



Sensitivity Analysis of the SVEIR Model on the Spread of Covid-19 Disease in Indonesia

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Abstract

The spread of Covid-19 is a serious global health problem, as well as in Indonesia. Mathematical modelling is one way to see how the spread of the Covid-19 disease is developing. Model used in this article is SVEIR models. In this article, we discuss the stability of the disease-free fixed point using the Routh Hurwitz criteria, while the stability of the endemic fixed point is examined using the Castillo-Chaves and Song theorems. It is confirmed that the disease-free fixed point is locally asymptotically stable if the basic reproduction number is less than one. In addition, the local asymptotically stable endemic fixed point if the basic reproduction number is more than one. Sensitivity analysis is performed to determine the parameters of the model that are most sensitive to the system. The results of numerical simulations show that the biggest influence on dynamics of spread of the disease is the contact rate of the spread of the disease.

Keywords: Covid-19; stability; sensitivity analysis.

1. Introduction

Covid-19 is one of the infectious disease identified in December 2019 in Wuhan, the capital city of Hubei, China. It was caused by severe acute respiratory syndrome coronavirus 2 (SARSCoV-2) which then spread throughout the world [1, 2]. Covid-19 occurs because of interactions that occur between agents, in this case the virus can be transmitted from human to human and has spread widely.

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On March 12, 2020, WHO declared Covid-19 a pandemic [3]. As of January 16, 2021, the total number of confirmed cases of Covid-19 in the world was 91.286.091 cases, 1.986.871 people died and there are 25.127.534 active cases [4]. Like China, this virus is also spreading in Indonesia. Indonesian data on January 16, 2021 showed that there were 14.224 new cases of Covid-19, bringing the number of Covid-19 cases in Indonesia to reach 896.642 people, as of the announcement of the first patient on March 2, 2020 [4, 5]. Covid-19 in Indonesia is very worrying where every month the number of infected people is increasing. Therefore, many researchers are interested in studying the transmission of the Covid-19 disease, so that its spread can be prevented or stopped, especially using mathematics.

Mathematical model is an abstract representation of a phenomenon that is built using equations to generate a general perspective of an epidemic event by investigating each influencing factor [6]. One of the problem that can be solved using mathematical model is models of the spread of Covid-19. Mathematical models can also help make it easier to find solutions in dealing with Covid-19. The basic model in endemic is the SIR model (Susceptible, Infectious, Recovered) which was introduced by Kermack and McKendrick in 1927 [7]. Furthermore, due to changes in model assumptions, they will change into the SEIR (Susceptible, Exposed, Infectious, Recovered), IA (Infectious, Aids), and SIS (Susceptible, Infectious, Susceptible) [8]. Diagne [9] studied the SEIR model on the spread of Covid-19 involving two groups of infections distinguished by symptoms, vaccination, treatment, and reinfection. The same analysis also done by Sasmita [10] whose model adds the assumption that there is an effect of misdiagnosis due to tool errors. Therefore, it can be concluded that several factors that influence the spread of Covid-19 are the presence of undetected cases of infection and sanitary conditions and infections with different symptoms from people who have been hospitalized [11], effectiveness and impact of vaccination [12], death [13], quarantine [14], and misdiagnosis [10]. The study in this article uses the SVEIR model which considers infected people with symptoms and infected without symptoms, vaccination, treatment, and reinfection [9, 10] and considers misdiagnosis [10]. This article discusses the stability of the fixed point on the SVEIR model and performs numerical simulations based on the analysis of the sensitivity of the model parameters.

2 Model Formulation

Suppose the population consists of six compartments, namely the susceptible human population S , the human population exposed to E , the infected human population without symptoms I_1 , the human population infected with symptoms I_2 , the human population that is cured R , the human population vaccinated against V , with assumption:

- 1) The population is infected with Covid-19, which is divided into two based on symptoms, namely, the presence of symptoms and the absence of symptoms.
- 2) There is a tool error that causes a misdiagnosis.
- 3) Vaccinated susceptible human populations are likely to be exposed.

From the assumptions above, the spread of Covid-19 can be illustrated in the compartment diagram in Figure 1.

