

Analysis and Forecast of Third Wave of COVID-19 Outbreak in Sri Lanka

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Abstract: *The coronavirus disease (COVID-19) is a respiratory viral disease first reported in Wuhan city in China on December 2019 and turned pandemic worldwide. The World Health Organization declared the COVID-19 outbreak as a pandemic on 11th February 2020. The first case of COVID-19 was reported in Sri Lanka on 27th January 2020, a Chinese female visiting the country. The first local patient was reported on 11th March 2020 thus bringing about unprecedented changes in the daily life in the country. However, Sri Lanka successfully managed to control the spread of the first and second waves of the virus and kept the number of patients and deaths at a minimum. Now, Sri Lanka struggles to respond effectively to COVID-19 third wave. A simple model for predicting COVID-19 epidemic is presented in this study. The prediction model is presented based on the classic Susceptible-Infectious-Recovered (SIR) model, which has been widely used to describe the epidemic time evolution of infectious diseases. The main purpose of this research is to estimate the parameters of SIR model and to predict the peak of the third wave of the COVID-19 pandemic in Sri Lanka using the data from 15th April 2021 to 25th June 2021. Data was obtained from daily situation reports of the Epidemiology Unit, Sri Lanka. The values of the rate of transmission and rate of removal are at 0.0966 and 0.07143, respectively. The peak of pandemic will be reached after approximately 142 days from its emergence in Sri Lanka. The percentage of infected persons at the peak of the third wave was estimated at 3.95% of the total population. The basic reproduction number was estimated at 1.3529. These results may be helpful to Sri Lankan authorities to adapt their strategies and may be taken into consideration in the future phase of discontentment. Further, it seems that this simple model is still reliable enough to describe the dynamics of the COVID-19 epidemic, not only qualitatively but also quantitatively with a high degree of correlation between actual data and prediction results*

Keywords: COVID-19, Pandemic, Parameters, Sri Lanka

1. Introduction

The coronavirus disease (COVID-19) is a respiratory viral disease first reported in Wuhan city in China on December 2019 and turned pandemic worldwide. At the inception itself, the COVID-19 pandemic became a global concern, and the World Health Organization declared internationally a public health emergency on 30th January 2020. Later on, new health and sanitation measures were taken in terms of imposing social distancing, lockdown, and curfew.

The first case of COVID-19 was reported in Sri Lanka on 27th January 2020, a Chinese female visiting the country. Almost six weeks later, Sri Lanka identified the first COVID-19 patient who contracted the disease locally. The number of COVID-19 cases reported since then showed a gradual increase and included both imported and locally transmitted cases. Although the first wave (from 27th January 2020 to 03rd October 2020) and second wave (from 04th October 2020 to 14th April 2021) of the COVID-19 pandemic progressed more slowly in Sri Lanka than the rest of the world, by mid-April, 2021, the third wave appeared to be much more aggressive with many more cases. The prediction of COVID-19 evolution is of great importance for providing information for the public authorities that could help them to adopt or revise their prevention measures.

The measures to control the COVID-19 pandemic involve a very complex process for several reasons. Firstly, no medicine can cure the disease caused by this new virus. Secondly, the origin of the virus that causes this disease is still unclear, although several hypotheses have been suggested that the virus originated in bats. This hypothesis

requires further detailed research to confirm this hypothesis. Thirdly, the incubation period of this disease is based on clinical studies in patients, and has been confirmed to be about 14 days; however, in most cases, symptoms only appear after 4–5 days after the patient is infected with the virus. During the incubation period, an asymptomatic patient may not know that they are infected, meaning that the patient can transmit the virus to other individuals without being aware. A recent study has found that this virus can remain on the surface of an object for 9 days, thus adding to the complexity of avoiding the spread of this virus. Other studies have also concluded that the rate of infection of the disease is very fast, resulting in a significant burden on health facilities hosting a number of infected patients.

The situation of a pandemic will increase the demand for epidemiological mathematical models, in order to explain the dynamics of the outbreak. This not only provides an explanation, but also has the potential to predict when an outbreak is new and is still in an active phase. This prediction aims to quickly estimate the impact of the COVID-19 pandemic on a population in the future. This is to ensure that the spread prevention measures that will be taken by the public health system are faster and more effective, such as tracing and quarantine for individuals who have come into contact with infected individuals.

