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MATHEMATICAL MODELLING OF THE OUTBREAK OF COVID-19: A CASE STUDY IN EAST JAVA

[1]Erna Setiawati, [2]Mardlijah

[1]Department of Mathematics, Institut Teknologi Sepuluh Nopember, Surabaya, Indonesia
[2]Department of Mathematics, Institut Teknologi Sepuluh Nopember, Surabaya, Indonesia

Email: [1]setiawati.erna689@gmail.com, [2]mardlijah@gmail.com

Abstract : Coronavirus disease (COVID-19) is an infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). In Indonesia, this case begin to develop since the end of February 2020 and until now there is still an increase in new infections. Several mathematical models of COVID-19 cases in Indonesia have been conducted, but the result are not yet fully accurate. This maybe due to different patterns in each region. The aim of this study is construct the Susceptible-Vaccinated-Infected-Recovered-Death (SVIRD) model for COVID-19, parameter estimation, stability analysis, and numerical simulation of the SVIRD model of the spread of COVID-19. The method used to estimate parameters is Kalman Filter, the analysis of the model uses the next generation matrix method to obtain the basic reproduction number and local stability of COVID-19 model. Numerical simulation model uses daily data of COVID-19 case in East Java. The estimation results of people infected by COVID-19 are close to actual value with a mean absolute percentage error (MAPE) value of 0.001%, so that the estimated value can be said to have a high level of accuracy. Therefore, the parameter estimation results can be used to predict the number of COVID-19 cases in East Java. In this study, the basic reproduction number is 1.1139 which indicate that East Java is in endemic of COVID-19. Sensitivity analysis is performed on the basic reproduction number and it can be concluded that the most sensitive parameters are the birth rate, the infection rate, and the proportion of individuals vaccinated twice.

Index Terms **- COVID-19, SVIRD Model, Basic Reproduction Number, Parameter Estimation, Kalman Filter, Sensitivity Analysis.**

I. INTRODUCTION

Infectious diseases are diseases caused by pathogenic microorganisms, such as bacteria, viruses, parasites or fungi; diseases can spread directly or indirectly from one person to another (WHO, 2015). One of the viruses that can cause infectious diseases is the corona virus. In December 2019, there were several cases of pneumonia with unknown causes in Wuhan, Hubei Province, China. In-depth sequencing analysis of lower respiratory tract samples revealed the presence of a new coronavirus called 2019 novel coronavirus (2019-CoV) (Huang, 2020). Then on February 11, 2020, WHO announced the official name for the disease, namely coronavirus disease (COVID-19) and the name of the virus that causes COVID-19 is severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The name of the virus was chosen because it is genetically related to the coronavirus that caused the SARS outbreak in 2003. SARS-CoV-2 is the seventh coronavirus known to infect humans; SARS-CoV, MERS-CoV and SARS-CoV-2 can cause severe illness, while HKU1, NL63, OC43 and 229E cause mild symptoms (Andersen, 2020).

COVID-19 can be transmitted through close human to human contact and based on the latest report from WHO, COVID-19 transmission includes droplet transmission, contact transmission, and aerosol transmission (Hu, 2020). COVID-19 is spread mainly through droplets of saliva or those that come out of the nose when an infected person sneezes (Lalwani, 2020). The spread of COVID-19 is very fast, one of which is caused by the large number of people traveling to and from China. On March 11, 2020, WHO declared COVID-19 a global pandemic and until now COVID-19 has spread to 47 countries including Indonesia.

COVID-19 was first detected in East Java on March 17, 2020. There were 6 positive cases of COVID-19 in East Java and all of them came from Surabaya. One day later, a positive case of COVID-19 was detected in Malang (detiknews, 2021). After that, positive cases of COVID-19 in East Java continued to increase from day to day until March 17, 2021, there were 135,464 positive confirmed cases and 9,549 people died. Efforts that can be made to tackle the spread of COVID-19 are implementing 3M (using masks, washing hands, and maintaining distance), quarantine, and Large-Scale Social Restrictions. These efforts have been made but in fact the positive cases of COVID-19 are still high. Currently a vaccine for COVID-19 has been found and phase 1 and phase 2 vaccinations are being carried out.

Many mathematical models of the spread of COVID-19 have been constructed and used to determine the dynamics of the spread of COVID-19, predict the peak of the COVID-19 pandemic, and when the COVID-19 pandemic will end. In addition, the results of the analysis of the mathematical model of the spread of COVID-19 can be used as a basis for taking a policy to reduce

the spread of COVID-19. In addition, the COVID-19 Cluster has been formed, one of which is to calculate the reproduction number. The reproduction number consists of two forms, namely the basic reproduction number (R_0) and the effective reproduction number (R_e). The reproduction number represents the average number of newly infected individuals due to the presence of one infected individual in the susceptible population. By calculating the basic reproduction number (R_0), it will be known that there will be endemic conditions or the disease will disappear from the population.

