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DYNAMICS OF A SIRV MODEL FOR THE SPREAD OF COVID-19 IN MALUKU PROVINCE

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ABSTRACT

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COVID-19 (Coronavirus Disease 2019) is caused by the SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2) coronavirus spreading around the world. In this study, the SIRV model was used, which is an epidemic model carried out by grouping the population into four subpopulations, namely the subpopulation of susceptible individuals who can be infected (Susceptible), the subpopulation of infected individuals (Infected), the subpopulation of individuals who recover from illness (Recovered), and the subpopulation of individuals who have been vaccinated (Vaccination). Based on the dynamic system analysis conducted, two equilibrium points were obtained, namely the disease-free equilibrium point and the endemic equilibrium point. In addition, based on data processing and model simulation results obtained, $R_0 = 0{,}00040$ *was obtained so that it can be concluded that the higher the number of vaccinated populations, the lower the level of Covid-19 spread, which means that vaccines can suppress cases of Covid-19 spread in Maluku Province.*

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1. INTRODUCTION

At the end of 2019, the world was shocked by the discovery of a new virus that initially hit marine fish market traders in Wuhan, China. On February 11, 2020, the spread of this virus became a concern of the *World Health Organization* (WHO) which informed the existence of a new virus called Coronavirus 2019 (Covid-19) [1].

Based on information published by the Covid-19 Handling Task Force in Indonesia since the first case of Covid-19 was reported in December 2019 until November 30, 2022, there were 6,664,844 people exposed to Covid-19 in Indonesia with a total death of 159,830 people. According to information from the Maluku Provincial Health Office, were 19,022 people exposed to Covid-19 in Maluku Province, with a total death of 307 people. Therefore, preventing and controlling this disease's spread is one of the current hot issues [2].

Among the current methods of prevention and treatment of infectious diseases, vaccine injection is one of the fast and most effective methods. For example, in the prevention and control of Covid-19, vaccine injection can reduce the transmission rate of the virus. However, although vaccines have been discovered and circulated, Covid-19 has not disappeared and almost all parts of the world are still fighting against Covid-19. Therefore, more and more researchers are considering vaccine injection in modeling infectious diseases [3] According to the perspective of Mathematics, the study of infectious diseases usually starts from the mechanism of disease transmission which is analyzed by building a mathematical model. The earliest epidemic model was constructed by Kermack and Mckendrick [4].

Several studies have discussed the mathematical model of Covid-19. Resmawan et al. [5] discussed the SEAQIR model as a Covid-19 transition involving quarantine intervention. Annas et al [6] also discussed the SEIR model for the spread of the Covid-19 pandemic in Indonesia. In the same year Resmawan and Yahya [7], discussed the SEAIQR model to conduct sensitivity analysis. In Zhang's research [8], a new mathematical model (SEIRD) was proposed, which was built with five classes including susceptible, exposed, infected, recovered, and dead to describe the probability of transmission. Bhadauria et al. [9] studied the SIQ model by using the stability theory of nonlinear ordinary differential equations. Li et al. [10] developed a numerical method for the stochastic SIQS epidemic model. Higazy [11] proved the existence of a stable solution for the fractional order Covid-19 SIDARTHE model. The θ-SEIHQRD model which is more relevant to Covid-19 was developed by Ramos et al. [12]. Nisar et al. [13] built and verified the SIRD model's correctness. Batistela et al. [14] proposed the SIRSi model for Covid-19. Pare et al. [15] proposed a traditional cohort model with continuous-time and discrete-time versions with non-trivial networks on a simple SIR-based model. Zhu et al. [16] constructed a time-delay reaction-diffusion model that more closely approximates the actual spread of the Covid-19 epidemic. Wei et al. [17] considered the time delay from susceptible individuals to infected individuals, thus, proposing the SVEIR epidemic disease model. Araz [18] discussed the mathematical model of the spread of Covid-19 and analyzed the global and local stability. Almocera et al. [19] studied the in-host model and the stability of the unique positive equilibrium point. Samanta [20] analyzed the stability of the proposed model to control the epidemic. Leon et al. [21] proposed the SEIARD mathematical model and tried to forecast the outbreak's evolution. Youssef et al. [22] performed numerical verification and prediction of the proposed SEIR model and compared the results with accurate data due to the spread of Covid-19 in Saudi Arabia. Carli et al., in their research [23], proposed a multi-region SIRQTHE model and optimal control approach, which supports the government in determining the most effective strategy to adopt during the post-lockdown mitigation phase in a multi-region scenario.

