

A suitable method to calculate the SIR model parameter in the investigation of COVID-19 disease in Sri Lanka

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Introduction

The world has been gripped by a pandemic since 2019. It was identified as a new corona virus disease -19 or COVID-19. While COVID-19 oriented in city of Wuhan in China, it has spread rapidly across the world, resulting in human tragedy and tremendous economic damage. People start to look for methods that are most effective in combating the outbreak or at least control the number of infections. Scientists have made tremendous progress in fight against disease. Yet, infectious diseases remain a major cause of mortality.

SIR Model is a Mathematical model that used to understand the behaviour of spreading infected disease. A successful formulation of such a model can be used to control the number of infections earlier. Mohammed Lounis, Dilipkumar Bagal (2020) had estimated different SIR model parameters for Covid-19 in Algeria and based on the daily reported cases in Algerian health ministry and predicted infectious situation using R_0 (Reproduction value). A. Annunziata, T. Asikainen (2020) had used different methods to use for reproduction value estimation. They had compared how their own estimate compares to an existing method. They tested those methods to different countries to check how their methods work in there. Nguemdjo.U.et al. [4] had analysed corona virus disease in Cameroon. They found the exponential increase in the total number of infected populations in Cameroon.

The first case of the virus has confirmed in Sri Lanka on 27th January 2020. Since then, the epidemiology unit provides daily suspected, infected, and recovery population data for Covid-19 in Sri Lanka. In this research, we aimed to find the SIR model parameters for covid-19 spread in Sri Lanka in two different ways using covid-19 data given by health

ministry of Sri Lanka from 10th March to 31st December and select a one which suits very much compared to the other.

Methodology

The general SIR model is given by,

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta}{N}S(t).I(t), \\ \frac{dI}{dt} &= \frac{\beta}{N}S(t).I(t) - \gamma I(t), \\ \frac{dR}{dt} &= \gamma I(t),\end{aligned}$$

$$N(t) = S(t) + I(t) + R(t),$$

where, $S(t)$ represents the number of susceptible people, $I(t)$ is the number of infected people, $R(t)$ is the number of removals (by recovering or by death) people and $N(t)$ is the national population at time t . Moreover, the constants β denotes the effective contact rate and γ represents the removal rate.

The reproduction number $R_0 = \beta/\gamma$ is a measure of how transferrable a disease is. That is, it gives the average number of people that a single infectious person will infects over the course of their infection. If $R_0 > 1$, one infected individual infects more than one individual. If $R_0 \leq 1$, the disease will surely die out without affecting a large share of population.

In order to calculate parameters (β, γ) of SIR Model, we consider two different methods, namely the log-plot method and JRC method.

For both methods, we initially assume that the susceptible population almost equal to the total population ($S \approx N$) and the number of infectious $I(t)$ first increases exponentially.

The log-plot method [1] used to evaluate the SIR parameters is determined by the equation

$$\ln(I) = mt + \ln(I_0),$$

where $m = \beta - \gamma$. The slope of the straight line drawn $\ln(I)$ versus t gives m .

In JRC method, the reproduction number $R_0 = \beta/\gamma$ is obtained by

$$R_0 = \frac{\beta}{\gamma} = \frac{[\log(I_2) - \log(I_1)]}{\gamma \cdot (t_2 - t_1)} + 1.$$

(See [2]). Using these two different methods,

We will choose one method that is more suitable for COVID situation in Sri Lanka considering the data taken between 10th March and 31st December, 2020.

Results and Discussion

According to the Health Ministry of Sri Lanka, incubation period (infectious period) for COVID-19 ranging from 2 to 14 days. We calculated the removal rate using average of incubation period and obtained $\gamma = \frac{1}{6} = 0.1667$.

Calculated parametric and reproduction values using log-plot method is tabulated in table 1.

The reproduction number R_0 calculated by JRC number is tabulated in table 2.

Table 1. Parameters of SIR model using log-plot method.

Month	Slope (m)	$\gamma [= \frac{1}{6 \text{ days}}]$	$\beta = m + \gamma$	R_0
March	0.2767	0.1667	0.4434	2.659868
April	0.1456	0.1667	0.3123	1.873425
May	0.1038	0.1667	0.2705	1.622675
June	0.0795	0.1667	0.2462	1.476905
July	0.0625	0.1667	0.2292	1.374925
August	0.0492	0.1667	0.2159	1.295141
September	0.0409	0.1667	0.2076	1.245351
October	0.0381	0.1667	0.2048	1.228554
November	0.0369	0.1667	0.2036	1.221356
December	0.0354	0.1667	0.2021	1.212358

Table 2. Parameters of SIR model using JRC method.

Month	R_0 Value	$\gamma [= \frac{1}{6 \text{ days}}]$	$\beta = [R_0 * \gamma]$
March	2.266652	0.1667	0.377851
April	1.71776	0.1667	0.286351
May	1.484034	0.1667	0.247388
June	1.306283	0.1667	0.217757
July	1.257888	0.1667	0.20969
August	1.16741	0.1667	0.194607
September	1.143388	0.1667	0.190603
October	1.213398	0.1667	0.202274
November	1.195496	0.1667	0.199289
December	1.179964	0.1667	0.1967

The number of infections for each day using log-plot, JRC methods and our collected data are plotted in figure 1. Note that, the deviation between the number of infections between log-plot curve data and given data is higher than deviation between number of infections between JRC curve data and given data provide by Health Ministry of Sri Lanka at every day from 10th March to 31st December 2020.

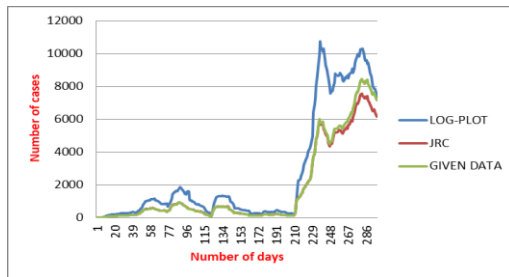


Figure 1. No of infection using JRC, log-plot and collected raw data.

Conclusion

The whole world has been suffering from the pandemic situation of COVID-19 for last two years. Modeling scientists try to develop governing models for the situation. The SIR model is one of the mostly accepted methods in Mathematical modeling to study Suspected, Infected and Recovered population of a region. In Sri-Lanka, the first case of COVID-19 was identified in January, 2020. Since then, the epidemiology unit of Health Ministry of Sri Lanka has been recorded daily suspected, infected, and recovery population data for Covid-19 in Sri Lanka. In this research, we found SIR model parameters in two different ways, namely using log-plot and JRC methods.

We compared both methods graphically with the plot of raw data and found that the JRC method plot is very close to the raw data plot than log-plot and hence concluded that JRC method is the most suitable method to investigate COVID-19 in Sri Lanka.

This model can be used to predict future epidemic situation and can take pre-cautions accordingly. However, the epidemic situation changes as per government policies such as imposing quarantine curfew, vaccinating process etc. Meantime, new variations of virus may negatively influence on the spread of diseases. Therefore, as per natural process of mathematical modeling, one needs to concentrate on the conditions of the situation and update the model accordingly.

References

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