In section 2, we formulate a model and investigate all equilibrium points with their local stability in section 3. Section 4 is mathematical simulation part. In particular, we show the simulation results of estimated value and actual value of each population. Then in section 5 we provide sensitivity analysis to reproduction number to find out the most sensitive parameter to reproduction number.

II. Model Formulation

The SVIRD model of the spread of COVID-19 is divided into five compartments namely Susceptible (S), Vaccinated (V), Infected (I), Recovered (R), and Death (D). COVID-19 transmission dynamics can be interpreted in Figure 1.

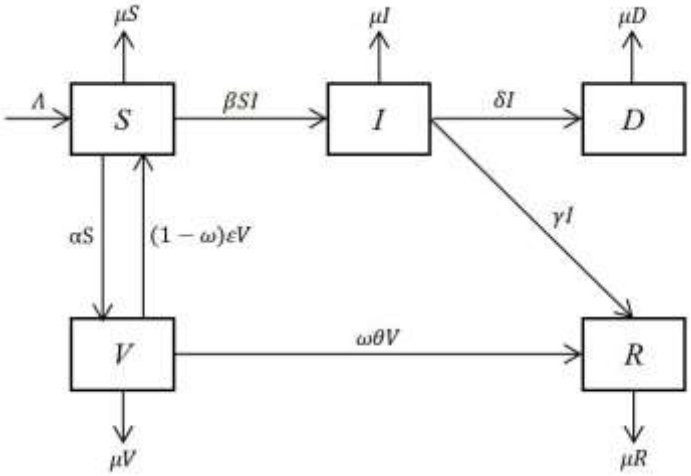

Figure 1: Compartmental Diagram for SVIRD Model Transmission of COVID-19

Based on compartmental diagram shown in Figure 1, the rate of change in the number of Susceptible, Vaccinated, Infected, Recovered, and Death population over time can be expressed as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda + (1-\omega)\varepsilon V - \beta SI - (\alpha+\mu)S \\
\frac{dV}{dt} &= \alpha S - \big((1-\omega)\varepsilon + \omega\theta + \mu\big)V \\
\frac{dI}{dt} &= \beta SI - (\gamma+\delta+\mu)I \qquad (1) \\
\frac{dR}{dt} &= \omega\theta V + \gamma I - \mu R \\
\frac{dD}{dt} &= \delta I - \mu D
\end{aligned}$$

Furthermore, in the system of Equation (1) the variable *R* and *D* do not appear in the other equations, which means that the number of individuals in the *R* and *D* compartments does not affect the rate of change of the number of individuals in the other compartments, so the *R* and *D* equations can be temporarily ignored from the system. Therefore, system of Equation (1) can be written as follows :

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda + (1-\omega)\varepsilon V - \beta SI - (\alpha+\mu)S \\
\frac{dV}{dt} &= \alpha S - \big((1-\omega)\varepsilon + \omega\theta + \mu\big)V \qquad (2) \\
\frac{dI}{dt} &= \beta SI - (\gamma+\delta+\mu)I
\end{aligned}$$

Definition of variables and parameters of SVIRD model for COVID-19 is presented in Table 1.

Table 1: Definition of Variable/ Parameter Used in Model

Variable/ Parameter	Definition
S	The number of Susceptible individuals at time t
V	The number of Vaccinated individuals at time t
R	The number of Recovered individuals at time t
I	The number of Infected individuals at time t
D	The number of Death individuals at time t
N	The total population at time t
Λ	Natural birth rate
β	Infection rate
γ	Recovery rate
δ	Death rate due to COVID-19
μ	Natural death rate
ε	The waning rate of the first dose of vaccine
θ	The rate of receiving second dose of vaccine
α	Proportion of individuals who receive the first dose of vaccine
ω	Proportion of individuals who are vaccinated twice
$(1-\omega)$	Proportion of individuals who are not vaccinated twice

III. Model Analysis

In this section, the system of Equations (2) is analyzed to find out the equilibrium points and then construct the basic reproduction number (R_0) to investigate the local stability of the equilibrium points. The system of Equation (2) has two equilibrium points, namely the disease free equilibrium point and the endemic equilibrium point. The equilibrium point of the system of Equations (2) can be obtained by setting :

$$\frac{dS}{dt} = \frac{dV}{dt} = \frac{dI}{dt} = 0$$

So, the system of Equations (2) can be written as :

$$\Lambda + (1-\omega)\varepsilon V - \beta SI - (\alpha+\mu)S = 0 \quad (3)$$

$$\alpha S - \big((1-\omega)\varepsilon + \omega\theta + \mu\big)V = 0 \quad (4)$$

$$\beta SI - (\gamma + \delta + \mu)I = 0 \quad (5)$$

1. Disease Free Equilibrium Point (DFE)

The disease free equilibrium point is the equilibrium point at which there is no disease in the population, so $I = 0$. Then $I = 0$ is substituted into Equation (3) and Equation (5) and we solve Equations (3-5), so we get the DFE point of the system of Equations (2) which is given by :

$$E_0(S,V,I) = ({S_0}^*, {V_0}^*, 0)$$

where ${S_0}^*$ and ${V_0}^*$ are given by Equation (6-7).

