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SUSCEPTIBLE VACCINATED INFECTED RECOVERED SUSCEPTIBLE MODEL: EQUILIBRIA POINTS AND APPLICATION ON COVID-19 CASE DATA IN INDONESIA

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ABSTRACT

Severe Respiratory Syndrome Coronavirus-2 is the infectious agent that causes COVID-19. A vaccine program is an effort to stop the spread of COVID-19 infections in Indonesia. The susceptible vaccinated infected recovered susceptible (SVIRS) model can be used to represent the spread of infectious diseases. This study aims to construct the SVIRS model, identify the equilibria points thus apply it to COVID-19 case data in Indonesia, and determine transmission patterns, model accuracy, and interpretation. Literature and applications are the research methodologies employed. First-order nonlinear differential equations form the obtained SVIRS model. The model has two equilibrium points: a disease-free equilibrium point, and the other is endemic equilibrium point. The SVIRS model on the spread of COVID-19 in Indonesia was obtained using daily secondary data from January 11 to November 30, 2022. The model is solved by the fourth-order Runge-Kutta method. The model's accuracy is accurate enough to explain the spread of COVID-19 in Indonesia with a mean average percentage error (MAPE) value of 43%. According to the transmission pattern, the number of COVID-19 cases in Indonesia peaked on July 27, 2022, then decreased to zero, obtaining an equilibrium point when no more cases of the disease were present.

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1. INTRODUCTION

Diseases known as infectious diseases are those that can be spread from one human to another and are brought on by microbes like viruses, bacteria, fungi, or parasites. Direct and indirect contact both have the potential to transmit disease. With a vaccine program, COVID-19 can be prevented from spreading. Coronavirus disease 2019 or COVID-19 is an infectious disease caused by the Severe Acute Respiratory Syndrome Coronaviruses-2 (SARS CoV-2) virus. According to WHO [1], COVID-19 can be transmitted through an infected person's mouth or nose in small fluid particles when coughing, sneezing, talking, or breathing. COVID-19 is an endemic infectious disease, which is a disease that spreads in a certain area for more than one year. Therefore, efforts are needed to reduce COVID-19 cases. Aside from reducing contact with infected individuals through quarantine and social distancing, efforts to prevent the spread of COVID-19 can be made by increasing the body's immunity through vaccination programs.

The spread of infectious diseases can be represented in the mathematical model. The model is susceptible infected recovered (SIR) model. The population is divided into three categories in the model: susceptible (S) individuals are those in good health who are susceptible to infection, infected (I) individuals are those who have the disease and can transmit it, and recovered (R) individuals are those who have recovered from the disease. Kermack and McKendrick [2] were the first to present the SIR model. Hethcote [3] also researched the SIR model for several kinds of infectious diseases, such as diphtheria and measles. Then, Liu et al. [4] constructed the susceptible vaccinated infected recovered (SVIR) model with the effect of vaccination, where those in the vaccination (V) compartment are those who have received the vaccine. The SVIR model has been the topic of many research studies. Islam [5] focused on the SVIR model with a population that is not constant, Henshaw and McClusky [6] analyzed it with immigration, Aryani and Widyaningsih [7] discussed it with vaccine failure and effectiveness, Husnulkhotimah [8] discussed it with immunity to the disease is not life-long, and Liu and Ding [9] analyzed it with time delay. In addition, the SVIR model is also applied to several infectious diseases-, for example, Tuberculosis [10], [11], Measles [12], Diphtheria [13], and Influenza [14].

Similar to Liu et al. [4], the population was considered to be constant in this study and migration factors were not taken into consideration. In contrast to Islam [5], the vaccine targets used in this research are individual S and individual R to formulate the SVIRS model. Then the model was applied to the spread of COVID-19 disease in Indonesia.

