Application of Modified Logistic Model's for an Analysing COVID-19 Transmission in Bangladesh

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Abstract

In Bangladesh, the logistic model is used to examine possible cases of COVID-19. The prototype is ready to spearhead the fight in Bangladesh against the COVID-19 strain. Direct computation with plausible COVID-19 data for Bangladesh from January 1st, 2022, to the end of the month provides the parameters for the model. In addition to a portrayal of the stability of equilibrium and propositions, this includes both a qualitative assessment of the modified logistic model as well as an analysis of the bifurcation of the modified logistic model. As it turns out, there is a wide chasm between the two. In addition to this, it was found that logistic curves were an appropriate way to describe the COVID-19 outbreak that was occurring in Bangladesh. The suggested model predicts Covid-19 duration and peak times in Bangladesh, which is compared to data. In conclusion, a numerical investigation of the logistic model for Corona virus cases in Bangladesh has been estimated, and its graphical representations have been provided. This model has been used to estimate the number of cases in Bangladesh. It has come to our attention that the cases that were anticipated and the ones that were investigated are extremely similar to one another in a number of important respects.

Keywords: Bifurcation, COVID-19, Novel corona virus, Modified logistic model, Stability Analysis.

Introduction

The newly reported Corona virus disease-2019 has spread all over the world after being discovered in Wuhan, China. Wuhan is where the disease was initially identified. On March 11, the World Health Organization (WHO) declared that they were treating the outbreak as if it were a pandemic [1]. Droplets from a person's respiratory system, vocal cords, or mouth can spread the virus [2]. Bangladesh's COVID-19 outbreak is part of the wider corona virus disease 2019 (COVID-19) pandemic, which was sparked by the SARS-CoV-2 virus. In March of 2020, the virus was predicted to spread to Bangladesh. On March 8, 2020, the country's epidemiology institute, IEDCR, announced the first three familiar precedents. Since

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then, the epidemic has spread over the entire country and the infected population has been booming. The novel corona virus is closely related to the kalong corona virus genetically and involves positive-sense single-stranded RNA. This virus family is well-known for spreading human illness, from the common cold to more severe respiratory conditions like severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) [3]. The plague caused by the Corona virus sickness is even more terrifying than the flu [4]. The rates of disease in a number of wealthy countries, including the United States of America, Brazil, Russia, India, Italy, France, and the United Kingdom, are frighteningly high. Isolation from society, closure of places of business and schools, travel restrictions, and activity limitations are among the preventative measures taken against COVID-19. Scores on the COVID-19 can be rather variable, both for individuals and countries [5]. Many academics from a variety of countries around the world have developed a wide variety of forecasting models in order to estimate the likely outcome of the COVID-19 epidemic [6]. Disease outbreak time series can now be predicted with the use of mathematical models trained with machine learning and deep learning [7].

As of the first of September in 2020, the logistic model has been finalized to fit the plague apocalypse cap of COVID-19 Nobel corona virus data. Scientists have created the "susceptible, un-quarantined infected, quarantined infected, con-firmed infected" model to better comprehend the particulars of each individual outbreak[8]. In the course of this specific research project, a logistic model was utilized in order to perform data analysis in Bangladesh. The RK-4 method was utilized in order to compile a list of all of the model's parameters. In order to analyze infectious illnesses, it is required to recapitulate the adhesions that were deduced from the conclusion. The COVID-19 corona virus sickness outbreak dispatch augmentation in Bangladesh was 1.05 on June 26th, which is a very good approximation for the value[9].Infection with COVID-19 can cause symptoms anywhere between 2 and 14 days following exposure. The symptoms of COVID-19 infection might vary from person to person, even in those who are exposed to the virus at the same time. Fever, chills, difficulty breathing, coughing, headache, loss of smell and taste, muscular or body aches, sore throat, nasal congestion, diarrhea, nausea, and vomiting are all treatable symptoms of noble corona virus illnesses [10]. Corona virus can be avoided with the use of COVID-19 vaccinations as those manufactured by Pfizer-BioNTech, Moderana, Oxford-AstraZeneca, BBIBP-CorV from Sinopharm, BBV152 from Bharat Biotech, CoronaVac from Sinova, Ad5-nCoV from CanSinoBiologics, and Sputnik V. These vaccines have proven to be effective by Regulatory Decision [11]. The steps of a logical model enact a characteristic vision of the possible outcomes with more grounded forms. It draws attention to a landmark achievement in the field of biomedical modeling. Capital accumulation, balanced growth, radioactive decay, statistics, neural networks, medicine (tumor growth modeling), chemistry, physics,