$${S_0}^* = \frac{\Lambda\big((1-\omega)\varepsilon + \omega\theta + \mu\big)}{\alpha(\omega\theta+\mu) + \mu\big((1-\omega)\varepsilon + \omega\theta + \mu\big)} \quad (6)$$

$${V_0}^* = \frac{\alpha\Lambda}{\alpha(\omega\theta+\mu) + \mu\big((1-\omega)\varepsilon + \omega\theta + \mu\big)} \quad (7)$$

2. Endemic Equilibrium Point (EE)

The endemic equilibrium point is the equilibrium point at which the disease spread in the population. Endemic disease means that in the population there are always individuals who are exposed to the disease, so the I at the endemic equilibrium point is ${I_1}^* > 0$. By solving Equations (3-5), we get the EE point of the system of Equations (2) which is given by :

$$E_1(S,V,I) = ({S_1}^*, {V_1}^*, {I_1}^*)$$

where ${S_1}^*, {V_1}^*$ and ${I_1}^*$ are given by Equation (8-10).

$${S_1}^* = \frac{\gamma + \delta + \mu}{\beta} \quad (8)$$

$$V_1^* = \frac{\alpha(\gamma+\delta+\mu)}{\beta\big((1-\omega)\varepsilon+\omega\theta+\mu\big)} \quad (9)$$

$$I_1^* = \frac{\big(\Lambda\beta-(\alpha+\mu)(\gamma+\delta+\mu)\big)\big((1-\omega)\varepsilon+\omega\theta+\mu\big)+\alpha\varepsilon(1-\omega)(\gamma+\delta+\mu)}{\beta(\gamma+\delta+\mu)\big((1-\omega)\varepsilon+\omega\theta+\mu\big)} \quad (10)$$

3. Basic Reproduction Number (R_0)

In this section, the basic reproduction is determined by finding the largest eigenvalue obtained using the next generation matrix method. The next generation matrix can be obtained from the infected subsystem equation. In the first step we derive equations that describe new infection cases and changes in the Infected compartment of the system. Furthermore, this system is called the infected subsystem. On the system of Equation (2), the infected subsystem are S and I. Then we rewrite the infected subsystem into the Equation (11) as follows :

$$\frac{dX}{dt} = T(X) - U(X) \quad (11)$$

where $T(X)$ and $U(X)$ are given by Equation (12-13).

$$T(X) = \begin{pmatrix} -\beta si \\ \beta si \end{pmatrix} \quad (12)$$

$$U(X) = \begin{pmatrix} (\alpha+\mu)s-(1-\omega)\varepsilon v-\Lambda \\ (\gamma+\delta+\mu)i \end{pmatrix} \quad (13)$$

In the Equation (11) , $T(X)$ is the disease transmission matrix (non-linear) and $U(X)$ is the transition matrix that describes the compartmental change (linear), where $X = (S, I)^T$.

In the second step, we determine the Jacobian matrices of $T(X)$ and $U(X)$ at the disease equilibrium point. The next generation matrix (NGM) is formulated by the partial derivatives of $T(X)$ and $U(X)$, namely $F = \left(\frac{\partial T(x^*)}{\partial X_i}\right)$ and $V = \left(\frac{\partial U(x^*)}{\partial X_i}\right)$ where x^* is the disease equilibrium point. So, we get F and V as shown in Equation (1-2).

$$F = \begin{pmatrix} 0 & -\dfrac{\Lambda\beta\big((1-\omega)\varepsilon+\omega\theta+\mu\big)}{\alpha(\omega\theta+\mu)+\mu\big((1-\omega)\varepsilon+\omega\theta+\mu\big)} \\ 0 & \dfrac{\Lambda\beta\big((1-\omega)\varepsilon+\omega\theta+\mu\big)}{\alpha(\omega\theta+\mu)+\mu\big((1-\omega)\varepsilon+\omega\theta+\mu\big)} \end{pmatrix} \quad (14)$$

$$V = \begin{pmatrix} \alpha+\mu & 0 \\ 0 & \gamma+\delta+\mu \end{pmatrix} \quad (15)$$

In the third step, we determine the basic reproduction number obtained from the largest eigenvalues of the matrix FV^{-1}. Before determining FV^{-1}, we first determining V^{-1} indicated by Equation (16).

$$V^{-1} = \frac{1}{(\alpha+\mu)(\gamma+\delta+\mu)}\begin{pmatrix} \gamma+\delta+\mu & 0 \\ 0 & \alpha+\mu \end{pmatrix} \quad (16)$$

Furthermore, by multiplying matrix F by V^{-1}, we obtain the matrix FV^{-1} represented by Equation (17).

