

# COVID-19

## PANDEMIC IN SRI LANKA: A QUANTITATIVE PERSPECTIVE



### Summary

This study explores the spread of the Novel SARS-CoV-2 (COVID-19) in Sri Lanka. The study offers a quantitative analysis of the disease transmission dynamics, and a discussion of the potential outcomes of the pandemic in Sri Lanka. A new extension of a mathematical model used in epidemiology is introduced, based on which, predictions regarding the spread of COVID-19 in Sri Lanka will be made. Predictions suggest a clear need for changes in the pandemic response in order to control transmission. Results also indicate that a sizable change in predicted transmission can be achieved through moderate changes in control measures.

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### Quantifying outbreaks

Epidemiologists use a number of metrics to quantitatively understand epidemics, amongst which a popularly used metric is the basic reproduction number,  $R_0$ . The reproduction number is defined as the average number of

secondary infections caused by an infected individual at an early stage of a disease outbreak. This single metric is often used to capture the dynamics of the infection as well as to gauge the effect of control measures. For instance, according to our estimates, the basic reproduction number for COVID-19 in Sri Lanka presently stands slightly above the critical value of 1. Given this, if the control measures succeed in bringing this value sufficiently below 1, it would bring the spread rapidly under control. However, if these measures do not succeed, Sri Lanka would risk an exponential increase in the number of cases. Whilst useful for getting a snapshot of the epidemic,  $R_0$  does not only reflect a single aspect of the spread of a disease. Rather, it is a combined measure of the contact rate, transmissibility, and the duration of the infection. Therefore, controlling any one of these factors would result in reducing  $R_0$ .

Whilst  $R_0$  is useful in capturing certain dynamics of the spread, it does not incorporate any information on the severity of the disease. For instance, the common cold has an  $R_0$  of around 2-3, implying its rapid spread in a population, yet its severity is much less than COVID-19. Epidemiologists often use two metrics to describe the severity of an infectious disease, the case fatality risk (CFR) and the infection fatality risk (IFR). CFR is defined as the percentage of individuals that eventually succumb to the disease out of all diagnosed cases. Similarly, IFR is defined as the percentage of individuals that eventually succumb to the disease out of all *infected* cases. It is interesting to note that for a disease like COVID-19 where many non-fatal cases go undiagnosed, CFR may be an overestimate of the lethality of the disease.

### Capturing disease dynamics with math

Although metrics such as the basic reproduction number ( $R_0$ ) and the case fatality risk (CFR) are useful for classifying and broadly understanding the severity of an outbreak, they provide little information about the future evolution of the disease. As a result, different types of deterministic and stochastic mathematical models have been developed to predict the spread and progression of a disease within a population over a given period of time. A compartmental model is one such mathematical model, where individuals in a population are classified into a few different discrete states based on their infection status, such as susceptible, infected, recovered etc. The model then evolves the number of individuals in each state according to a deterministic differential equation or a stochastic process.

A widely-used compartmental model is the SEIR model, where the population is categorized into 4 compartments: susceptible (S), exposed (E), infected (I), and removed (R). The susceptible category consists of individuals who have not been exposed to the disease, while the exposed category contains individuals who have contracted the disease but are not infectious yet. Individuals in the infected category

have been infected with the disease, and can transmit it to individuals in the susceptible category. Finally, the removed category contains individuals who have either fully recovered or deceased. It is assumed that these removed individuals cannot contract the disease again or transmit it to others. Other variations of compartmental models also exist, such as the SIR model, where there is no significant incubation period, and the SEIS model, where recovered individuals return to the susceptible (S) state in the case of diseases where there is no long-term immunity.

