RESEARCH ARTICLE • OPEN ACCESS

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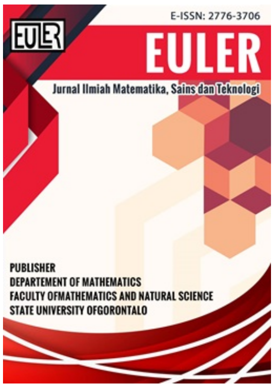
Volume 13, Issue 3, pp. 311–318, Dec. 2025

Received 14 August 2025, Revised 28 October 2025, Accepted 1 November 2025, Published 1 December 2025

To Cite this Article : N. A. Purnami, et al.,"Mathematical Model of COVID-19 with the Influence of Vaccination", *Euler J. Ilm. Mat. Sains dan Teknol.*, vol. 13, no. 3, pp. 311–318, 2025, *https://doi.org/10.37905/euler.v13i3.34182*

JOURNAL INFO • EULER : JURNAL ILMIAH MATEMATIKA, SAINS DAN TEKNOLOGI



Homepage : http://ejurnal.ung.ac.id/index.php/euler/index
Journal Abbreviation : Euler J. Ilm. Mat. Sains dan Teknol.
Frequency : Three times a year
Publication Language : English (preferable), Indonesia
DOI : https://doi.org/10.37905/euler
Online ISSN : 2776-3706
Publisher : Department of Mathematics, Universitas Negeri Gorontalo
Country : Indonesia
OAI Address : http://ejurnal.ung.ac.id/index.php/euler/oai
Google Scholar ID : QF_r-_gAAAAJ
Email : euler@ung.ac.id

Euler : Jurnal Ilmiah Matematika, Sains dan Teknologi, Volume 13, Issue 3, Pages 311–318, Dec. 2025 *https://doi.org/10.37905/euler.v13i3.34182*

Research Article

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Mathematical Model of COVID-19 with the Influence of Vaccination

Ndaru Atmi Purnami[1,*], **Luqman Nuradi Prawadika**[1], **Irvandi Gorby Pasangka**[2], **Findasari**[3], **Eka Kusumawati**[4], **Ilham Yoga Pratama**[5], **Ridho Suharis**[1], **Nadhira Hasna Maturbongs**[1]

[1]*Department of Mathematics, Universitas Negeri Jakarta, Jakarta Timur 13220, Indonesia*
[2]*Department of Mathematics, Universitas Nusa Cendana, Kupang 85111, Indonesia*
[3]*Department of Mathematics, Universitas Muhammadiyah Kudus, Kudus 59316, Indonesia*
[4]*Madrasah Aliyah Nahdlatul Ulama Banat Kudus, Kudus 59314, Indonesia*
[5]*Electrical Engineering Study Program, Institut Teknologi Dirgantara Adisutjipto, Bantul 55198, Indonesia*

ARTICLE HISTORY
Received 14 August 2025
Revised 28 October 2025
Accepted 1 November 2025
Published 1 December 2025

KEYWORDS
COVID-19
SEVIRD
Coronavirus
Vaccination
Mathematical Modeling

ABSTRACT. *The COVID-19 pandemic, which first emerged at the end of 2019, has had a significant impact on people's lives around the world. In Indonesia, the outbreak began to develop in February 2020. Although the pandemic has now passed and people have started to resume their normal activities, some individuals are still being infected with COVID-19, even though the number of cases is now under control. One of the key factors in controlling COVID-19 is vaccination. The extent to which vaccination affects COVID-19 transmission will be discussed in this study. Furthermore, a numerical simulation will be conducted on this mathematical model to observe the impact of vaccination on COVID-19. The mathematical model of COVID-19 with vaccination influence will describe the interaction between six population classes, namely: the class of susceptible individuals who can be infected (Susceptible – S), the class of exposed individuals (Exposed – E), the class of vaccinated individuals who have never been infected (Vaccinated – V), the class of infected individuals (Infected – I), the class of individuals who have recovered (Recovered – R), and the class of infected individuals who have died (Death – D). It is important to note that COVID-19 is a disease caused by infection with the coronavirus. A person who has not yet been infected with the virus has the potential to be exposed. One way to prevent exposure is through vaccination. In Indonesia, vaccination has been made mandatory three times: the first dose, the second dose, and the booster. However, because the coronavirus has an incubation period, there is no guarantee that a vaccinated person has not already been exposed to the virus. Exposed individuals will become infected with COVID-19 once the incubation period ends. Infected individuals may show symptoms or be asymptomatic. An infected individual has two possible outcomes: recovery or death. The modeling is based on the SEVIRD model, with its parameters estimated using data. This study produces a mathematical model of COVID-19 with vaccination influence, showing that vaccination plays a role in controlling the spread of COVID-19.*