$$FV^{-1} = \begin{pmatrix} 0 & -\dfrac{\Lambda\beta\big((1-\omega)\varepsilon+\omega\theta+\mu\big)}{\Big(\alpha(\omega\theta+\mu)+\mu\big((1-\omega)\varepsilon+\omega\theta+\mu\big)\Big)(\gamma+\delta+\mu)} \\ 0 & \dfrac{\Lambda\beta\big((1-\omega)\varepsilon+\omega\theta+\mu\big)}{\Big(\alpha(\omega\theta+\mu)+\mu\big((1-\omega)\varepsilon+\omega\theta+\mu\big)\Big)(\gamma+\delta+\mu)} \end{pmatrix} \quad (17)$$

After obtaining FV^{-1}, we determine the largest eigenvalue of FV^{-1}. based on the elements of matrix FV^{-1}, we can see that the matrix FV^{-1} is an upper triangular matrix, so that the eigenvalues of FV^{-1} are the elements that lie on the main diagonal of the matrix FV^{-1}. therefore, we obtain the largest eigenvalue (ρ) of the matrix FV^{-1} represented in Equation (18).

$$\rho(FV^{-1}) = \frac{\Lambda\beta\big((1-\omega)\varepsilon+\omega\theta+\mu\big)}{\Big(\alpha(\omega\theta+\mu)+\mu\big((1-\omega)\varepsilon+\omega\theta+\mu\big)\Big)(\gamma+\delta+\mu)} \quad (18)$$

Thus, we obtain the basic reproduction number represented by Equation (19).

$$R_0 = \frac{\Lambda\beta\big((1-\omega)\varepsilon+\omega\theta+\mu\big)}{\Big(\alpha(\omega\theta+\mu)+\mu\big((1-\omega)\varepsilon+\omega\theta+\mu\big)\Big)(\gamma+\delta+\mu)} \quad (19)$$

IV. Simulation And Discussion

In this section, we perform numerical analysis and simulations to obtain an estimate of the parameters of the mathematical model of the spread of COVID-19 which is linear and discrete in which there is an output value that can be determined. After that, we take a stochastic approach to the model by adding random or unpredictable output values where the noise used is normally distributed. The method used in the analysis and results of this numerical solution is the Kalman Filter method. Due to unknown parameter data, we estimate parameters based on daily cumulative data on COVID-19 cases and vaccination data in East Java from 23 February 2021 to 22 June 2021.

The process of the Kalman Filter method uses initial data, then estimates the situation in the future. The advantage of the Kalman Filter method is that there are two stages in the estimation. The first stage is the prediction stage where in this stage the predicted value is generated from the parameter estimate. The second stage is the correction stage where the value from the prediction stage is adjusted to the measurement data, namely the cumulative value data for humans infected with COVID-19 in East Java from 23 February 2021 to 22 June 2021. So the final estimation result is the estimation result after correction of the existing data. Table 2 is the initial value of the variables and parameters that we used in the model.

Table 2: Variable/ Parameter Used in Model Simulations

Variable/ Parameter	Value	Unit
S	40,665,696	person
V	40,060,116	person
R	199,368	person
I	127,013	person
D	270,241	person
N	8,958	person
Λ	0.039×10^{-3}	person × day^{-1}
β	0.27	$person^{-1} \times day^{-1}$
γ	1/9	day^{-1}
δ	19×10^{-5}	day^{-1}
μ	0.024×10^{-3}	day^{-1}
ε	0.01667	dimensionless
θ	0.00063	dimensionless
α	0.00151	day^{-1}
ω	0.50851	day^{-1}
$(1-\omega)$	0.49149	day^{-1}

The following is the result of the correction stage which is shown through a graph using the initial values of the state variables and parameters in Table 2.

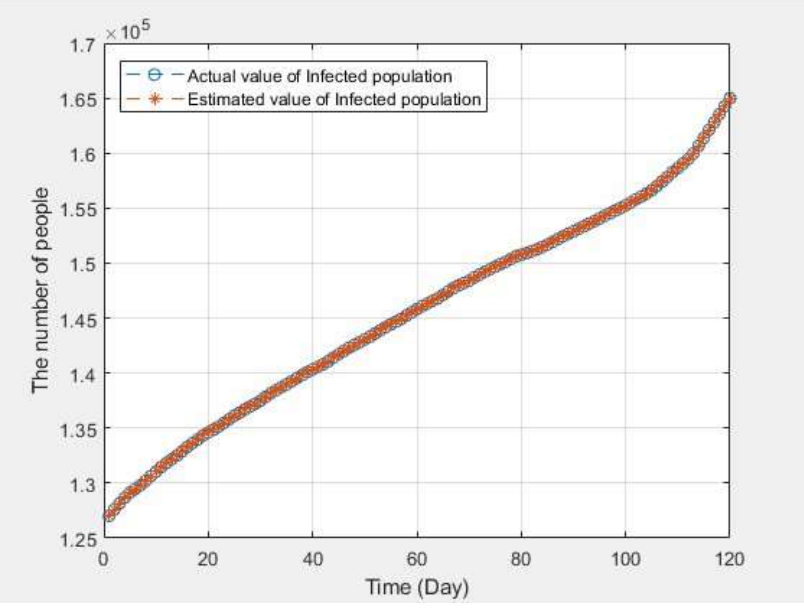

Figure 2: The Comparison Between Actual Value and Estimated Value of Infected Population

