A Modified SIRD Model for the COVID-19 Contagion in Kerala, India

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Abstract

The purpose of this work is to give a contribution to understanding the COVID-19 contagion in Kerala, India. By following the setups in the research paper *A Modified SIR Model for the COVID-19 Contagion in Italy*, our group attempted to make a Susceptible-Infectious-Recovery-Death(SIRD) model and modified it to a Susceptible-Infectious-Recovery-Death-Vaccination(SIRDV) model to better predict the change in existing infection cases. We performed numerical simulation using the official data of COVID-19 provided by the Kerala government, and build our model with some parameters fixed according to biomedical research of the property of COVID-19 virus, and others optimized by numerical solution as an inner step. We also performed a sensitivity analysis to the parameters in the SIRDV model, to investigate how to control the increment of infectious in practice.

1. Introduction

COVID-19 has become a serious health problem threatening the world due to its rapid spread. In our research project, we have chosen Kerala, the city with a relatively large population and has the largest COVID-19 testing rate in India, as our preference to investigate, since the data is more comprehensive. Kerala had reportable data of COVID-19 since January 30th, 2021. Until the end of October 2021, the total infection curve has three obvious waves as shown below in Figure 1. We chose to look closer into the second wave. From April 30th, 2021 to May 30th, 2021, the number of existing infection cases had increased from $3*10^5$ to $4.5*10^5$, then dropped down to $2.2*10^5$, which has an obvious turning point. The total number of death cases had increased from 5308 to 8641. The curve in this period is smoother compared to the third wave, and the initial condition during this period is better to use in our numerical simulation than the first wave since the number of deaths was relatively large that cannot be neglected. Thus, we perform numerical simulations with data in Kerala from April 30th, 2021 to May 30th, 2021.

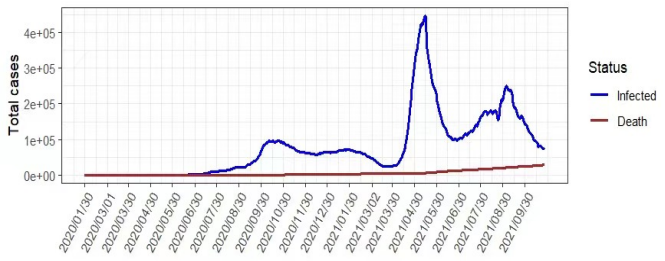

Figure 1: The Infected and Death Amount of Kerala State

A mathematical model is a tool to provide clear figures and tendencies for researchers to make a significant reduction of infected people and the death. According to the research paper *A Modified SIR Model for the COVID-19 Contagion in Italy*, our group attempted to make a SIRD model and modify it to a SIRDV model. Here are our assumptions to build mathematical models: Following the basic assumption of the SIRD model, the total population(N) of Kerala was 35336581 in April 2021 which was considered as the immutable total population during the whole period we were investigating. The total population(N) is equal to the sum of the Susceptible(S), the Infectious(I), the Recovery(S), and the Death(D), which in symbol words, is N=S+I+R+D. We assumed that the death rate, vaccination rate, and vaccination effectiveness rate, and other parameters we are using are constant and fixed. Moreover, we assumed that people who are infected by COVID-19 will not be infected again, and people who are recovered from COVID-19 do not need to be vaccinated. We defined β as transmission rate of COVID-19, γ as recovery rate, μ as death rate, η as vaccine effectiveness, α as vaccine rate. The variables involved in our model and the parameters are summarized in the following tables:

parameters	Description
β	Transmission rate of COVID-19 – It depends on basic reproduction number of COVID-19 and *gamma*
γ	Recovery rate – inverse of the COVID infectious period
μ	Death rate – depends on COVID-19
α	The vaccination rate
η	The vaccine effectiveness

Table 1: Parameters of the mathematical model

variables	Description
$S(t)$	the population of individuals susceptible of contracting the infection at time t
$I(t)$	the population of infected individuals that are active at time t
$R(t)$	the cumulative population of individuals that recovered from the disease up to time t
$D(t)$	the cumulative population of individuals that deceased due to the disease, up to time t
$V(t)$	the population of vaccinated individuals at time t
D	the duration of infection

