InPrime: Indonesian Journal of Pure and Applied Mathematics
Vol. 5, No. 1 (2023), pp. 1 – 21, doi: 10.15408/inprime.v5i1.27192
p-ISSN 2686-5335, e-ISSN: 2716-2478

Model and Simulation of COVID-19 Transmission with Vaccination and Quarantine Interventions in Jember

Faizal Rifky Fahreza*, Moh. Hasan, and Kusbudiono
Department of Mathematics, Jember University, Jl. Kalimantan 37, Jember, Indonesia
Email: faizalrifky.f@gmail.com

Abstract

In this study, we model the transmission of COVID-19 by considering vaccination and quarantine interventions. The focus of our study is to measure the effect of these two interventions on controlling the spread of COVID-19. We demonstrate the use of the Kermack-McKendrik model as an SIR model for the number of people infected with COVID-19 applied in Jember, Indonesia. The model parameters are estimated using the Levenberg-Marquardt approach and the model equations are solved using the Runge-Kutta 4th-order method. Through the simulation study, we can determine the peak of the spread of COVID-19 cases and obtain several parameters related to vaccination and quarantine interventions that significantly affected the transmission rate of COVID-19. It is found that a faster rate of vaccinations will reduce the rate of transmission of COVID-19. Moreover, COVID-19 can be fully controlled if the infected patients carry out proper quarantine procedures.
Keywords: COVID-19; Kermack-McKendrik; Levenberg-Marquardt; quarantine; SIR; vaccination

Abstrak

Dalam penelitian ini, kami memodelkan penularan COVID-19 dengan mempertimbangkan intervensi vaksinasi dan karantina. Fokus dari penelitian kami adalah untuk mengukur pengaruh dari kedua intervensi tersebut dalam mengontrol penyebaran COVID-19. Kami mendemonstrasikan penggunaan model Kermack-McKendrik sebagai model SIR untuk kasus pasien yang terinfeksi COVID-19 di Jember, Indonesia. Parameter model diestimasi menggunakan pendekatan Levenberg-Marquardt dan menyelesaikan model menggunakan metode orde-4 Runge-Kutta. Melalui studi simulasi, kami dapat menentukan waktu puncak penyebaran kasus COVID-19 dan mendapatkan beberapa parameter terkait intervensi vaksinasi dan karantina yang berpengaruh signifikan terhadap laju penularan COVID-19. Hasil simulasi menunjukan bahwa laju vaksinansi yang cepat akan mengurangi laju penyebaran COVID-19. Selain itu, COVID-19 dapat dikontrol dengan penuh jika pasien melakukan prosedur karantina yang tepat.
Kata Kunci: *COVID-19;* Kermack-McKendrik; Levenberg-Marquardt; *karantina; vaksinasi*

2020MSC: 00A71, 92B05

1. INTRODUCTION

The SARS-CoV-2 case first appeared in Wuhan, Hubei Province, China, in December 2019 [1] [2]. SARS-CoV-2 causes infected individuals to transmit Coronavirus Disease (COVID-19) through several modes of transmission, namely through direct contact, indirect contact, or close contact with infected individuals [3] [4]. As a result, SARS-CoV-2 can quickly spread in a population in a short time. This transmission process can be modeled mathematically to determine the peak point of its spread, determine the parameters that have a significant effect and determine the steps to control the rate of spread [5], [6], [7]. From this model, we can provide disease transmission mechanisms, determine

* Corresponding author
Submitted July 18th, 2022, Revised January 25th, 2023, Accepted for publication January 27th, 2023.

transmission processes, suggest effective control and prevention measures, and estimate the severity and scale of potential epidemics [8].

Most infectious disease transmission models use a deterministic model because this model requires fewer data, is relatively easy to set up, and software is widely available and easy to use to complete this model [9]. One example of deterministic models is the Kermack-McKendrick model or the SIR model. Another example of a deterministic model is a disease transmission model by adding a control compartment such as the model with the implementation of vaccination and quarantine interventions [10] [11]. This study models the spread of COVID-19 using the Kermack-McKendrick model involving vaccination and quarantine interventions and finds the effect of these two interventions on the transmission process in Jember, Indonesia. We estimate the parameters in the SIR model using the Levenberg-Marquardt method, which is a method for solving non-linear least squares problems [12] [13]. These problems usually arise in data fitting by adjusting m observations and n parameters in non-linear models [14].

Our study seeks to find the basic reproduction number, $\mathcal{R}_0$, and the effective reproduction number, $\mathcal{R}^*$. The $\mathcal{R}_0$ can be interpreted as the average number of secondary infections caused by one infected individual in the susceptible population exposed during the mean infection period [8], and the $\mathcal{R}^*$ is interpreted as the number of secondary infections by a single infection during the pandemic with time-dependent control interventions. In fact, $\mathcal{R}^*$ is $\mathcal{R}_0$ multiplied by $\frac{S}{N}$ [15]. In general, conditions that may occur from the basic reproduction number are $\mathcal{R}_0 < 1$ so that the number of infected individuals will decrease so that the disease will disappear, or $\mathcal{R}_0 > 1$, then the number of infected individuals will increase; the disease becomes epidemic. This basic reproduction number $\mathcal{R}_0$ can be found using the next-generation matrix $\boldsymbol{K} = \boldsymbol{F}\boldsymbol{V}^{-1}$ [16]. The $\mathcal{R}_0$ is the spectral radius of the $\boldsymbol{K}$ matrix, or the maximum modulus of the real and complex numbers at the eigenvalues of the $\boldsymbol{K}$ matrix, with $\boldsymbol{F}$ and $\boldsymbol{V}$ being a Jacobian matrix of the infected and uninfected compartment subpopulation [17].

2. METHODS

The data used in this study is a daily data obtained from the district health office of Jember, Indonesia, from July 1, 2021, until August 14, 2021. The data contains the population number in Jember, the number of people receiving COVID-19 vaccination for dose 1 and 2, the number of confirmed cases of COVID-19, the number of COVID-19 patients, the number of COVID-19 patients with mild, moderate, and severe symptoms, the number of recovered COVID-19 patients, and the number of patients who died from COVID-19.

This study utilizes the Levenberg-Marquardt method to model the COVID-19 transmission using a compartmental approach, which can be written as follows:

$$\frac{dS}{dt} = -\lambda IS \frac{dI}{dt} = \lambda IS - \gamma I \frac{dR}{dt} = \gamma I. \tag{1}$$

This model divides the host population into three compartments: S as the susceptible compartment, I as the infected compartment, and R as the recovered compartment. Each of these compartments indicates the number of individuals in that compartment and has a non-negative value. The constants

λ and γ are model parameters that indicate the rate of movement from one compartment to another, where λ is the rate of infection and γ is the rate of recovery. The parameters in model (1) are estimated using the following equation:

$$\left(\mathbf{J}^{\mathrm{T}}\mathbf{J} + \mu\mathbf{I}\right)\mathbf{h}_{\mathrm{lm}} = -\mathbf{J}^{\mathrm{T}}\mathbf{f} \tag{2}$$

Since the Levenberg-Marquardt method uses the principles of the Gauss-Newton method, equation (2) is obtained from a linear approximation for the vector $\mathbf{f}$, which is then added to the damping parameter μ. So that $\mathbf{J}$ is the Jacobian matrix of vector $\mathbf{f}$, and $\mathbf{h}_{\mathrm{lm}}$ is the approximate result. The non-linear least square problem using the Levenberg-Marquardt method can be solved using the *lmfit* library in Python.

We solve the SIR model using the Runge-Kutta 4th-order method. The Runge-Kutta method is a numerical method for approximating the exact solution of an ordinary differential equation [18]. The Runge-Kutta 4th-order method can be built from the explicit Runge-Kutta method by setting the order of 4 and using the Runge-Kutta-4 coefficient according to the butcher table [19]. The Runge-Kutta 4$^{\text{th}}$-order is obtained as follows:

$$\begin{aligned}
K_1 &= y_n, \\
K_2 &= y_n + \frac{h}{2} f(t_n, K_1), \\
K_3 &= y_n + \frac{h}{2} f\left(t_n + \frac{h}{2}, K_2\right), \\
K_4 &= y_n + hf\left(t_n + \frac{h}{2}, K_3\right), \\
y_{n+1} &= y_n + \frac{h}{6} f(t_n, K_1) + \frac{h}{3} f\left(t_n + \frac{h}{2}, K_2\right) + \frac{h}{3} f\left(t_n + \frac{h}{2}, K_3\right) + \frac{h}{6} f(t_n + h, K_4),
\end{aligned} \tag{3}$$

where y_{n+1} approximates the Runge-Kutta 4th-order for the function f. This method evaluates each derivative step 4 times on K_1, K_2, K_3, and K_4.

