**Title:** Estimation of the Basic Reproduction Number of SARS-CoV-2 in Bangladesh Using Exponential Growth Method.

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**Authors:** Riaz Mahmud¹*, H. M. Abrar Fahim Patwari²

**Affiliations:**

¹ Department of Mathematics, Faculty of Mathematics and Computer Science, South Asian University, New Delhi 110021, India.

² Department of Applied Mathematics, Faculty of Science, Noakhali Science and Technology University, Noakhali 3814, Bangladesh.

**Corresponding Author:**

Riaz Mahmud

Address: Department of Mathematics, South Asian University, Akbar Bhawan, Chanakyapuri, New Delhi-110021, India.

E-mail: riaz.mh@students.sau.ac.in

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Estimation of the Basic Reproduction Number of SARS-CoV-2 in Bangladesh Using Exponential Growth Method

Abstract:

Objectives: In December 2019, a novel coronavirus (SARS-CoV-2) outbreak emerged in Wuhan, Hubei Province, China. Soon, it has spread out across the world and become an ongoing pandemic. In Bangladesh, the first case of novel coronavirus (SARS-CoV-2) was detected on March 8, 2020. Since then, not many significant studies have been conducted to understand the transmission dynamics of novel coronavirus (SARS-CoV-2) in Bangladesh. In this study, we estimated the basic reproduction number \( R_0 \) of novel coronavirus (SARS-CoV-2) in Bangladesh.

Methods: The data of daily confirmed cases of novel coronavirus (SARS-CoV-2) in Bangladesh and the reported values of generation time of novel coronavirus (SARS-CoV-2) for Singapore and Tianjin, China, were collected. We calculated the basic reproduction number \( R_0 \) by applying the exponential growth (EG) method. Epidemic data of the first 76 days and different values of generation time were used for the calculation.

Results: The basic reproduction number \( R_0 \) of novel coronavirus (SARS-CoV-2) in Bangladesh is estimated to be 2.66 [95% CI: 2.58-2.75], optimized \( R_0 \) is 2.78 [95% CI: 2.69-2.88] using generation time 5.20 with a standard deviation of 1.72 for Singapore. Using generation time 3.95 with a standard deviation of 1.51 for Tianjin, China, \( R_0 \) is estimated to be 2.15 [95% CI: 2.09-2.20], optimized \( R_0 \) is 2.22 [95% CI: 2.16-2.29].

Conclusions: The calculated basic reproduction number \( R_0 \) of novel coronavirus (SARS-CoV-2) in Bangladesh is significantly higher than 1, which indicates its high transmissibility and contagiousness.

Keywords: Basic reproduction number, SARS-CoV-2, COVID-19, Coronavirus disease 2019
Introduction:

Coronavirus disease 2019 (COVID-19) is a highly infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [1]. COVID-19 was first identified in December 2019, Wuhan, Hubei Province, China [2]. Eventually, it resulted in an ongoing pandemic [3]. Up until the 25th of August 2020, more than 23.9 million cases were confirmed across 213 countries and territories. The death toll is high, with more than 820,000 deaths. Moreover, more than 16.4 million people have recovered from it [4]. However, as COVID-19 has spread out across the world, Bangladesh is not an exception. Ever since 8th March, the first case spotted, there has been a report of 299,628 confirmed cases, 4,028 deaths, and 186,756 recoveries from COVID-19 as of 25th August 2020 [5]. SARS-CoV-2 infects the host's respiratory system. It spreads between people when they come to close contact with an infected person (symptomatic or not) by inhaling small droplets produced by coughing, sneezing, or talking [6].

Most of the mathematical models on how a contagious disease spreads on a population are based on the basic reproduction number (R\(_0\)). R\(_0\) defines the secondary cases generated by an infected person over his entire period of infectiousness in a completely susceptible population [7]. The significance of R\(_0\) lies within its threshold. If R\(_0\) > 1, the infected population number will grow. And if R\(_0\) < 1, the number will decrease [8]. In the study of epidemiology, R\(_0\)<1 is the favorable ratio. An epidemic with high basic reproduction number R\(_0\) is potentially a civilization-ending threat. Several control methods can be taken to minimize the R\(_0\). We experienced numerous highly infectious disease outbreak in the last two decades. Globalization has enabled us with high connectivity. However, this fruit of civilization could become the doom for us instantaneously without proper control measures. We must know what we are up against to implement proper control methods. And \(R_0\) gives an explicit idea about the transmission of the virus.
There are many popular methods for estimating the $R_0$ value. For this research purpose, we shall use the exponential growth (EG) method. Using the EG has adequacy because researchers found from the simulation that it is less prone to bias [9]. In the EG method, we need generation time (or generation interval) $GT$, to formulate $R_0$. GT defines the time interval between symptoms recorded on an infected person and a secondary case [10].