1. Introduction

In 2019, COVID-19 became a serious global issue [1]. This disease outbreak was caused by an infection of the SARS-CoV-2 virus, which was first detected in Wuhan, China [2]. Currently, COVID-19 has been brought under control, and people have resumed normal activities, including in Indonesia. One of the ways to control COVID-19 is through vaccination [3]. Several studies have been conducted to understand the characteristics and strategies for managing this disease, so that it can be controlled effectively. One such study explores optimistic and pessimistic scenarios using a modeling approach based on the SIR Model, as written by Kusumo et al. [4]. In addition, Bagal et al. [5] presented the classical SIR Model to estimate the epidemiological parameters of COVID-19 in India during various phases of government lockdown, and to assess the impact of strict interventions on the outbreak dynamics. From this study, the classical SIR Model is shown to be fairly representative for modeling COVID-19 within the context of lockdown interventions, which have proven effective in significantly reducing the transmission rate. However, to achieve outbreak elimination, a combination of strategies is needed, such as contact tracing, testing, isolation, and vaccination. On the other hand, an extension of the classical SIR Model was presented by Cooper et al. [6], which modifies the assumption of a constant population. This allows the susceptible class to increase again during surges, such as due to reopening regions or the entry of new cases into Indonesia. This modified SIR Model is more realistic when applied to communities experiencing wave-like outbreaks, where the susceptible population does not necessarily decrease monotonically. The classical SIR Model can be robust enough if its parameters and population assumptions are adjusted according to real-time data.

A study on the SEIRV Model, which has proven to be more realistic and effective in modeling the dynamics of the COVID-19 pandemic with vaccination interaction, was presented by Saharan et al. [7]. In that study, the developed model helps assess the effectiveness of vaccines, showing that vaccination can reduce cases and significantly alter the trajectory of the pandemic com-

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[*] Corresponding Author.

Email : *ndaru.atmi@unj.ac.id* (N. A. Purnami)

Homepage : http://ejurnal.ung.ac.id/index.php/euler/index / E-ISSN : 2776-3706

pared to a scenario without vaccination. Furthermore, the study discusses how the SEIR Model outperforms Holt's trend method for short- and medium-term predictions, while the SEIRV Model is more suitable for policy analysis related to vaccination. In the development of the SEIRV Model, a new class P was added to represent protective behavior (self-protection) [8]. This model development incorporates vaccination and optimal control strategies to minimize both the number of COVID-19 infections and the cost of interventions. On the other hand, the development of the SEIRV Model was also discussed by Poonia et al. [9]. This enhancement extends the SEIRV Model to predict the spread of COVID-19, particularly by taking into account the effects of vaccination and the implementation of social distancing.

In the formulation of the SIR, SEIR, and their variant models, the Basic Reproduction Number (R_0) must be calculated to determine the average number of new infections caused by a single infected individual in a fully susceptible population. The Next Generation Matrix (NGM) is constructed and used to calculate a mathematically valid and structured R_0 [10]. A study on the fundamental concepts, model development, and R_0 calculation was presented by [11].

The Taylor matrix and collocation numerical methods are used to obtain robust numerical solutions in solving the SIR Model with time-dependent parameters and recovery rates [12]. Numerical simulations based on daily COVID-19 data in Indonesia were studied by Annas et al. [13]. This study discusses the criteria under which COVID-19 would become endemic without intervention. The SEIR Model was used in this study with the aim of evaluating how interventions such as vaccination and isolation affect the spread of COVID-19 in Indonesia. These findings can serve as a guide for early prevention policies and epidemic intervention strategies.

Based on the literature review conducted, this study will discuss a mathematical model of COVID-19 using the SEVIRD Model. One of the key differences between this study and previous research lies in the addition of the Death (D) class, with the assumption that each individual infected with COVID-19 has the possibility of either recovering or dying from the disease. The mathematical modeling of COVID-19 in this study begins with determining the assumptions and parameters to be used. Based on these assumptions and parameters, a transfer diagram is constructed to formulate the mathematical model of COVID-19 with the influence of vaccination. Once the model is established, the disease-free equilibria point and the basic reproduction number R_0 will be calculated. In addition, R_0 will also be used for analysis in the numerical simulation results. The parameters used for the numerical simulations are obtained from [14–19]. To determine the accuracy of the SEVIRD Model, the Root Mean Square Error (RMSE) method is used. The RMSE calculation is employed to measure the error difference between the SEVIRD simulation results and the actual data. This study is expected to show that the mathematical model of COVID-19, incorporating the influence of vaccination, can demonstrate the role of vaccination in controlling the spread of COVID-19.

2. Methods

The research flow was divided into five stages: data collection method, model formulation, data analysis method, computational method, and system performance evaluation method.