To model the transmission of COVID-19 with vaccination and quarantine interventions, several assumptions are made:

a. Population not exposed to SARS-CoV-2 are grouped into the $S(t)$ compartment. Population infected with SARS-CoV-2 are grouped into compartment $I(t)$ with an infection rate of λ. Population recovered from COVID-19 or COVID-19 survivors are grouped into the $R(t)$ compartment with a recovery rate of γ.
b. The population is constant, i.e., the population growth rate due to birth or population migration (Λ) and the regular death rate (μ) are assumed to be the same.
c. Each individual in the $S(t)$ compartment is vaccinated with two doses (with vaccination rates of φ_1 and φ_2), so, there are two compartments for the vaccinated individuals, i.e., $V_1(t)$ for individuals receiving dose 1 and $V_2(t)$ for individuals receiving dose 2.
d. Individuals in compartment $V_1(t)$ may not get proper protection from COVID-19 optimally, but it is assumed that the possibility of infection rate can be reduced due to the first dose of vaccination with parameter of p.
e. Individuals receiving the second dose of vaccination are not 100% protected from COVID-19, so it is also assumed that there is a parameter to reduce the possibility of being infected

with COVID-19 better than parameter p, i.e., parameter r.

f. Individuals who receive quarantine intervention enter into the $Q(t)$ compartment. Individuals in this compartment tested positive for COVID-19 but have no symptoms or mild symptoms. Individuals in this compartment are assumed to only partially avoid contact with others so they still have the possibility to spread COVID-19. However, the ability to spread COVID-19 can be reduced, so that there is a parameter q which indicates a reduction in this compartment's spread rate.
g. Individuals infected with COVID-19 with mild or no symptoms will be quarantined, thus there is a shift from compartment $I(t)$ to $Q(t)$ at a rate of τ_1.
h. Individuals in the Q(t) compartment are assumed to be completely recovered. Displacement from compartment $Q(t)$ to compartment $I(t)$ is possible with a movement rate of τ_2.
i. COVID-19 survivors are not 100% free from SARS-CoV-2. There is a possibility that COVID-19 survivors are exposed to the SARS-CoV-2 virus, so there may be a movement from $R(t)$ to $S(t)$ compartment at a rate of ρ.
j. Individuals in compartments $I(t)$ and $Q(t)$ do not entirely go to $R(t)$. There is a possibility that individuals in this compartment do not survive. Therefore, they are grouped into compartment $D(t)$ with death rate due to COVID-19 being ζ.
k. Based on the previous assumptions, individuals in the $Q(t)$ compartment are asymptomatic individuals with mild symptoms. The effect of the two-dose vaccinations can reduce the risk of individuals exposed to COVID-19 from getting severe symptoms to death. The reduced-risk is denoted by a parameter d, which described the rate of movement from compartment $Q(t)$ to $D(t)$.

We estimate the parameters of infection rate parameter (λ), vaccination rate at dose one and dose two (φ_1 and φ_2, respectively), recovery rate (γ), transfer rate from $I(t)$ to $Q(t)$ (τ_1), and the death rate due to COVID-19 (ζ) using the Levenberg-Marquardt method and solve the model using the Runge-Kutta method of order 4. The $\mathcal{R}_0$ value of the COVID-19 transmission model with vaccination and quarantine interventions is also estimated in this study. Additionally, we conduct a simulation study for COVID-19 transmission model by varying the values of the vaccination rate parameters for dose 1 and 2 (φ_1 and φ_2, respectively), the transfer rate from $I(t)$ to $Q(t)$ (τ_1), and reducing the infection rate due to quarantine (q), and extending the time on the model.

3. RESULTS AND DISCUSSIONS

3.1 COVID-19 Transmission Model with Vaccination and Quarantine Intervention

The COVID-19 transmission model was built with a compartmental approach. The model is built from a modified SIR infectious disease transmission model based on the assumptions written in the methodology. Furthermore, based on the assumptions, the transmission model is:

$$\begin{aligned}\frac{dS}{dt} &= \Lambda - \frac{\lambda SI}{N} - \frac{\lambda qSQ}{N} - \varphi_1 S + \rho R - \mu S,\\ \frac{dV_1}{dt} &= \varphi_1 S - \frac{\lambda pV_1 I}{N} - \frac{\lambda pqV_1 Q}{N} - \varphi_2 V_1 - \mu V_1,\end{aligned} \tag{4}$$

$$\frac{dV_2}{dt} = \varphi_2 V_1 - \frac{\lambda r V_2 I}{N} - \frac{\lambda r q V_2 Q}{N} - \mu V_2,$$

$$\frac{dI}{dt} = \frac{\lambda SI}{N} + \frac{\lambda p V_1 I}{N} + \frac{\lambda r V_2 I}{N} + \frac{\lambda q SQ}{N} + \frac{\lambda p q V_1 Q}{N} + \frac{\lambda r q V_2 Q}{N} - \tau_1 I + \tau_2 Q - \gamma I - \zeta I - \mu I,$$

$$\frac{dQ}{dt} = \tau_1 I - \tau_2 Q - \gamma Q - \zeta d Q - \mu Q,$$

$$\frac{dR}{dt} = \gamma I + \gamma Q - \rho R - \mu R,$$

$$\frac{dD}{dt} = \zeta I + \zeta d Q.$$

Based on the assumption of the second point, because the population is assumed to be constant so that the regular birth rate and regular death rate can be assumed to be the same, then the total population or $N = S + V_1 + V_2 + I + Q + R + D$ can be expressed as $\frac{dN}{dt} = \Lambda - \mu N$, with the value $\Lambda = \mu N$ because N is constant.

3.2 Parameter Estimation

Parameters in the COVID-19 transmission model were then estimated using the Levenberg-Marquardt method. The parameters to be estimated are shown in Table 1.

Table 1. Parameters to be estimated

Parameter	Description
λ	Infection rate
φ_1	Single-dose vaccination rate
φ_2	Double-dose vaccination rate
τ_1	Rate of movement from $I(t)$ to $Q(t)$
γ	Recovery rate
ζ	The death rate due to COVID-19

Before performing data fitting, assuming the parameters that are not estimated is necessary. The parameters whose values are assumed are presented in Table 2.

Table 2. Parameters value assumption

Parameter	Value	Description
τ_2	0.002857	Rate of movement from $Q(t)$ to $I(t)$
ρ	0.590071	Reinfection rate [20]
p	0.180143	Reduction of infection rate due to single-dose vaccine
r	0.05	Reduction of infection rate due to a two-dose vaccine
q	0.02	Reduction of infection rate due to quarantine
d	0.0065	Reducing the death rate from vaccines
Λ	0	Normal birth rate
μ	0	Normal death rate

The initial value for each compartment is required for the fitting data. The initial value will be taken from COVID-19 data in Jember from July 1, 2021, to August 14, 2021, with the data used as the initial value being July 1, 2021. In contrast, the initial value for compartment $S(t)$ is taken from the total population in Jember minus the initial value of all compartments. The first data for each compartment will be used as the initial value for each compartment, so the initial value for each can be seen in Table 3.

Table 3. Compartment initial values

Compartment	Initial Value
$S(0)$	2.286.948
$V_1(0)$	164.243
$V_2(0)$	66.485
$I(0)$	7.512
$Q(0)$	4.319
$R(0)$	6.695
$D(0)$	527.

The parameters in Table 1 are estimated for range $[0,1]$ by using the initial guess of each parameter as 1. We use the *lmfit* library in Python to estimate the parameters and the results shown in Table 4.

Table 4. Estimation of parameters

Parameter	Estimation
φ_1	0.001393
φ_2	0.007576
λ	0.030111
τ_1	0.005444
γ	0.008703
ζ	0.001293

3.3 Model Solution Using Runge-Kutta Order 4

The COVID-19 transmission model with known values for each parameter can then be found as a solution using the Runge-Kutta method of order 4. The solution from the model will be solved in the range $[0,44]$ according to the length of the data. Figure 1 shows the solutions of each compartment compared to the COVID-19 data for 45 days, except for the $S(t)$ compartment, which is presented without comparison data.

3.4 The basic Reproduction Number $\mathcal{R}_0$ of the COVID-19 Transmission Model

The basic reproduction number $\mathcal{R}_0$ of the COVID-19 transmission model will be searched using the next-generation matrix. First, determine which compartments are included in the infected compartment. Based on equation (4), two compartments are infected, namely compartments $I(t)$ and $Q(t)$.

$$\frac{dI}{dt} = \frac{\lambda SI}{N} + \frac{\lambda pV_1 I}{N} + \frac{\lambda rV_2 I}{N} + \frac{\lambda qSQ}{N} + \frac{\lambda pqV_1 Q}{N} + \frac{\lambda rqV_2 Q}{N} - \tau_1 I + \tau_2 Q - \gamma I - \zeta I - \mu I,$$

$$\frac{dQ}{dt} = \tau_1 I - \tau_2 Q - \gamma Q - \zeta dQ - \mu Q.$$

Furthermore, vector $\boldsymbol{\mathcal{F}}$ is obtained, the rate of a new infection, and vector $\boldsymbol{\mathcal{V}}$, the transition to the infected compartment.

$$\boldsymbol{\mathcal{F}} = \begin{bmatrix} \frac{\lambda SI}{N} + \frac{\lambda pV_1 I}{N} + \frac{\lambda rV_2 I}{N} + \frac{\lambda qSQ}{N} + \frac{\lambda pqV_1 Q}{N} + \frac{\lambda rqV_2 Q}{N} \\ 0 \end{bmatrix}, \boldsymbol{\mathcal{V}} = \begin{bmatrix} \tau_1 I - \tau_2 Q + \gamma I + \zeta I + \mu I \\ -\tau_1 I + \tau_2 Q + \gamma Q + \zeta dQ + \mu Q \end{bmatrix}.$$

