

BREAKPOINT ESTIMATION USING SIR MODEL ON COVID-19 EPIDEMIC IN BANGLADESH

Tonushree Roy^{1*}, Md Abdul Masud², Mohammad Jamal Hossain³, Md Samsuzzaman⁴

^{1,2&3}Department of Computer Science and Information Technology (CSIT), Patuakhali Science and Technology University. E-mail: tanusire6240@cse.pstu.ac.bd, masud@pstu.ac.bd, jamalpstu07@pstu.ac.bd

⁴Department of Computer Science and Communication Engineering (CCE), Patuakhali Science and Technology University, Bangladesh. E-mail: sobuz@pstu.ac.bd

*Correspondence: E-mail: tanusire6240@cse.pstu.ac.bd

Abstract: Covid-19 destroyed the harmonic rhythm of civilized globes. The impact of this omnivorous pandemic situation has flown down all over the world along with Bangladesh. Covid-19 prediction and breakpoint estimation has drawn much attention for recovering a normal and healthy life. Generally, the SIR (Susceptible-Infected-Removed/Recovered) model is an epidemiological model that is used for breakpoint estimation and prediction of different infectious diseases. Breakpoint estimation means the break of the flow of the curve which means it reaches its highest peak position. In this paper, we apply the SIR model for breakpoint estimation as well as prediction of the Covid-19 epidemic in Bangladesh. Then we compare our predicted curve with the actual data points. The result shows that our predicted curves estimate breakpoints quite well which is close to the actual breakpoints. The SIR model allows a change in the rate of expansion that helps to predict the pictorial view of the overall situation in the following days. The prediction of Covid-19 helps raise the consciousness among people to understand the gruesomeness of this pandemic. For that reason, we have been motivated to estimate the breakpoint on the COVID-19 epidemic in Bangladesh.

Keywords: Breakpoint, Recovery rate, SIR model, Susceptible, Transition rate.

Introduction

The first case of COVID-19 was reported on December 31. The source of the outbreak has been confirmed to be a wet market in Wuhan (China). But in Bangladesh, the first coronavirus was detected in March 2020. IEDCR (Institute of Epidemiology, Disease Control and Research), the nation's epidemiology institute, announced the first three confirmed cases on March 8, 2020. Since the initially reported cases, the country's situation has gotten worse and is constantly affecting the social and economic life of people. But it is not a brand-new phenomenon brought on by the pandemic we are currently experiencing. Disease outbreaks have occurred in the past and will continue to do so. So being able to forecast how severe they are and how they might spread, is important for helping the healthcare system prepare.

For example, Siedner et al. (2020) discussed an interrupted time series model. Then they attempted to compare the daily growth rate of COVID-19 instances with the social exclusion policies in the USA. Weiming et al. (2020) conducted an analysis of the Covid-19 outbreak's fluctuating tendencies. For Hubei and non-Hubei regions, they employed a join-point regression model in China. Young Joo Kim et al. (2020) used the SIR model with a breakpoint to assess the COVID-19 spreading pattern in South Korea while taking into account the potential effects of policy interventions on transmission rates.

Simsek et al. (2020) analyzed intubation rates, the number of patients in the intensive care unit, daily active cases, death rates, and recovered rates in Turkey between the 27 March 2020 to 26 April 2020 dates using breakpoint regression model and made a comparison to 9 pandemic countries (Italy, China, Germany, South Korea, Iran, Spain, France, United Kingdom, and the United States of America).

Ian Cooper et al. (2020) analyzed the efficiency of the modeling approach based on the SIR (susceptible-infected-removed/Recovered) model that helped them to investigate the Covid-19 outbreak's spread within a community.

Christos Katris (2021) applied the SIR model to track the outbreak of Covid-19 in Greece. At first, he used a univariate time series model but for a more accurate result, he included other time series models like ARIMA (Autoregressive Integrated Moving Average) and Exponential Smoothing techniques from the classical models, also Multivariate Adaptive Regression (MAR) and Feed-Forward Neural (FFN) Network from the machine learning approaches to estimating the termination of the outbreak.

Venkatbharat Poleneni et al. (2021) used the ARIMA model for controlling the threat to human life. To make this contribution happen, they analyzed the rising number of susceptible in India and forecasted the upcoming 15 days situation to grasp the overall situation of Covid-19. Julshan Alam Ratu et al. (2021) predicted daily confirmed cases in Bangladesh using the ARIMA model among three different Covid-19 datasets.

Giuseppe C. Calafiore et al. (2020) developed the SIR model named SIRD (Susceptible-Infected-Recovered-Deceased). They identified the characteristics of their suggested model using official data from the pandemic in Italy up to March 30, 2020. They took into account the population at risk, the initial transmission rate, and the actual number of affected persons. Leonardo Lopez and Xavier Rodo (2020) used a modified SEIR compartmental model to account for the transmission of infection during the latent phase. This model additionally takes into consideration the impacts of different containment levels. To account for the uncertainty in case reporting and to examine the scenario forecasts for the various locations, they fitted data reported infected populations at the start of the first pandemic peak. Their model's objective is to analyze the confinement rate during the early phases of an epidemic outbreak in order to explore scenarios that reduce both incidence and death.

The SIR (Susceptible-Infected-Recovered/Removed) model, which is heavily regarded for the assessment of COVID-19 casualties, was initially evaluated and examined by Onder Tutsoy et al. (2020). Then they provide the Suspicious-Infected-Death (SpID) model that is revolutionary, comprehensive, higher-order, multi-dimensional, tightly linked, and parametric in nature. The COVID-19 dynamics are inside the moderately cyclical, stable region, according to the results of the mathematical study that was done using the deaths in Turkey, even if some of the dynamics are near the unstable region.

There are some other people who work with the basic reproduction number. When the values of the fundamental reproduction number are less than one, the disease is predicted to terminate, whereas when the values are greater than one, the sickness is predicted to become an epidemic. Marwan Al-Raei (2020) used the SIRD epidemiology model to estimate the novel coronavirus disease's basic reproduction number for eight countries (The Syrian Arab Republic, India, France, the United States, Nigeria, Yemen, Russia, and China). Yi-Cheng Chen et al. (2020) conducted mathematical and numerical analyses of COVID-19. They suggested a time-dependent SIR model that monitors the transmission and recovery rate at time t in order to forecast the COVID-19 trend. They demonstrated that their one-day prediction errors are almost less than 3% using the data provided by the Chinese authority. Their model predicts the peak and the overall number of confirmed cases in China. They illustrated an outbreak's phase transition diagram and demonstrated that multiple nations will likely have COVID-19 outbreaks on March 2, 2020.