economics (innovation diffusion), and the list goes on and on are all real-world applications of population dynamics. This paper discusses the edict for modeling as a means of comprehending processes, since this is the only way to make an unarguable forecast [12]. It is generally agreed that isolation and guarantine are two separate types of confinement. Others who have been infected with COVID-19 are separated from others who have not been through isolation. The quarantine's goal is to stop the rapid spread of COVID-19 among those who may have been briefly exposed to it [13-14].Biologically meaningful equilibrium states must be both stable and unstable [15-16]. The study of bifurcations has been incorporated into the dynamic analysis of the model that has been proposed [17-18]. The epidemic model is used when conducting research on the study of biological system [19]. The infectious agent, transmission method, latent period, infectious period, susceptibility, resistance, social, cultural, demographic, economic, and geographic factors propagate infectious illness [20]. The centre manifold theorem and bifurcation theory show that the SIS epidemic model flips and Hopfs [21]. A model that could be depended upon to reliably forecast the amount of persons who will fall ill with the Corona virus in Bangladesh was the overarching purpose of the article. This goal was accomplished by constructing the model.

Methodology

The overarching purpose of this research is to develop a time-adjusted logistic model in an effort to incorporate the most helpful characteristics associated with the magnitude of the epidemic, the population density, and the rate of transmission. This model will be constructed using a tailored logistic model that incorporates time series data. The mathematical formulations of the problem have been established prior to submitting the research paper. This is crucial for developing a mathematical formulation of the issue. In order to make a prediction regarding COVID-19 situations, it then utilized numerical methods such as the RK-4 approach. Following this, the basic equations that were derived from the modified logistic model will have the parameters substituted in. Make an effort to describe the transmission dynamics of COVID-19 using the updated model by employing mathematical software such as MATHEMATICA and MATLAB. It carries out an in-depth examination of the updated logistic model and demonstrates its application by making use of data that was made public in January 2022 and came from MIS-Health, which is part of Bangladesh's Directorate General of Health Services (DGHS).

Formulation of the Modified Logistic Model

To assume that the size of the existing population is the only factor that influences population growth. When it comes to really straightforward creatures like microbes, such an assumption might not be that irrational at all. This is definitely an oversimplification when applied to more complicated creatures such as plants, animals, or human beings because it ignores intra-species competition for resources in addition to other crucial aspects, such as age structure. The application of this to more complex creatures such as plants, animals, or human beings is certainly an oversimplification. It is possible that the size of other populations that interact with the population that is the focus of this study could have an effect on the birth and death rates of that group. This is significant because the size of other populations has the potential to have an impact on the birth and mortality rates. In light of the fact that the significance of this component cannot be overstated, giving it the attention it deserves is an imperative requirement. Because, despite its flaws, the model is able to accurately predict the qualitative behavior of real populations like COVID-19, researchers are concentrating their efforts on a model in which the infection rate is the only feature that is dependent on population size. This is as a result of the model's success in accurately forecasting the qualitative behavior of real-world populations.

The population growth can be modeled embedding the logistic growth model which is a sigmoid curve. The logistic growth model is engaged for biological schemes.

$$\frac{dC}{dt} = rC\left(1 - \frac{C}{K}\right) + \frac{C}{K}$$
(1)

Where, C -accumulated number of cases,

r-Pestilence rate, *t*-time and

K is the final pestilence size.

The pace at which the population is increasing or decreasing over time is represented by

$$\frac{dC}{dt}$$

If the elementary number of cases is given by $C|t = 0 = C_0$, then the solution (1) is

$$C(t) = \frac{e^{\frac{t}{K} + rt} (1 + Kr)}{e^{\frac{t}{K} + rt} r - \left(\frac{-1 - Kr + C_0 r}{C_0}\right)^{\frac{1}{1 + Kr} + \frac{Kr}{1 + Kr}}}$$
(2)