2.1. Data Collection Method

This study is supported by a literature review by reading and analyzing literature on mathematical modeling of COVID-19, with or without interventions as disease control measures, in order to obtain information relevant to the topic. The mathematical modeling process begins by defining the population classes, determining the assumptions used, identifying the parameters that influence the mathematical model, creating a transfer diagram, and formulating the mathematical model. Next, numerical simulations are conducted to understand the medical interpretation of the mathematical model, allowing for comparison with actual medical facts. After the literature review is completed, data is collected for use in the numerical simulation. Data collection for this simulation is carried out qualitatively from journals written by [14–19].

2.2. Model Formulation

The transmission process of COVID-19 begins when a susceptible individual becomes infected with the SARS-CoV-2 virus. This virus has an incubation period. When the incubation period ends, the individual may become infected with the COVID-19 disease. Prior to infection, vaccination is administered as one method of controlling the spread of COVID-19. The individuals who receive the vaccine are those in the susceptible class. However, it is still possible for individuals who are already infected with the SARS-CoV-2 virus to receive the vaccine. This is because symptoms of the disease may not appear during the incubation period, allowing an individual who is vaccinated to still become infected with COVID-19. An individual infected with COVID-19 has two possible outcomes: recovery or death due to the disease.

The classification in the mathematical model of COVID-19 with the influence of vaccination is divided into six compartments: Susceptible (S), Exposed (E), Vaccinated (V), Infected (I), Recovered (R), and Death (D). The Susceptible (S) class is defined as the vulnerable group—individuals who have not been infected by the virus and are still at risk of infection. The Exposed (E) class refers to individuals who have been exposed to the virus but have not yet shown symptoms of infection—in other words, individuals in the incubation phase. The Vaccinated (V) class includes individuals who have been vaccinated but have never been infected with COVID-19. The Infected (I) class is defined as individuals who are currently infected with COVID-19. The Recovered (R) class includes individuals who have recovered from COVID-19. The Death (D) class refers to individuals who have died as a result of COVID-19 infection.

Next, let $S\left(t\right)$ represent the number of susceptible individuals at time t, $E\left(t\right)$ the number of individuals exposed to COVID-19 at time t, $V\left(t\right)$ the number of vaccinated individuals at time t, $I\left(t\right)$ the number of individuals infected with COVID-19 at time t, $R\left(t\right)$ the number of individuals recovered from COVID-19 at time t, and $D\left(t\right)$ the number of individuals who died from COVID-19 at time t. From this point forward, $S\left(t\right), E\left(t\right), V\left(t\right), I\left(t\right), R\left(t\right)$ and $D(t)$ will be simply denoted as S, E, V, I, R and D, respectively. In this model, the following assumptions are made:

1. The population is closed, meaning there is no immigration

or emigration.

2. There is interaction between susceptible individuals and infected individuals, as well as between susceptible individuals and vaccinated individuals.
3. The probability of infection depends on the number of susceptible individuals and the number of infectious individuals.
4. Individuals who have recovered cannot become susceptible again.
5. Multiple vaccine doses (second dose or booster) are not considered; thus, the vaccinated class includes all individuals who have received any dose, whether only the first, the second, or up to the booster.
6. There is a possibility that exposed individuals receive the vaccine because symptoms do not appear (i.e., they are unaware of having been exposed to the SARS-CoV-2 virus), meaning that vaccinated individuals may still become infected with COVID-19.

The following are the parameters used in the mathematical model of COVID-19 with the influence of vaccination.

Table 1. Parameters used

Parameter	Definition
Λ	Natural birth rate
β	Transmission rate
ρ	Vaccination rate
δ	Rate at which exposed individuals get vaccinated
σ	Rate at which exposed individuals become infected with COVID-19
ω	Rate at which vaccinated individuals become infected with COVID-19
α	Death rate due to COVID-19
γ	Recovery rate
μ	Natural death rate

Based on the assumptions above, the transfer diagram is obtained on Figure 1.

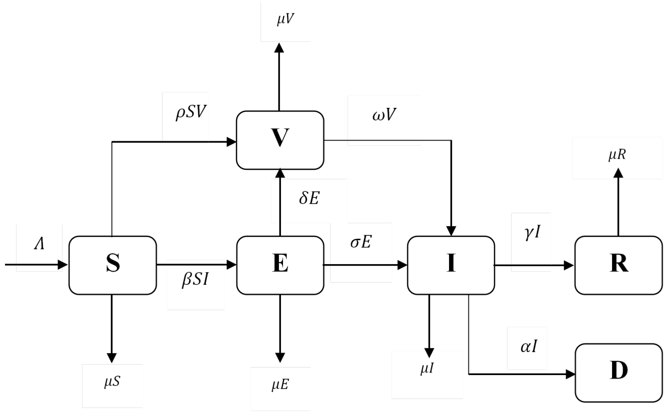


Figure 1. Transfer diagram of the COVID-19 mathematical model with the influence of vaccination

