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Research Paper

Susceptible Vaccine Infected Removed (SVIR) Model for COVID-19 Cases in Indonesia

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Abstract
Analysis of data on COVID-19 cases in Indonesia is shown by using the Susceptible Vaccine Infected Removed (SVIR) in this article. In the previous research, cases in the period March-May 2021 were studied, and the reproduction number was computed based on the Susceptible Infected Removed (SIR) model. The prediction did not agree with the real data. Therefore the objective of this article is to improve the model by adding the vaccine variable leading to the new model called the SVIR model as the novelty of this article. The used data are collected from COVID-19 cases of the Indonesian population published by the Indonesian government from March 2020-April 2022. However, the vaccinated persons with COVID-19 cases have been recorded since January 2022. Therefore the models rely on the period January 2021-March 2022, where the parameters in the SIR and SVIR models are determined in this period. The method used is discretizing the models into linear systems, and these systems are solved by Ordinary Least Square (OLS) for time-dependent parameters. It is assumed that the birth rate and death rate in the considered period are constant. Additionally, individuals who have recovered from COVID-19 will not be infected again, and vaccination is not necessarily twice. Furthermore, individuals who have been vaccinated will not be infected with the COVID-19 virus. The SVIR model has captured 3 waves of COVID-19 cases that are appropriate to the real situation in Indonesia from January 2021-March 2022. Additionally, the reproduction numbers as functions of time have been generated. The fluctuations of reproduction numbers agree with the real data. For further research, different regions such as districts in Java and other islands will also be analyzed as the implication of this research.

Keywords
COVID-19, SIR, SVIR, Vaccination, Reproduction Number

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1. INTRODUCTION

The pandemic status that has not been revoked by the Indonesian government encourages research to be carried out continuously to obtain answers and solutions to the phenomena that occur. It is known that the COVID-19 pandemic has attacked not only the public health sector but also various main sectors in Indonesia. Losses were experienced by almost everyone, and the loss of relatives was also caused by the outbreak of this virus. According to Karim and Karim (2021), the emergence of the alpha, beta, and delta variants of the VoC SARS-CoV-2 is associated with a new wave (Ito et al., 2022). Moreover, there are rumors that there will be an explosion of infection waves due to the appearance of the Omicron variant (World Health Organization, 2022). One example of research on this was shown in the cases of COVID-19 in Norwegia (Jørgensen et al., 2022). So, the COVID-19 phenomenon in Indonesia and the world still need further research due to the presence of severe variant. Therefore, it is hoped that this research can produce outputs that can be considered by the government as policymakers to suppress and reduce the risk so that the pandemic ends soon, and finally, the situation is becoming normal and improve people's welfare.

There have been many studies conducted predicting how the next COVID-19 will occur, such as the research conducted by Parhusip (2020). The research predicted the number of COVID-19 cases that appeared at a certain time by comparing 3 different regions indicating different mobilities of the population in the regions. Other researchers Sifriyani et al. (2020) predict the growth rate of COVID-19 cases without discussing the effect of vaccination, even though it is known that there is a decrease in the growth rate of COVID-19 cases. The reproduction number has been computed Trihandaru et al. (2021) using the SIR model as a function of time which improves the existing SIR models with constant parameters.

However, this research has the contribution of the vaccinated variable since vaccination has not been obligated in that period (2020-2021). Motivated by those researches, this study aims to identify and analyze the effect of vaccines on the growth rate of confirmed COVID-19. The research here refers to the existing SIR model, which was expanded to SEIR with the addition of the Exposed variable and SVIR with the addition of the Vaccinated variable (Overton et al., 2020; Etbaigha et al., 2018; Witbooi et al., 2015; Jannah et al., 2021). The used data are determined by 4 variables data on new cases, recovered, died, and vaccination, which is recorded daily from Indonesian data taken from several resources published by the Indonesian government. Computing and visualization will be performed using Matlab, Microsoft Excel, and Tableau. Additionally, a data bank will also be created where all variables in all regions (provinces) in Indonesia are mined and collected and can be accessed by anyone through the Github platform for free for research purposes and others. The data bank was created on our own due to the difficulty of obtaining data on COVID-19 variables, which include deaths, new cases, recovered, vaccination, and others. Based on information circulating in society, the authors argue that the function of vaccines is not to slow the rate of COVID-19, but to reduce the risk of severe symptoms and death for people with COVID-19. Through this research, we examine the influence of vaccination rates on the growth rate of COVID-19 in Indonesia.