### The augmented SEIR model

Research suggests that the SEIR model best captures the different stages of a person infected with COVID-19 in most settings<sup>1</sup>. However, the basic SEIR model is not capable of accounting for certain subtle yet important dynamics of the COVID-19 pandemic, such as the presence of asymptomatic infections, mass testing, and quarantine protocols. Given this, we developed an augmented SEIR model which aims to capture these more complex dynamics through additional states and pathways between states. In particular, our augmented SEIR model extends the standard SEIR model in the following ways:

- The exposed (E) state is first subdivided into two states that separately represent exposed individuals who are not infectious (**E<sub>0</sub>**), and exposed individuals who are infectious (**E<sub>1</sub>**).

- The infected (I) state is subdivided into four separate states depending on the nature of the symptoms: asymptomatic (**I<sub>0</sub>**), mild (**I<sub>1</sub>**), severe (**I<sub>2</sub>**), and critical (**I<sub>3</sub>**). It is assumed that individuals in I<sub>2</sub> require hospitalization, and those in I<sub>3</sub> require ICU admission.

- Recovered individuals and deceased individuals are classified separately using the (R) and (D) states respectively.

- All of the infectious states described above (E<sub>1</sub>, I<sub>0</sub>, I<sub>1</sub>, I<sub>2</sub>, I<sub>3</sub>), and the recovered and deceased states are further subdivided into unreported (sub U) and reported (sub R) categories, such as E<sub>1U</sub> and E<sub>1R</sub>, I<sub>0U</sub> and I<sub>0R</sub> etc. The unreported category represents individuals who have not been tested for COVID-19, and are therefore silent transmitters of the disease within the population (if infectious). Individuals in the reported category are assumed to have tested positive for COVID-19 and subsequently placed in quarantine. Furthermore, it is assumed that the "reported" individuals do not transmit the disease to others.

A schematic of the new model is given in Figure 1, which shows the various states individuals can be in, at a given point in time, and the pathways that connect these states.

Our SEIR model has two main use cases. First, it can quantitatively gauge the current state of the epidemic. Secondly, it can be used to project the future evolution of the epidemic.

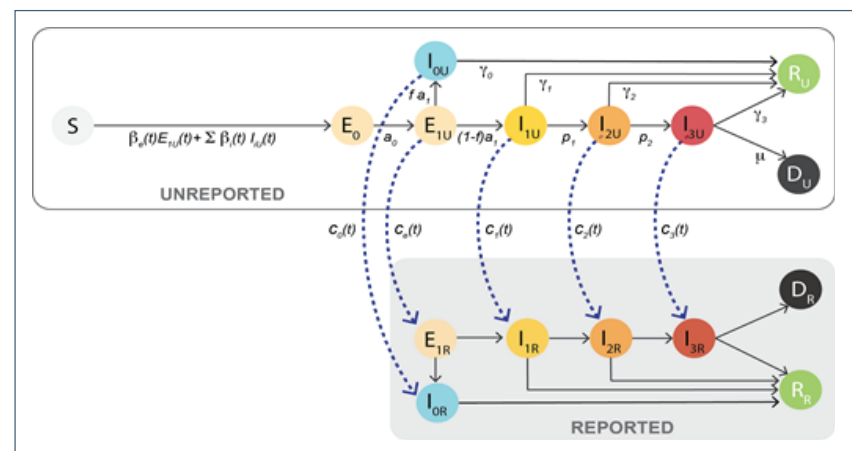


Figure 1 - A schematic of the augmented SEIR model

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## COVID-19 in Sri Lanka: Basic descriptives

Data provided by the National Operation Centre for Prevention of COVID-19 Outbreak and the Research Analysis Projection & Development Branch – SL Army, was used to derive demographic insights into the spread of COVID-19 in Sri Lanka. The dataset contained 35,572 recorded positive cases up to the 26<sup>th</sup> of December 2020. Records contained information on the location, district secretariat division (DSD) and district of all recorded cases, including other demographic information such as the gender and identified cluster for some records. Figure 2 below shows the breakdown of positive cases by DSD. About 80% of the cumulative cases reported in the data were recorded from the 11 DSDs indicated in the figure, out of which 10 belonged to the Western province of Sri Lanka.