Figure 2 shows a comparison of the estimated value of infected individuals and actual data of individual infected by COVID-19 based on daily cumulative data on COVID-19 cases in East Java province in the period 23 February 2021 - 22 June 2021. From the graph it can be seen that the human population is infected by COVID-19 continues to increase. Within 120 days, the infected human population had increased by 30%. This increase occurred due to direct contact between susceptible individuals and infected individuals, so that the susceptible population decreased and moved to the infected population. Based on Figure 2, the estimated value and the actual data for the Infected population in East Java are similar. This shows that the SVIRD model in cases of the spread of COVID-19 in East Java can be used to predict the number of COVID-19 cases in East Java, so that the government can take a strategy to prevent the COVID-19 pandemic. It can also be seen from the simulation results that the MAPE value is 0.001% so that the estimated value can be said to have high forecasting accuracy.

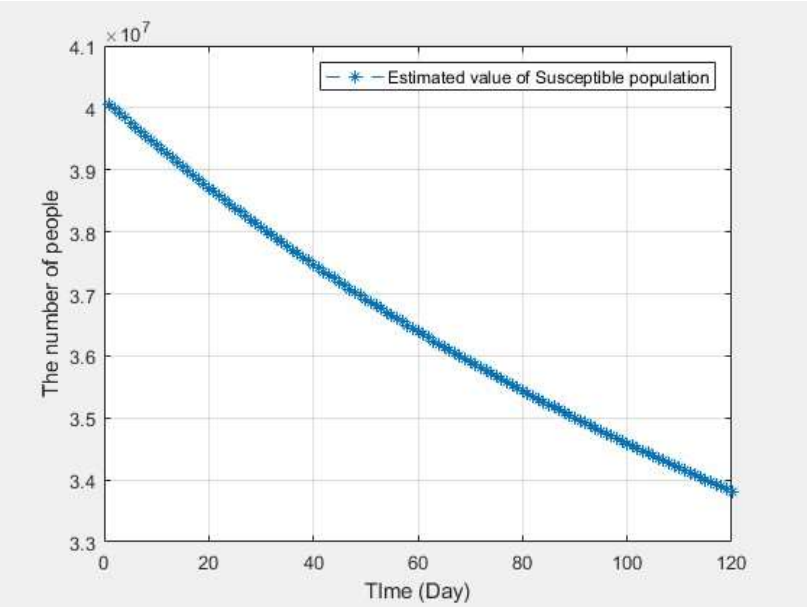

Figure 3: The Comparison Between Actual Value and Estimated Value of Susceptible Population

Figure 3 shows that the results of the estimation of susceptible individuals in East Java province decreased from 23 February 2021 to 22 June 2021. The decrease in the number of vulnerable populations was influenced by contact between susceptible individuals and infected individuals so that the susceptible human population decreased and shifted to the human population. infected. On 23 February 2021, there were 40,060,116 vulnerable people and a decrease of 16% so that on 22 June 2021 there were 33,813,204 vulnerable people.

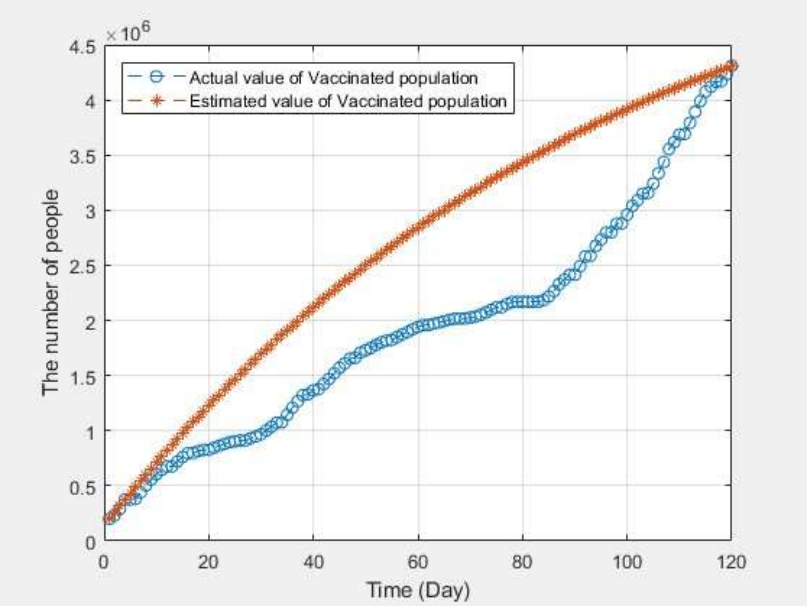

Figure 4: The Comparison Between Actual Value and Estimated Value of Vaccinated Population