Stability of Equilibrium

Stability occurs when
$$\frac{dC}{dt} = 0$$

$$\Rightarrow rC\left(1 - \frac{C}{K}\right) + \frac{C}{K} = 0$$

$$\Rightarrow rC\left(\frac{K - C}{K}\right) + \frac{C}{K} = 0$$

$$\Rightarrow \frac{rC(K - C) + C}{K} = 0$$

$$\Rightarrow rC(K - C) + C = 0$$

$$\Rightarrow C\left\{r(K - C) + 1\right\} = 0$$
Either $C = 0$ or $\Rightarrow r(K - C) + 1 = 0$

$$\Rightarrow r(K - C) = -1$$

$$\Rightarrow K - C = -\frac{1}{r}$$

$$\Rightarrow -C = -\frac{1}{r} - K$$

$$\therefore C = 0, C = \frac{1}{r} + K$$

(3)

The process of linearization is unstable as C rises exponentially from any tiny beginning value and C = 0 is the starting point. The population has a tendency to move closer to the reciprocal of the rate of growth that is inherent and the maximum, which is the equilibrium number of individuals of a particular species that can be maintained indefinitely in a particular environment. In other words, the population moves closer to the reciprocal of the rate of growth that is inherent and the

maximum. Since the time is infinite, the equation $C = \frac{1}{K} + K$ cannot change (stable).

Proposition 1: When $t \to \infty$ then $C(t) = \frac{1}{r} + K$

From the equation (2) we have,

$$C(t) = \frac{e^{\frac{t}{K} + rt} (1 + Kr)}{e^{\frac{t}{K} + rt} r - \left(\frac{-1 - Kr + C_0 r}{C_0}\right)^{\frac{1}{1 + Kr} + \frac{Kr}{1 + Kr}}}$$

$$\Rightarrow C(t) = \frac{(1 + Kr)}{r - e^{-\frac{t}{K} - rt} \left(\frac{-1 - Kr + C_0 r}{C_0}\right)^{\frac{1}{1 + Kr} + \frac{Kr}{1 + Kr}}}$$

When $t \to \infty$ then $C(t) = \frac{(1+Kr)}{r-0}$

$$\Rightarrow C(t) = \frac{(1+Kr)}{r-0}$$
$$\Rightarrow C(t) = \frac{1+Kr}{r}$$
$$\Rightarrow C(t) = \frac{1+Kr}{r}$$

That is to say, we have demonstrated that when time is not a constraint, the population tends to approach the summation of reciprocal of the intrinsic growth rate

and the maximum, which is the equilibrium number of individuals of a certain species that can be maintained eternally in a particular habitat.

Proposition 2:*If the modified logistic model has a carrying capacity of K, and if*

$$0 < C_0 < \frac{K}{2}, \text{ then the amount of time } t = \frac{1}{\left(\frac{1}{K} + r\right)} \ln \frac{2\left(1 + Kr - C_0 r\right)}{\left(1 + Kr - 2C_0 r\right)} \text{ for the } t$$

doubling population.

From the equation (2) we have,

$$C(t) = \frac{e^{\frac{t}{K} + rt} (1 + Kr)}{e^{\frac{t}{K} + rt} r - \left(\frac{-1 - Kr + C_0 r}{C_0}\right)^{\frac{1}{1 + Kr} + \frac{Kr}{1 + Kr}}}$$

At time *t*, set for doubling population $C(t) = 2C_0$

$$C(t) = \frac{e^{\frac{t}{K} + rt} (1 + Kr)}{e^{\frac{t}{K} + rt} r - \left(\frac{-1 - Kr + C_0 r}{C_0}\right)^{\frac{1}{1 + Kr} + \frac{Kr}{1 + Kr}}}$$

$$\Rightarrow \frac{e^{\frac{t}{K}+rr}(1+Kr)}{e^{\frac{t}{K}+rr}r - \left(\frac{-1-Kr+C_{0}r}{C_{0}}\right)^{\frac{1}{1+Kr}+\frac{Kr}{1+Kr}}} = 2C_{0}$$

$$\Rightarrow e^{\frac{t}{K}+rr}(1+Kr) = 2C_{0}e^{\frac{t}{K}+rr}r - 2C_{0}\left(\frac{-1-Kr+C_{0}r}{C_{0}}\right)$$

$$\Rightarrow e^{\frac{t}{K}+rr}(1+Kr) = 2C_{0}e^{\frac{t}{K}+rr}r - 2(-1-Kr+C_{0}r)$$

$$\Rightarrow e^{\frac{t}{K}+rr}(1+Kr) - 2C_{0}e^{\frac{t}{K}+rr}r = -2(-1-Kr+C_{0}r)$$