Records indicate a marginally higher proportion of males (57% of 3,363 cases reporting gender) among those infected. This is similar to the gender breakdown of COVID-19 deaths reported by the Epidemiology Unit of Sri Lanka. In order to descriptively assess the relative transmissibility of the virus, information regarding the place of residence of infected persons, where reported, is used. This allows to identify incidences of multiple cases being reported within the same household/workplace/village. Out of 4,592 records with reported place of residence, 46% reported multiple positive cases in the same household, workplace or village, which indicates a reasonably high transmissibility of the virus (see Figure 3).

The dataset also provides limited information on identified clusters based on which 7 major clusters were identified (based on 1,775 (approx.) records with an identified cluster). These include Minuwangoda Brandix, Mahara Prison, Welikada Prison, Atulugama, Bloemendhal, Katunayake BOI, and the Peliyagoda Fish Market clusters. The Minuwangoda Brandix cluster is identified as the biggest, followed by the prison clusters.

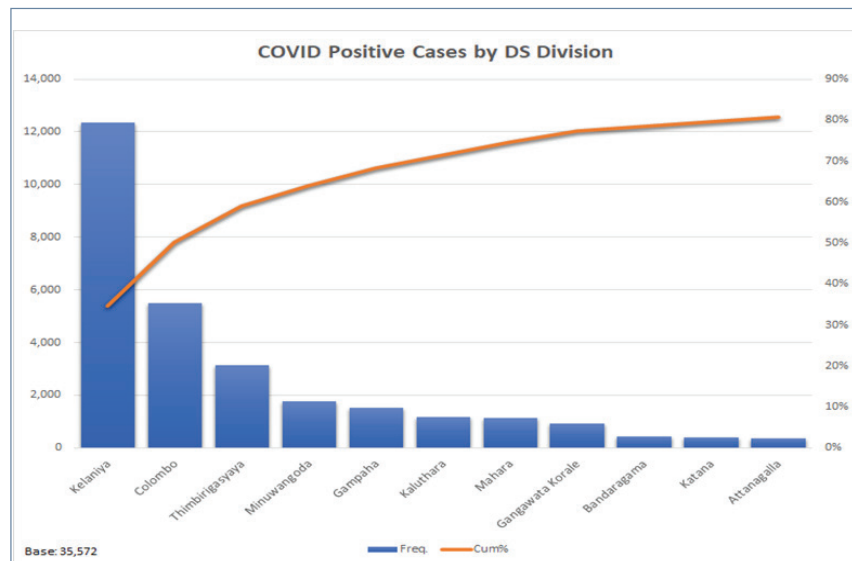


Figure 2 - Positive cases by district secretariat division

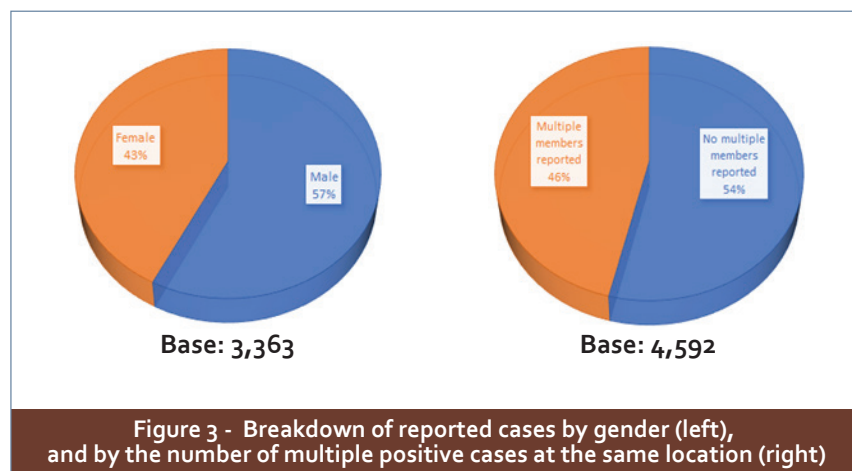


Figure 3 - Breakdown of reported cases by gender (left), and by the number of multiple positive cases at the same location (right)