2. EXPERIMENTAL SECTION

2.1 Data Source

The article here will address the COVID-19 cases in the Indonesian population for a certain period. The data source initially was taken from https://www.worldometers.info/coronavirus/country/indonesia/. We use also data on COVID-19 cases, which are published by the Indonesian government,i.e. https://covid19.go.id/. In this link, we get only a figure describing each day of the COVID-19 cases in Indonesia. The given data cannot be analyzed directly by the used code. To use the information given by the figure each day, one needs to retype again for each case per day in excel such that we can have a data set related to Indonesian COVID-19 cases. The data are collected from March 2020-March 2022. However, we do visualization and analysis of the COVID-19 cases starting from January 2021. We visualize some data of COVID-19 cases in this article which are illustrated using Figure 1. Figure 2 depicts the number of people who are recovered from COVID-19 cases after infected in the period January-December 2021. The number of Indonesian people who are dead is shown in Figure 3 in the same period. This figure shows that the maximum increment of death of people infected by COVID-19 cases occurred in July 2021.

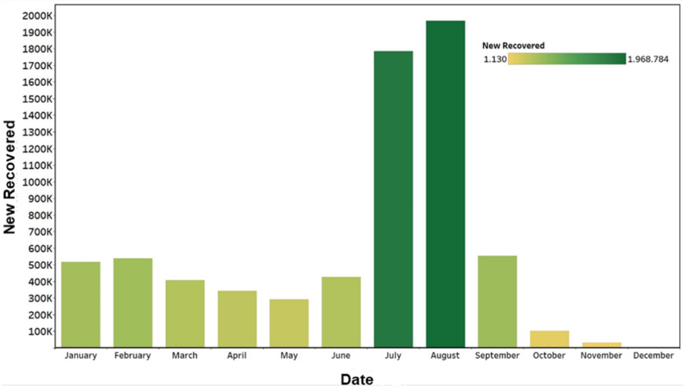


Figure 1. The Number of Recovered from COVID-19 Where the Vertical Line Describes the New Cases of Each *X*-Thousand (Denoted by *K* After the Number) and the Horizontal Line Indicates the Months to Do Observation, i.e. January-December 2021

Other features such as COVID-19 cases for the number of dead people and the number of vaccinated can also be drawn in different ways to get the first outlook on-the distribution of the population who were dead and vaccinated. Figure 3 uses a pie chart to illustrate the number of dead people who were caused by COVID-19. In August 2021, we obtained the maximum number. One may conclude that this result relates to the case of the maximum number who were infected in July 2021.

The vaccinated persons were not yet presented in the graphic. As one may observe in the national news about COVID-19 cases in Indonesia that the vaccination program was intensively started in early 2022. The authors here have referred to the particular link to obtain the number of vaccinated persons of COVID-19 in Indonesia, i.e. https://ourworldindata.org/covid-vaccinations. In the modeling and analysis below, we extend the data above until March 2022, since the data of vaccinated persons can be obtained regularly in that period.

2.2 SIR Model for COVID-19 Cases in Indonesia

The SIR model has been used by several authors to describe the behavior of spreading viruses in several cases including for COVID-19 cases (Bagal et al., 2020; Britton et al., 2020; Cooper et al., 2020; Pambuccian, 2020). SIR model explains the spread of disease from susceptible individuals to infected, then infected individuals will be recovered. In the SIR model, susceptible is a person who is sick (S), infected is a person who is infected or transmits the disease (I), and recovered is a person who is free from disease (R) which is shown in Figure 4 (Overton et al., 2020).

This model considers the following assumptions:

a. Closed population and constant individuals
b. The population is homogeneous
c. The birth and death rates at times t are neglected
d. There is only one disease that spreads