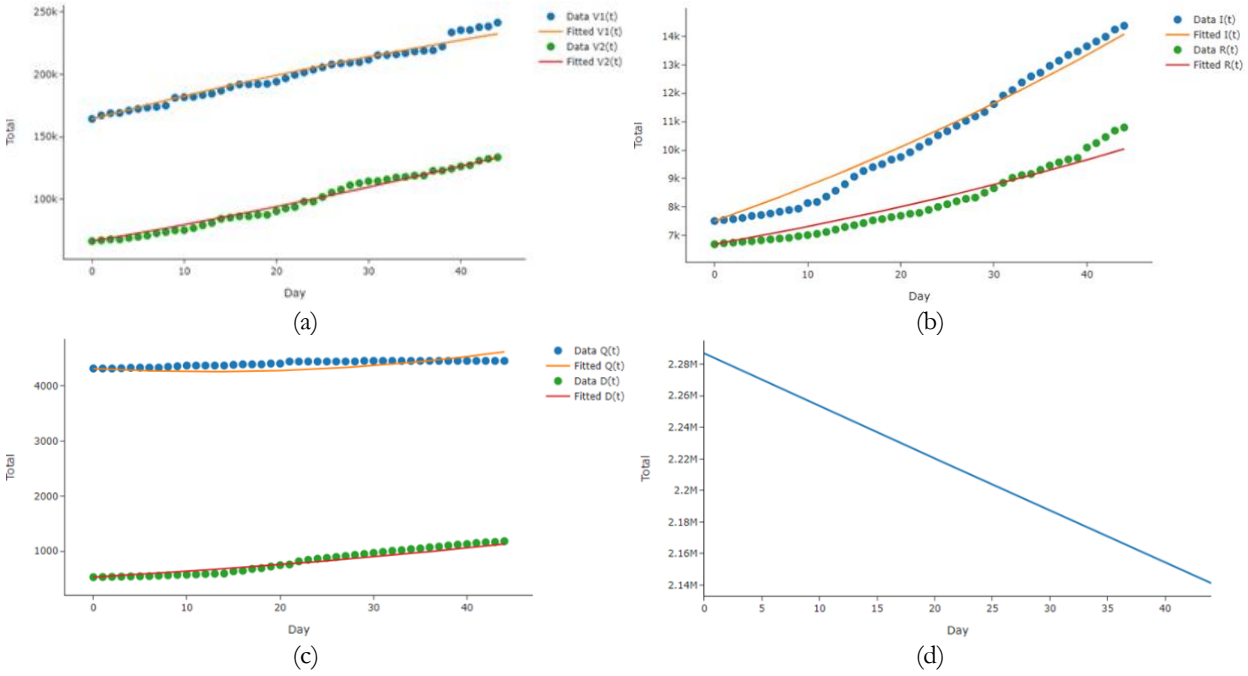

Figure 1. (**a**) The graphs of the solution compartments $V_1(t)$ and $V_2(t)$; (**b**) Solution plot of compartments $I(t)$ and $R(t)$; (**c**) $Q(t)$ and $D(t)$ compartment solution plots; (**d**) $S(t)$ compartment solution plot.

The matrix $\boldsymbol{F}$ and $\boldsymbol{V}$ can be obtained as follows.

$$\boldsymbol{F} = \begin{bmatrix} \frac{\partial \mathcal{F}_1}{\partial I} & \frac{\partial \mathcal{F}_1}{\partial Q} \\ \frac{\partial \mathcal{F}_2}{\partial I} & \frac{\partial \mathcal{F}_2}{\partial Q} \end{bmatrix} = \begin{bmatrix} \frac{\lambda S + \lambda pV_1 + \lambda rV_2}{N} & \frac{\lambda qS + \lambda pqV_1 + \lambda rqV_2}{N} \\ 0 & 0 \end{bmatrix},$$

$$\boldsymbol{V} = \begin{bmatrix} \frac{\partial \mathcal{V}_1}{\partial I} & \frac{\partial \mathcal{V}_1}{\partial Q} \\ \frac{\partial \mathcal{V}_2}{\partial I} & \frac{\partial \mathcal{V}_2}{\partial Q} \end{bmatrix} = \begin{bmatrix} \tau_1 + \gamma + \zeta + \mu & -\tau_2 \\ -\tau_1 & \tau_2 + \gamma + \zeta d + \mu \end{bmatrix}.$$

The next-generation matrix is

$$\boldsymbol{K} = (\boldsymbol{FV^{-1}}) = \begin{bmatrix} \dfrac{\lambda(pV_1 + rV_2 + S)(d\zeta + q\tau_1 + \gamma + \mu + \tau_2)}{N\left(d\zeta^2 + \left((d+1)\gamma + (d+1)\mu + d\tau_1 + \tau_2\right)\zeta + (\mu+\gamma)(\mu+\gamma+\tau_1+\tau_2)\right)} & 0 \\ \dfrac{(pV_1 + rV_2 + S)\lambda\left((\gamma+\mu+\zeta+\tau_1)q + \tau_2\right)}{N\left(d\zeta^2 + \left((d+1)\gamma + (d+1)\mu + d\tau_1 + \tau_2\right)\zeta + (\mu+\gamma)(\mu+\gamma+\tau_1+\tau_2)\right)} & 0 \end{bmatrix}^{\mathrm{T}}.$$

From the next generation matrix, we get the basic reproduction number $\mathcal{R}_0$. It is necessary to find the eigenvalues of the $\boldsymbol{K}$ matrix as follows.

$$\boldsymbol{EigVal} = \begin{bmatrix} 0 \\ \dfrac{\lambda(pV_1 + rV_2 + S)(d\zeta + q\tau_1 + \gamma + \mu + \tau_2)}{N\left(d\zeta^2 + \left((d+1)\gamma + (d+1)\mu + d\tau_1 + \tau_2\right)\zeta + (\mu+\gamma)(\mu+\gamma+\tau_1+\tau_2)\right)} \end{bmatrix}.$$

The basic reproduction number $\mathcal{R}_0$ is obtained from the largest eigenvalue or spectral radius so that the basic reproduction number of the model (4) is

$$\mathcal{R}_0 = \frac{\lambda(pV_1 + rV_2 + S)(d\zeta + q\tau_1 + \gamma + \mu + \tau_2)}{N\left(d\zeta^2 + \left((d+1)\gamma + (d+1)\mu + d\tau_1 + \tau_2\right)\zeta + (\mu+\gamma)(\mu+\gamma+\tau_1+\tau_2)\right)}. \tag{5}$$

The R_0 can be obtained by substituting the previously known parameter values. By substituting the value of each parameter and compartment required into equation (5), the value of $\mathcal{R}_0$ at $t = 0$ is $\mathcal{R}_0 = 2.064658 \approx 2$. This means each infected individual can infect or produce two new infected individuals. In addition, because $\mathcal{R}_0 > 1$, it can be concluded that the number of infected individuals will continue to increase, and the disease will become epidemic.

Next, the effective reproduction number $(\mathcal{R}^*)$ in time range t=[0,44] is obtained by using equation (6) along $with\ t$ as follows.

$$\mathcal{R}^* = \mathcal{R}_0 \cdot \frac{S}{N}. \tag{6}$$

The plot of $\mathcal{R}^*$ in the range t is shown in Figure 2. Based on this figure, the value of $\mathcal{R}^*$ continues to decrease, with the value at $t = 0$ being $\mathcal{R}^* = 1.86$ and the value at $t = 44$ being $\mathcal{R}^* = 1.74$. It can also be concluded that the average secondary infection that occurred in the time $t = [0,44]$ or July 1, 2021 – August 14, 2021, continued to decline. However, the curve in Figure 2 does not decrease linearly, and there is still a possibility that the curve is stable at one point or close to 0.

3.5 Model Simulation

Simulations on the COVID-19 transmission model were carried out by varying the values of several parameters related to quarantine and vaccination interventions and varying the time (t) to discover the process of spreading COVID-19 when t was more than the amount of data according to the COVID-19 transmission model. The parameters will be varied in the interval $[0,2\alpha]$, where α is the value of the parameter being varied (see Table 5).

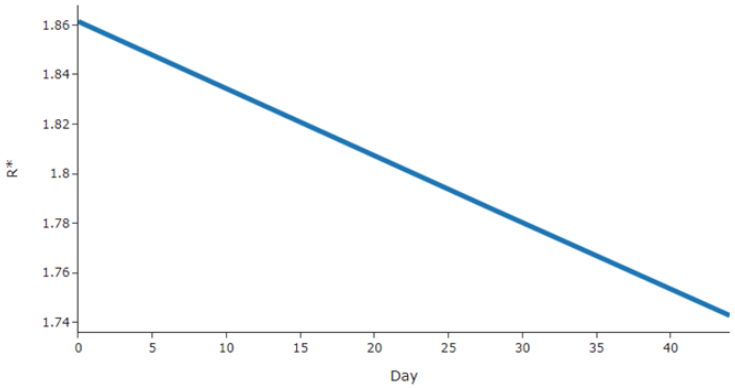

Figure 2. Plot $\mathcal{R}^*$ over the range $t = [0,44]$.

Table 5. Parameters with varied values

Parameter	Description	Value
φ_1	Single-dose vaccination rate	0.001393
φ_2	Double-dose vaccination rate	0.007576
τ_1	Rate of movement from $I(t)$ to $Q(t)$	0.005444
q	Reduction of infection rate due to quarantine	0.05

The first simulation to be carried out is to widen the time interval (t) for the solution from the COVID-19 transmission model to $[0,1200]$. The extended time in this simulation will start from July 1, 2021, as $t = 0$, so the model's simulation results are as in Figure 3. Based on Figure 3, it can be seen that under the parameter values according to the estimation results, cases of infection or spread of COVID-19 reached a peak on the 454th day with a total of 184,018 cases with individuals in the quarantine compartment reaching its peak on the 546th-day with the total number of cases reached 81,002 people, while for individuals who recovered from COVID-19 the peak was on the 638th day with a total of 303,085 people who recovered. In contrast to the previous three compartments, compartment $D(t)$ or individuals who died from COVID-19 up to day 1200 have not yet touched the top of the curve. Then the number of individuals vaccinated against COVID-19 dose 1 peaked on the 174th day, reaching 298,671 people. At the same time, the number of individuals vaccinated with dose 2 continued to increase until the 1200th day, with the number of individuals on the 1200th day reaching 1,416,182 people.