$$\Rightarrow e^{\frac{t}{K} + rt} \left(1 + Kr - 2C_0 r\right) = -2\left(-1 - Kr + C_0 r\right)$$
$$\Rightarrow e^{\frac{t}{K} + rt} = \frac{-2\left(-1 - Kr + C_0 r\right)}{\left(1 + Kr - 2C_0 r\right)} \Rightarrow \frac{t}{K} + rt = \ln \frac{-2\left(-1 - Kr + C_0 r\right)}{\left(1 + Kr - 2C_0 r\right)}$$
$$\Rightarrow t \left(\frac{1}{K} + r\right) = \ln \frac{-2\left(-1 - Kr + C_0 r\right)}{\left(1 + Kr - 2C_0 r\right)}$$
$$\Rightarrow t = \frac{1}{\left(\frac{1}{K} + r\right)} \ln \frac{2\left(1 + Kr - C_0 r\right)}{\left(1 + Kr - 2C_0 r\right)}$$

This is the minimum amount of time needed for the population to double.

Results and Discussions

A Qualitative Analysis of the Modified Logistic Model

It is an absolute necessity that the values of r, K, and C_0 all be subject to varying degrees of imprecision. This is the case even if it may seem counterintuitive. Errors in r and C_0 do not have any impact on the reliability of the forecast of the final COVID-19 population size K. Despite this, the accuracy of the prediction is unaffected. When the conditions of $t \to \infty$ are applied to a solution, we call that solution stable if it undergoes only time changes in its initial size, C_0 , as a direct result of the application of these requirements. If the solution does not undergo these time changes, then we do not consider that solution to be stable. Any answer that provides a description of something that is of significance to biology must first demonstrate that it is stable. It would be unreasonable to consider the solution meaningful if even a very slight disturbance may result in a large change to the solution. If this were the case, the solution would be meaningless. It must be taken to retain that the modified logistic model is not an application of a fundamental law in a direct manner; rather, it is a shape that is adopted. This is crucial information to remember at all times. In order to do this, the COVID-19 model's broader classes are considered, and features that are valid for these classes are evaluated, rather than attributes that depend on the specifics of the modified logistic model. Because of this, it will be able to accomplish its objective. That is, it seeks to learn more about the characteristics shared by the larger classes as a whole.

Application of Modified Logistic Model's for an Analysing COVID-19

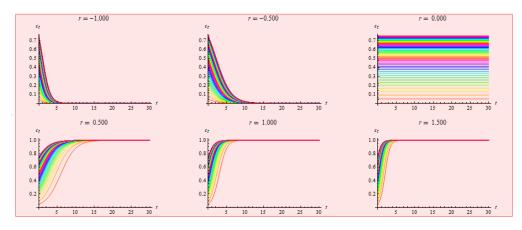
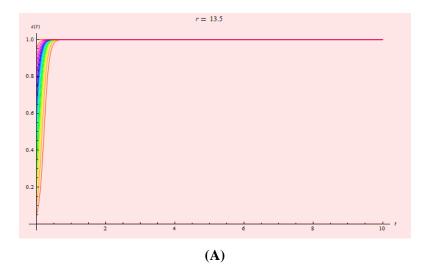


Figure 1. Solution curves of the equation (2) for arbitrary growth rates.

For the range $-1 \le r \le -0.5$ in Figure 1, the exponential decline of x(t) is given by the following equation (2). As time goes on, x(t) progressively increases in an exponential fashion for the range $0.5 \le r \le 1.5$.

If C is larger than K for some value of t, then the graph of C will always show an increase as t increases because the line joining C and K cannot be crossed by the graph of C. If C is less than K, then the line can be crossed at any time t. Therefore, as time goes on into the infinite future, C approaches the bound.





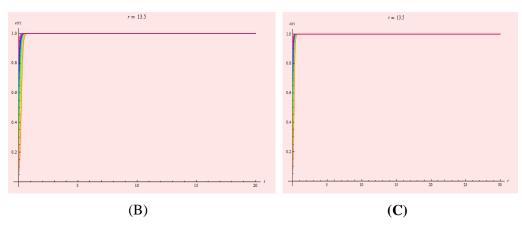


Figure 2. COVID-19 solution curves of the equation (2) for r = 13.5.