2. RESEARCH METHODS

The methods used in this research are literature and applied studies. The literature study: identify the infected disease characteristics, change and add assumptions, add parameters on the SIR model, and define new compartment V so that formed SVIRS model. Next, determine the equilibria points of the SVIRS model. Daily secondary data from the *Satuan Tugas Penanganan* COVID-19 [15] and Worldometer [16] were used in the applied study, which ranged from January 11th through November 30th, 2022. The flowchart of the research method in Figure 1 shows the steps of the research in more detail.

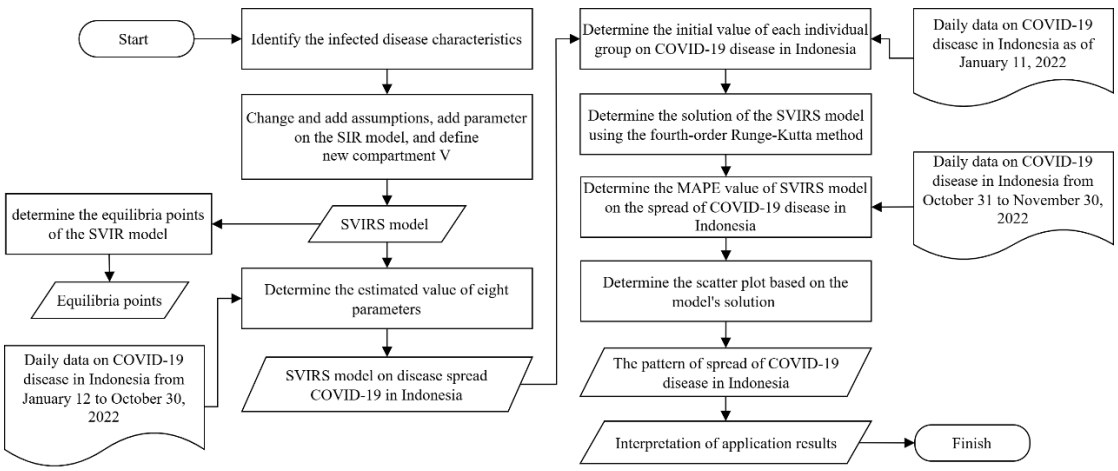


Figure 1. Research Method Flowchart

3. RESULTS AND DISCUSSION

This section presents the formulation of the SVIRS model, equilibria points, and application of the model in data on the spread of COVID-19 disease in Indonesia.

3.1 SVIRS Model

Formulation of an SVIR model based on the SIR model by Hethcote [17]. Similar to Hethcote [17], this model population is assumed to be constant (N) without considering migration factors. Thus, the natural death rate (μ) equals the birth rate. In this research, we consider the death rate due to disease, so if δ is the death rate due to disease, then the number of individuals I decrease by δI.

A vaccination program is an attempt to prevent the spread of disease infectious. In 2008, Liu et al. [4] formulated a SIR model with the effect of vaccination called the SVIR model. Individual S is the vaccine's target in the model. People who have been infected and recovered from some infectious diseases can get vaccinated again to boost immunity. Thus, different from Liu et al. [4], in this study, the initial assumption that the vaccine target was only individual S changed to the vaccine target was individual S and individual R. If the vaccination rate of individuals S and R is θ then the number of vaccinated individuals is θ(S+R). In addition, it is also assumed that the success of vaccination is 100%, so the vaccination rate is only determined by the percentage of the number of individuals vaccinated. Thus, every vaccinated individual will definitely not be infected within a certain period. Similar to Aryani and Widyaningsih [7], in this research also considered the end of vaccine effectiveness. If λ is the end of the vaccine effectiveness rate then as many λV individuals V lose vaccine effectiveness and become individuals S. But unlike with Aryani and Widyaningsih [7], in this research assumed that individuals R only had temporary immunity. If the body immunity waning rate is σ then the number of recovered individuals who are again susceptible is σR. So, the number of individuals R decreases by σR and the number of individuals S increases by σR. Thus, the SVIRS model on the spread of infectious diseases is written as