Vishaal Ram and Laura P. Schaposnik (2020) developed a modified age-structured SIR model. Rajesh Singh and R. Adhikari (2020) employed an age-structured SIR model with social interaction matrices acquired from Bayesian imputation and surveys to examine the COVID-19 epidemic's growth in India. For the dynamics of the COVID-19 pandemic, Rohit Parasnis et al. (2021) developed a theoretical foundation and carried out an empirical validation of the age-structured SIR model, a variation of the traditional Susceptible-Infected-Recovered (SIR) model of epidemic transmission.

For forecasting and predicting the outbreak, S M Abdullah Al Shuaeb (2020) et al. used a machine learning (ML) linear regression model. The main objective of their paper is how to predict the recovery cases, virus-affected cases, tested cases, and death cases and forecast the future circumstance of Bangladesh.

There are also some limitations in SIR model prediction that have been improving day by day. For example, in the SIR model, the analysis does not include cases that have not been recorded. If the proportion of undetected cases changes over time, this can distort the curve and thus the determination of the change points. It is presumably that infectious people interact freely with susceptible people. where a small number of infected people infect a huge number of susceptible people. (Zhang Y et al., 2020; Lau MSY et al., 2020; Adam DC et al., 2020) Another crucial premise is that after being infected and recovering, a person is no longer vulnerable to infection. This assumption, however, does not seem to be seriously violated. The danger of reinfection is regarded as low (McMahon A & Robb NC, 2020), despite the fact that some instances of SARS-CoV-2 infection have been documented more than once (Gousseff Met et al., 2020; Murillo-Zamora E et al., 2020).

Overall, the SIR model strikes a balance between the computational ease of use and the accuracy of portraying the actual complexity of a real-life pandemic. In this paper, we apply the SIR model for predicting the possible outcome of maximum peak and then compare the outcome with the actual dataset to see the compatibility of the SIR model.

The objective of this study is to examine the transmission dynamics of COVID-19 and predict the breakpoint of the infection in Bangladesh using publicly available data through the SIR model.

Materials and Method

SIR (Susceptible-Infected-Removed/Recovered) Model

In this paper, we formulate the SIR model for estimating the breaking point of the COVID-19 spreading scenario. The SIR model is mainly a compartment model which represents the basic building block of epidemiology. Inhere, the population is divided into a set of states of groups. The standard SIR model assigns the population into the following groups: (Herbert W. Hethcote (2000))

- 1) Susceptible (S)
- 2) Infected (I)
- 3) Recovered or removed (R)

Susceptible is defined by S which means the number of susceptible individuals. When a susceptible and an infectious individual come into "infectious contact", the susceptible individual transmits the disease and the transitions come to the infectious compartment.

Infected is defined by I which means the number of infected individuals, these are individual peoples who have been infected and are capable of infecting susceptible individuals.

Recovered (removed) is defined by R which means the number of recovered (removed) individuals, these are individuals who have been infected. When they have been infected, they have either recovered from the disease or entered the removed compartment which means he/she has died. But when we assume the whole situation, we will see that the number of deaths is negligible concerning the total population.

A model with these types is referred to as a SIR model and represents many viral infectious diseases like measles, influenza, chicken pox, and COVID-19.

The number of people in each compartment at a particular time is represented by the variables S, I, and R. To represent that the number of susceptible, infectious, and removed individuals may vary over time (even if the total population size remains constant), we make the precise numbers a function of t (time): S (t), I (t) and R (t). As implied by the variable function of t, the model is dynamic in that the numbers in each compartment may fluctuate over time.

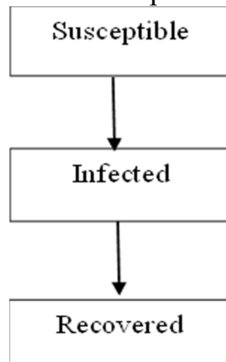


Figure 1. Simple structure of SIR model

Everybody who has the potential to contract the infection is represented by susceptible. In this case, it is assumed that there are susceptible individuals who are able to spread the infection to everyone. Thus, everyone will be susceptible at first. Then we have the second category of people who are infected. When people become infected, they leave the susceptible category. Most diseases are not contagious again once people have been exposed to them once. They are only ever infected once. If we assume that the death rate is low in comparison to the number that is being recovered, people who have the infectious disease will eventually transition, ideally into a recovery condition. Therefore, we simply assume that everything and everyone is susceptible at first. They have two options in this scenario: either they spread the infection to others or they leave and recover. In other cases, they are unable to contract the illness themselves or pass it on to someone else. These are the underlying presumptions of this model. This presumption can be expressed mathematically by saying that the total number of susceptible, infected, and recovered individuals equals N. Here, the term “N” refers to every person in a town, city, or state.

$$S(t)+I(t)+R(t) = N \quad (1)$$

One of the things that would be helpful for us is to provide some labels for what will happen to these variables when time t equals 0. These are referred to as the initial conditions at the beginning. The underlying premise is that there are no recovery people at the beginning. Because there will initially be a very limited number of infected individuals. Most likely simply one at the beginning. However, it's possible that we will not begin collecting data for a long time. In this case, the initial node of infected individuals may only be a tiny number.

$$\begin{aligned} (0) &= S_0 \\ (0) &= I_0 \\ (0) &= R_0 \end{aligned} \quad (2)$$

From that angle, the susceptible condition is different. That implies that there weren't exactly zero susceptible people there at the moment. Compared to everyone else, we saw a really large quantity. As a result, we attempted to illustrate what is happening. People develop susceptibility, susceptible individuals contract an infection, and the infection subsequently spreads to further individuals in a cascading manner. Therefore, some of those infected individuals later recover. However, what we really want to do is make an effort to create equations that aim to capture the behavior of this S of t, I of t, and R of t. An area of mathematics called a system of differential equations will be used in this case. After dividing it into three concepts, we want to measure the rate of change with respect to time (t).