Since the right side of the differential equation is zero only for two values of x, we are limited to using C = 0 and K = 0 as limits. Upper and lower bounds cannot be calculated from any other values of x that do not satisfy both conditions. These solutions must increase toward K as time approaches infinity, since they cannot decrease toward zero. This happens because solutions close to C = 0 have a tendency to go farther away from C = 0. Therefore, these solutions can never converge to zero.

According to Figure 1, when the infection rate is negative and the time range is between 0 and 30, the population decreases at an exponential rate. The population has remained in the same condition as before despite the fact that there is no longer any danger of infection. The rate of infection will continue to climb, which will result in a further slowing of the rate of population growth.

It is clear from looking at Figure 2(a) that the rise in population is occurring at an exponential rate when r = 13.5 is used, and that the time range is $0 < r \le 10$. Figure 2(b) and (c) show that even though the infection rate has remained the same, there has been a gradual decrease in the population over time.

Bifurcation Analysis of the Modified Logistic Model

Bifurcation describes a qualitative change in iteration dynamics as a result of a perturbation to a parameter. Whenever there is a shift in the orbital structure of a system, scientist's use the term "bifurcation" to describe it. The structure and transitional behavior of dynamic evolution are important to its comprehension. There is a change from one stable condition to another at the bifurcation point. Bifurcation points can cause significant changes in the fixed point's behavior and the characteristics of the trajectories.

Choose K = 2650 is the final pestilence size and transmission rate, r = 13.50, it is considered that the data on January 2022 from Bangladesh.

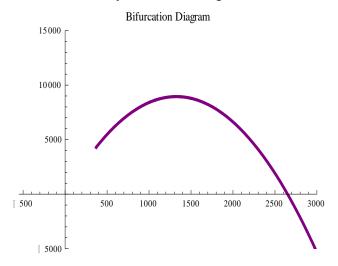


Figure 3. Bifurcation diagram of the modified logistic equation (1).

Putting the value of K = 2650 and r = 13.50 in the equation (3) it contains two points C = 0 and C = 2650.07.

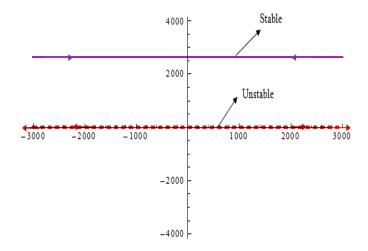


Figure 4. Bifurcation diagram of the equation (3).

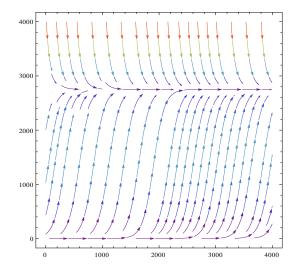


Figure 5. Bifurcation at C = 2650.07 (a sink) and C = 0 (a source) described by the equation (1).

Figure 3 reveals that the greatest number of people who would be impacted by the pandemic is 2650, and that the point at which transmission begins is C=370. Because seemingly inconsequential shifts in the parameter values can have a significant impact on the behavior of the solutions, the behavior of the solutions can be extremely sensitive to change. This sensitivity to change can make the behavior of the solutions extremely difficult to predict. From the Figure 4 and Figure 5 the observation was made that the node with the point C = 0 is an unstable node, whereas the observation was made that the node with the point C = 2650.07 is a stable node.

Modified Logistic Model for the COVID-19 of Bangladesh

Simply obtaining the logistical form is sufficient, which provides insight into a critical aspect of modeling in biological schemes. The turn of events was for the better. The logistic form in equation 1 includes three parameters, C_0 , K, and r, and these are the only ones that can be used to correlate hypothetical situations with real-world cases.

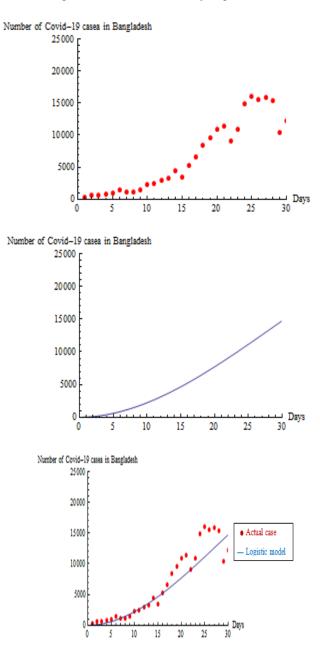
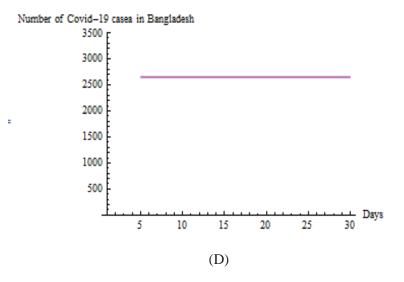


Figure 6. Modified Logistic Model for the COVID-19 of Bangladesh.