Figure 4 shows a comparison of the estimated value and actual data of individuals who received the first dose of vaccination based on daily cumulative data on the implementation of the first dose of vaccination in East Java province in the period 23 February 2021 - 22 June 2021. From the graph it can be seen that the human population infected by COVID-19 is continue to increase. The increase in the number of vaccinated populations is influenced by susceptible individuals who receive the first dose of vaccination. If it is calculated based on actual data on individuals who get vaccinated with the first dose from 23 February 2021 to 22 June 22 2021, there is an increase in the Vaccinated population by 2.062%, while if it is calculated based on the estimated value, there is an increase in the Vaccinated population on 23 February 2021 to 22 June 2021 by 2.060%. So, there is an increase in the difference between the actual data and the estimated value of the Vaccinated population of 2%. It can also be seen from the simulation results of the Vaccinated population that the MAPE value is 30.813% so that the estimated value can be said to have an ordinary forecasting accuracy.

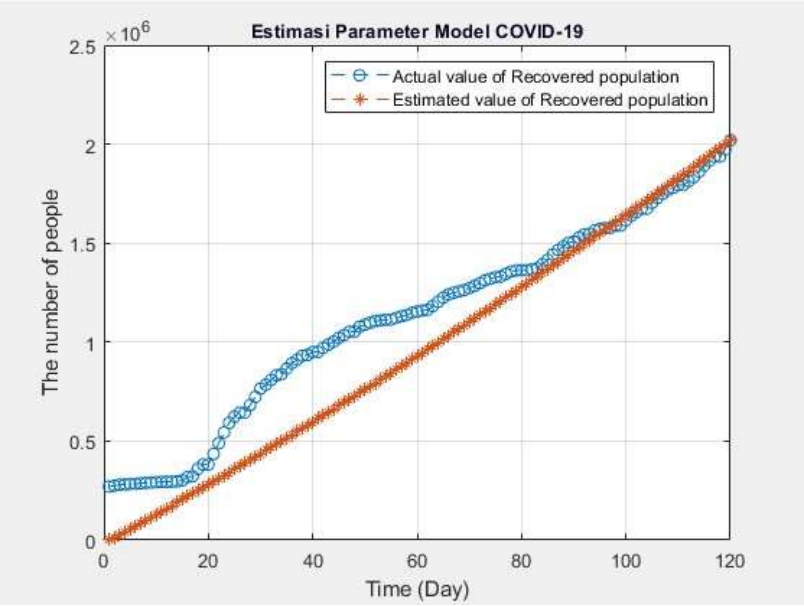

Figure 5: The Comparison Between Actual Value and Estimated Value of Recovered Population

Figure 5 shows that the estimation results in humans who recovered from COVID-19 increased from 23 February 2021 to 22 June 2021 in the province of East Java. This is in accordance with actual data from the human population who recovered from COVID-19, which has also increased. The increase in the recovered population was influenced by individuals who had received the first dose of vaccination in the Vaccinated population who received the second dose of vaccination. If it is calculated based on the actual data of the Recovered population from 23 February 2021 to 22 June 2021, there is an increase in the Recovered population by 647%. The actual data on 23 June 2021 shows a recovered population of 2,019,532 people where 7% of people who recovered from COVID-19 and 93% of people who received the second dose of vaccination. It can also be seen from the simulation results of the Recovered population that the MAPE value is 22.945% so that the estimated value can be said to have an ordinary forecasting accuracy.

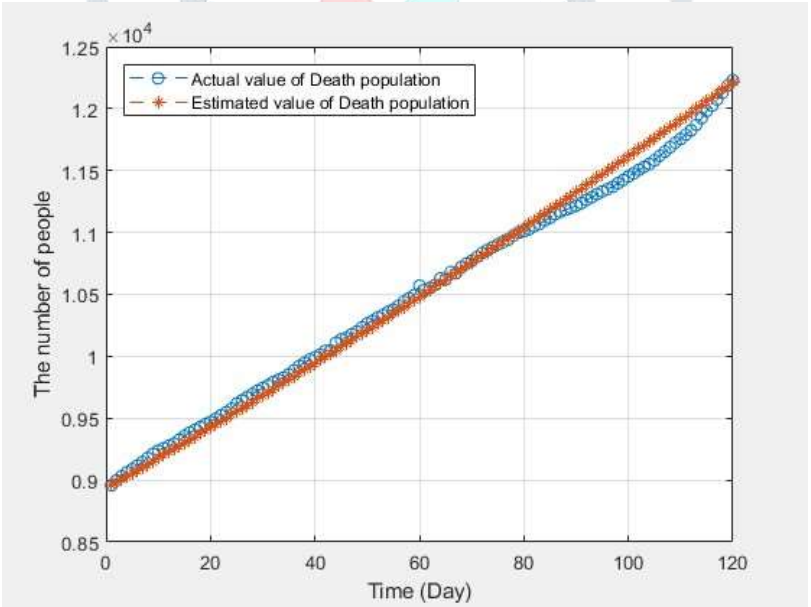

Figure 5: The Comparison Between Actual Value and Estimated Value of Death Population