## COVID-19 in Sri Lanka: Where are we now, and where to next?

Accurately estimating even the most basic metrics of a disease outbreak such as COVID-19 can be notoriously difficult. At the time of writing this article, there still seems to be no consensus over the value of the basic reproduction numbers and the COVID-19 death rate in Sri Lanka. One way of estimating these metrics is to fit the available data streams to the predicted counterparts of a mathematical model such as ours. Then, one can use the parameters of the model to estimate the values of the quantitative metrics of interest. Our model currently estimates the  $R_0$  value as

1.15. However, it should be noted that this estimate is highly volatile as it depends on the changing dynamics of the transmission rate. Based on the data of the current wave in Sri Lanka, our model also estimates a CFR value of 0.66%, and an IFR value of 0.55%, which suggests an under-reporting of cases. More interestingly, given the current trend, we can also use our augmented SEIR model to predict the future evolution of the spread. However, it is worth emphasizing that although necessary steps have been implemented to improve the accuracy of model predictions at the time of modelling, there are many uncertainties around the infection and transmission of COVID-19 which could impact the accuracy of the predictions.

Figure 4 shows how the model propagates for the next 9 months with its parameters tuned to the data from the Johns Hopkins University dataset as of January 2021. According to this, despite having somewhat controlled the spread in December 2020, Sri Lanka currently seems to be heading towards an exponential growth of cases. Based on model predictions, the current trajectory will likely reach its peak in early August 2021, with more than 25,000 projected daily cases per-day, and over 150 daily fatalities. This would also likely overwhelm our healthcare system with about 28,000 hospitalizations at the peak.

The model predictions clearly indicate a need for changing the COVID response in Sri Lanka. However, our model also indicates that a relatively moderate positive change in the control measures could elicit a considerable change in this dire prediction. For instance, bringing the  $R_0$  value down to 0.8 through slightly more stringent control measures such as, stricter and longer lockdowns, work from home orders to all possible situations, and strict enforcement of masking, the spread can be slowed down and brought under control by mid-June 2021 (see Figure 5).

Given that effective vaccines are the only fool-proof solution for overcoming the pandemic, we also extend our model to account for a mass vaccination program. Interestingly, the model predicts that if 20% of the population can be vaccinated before the end of June 2021 whilst maintaining the same level of control measures currently in place, the spread of the virus could be brought under control by early October (see Figure 7). However, this does not suggest that we are out of the woods yet. Even with 20% of the population vaccinated, there are still plenty of susceptible individuals to start a third wave. In fact, the model predicts that even a slight increase of  $R_0$  to 1.5, post 1<sup>st</sup> August 2021, could trigger a catastrophic third wave, even with 20% of the population vaccinated.