$\frac{dS}{dt}$ denotes the rate of change of susceptible at a time.

$\frac{dI}{dt}$ represents the number of infected people changing at a time.

$\frac{dR}{dt}$ represents the number of recovered individuals changing with respect to time.

Therefore, we believe that this should be based on the idea that the more connections between people there are, the more the S and the I will grow together to produce additional interactions. The greater the chance that a number of people may develop an infection. Thus, using that presumption, we can formulate the following equation. (Ross Beckley et al. (2013), Herbert W. Hethcote (2000))

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \quad (3)$$

This indicates that the susceptibility is decreasing with time, indicating a negative change in the susceptibility rate. Here β represents the transmission rate (a positive constant). I and S are both numbers that represent infected and susceptible in a population. The three factors are all positive, but the susceptibility's rate of change is always declining. This demonstrates that S must always be less than its starting value. Naturally, this makes perfect sense because during the beginning of an outbreak, theoretically, every member of the population is susceptible to the virus, particularly when it involves a novel strain like COVID-19 that has never been observed before. As a result of its negative change rate, S will always decrease. (Ross Beckley et al. (2013), Herbert W. Hethcote (2000))

When we think about infected people, one way we can get infected people is that susceptible people transit to the infected region. So, if we can lose $-\frac{\beta SI}{N}$ out of the susceptible, then we are going to gain it here in the infected as well we get a plus γI (it's a recovery rate) as I. but that is not the only factor that affects infecting people

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \quad (4)$$

There are newly infected people coming in when the transition moves from susceptible to infecting it. But there are also losses of infected people when they get recovered from the disease when their immune system sort of kicks in and they fight it off. And then they are no longer capable of infecting anybody. And so, when this happens, we also have a loss of infected people which is a good thing. And therefore, a negative γI turn. The more infected there are, the bigger the frequency of change of infected leaving. But then for the recovered people if we are

losing γI from the infected, we give them right back into the recovery state. (Ross Beckley et al. (2013), Herbert W. Hethcote (2000)).

So, we get

$$\frac{dR}{dt} = \gamma I \quad (5)$$

We initially say everybody is sort of susceptible. So if we imagine we have got a town of about 500 people and we are going to imagine the course of an epidemic that lasts 60 days (Figure 2).

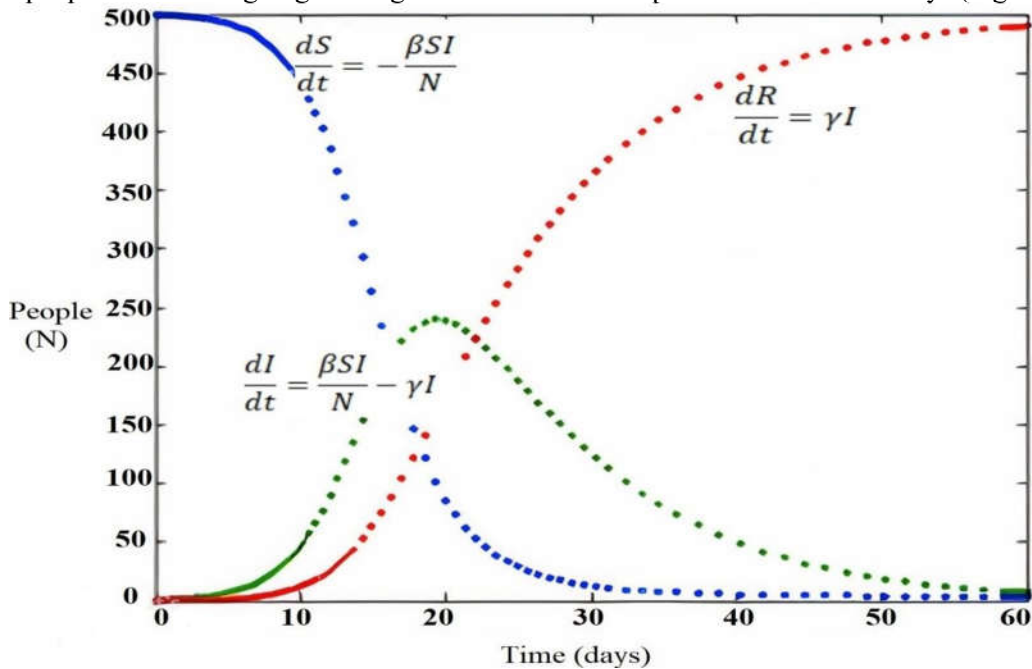


Figure 2. Pictorial view of SIR model (Wikipedia (2021)).

So, if we look at the blue line, what is happening here is that it starts at approximately 500, and then it drops. As time goes along the number of susceptible people goes less and less. And we are going to imagine any section sweeps through this particular town and it is going to infect everybody. At the end of the day, the number of susceptible people goes to 0 because at some point everybody in the town has been infected. Likewise for the recovered people if everyone has gotten infected and then gone through that process of becoming recovered, their immune system kicks in. Then the number of recovered people which initially was 0 goes up and gets close to 500 (The red line). Now if we look at dI/dt , that's got two different terms positive and negative and for the first portion, the number of susceptible is large. That positive term that includes the number of susceptible dominates and so the number of infected people goes up and up. But as time goes on the number of susceptible is going to go down. Then the negative term starts to dominate the positive term then the infected people go down in quantity as they transition to be recovered more quickly than they get new cases from people transitioning out of being susceptible.

Breakpoint Estimation of SIR model

There is an inflection point in the graph of infected people; we find the local maximum (I_{max}). That means at some point the growth of the number of infected must stop. The condition that will cause this growth to stop is $dI/dt = 0$. Because, if the infected people stopped growing that means $dI/dt=0$.