Table 2: Involved variables

2. An Approach Using the Regular SIRD Model

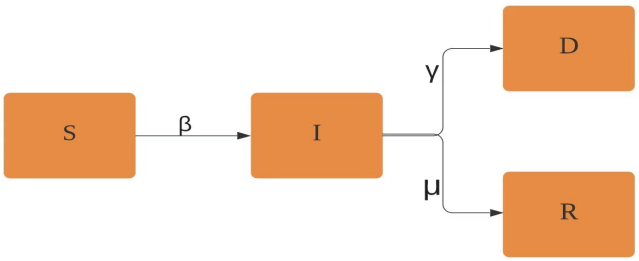

Figure 2: Framework of SIRD model

The basic framework of the SIRD model as described in the original paper is shown in Figure 2. Our SIRD model for a region/population is described by the following equations:

$$\begin{aligned}
\frac{dS}{dt} &= -\beta\frac{S}{N}I \\
\frac{dI}{dt} &= \beta\frac{S}{N}I - \gamma I - \mu I \\
\frac{dR}{dt} &= \gamma I \\
\frac{dD}{dt} &= \mu I \\
N &= S + I + R + D
\end{aligned}$$

Where β is the transmission rate, γ is the recovery rate, and μ is the death rate. The parameter $\beta > 0$ and $\gamma > 0$. For the recovery rate γ, $\gamma = \frac{1}{D}$, where D is the duration of infection. After reading some biomedical research papers, we found that the duration of infection in Kerala is approximately 22 days, and the death rate is 0.31%. Therefore our $\gamma = \frac{1}{D} = \frac{1}{22}$, and $\mu = 0.0031$. To find the optimized β to build our model, we will find its numeric solution. During the time period we investigated, the susceptible population is approximately equal to the total population, that is, N≈S. Thus $\frac{S}{N} \approx 1$. Then we can simplify the relationship between the number of infections and time:

$$\frac{dI}{dt} = \beta\frac{S}{N}I - \gamma I - \mu I \approx (\beta - \gamma - \mu)I$$

The approximate number of infected people is:

$$I(t) = exp(\beta - \gamma - \mu)t$$

After the value of the death rate μ and the recovery rate γ were plugged in, the transmission rate β was found to be 0.075663.

Let R_0 represent the Basic reproduction number(the average number of people that an infected individual would infect), where $R_0 = \frac{\beta}{\gamma}$. We need to get the overall data of the COVID-19 to get R_0 in real cases. In our case, using the parameters we found, $R_0 = \frac{\beta}{\gamma} = \frac{0.075663}{\frac{1}{22}} = 1.6646$, which indicates the expected number of cases directly generated by one case was around 1.6646 in Kerala. This shows the spreading properties of COVID-19 contagion in Kerala implied by our mathematical model.

With the parameters found above, we applied the regular SIRD model in RStudio to analyze the infected proportion of the population in Kerala. The numeric simulation result is shown below:

Figure 3: Prediction and Real Value of I after Applying Regular SIRD Model

Obviously, after applying the regular SIRD model to predict the existing infection proportion, the result was far from real values. A turning point occurs in the real infection curve, while the predicted infection cases kept increasing. Thus there must be other variables teat contribute to the change of existing infected proportion. As we were checking the news of that time, we found out that India dramatically increased the vaccination proportion during the time we investigated. Thus it was necessary to add the effect of vaccination to the model to better mimic the tendency of infected proportion and better decide what variables need to be controlled to make the infected proportion grow slower.

3. An Approach Using a Modified SIRDV Model

As shown in Figure 4, our model extends the general SIRD framework by adding the effect of vaccination.

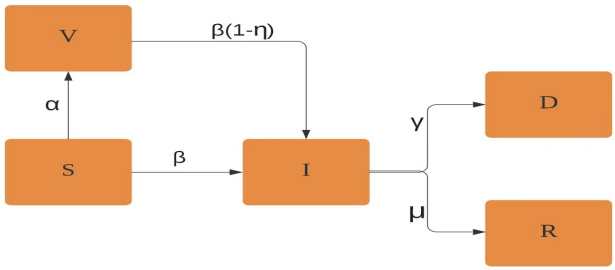

Figure 4: Framework of SIRDV model

To make the model more practical, the effect of vaccination needs to be considered. However, due to the lack of vaccines and the low rate of complete vaccination, we considered the population who get one shot as the vaccinated population in India. By the characteristic of vaccination, we assumed that η is the proportion of efficient vaccinations, and the population that is vaccinated, denoted by V, comes from S and reduces the infection proportion according to its efficiency. Our modified SIRDV model for a region/population is described by the following equations:
$V(t)$: the population of vaccinated individuals at time t;

$$\begin{aligned}
\frac{dS}{dt} &= -\beta\frac{S}{N}I - \alpha \\
\frac{dI}{dt} &= \beta\frac{S}{N}I + \beta(1-\eta)\frac{V}{N}I - \gamma I - \mu I \\
\frac{dV}{dt} &= -\beta(1-\eta)\frac{V}{N}I + \alpha \\
\frac{dR}{dt} &= \gamma I \\
\frac{dD}{dt} &= \mu I
\end{aligned}$$