$$\begin{aligned} \frac{dS}{dt} &= \mu N + \lambda V + \sigma R - \beta \frac{SI}{N} - \theta S - \mu S, \\ \frac{dV}{dt} &= \theta(S+R) - \lambda V - \mu V, \\ \frac{dI}{dt} &= \beta \frac{SI}{N} - \gamma I - \delta I - \mu I, \\ \frac{dR}{dt} &= \gamma I - \sigma R - \theta R - \mu R. \end{aligned} \tag{1}$$

with $S(0) \geq 0, V(0) \geq 0, I(0) > 0, R(0) \geq 0$ and parameters $\mu, \beta, \gamma, \delta, \theta, \lambda, \sigma > 0$. These parameters in a row are the rate of natural birth/death, contact rate, recovery rate, death rate due to the disease, vaccine rate, end-of-vaccine effectiveness rate, and body immunity waning rate. SVIRS **Equation (1)** is a first-order nonlinear differential equation system with independent variable t and dependent variables S, V, I, and R. Where S(t), V(t), I(t), and R(t) are the number of individuals in each group at the time t, such that $S(t) + V(t) + I(t) + R(t) = N$.

3.2 Equilibria Points

According to Meyer [18], a dynamic system is said to be in equilibrium condition if it does not change as time proceeds. Mathematically the absence of change in **Equation (1)** is expressed by

$$\begin{aligned} \frac{dS}{dt} &= 0, \\ \frac{dV}{dt} &= 0, \\ \frac{dI}{dt} &= 0, \end{aligned} \tag{2}$$

$$\frac{dR}{dt} = 0.$$

By considering the **Equation (2)** and **Equation (1)**, it obtained a system of nonlinear equation

$$\begin{aligned} \mu N + \lambda V + \sigma R - \beta \frac{SI}{N} - \theta S - \mu S &= 0, \\ \theta(S + R) - \lambda V - \mu V &= 0, \\ \beta \frac{SI}{N} - \gamma I - \delta I - \mu I &= 0, \\ \gamma I - \sigma R - \theta R - \mu R &= 0. \end{aligned} \tag{3}$$

There are two equilibria points of the **Equation (3)**.

1. $E_0 = (S_0, V_0, I_0, R_0) = \left(\frac{N(\lambda+\mu)}{\theta+\lambda+\mu}, \frac{N\theta}{\theta+\lambda+\mu}, 0, 0\right).$ (4)

   The value of $I_0 = 0$. It means that no more infected individuals so that there is no spread of the disease all the time in the population. Therefore, E_0 is called the disease-free equilibrium point.

2. $E = (S, V, I, R)$
   with,

$$S = \frac{N(\gamma + \delta + \mu)}{\beta},$$

$$V = \frac{N\theta\left(\beta\gamma\mu + \gamma(\delta+\mu)(\theta+\mu+\sigma) + (\delta+\mu)^2(\theta+\mu\sigma)\right)}{\beta\left(\gamma\mu(\theta+\lambda+\mu) + \delta(\lambda+\mu)(\theta+\mu+\sigma) + \mu(\lambda+\mu)(\theta+\mu+\sigma)\right)},$$

$$I = -\frac{N\mu\left(-\beta(\lambda+\mu) + (\gamma+\delta+\mu)(\theta+\lambda+\mu)\right)(\theta+\mu+\sigma)}{\beta\left(\gamma\mu(\theta+\lambda+\mu) + \delta(\lambda+\mu)(\theta+\mu+\sigma) + \mu(\lambda+\mu)(\theta+\mu+\sigma)\right)},$$

$$R = -\frac{N\gamma\mu\left(-\beta(\lambda+\mu) + (\gamma+\delta+\mu)(\theta+\lambda+\mu)\right)}{\beta\left(\gamma\mu(\theta+\lambda+\mu) + \delta(\lambda+\mu)(\theta+\mu+\sigma) + \mu(\lambda+\mu)(\theta+\mu+\sigma)\right)}.$$

The value of $I, R > 0$, with $(\gamma + \delta + \mu)(\theta + \lambda + \mu) < \beta(\lambda + \mu)$. It means that are still infected individuals so this point is called the endemic equilibrium point.