**Materials and Methods:**

**Data Sources:**

Data used in this paper is the daily confirmed cases of infection of SARS-CoV-2 in Bangladesh (from the 1st day of the outbreak to the 76th day). The data were gathered from https://ourworldindata.org/coronavirus-source-data. This website provides real-time data and statistics on various topics.

**Estimation of the Basic reproduction number $R_0$:**

The use of the basic reproduction number $R_0$ is one of the most important concepts in the study of demography, ecology, and epidemiology. In epidemiology, $R_0$ defines the secondary cases generated by an infected person over his entire period of infectiousness in a completely susceptible population [7]. $R_0$ expresses the transmissibility of a disease. The basic reproduction number is the common buzzword during a pandemic. Because the nature of the virus is explicit with it. There are many existing methods for estimating $R_0$. Among them are Exponential Growth (EG), Maximum Likelihood estimation (ML), Sequential Bayesian method (SB), the Time-Dependent method (TD), and so on. For this particular paper, we shall apply the EG method. Also, the EG method requires Generation Time (GT), also known as Generation Interval, of the virus for the estimation.

**Exponential Growth:**

The count of cases increases exponentially in the early stages of an epidemic. The exponential growth (EG) model is a simplified model. If something grows with a consistent rate, then it is said...
to be an exponential growth. The basic reproduction number $R_0$ can be interpreted indirectly from the exponential curve of epidemic growth. As reported by Wallinga and Lipsitch, 2007 [11], the exponential growth of an epidemic at the early stage is linked to $R_0$ as the following manner,

$$R_0 = \frac{1}{M(-r)}$$

Here, $M$ = moment generating function of GT distribution and $r$ = exponential growth rate. The daily confirmed cases data are integers. So Poisson regression is used to fit the value of the growth rate, $r$.

**Generation Time:**

Generation Time (GT) of a virus shapes how a pandemic spread in a population. The measure of GT is critical in the estimation of $R_0$. We relied upon a paper that evaluated the generation time of SARS-CoV-2. Researchers found that the GT of SARS-CoV-2 differs. For the data of Singapore, they estimated the generation time (GT) of SARS-CoV-2 to be 5.20 with a standard deviation (SD) 1.72 and the generation time (GT) 3.95 with a standard deviation 1.51 is calculated for the data of Tianjin, China [12].

**R0 Package:**

R software (version 4.0.2), along with the R0 package, have been used for the estimation of $R_0$ and analyzing the data [9].

**Results:**

Using reported generation time of novel coronavirus (SARS-CoV-2) for Singapore and Tianjin, China, 5.2, and 3.95 with a standard deviation of 1.72 and 1.51 respectively, the basic reproduction number $R_0$ of novel coronavirus (SARS-CoV-2) in Bangladesh are estimated. For the estimation, the data of the first 76 days of novel coronavirus (SARS-CoV-2) outbreak in Bangladesh is used. The optimal time interval is calculated to be from day 2 of the outbreak to day 44. Hence, the optimal $R_0$ is calculated in the optimal time interval.
The value of $R_0$ is estimated to be $2.66$ [95% CI: 2.58-2.75] with the optimal value of $2.78$ [95% CI: 2.69-2.88], using the reported generation time of SARS-CoV-2 for Singapore. Furthermore, using the reported generation time of SARS-CoV-2 for Tianjin, China, the estimated $R_0$ is $2.15$ [95% CI: 2.09-2.20] with the optimal value of $2.22$ [95% CI: 2.16-2.29] (Table 1).