While the value in the $S(t)$ compartment continues to decrease, with the highest value being on day 0 with a total of the initial value of the $S(t)$ compartment, furthermore, if you look at the compartment curves that have reached a peak, such as the $R(t)$ curve and the $V_1(t)$ curve, it shows a decrease in the number of individuals in that compartment. The displacement in the COVID-19 transmission model causes a decrease in the number of individuals in a compartment. Then $\mathcal{R}^*$ in this transmission model will also be simulated at $t = [0,1200]$. Figure 3 shows the simulation of the $\mathcal{R}^*$ value in the COVID-19 transmission model. Based on Figure 3, the value of $\mathcal{R}^*$ begins to be below one on the 464th day, namely $\mathcal{R}^*$ of 0.999066. If the value of $\mathcal{R}^*$ is already below 1, starting from day

464, individuals infected with COVID-19 will decrease so that the COVID-19 disease can slowly disappear.

The next model simulation will be made by changing the parameter values in Table 5. The parameter values that have been changed will be symbolized by variables φ_{1S}, φ_{2S}, τ_{1S}, and q_S. The first parameter simulation will be carried out by varying the value of the vaccination rate parameter at dose one or φ_1. The estimated value of the parameter $\varphi_1 = 0.001393$, so that the parameter φ_1 will be varied from 0 to $2\varphi_1 = 0.002786$. The following will present the simulation results of the COVID-19 transmission model by varying the value of φ_1.

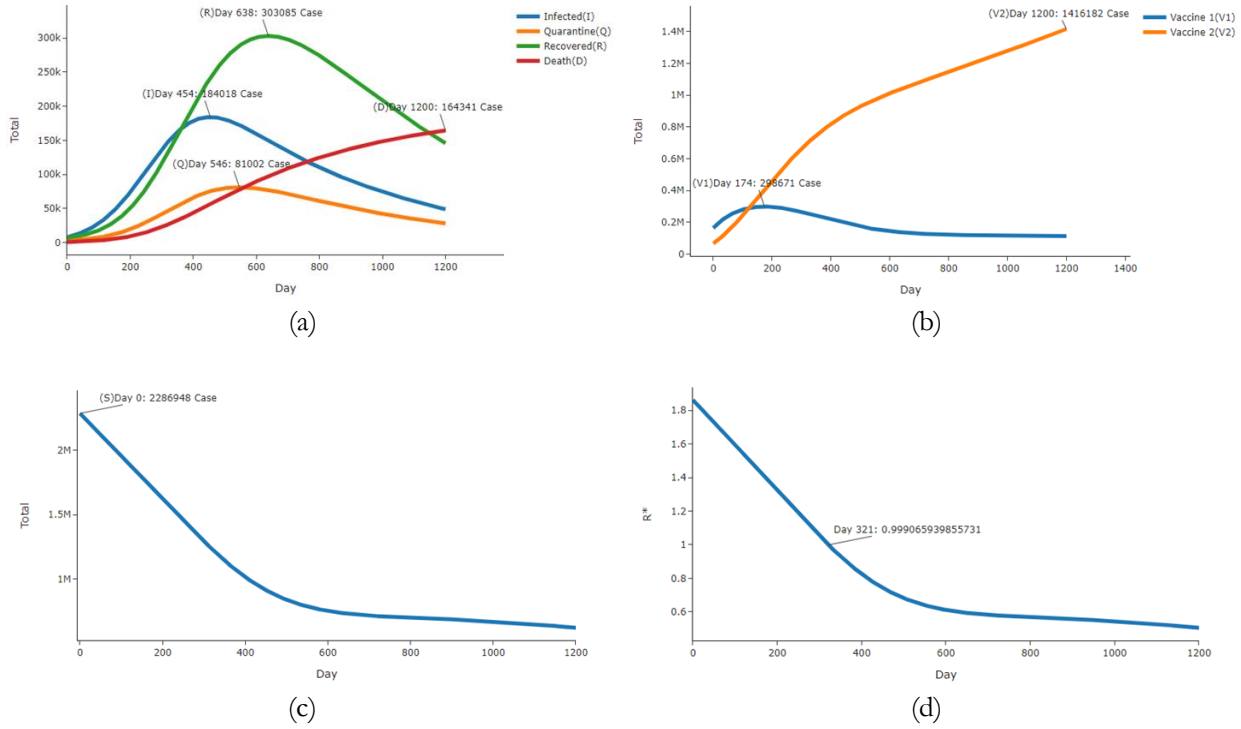

Figure 3. (**a**) Model simulation at $t = [0,1200]$ for $I(t), Q(t), R(t)$, and $D(t)$; (**b**) Model simulation at $t = [0,1200]$ for $V_1(t)$ and $V_2(t)$; (**c**) Model simulation at $t = [0,1200]$ for compartment $S(t)$; (**d**) Simulation of $\mathcal{R}^*$ values in the range $t = [0,1200]$.

Figure 4 shows the results of the variation of $\varphi_{1S} < \varphi_1$, namely the value of φ_{1S} is reduced by 70% from the φ_1 or $\varphi_{1S} = 0.000418$. Based on Figure 4, the condition of the spread of COVID-19 or compartment $I(t)$, whose simulation is depicted by blue and purple curves, experienced an increase in total cases at the peak of the spread by 86.93% to 343,985 people, with the peak t shifting longer to 462 days. Meanwhile, for the quarantine compartment depicted by orange and brown curves, the peak of the curve shifted to day 557, with total cases increasing by 84.29% to 149,275 people.

Then the compartment for individuals who recovered from COVID-19, depicted by the green and pink curves, also experienced an increase in cases at 82.52% to 553,191 people, with the peak

shifting longer to the 660th day. Next is the compartment of individuals who died from COVID-19, depicted by red and silver colored curves. In the $D(t)$ compartment simulation, cases also increased by 97.97%. It can be seen on the 1200th-day cases, which rose to 325,351 people.

Compartment $V_1(t)$ or individuals vaccinated with dose one are depicted by a blue curve at φ_1 and green when $\varphi_{1_S} < \varphi_1$. These two curves show a decrease in the number of individuals vaccinated with dose 1. It can be seen from the highest number on both curves, which is larger than the curve at the initial condition. Similar to compartment $V_1\ (t)$, in compartment $V_2\ (t)$, which is depicted by an orange curve at φ_1 and red when $\varphi_{1_S} < \varphi_1$ also decreases by 65% at $t = 1200$.

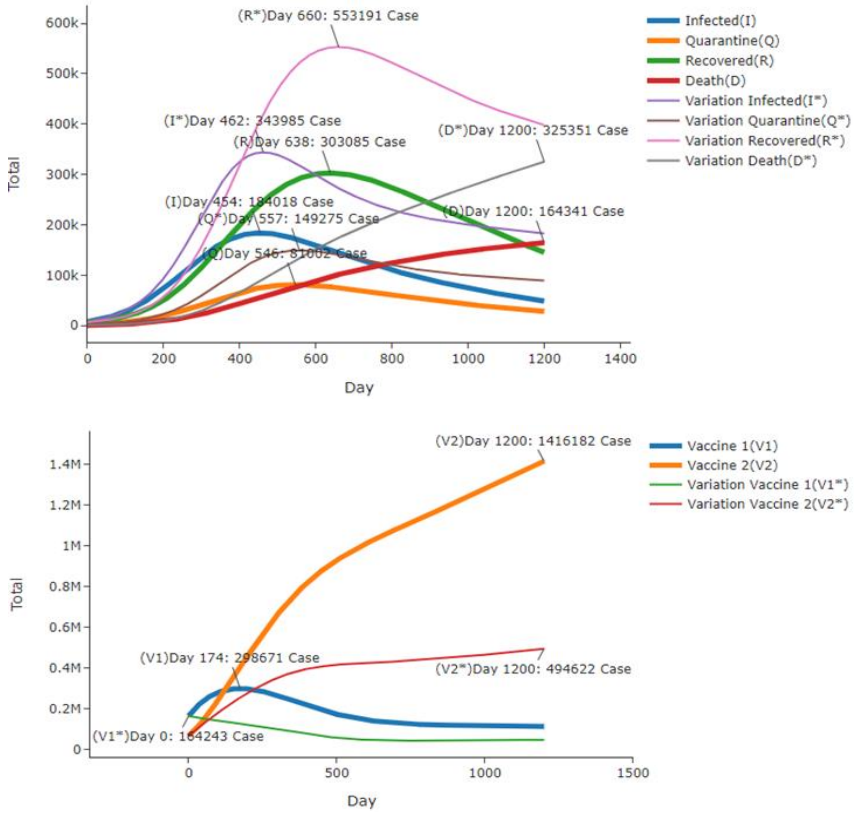

Figure 4. The top plot shows a model simulation for $I(t), Q(t), R(t),$ and $D(t)$ when $\varphi_{1_S} < \varphi_1$. The bottom plot shows a model simulation for $V_1\ (t)$ and $V_2(t)$ when $\varphi_{1_S} < \varphi_1$.