By considering these assumptions, the SIR model can be for-

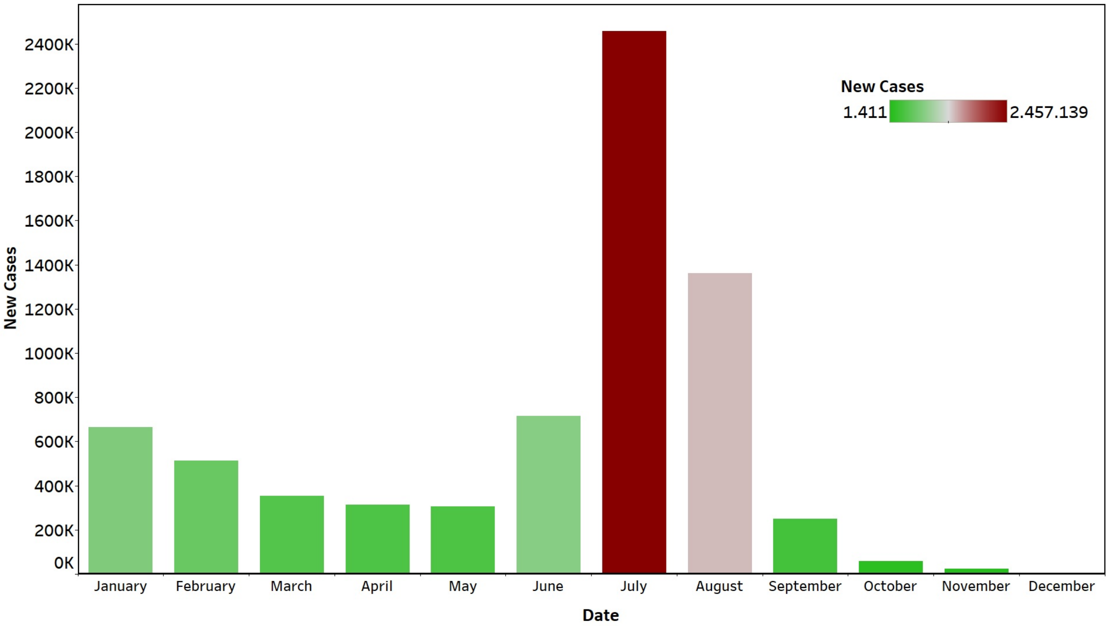


Figure 2. The Number of Infected People with COVID-19 Cases Where the Horizontal Describes the New Cases of Each X-Thousand (Denoted by K After the Number)

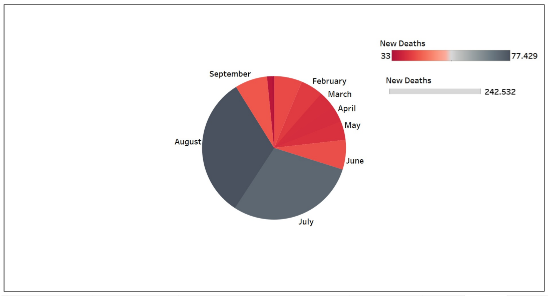


Figure 3. The Number of Dead People to COVID-19 Cases in Indonesia in the Year 2021

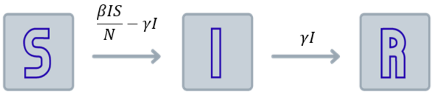


Figure 4. Transfer Diagram of the State of the SIR Model

mulated as follows

$$\frac{dS}{dt} = -\frac{\beta IS}{N} \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

where β is the contact rate, and $1/\gamma$ is the average infection over time. Since the total population is N, so it implies

$$N = S + I + R = \text{constant} \tag{4}$$

Denote that the initial values for S, I, and R anre $S(0)= S_0$, $I(0)= I_0$, $R(0)= R_0$ in time t, respectively. Eliminate I from Equations (1)–(3):

$$S = S_0 \exp\left[-\frac{\beta}{N\gamma}(R - R_0)\right] \tag{5}$$

When t goes to ∞ the number of remaining suspects is:

$$S_\infty = S_0 \exp\left[-\frac{\beta}{N\gamma}(R_\infty - R_0)\right] \tag{6}$$

The value R_∞ means the last number R (cured + died) and the last number of infected people is zero, then Equations (4) and (6) apply to:

$$N = S_\infty + R_\infty \tag{7}$$

$$R_\infty = N - S_0 \exp\left[-\frac{\beta}{N\gamma}(R_\infty - R_0)\right] \tag{8}$$

For the model to be usable, it is necessary to estimate the model parameters, β, γ, and the initial values S_0 and I_0 from the available data (given the values R_0= 0 and I_0= 0).

The data that needs to be prepared is a time series of total cases named C, where C= I+R. Estimation of parameters and initial values is to minimize the difference between the actual and predicted numbers in many cases, so that: $\|C_t\text{-}\hat{C}_t(\beta, \gamma, S_0)\|^2$= minimum, where C_t= $(C_1, C_2, C_3, \cdots, C_n)$ is the number of cases at time $t_1, t_2, t_3, \cdots, t_n$ and $\hat{C}_t$= $(\hat{C}_1, \hat{C}_2, \hat{C}_3, \cdots, \hat{C}_n)$ corresponds to the calculated estimation in the model.

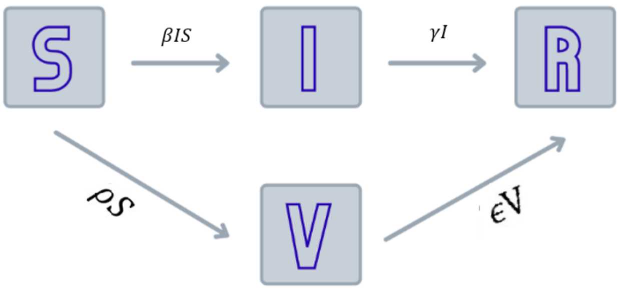


Figure 5. Transfer Diagram of the State of the SVIR Mathematical Model

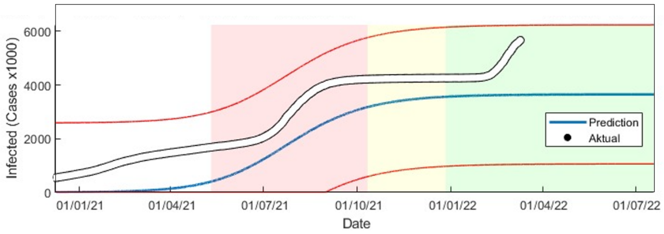


Figure 6. SIR Model Using Data Indonesian Covid-19 Cases 1^{st} January 2021-to 4^{th} March 2022 Using R= 0.71, R_0= 1.36, β= 0.107, γ= 0.078, N= 7.62079×10^6, C_{end}= 3.65304×10^6, S_{end}= 3.96735×10^6, RMSE= 866,637