We can look at when $\frac{dI}{dt} = 0$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$

$$\text{or, } 0 = \frac{\beta SI}{N} - \gamma I$$

$$\text{or, } 0 = I \left(\frac{\beta S}{N} - \gamma \right)$$

$$I = 0 \text{ or } \left(\frac{\beta S}{N} - \gamma \right) = 0$$

$$\text{or } \frac{\beta S}{N} = \gamma$$

$$\text{or } S = \frac{N\gamma}{\beta}$$

When these conditions are satisfied, the rate at which susceptible become infected precisely balances the rate of recovery. So, the number of infected individuals remains constant. So, we can see from equation 6 that the number of infected people stops when $I=0$ or S equals $N\gamma/\beta$. (Ross Beckley (2013), Herbert W. Hethcote (2000))

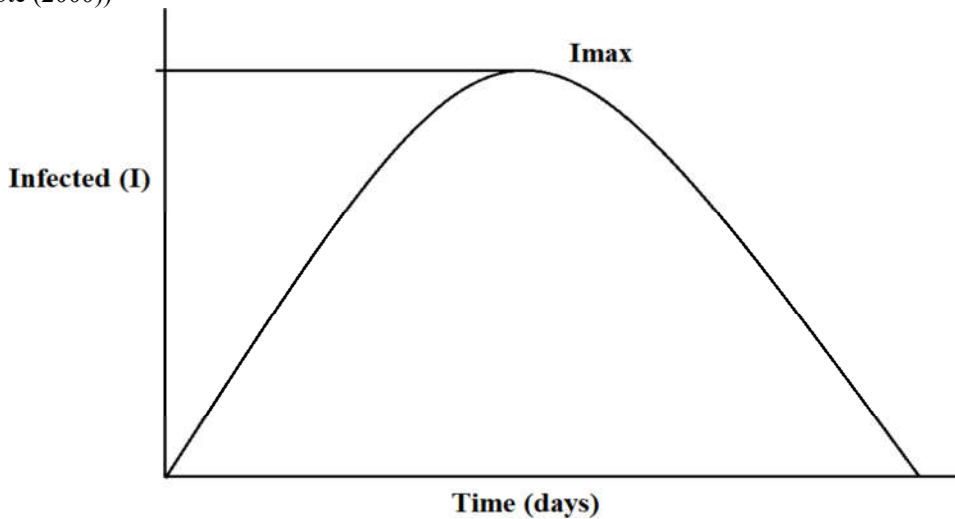


Figure 3. Figure of I maximum (Infected maximum).

Results and Discussion

In this section, we present the experimental results of the SIR model on the Covid-19 dataset including data collection, experimental settings, and experimental result analysis with real data.

Collection of data

We have collected all the data from the WHO (World Health Organization) and IEDCR (Institute of Epidemiology, Disease Control and Research) website. Every dataset consists of four features: Date, Suspected, Infected and Removed. Every dataset has the same features, but the records are different. The first wave dataset represents records from 20 April 2020 to 21 February 2020. The second wave dataset represents records from 7 February 2021 to 5 May 2021. The third wave dataset represents records from 15 May 2021 to 29 November 2021. Therefore, the last and fourth wave dataset represents records from 18 December 2021 to 24 February 2022.

Table 1. Covid-19 first wave dataset in Bangladesh.

Date	Susceptible	Infected	Removed
01-04-2020	434	9	2
02-04-2020	367	18	1
03-04-2020	468	35	3
04-04-2020	679	41	5
05-04-2020	981	54	3
06-04-2020	905	112	1
07-04-2020	1184	94	6
.	.	.	.
.	.	.	.
.	.	.	.
27-08-2020	11934	1897	42
28-08-2020	12454	2174	33

Table 2. Covid-19 second wave dataset in Bangladesh.

Date	Susceptible	Infected	Removed
07-02-2021	12404	292	15
08-02-2021	13762	316	16
09-02-2021	14468	387	8
10-02-2021	14999	388	10
11-02-2021	15776	418	9
12-02-2021	14328	112	5
13-02-2021	12871	404	13
.	.	.	.
.	.	.	.
.	.	.	.
13-05-2021	11934	1897	42
14-05-2021	12454	2174	33

Table 3. Covid-19 third wave dataset in Bangladesh.

Date	Susceptible	Infected	Removed
15-05-2021	3758	261	22
16-05-2021	5430	363	25
17-05-2021	10347	698	32
18-05-2021	16855	1272	30
19-05-2021	20528	1608	37
20-05-2021	19437	1457	36
21-05-2021	18294	1504	26
.	.	.	.
.	.	.	.
.	.	.	.
16-12-2021	25203	257	3
17-12-2021	16310	191	2

Table 4. Covid-19 fourth wave dataset in Bangladesh.

Date	Susceptible	Infected	Removed
18-12-2022	13991	122	4
19-12-2022	17332	211	1
20-12-2022	19955	260	2
21-12-2022	20909	291	1
22-12-2022	18779	352	1
23-12-2022	19624	382	2
24-12-2022	16913	342	1
.	.	.	.
.	.	.	.
.	.	.	.
28-02-2022	25203	257	3
01-03-2022	16310	191	2

By using this dataset, we estimated the breakpoint among different waves in Bangladesh. Mainly we have focused here on the Infected column to see how severe the spread of infection is and then compare it with its actual data to see the comparison.

Experimental Settings

For SIR model prediction, we first consider parameters called infection rate beta (β) and recovery rate gamma (γ) (Weston C. Roda et al. (2020)). The transmission rate (β) is the rate of the spread of diseases. This variable takes into account both the mean number of contacts per person and the disease's transmissibility. That means the average number of contacts per person per time. The other parameter gamma (γ) is the recovery rate. If an individual is infectious for an average time period of D, then $\gamma = 1/D$. Simply, beta (β) is the rate at which susceptible individuals get infected. And gamma (γ) is the rate at which infected individuals recover or (die).

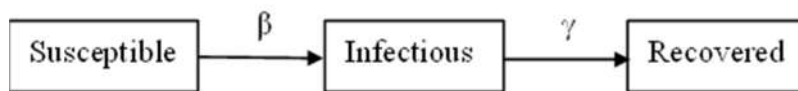


Figure 4. Parameter of SIR model

By observing some following days, we calculated beta and gamma values for every wave. By calculating this infection rate and recovery rate, we constructed the SIR model using equations 1, 2, 3, 4, and 5 (Ross Beckley (2013), Herbert W. Hethcote (2000)).