Figure 5 presents the simulation results of the COVID-19 transmission model when $\varphi_{1_S} > \varphi_1$. Figure 5 shows the simulation results of the COVID-19 transmission model with the value of φ_{1_S} increased by 80% to $\varphi_{1_S} = 0.002507$. The first compartment is $I(t)$, depicted by a blue curve at φ_1 and purple when $\varphi_{1_S} > \varphi_1$. This compartment experienced a decrease in the number of cases at the peak point, and the peak of infection cases passed more quickly, namely on the 380th day, with the total cases dropping by 49.58% to 92,791 people.

There is the quarantine compartment or $Q(t)$, which is depicted by an orange curve at φ_1 and brown when $\varphi_{1_S} > \varphi_1$. Based on the $Q(t)$ compartment curve, the peak of the curve is at day 466, faster than the initial condition. Meanwhile, the total cases at the peak of the curve also decreased by 50% to 40,504 people. The third compartment is the $R(t)$ compartment or individuals who have recovered from COVID-19, represented by a green curve at φ_1 and pink when $\varphi_{1_S} > \varphi_1$. Similar to the previous two compartments, the peak point also shifted earlier to day 546, with the total recovered cases dropping by 50.71% to 149,378 people. The last compartment is for individuals who died due to COVID-19, depicted by a red curve at φ_1 and silver when $\varphi_{1_S} > \varphi_1$. This compartment also experienced a decrease in death cases due to COVID-19. It can be seen from the total cases on the 1200th day, which decreased by 56.91%. Based on Figure 5, compartment $V_1\ (t)$ is depicted by a blue curve at φ_1 and green when $\varphi_{1_S} > \varphi_1$ increases the number of individuals vaccinated with dose one at the peak point of 52.84% with the peak point being on day-169. Same as compartment $V_1\ (t)$, in compartment $V_2\ (t)$, which is depicted by an orange curve at φ_1 and red when $\varphi_{1_S} > \varphi_1$ also increases. It can be seen from the increase in the number of individuals vaccinated with dose 2 of 48.44 % at time $t = 1200$.

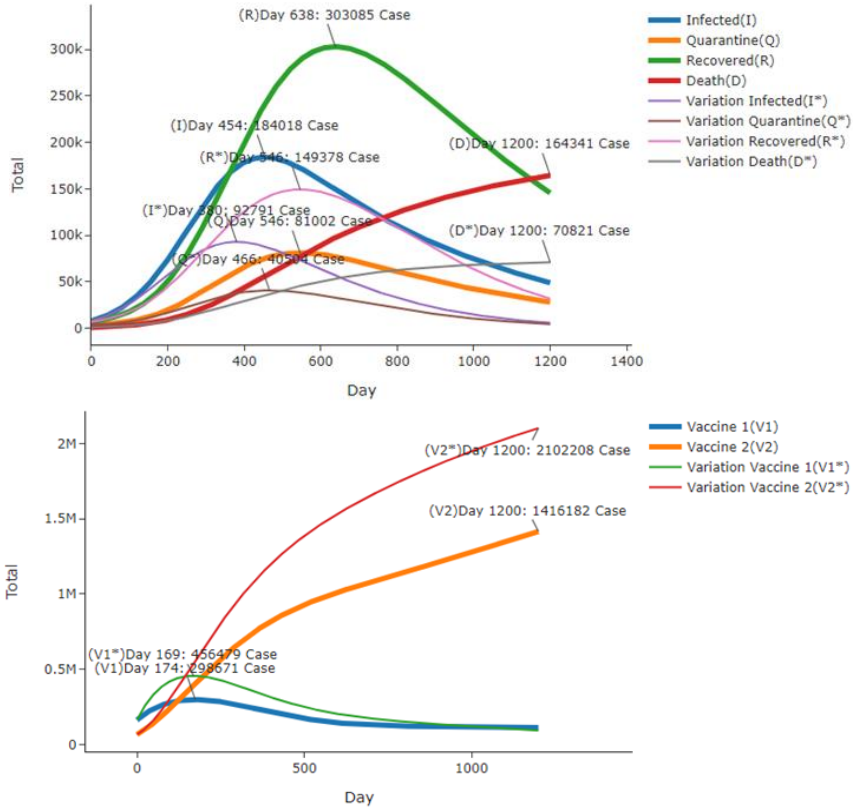

Figure 5. The top plot shows a model simulation for $I(t), Q(t), R(t)$, and $D(t)$ when $\varphi_{1_S} > \varphi_1$; The bottom plot shows a model simulation for $V_1\ (t)$ and $V_2(t)$ when $\varphi_{1_S} > \varphi_1$.

The next parameter variation is done by varying the value of the vaccination rate parameter at dose two or φ_2. The parameter φ_2 value is varied from 0 to $2\varphi_2 = 0.015152$. The following will present the results of the simulation of the COVID-19 transmission model for the variation of the φ_2 parameter. Figure 6 presents the simulation results of the COVID-19 transmission model at φ_2 and when $\varphi_{2_S} < \varphi_2$ for compartments $I(t), Q(t), R(t)$, and $D(t)$. The parameter value φ_{2_S} in this condition is reduced by 90% to $\varphi_{2_S} = 0.000758$. The first compartment is for confirmed cases of COVID-19 or $I(t)$. Based on the $I(t)$ curve, in the condition $\varphi_{2_S} < \varphi_2$, there was an increase in the number of cases at the top of the curve by 61.81% to 297,764 people, with the peak point being on day 487, with the peak point being longer than φ_2.

Then the $Q(t)$ and $R(t)$ compartments experienced the same thing: an increase in the number of cases for each compartment with the peak point shifting further away compared to $the\ \varphi_2$ condition. The increase in the number of cases in these two compartments, namely $Q(t)$ and $R(t)$, was 62.11% and 63.45%, respectively, with peaks for these two compartments when $\varphi_{2_S} < \varphi_2$ were on the day of 586th and 694th day. The next compartment, namely $D(t)$, also experienced an increase in cases like the others. The $D(t)$ curve shows an increase in deaths due to COVID-19 by 78.66% at $t = 1200$.

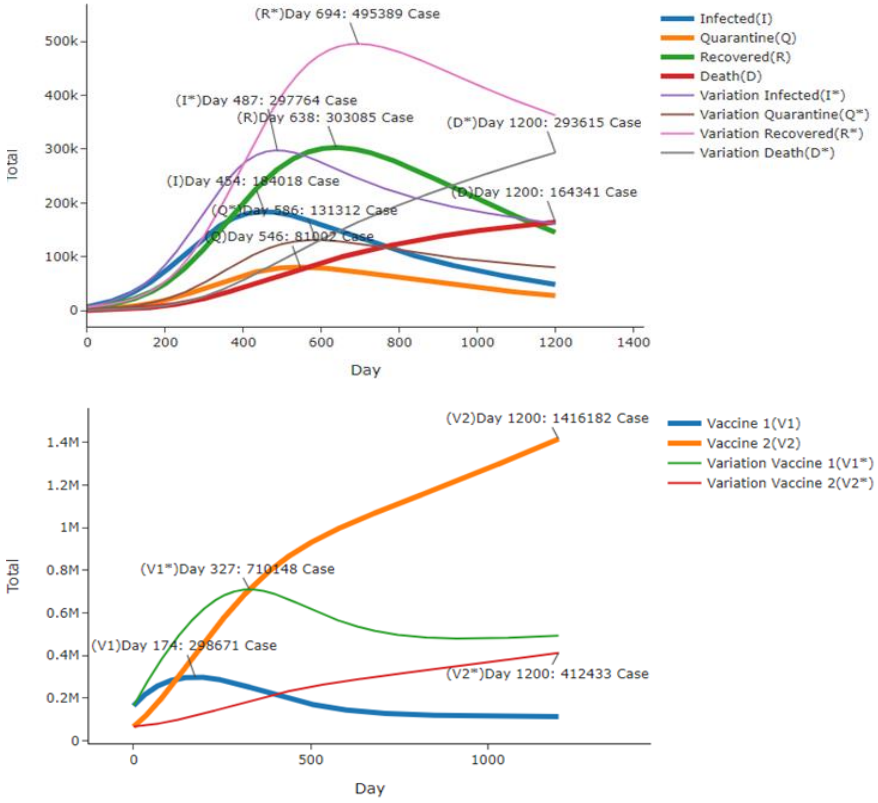

Figure 6. The top plot shows a model simulation for $I(t), Q(t), R(t)$, and $D(t)$ when $\varphi_{2_S} < \varphi_2$. The bottom plot shows a model simulation for $V_1\ (t)$ and $V_2(t)$ when $\varphi_{2_S} < \varphi_2$.

The following simulation results show the $V_1(t)$ and $V_2(t)$ compartments at φ_2 and the condition $\varphi_{2_S} < \varphi_2$. Based on the $V_1(t)$ curve, it can be seen that there was an increase in the number of individuals vaccinated with dose 1. It can be seen from the number of individuals at the peak point, which increased by 137.77% to 710,148 people, with the peak position shifting further to the 327th day. In contrast to the $V_1(t)$ compartment, the $V_2\ (t)$ compartment experienced a decrease in the number of individuals. At $t = 1200$, the number of individuals who received vaccine dose 2 decreased by 70.88% to 412,433 people. Next is the COVID-19 transmission model simulation with variations when $\varphi_{2_S} > \varphi_2$.