Multiple forecasting methods were used to analyze and predict the future trends of COVID-19. A variety of models have been developed, ranging from very simple models to complex models that include many variables and parameters. However, complex models can include many parameters and variables, hence; the process of estimating these parameters

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requires detailed statistics and validation. Factors affecting the statistics of these parameters and variables should have real data available. This may not be available in every country, as there may be very limited data available. Therefore, support for the application of a simple model in the form of a compartment regression, which is commonly referred to as the Susceptible-Infectious-Recovered (SIR) and Susceptible-Exposed-Infectious-Recovered (SEIR) models, is still very relevant. These epidemiological models are in the form of ordinary differential equations and contain several parameters and variables; furthermore, these parameters have information that is immediately available to be applied in measures in order to prevent the spread of an outbreak.

The main objective of this research is to estimate the SIR model's parameters such as rate of transmission and rate of removal. Further, we aimed to calculate the basic reproduction number for the spread of third wave in Sri Lanka, the percentage of infected persons at the peak, the total number of cases caught by the pandemic and the extinction date of the COVID-19 pandemic in Sri Lanka using the data from April 15th, 2021 to June 25th 2021. Data was obtained from daily situation reports of the Epidemiology Unit, Sri Lanka.

Section 2 describes the materials and methods, starting with introducing the equations of the SIR model and then the method for deriving two parameters of the model that plays an important role in understanding the characteristics of an epidemic in an area. Section 3 describes the results and discussion. The last section, Section 4, contains the conclusions

2. Materials and Methods

2.1 Susceptible-Infected-Recovered Compartmental Model

The classical SIR model was introduced by Kermack and McKendrick, depending on the fact that any population can be divided into three compartments susceptible, infected and recovered, each containing individuals that are identical in terms of their status with respect to the disease. This simple model can be applied easily to gain insight into how the COVID-19 virus spreads in a population as a function of time. This classic SIR model is also useful for predicting the spread of the virus, both qualitatively and quantitatively. The classic SIR model describes an infectious disease that spreads in a population with permanent immunity. The number of infected persons decreases with recoveries and deaths. Recovered individuals can also no longer change to the susceptible state.

The classic SIR model is composed of a system of equations, consisting of the three coupled ordinary differential equations (ODEs). In this mathematical model, we assumed that all the clinically tested positive patients for COVID-19 virus are homogeneous with no impact of age, gender, and history of chronic diseases on the disease progression.

Natural birth and death process was considered to be negligible, and those who recovered have developed complete immunity against the virus. In this simple model, the susceptible individual may become exposed to the novel coronavirus at a rate of β . As a result of treatments or due to the immunity, the patient can recover at a rate of γ .

The epidemiological model in compartment form for the SIR model can be defined as follows:

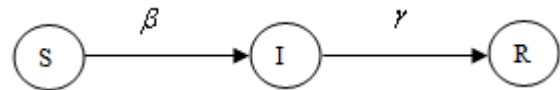


Figure 1: Transfer diagram: SIR model

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

2.2 Determination of Model Parameters

When the infectious occurs, the susceptible population is almost equal to the total population $S \approx N$. Subsequently, the number of infectious individuals $I(t)$ first increases exponentially.

$$\frac{dI}{dt} \approx (\beta - \gamma)I \tag{4}$$

$$I = I_0 e^{(\beta - \gamma)t} \tag{5}$$

$$\ln I = (\beta - \gamma)t + \ln I_0 \tag{6}$$

We can calculate the value of $\beta - \gamma$ from the log-plot data and for the best-line fit we can use, for example, the least squares.

If we suppose that I is a constant ($I(t) = I_0$), we obtain the equation:

$$\frac{dR}{dt} = \gamma I_0 \tag{7}$$

By integrating:

$$R(t) = \gamma I_0 t \tag{8}$$

If the time of recovery $t = T$ days, and $R(T) = I_0$, or $\gamma T = 1$. Therefore, γ is defined as the inverse of the duration of recovery. That is, $\gamma = \frac{1}{T}$.

2.3 Estimation of Percentage Infected Persons at the Peak of the Pandemic

Estimation of I_{\max} (percentage of infected persons at the peak of the epidemic) can be calculated as follows:

We divide the equation (2) by (1):

$$\frac{dI}{dS} = -1 + \frac{\gamma}{\beta S} \quad (9)$$

If we integrate both sides, we obtain the Equation:

$$I_{\max} = 1 + \frac{\gamma}{\beta} \left(\ln \frac{\gamma}{\beta} - 1 \right) \quad (10)$$

2.4 Determination of the Basic Reproduction Number (R_0)

R_0 or the basic reproduction number is defined as the average number of people infected by a single individual. It is used to determine the ability of a disease to spread within a given population. It represents the transmissibility of a disease. Also, it is a dimensionless number and an indicator of the contagiousness of a pathogen.