For constructing the SIR model, in the first wave, we have set beta 0.38 and gamma 0.25, in the second wave beta 0.4 and gamma 0.22, in the third wave beta 0.6 and gamma 0.4 and last wave or fourth wave beta 0.5 and gamma 0.18 by following above instructions. All the experiments are carried out using R (R core Team 2013).

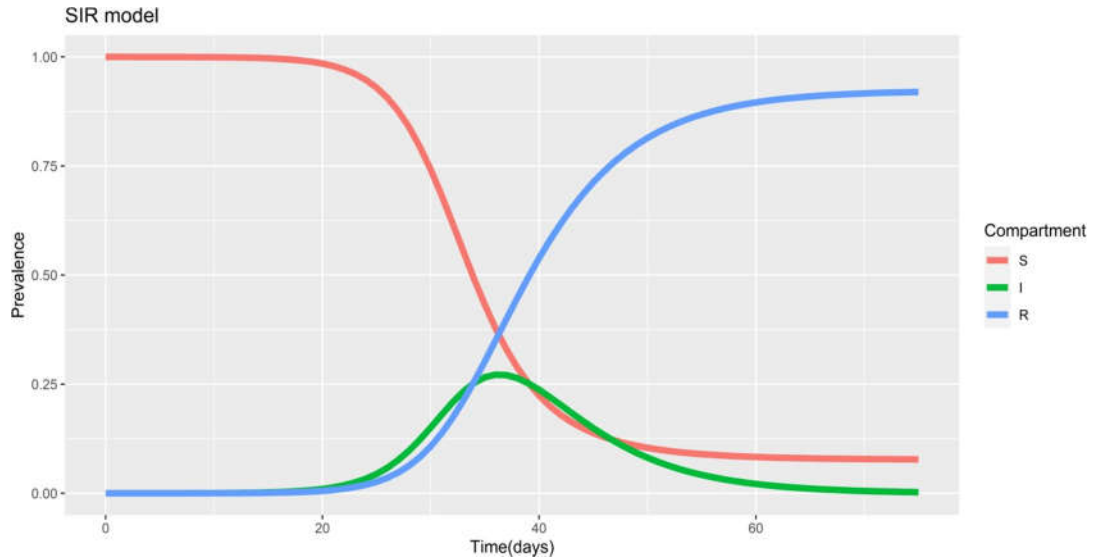
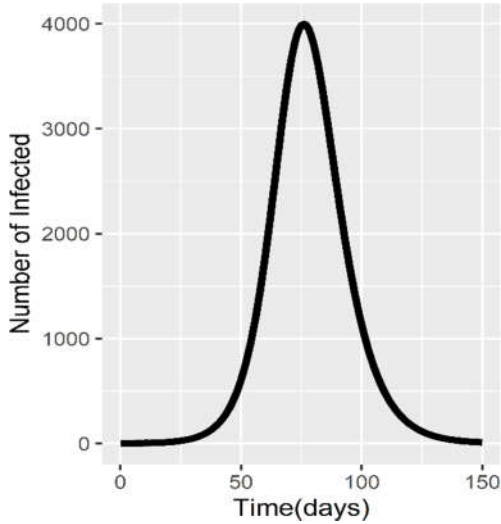
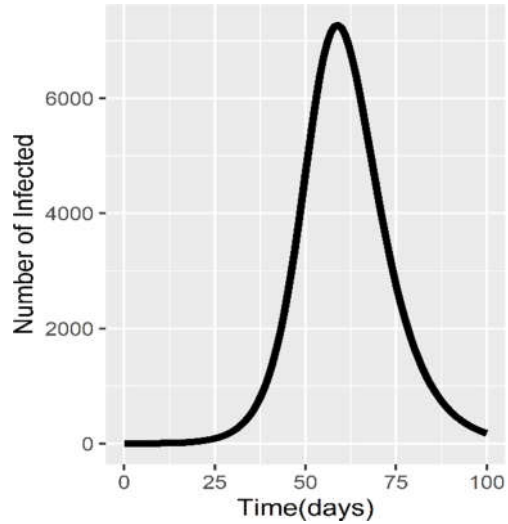


Figure 5. SIR model prediction of Covid-19 in Bangladesh.

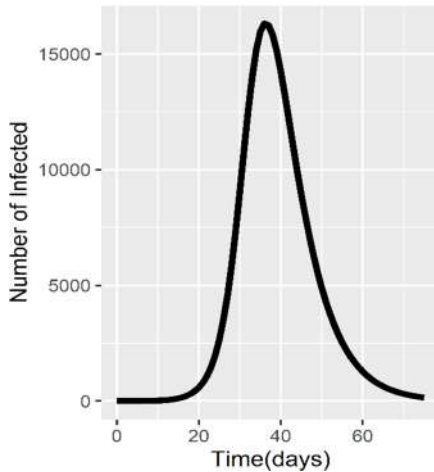
Figure 5 shows the Overall view of the SIR predicted model on fourth wave. Fourth wave represents dataset from 18 December 2021 to 1 May 2022. The red line shows the suspected people, the green line shows the infected and the blue line recovered. As expected, the suspected rate is very high from the beginning. But as time goes on the number of suspects will decrease where recovered people will increase. On the other hand, the number of infected people first increases and then reaches its highest peak. After that, it will decrease, which means the infection rate will slow down.