The value of φ_{2_S} in the simulation results shown in Figure 7 is increased to $2\varphi_2$ or 100%. Based on Figure 7, compartment $I(t)$ has decreased. At φ_2, the peak point of this compartment was on day 454, while when the condition $\varphi_{2_S} > \varphi_2$ peak point for this compartment was on day 453, the number of cases decreased by 14,39% compared to $the\ \varphi_2$ condition. Similar to compartment $I(t)$, the $Q(t)$ and $R(t)$ compartments also experienced a decrease in the number of cases. The decrease in the peak of individual quarantined cases in this condition occurred by 14.08% from φ_2, with the peak shifting one day earlier to the 545th day.

Meanwhile, the $R(t)$ compartment experienced a decrease in cases. The decrease in the peak number of individuals who recovered from COVID-19 in this condition occurred by 13.78%, with the peak shifting two days earlier to the 636th day. Next is the D(t) compartment. This compartment has also decreased in number. It can be seen from the number of individuals who died from COVID-19 at $t = 1200$, which decreased by 14.29% to 140,849 people. Based on Figure 7, the number of individuals in compartment $V_1(t)$ has decreased. The $V_1\ (t)$ curve shows a decrease in the number of individuals vaccinated with dose one at 37.91% to 185,455 people, with the peak point getting faster to the 76th day. In contrast to the $V_1(t)$ compartment, the $V_2(t)$ compartment experienced an increase in the number of individuals. Based on the $V_2(t)$ curve, the $V_2(t)$ compartment experienced an increase in individuals by 10.95% to 1,571,284 people on the 1200th day.

The third parameter variation is to vary the parameter τ_1, which is the rate of movement from $I(t)$ to $Q(t)$ or the quarantine rate. The value of this parameter will be simulated from 0 to $2\tau_1 = 0.010888$. The simulation results for the COVID-19 transmission model when $\tau_{1_S} < \tau_1$ can be seen in Figure 8. Figure 8 shows the simulation of the transmission model for compartments $I(t), Q(t), R(t),$ and $D(t)$ when the value of τ_{1_S} is reduced by 80% to 0.001089. Based on Figure 8, the $Q(t)$ compartment experienced a decrease in cases. This $Q(t)$ curve shows a decrease in the number of cases at the peak of 54.76%, with the peak point being faster on the 523rd day. In contrast to the $Q(t)$ compartment, the other three compartments experienced increased total cases. Compartment $I(t)$ experienced an increase in infection cases by 129.99%, with its peak shifting earlier to day 425, and compartment $R(t)$, which experienced an increase in cases at its peak of 69.14%, with its peak shifting earlier to 601st day.

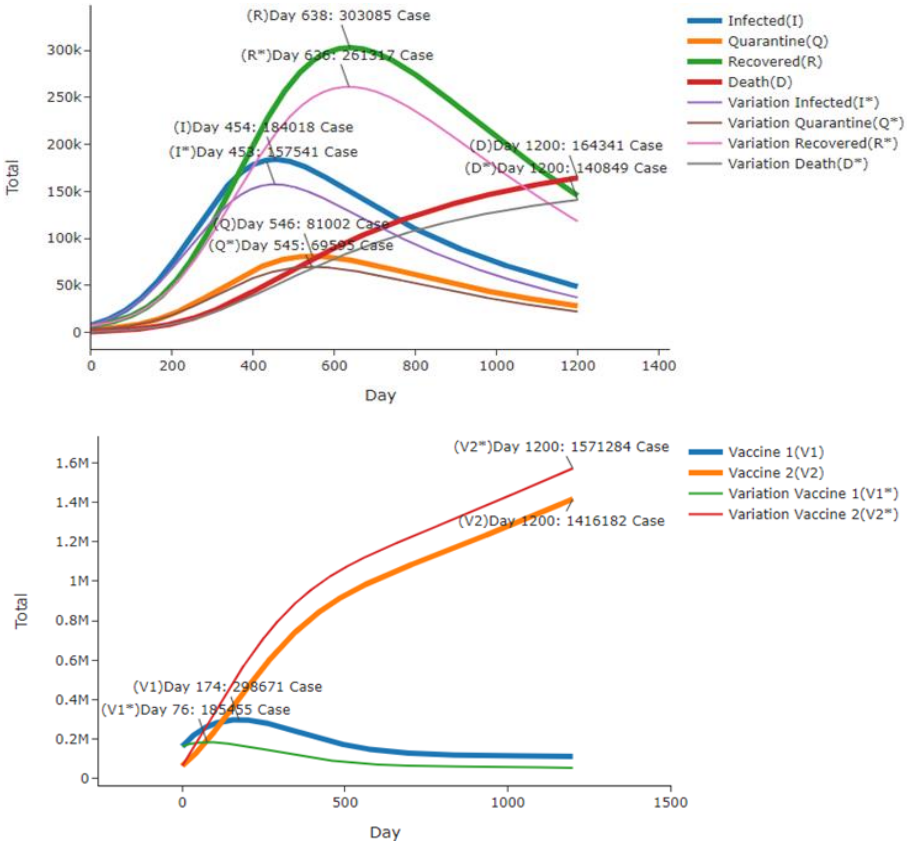

Figure 7. The top plot shows a model simulation for $I(t), Q(t), R(t)$, and $D(t)$ when $\varphi_{2_S} > \varphi_2$. The bottom plot shows the model simulation for $V_1(t)$ and $V_2(t)$ when $\varphi_{2_S} > \varphi_2$.

Furthermore, in the $D(t)$ compartment, the $D(t)$ curve shows an increase in the number of cases in this compartment by 138.64% on the 1200th day to 392,177 people. Based on Figure 8, compartments $V_1(t)$ and $V_2(t)$ experienced a decrease in individuals. The decrease at the peak of the $V_1(t)$ compartment was 1.70% to 293,591 people, with the peak shifting earlier to the 158th day. At the same time, the decrease in the total individual in compartment $V_2(t)$ can be seen at $t = 1200$ in the orange curve at τ_1 and the red curve for $\tau_{1_S} < \tau_1$. The decrease that occurred in the $V_2(t)$ compartment was 35.44%.

The following simulation is done by varying the value of $\tau_{1_S} > \tau_1$. The value of τ_{1_S} will be increased by 80% from τ_1 to 0.009799. The following will present the simulation results of the COVID-19 transmission model when the value of $\tau_{1_S} > \tau_1$. Figure 9 shows the simulation results of the COVID-19 transmission model with the value $\tau_{1_S} > \tau_1$ for compartments $I(t), Q(t), R(t)$, and $D(t)$. In this condition, compartment $I(t)$ experienced a decrease in cases at the peak point of 64.21%, with the peak of cases shifting earlier on the 429th day. Likewise, the $R(t)$ compartment experienced a decrease in the number of cases at the top of the curve. Based on the $R(t)$ curve, the

decrease in total cases at the peak of the $R(t)$ compartment occurred by 54.60%, with the peak being on the 612th day, with a shift in peak faster than τ_1.

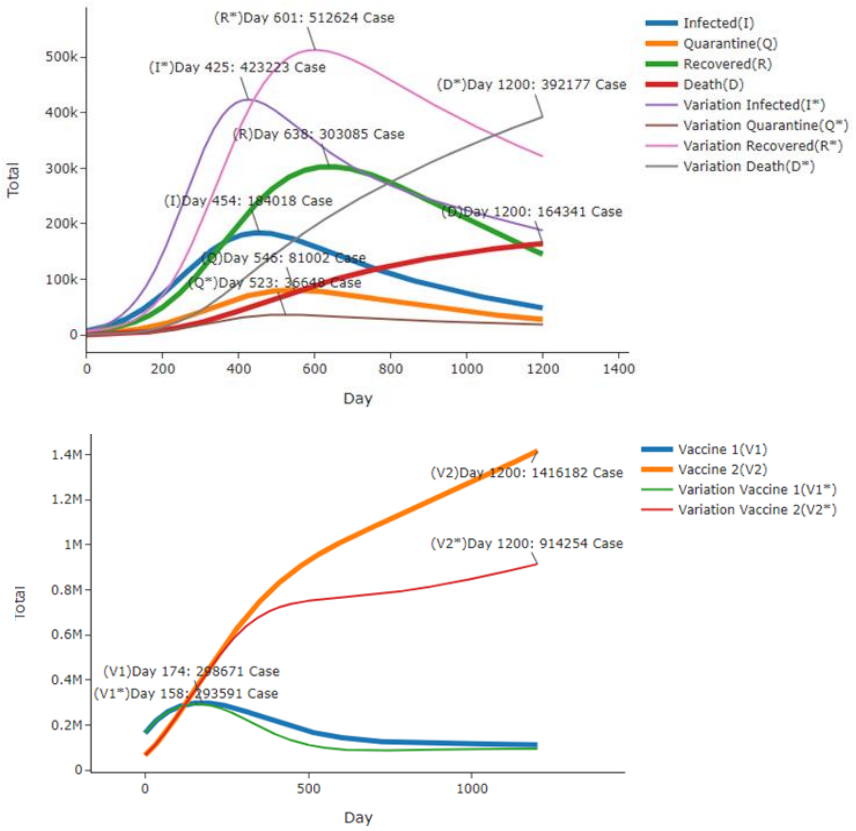

Figure 8. The top plot shows the model simulation for $I(t), Q(t), R(t)$, and $D(t)$ when $\tau_{1_S} < \tau_1$. The bottom plot shows the model simulation for $V_1\ (t)$ and $V_2(t)$ when $\tau_{1_S} < \tau_1$.