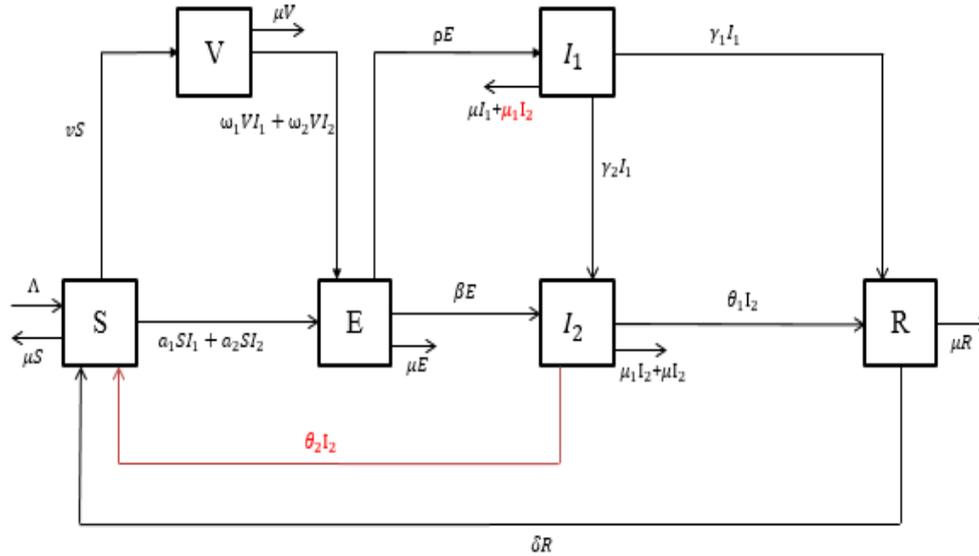


Figure 1: Compartment Diagram on Covid-19 models.

Based on Figure 1, the mathematical model has the form:

$$\frac{dS}{dt} = \Lambda + \delta R + \theta_2 I_2 - \alpha_1 S I_1 - \alpha_2 S I_2 - vS - \mu S$$

$$\frac{dV}{dt} = vS - \omega_1 V I_1 - \omega_2 V I_2 - \mu V$$

$$\frac{dE}{dt} = \alpha_1 S I_1 + \alpha_2 S I_2 + \omega_1 V I_1 + \omega_2 V I_2 - \beta E - \rho E - \mu E$$

(1)

$$\frac{dI_1}{dt} = \rho E - \gamma_1 I_1 - \gamma_2 I_1 - \mu I_1 - \mu_1 I_1$$

$$\frac{dI_2}{dt} = \beta E + \gamma_2 I_1 - \theta_1 I_2 - \theta_2 I_2 - (\mu + \mu_1) I_2$$

$$\frac{dR}{dt} = \gamma_1 I_1 + \theta_1 I_2 - \delta R - \mu R.$$

The total population is acquired by totaling the six equation, $(N = S + V + E + I_1 + I_2 + R \geq \frac{\Lambda}{\mu})$ where all parameters are positive and constant. The parameters used in equation (1) are shown in Table 1

Table 1: Description of Parameters on Covid-19 models.

Symbol	Description
Λ	Natural birth rate
μ	Natural death rate
μ_1	The death rate due to human disease
a_1	Contact rate with no symptom
a_2	Contact rate with symptom
v	Vaccination rate
β	The rate of disease transmission
δ	Reinfection rate
γ_1	The rate of the group recovering due to the presence of immunity
γ_2	The rate of a group of asymptomatic carriers being reported
θ_1	Proportion of recovered individuals
θ_2	Proportion of individual errors recovered
ω_1	The rate of contact of vaccination individuals with no symptom
ω_2	The rate of contact of vaccination individuals with symptom

3. Result and Discussion

3.1 Dynamics Properties

The disease-free fixed point of equations (1) is: $T^0(S, V, E, I_1, I_2, R) = (\frac{\Lambda}{v+\mu}, \frac{v\Lambda}{\mu(v+\mu)}, 0, 0, 0, 0)$ while the endemic fixed point is $T^*(S, V, E, I_1, I_2, R) = (S^*, V^*, E^*, I_1^*, I_2^*, R^*)$ with

$$S^* = \frac{R^*\delta + I_2^*\theta_2 + \Lambda}{v + I_1^*\alpha_1 + I_2^*\alpha_2 + \mu} \qquad I_1^* = \frac{E^*\rho}{\gamma_1 + \gamma_2 + \mu + \mu_1}$$

$$V^* = \frac{S^*v}{\mu + I_1^*\omega_1 + I_2^*\omega_2} \qquad I_2^* = \frac{E^*\beta + I_1^*\gamma_2}{\theta_1 + \theta_2 + \mu + \mu_1}$$

$$E^* = \frac{I_1S^*\alpha_1 + I_2S^*\alpha_2 + I_1^*V^*\omega_1 + I_2^*V^*\omega_2}{\beta + \mu + \rho} \qquad R^* = \frac{I_1^*\gamma_1 + I_2^*\theta_1}{\delta + \mu}.$$