A new model introduced in this study refers to the modified model [24] by adding a vaccine subpopulation class that represents individuals who have been vaccinated. This vaccine protects the body from getting sick from Covid-19 by generating or stimulating specific immunity. Based on the model, the equilibrium point of each compartment was sought in a disease-free and endemic state and the basic reproduction number of the model. Furthermore, from the equilibrium point obtained, the stability of the equilibrium point was sought. After that, numerical simulations were carried out using parameter values.

2. RESEARCH METHODS

The research methods used in this research are literature studies and case studies. The data used in this study are data on patients infected with Covid-19, patients who died from Covid-19 infection, patients who recovered after Covid-19 infection, and vaccination data from March 2022 to November 2022. This data was obtained from the Maluku Provincial Health Office. The research procedure used in this study is described in the following flowchart.

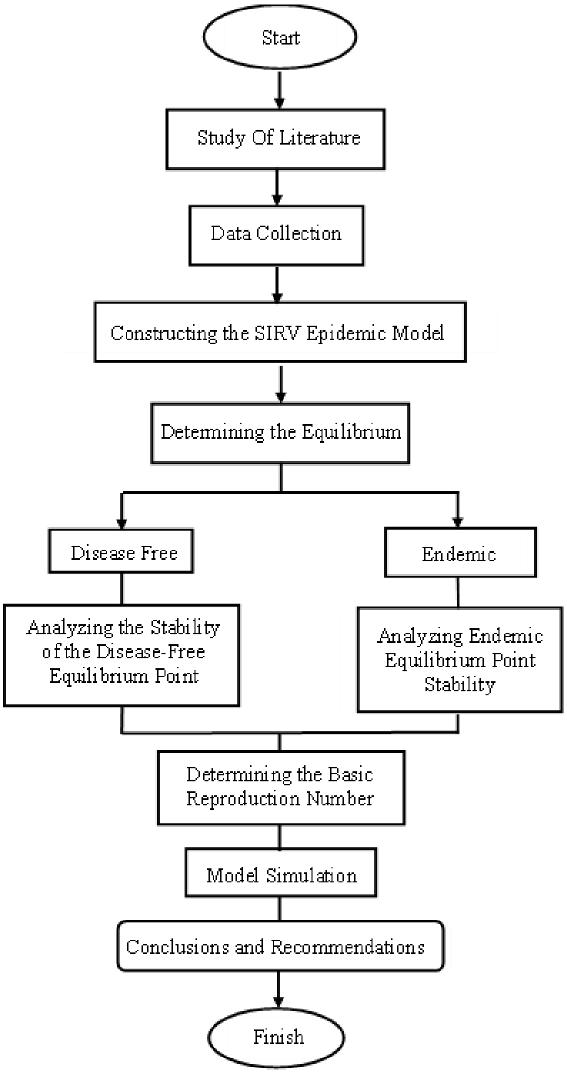


Figure 1. Research flowchart

Based on the research flowchart, after constructing the SIRV model of the spread of Covid-19, the next step is to determine the disease-free equilibrium point. Then, the stability of each equilibrium point is analyzed. The next is finding the basic reproduction number and performing simulations using Matlab software.

3. RESULTS AND DISCUSSION

3.1 Mathematical Model of Covid-19 Spread with Vaccination

The SIRV model of the spread of Covid-19 with vaccination described in this study consists of 4 subpopulations with the following assumptions:

a. The natural mortality rate is present in each subpopulation.

b. Susceptible *(S)* subpopulations may increase due to births.

c. Individuals in the susceptible subpopulation *(S)* are infected with Covid-19 when interacting with individuals in the infected subpopulation *(I)* with an infection rate equal to α. The death rate due to Covid-19 is assumed to be equal to μ_c.

d. Infected individuals can experience death from Covid-19 due to poor treatment or a decreased immune system.

e. Individuals in the *Infected (I)* subpopulation move to the *Recovered (R)* subpopulation because they have received treatment and care from the medical team or their families.

f. Individuals in the *Recovered (R)* subpopulation will move to the *Vaccination (V)* subpopulation because they have been vaccinated to strengthen their immunity.

g. Individuals in the susceptible subpopulation *(S)* can also vaccinate to prevent being infected with Covid-19.

h. Individuals who have recovered from Covid-19 and have been vaccinated will not be susceptible again.

Based on these assumptions, the spread of Covid-19 is schematically presented in the compartment section as shown in **Figure 2**.