Figure 6 illustrates these conclusions for the Corona virus cases that occurred in Bangladesh. It does so by making a comparison between the actual cases and the logistic model. It has been discovered that there is a sizeable number of people who have been invaded in the actual happenings that have taken place. The distance between the data points and the curve produced by the logistic model is shrinking to an exceedingly small value. This modeling commandment, which is discussed in this research study, is to further comprehend the underlying scheme because it is only in this way that justifiable projections can be assembled. This is the only method that this can be accomplished. This conversation's overarching objective is to bring about a deeper comprehension of the system.

Logistic Curves Fitted for COVID-19 Cases of Bangladesh

It assumes that a population can in fact be described by a modified logistic model when using the modified logistic model and then seeks to identify the parameters r and K as well as the beginning population size C_0 in order to get the best match with experimental data. This is done by using the logistic model with some modifications. The utilization of the modified logistic model serves to accomplish this goal. In order to accomplish this objective, one needs to select the criteria that, when combined with the data, will produce the best accurate match that can possibly be made.



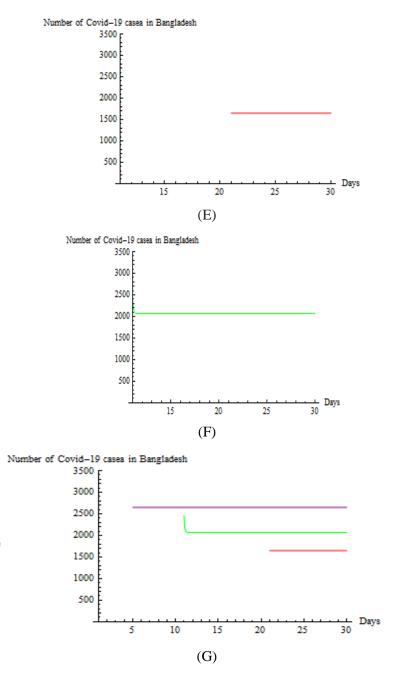


Figure 7. Logistic curves fitted of (D-G) for COVID-19 corona virus of Bangladesh.

As may be shown in Figure 7(D), about 2500 people have been infected between days 5 and 30 after infection. As can be seen in Figure 7(E), the number of infected people rises above 2000 between days 15 and 30. By t=20-30 days, as shown in Figure 7(F), the number of infected individuals had risen to about 1500.

A cursory examination of the picture makes it clearly clear that the logistic model forecasts the number of COVID-19 cases in Bangladesh to be fairly irregularly distributed over a reasonably extended period of time. This is something that can be seen by taking a short look at the chart. It is possible to monitor it for a constrained amount of time with the purpose of determining the logistic curve that is best suitable to fit COVID-19 patients in Bangladesh. The purpose of this endeavor is doable. Observation is the method that can be used to do this. Because it estimated the parameters based on a combination of intuition and observation, it is unable to precisely characterize how many curves could be fitted to explain the COVID-19 cases in Bangladesh. This is because intuition and observation were both used in the estimation process. This is due to the fact that it approximated the parameters by utilizing each of the aforementioned methods simultaneously. In addition to this, it is projected that the number of cases that are reported each day in Bangladesh would reach its highest point in the month of January 2022.

Estimated numerical study of Logistic model for corona virus cases in Bangladesh

Choose K = 2650 is the final pestilence size.

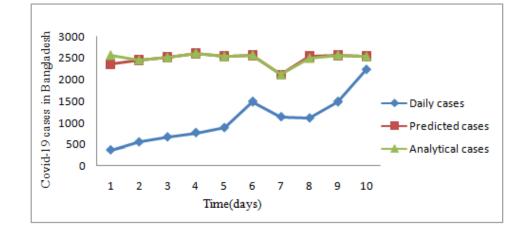
r = 13.50, it is considered that the data on January 2022 from MIS-Health, Directorate General of Health Services (DGHS) in Bangladesh.