**Table 1. Estimation of basic reproduction number $R_0$ of SARS-CoV-2 in Bangladesh by exponential growth method using different reported values of generation time of SARS-CoV-2.**

| Generation Time | Source | Remark | Estimated $R_0$ [95% CI] | Optimal $R_0$ [95% CI] |
|-----------------|--------|--------|--------------------------|-------------------------|
| GT 5.20, SD 1.72 | [12]   | GT was reported for Singapore. | 2.66 [2.58-2.75]        | 2.78 [2.69-2.88]        |
| GT 3.95, SD 1.51 | [12]   | GT was reported for Tianjin, China. | 2.15 [2.09-2.20]        | 2.22 [2.16-2.29]        |

**Sensitivity Analysis:**

To analyze the sensitivity, we estimated $R_0$ of SARS-CoV-2 for the same data using previously reported generation time of MERS and SARS coronavirus 7.6 and 8.4 with a standard deviation of 3.4 and 3.8, respectively [13, 14]. The estimated $R_0$ is $3.65$ [95% CI: 3.51-3.80] and $4.07$ [95% CI: 3.90-4.25] with optimal value $3.86$ [95% CI: 3.70-4.04] and $4.32$ [95% CI: 4.13-4.53] corresponding to the generation time of MERS and SARS coronavirus respectively (Table 2).

**Table 2. Estimation of basic reproduction number $R_0$ of SARS-CoV-2 in Bangladesh by exponential growth method using generation time of MERS and SARS coronavirus.**

| Generation Time | Source | Remark | Estimated $R_0$ [95% CI] | Optimal $R_0$ [95% CI] |
|-----------------|--------|--------|--------------------------|-------------------------|
| GT 7.6, SD 3.4  | [13]   | GT of MERS. | 3.65 [3.51-3.80]        | 3.86 [3.70-4.04]        |
| GT 8.4, SD 3.8  | [14]   | GT of SARS. | 4.07 [3.90-4.25]        | 4.32 [4.13-4.53]        |
We found that the value of $R_0$ varies with the change of generation time. Using the EG method, for generation time 3.95, the value of $R_0$ is estimated to be 2.15, and this value is almost doubled and estimated to be 4.07 for generation time 8.4 (Figure 1).

![Sensitivity of the Basic Reproduction Number of SARS-CoV-2](image)

**Figure 1.** Different values of $R_0$ corresponding to different values of generation time is illustrated. The values of $R_0$ corresponding to generation time 3.95, 5.20, 7.60, and 8.40 represented by red, purple, blue, and black dots, respectively.

The analysis shows that $R_0$ is sensitive to generation time. Hence, generation time needs to be estimated accurately to estimate $R_0$ more precisely.

**Discussion:**

The estimated value of the basic reproduction number $R_0$ of SARS-CoV-2 in Bangladesh using the exponential growth method is ranging from 2.22 to 2.78. This result is quite similar to the previously reported $R_0$ using the same method in China 2.24 and 2.90 [15, 16]. This estimated value of $R_0$ is significantly greater than 1, which is evidence of the high transmissibility and
contagiousness of SARS-CoV-2 in Bangladesh. In this study, we found that $R_0$ shows some sensitivity to generation time. Thus, a more precise estimation of generation time is needed to estimate $R_0$ with more accuracy.

The estimation of $R_0$ can be used to estimate other transmission dynamical parameters of SARS-CoV-2 in Bangladesh. It also can help to determine an optimum strategy for vaccination. From the epidemiological study, we have, $c > (1 - R_0^{-1}) / (1 - r)(1 - s)$ [17]. Where $c$ is the minimum coverage of elimination, $r$ is the fraction of individuals who are completely immunized, and $s$ is the susceptible individuals.

This study has some strong points. First, in this study the quantification of the basic reproduction number $R_0$ of SARS-CoV-2 in Bangladesh has been done using the reported generation time of SARS-CoV-2. This increases the possibility of better accuracy of the study. Second, the sensitivity analysis was done for different generation time values, which gives a hint for further betterment of the estimation of $R_0$. Last, this study gives a hint for the optimal vaccination strategy. This can be helpful if the vaccine arrives in the near future.

This study has several limitations too. First is the quality of data. We collected data from a public resource. The quality of data is not ensured. There is a possibility that some confirmed cases remained unreported. This can affect our estimation. Second, the reported values of generation time vary from 3.95 to 5.20. This is not quantified precisely.

In summary, using the exponential growth method, the basic reproduction number $R_0$ of SARS-CoV-2 is estimated. $R_0$ has shown some sensitivity to generation time. This study can be helpful for further understanding of the transmission dynamics of SARS-CoV-2 in Bangladesh. The estimated $R_0$ is significantly larger than 1, which is evidence of its high transmissibility and contagiousness. Either vaccination should be done, or more preventive control measures should be taken to reduce the epidemic size.
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