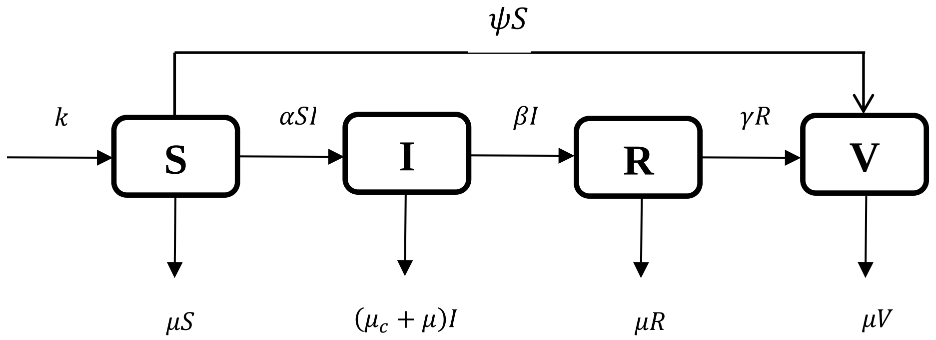


Figure 2. SIRV model

Based on the compartmental chart above, a Mathematical Model of Covid-19 Spread with Vaccination is formed, written in the form of differential equations as **Equation (1)** to **Equation (4)**.

$$\frac{dS}{dt} = k - \mu S - \alpha SI - \psi S \tag{1}$$

$$\frac{dI}{dt} = \alpha SI - (\mu_c + \mu)I - \beta I \tag{2}$$

$$\frac{dR}{dt} = \beta I - \mu R - \gamma R \tag{3}$$

$$\frac{dV}{dt} = \gamma R - \mu V + \psi S \tag{4}$$

where,

S = Number of vulnerable subpopulations
I = Number of infected subpopulations
R = Number of recovered subpopulations
V = Number of vaccinated subpopulations
k = Birth rate
α = Disease infection rate
β = Healing rate
γ = Vaccination rate after infection
ψ = Vaccination rate before the infection
μ = Natural mortality rate
μ_c = The death rate due to Covid-19

3.2 Equilibrium Point Analysis of The Mathematical Model of Covid-19 Spread with Vaccination

Its equilibrium points are time-invariant. Thus, the equilibrium points are obtained when $\frac{dS}{dt} = 0, \frac{dI}{dt} = 0, \frac{dR}{dt} = 0, \frac{and\ dV}{dt} = 0$. There are two equilibrium points, namely, the disease-free equilibrium point and the endemic equilibrium point. The analysis of the stability of the equilibrium point, the Jacobian matrix of **Equation (1)** to **Equation (4)** can be formed as follows:

$$J_{(S,I,R,V)}=\begin{bmatrix}\frac{\partial S(t)}{\partial S} & \frac{\partial S(t)}{\partial I} & \frac{\partial S(t)}{\partial R} & \frac{\partial S(t)}{\partial V}\\ \frac{\partial \hat{I}(t)}{\partial S} & \frac{\partial \hat{I}(t)}{\partial I} & \frac{\partial \hat{I}(t)}{\partial R} & \frac{\partial \hat{I}(t)}{\partial V}\\ \frac{\partial R(t)}{\partial S} & \frac{\partial R(t)}{\partial I} & \frac{\partial R(t)}{\partial R} & \frac{\partial R(t)}{\partial V}\\ \frac{\partial V(t)}{\partial S} & \frac{\partial V(t)}{\partial I} & \frac{\partial V(t)}{\partial R} & \frac{\partial V(t)}{\partial V}\end{bmatrix}=\begin{bmatrix}-\mu-\alpha I-\psi & -\alpha S & 0 & 0\\ \alpha I & \alpha S-\mu_c-\mu-\beta & 0 & 0\\ 0 & \beta & -\mu-\gamma & 0\\ \psi & 0 & \gamma & -\mu\end{bmatrix}$$

3.2.1 Disease-free Equilibrium Point

If $I=0$, then a disease-free equilibrium point will be obtained where all populations infected with the Covid-19 virus no longer exist in this state. To obtain the equilibrium point, from **Equation (1)**, we obtain $k-\mu S-\psi S=\alpha SI$. Because $I=0$ then $k-\mu S-\psi S=0$ so $=\frac{k}{(\mu+\psi)}$. Furthermore, from **Equation (3)**, it is obtained $\gamma R=\beta I-\mu R$. Because $I=0$, it is obtained that $R=0$. Furthermore, from **Equation (4)**, it is obtained $\mu V=\gamma R+\psi S$. Because $R=0$, then $V=\frac{\psi k}{\mu(\mu+\psi)}$. Thus, the virus-free equilibrium point is obtained, namely $E_0\big(S(t),I(t),R(t),V(t)\big)=(\frac{k}{\mu+\psi,}\ 0{,}0,\frac{\psi k}{\mu(\mu+\psi)})$.