Based on the transfer diagram in Figure 1, the mathematical model of COVID-19 with the influence of vaccination is formulated as follows:

$$\frac{dS}{dt} = \Lambda - \rho SV - \beta SI - \mu S, \tag{1}$$

$$\frac{dE}{dt} = \beta SI - \delta E - \sigma E - \mu E, \tag{2}$$

$$\frac{dV}{dt} = \rho SV + \delta E - \omega V - \mu V, \tag{3}$$

$$\frac{dI}{dt} = \sigma E + \omega V - \gamma I - \alpha I - \mu I, \tag{4}$$

$$\frac{dR}{dt} = \gamma I - \mu R, \tag{5}$$

$$\frac{dD}{dt} = \alpha I. \tag{6}$$

with initial conditions $S(0) = S_0$, $E(0) = E_0$, $V(0) = V_0$, $I(0) = I_0$, $R(0) = R_0$, $D(0) = D_0$, and $S > 0$, $E \geq 0$, $V \geq 0$, $I \geq 0$, $R \geq 0$, $D \geq 0$.

2.3. Data Analysis Method

Two methods are used for data analysis. First, the disease-free equilibria point is determined. Second, the Basic Reproduction Number (R_0) is calculated and used to analyze the results of the numerical simulation.

In determining the disease-free equilibria point, the condition for finding the equilibrium point of the system of eq. (1) – eq. (6) is $\frac{dS}{dt} = 0$, $\frac{dE}{dt} = 0$, $\frac{dV}{dt} = 0$, $\frac{dI}{dt} = 0$, $\frac{dR}{dt} = 0$, and $\frac{dD}{dt} = 0$, resulting in

$$\Lambda - \rho SV - \beta SI - \mu S = 0, \tag{7}$$

$$\beta SI - \delta E - \sigma E - \mu E = 0, \tag{8}$$

$$\rho SV + \delta E - \omega V - \mu V = 0, \tag{9}$$

$$\sigma E + \omega V - \gamma I - \alpha I - \mu I = 0, \tag{10}$$

$$\gamma I - \mu R = 0, \tag{11}$$

$$\alpha I = 0. \tag{12}$$

The solution to the eq. (7) – eq. (8) represents the equilibrium point of the system of eq. (1) – eq. (6). The equilibrium point is divided into two types: the disease-free equilibria and the endemic equilibrium. This study focuses only on determining the disease-free equilibria, which is denoted by TE_0. The disease-free equilibria refers to the equilibrium point of the system of eq. (1) – eq. (6) where no individuals are exposed to or infected with COVID-19. In other words, $E = 0$, $I = 0$, and $D = 0$. The disease-free equilibria is obtained by substituting $E = 0$, $I = 0$, and $D = 0$ into eq. (7) – eq. (12). After TE_0 is obtained, its existence will be tested and interpreted based on the results of the existence test. On the other hand, the COVID-19 endemic equilibrium point is the equilibrium point of the System of eq. (1) – eq. (6) where there are individuals who are exposed to and infected with COVID-19. In other words, $E \neq 0$ and $I \neq 0$. To find the COVID-19 endemic equilibrium point, one can solve the System of eq. (7) – eq. (8). Furthermore, the discussion regarding the existence and interpretation of this endemic equilibrium point will be addressed in future research, accompanied by a stability analysis of all equilibrium points—both the COVID-19-free equilibria and the COVID-19 endemic equilibrium.

The next method used after calculating TE_0 is to compute the Basic Reproduction Number (R_0), which represents the average number of new infections caused by a single infected individual in a fully susceptible population. The Next Generation Matrix (NGM) is used to calculate R_0. To calculate R_0 using the

NGM, the first step is to ensure that there is a dynamic system in the form of an ordinary differential equation model. The second step is to divide this dynamic system into two components:

1. the rate of appearance of new cases (new infections), represented by the matrix $F(x)$, and
2. the rate of transitions between health states (recovery, death, moving to other classes), represented by the matrix $V(x)$.

The next step is to evaluate the Jacobian matrices of $F(x)$ and $V(x)$ at the disease-free equilibria. Then, the Next Generation Matrix K is determined using the following equation:

$$K = F(x).V^{-1}(x). \tag{13}$$

The largest eigenvalue (in norm) of K is R_0.

2.4. *Computational Method*

This section explains the computational method used in the study. The computation was carried out using Python software. The computational method begins by utilizing the NumPy, SciPy, and Matplotlib libraries. The NumPy library is a Python library for mathematical and array operations, such as vectors and matrices. In this program, NumPy is used to generate a sequence of numbers from 0 to 120 with 121 points (representing a simulation period of 120 days). The selection of a 120-day simulation period is based on the minimum duration of COVID-19, which ranges from 120 to 180 days. With NumPy, the program can perform efficient numerical computations. The odeint function, part of the SciPy library, is used to numerically solve ordinary differential equations. In this program, odeint is used to solve the SEVIRD equations over time. The function works by inputting the SEVIRD model function, initial conditions (y_0), and the time range (t). Odeint then returns an array of solution values for each compartment at each time step. The Matplotlib library is used to generate plots and visualizations of the simulation results.