Figure 5 shows a comparison of the estimated value and actual data of people who died from COVID-19 based on daily cumulative data of COVID-19 cases in East Java province for the period 23 February 2021 - 22 June 2021. From the graph it can be seen that the human population who died from COVID -19 continues to increase. The increase in the human population who died from COVID-19 was influenced by the number of individuals infected with COVID-19 who died. If it is calculated based on actual data on humans who died due to COVID-19 from 23 February 2021 to 22 June 2021, there will be an increase in the Death population by 37%, while if it is calculated based on the estimated value, there will be an increase in the Death population from 23 February 2021 to 22 June 2021 of 36%. So, there is an increase in the difference between the actual data and the estimated value of the Death population of 1%. It can also be seen from the simulation results of the Death population that the MAPE value is 0.273% so that the estimated value can be said to have high forecasting accuracy.

Next, we determine the value of the equilibrium point and the value of the basic reproduction number to determine the type of stability of the equilibrium point. We determine the value of the disease free equilibrium point by substituting the parameter values in Table 2 into Equation (6-7), so we get the disease free equilibrium point as follows.

$$E_0(S, V, I) = (0.48344, \quad 0.08552, \quad 0)$$

With the same procedure, we determine the endemic equilibrium point by substituting the parameter values in Table 2 into Equation (8-10), so we get the endemic equilibrium point as follows.

$$E_1(S,V,I) = (0.412315, \quad 0.072939, \quad 0.00036)$$

After getting the value of the equilibrium point, we determine the value of the basic reproduction number (R_0) by substituting the parameter values in Table 2 into Equation (11) to obtain:

$$R_0 = 1.1139$$

This means that if someone is infected with COVID-19 then that person will infect 1.1139 other people, so the infected population will decrease and eventually disappear from the population at a certain time. Based on the value of R_0, if $R_0 > 1$ then the system of Equations (2) has two equilibrium points that exist, namely a disease free equilibrium point which is unstable and an endemic equilibrium point which is asymptotically stable.

Next, the parameter sensitivity analysis will be carried out on the basic reproduction number (R_0) to determine the parameters that affect changes in the value of the basic reproduction number (R_0).

V. SENSITIVITY ANALYSIS

In this section, we discuss sensitivity analysis. Sensitivity analysis is a method for measuring uncertainty in all types of complex models. Sensitivity analysis is used to identify which parameter has the most significant influence on a measured variable which is then used as an intervention. There are two types of sensitivity analysis, namely local sensitivity analysis and global sensitivity analysis (Marino et al., 2008). Local sensitivity analysis is carried out by exploring the value of one or two parameters together and the other parameter values are fixed or constant. Meanwhile, global sensitivity analysis is carried out by varying all parameters simultaneously and seeing their effect on the output under study. In this study, the sensitivity analysis carried out is a local sensitivity analysis. The sensitivity index allows us to measure the relative change in a state variable as the parameter changes. If the sensitivity index value is greater, then the parameter is an influential parameter (Malorung et al., 2018). The relationship between the parameters and the variables analyzed is indicated by positive and negative signs. Local sensitivity analysis can be performed using the partial derivation technique.

Definition. The normalized forward sensitivity index of a variable, V, that depends differentiable on a parameter, p, is defined as:

$$C_p^V = \frac{\partial V}{\partial p} \times \frac{p}{V} \qquad (20)$$

where, V is the variable to be analyzed to the parameter p (Chitnis et al., 2008).

In this study, we analyze the sensitivity of the parameters to the basic reproduction number (R_0). Based on Equation (20), the sensitivity index of the parameter β is

$$C_\beta^{R_0} = \frac{\Lambda\big((1-\omega)\varepsilon + \omega\theta + \mu\big)}{\Big(\alpha(\omega\theta+\mu) + \mu\big((1-\omega)\varepsilon + \omega\theta + \mu\big)\Big)(\gamma+\delta+\mu)} \times \frac{\Big(\alpha(\omega\theta+\mu) + \mu\big((1-\omega)\varepsilon + \omega\theta + \mu\big)\Big)(\gamma+\delta+\mu)}{\Lambda\big((1-\omega)\varepsilon + \omega\theta + \mu\big)} = 1$$

With the same procedure, the sensitivity expressions for the other parameters were obtained. The expression of the sensitivity of the parameters to the basic reproduction number is presented in Table 3.