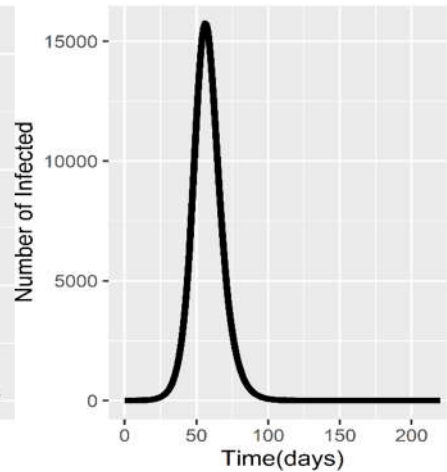
(a) First wave infected curve



(b) Second wave infected curve

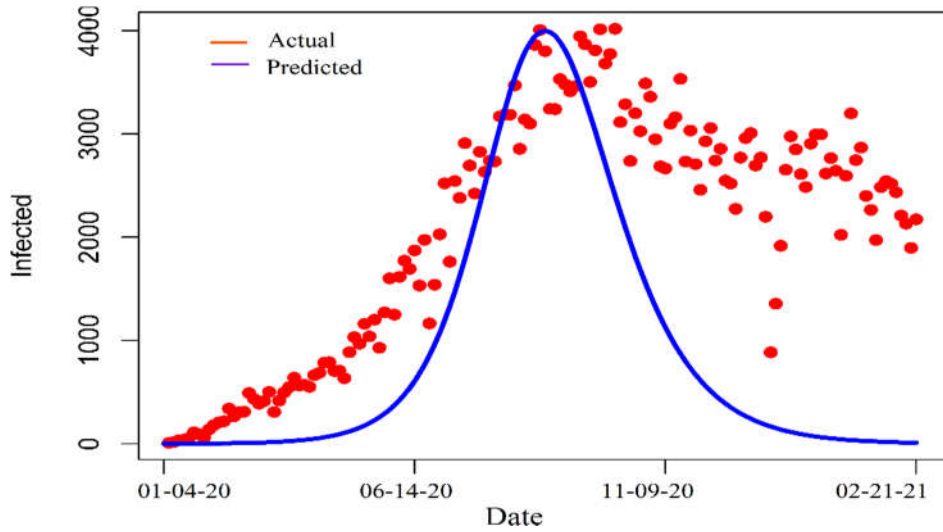


(c) Third wave infected curve

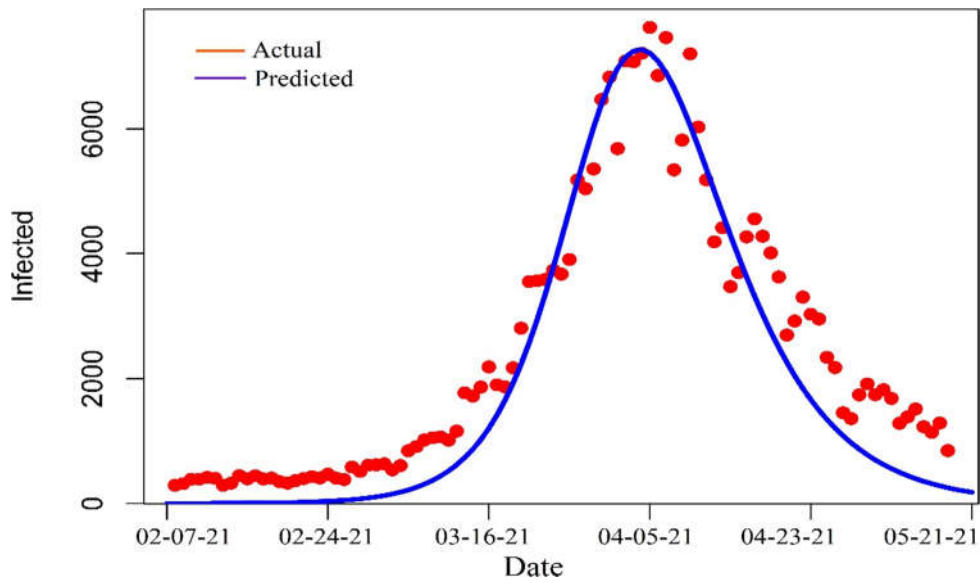


(d) Fourth wave infected curve

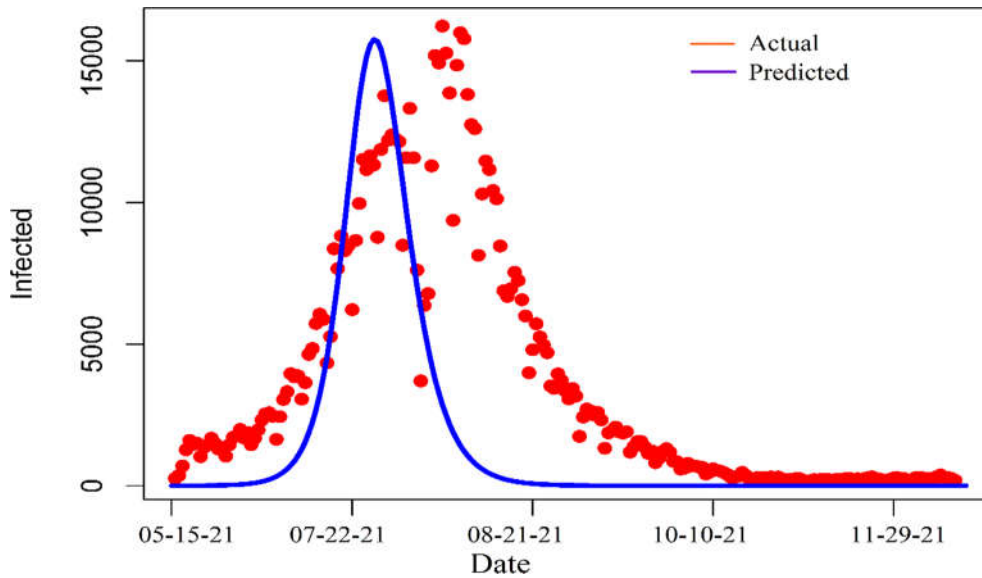
Figure 6. Number of infected people. Figure 6(a) represents the infected growth rate from 1 April 2020 to 6 February 2021. Figure 6(b) 7 February 2021 to 14 May 2021. Figure 6(c) 15 May 2021 to 17 December 2021. Figure 6(d) 18 December 2021 to 1 March 2022. From figure 6(a) we can see that the peak point is approximately 4000. Similarly, approximately 7000, 15500, 16000 respectively for figure 6(b), 6(c) and 6(d).