The parameters used in the numerical simulation are taken from [14–19], as shown in Table 2.

Table 2. Parameter values used

Parameter	Value	Unit
Λ	20	people
β	0.3	per day
ρ	0.75	per day
δ	0.01	per day
σ	$\frac{1}{5.2}$	per day
ω	0.005	per day
α	0.01	per day
γ	0.1	per day
μ	0.01	per day

The initial conditions used in the numerical simulation are: $S_0 = 999000$, $E_0 = 500$, $V_0 = 0$, $I_0 = 500$, $R_0 = 0$, and $D_0 = 0$.

2.5. *System Performance Evaluation Method*

The forecast accuracy matrix is used to compare the forecasting performance of each method employed [20]. Based on [7, 20–22], the forecasting evaluation is conducted on the test data to identify the model with the best forecasting performance using Mean Absolute Error (MAE), Root Mean Square Error (RMSE), and Mean Absolute Percentage Error (MAPE). The equations used to calculate these metrics are:

$$\text{MAE} = \frac{1}{N}\sum_{t=1}^{N} |\hat{y}_t - y_t|, \tag{14}$$

$$\text{RMSE} = \sqrt{\frac{1}{N}\sum_{t=1}^{N} (\hat{y}_t - y_t)^2}, \tag{15}$$

$$\text{MAPE} = \frac{1}{N}\sum_{t=1}^{N} \frac{|\hat{y}_t - y_t|}{y_t}. \tag{16}$$

Based on eq. (14) – eq. (16), y_t is the actual number of cases at time-t, $\hat{y}_t$ is the predicted number of cases at time-t, and N is the number of test data points.

3. Results and Discussion

This section discusses the COVID-19 Disease-Free Equilibria Point (TE_0), the Basic Reproduction Number (R_0), numerical simulations of the effect of vaccination on COVID-19, and the performance testing of the SEVIRD Model. The following provides explanations regarding these four topics.

3.1. *COVID-19 Disease-Free Equilibria Point (TE_0)*

The disease-free equilibria point is given in the following theorem.

> **Theorem 1.** *The equilibria point $TE_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0\right)$ is the COVID-19 disease-free equilibria point for the system of eq. (1) – eq. (6).*

Proof. By substituting $E = 0$ and $I = 0$ to eq. (10), we obtain

$$\sigma(0) + \omega V - \gamma(0) - \alpha(0) - \mu(0) = 0 \Rightarrow \omega V = 0.$$

Since $\omega \neq 0$, it follows that $V = 0$.

Next, substitute $I = 0$ to eq. (11) to obtain

$$\gamma(0) - \mu R = 0 \Rightarrow -\mu R = 0.$$

Since $\mu \neq 0$, then $R = 0$.

Then, substitute $I = 0$ and $V = 0$ to eq. (7) to obtain

$$\begin{aligned} \Lambda - \rho S(0) - \beta S(0) - \mu S = 0 &\Rightarrow \Lambda - \mu S = 0 \\ &\Rightarrow \mu S = \Lambda \\ &\Rightarrow S = \frac{\Lambda}{\mu}. \end{aligned}$$

As a result, the COVID-19 disease-free equilibria point of the system of eq. (1) – eq. (6) is $TE_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0\right)$. ☐

The COVID-19 disease-free equilibria point $TE_0 = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0\right)$ always exists. This has a medical interpretation that, under steady-state conditions, the number of susceptible individuals is $\frac{\Lambda}{\mu}$ people, while the number of exposed individuals, vaccinated individuals, infected individuals, recovered individuals, and individuals who have died due to COVID-19 are all zero (none). This equilibria point indicates a state where COVID-19 does not occur. The natural birth rate and the natural death rate of susceptible individuals are factors that influence this condition.

3.2. Basic Reproduction Number (R_0)

The Basic Reproduction Number (R_0) is given in the following theorem.

Theorem 2. *The value* $R_0 = \dfrac{\beta\sigma\Lambda}{\mu(\sigma+\mu)(\gamma+\alpha+\mu)}$ *is the Basic Reproduction Number for the system of eq. (1) – eq. (6).*

Proof. To calculate R_0, the focus is only on the classes that are directly infectious or that generate infectious individuals, namely the Exposed (E) class and the Infected (I) class. If we define $x = (E, I)^T$, then $F(x)$ represents the new infections, expressed as follows:

$$F(x) = \begin{pmatrix} \beta SI \\ 0 \end{pmatrix}.$$

If $V(x)$ represents the transfer between compartments, then $V(x)$ can be expressed as follows:

$$V(x) = \begin{pmatrix} (\sigma+\mu)E \\ -\sigma E + (\gamma+\alpha+\mu)I \end{pmatrix}.$$