The next compartment is the $Q(t)$, the same as the previous two compartments. This compartment also experiences a decrease in the total number of cases at its peak. Based on the $Q(t)$ curve, the total cases at the top of the compartment decreased by 34.99%, with the peak of cases shifting earlier to day 517. The next compartment is the $D(t)$ compartment. Based on the $D(t)$ curve, cases in this compartment also decreased. It can be seen on the 1200th day, which shows a decrease in individual cases of dying from COVID-19 by 65.16%.

The following simulation results are compartments $V_1(t)$ and $V_2(t)$. Based on Figure 9, compartment $V_1(t)$ experienced a slight increase in the total number of individuals vaccinated at dose 1. From the curve $V_1(t)$, the increase in the number of individuals at the peak of compartment $V_1(t)$ was 1.41% to 302,894 people, with the curve peak shifting longer to be the 188th day. Like compartment $V_1(t)$, compartment $V_2(t)$ also experienced an increase in the total number of

individuals in this compartment. The increase in the number of individuals in this compartment can be seen on the 1200th day, with an increase of 24.86% to 1,768,307 people.

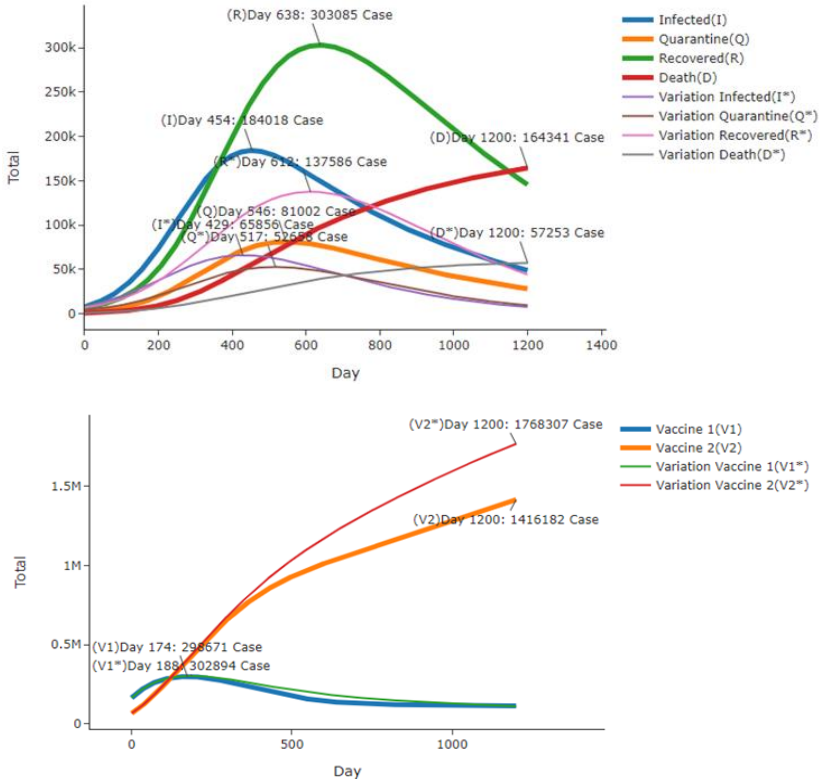

Figure 9. The top plot shows the model simulation for $I(t), Q(t), R(t)$, and $D(t)$ when $\tau_{1_S} > \tau_1$. The bottom plot shows the model simulation for $V_1\ (t)$ and $V_2(t)$ when $\tau_{1_S} > \tau_1$.

The last parameter variation is done by varying the value of the q parameter or reducing the infection rate due to the quarantine intervention. The value of the q parameter is varied from 0 to $2q = 0.1$. Next, the model simulation for the parameter $q_S < q$ variation is shown in Figure 10. Figure 10 is a simulation for compartments $I(t), Q(t), R(t)$, and $D(t)$ with the parameter q values used as 0.01. This value is down by 80% from q. Based on Figure 10, it can be seen that there was a decrease in cases in the four compartments. In compartment $I(t)$, there was a decrease in the number of cases at the peak of 5.98%, with the peak shifting longer on the 456th day. Then for the $Q(t)$ compartment, the number of cases also decreased at the peak point, with a decrease in cases that occurred by 5.89% at the peak point, which shifted longer to day 548. The next compartment is the $R(t)$ compartment. Compartment $R(t)$ experienced a decrease in the number of cases at the peak of 5.82%, with the peak of cases shifting to the 639th day. Furthermore, in the $D(t)$ compartment, there was a decrease in cases seen on the 1200th day cases, which decreased by 6.62%.

Based on Figure 10, the simulation results for the $V_1(t)$ and $V_2(t)$ compartments at $q_S < q$ do not have a significant change in cases. Compartment $V_1(t)$ only experienced an increase in the number

of individuals by 0.19% to 299,241 people, with the peak shifting to the 175th day. Furthermore, for the $V_2(t)$ compartment, it increased by 2.77% on the 1200th day.

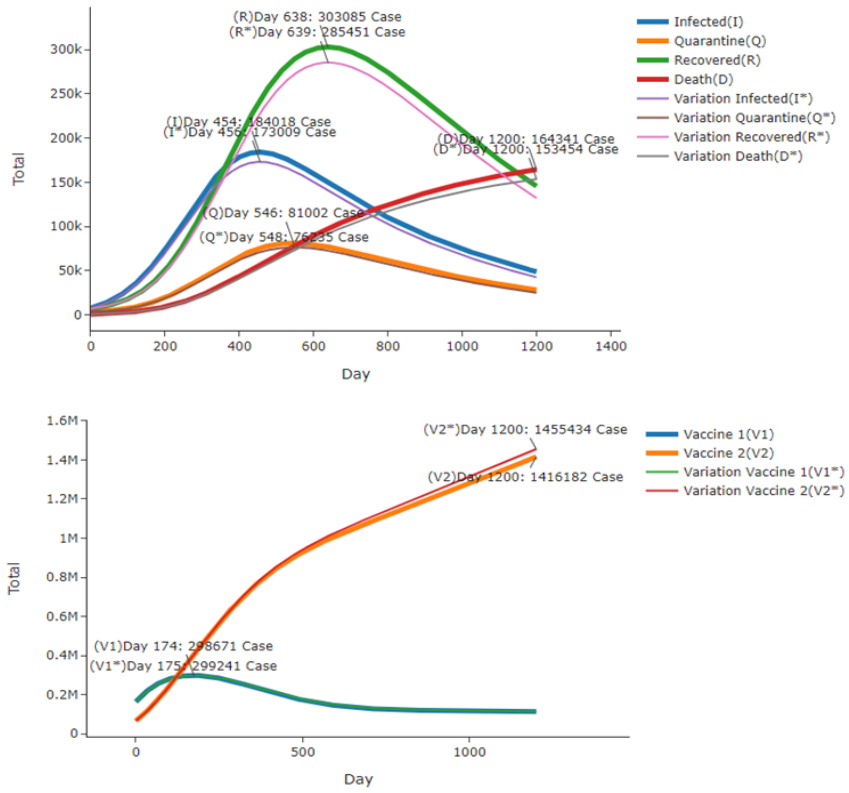

Figure 10. The top plot shows the model simulation for $I(t), Q(t), R(t)$, and $D(t)$ when $q_S < q$. The bottom plot shows the model simulation for $V_1(t)$ and $V_2(t)$ when $q_S < q$.

The following simulation is a simulation when the parameter value $q_S > q$. Figure 11 shows the simulation results of the COVID-19 transmission model for compartments $I(t), Q(t), R(t)$, and $D(t)$ when the parameter value $q_S > q$. The value of the q_S parameter in Figure 11 is 0.09, which is an increase of 80% from q. Based on Figure 11, the four compartments experienced a rise in cases. In the compartment, $I(t)$ cases increased at the peak point of 5.96%, with the peak point occurring earlier than the 450th day. Furthermore, for the $Q(t)$ compartment, there was an increase in cases at the peak of 5.84% to 85,732 people, with the peak shifting faster to the 544th day. The third compartment, the $R(t)$, also experienced an increase in the number of individuals at the peak of 5.76%, with the peak shifting to the 637th day. The last compartment is compartment $D(t)$. Based on the $D(t)$ curve, the $D(t)$ compartment also experienced an increase in cases of 6.65% on the 1200th day.

Furthermore, the COVID-19 transmission model simulation results for compartments $V_1(t)$ and $V_2(t)$. Based on Figure 11, both compartments experienced a decrease in individuals. The curve in compartment $V_1(t)$ shows a decline in the number of individuals at the peak point by 0.19% to

298,102 people, with the peak point shifting to day 172. Furthermore, for compartment $V_2(t)$, there is also a decrease in the number of individuals. This compartment decreased by 2.76%, which occurred on the 1200th day.