The basic reproduction number is determined using the next generation matrix, where the basic reproduction number is the dominant eigenvalue of $G = FV^{-1}$ where

$$F = \begin{pmatrix} 0 & \alpha_1S^0 + \omega_2V^0 & \alpha_2S^0 + \omega_3V^0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} ; V = \begin{pmatrix} k_1 & 0 & 0 \\ -\rho & k_2 & 0 \\ -\beta & -\gamma_2 & k_3 \end{pmatrix},$$

with:

$$k_1 = \beta + \mu + \rho$$

$$k_2 = \gamma_1 + \gamma_2 + \mu + \mu_1$$

$$k_3 = \theta_1 + \theta_2 + \mu + \mu_1.$$

The basic reproduction number is

$$\mathcal{R}_0 = \frac{\Lambda(k_2\beta(\alpha_2\mu + v\omega_2) + \rho(k_3\alpha_1\mu + \alpha_2\gamma_2\mu + k_3v\omega_1 + v\gamma_2\omega_2))}{k_1k_2k_3\mu(v + \mu)}$$

The following is the stability theorem of the disease-free fixed point and the endemic fixed point based on the value of the basic reproduction number.

Theorem 1: The disease-free fixed point T^0 in equations (1) is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$

Proof.

Stability of the disease-free fixed point can be determined by linearizing the system at (T^0) . The Jacobi Matrix is obtained as follows:

$$J_{T^0} = \begin{bmatrix} k_{11} & 0 & 0 & k_{14} & k_{15} & k_{16} \\ k_{21} & k_{22} & 0 & k_{24} & k_{25} & 0 \\ 0 & 0 & k_{33} & k_{34} & k_{35} & 0 \\ 0 & 0 & k_{43} & k_{44} & 0 & 0 \\ 0 & 0 & k_{53} & k_{54} & k_{55} & 0 \\ 0 & 0 & 0 & k_{64} & k_{65} & k_{66} \end{bmatrix},$$

with;

$$\begin{aligned} k_{j_{11}} &= -v - \mu; & k_{22} &= -\mu; & k_{35} &= \alpha_2 S^0 + \omega_2 V^0; & k_{55} &= -\theta_1 - \theta_2 - \mu - \mu_1; \\ k_{14} &= -\alpha_1 S^0; & k_{24} &= -\omega_1 V^0; & k_{43} &= \rho; & k_{64} &= \gamma_1; \\ k_{15} &= -\alpha_2 S^0; & k_{25} &= -\omega_2 V^0; & k_{44} &= -\gamma_1 - \gamma_2 - \mu - \mu_1; & k_{65} &= \theta_1; \\ k_{16} &= \delta; & k_{33} &= -\beta - \mu - \rho; & k_{53} &= \beta; & k_{66} &= -\mu - \delta. \\ k_{21} &= v; & k_{34} &= \alpha_1 S^0 + \omega_1 V^0; & k_{54} &= \gamma_2; \end{aligned}$$

Determination of the eigenvalues can be obtained by $|J_{T^0} - \lambda I| = 0$ so that the equation is obtained:

$$(k_{11} - \lambda)(k_{22} - \lambda)(k_{66} - \lambda)(\lambda^3 + c_1\lambda^2 + c_2\lambda + c_3) = 0.$$

From the equation, there are six eigenvalues with three negative eigenvalues, namely, $\lambda_1 = -v - \mu, \lambda_2 = -\mu, \lambda_3 = -\mu - \delta$, while the other three eigenvalues are obtained by solving the following characteristic equation with the following Routh-Hurwitz criteria:

$$(\lambda^3 + c_1\lambda^2 + c_2\lambda + c_3) = 0$$

with

$$c_1 = k_1 + k_2 + k_3,$$

$$c_2 = k_1k_2(1 - \mathcal{R}_{02}) + k_1k_3(1 - \mathcal{R}_{01}) + k_2k_3,$$

$$c_3 = k_1k_2k_3(1 - \mathcal{R}_0).$$

Because all positive parameter values, then $c_1, c_2, c_3 > 0$. In accordance with the Routh-Hurwitz criteria, with the condition that $\mathcal{R}_0 < 1$, it can be concluded that the equation will have negative eigenvalues. This indicates that the disease-free fixed point will be locally asymptotically stable.