The matrix F is the Jacobian of $F(x)$ which is expressed as follows:

$$F = \frac{\partial F(x)}{\partial(E,I)} = \begin{pmatrix} 0 & \beta S \\ 0 & 0 \end{pmatrix}. \tag{17}$$

Next, substitute $T_{E_0} = (\Lambda/\mu, 0, 0, 0, 0, 0)$ to eq. (17) to obtain

$$F = \begin{pmatrix} 0 & \dfrac{\beta\Lambda}{\mu} \\ 0 & 0 \end{pmatrix}. \tag{18}$$

The matrix V is the Jacobian of $V(x)$ which is expressed as follows:

$$V = \frac{\partial V(x)}{\partial(E,I)} = \begin{pmatrix} \sigma+\mu & 0 \\ -\sigma & \gamma+\alpha+\mu \end{pmatrix}.$$

Then, the determinant of matrix V is calculated as

$$\det(V) = (\sigma+\mu)(\gamma+\alpha+\mu),$$

Therefore, the inverse of matrix V is

$$\begin{aligned} V^{-1} &= \frac{1}{(\sigma+\mu)(\gamma+\alpha+\mu)} \begin{pmatrix} \gamma+\alpha+\mu & 0 \\ \sigma & \sigma+\mu \end{pmatrix} \\ &= \begin{pmatrix} \dfrac{1}{\sigma+\mu} & 0 \\ \dfrac{\sigma}{(\sigma+\mu)(\gamma+\alpha+\mu)} & \dfrac{1}{\gamma+\alpha+\mu} \end{pmatrix}. \end{aligned} \tag{19}$$

From eq. (18) and eq. (19), the Generation Matrix K is obtained as follows

$$\begin{aligned} K &= \begin{pmatrix} 0 & \dfrac{\beta\Lambda}{\mu} \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \dfrac{1}{\sigma+\mu} & 0 \\ \dfrac{\sigma}{(\sigma+\mu)(\gamma+\alpha+\mu)} & \dfrac{1}{\gamma+\alpha+\mu} \end{pmatrix} \\ &= \begin{pmatrix} \dfrac{\beta\sigma\Lambda}{\mu(\sigma+\mu)(\gamma+\alpha+\mu)} & \dfrac{\beta\Lambda}{\mu(\gamma+\alpha+\mu)} \\ 0 & 0 \end{pmatrix}. \end{aligned} \tag{20}$$

From eq. (20), the eigenvalues of matrix K are obtained as

$$\lambda_1 = \frac{\beta\sigma\Lambda}{\mu(\sigma+\mu)(\gamma+\alpha+\mu)} \quad \text{and} \quad \lambda_2 = 0.$$

Since $\lambda_1 > \lambda_2$, then

$$R_0 = \lambda_1 = \frac{\beta\sigma\Lambda}{\mu(\sigma+\mu)(\gamma+\alpha+\mu)}.$$

If vaccination is implemented in the population, the number of susceptible individuals at steady state will be lower. In other words, this condition can reduce the value of R_0, which aligns with medical expectations. ☐

The Basic Reproduction Number $R_0 = \dfrac{\beta\sigma\Lambda}{\mu(\sigma+\mu)(\gamma+\alpha+\mu)}$ represents the average number of susceptible individuals who will be directly infected by a single individual with COVID-19 in a completely susceptible population (i.e., no one has been vaccinated). Thus, R_0 is a measure of the disease's transmission potential. If $\beta\sigma\Lambda > \mu(\sigma+\mu)(\gamma+\alpha+\mu)$, COVID-19 spreads rapidly and tends to become widespread. If $\beta\sigma\Lambda < \mu(\sigma+\mu)(\gamma+\alpha+\mu)$, individuals recover or die quickly. In other words, the infectious period of COVID-19 is short. If $\beta\sigma\Lambda = \mu(\sigma+\mu)(\gamma+\alpha+\mu)$, the disease reaches a critical point (the number of cases remains stable). If vaccination is implemented in the population, the value of Λ/μ will decrease, thereby reducing the value of R_0, as desired.

3.3. Numerical Simulation of the Effect of Vaccination on COVID-19

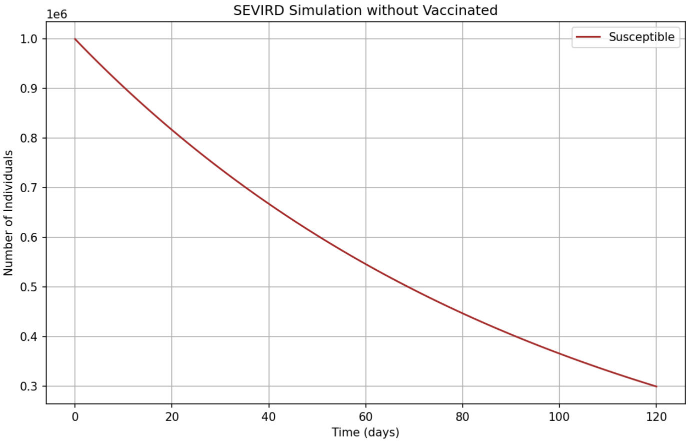
The parameter values are provided in Table 2. In the numerical simulation, two cases will be considered: a numerical simulation of System of eq. (1) – eq. (6) without vaccination and with vaccination. For the numerical simulation of System of eq. (1) – eq. (6) without vaccination, the simulation plot is presented as follows.