3.2.2 Endemic Equilibrium Point

The endemic equilibrium point is affected by the population infected with the Covid-19 virus by $I\neq 0$. So, **Equation (1)** is obtained:

$$I=\frac{k-\mu S-\psi S}{\alpha S}\tag{5}$$

For **Equation (2)**, it is obtained $[\alpha S-(\mu_c+\mu+\beta)]I=0$. Since $I=0$, then$\alpha S-(\mu_c+\mu+\beta)=0$ so, it is obtained:

$$S=\frac{(\mu_c+\mu+\beta)}{\alpha}\tag{6}$$

From **Equation (5)**, it is obtained:

$$I=\frac{ka-\mu\mu_c-\mu^2-\mu\beta-\psi\mu_c-\psi\mu-\psi\beta}{\alpha(\mu_c+\mu+\beta)}\tag{7}$$

By substituting **Equation (7)** into **Equation (3)**, it is obtained:

$$R=\frac{\beta(k\alpha-\mu^2-\mu\mu_c-\beta\mu-\psi\mu_c-\psi\mu-\psi\beta)}{\alpha(\mu_c+\mu+\beta)(\mu+\gamma)}\tag{8}$$

Furthermore, by substituting **Equation (8)** into **Equation (4)**, it is obtained:

$$V=\frac{\gamma\left(\frac{k\alpha\beta-\mu^2\beta-\mu\mu_C\beta-\beta^2\mu-\psi\mu_C\beta-\psi\mu\beta-\psi\beta^2}{\alpha(\mu_C+\mu+\beta)(\mu+\gamma)}\right)+\psi\left(\frac{\mu_C+\mu+\beta}{\alpha}\right)}{\mu}\tag{9}$$

Thus, the endemic equilibrium point is obtained, namely:

$$E_1\ (S(t),I(t),R(t),V(t))=\left\{\begin{matrix}\left(\frac{\mu_c+\mu+\beta}{\alpha}\right),\left(\frac{k\alpha-\mu\mu_c-\mu^2-\mu\beta-\psi\mu_c-\psi\mu-\psi\beta}{\alpha(\mu_c+\mu+\beta)}\right),\left(\frac{\beta\left(k\alpha-\mu^2-\mu\mu_c-\beta\mu-\psi\mu_c-\psi\mu-\psi\beta\right)}{\alpha(\mu_c+\mu+\beta)(\mu+\gamma)}\right),\\ \left(\frac{\gamma\left(\frac{k\alpha\beta-\mu^2\beta-\mu\mu_c\beta-\beta^2\mu-\psi\mu_c\beta-\psi\mu\beta-\psi\beta^2}{\alpha(\mu_c+\mu+\beta)(\mu+\gamma)}\right)+\psi\left(\frac{\mu_c+\mu+\beta}{a}\right)}{\mu}\right)\end{matrix}\right\}$$

3.2.3 Stability Analysis of Disease-Free Equilibrium Point

Based on the disease-free equilibrium point obtained, the following jacobian matrix is formed:

$$J_{(S,0,0,V)}=\begin{bmatrix} -\mu-\psi & -\alpha\left(\dfrac{k}{\mu+\psi}\right) & 0 & 0 \\ 0 & \alpha\left(\dfrac{k}{\mu+\psi}\right)-\mu_c-\mu-\beta & 0 & 0 \\ 0 & \beta & -\mu-\gamma & 0 \\ \psi & 0 & \gamma & -\mu \end{bmatrix}$$

From the jacobian matrix, by using $det\left(\lambda I-J_{(S,0,0,V)}\right)=0$, then it is obtained :

$$\det\begin{bmatrix} \lambda+\mu+\psi & \alpha\left(\dfrac{k}{\mu+\psi}\right) & 0 & 0 \\ 0 & \lambda-\alpha\left(\dfrac{k}{\mu+\psi}\right)+\mu_c+\mu+\beta & 0 & 0 \\ 0 & -\beta & \lambda+\mu+\gamma & 0 \\ -\psi & 0 & -\gamma & \lambda+\mu \end{bmatrix}=0$$

Furthermore, the characteristic equation is obtained with the cofactor expansion method.

$$\left(\lambda-\alpha\left(\frac{k}{\mu+\psi}\right)+\mu_c+\mu+\beta\right)(\lambda+\mu+\psi)(\lambda+\mu+\gamma)(\lambda+\mu)$$