2.3 SVIR (Susceptible-Vaccine-Infected-Removed) Model

The second used model in the spread of the COVID-19 virus is the SVIR (Susceptible Vaccine Infected Removed). This model is derived as an extension of the SIR (Susceptible Infected Removed) model for the spread of the COVID-19 virus. Before doing the modeling, we need to define the assumptions used in the research because assumptions are so basic that, without them, the research problem itself could not exist (Leedy and Ormrod, 2019; Simon, 2011). The following are the used assumptions, namely:

1. It is assumed that the birth rate and death rate in the considered period are constant, so there are no births or deaths
2. The number of COVID-19 cases is only counted in Indonesia, and there are no cases outside Indonesia
3. Individuals will be infected if they interact with infected individuals, either directly or indirectly
4. Individuals who recover from COVID-19 will not be infected again
5. Vaccination is not necessary twice to be counted
6. It is assumed that individuals who have been vaccinated will not be infected with the COVID-19 virus

Furthermore, the variables and parameters used in the COVID-19 spread model with vaccination will be determined, namely:

$N(t)$: Total population at the time t
$S(t)$: The number of vulnerable populations at the time t
$I(t)$: The number of people infected at the time t

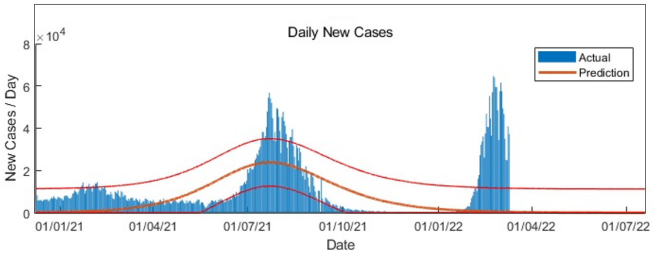


Figure 7. Daily New Cases for SIR Model Using Data Indonesian COVID-19 Cases 1^{st} January 2021-to 4^{th} March 2022 Using R= 0.71, R_0= 1.36, β= 0.107, γ= 0.078, N= 7.62079×10^6, C_{end}= 3.65304×10^6, S_{end}= 3.96735×10^6, RMSE= 866,637

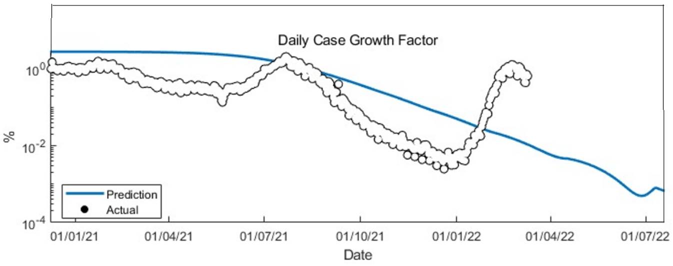


Figure 8. Daily Cases of Growth Factor for SIR Model Using Data Indonesian COVID-19 Cases 1^{st} January 2021-to 4^{th} March 2022 Using R= 0.71, R_0= 1.36, β= 0.107, γ= 0.078, N= 7.62079×10^6, C_{end}= 3.65304×10^6, S_{end}= 3.96735×10^6, RMSE= 866,637

$R(t)$: The number of people who recovered from COVID-19 and who died from COVID-19 at the time t
$V(t)$: The rate of the population who have been vaccinated at the time t
β: The rate of growth of the population infected with COVID-19
ρ: The rate of movement of the vulnerable population to the population who has vaccination
γ: The rate of movement from the infected population to the Removed population (cured or dead) from COVID-19
ϵ: The rate of transfer of vaccinated and uninfected individuals to removed individuals

We propose the SVIR model as the extension of the SIR model where vaccination is taken into account in the model. The diagram model in Figure 5 is developed to figure out the idea of this extension which shows the novelty of this article.