Where β is the transmission rate, γ is the recovery rate, μ is the death rate, α is the vaccination rate, η is the vaccine effectiveness. For $\frac{dV}{dt} = -\beta(1-\eta)VI + \alpha$, $(1-\eta)V$ represents for the population that who is vaccinated but fails to immunization, thus they are people in V population but response to virus same as S population. α represents for the vaccination rate. After doing some research, the vaccination rate during the month that we were investigating was around 10% and the vaccine effectiveness rate was approximately 75%. Thus, adding these two parameters along with the parameters found in the prior section, we applied the SIRDV model in RStudio to analyze the infected proportion of the population in Kerala. The numeric simulation result is shown below:

Figure 5: Prediction and Real Value of I after Applying Regular SIRD Model

The tendency of the infected proportion significantly decreases after increasing and a turning point appears, which is closer to the pattern of real situation. Thus this modified model can better describe the infected proportion, and we can change the parameters of the model to see which of them should be controlled to flatten the infection curve.

4. Sensitivity Analysis

After successfully building the SIRDV model, our next goal was to find what parameters of the model could be changed to make the infection curve flatter. That is trying to decrease the existing infection cases by altering parameters so that hospitals will not be running at full capacity and more patients can be cured.

We chose to investigate α, the vaccination rate, and β, the transmission rate of COVID-19 since the other parameters should be fixed and based on the internal properties of the COVID-19 virus. We believe it would be functional to find out how changes in those two parameters affect our SIRDV model. This would give us an idea on how to control the increment of infectious in practice.

To start with, we analyzed the infection graph after changing the vaccination rate α. The result is shown below:

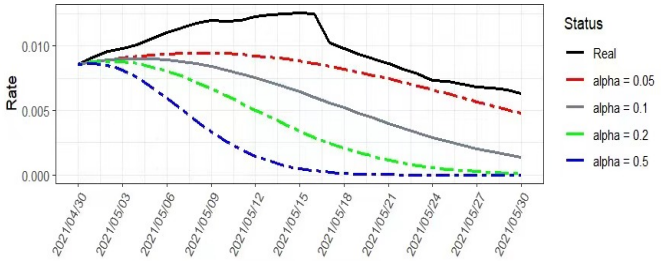

Figure 6: Infection rates after Changing α

Clearly, as α increases, the infection proportion curve goes flatter, meaning that the spreading of virus has been slowed down, thus getting more people to be vaccinated can flatten the infection curve. We can expect some portion of the population to be unwilling or unable to receive

a COVID-19 vaccine. If large populations refuse vaccination, the duration of the pandemic can be prolonged.

Then we changed β, the transmission rate of the virus. The result is shown below:

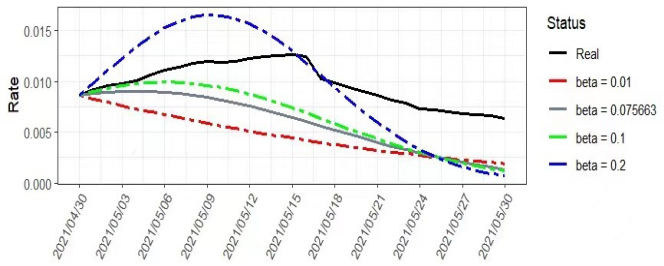

Figure 7: Infection rates after Changing β

As β increases, infection proportion also increases. Thus to decrease the infection proportion, policies need to be established to decrease the transmission rate or transmission rate of the virus, including quarantine and encouraging people to wear masks.