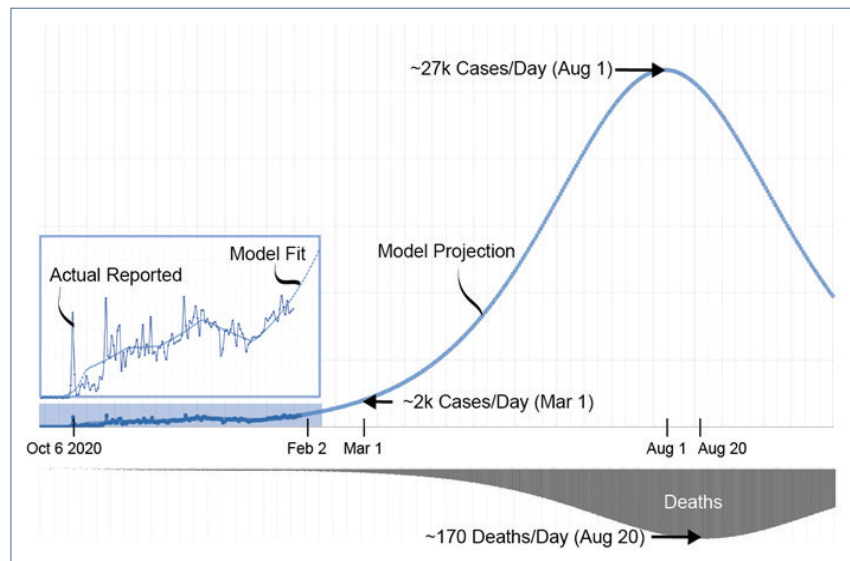


Figure 4 - Predictions from model based on January 2021 parameters

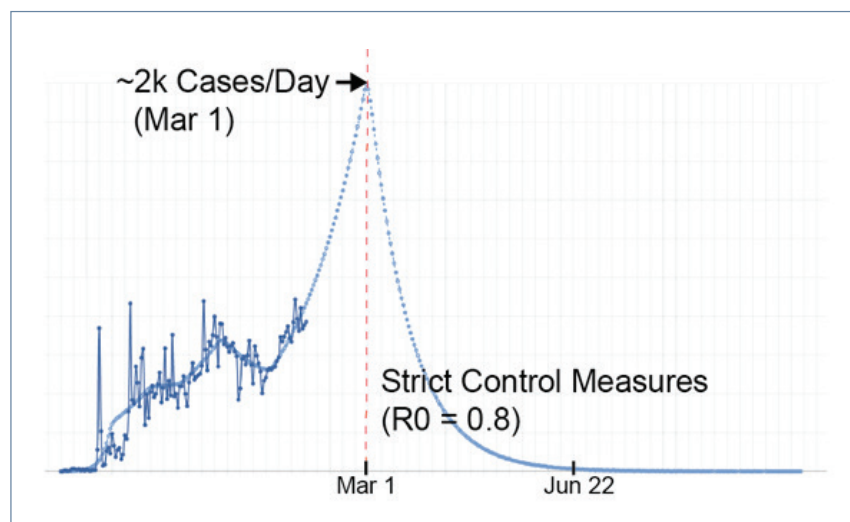


Figure 5 - Effect of stricter control measures

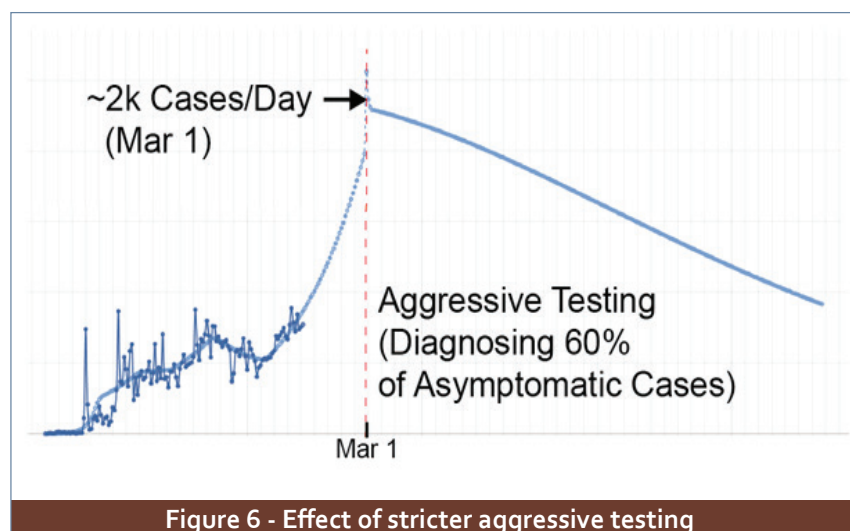


Figure 6 - Effect of stricter aggressive testing

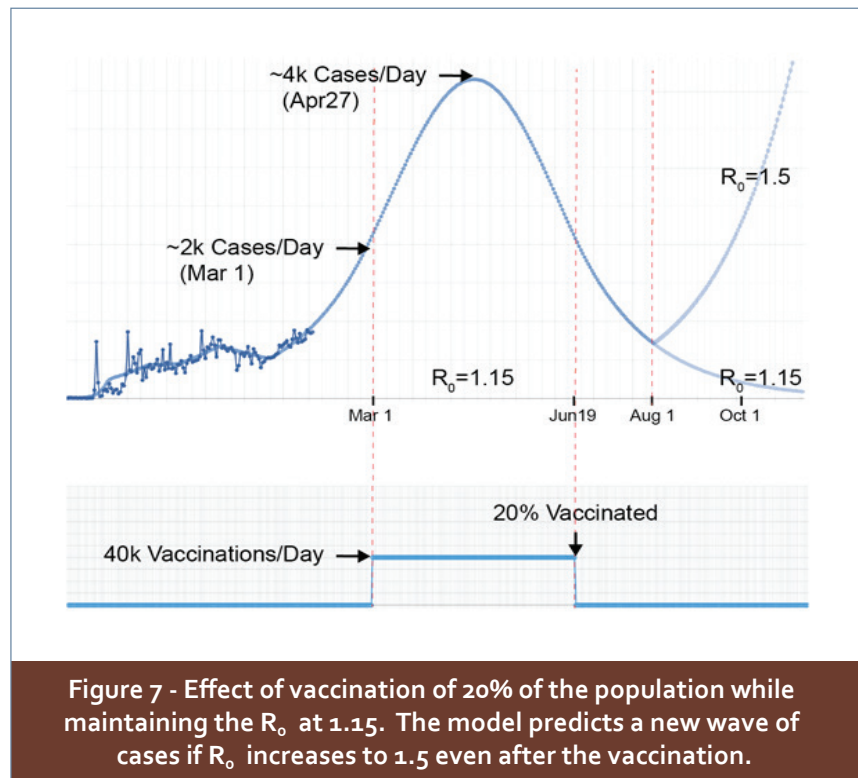
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## Conclusion

Our models suggest a clear need to reevaluate the COVID-19 control measures currently in place in Sri Lanka, in order to change the current trajectory of the disease within the country. Implementing more stringent control measures, increasing current rates of testing, aggressive contact tracing and quarantining, and setting a clear vaccination goal to vaccinate 20% or more of the population by June 2021, are among some of the measures which can be useful in bringing the spread under control. It should also be noted that our models do not account for the relaxing of certain COVID-19 restrictions such as the reopening of borders and admittance of international travellers to Sri Lanka that came into effect in January 2021. Whilst these impacts have not been accounted for in the models, it is safe to assume that the impact of these relaxations will result in further aggravating the current situation, given the discovery of the more virulent UK and South African COVID-19 strains.