Figure 5 shows the SIR mathematical model with vaccination and it is called the SVIR model. Thus, from the diagram above, a mathematical model can be formed in the following system of nonlinear ordinary differential Equations (Sundnes, 2020), i.e:

$$\begin{aligned}
\frac{dS}{dt} &= -\frac{\beta SI}{N} - \rho S \\
\frac{dI}{dt} &= -\frac{\beta SI}{N} - \gamma I \\
\frac{dR}{dt} &= \gamma I + \epsilon V \\
\frac{dV}{dt} &= \rho S + \epsilon V
\end{aligned} \tag{9}$$

Note that all parameters are functions of time in this research. To be able to calculate the parameters, and from the data that has been collected, the left-hand side of Equation (9) can be written discretely for each i-th variable as follows:

$$\frac{dS}{dt} = \frac{\Delta S_i}{\Delta t}, \frac{dI}{dt} = \frac{\Delta I_i}{\Delta t}, \frac{dR}{dt} = \frac{\Delta R_i}{\Delta t}, \frac{dV}{dt} = \frac{\Delta V_i}{\Delta t} \tag{10}$$

Since the vaccinated population will form an immunity for one month after complete vaccination, the value of $\epsilon_{i+1}V_i$=$\rho_i V_{i-1}$. By using the application of the standard difference numerical method, it is obtained that:

$$\frac{\Delta S_i}{\Delta t} = -\frac{\beta_{i+1}}{N} S_i I_i - \rho_{i+1} S_i, \Delta S_{i+1} = S_{i+1} - S_i, \tag{11}$$

$$\frac{\Delta I_{i+1}}{\Delta t} = -\frac{\beta_{i+1}}{N} S_i I_i - \gamma_{i+1} I_i, \Delta I_{i+1} = I_{i+1} - I_i, \tag{12}$$

$$\frac{\Delta R_{i+1}}{\Delta t} = \gamma_{i+1} I_i + \epsilon_i V_{i-1}, \Delta R_{i+1} = R_{i+1} - R_i, \tag{13}$$

$$\begin{aligned}\frac{\Delta V_{i+1}}{\Delta t} &= \rho_{i+1} S_i - \epsilon_{i+1} V_i = \rho_{i+1} S_i - \rho_i V_{i-1}, \Delta V_{i+1} \\ &= V_{i+1} - V_i\end{aligned} \tag{14}$$

2.4 Discretization of the SVIR Model Into a Linear Equation and the Reproduction Number

Numerically, we can write: $S(t+\Delta t)= S_{i+1}$, $S(t)= S_i$ and other variables follow similarly, i.e. $I(t+\Delta t)= I_{i+1}$, $I(t)= I_i$, $R(t+\Delta t)= R_{i+1}$, $R(t)= R_i$, $V(t+\Delta t)= V_{i+1}$, $V(t)= V_i$. Therefore discretization can be employed in Equation (9) leading to the linear system for computing the parameters for each iteration. This means that the parameters in the SVIR model can be determined by solving the linear system for each Δt. Suppose taken Δt= 1, Equation (11)-(14) become:

$$-\frac{\beta_{i+1}}{N} S_i I_i - \rho_{i+1} S_i = \Delta S_{i+1} = S_{i+1} - S_i, \tag{15}$$

$$-\frac{\beta_{i+1}}{N} S_i I_i - \gamma_{i+1} I_i = \Delta I_{i+1} = I_{i+1} - I_i, \tag{16}$$

$$\gamma_{i+1} I_i + \epsilon_i V_{i-1} = \Delta R_{i+1} = R_{i+1} - R_i, \tag{17}$$

$$\begin{aligned}\rho_{i+1} S_i - \epsilon_{i+1} V_i &= \rho_{i+1} S_i - \rho_i V_{i-1}; \Delta V_{i+1} \\ &= V_{i+1} - V_i\end{aligned} \tag{18}$$

Simplifying the notation of parameters and collecting the known variables from Equations (15)-(18), one yield

$$\frac{\beta}{N}\begin{bmatrix} -S_i I_i \\ S_i I_i \\ 0 \\ 0 \end{bmatrix} + \rho \begin{bmatrix} -S_i \\ 0 \\ 0 \\ S_i \end{bmatrix} + \gamma \begin{bmatrix} 0 \\ -I_i \\ I_i \\ 0 \end{bmatrix} + \epsilon \begin{bmatrix} 0 \\ 0 \\ -V_i \\ V_i \end{bmatrix} = \begin{bmatrix} S_{i-1} - S_i \\ I_{i-1} - I_i \\ R_{i-1} - R_i \\ V_{i-1} - V_i \end{bmatrix} \tag{19}$$

Thus the obtained linear Equations are as follows:

$$\begin{bmatrix} -S_i I_i & -S_i & 0 & 0 \\ S_i I_i & 0 & -I_i & 0 \\ 0 & 0 & I_i & -V_i \\ 0 & S_1 & 0 & V_i \end{bmatrix} \begin{bmatrix} \frac{\beta}{N} \\ \rho \\ \gamma \\ \epsilon \end{bmatrix} = \begin{bmatrix} S_{i-1} - S_i \\ I_{i-1} - I_i \\ R_{i-1} - R_i \\ V_{i-1} - V_i \end{bmatrix} \tag{20}$$

Let us denote

$$A = \begin{bmatrix} -S_i I_i & -S_i & 0 & 0 \\ S_i I_i & 0 & -I_i & 0 \\ 0 & 0 & I_i & -V_i \\ 0 & S_1 & 0 & V_i \end{bmatrix}, \vec{x} \begin{bmatrix} \beta \\ \rho \\ \gamma \\ \epsilon \end{bmatrix}, \text{and} \quad \vec{b} = \begin{bmatrix} S_{i-1} - S_i \\ I_{i-1} - I_i \\ R_{i-1} - R_i \\ V_{i-1} - V_i \end{bmatrix}$$