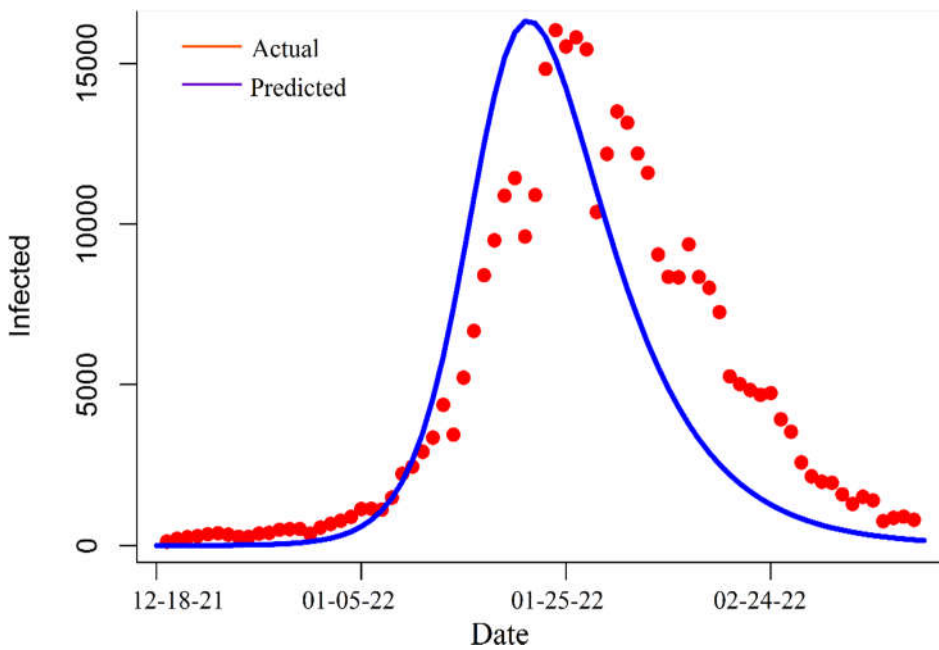
(a) First wave comparison between predicted curve with actual data points



(b) Second wave comparison between predicted curve with actual data points



(c) Third wave comparison between predicted curve with actual data points



(d) Fourth wave comparison between predicted curve with actual data points

Figure 7. Comparison between predicted curve with actual data points. Figures 7(a), 7(b), 7(c), and 7(d) represent the comparison between the predicted curve with the actual or real data points respectively for the first wave, second wave, third wave, and fourth wave. The red points indicate the actual data points whereas the blue line indicates the predicted model curve.

Table 5. Comparison table between real data and predicted model

Date	Estimated Breakpoint	Actual Breakpoint	Matching peak data point with actual and predicted
4 April 20-6 Feb 21	3999	4019	77
7 Feb 21- 14 May 21	7270	7626	60
15 May 21- 17 Dec 21	15749	16230	57
18 Dec 21- 1 May 22	16310	16033	37

Table 5. shows that there remains pretty much similarity between the estimated breakpoint (peak value) and actual breakpoint (peak value). Thus, our findings are based on finding the breakpoint that highlights the role of the virus outbreak that can be useful to avoid a massive collapse in Bangladesh and the rest of the world.

Conclusion

Nowadays, COVID-19 has become a burning issue in the world. This virus originated in Wuhan, China on 31 December 2019. This virus has created severe circumstances in the whole world, especially in Bangladesh. The development of good prediction models has become necessary to control this outbreak better and get insights into the outbreak and consequences of the infectious disease. For that reason we have tried to measure the effectiveness of the model and how much the real data matched the predicted value. As a result, we can get advanced forecasting for preparing ourselves mentally to face this crisis. This will also help people to understand the gruesomeness of this fatal death-like outbreak. Although there is a high level of uncertainty in the available data and also a lack in the availability of important data, it will affect the accuracy of standard epidemiological models. However, this will give us a whole view of the Covid-19 pandemic and how important it is to take the immediate step for normalizing this situation.

The current analysis can be extended by following to overcome these limitations: In our SIR model, we do not consider asymptomatic individuals and the possibility of re-infection (which in the case of COVID-19, one may want to consider (Marie Gousseff et al. (2020)). The proposed model is developed by taking into consideration the suspicious, infected, and death casualties, but it does not take into account the intensive care and intubation casualties. In the Removed or Recovered compartment of SIR, there is no specific separation between Removed or Recovered.

References

Adam, D. C., Wu, P., Wong, J. Y., Lau, E. H., Tsang, T. K., Leung, G. M., . . . Cauchemez, S.(2020). Clustering and superspreading potential of SARS-CoV-2 infections in Hong Kong. *Nature Medicine*. doi:<https://doi.org/10.1038/s41591-020-1092-0>

Al-Raei, M. (2021). The basic reproduction number of the new coronavirus pandemic with mortality for India, the Syrian Arab Republic, the United States, Yemen, China, France, Nigeria and Russia with different rate of cases. *Clinical Epidemiology and Global Health*, 9, 147-149. doi:<https://doi.org/10.1016/j.cegh.2020.08.005>.

Beckley, R., Weatherspoon, C., Alexander, M., Chandler, M., Johnson, A., & Bhatt, G. S.(2013). Modeling epidemics with differential equations. Retrieved from <https://www.semanticscholar.org/paper/Modeling-epidemics-with-differential-equations-Beckley-Weatherspoon/36913fd956c2373a7a7597d167a82e7b000b3983>