Time(days)	Actual cases: Bangladesh	Prediction of infected cases of C(t)(Numerical value)	Analytical Cases
1	370	2355	2567
2	557	2457	2458
3	674	2517	2518
4	775	2608	2610
5	892	2546	2540
6	1140	2549	2548
7	1146	2109	2116
8	1116	2549	2499
9	1491	2567	2569
10	2231	2549	2539
11	2458	2601	2549
12	2916	2603	2604

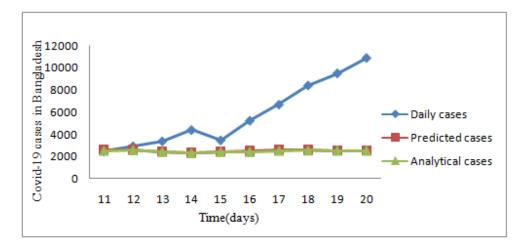
Table 1. Results of daily modified logistic model for Bangladesh

Time(days)	Actual cases: Bangladesh	Prediction of infected cases of C(t)(Numerical value)	Analytical Cases
13	3359	2442	2449
14	4378	2349	2333
15	3447	2467	2449
16	5222	2478	2450
17	6,676	2585	2549
18	8407	2569	2570
19	9500	2549	2551
20	10888	2555	2556
21	11434	2539	2540
22	9614	2540	2550
23	10906	2560	2590
24	14848	2650	2650
25	16033	2650	2650
26	15609	2650	2650
27	15807	2650	2650
28	15440	2650	2650
29	10378	2650	2650
30	12183	2650	2650

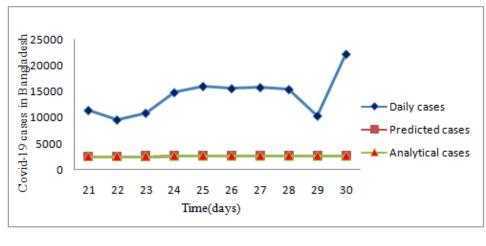
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(A)



(B)



(C)

Figure 8. Predicted evaluation of corona virus epidemic in Bangladesh on January 2022 (A) 1-10 days, (B) 11-20 days and (C) 21-30 days.

The states and projected transmission rates are treated as if they exist in the same hypothetical environment as in the actual, predicted, and analytical scenarios. The projected impact of the January 2022 corona virus outbreak in Bangladesh is displayed. According to the numbers, the daily real instances on January 1, 2022, were 370, while the expected number of cases was 2355 and the analytical figure was 2567. The actual number of cases on January 2, 2022 was 557, while the predicted and evaluated numbers were 2457 and 2458, respectively. The analytical number for January 10, 2022 was 2539, while the projected number of cases was 2549. On that day, there were actually 2,231. The analytical and predicted numbers of cases for January 25, 2022, were both 2650; however, the actual number of cases for that day was 16033. According to the chart, January 1st has the fewest transmissions and January 25th has the most. From January 24th to 30th, the graph reveals no reduction in the number of predicted and analyzed instances. The RK-4 approach shows promise when applied to the logistic model. An epidemic caused by the Corona virus has hit Bangladesh.

Conclusions

In order to better understand the evaluation of suspected cases and to account for the possibility of contagious incidents in which no symptoms are present, the COVID-19 logistic model was created in Bangladesh. The model description includes a discussion of the symptomatic contagious. Indicated and unindicted instances are also differentiated from the contagious. In order to better fit the IEDCR indicated case data for all of Bangladesh, the modified logistic model simulations started on January 1, 2022. It is necessary for the transmission rate to be negative, and the time range must be between one and thirty while the population is falling at an exponential rate. The rate of transmission is consistently increasing, which suggests that the rate of population expansion will be slowed even further in the next time. When the formula r = 13.5 is applied, it becomes immediately apparent that the rise in population is occurring at an exponential rate, and the range of time from 1 to 30 days is being taken into consideration here. This indicates that over the course of time, even though the rate of transmission has remained the same, there has been a gradual but consistent decrease in the population despite the fact that there has been no change in the transmission rate. The bifurcation graphs illustrate two distinct equilibrium locations, each of which has a node that is either stable or unstable. The COVID-19 epidemic in Bangladesh was the target of a tailored logistical concept. Bangladesh is included in the logistic model since covid-19 can spread to any area where people live. The incidence of COVID-19 in Bangladesh was analyzed using a modified logistic model. Dissimilarities between the analyzed and anticipated cases (RK-4) are found to be quite minor. Isolation and guarantine at home can help reduce the spread of new corona viruses. Despite the decline in new cases of corona virus, the recovery rate is not encouraging. Researchers have discovered that vaccination is not the only

way to prevent corona virus infections. Corona virus disease can be reduced by following health standards in addition to getting vaccinated.