Therefore, Equation (20) can be solved and the values of parameters ρ, β, γ, and ϵ will be obtained for each iteration indicating that these parameters vary over time. Additionally, it must be checked that the matrix A above is not singular for each iteration. Then, the values of ρ, β, γ, and ϵ will change for every i and i+1 data pair. Therefore Equation (20) above will be solved as in the section below. As stated in the previous research Trihandaru et al. (2021), the reproduction number was formulated by the proportion of beta and gamma for the basic formula, though other formulations also have been proposed by other authors (Djilali and Bentout, 2021).

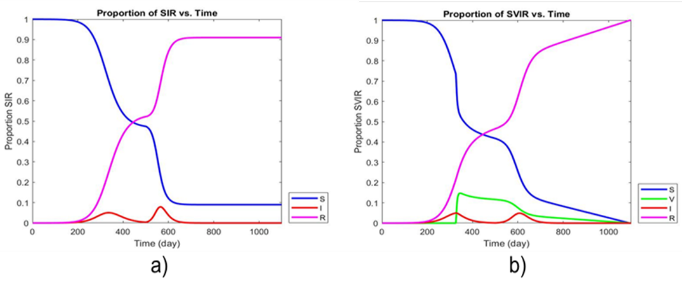
3. RESULTS AND DISCUSSION

3.1 Solutions of SIR Model and SVIR Model

For learning the first simulation, the authors are introducing the SIR model where the parameters are constants. These constants are initially given in the SIR model for illustrating the dynamic of each variable. In the real data of COVID-19 cases, these constants must be determined such that the SIR model is fitted to the real cases. Therefore, the SIR model here uses a set of training constants.

Figure 6-Figure 8 depict the first and second waves that have been modeled quite well. However, near the end, the third wave was not successfully modeled indicating underfitting. According to Emmert-Streib and Dehmer (2019) underfitting is a situation where the model has high bias and low variance or the model is said to be too simple. It was stated that underfitting is a fundamental problem that trips up even experienced data analysis (Koehrsen, 2018). We conclude that the SIR model needs to be further expanded by considering several variables and reducing assumptions.

Next, we will look for R_0 (Reproduction number) containing information on the spread of infectious disease outbreaks. Reproduction number is the average number of susceptible individuals infected (cases secondary) directly by another infected individual (primary case) in a susceptible population (Fajar and Padjadjaran, 2020; Giesecke, 2017). By computing



a) b)

Figure 9. The SIR Model (a) and the SVIR Model (b) Which Parameters Adjusted to Case of Indonesia Using Data Indonesian COVID-19 Cases 1^{st} January 2021-to 4^{th} March 2022 Using R= 0.71, R_0= 1.36, β= 0.107, γ= 0.078, N= 7.62079× 10^6, C_{end}= 3.65304×10^6, S_{end}= 3.96735×10^6, RMSE =866,637

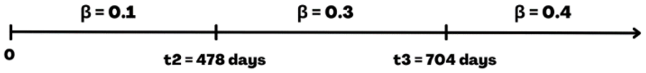


Figure 10. Time Plot of Intervention

R_0 using the formula R_0=$|\frac{\beta}{\gamma N}|$, then we get (R_0) of 1.36. This number states the number of susceptible individuals who are directly infected by infected individuals and is one indicator of an outbreak. The condition R_0 = 1.36>1 indicates that each infected individual will produce on average more than one new infected individual during the transmission period, so that the virus will attack the population, in other words, the virus will develop into an epidemic.

The next modeling is the addition of vaccinated variables and carried out in the conditions and phenomena that occur in Indonesia. The SVIR model with the assumptions described in section 2, is compared with the basic SIR model with the same parameters resulting in Figure 9.

There are two simple interventions which are timescales to describe two waves or large spikes in the growth of COVID-19 cases in Indonesia, which divides the entire modeling time into three parts. Intervention on the model has also been carried out by Sennott et al. (2016) and specifically in modeling the future of the pandemic (Kretzschmar et al., 2022). The intervention referred to here is shown in Figure 10 and the vaccination movement and its rate agree with the dynamic of the wave of infection cases.

In mid-May or 478 days since the first COVID-19 was detected, the second wave of COVID-19 cases occurred. Similarly, at the beginning of 2022, or 704 days, the third wave began. The growth rate or parameter is set differently each period while still adjusting the situation in real terms based on the data.