3.3 Application Model

In this section, the **Equation (1)** is applied to data on COVID-19 in Indonesia. Daily secondary data from January 12th – October 30th, 2022 were used to estimate parameter values. The natural birth/death rate is determined by crude birth rate (CBR) sourced from Worldometer **[16]**, the contact rate is determined by the number of new cases, the recovery rate is determined by the number of recovered individuals divided by the number of infected individuals, the death rate due to the disease is determined by the number of deaths due to COVID-19, and the vaccination rate is determined by the number of vaccinated individuals divided by the number of susceptible individuals (S) and recovered individuals (R). Data on the number of new cases, the number of recovered individuals, the number of infected individuals, the number of deaths due to COVID-19, and the number of vaccinated individuals sourced from the *Satuan Tugas Penanganan* COVID-19 **[15]**. Then, according to Doria-Rose et al. **[19]**, the COVID-19 vaccine can provide protection for 6 months, so that the end-of-vaccine effectiveness rate is determined through one divided period of vaccine effectiveness. Meanwhile, the rate of expiration of vaccine effectiveness sourced from Associate Director of the NCI's Surveillance Research Program (SRP) **[20]** is 3%. The estimation results of seven parameters are presented in **Table 1**.

Table 1. Estimated Value of Seven Parameters

Parameter	Definition	Value
μ	natural human birth/death rate	0.000047
β	contact rate	0.103488
γ	recovery rate	0.092820
δ	death rate due to the disease	0.000831
θ	vaccination rate	0.000843
λ	end of vaccine effectiveness rate	0.005556

σ	body immunity waning rate	0.030000

For these parameters in **Table 1**, model SVIRS for the spread of COVID-19 in Indonesia could be represented as

$$\begin{aligned}\frac{dS}{dt} &= 0{,}000047N + +0{,}005556V + 0{,}030000R - 0{,}1038488\frac{SI}{N} - 0{,}000843S - 0{,}000047S,\\ \frac{dV}{dt} &= 0{,}000843(S+R) - 0{,}005556V - 0{,}000047V,\\ \frac{dI}{dt} &= 0{,}103488\frac{SI}{N} - 0{,}092820I - 0{,}000831I - 0{,}000047I,\\ \frac{dR}{dt} &= 0{,}092820I - 0{,}030000R - 0{,}000843R - 0{,}000047R.\end{aligned} \tag{5}$$

with the initial values from the number of individuals S, V, I, and R on January 11th, 2022 that are

$$S(0) = 280.662.755, \quad V(0) = 1.657, \quad I(0) = 6.659, \quad R(0) = 446. \tag{6}$$

The solution of **Equation (5)** with initial value **Equation (6)** is determined using the Runge-Kutta method of fourth order. The MAPE value of the model numerical solution is 43%. It means the model is accurate enough to explain the spread of COVID-19 in Indonesia. The solution of the model is the pattern of the spread of COVID-19 disease in Indonesia. **Figure 2** and **3** are the number of individuals in each group S, V, I, and R for $0 \leq t \leq 3500$ days (January 11th, 2022-February 28th, 2032).