References

- [1] He, S., Tang, S, Rong,: A discrete stochastic model of the COVID-19 outbreak: forecast and control. Math Bios and Eng, 2020, 17, 2792-2804.
- [2] Zhu, N., Zhang, D., Wang, W.: A Novel Corona virus from Patients with Pneumonia in China. The New Eng J of Med, 2020,382, 727–733.
- [3] Zhang, S., Diao, W., Yu., L., Pei, Z., Lin, Chen, D.: Estimation of the reproductive number of novel corona virus (COVID-19) and the probable outbreak size on the diamond princess cruise ship: data-driven analysis. Int J Infect Dis,2020, 93, 201-204.
- [4] Wang, P., Zheng, X., Jiavang, Li, Zhu, B.:Logistic model and machine learning technics. Ch, Sols and Fras 2020,139, 110-125.
- [5] Yang, Z., Zeng, Z., Wang, K., Wong, S., Lian, W., Zanin, M.: Modified seir and al prediction of the epidemics trend of COVID-19 in China under public health interventions. J Thorac Dis., 2020,12, 165-174.
- [6] Giuliani, D., Dickson, M.,M., Espa, G., Santi, F.: Modeling and predicting the spatiotemporal spread of corona virus disease 2019(COVID-19) in Italy. BMC Inf Dis., 2020, 20, 70-92.
- [7] Fanelli, D., Piazza, F.: Analysis and forcast of COVID-19 spreading in China, Italy and France. Ch Sols and Fras., 2020, 134, 109-121.
- [8] Yousaf, M., Zahir, S., Riaz, M.: Statistical analysis of forecasting COVID-19 for upcoming month in Pakistan. Cha sols and Fras., 2020, 138, 109-126.
- [9] Zhao, S., Chen, H.: Modeling and epidemic dynamics and control of COVID-19 outbreak in China. Quan Bio., 2020, 8, 11-19.
- [10] Shen, CY.: Logistic growth modelling of COVID-19 proliferation in China and its international implications. Int J Infect Dis., 2020,96, 582-589.
- [11] Regulatory Decision summary-Pfizer-BioNTech COVID-19 Vaccine. Health Canada Government of Canada, 2020.
- [12] World Health Organisation Corona virus disease (Covid-19): Vaccines, 2020.
- [13] Hasan, M.,M., Ahmed, M., Urmy, S.,A.: Efficacy of limited antiviral, testing, hospitalization, and social distancing for covid-19 pandemic, Sens Inte., 2021,2, 10-22.

- [14] Genga, X., Katulb, G.,G., Gergesa, F., Zeide, E, Nassif, H., Boufadela, M.,C.: A kernel-modulated SIR model for Covid-19 contagious spread from county to continent. PANAS., 2021,118,1-9.
- [15] Murry, J.,D.: Mathematical Biology I: An Introduction, Springer, New York, 2007.
- [16] Fred, B., Carlos, C-C. Mathematical Models in Population Biology and Epidemiology, Springer, New York. 2012.
- [17] Malek, A., Haque, A. Model development and prediction of COVID-19 pandemic in Bangladesh with nonlinear incident. Ira J of Sc., 2023, 47, 249-258.
- [18] Postlethwaite, C.M., Rucklidge, A.M.: A trio of heteroclinic bifurcations arising from a modelof spatially-extended Rock-Paper-Scissors. Nonlinearity, 2019, 32,1375-1407.
- [19] Ritchie, M., Berthouze, L., House, T., Kiss, I.,Z.: Higher-order structure and epidemic dynamics in clustered networks. J of Thel Bio. 2014, 318, 21-34.
- [20] Hethcote, H.,W. Three Basic epidemiological models. App math eco, 1989,18, 119-144.
- [21] Hu, Z., Teng, Z., Jia. C., Zhang, C., Zhang: Dynamical analysis and chaos control of a discrete SIS epidemic model Ad in Dif eqs., 2014,58, 1687-1847.

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