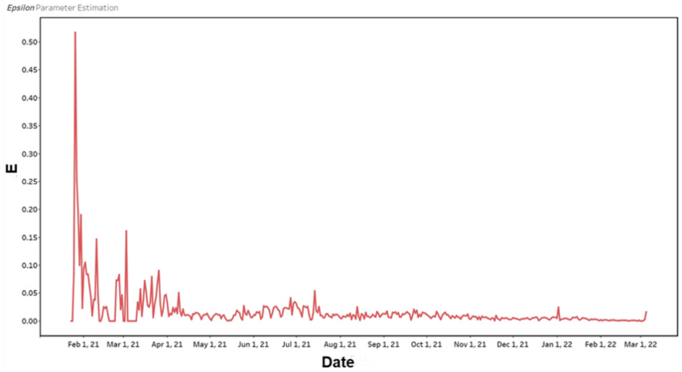


Figure 11. The Dynamic of Epsilon Parameter Estimation of SVIR Model Based on the Real COVID-19 Data Cases in Indonesia in Period 13^{rd} January 2021–2^{nd} March 2022. The Values are Obtained by Solving Equation (20)

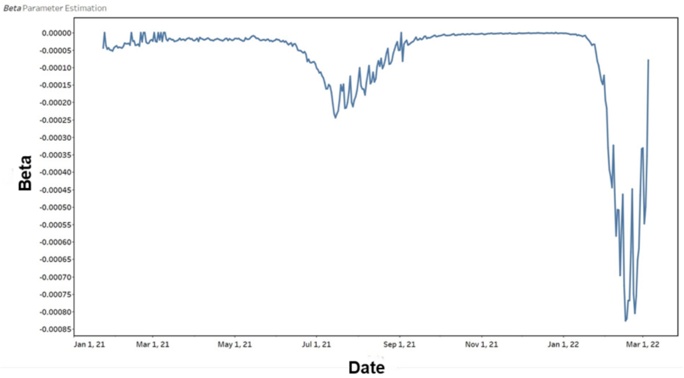


Figure 12. The Dynamic of Beta Parameter Estimation of SVIR Model Based on the Real COVID-19 Data Cases in Indonesia in Period 13^{rd} January 2021–2^{nd} March 2022. The Values are Obtained by Solving Equation (20)

3.2 The Parameters of the SVIR Model

Since the matrix is not singular for each iteration in Equation (20), we can use the OLS (Ordinary Least Square) because OLS point estimates are assumed to be unbiased in a properly specified model forming OLS has the following steps (Huang, 2018): Multiply the left and right sides by the transpose of matrix A which is symbolized by A^T, so the Equation $A\vec{x}$= $\vec{b}$ becomes A^T $A\vec{x}$= $A^T\vec{b}$. By inverting both sides of the matrix (assuming A^T A has an inverse) then the following equation is obtained:

$$\vec{x} = (A^T A)^{-1} A^T \vec{b} \tag{21}$$

Now, the two models are compared. The SIR model shows that the S variable is constant after the third wave and no longer shows the rate of decline. This result describes unreasonably meaning vulnerable people are still the same. On the other hand, all components in the SVIR model provide reasonable values. Additionally, the SVIR model predicts that the situation

Table 1. Descriptive Statistics for the Estimated Parameter Values

	Computed in all period				Computed from 3^{rd} September 2021–2^{nd} March 2022 (horizontal) where N= 20,000,000
	β	γ	ρ	ϵ	R_0
Mean	7.876×10^{-5}	9.671×10^{-10}	5.278×10^{3}	0.0165	0.584
Standard deviation	0.000151719	9.3263×10^{-10}	6432.510993	0.0359367	0.431
Maximum	8.258×10^{-4}	8.942×10^{-9}	3.080×10^{4}	0.5170	4.86

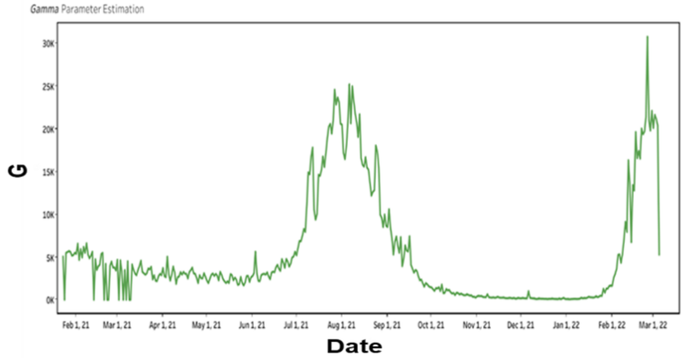


Figure 13. The Dynamic of Gamma Parameter Estimation of SVIR Model Based on the Real COVID-19 Data Cases in Indonesia in Period 13^{rd} January 2021–2^{nd} March 2022