Theorem 2: The endemic fixed point T^* in equations (1) is locally asymptotically stable if $\mathcal{R}_0 > 1$

Proof.

The proof uses the Castillo-Chaves and Song theorem [15]. Let $\varphi = a_1$ be the bifurcation parameter. Based on $\mathcal{R}_0 = 1$ it gives

$$a_1 = \varphi^* = \frac{k_1k_2k_3 - k_2\beta(S^0\alpha_2 + V^0\omega_2) - \rho S^0\alpha_2\gamma_2 - \rho k_3V^0\omega_1 - \rho\gamma_2\omega_2}{\rho k_3}.$$

The fixed point T^0 has six eigenvalues if $\mathcal{R}_0 = 1$ or $a_1 = \varphi^*$. The eigenvalues have right eigenvectors $(u_1, u_2, u_3, u_4, u_5, u_6)$ and left eigenvectors $(v_1, v_2, v_3, v_4, v_5, v_6)$ that are related to each other. The right eigenvector $\lambda = 0$ is obtained by solving the equation $(J_{T^0} - \lambda I)u = 0$.

Let $u_4 > 0$, it gives

$$u_3 = \frac{k_2}{\rho} u_4 > 0, \quad u_1 = -\frac{(-\alpha_1 S^0)}{(-v - \mu)} u_4 - \frac{(-\alpha_2 S^0)}{(-v - \mu)} u_5 - \frac{\delta}{(-v - \mu)} u_6 < 0$$

$$u_5 = \left(\frac{\beta k_2}{k_3 \rho} + \frac{\gamma_2}{k_3}\right) u_4 > 0, \quad u_2 = -\frac{v}{-\mu} u_1 - \frac{-\omega_1 V^0}{-\mu} u_4 - \frac{-\omega_2 V^0}{-\mu} u_5 < 0,$$

$$u_6 = -\frac{\gamma_1}{(-\mu - \delta)} u_4 - \frac{\theta_1}{(-\mu - \delta)} u_5 > 0.$$

The left eigenvector $\lambda = 0$ is obtained by solving the equation $(J_{T^0} - \lambda I)^T u = 0$

Let $v_5 > 0$, gives

$$j_{22}v_2 = 0, \text{ so } v_2 = 0; v_1 = -\frac{j_{21}}{j_{11}} v_2 = 0; v_6 = -\frac{j_{16}}{j_{66}} v_1 = 0$$

$$v_3 = -\frac{(-\theta_1 - \theta_2 - \mu - \mu_1)}{\alpha_2 S^0 + \omega_2 V^0} v_5 > 0; \quad v_4 = -\frac{\beta}{\rho} v_5 - \frac{(-\beta - \mu - \rho)}{\rho} v_3 > 0.$$

Let

$$x_1 = S; x_2 = V; x_3 = E; x_4 = I_1; x_5 = I_2; x_6 = R,$$

then

$$\begin{aligned} f_1 &= \frac{dx_1}{dt} = \Lambda + \delta x_6 + \theta_2 x_5 - \varphi x_1 x_4 - \alpha_2 x_1 x_5 - v x_1 - \mu x_1, \\ f_2 &= \frac{dx_2}{dt} = v x_1 - \omega_1 x_2 x_4 - \omega_2 x_2 x_5 - \mu x_2, \\ f_3 &= \frac{dx_3}{dt} = \varphi x_1 x_4 + \alpha_2 x_1 x_5 + \omega_1 x_2 x_4 + \omega_2 x_2 x_5 - \beta x_3 - \rho x_3 - \mu x_3, \\ f_4 &= \frac{dx_4}{dt} = \rho x_3 - \gamma_1 x_4 - \gamma_2 x_4 - \mu x_4 - \mu_1 x_4, \\ f_5 &= \frac{dx_5}{dt} = \beta x_2 + \gamma_2 x_4 + \delta x_6 - \theta_1 x_5 - \theta_2 x_5 - (\mu + \mu_1) x_5, \\ f_6 &= \frac{dx_6}{dt} = \gamma_1 x_4 + \theta_1 x_5 - \delta x_6 - \mu x_6. \end{aligned}$$