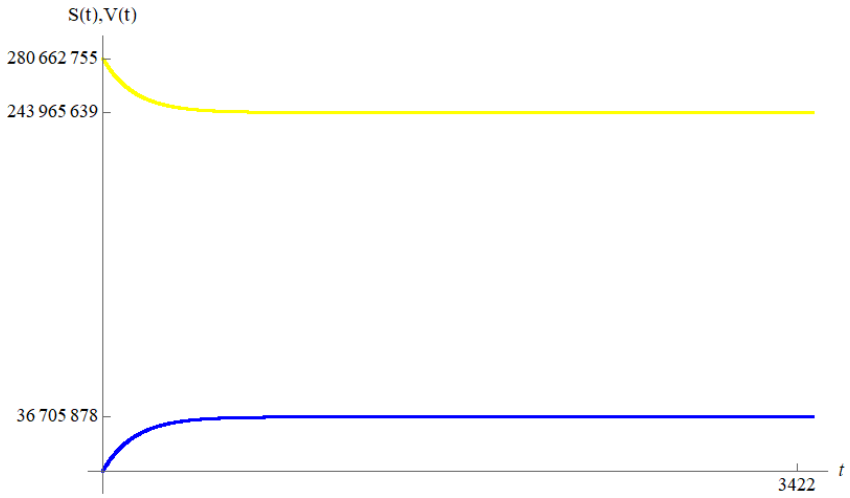


Figure 2. Scatter Plot of the Number of S (yellow) and V (blue) Individuals for 3500 days

Based on **Figure 2**, the number of susceptible individuals (S) decreases from the initial value (280.662.755 individuals) till the 3422nd day or May 26th, 2031 (243.965.639 individuals) then after the day it stays all the time. A decreasing number of S occurred due to susceptible individuals getting a vaccine, so became vaccinated individuals (V). The number of V increased to 36.705.878 on day 3422 or May 26th, 2031, and began to remain all the time due to the presence of individuals S and R receiving the vaccine then moved to V.

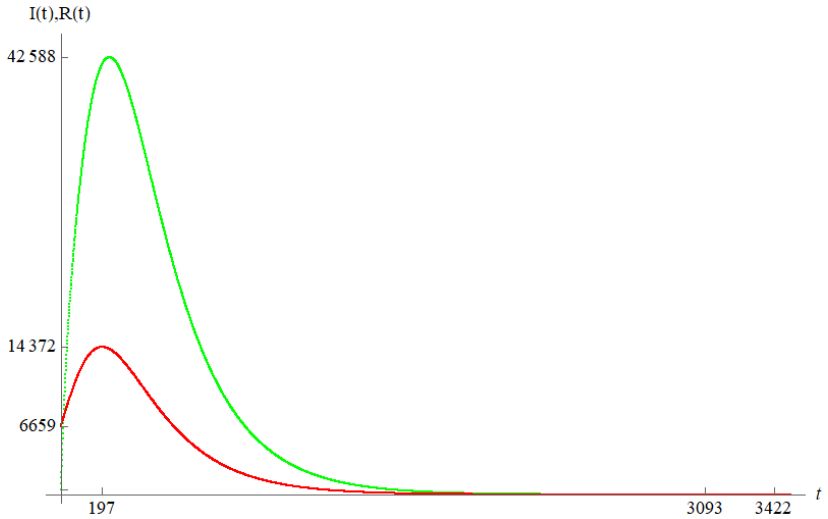


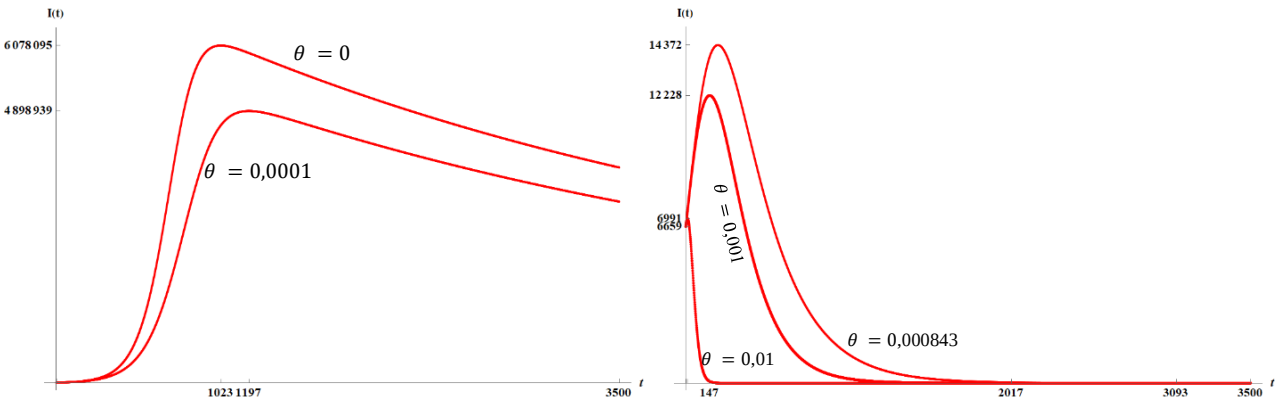
Figure 3. Scatter Plot of the Number of I (red) and R (green) Individuals for 3500 days