The two uses of R_0 are (1) to assess the ability of an infectious disease to invade the community and (2) to determine the fraction of the community which should be vaccinated in order to prevent the growth of the epidemic. Further, If $R_0 > 1$, then an epidemic will occur. If $R_0 < 1$, then an epidemic will not occur.

Mathematically, it represents the ratio of transmission and recovery rates.

$$R_0 = \frac{\beta}{\gamma} \quad (11)$$

3. Results and Discussion

In this research, we applied the SIR model to estimate different parameters related to the third wave of COVID-19 epidemic of Sri Lanka.

The values of the rate of transmission and rate of removal are at 0.0966 and 0.07143, respectively. The peak of pandemic will be reached after approximately 142 days from its emergence in Sri Lanka. That is, 03rd Sep. 2021 (Predicted date) from its emergence (15th Apr. 2021). The percentage of infected persons at the peak of the third wave was estimated at 3.95%.

Taking into account the total number of the Sri Lankan population, the number of sick peoples will be 861,100 persons. Finally, the basic reproduction number was estimated at 1.3529. By approximating directly from the dataset of Sri Lanka, we obtained the values of S, I, and R plotted in Fig 2.

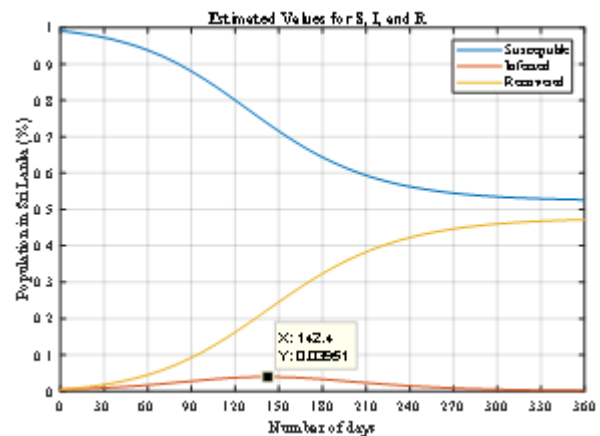


Figure 2: Estimated values for S, I, and R

4. Conclusion

The world has been facing a devastating COVID-19, caused by SARS-CoV-2, since its emergence in the Wuhan city of China at the end of 2019. The pandemic, which has rapidly spread to almost all countries in the world, continues to inflict severe public health and socio-economic burden in many parts of the world, including in Sri Lanka. In the absence of a safe and effective vaccine or antiviral for use against the pandemic in humans, control efforts are focused on the use of non-pharmaceutical interventions, such as social (physical)-distancing, community lockdown, contact tracing, quarantine of suspected cases, isolation of confirmed cases and the use of face masks in public. Sri Lanka is one of the countries in South Asia that is hardest hit with the burden of the COVID-19 pandemic.

We developed a mathematical model for analyzing the COVID-19 pandemic in Sri Lanka. The SIR compartmental epidemic model we developed in this study, which takes the form of a deterministic system of nonlinear differential equations. The numerical results show that if public health authorities toughen the control measures, they can delay the peak and thereby flatten the curve.

References

- [1] Y. Asahiro, K. Iwama, H. Tamaki, and T. Tokuyama, "Greedy finding a dense subgraph," *Journal of Algorithms*, vol. 34, pp. 203–221, 2000.
- [2] Y. Asahiro, R. Hassin, and K. Iwama, "Complexity of finding dense subgraphs," *Discrete Applied Mathematics*, vol. 121, pp. 15–26, 2002.
- [3] W. Hu and X. Jiashu, "Research of network hotspot detection and tracking model based on the characteristics of events," in *ICCSM*, vol. 1, pp. 304–308, 2010.
- [4] R. T. Handayanto, Haryono, and J. Prianggono, "Real time neural network-based network analyzer for hotspot area," in *ICACSIS*, pp. 323–330, 2011.
- [5] H. Hu, X. Yan, Y. Huang, J. Han, and X. J. Zhou, "Mining coherent dense subgraphs across massive biological networks for functional discovery," *Bioinformatics*, vol. 21, no. Suppl. 1, pp. i213–i221, 2005.

Author Profile



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