Based on the equation obtained partial derivative

$$\frac{\partial^2 f_3}{\partial x_2 x_4} (T^0, \varphi^*) = \omega_1 \qquad \frac{\partial^2 f_3}{\partial x_1 x_4} (T^0, \varphi^*) = \varphi^*$$

$$\frac{\partial^2 f_3}{\partial x_2 x_5} (T^0, \varphi^*) = \omega_2 \qquad \frac{\partial^2 f_3}{\partial x_1 x_5} (T^0, \varphi^*) = \alpha_2$$

Therefore:

$$\begin{aligned} a &= v_3 u_2 u_4 \frac{\partial^2 f_3}{\partial x_2 x_4} (T_0, \varphi^*) + v_3 u_2 u_5 \frac{\partial^2 f_3}{\partial x_2 x_5} (T_0, \varphi^*) + v_3 u_1 u_4 \frac{\partial^2 f_3}{\partial x_1 x_4} (T_0, \varphi^*) \\ &+ v_3 u_1 u_5 \frac{\partial^2 f_3}{\partial x_1 x_5} (T_0, \varphi^*). \end{aligned}$$

$$b = v_3 u_1 \frac{\partial^2 f_1}{\partial x_1 \varphi} (T_0, \varphi^*) + v_3 u_4 \frac{\partial^2 f_3}{\partial x_4 \varphi} (T_0, \varphi^*) = v_3 u_4 \frac{\partial^2 f_3}{\partial x_4 \varphi} (T_0, \varphi^*)$$

with $u_3, u_4, u_5, v_3 > 0$ and $u_2 < 0$ so $a < 0$ and $b > 0$

The values of a and b obtained with $a < 0$ and $b > 0$ are in accordance with case 4 of the Castillo-Chaves and Song theorem [15]. As a result, when changes from $\varphi < \varphi^* (\mathcal{R}_0 < 1)$ to $\varphi < \varphi^* (\mathcal{R}_0 > 1)$, the unstable endemic fixed point T^* changes from negative to positive and locally asymptotically stable. So it is proven that if $R_0 > 1$ then the endemic fixed point T^* is local asymptotically.

3.2 Numerical Analysis

Numerical simulation is carried out with the parameter values presented in Table 2.

Table 2: Parameter Value on Covid-19 Model.

Symbol	Value		Reference
	$\mathcal{R}_0 < 1$	$\mathcal{R}_0 > 1$	
a_1	0,0104	0,0104	[10]
a_2	0,0731	0,0731	[10]
v	0,0002	0,0002	[14]
β	0,4	0,4	[10]
μ	0,006567	0,006567	[14]
γ_1	0,075	0,075	[10]
γ_2	0,036	0,036	[10]
Δ	0,9629	0,9629	[16]
ρ	0,0285	0,0285	[11]
ω_1	0,00047	0,00047	[14]
ω_2	0,00334	0,00334	[14]
Λ	0,01755	0,01755	[17]
μ_1	0.087	0.0002211	[10, 18]

Parameter values will be used to perform numerical analysis, where the initial value for each sub-population is $S(0) = 0.993, V(0) = 0.762, E(0) = 0.052, I_1(0) = 0.036, I_2(0) = 0.125, R(0) = 0$ [20, 21]. Furthermore, we also analyze the sensitivity of the parameters to the basic reproduction number (\mathcal{R}_0). This sensitivity analysis was carried out to find out how much influence each parameter has on \mathcal{R}_0 . The following is the result of the sensitivity value at \mathcal{R}_0 .

Table 3: Sensitivity Index.

Parameter	Sensitivity Index
a_1	+0,008163
a_2	+0,990446
v	-0.028165
β	+0,051288
γ_1	-0.018664
γ_2	0.012179
ω_1	+0.000011
ω_2	+0.001379

Table 3 gives parameters that have a significant influence on \mathcal{R}_0 are a_2 and μ . Meanwhile, a_2 is contact rate with symptom from susceptible to expose. The positive sign on the sensitivity index means that if the parameter value is increased, then the \mathcal{R}_0 value will be increased. Conversely, a negative sign on the sensitivity index means that when the parameter value is increased, \mathcal{R}_0 will also decrease. The effect of contact rate (a_2) on dynamics the spread of the Covid-19 disease.