If you would like to learn more about our mathematical model and explore the future evolution of COVID-19 in



**Figure 7 - Effect of vaccination of 20% of the population while maintaining the  $R_0$  at 1.15. The model predicts a new wave of cases if  $R_0$  increases to 1.5 even after the vaccination.**

Sri Lanka, visit our interactive COVID-19 simulator: [www.slcovidmodel.com](http://www.slcovidmodel.com).

## References

1. Hill, Alison L. "The math behind epidemics." *Physics Today* (2020):

28-34.

2. Dong E, Du H, Gardner L. An interactive web-based dashboard to track COVID-19 in real time. *Lancet Inf Dis.* 20(5):533-534. ■

The National Cancer Control Programme developed and published the National Guideline on Cancer Early Detection & Referral Pathways to be distributed among the General Practitioners and other Primary Care Doctors. A number of our members actively contributed to the development of this document.

500 copies of the guideline were issued to the College of General Practitioners of Sri Lanka (CGPSL), aiming to be circulated among the membership. The copies of the book are available in the office of the CGPSL. Kindly collect your copy!

**Use the link below to download the e-version:**

<https://www.nccp.health.gov.lk/storage/post/pdfs/National%20guideline%20on%20cancer%20early%20detection%20and%20referral%20pathways%20printed%20book.pdf>