- Calafiore, G. C., Novara, C., & Possieri, C. (2020). A Modified SIR Model for the COVID-19 Contagion in Italy. *2020 59th IEEE Conference on Decision and Control (CDC)*, 3889- 3894. doi:10.1109/CDC42340.2020.9304142
- Chen, Y.-C., Lu, P.-E., Chang, C.-S., & Liu, T.-H. (2020). A Time-Dependent SIR Model for COVID-19 With Undetectable Infected Persons. *IEEE Transactions on Network Science and Engineering*, 7(4), 3279-3294. doi:10.1109/TNSE.2020.3024723.
- Christos, K. (2021). A time series-based statistical approach for outbreak spread forecasting: Application of COVID-19 in Greece. *Expert Systems With Applications*, 166. doi:https://doi.org/10.1016/j.eswa.2020.114077
- Cooper, I., Mondal, A., & Antonopoulos, C. G. (2020). A SIR model assumption for the spread of COVID-19 in different communities. *Chaos, Solitons and Fractals*. doi:10.1016/j.chaos.2020.110057
- Gousseff, M., Penot, P., Gallay, L., Batisse, D., Benech, N., Bouiller, K., . . . Vig, N. (2020). Clinical recurrences of COVID-19 symptoms after recovery: Viral relapse, reinfection or inflammatory rebound? *Journal of Infection*, 81(5), 816-846. doi:https://doi.org/10.1016/j.jinf.2020.06.073
- Hethcote, H. W. (2000). The Mathematics of Infectious Diseases. *42*(4), 599-653. doi:https://doi.org/10.1137/S0036144500371907 https://simple.wikipedia.org/wiki/SIR_model (January 2021) IEDCR (Institute of Epidemiology Disease Control And Research), https://dghs-dashboards.com/pages/covid19.php
- Kim, Y.-J., Seo, M. H., & Yeom, H.-E. (2020). Estimating a breakpoint in the pattern of spread of COVID-19 in South Korea. *International Journal of Infectious Diseases*, 97, 360- 364. doi:https://doi.org/10.1016/j.ijid.2020.06.055.
- Lau, M. S., Grenfell, B., Thomas, M., Bryan, M., Nelson, K., & Lopman, B. (2020). Characterizing superspreading events and age-specific infectiousness of SARS-CoV-2 transmission in Georgia, USA. *Proceedings of the National Academy of Sciences*. doi: https://doi.org/10.1101/2020.06.20.20130476
- López, L., & Rodó, X. (2021). A modified SEIR model to predict the COVID-19 outbreak in Spain and Italy: Simulating control scenarios and multi-scale epidemics. *Results in Physics*, 21. doi:https://doi.org/10.1016/j.rinp.2020.103746.
- McMahon, A., & Robb, N. (2020). Reinfection with SARS-CoV-2: Discrete SIR (Susceptible, Infected, Recovered) Modeling Using Empirical Infection Data. *JMIR Public Health and Surveillance*, 6. doi:10.2196/21168.
- Murillo-Zamora, E., Mendoza-Cano, O., Delgado-Enciso, I., & Suárez, C. M. (2021). Predictors of severe symptomatic laboratory-confirmed SARS-CoV-2 reinfection. *Public Health*, 193, 113-115. doi:https://doi.org/10.1016/j.puhe.2021.01.021
- Parasnis, R., Sakhale, A., Kato, R., Franceschetti, M., & Touri, B. (2021). A Case for the Age-Structured SIR Dynamics for Modelling COVID-19. *2021 60th IEEE Conference on Decision and Control (CDC)*, 5508-5513. doi:10.1109/CDC45484.2021.9683725.
- Poleneni, V., Rao, J. K., & Hidayathulla, S. A. (2021). COVID-19 Prediction using ARIMA Model. *2021 11th International Conference on Cloud Computing, Data Science & Engineering (Confluence)*, 860-865. doi:10.1109/Confluence51648.2021.9377038
- Ram, V., & Schaposnik, L. P. (2021). A modified age-structured SIR model for COVID-19 type viruses. *Scientific Reports*, 11, 15194. doi:https://doi.org/10.1038/s41598-021- 94609-3
- Ratu, J. A., Masud, M. A., Hossain, M. M., & Samsuzzaman, M. (2021). Forecasting the COVID-19 Pandemic in Bangladesh Using ARIMA Model. *2021 3rd International Conference on Sustainable Technologies for Industry 4.0 (STI)*, 1-6. doi:10.1109/STI53101.2021.9732576
- Roda, W. C., Varughese, M. B., Han, D., & Li, M. (2020). Why is it difficult to accurately predict the COVID-19 epidemic? *Infectious Disease Modeling*, 271-281. doi:10.1016/j.idm.2020.03.001
- Shuaeb, S. M., Kamruzaman, M., & Al-Amin, M. (2020). COVID-19 Outbreak Prediction and Forecasting in Bangladesh using Machine Learning Algorithm. *International Journal of Trend*

- in Scientific Research and Development (IJTSRD)*, 5(1), 829-835. Retrieved from www.ijtsrd.com/papers/ijtsrd38068
- Siedner, M. J., Harling, G., Reynolds, Z., Gilbert, R. F., Haneuse, S., Venkataramani, A. S., & Tsai, A. C. (2020). Social distancing to slow the U.S. COVID-19 epidemic: longitudinal pretest-posttest comparison group study. *PLOS MEDICINE*. doi:10.1371/journal.pmed.1003244
- Simsek, E. E., Guner, A. E., Kul, S., Karakurt, Z., Tekesin, K., & Birinci, S. (2020). A comparative analysis of the COVID-19 pandemic response: The case of Turkey. *NORTHERN CLINICS OF İSTANBUL*, 443–451. doi:10.14744/nci.2020.87846
- Singh, R., & Adhikari, R. (2020, 3). Age-structured impact of social distancing on the COVID-19 epidemic in India. Retrieved from <https://arxiv.org/abs/2003.12055>
- Tang, W., Liao, H., Marley, G., Wang, Z., Cheng, W., Wu, D., & Yu, R. (2020). The Changing Patterns of Coronavirus Disease 2019 (COVID-19) in China: A Tempogeographic Analysis of the Severe Acute Respiratory Syndrome Coronavirus 2 Epidemic. *Clinical Infectious Diseases*, 71(15), 818–824. doi:<https://doi.org/10.1093/cid/ciaa423>
- To, K. K.-W., Hung, I. F.-N., Ip, J. D., Chu, A. W.-H., Chan, W.-M., Tam, A. R., . . . To, W.-K. (2021). Coronavirus Disease 2019 (COVID-19) Re-infection by a Phylogenetically Distinct Severe Acute Respiratory Syndrome Coronavirus 2 Strain Confirmed by Whole Genome Sequencing. *Clinical Infectious Diseases*, 73(9), e2946–e2951. doi:<https://doi.org/10.1093/cid/ciaa1275>
- Tutsoy, O., Çolak, Ş., Polat, A., & Balikci, K. (2020). A Novel Parametric Model for the Prediction and Analysis of the COVID-19 Casualties. *IEEE Access*, 8, 193898-193906. doi:10.1109/ACCESS.2020.3033146. World Health Organization (<https://covid19.who.int/region/searo/country/bd>)
- Zhang, Y., Li, Y., Wang, L., Li, M., & Zhou, X. (2020). Evaluating Transmission Heterogeneity and Super-Spreading Event of COVID-19 in a Metropolis of China. *International Journal of Environmental Research and Public Health*. doi:<https://doi.org/10.3390/ijerph17103705>