In Figure 2, the number of susceptible individuals without vaccination tends to decrease over time. This reduction is caused by susceptible individuals becoming exposed individuals. On the other hand, the number of exposed individuals increases until it reaches its peak before the fifth day. After the fifth day, the number of susceptible individuals continues to decline until approximately the thirtieth day. Meanwhile, the number of exposed individuals remains significantly present without decreasing. The decrease in exposed individuals is due to the end of the incubation period. In other words, many exposed individuals transition into COVID-19 infected individuals, and the mortality rate due to COVID-19 increases daily. However, the number of individuals recovering from COVID-19 is much lower than those who die from the disease. In other words, without vaccination, a large number of individuals will die from COVID-19. Next, the numerical simulation of System of eq. (1) – eq. (6) with the effect of vaccination will be conducted.

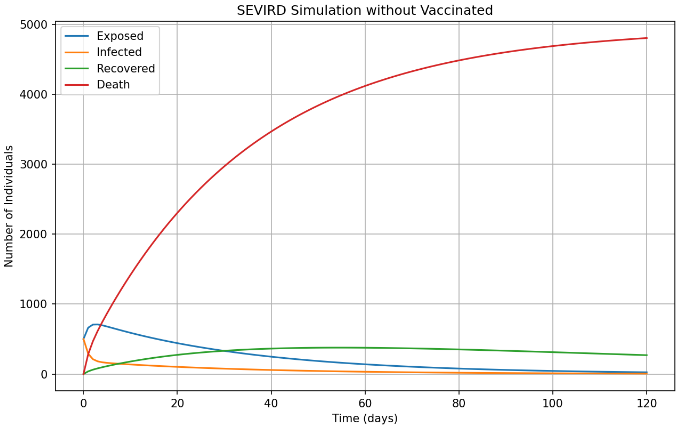
For the numerical simulation of System of eq. (1) – eq. (6) with the effect of vaccination, the simulation plot is presented as follows.

Table 3. Performance evaluation for the SEVIRD Model

No.	Case Type	$RMSE$	MAE	$MAPE$
1.	Daily COVID-19 infected cases (I)	3877.49	3229.64	17.61%
2.	Daily recovery cases (R)	17768.13	14363.76	16.19%
3.	Daily COVID-19 death cases (D)	1574.57	1202.80	9.80%



(a)



(b)

Figure 2. Simulation based on SEVIRD model without vaccination

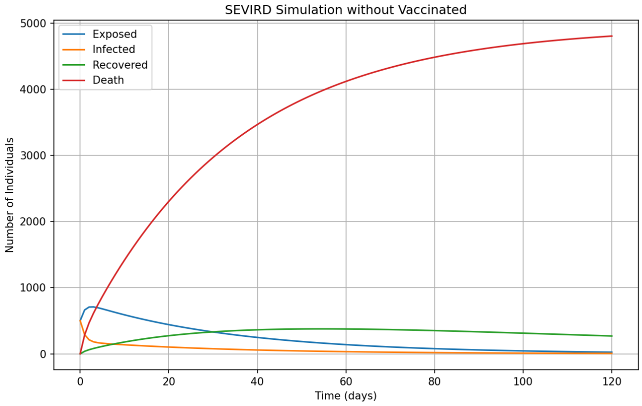


Figure 3. Simulation based on SEVIRD model with vaccination

In Figure 3, the number of susceptible individuals decreases to nearly zero because almost all susceptible individuals have been vaccinated, resulting in an increase in vaccinated individuals. Vaccinated individuals can still become infected, but in small numbers. One reason is that some vaccinated individuals were already exposed but asymptomatic, so they got vaccinated without knowing they were already exposed; as a result, after vaccination, these individuals become infected with COVID-19. There are almost no exposed individuals who are unvaccinated because many susceptible individuals were vaccinated before being exposed to COVID-19. Additionally, exposed individuals complete their incubation period and then become infected with COVID-19. Although there are infected individuals, many more recover compared to those who die from COVID-19. In other words, vaccination helps control the spread of COVID-19.

3.4. Performance Testing of the SEVIRD Model

In the SEVIRD Model, the model's performance can be assessed using the values of Root Mean Squared Error (RMSE), Mean Absolute Error (MAE), and Mean Absolute Percentage Error (MAPE), as shown in Table 3.