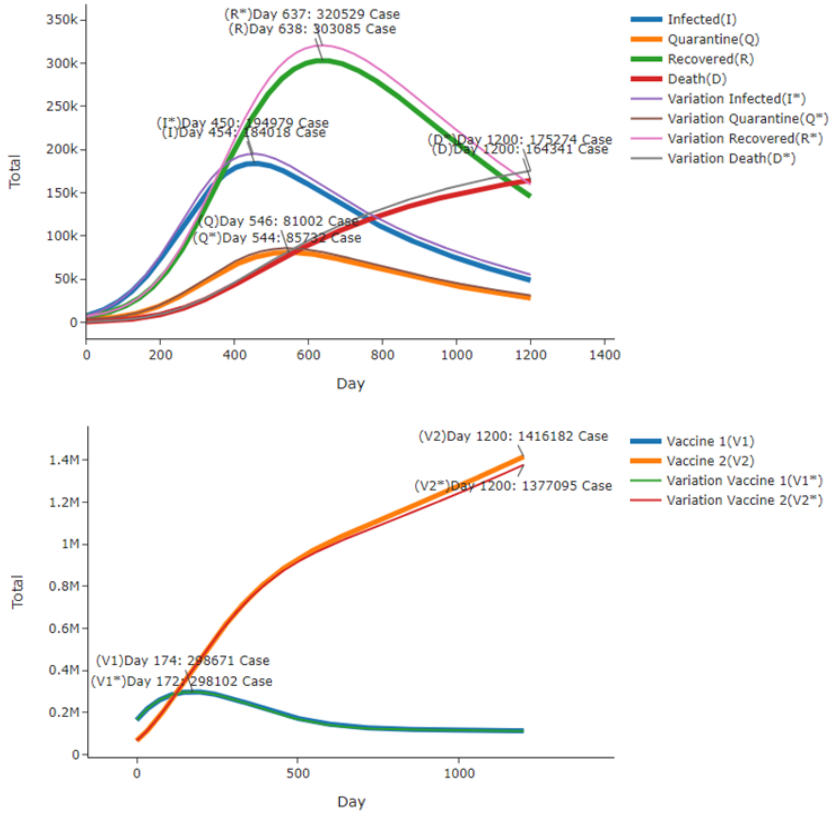

Figure 11. The top plot shows the model simulation for $I(t), Q(t), R(t)$, and $D(t)$ when $q_S > q$. The bottom plot shows the model simulation for $V_1\ (t)$ and $V_2(t)$ when $q_S > q$.

Based on the simulations carried out on the COVID-19 transmission model by varying the values of the four parameters, several parameters significantly influence the rate of spread of COVID-19. Parameter φ_1 is the rate of vaccination of dose 1, φ_2 is the rate of vaccination of dose 2, and τ_1 is the rate of quarantine or transfer from $I(t)$ to $Q(t)$, giving a more significant effect than parameter q. Then if you pay attention to the rate of spread of COVID-19, the rate of spread of this disease can be suppressed or based on its spread curve. To do that, several things can be done, including the following,

1. Accelerate the process of vaccination dose of 1 COVID-19 per day or increase the value of φ_1,
2. Accelerate the process of vaccination dose of 2 COVID-19 per day or increase the value of φ_2,
3. Increase the number of quarantined individuals due to positive COVID-19 with asymptomatic status or mild symptoms, or increase the value of τ_1.

When we implement the three efforts above, the simulation of the spread of COVID-19 is shown in Figure 12. This figure shows the compartment curve $I(t)$ during the initial conditions and after

implementing the three efforts. Cases at the peak are much lower than in the previous simulation, with a total of 28,463 cases, and this figure decreased by 84.53% from the total cases in the initial conditions. Then the q parameter does not significantly affect the last three parameters. Still, this parameter shows that the smaller the value, the slightly lower the spread of COVID-19, which means that the fewer individuals who violate quarantine procedures, the less the spread of COVID-19.

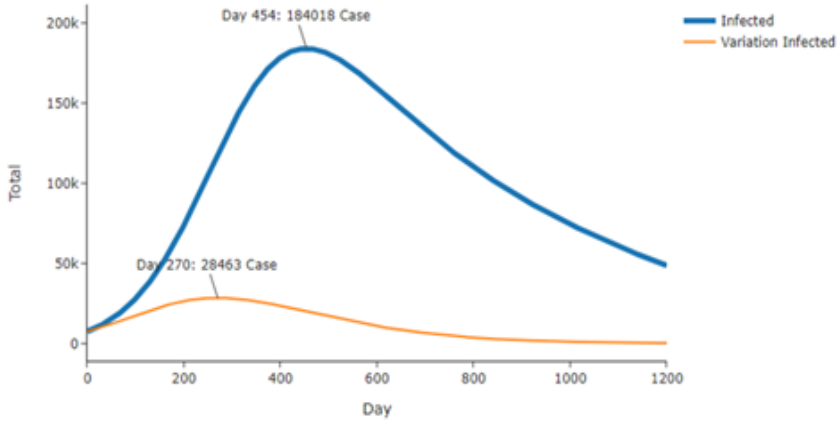

Figure 12. Model simulation implemented the three prevention efforts: vaccination dose 1, dose 2, and individual quarantine.

4. CONCLUSIONS

The COVID-19 transmission model with vaccination and quarantine interventions can be used to describe future conditions in Jember. The results of the simulation study yield a better spread scenario than the initial conditions by varying different parameter values. It is found that vaccination and quarantine interventions greatly influence the transmission of COVID-19. A faster rate of vaccinations will reduce the rate of transmission of COVID-19. In terms of quarantine interventions, if individuals who are tested positive for COVID-19 with mild or asymptomatic symptoms carry out proper quarantine procedures, the tracking process for individuals who are confirmed with COVID-19 can be further expanded to maximize quarantine interventions. As a result, the rate of spread of COVID-19 can be reduced.

REFERENCES

[1] A. Susilo, M. Rumende, C. W. Pitoyo, W. D. Santoso, M. Yulianti, Herikurniawan, R. Sinto, G. Singh, L. Nainggolan, E. J. Nelwan, L. K. Chen, A. Widhani, E. Wijaya, B. Wicaksana, M. Maradewi, F. Annisa, C. O. Jasirwan and E. Yunihastuti, "Coronavirus Disease 2019: Review of Current Litertures," *Jurnal Penyakit Dalam Indonesia,* vol. 7, pp. 45-67, 2020.

[2] N. Zhu et al., "A novel coronavirus from patients with pneumonia in China, 2019," *N Engl. J. Med,* vol. 382, no. 8, p. 727–733, 2020.

[3] WHO, "Transmission of SARS-CoV-2: implications for infection prevention precautions," World Health Organization, 2020.

[4] L. Zhang, J. Huang, H. Yu, X. Liu, Y. Wei, X. Lian, C. Liu and Z. Jing, "Optimal parameterization of COVID-19 epidemic models," *Atmospheric and Oceanic Science Letters,* 2020. doi: https://doi.org/10.1016/j.aosl.2020.100024.

[5] Y. Yulida and M. A. Karim, "PEMODELAN MATEMATIKA PENYEBARAN COVID-19 DI PROVINSI KALIMANTAN SELATAN," *Media Bina Ilmiah,* vol. 14, pp. 3257-3264, 2020.

[6] A. A. Gebremeskel, H. W. Berhe and H. A. Atsbaha, "Mathematical modelling and analysis of COVID-19 epidemic and predicting its future situation in Ethiopia," *Results in Physics,* vol. 22, 2021.

[7] S. Tyagi, S. C. Martha, S. Abbas and A. Debbouche, "Mathematical modeling and analysis for controlling the spread of infectious diseases," *Chaos, Solitons and Fractals,* vol. 144, 2021.

[8] M. Y. Li, An Introduction to Mathematical Modeling of Infectious Diseases, Canada: Springer Nature, 2018.

[9] H. Trottier and P. Philippe, "Deterministic Modeling Of Infectious Diseases: Theory And Methods," *The Internet Journal of Infectious Diseases,* vol. 1, 2000.

[10] D. Aldila and D. Asrianti, "A deterministic model of measles with imperfect vaccination and quarantine intervention," *Journal of Physics: Conference Series,* 2019.

[11] M. Zevika, A. Triska, N. Nuraini and G. Lahodny Jr, "On The Study of Covid-19 Transmission Using Deterministic and Stochastic Models with Vaccination Treatment and Quarantine," *Communication in Biomathematical Sciences,* vol. 5, no. 1, pp. 1-19, 2022.

[12] K. Madsen, H. B. Nielsen and O. Tingleff, Methods for Non-Linear Least Squares Problems, 2nd ed., Denmark: Technical University of Denmark, 2004.

[13] M. Umar, Z. Sabir, M. A. Z. Raja, M. Gupta, D.-N. Le, A. A. Aly and Y. Guerrero-Sánchez, "Computational Intelligent Paradigms to Solve the Nonlinear SIR System for Spreading Infection and Treatment using Levenberg–Marquardt Backpropagation," *Symmetry ,* vol. 13, no. 618, p. sym13040618, 2021.

[14] C. T. Kelley, Iterative Methods for Optimization, Philadelphia: SIAM Frontiers in Applied Mathematics, 1999.

[15] F. Brauer, P. v. d. Driessche and J. Wu, Mathematical Epidemiology, Berlin: Springer, 2008.

[16] M. Martcheva, An Introduction to Mathematical Epidemiology, New York: Springer, 2015.

[17] P. J. Olver and C. Shakiban, Applied Linear Algebra, 2nd ed., Cham: Springer, 2018.

[18] A. Iserles, A First Course in the Numerical Analysis of Differential Equations, 2nd ed., New York: Cambridge University Press, 2009.

[19] J. C. Butcher, Numerical Methods for Ordinary Differential Equations, 2nd ed., Chichester: John Wiley & Sons Ltd, 2008.

[20] Y. Mao, W. Wang, J. Ma, S. Wu and F. Sun, "Reinfection rates among patients previously infected by SARS-CoV-2: systematic review and meta-analysis," *Chinese Medical Journal,* vol. 135, pp. 145-152, 2022.