5. Conclusion

Firstly, we fitted a SIRD model to our Kerala data following the setup in "A Modified SIR Model for the COVID-19 Contagion in Italy". The model was not satisfactory. The total infection rate kept increasing while the real data encountered a turning point on May 15th, 2021. Since India dramatically increased the vaccination rate during the time we investigated, it is necessary to add the effect of vaccination to the model to better mimic the tendency of the infected rate. Therefore we had modified the model by adding the effect of vaccination. Under a vaccination rate of 10% and a vaccine effective rate of 75%, the total infection rate predicted by our modified SIRDV model followed the same pattern with the real data. A turning point had occurred and the infection rate kept decreasing after May 5th, 2021. We have successfully modified the original model in the paper to better fit the real data.

To better evaluate which parameter is significant in lowering the infection rate, we chose to investigate α, the vaccination rate, and β, the transmission rate of COVID-19. After adjusting parameters and performing numerical simulation with Kerala data, we have concluded that: As the vaccination rate increases, and as the transmission rate decreases, the infection proportion would be significantly lowered based on our SIRDV model.

The results allow new insights into future COVID-19 trends and the sensitivity of pandemic dynamics to various behavioral and other model parameters. As more exact information becomes available, new data can be directly incorporated into our model to produce more accurate results. The numerical values and ranges for the model parameters found in this study could be used as estimates to predict potential infection outcomes for scenarios where limited data is available (e.g., future pandemics). As model-based predictions get increasingly accurate, we expect that they will help guide informed policy decisions for the general public.

6. Limitation

Although the current model better simulates the real situation than the regular SIRD model, it has some obvious limitations. The turning point of predicted infection proportion is around one week before the real situation's turning point. The inaccuracy of this might be caused by our assumption that the vaccine works after just the first shot that overestimated the efficiency of vaccination. Also, although the testing rate of Kerala is one of the highest in India, it is not high enough to get an accurate value. We couldn't assume the total number of infected people by simply dividing the tested positive number by test rate since most people would test for COVID-19 if they do not feel well, but we do not know the exact rate, thus throughout the whole progress, the infection rate remains highly inaccurate. Moreover, in the real situation, all parameters like α, β, and so on are dynamic, but for easier implementation, we simplified them to be fixed. The family of curves represented by our equations with constant parameters is considerably limited as it assumes that the population does not change its behavior at all over the course of the outbreak. The simplicity of the SIRD and SIRDV model makes it easy to compute, but also likely oversimplifies complex disease processes. Our model does not, for example, incorporate the latent period between when an individual is exposed to a disease and when that individual becomes infected and contagious.

Another inconsistency with the real world data was the Basic reproduction number(the average number of people that an infected individual would infect) calculated with our optimal β and chosen γ. Based on the formula, our $R_0 = \frac{\beta}{\gamma} = 1.6646$. However, in the real world the basic reproduction number in Kerala, India was 5.7, which indicates the expected number of cases directly generated by one case was 5.7 in Kerala where all individuals are susceptible to infection. Our number was much lower than 5.7, and it seems impossible that the expected number of cases directly generated by one case was 1.7 in Kerala due to the large population and low quarantine rate. This inconsistency might be because Kerala has a relatively low test rate of COVID-19, which means the data we got might not represent what really happened in the spreading of COVID-19 in that area. If the testing rate in Kerala increases, we might end up with a better model using more accurate data.

7. Data availability

COVID data was obtained from the Government of Kerala COVID-19 Data.
The data contains the confirmed, recovered and deceased cases of Covid-19 cases in Kerala, India from January 31, 2020 to October 27, 2021 . This dataset can be used for EDA and time series analysis. All our plots and model simulations were done using RStudio.
https://dashboard.kerala.gov.in/index.php

References

[1] A Modified SIR Model for the COVID-19 Contagion in Italy
https://arxiv.org/pdf/2003.14391.pdf

[2] SIR Model-based Prediction of Infected Population of Coronavirus in Hubei Province
https://arxiv.org/abs/2003.06419

[3] A model and predictions for COVID-19 considering population behavior and vaccination
https://www.nature.com/articles/s41598-021-91514-7

[4] Lyapunov Stability Analysis of Covid 19 SIR Modeling
https://eds.a.ebscohost.com/eds/detail/detail?vid=0sid=1608e158-4127-46f0-ab95-0c6f7c549dbf%40sessionmgr4008bdata =JnNpdGU9ZWRzLWxpdmU%3dAN=149824033db=a9h

[5] Measuring and Preventing COVID-19 Using the SIR Model and Machine Learning in Smart Health Care
https://www.hindawi.com/journals/jhe/2020/8857346/