Table 4: Contact rate (a_2) effect on \mathcal{R}_0 .

Parameter a_2	\mathcal{R}_0
0,07305	1,83757
0,05113	1,29157
0,02922	0,74556

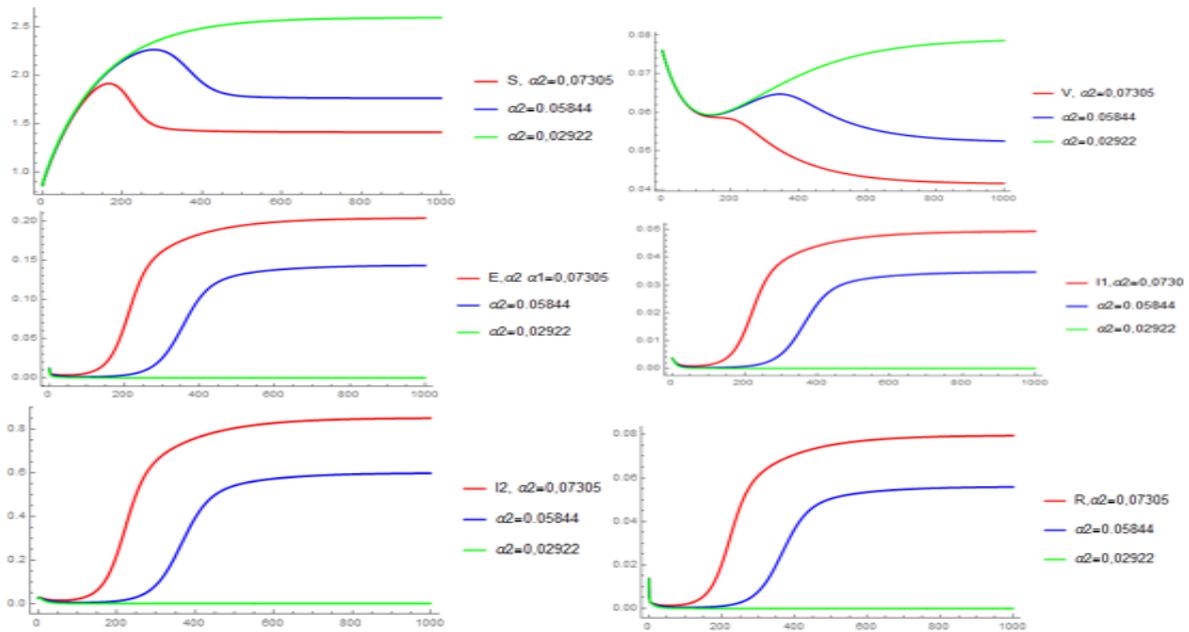


Figure 2: The dynamics of population due to changes in the value of α_2 .

Figure 2 shows that if the α_2 value is lowered, the proportion of the infected human population will decrease because fewer individuals are in contact with the infection, as a result, the infected individuals will be smaller as well. The proportion of the susceptible human population that has contact with infected people can affect the proportion of the infected human population to decrease, even experiencing extinction when $\alpha_2 = 0.02922$. As a result of no spread, the number of deaths will decrease and result in an increase in the number of vulnerable populations.

4. Conclusion

SVEIR model has been used in modeling the spread of the Covid-19 disease by considering two infected individuals, namely with symptoms and without symptoms. This model also considers vaccination in susceptible human populations and considers population immunity. In this modified model, there are two fixed points, namely a disease-free fixed point that is locally asymptotically stable when $\mathcal{R}_0 < 1$, and a disease-endemic fixed point that is locally asymptotically stable at conditions $\mathcal{R}_0 > 1$. The results of the simulations carried out show results that are in accordance with the theorem.

Sensitivity analysis that produces the largest sensitivity index value is the transition rate parameter to the dynamics of the spread of disease, quarantine, vaccination effectiveness, and the effect of body immunity in each population. Therefore, these three parameters have a big influence on \mathcal{R}_0 . The value of \mathcal{R}_0 is also influenced by several parameters but does not have a significant effect such as the rate of quarantine causing death, however this rate must also be suppressed so as not to affect the dynamics of the disease. The numerical simulation also shows that the biggest influence on the dynamics of the spread of the disease is the transition of the spread of the disease. Therefore, every population must maintain or at least reduce contact with individuals is an effective measure to prevent the spread of Covid-19 disease based on this model and analysis.

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