From **Figure 3**, appears that the number of infected individuals (I) increased to 14.372 individuals on the 197th day or July 27th, 2022. However, according to *Satuan Tugas Penanganan* COVID-19 **[15]**, there are still 46.024 individuals who are infected. This difference may exist because each person is unaware of the importance of vaccination. Additionally, this is comparable to the MAPE goodness of the model value, which is just enough accurate, therefore it makes sense that the value predicted is not equal to the facts. Then the number of I decreased to zero individuals on the 3093th day or July 1st, 2030 and the number has not changed over time. This means that no individuals have been infected with COVID-19. The number of R increases to 42.588 individuals and then decreases to zero individuals on the 3422nd day or May 26th, 2031, and does not change again all the time. The increase occurred because more individuals recovered from COVID-19 infection than recovered individuals who were vaccinated. Conversely, the decline occurred because recovered individuals were vaccinated and lost more immunity than infected individuals who recovered.

Starting on day 3422nd day or May 26th, 2031 the number of individuals S, V, I, and R remain constant at all times, so it can be said that the system is in equilibrium condition. The number of individuals S at equilibrium condition is 243.965.639, V is 36.705.878 individuals, and I and R is 0 individuals. Therefore, $E_0 = (S_0,\ V_0,\ I_0,\ R_0) = (243.965.639, 36.705.878, 0, 0)$ is a disease-free equilibrium point. It is the same if the point E_0 (4) calculated with parameter in **Table 1**. It indicates that when equilibrium conditions are no longer there are individual I so that Indonesia can be free from COVID-19 disease.

3.4 Simulation

Simulations were run for various values of the vaccination rate parameter (θ) using seven additional parameters similar to those used in the application section. Simulation of θ with four different value ranges: 0 (vaccination-free), 0,0001, 0,001, and 0,01. **Figure 4** shows the outcomes of the simulation.



(a) **(b)**

Figure 4. Scatter Plot of the Number of I Individuals for 3500 days
(a) $\theta = 0, \theta = 0.0001$ (b) $\theta = 0.001, \theta = 0.01$

Figure 4 shows that if there is no vaccination ($\theta = 0$), the number of infected individuals significantly increases up to 6,078,095 people on day 1197, or April 22, 2025. The existence of vaccination can prevent the spread of disease so that the number of infected individuals is reduced. The greater θ value, the faster it decreases the number of infected individuals. As a result, the vaccination program has an impact on reducing and even preventing the spread of COVID-19 disease in Indonesia.

4. CONCLUSIONS

Based on the study and application above, the following conclusions are obtained.

1. The SVIRS model for the spread of infectious disease is (1), which is a system of first-order nonlinear differential equations.
2. The SVIRS model has two equilibrium points, namely the disease-free equilibrium point and the endemic equilibrium point.
3. Based on the study and application of the COVID-19 disease shows that the peak of COVID-19 cases in Indonesia occurred on July 27th, 2022, and then decreased to zero individuals. The MAPE value is 43% which means the model is accurate enough to explain the spread of COVID-19 in Indonesia. The spread of COVID-19 in Indonesia has the disease-free equilibrium point $E_0 = (S_0, V_0, I_0, R_0) = (243.965.639, 36.705.878, 0, 0)$ so that Indonesia can be free from COVID-19 disease. Based on simulations, it was found that COVID-19 could disappear faster from Indonesia if the vaccination rate was greater (more individuals were vaccinated).

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