From Table 3, for the daily COVID-19 infected cases, the RMSE value is 3877.49. This indicates that, on average, the model's predictions deviate by approximately ± 3878 individuals from the actual data. The MAE value of 3229.64 means that, on average, the model's predictions deviate by about ± 3230 individuals, without amplifying the effect of outliers. The MAPE value of 17.61% indicates that the model's predictions are proportionally very close to the actual data, with a percentage error of 17.61%. In other words, for the infected individuals category, the model has an accuracy of 82.39%.

For the daily recovery cases, the RMSE value is 17768.13. This indicates that, on average, the model's predictions deviate by approximately ± 17769 individuals from the actual data. The MAE value of 14363.76 means that, on average, the model's predictions deviate by about ± 14364 individuals, without amplifying the effect of outliers. The MAPE value of 16.19% indicates that the model's predictions are proportionally close to the actual data, with a percentage error of 16.19%. In other words, for the category of individuals recovering from COVID-19, the model has an accuracy of 83.81%.

For the daily COVID-19 death cases, the RMSE value is 1574.57. This indicates that, on average, the model's predictions deviate by approximately ± 1575 individuals from the actual data. The MAE value of 1202.80 means that, on average, the model's predictions deviate by about ± 1203 individuals, without amplifying the effect of outliers. The MAPE value of 9.80% indicates that the model's predictions are proportionally close to the actual data, with a percentage error of 9.80%. In other words, for the category of individuals who died from COVID-19, the model has an accuracy of 90.20%.

3.5. Comparison with Standard SEIRV Models

The SEVIRD model is an extension of the basic SEIRV model by adding a new compartment, namely the Death (D) class, which represents the number of individuals who have died due to COVID-19. In the SEIRV model, it is assumed that all infected individuals will eventually recover and gain immunity. However, in the SEVIRD model, a portion of the individuals in the Infected (I) class can transition to the Death (D) class at a disease-induced death rate.

The addition of this compartment makes the SEVIRD model more realistic in representing the spread of COVID-19, particularly considering its significant fatality rate. Simulation results show that the SEVIRD model predicts a faster decline in the number of infected individuals compared to the SEIRV model, as some individuals move to the Death (D) class. Moreover, the number of recovered individuals (R) in the SEVIRD model tends to be lower than in the SEIRV model because some individuals do not recover from the infection.

Overall, the SEVIRD model provides a more comprehensive depiction of disease dynamics by accounting for both possible outcomes of infection: recovery or death. However, the SEIRV model remains relevant when the death rate is relatively low or when the primary focus of the study is on vaccine effectiveness and population immunity development, rather than on disease fatality.

During the pandemic, COVID-19 had a very high disease-induced death rate. By adding the Death (D) compartment, the SEVIRD mathematical model offers a more realistic interpretation of real-world conditions, with higher accuracy compared to the SEIRV model.

4. Conclusion

The results of the COVID-19 mathematical model incorporating the effect of vaccination show that vaccination plays a significant role in controlling the spread of COVID-19. Without vaccination, the number of individuals who die from COVID-19 is higher than the number of those who recover. With vaccination, although some individuals still become infected, the number of recoveries exceeds the number of deaths due to COVID-19. In other words, the SEVIRD model is suitable for analyzing vaccination-related policies and has a strong impact on COVID-19 disease control strategies. At steady state, the disease-free equilibria point is influenced by the natural birth rate and the natural death rate of susceptible individuals. If vaccination is present in the population, the number of susceptible individuals at steady state will be lower. The SEVIRD model achieves an average accuracy of 85.47%.

Author Contributions. **Ndaru Atmi Purnami**: Conceptualization, methodology, writing–original draft preparation, supervision, and funding acquisition. **Luqman Nuradi Prawadika**: writing–original draft preparation and writing–review and editing.**Irvandi Gorby Pasangka**: formal analysis and supervision. **Findasari**: validation and data curation. **Eka Kusumawati**: validation. **Ilham Yoga Pratama**: software and visualization. **Ridho Suharis**: software and visualization. **Nadhira Hasna Maturbongs**: investigation, resources, and project administration. All authors discussed the results and contributed to the final manuscript.

Acknowledgement. This research is supported by Lembaga Penelitian dan Pengabdian Masyarakat Universitas Negeri Jakarta with contract number 1386/UN39/HK.02/2025. We would like to thank Muhammad Rizky Ardiansyah from Program Studi Matematika Universitas Negeri Jakarta for his assistance during the research. We would like to express our sincere gratitude to the editor and reviewers for their insightful comments and helpful suggestions that greatly improved the quality of this manuscript.

Funding. This research was an independent study funded by the authors and supported by Lembaga Penelitian dan Pengabdian Masyarakat Universitas Negeri Jakarta with contract number 1386/UN39/HK.02/2025.

Conflict of interest. The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability. The data presented in this study are available on request from the corresponding author. The data are not publicly available due to privacy or institutional restrictions.

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