Table 3: Parameter Sensitivity Expression to Basic Reproduction Number

Variable/ Parameter	Sensitivity Expression	Sensitivity Index	$R_0 = 1.1139$	
			P-10%	P+10%
Λ	1	+1	1.0025	1.2253
β	1	+1	1.0025	1.2253
γ	$-\frac{\gamma}{(\gamma+\delta+\mu)}$	−0.9981	1.2374	1.0128
δ	$-\frac{\delta}{(\gamma+\delta+\mu)}$	−0.0017	1.1141	1.1137
μ	$\frac{(\Lambda\beta p_2 - p_1 p_3)\mu}{p_1 p_2}$	−0.3308	1.1520	1.0782
ε	$\frac{(\Lambda\beta(1-\omega)p_2 - p_1 p_4)\varepsilon}{p_1 p_2}$	+0.6884	1.0351	1.1885
θ	$\frac{(\Lambda\beta\omega p_2 - p_1 p_5)\theta}{p_1 p_2}$	−0.6405	1.1904	1.0471
α	$-\frac{(p_1 p_6)\alpha}{p_1 p_2}$	−0.7174	1.2	1.0393
ω	$\frac{(\Lambda\beta(\theta-\varepsilon)p_2 - p_1 p_7)\omega}{p_1 p_2}$	−1.3527	1.2708	0.9690

where the value of $p_1, p_2, p_3, p_4, p_5, p_6$, and p_7 as follows :

$$p_1 = \Lambda\beta\big((1-\omega)\varepsilon + \omega\theta + \mu\big)$$

$$p_2 = \Big(\alpha(\omega\theta + \mu) + \mu\big((1-\omega)\varepsilon + \omega\theta + \mu\big)\Big)(\gamma + \delta + \mu)$$

$$p_3 = 3\mu^2 + 2\Big(\alpha + \gamma + \delta + \big((1-\omega)\varepsilon + \omega\theta + \mu\big)\Big)\mu + \Big(\big((1-\omega)\varepsilon + \omega\theta + \mu\big)(\gamma + \delta) + \alpha\omega\theta\Big)$$

$$p_4 = \mu(1-\omega)(\gamma + \delta + \mu)$$

$$p_5 = \omega(\alpha + \mu)(\gamma + \delta + \mu)$$

$$p_6 = (\omega\theta + \mu)(\gamma + \delta + \mu)$$

$$p_7 = (\alpha\theta + (\theta - \varepsilon)\mu)(\gamma + \delta + \mu)$$

From Table 3, it can be seen that each parameter has a varying effect on the value of the basic reproduction number (R_0). The sensitivity index with a positive value indicates the effect of changes in parameter values that are directly proportional to changes in the value of the basic reproduction number (R_0), meaning that if the parameter value is increased (decreased) while other parameters are remain constant, it will contribute to an increase (decrease) in the value of R_0. However, a negative sensitivity index indicates that there is an effect of changing the parameter value which is inversely proportional to the change in the value of the basic reproduction number (R_0), meaning that if the parameter value is increased (decreased) while other parameters are remain constant, it will contribute to a decrease (increase) in the value of R_0.

The sensitivity analysis shown in Table 3 shows that the most influential or sensitive parameters to the basic reproduction number (R_0) are birth rate (Λ), infection rate (β), and the proportion of individuals who were vaccinated twice (ω). Parameters and have a positive relationship while the parameter (ω) has a negative relationship with R_0. This means that if the value of the parameter and/or increases, the value of R_0 will also increase. Conversely, if the value of the parameters and/or decreases, the value of R_0 will also decrease. The opposite is true for the parameter . If the value of the parameter increases, the value of R_0 decreases, otherwise if the value of the parameter decreases, the value of R_0 increases. The sensitivity index $C_\beta^{R_0} = 1$ indicates that if the value of β is increased by 10%, it will increase the value of R_0 by 10%. The same applies to the sensitivity index $C_\Lambda^{R_0} = 1$ indicates that if the value of Λ is increased by 10%, it will increase the value of R_0 by 10%. Furthermore, for the sensitivity index $C_\omega^{R_0} = 1.3527$, it shows that if the value of is 10%, it will reduce the R_0 value by 13.527%. This proves that the results of the analysis are appropriate with the test results on the value of the basic reproduction number (R_0).

VI. Conclusion

In this study, we have formulated a deterministic mathematical model for dynamic transmission of COVID-19. From the model, we derive the basic reproduction number (R_0) formula. After substituting the parameter value into the R_0 formula, the value of $R_0 = 1.1139 > 0$ so that COVID-19 will continue to exist in the population, which in this case is the East Java population. Based on the R_0 value, it can be concluded that the SVIRD mathematical model has two existing equilibrium points, namely the endemic equilibrium point which is asymptotically stable and the disease free equilibrium point which is unstable. In addition, a sensitivity analysis of the parameters is carried out on the basic reproduction number (R_0) and from the results of the sensitivity analysis it is concluded that the most influential parameters on the value of the basic reproduction number (R_0) are the birth rate (Λ) and the infection rate (β) which are directly proportional to changes in the value of the basic reproduction number (R_0) and the proportion of individuals who are vaccinated twice (ω) which is inversely proportional to the change in the value of the basic reproduction number (R_0).

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