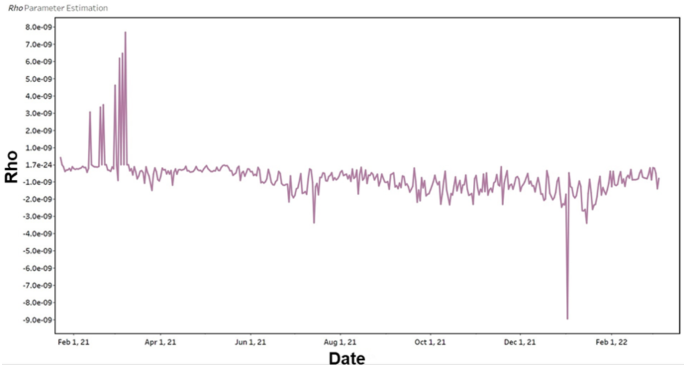


Figure 14. The Dynamic of Rho Parameter Estimation of SVIR Model Based on Real COVID-19 Data Cases in Indonesia in Period 13^{rd} January 2021–2^{nd} March 2022

of many vulnerable people is closer to zero on the 1000^{th} day and after, which means after (max) 1000^{th} days we will move to endemic. Here, the government can initiate efforts in the transition from pandemic to endemic and revoke the status of the pandemic by getting attention to the Suspect variable in the modeling graph. Finally, the estimation results using the method described above and the application of OLS, the dynamic parameters concerning time are depicted in Figure 11-Figure 15.

Consider those parameters illustrated in Figure 11-Figure 15. The behavior of 3 waves in the real data is captured by the Gamma parameter shown in Figure 13. Critical situations are also depicted in the same period for all parameters, i.e. January 2022-March 2022 except for the epsilon parameter tends to zero. The rate of reproduction number is decreasing in the period February 2021-July 2021 and again increasing with a higher maximum than before in the period July 2021-September 2021. As we also noticed in real data, the reproduction number is decreasing from September 2021 until February 2022 indicating the vaccination reducing the number of infected people. Though there exists a slowly increasing rate of the reproduction number from February 2021-March 2022, the rate of change is not as high as in the previous period. Unfortunately, the data in April 2022 have not contributed to the model, such that we cannot identify its behavior after April 2022. We observe that the COVID-19 cases and its variant are not frequently reported indicating the reduction in reproduction numbers in society. In this article, we can only provide descriptive statistics on the acquisition of each parameter and the values are presented in Table 1.

The mean, standard deviation, and maximum reproduction number shown in Table 1 describe the behavior of the COVID-19 cases in 3 periods where the maximum reproduction number occurred in the period January-March 2022. This agrees with the real data of COVID-19 cases in the Indonesian population in this period. The third wave of COVID-19 cases such as Omicron infected some people in Indonesia vary rapidly. Therefore the SVIR model has shown a better model for COVID-19 cases in Indonesia in the period January 2021-March 2022 indicating the objective of this research is satisfied, i.e. using the vaccination to be the considered variable to develop the SVIR model as the novelty of this article.

The SVIR model is a model of ordinary differential equations which is normally discussed its stability as the global dynamics of the system (Djilali and Bentout, 2021). In this article, we mimic the vaccine variable involves in the model to give a better approximation due to the latest development of the data where the vaccine variable takes place. The result here can be used for further research where the user data are taken from different regions or districts in Indonesia to provide analysis

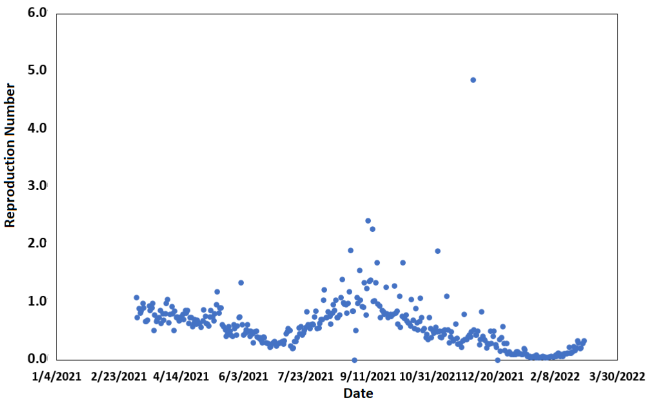


Figure 15. The Dynamic of Reproduction Number Estimation Per Day of SVIR Model (Vertical) Based on Real COVID-19 Data Cases in Indonesia in the Period February 2021–March 2022 (Horizontal) Where N= 20,000,000

for each district.

4. CONCLUSIONS

This article describes the modeling of SIR (Susceptible, Infected, and Removed) and SVIR (Susceptible, Vaccine, Infected, and Removed) for data on COVID-19 cases in Indonesia within the period January 2021-March 2022. The results show that the vaccination variable has provided better results compared to the basic SIR model. Additionally, the SVIR model also provides a more logical graphic or illustration for the same parameters and conditions compared to the SIR model. Therefore, the SVIR model provides a better model than the SIR model. Finally, we conclude that the four parameters of the SVIR model are well estimated since the values can be iteratively computed for each iteration. Thus, the estimation of SVIR parameters using the OLS (Ordinary Least Square) produces well-estimated parameters.

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