Since all parameters are positive, then $\lambda_2, \lambda_3,$ and λ_4 are negative. Therefore, the disease-free equilibrium point $(I=0)$ will be locally asymptotically stable if

$$\alpha\left(\frac{k}{\mu+\psi}\right)+\mu_c+\mu+\beta<0 \text{ or } \frac{\alpha k}{(\mu+\psi)(\mu_c+\mu+\beta)}<1$$

3.2.4 Stability Analysis of Endemic Equilibrium Point

Based on the endemic equilibrium point obtained, the following Jacobian matrix is formed:

$$J_{(S,I,R,V)}=\begin{bmatrix} -\dfrac{k\alpha}{\mu_c+\mu+\beta} & -\mu_c-\mu-\beta & 0 & 0 \\ \dfrac{k\alpha-\mu\mu_c-\mu^2-\mu\beta-\psi\mu_c-\psi\mu-\psi\beta}{\mu_c+\mu+\beta} & 0 & 0 & 0 \\ 0 & \beta & -\mu-\gamma & 0 \\ \psi & 0 & \gamma & -\mu \end{bmatrix}$$

From the Jacobian matrix, by using $\det(\lambda I-J_{(S,I,R,V)})=0$ then it is obtained:

$$\det\left(\begin{bmatrix} \lambda+\dfrac{k\alpha}{\mu_c+\mu+\beta} & \mu_c+\mu+\beta & 0 & 0 \\ \dfrac{-k\alpha+\mu\mu_c+\mu^2+\mu\beta+\psi\mu_c+\psi\mu+\psi\beta}{\mu_c+\mu+\beta} & \lambda & 0 & 0 \\ 0 & -\beta & \lambda+\mu+\gamma & 0 \\ -\psi & 0 & -\gamma & \lambda+\mu \end{bmatrix}\right)=0$$

Furthermore, with the cofactor expansion method, the characteristic equation is obtained, namely

$$=(\lambda+\mu+\gamma)(\lambda+\mu)\left(\lambda^2+\frac{k\alpha}{\mu_c+\mu+\beta}\lambda+k\alpha-\mu\mu_c-\mu^2-\mu\beta-\psi\mu_c-\psi\mu-\psi\beta\right)$$

Since all parameters are positive, then λ_1 and λ_2 are negative. Therefore, the endemic equilibrium point $(I\neq 0)$ will be locally asymptotically stable if

$$k\alpha-\mu\mu_c-\mu^2-\mu\beta-\psi\mu_c-\psi\mu-\psi\beta<0 \text{ atau } \frac{\alpha k}{(\mu+\psi)(\mu_c+\mu+\beta)}<1$$

3.3 Reproduction Numbers (R_0)

Reproduction Numbers are grouped in three forms. If ($R_0 < 1$), this indicates the spread of Covid-19 will still occur, but over time it will disappear. If ($R_0 > 1$), it shows the potential spread of Covid-19 continues to increase until it is related to death, and if ($R_0 = 1$), then it indicates the occurrence of endemic Covid-19) and remains in the population. The primary reproduction number will be determined using the *Next Generation Matrix*. In determining the reproduction number, subpopulation *I* is considered. Then, the Jacobian matrix substitutes the value of the disease-free equilibrium point into the linearization with *J (I)* in subpopulation *I* so that it is obtained:

$$J = \frac{\alpha k}{\mu + \psi} - \left(\mu_c + \mu + \beta\right)$$

Then, the Jacobian matrix decomposition is carried out into ***J***=***F***-***V***, where *F is* the infection rate that increases in infection cases, and *V* is the infection rate that results in a reduction in infection so that the following is obtained:

$$F = \frac{\alpha k}{\mu + \psi}$$

$$V = (\mu_c + \mu + \beta)$$

In **Equation (8)**, it is obtained the form of a *Next Generation Matrix* with $K = FV^{-1}$as follows:

$$K = \frac{\alpha k}{\mu + \psi\left(\mu_c + \mu + \beta\right)}$$

Based on the calculation, the basic reproduction number is obtained as follows:

$$R_0 = \frac{\alpha k}{(\mu + \psi)(\mu_c + \mu + \beta)}$$

3.4 Simulation Model of Covid-19 Virus Spread in Maluku Province

A simulation of the Maluku Province Covid-19 virus spread model was carried out at this stage. The simulation was carried out by giving parameter values to the model to explain the condition of the spread of the disease, which is displayed in the form of a curve based on the data summarized in **Table 1** below.

Table 1. Parameter Estimation

Parameters	Definition	Value
k	The rate of Individual birth	0,01676
α	The rate of susceptible individuals to infected individuals	0,00011
β	The cure rate of infected individuals	0,84314
γ	The rate of individual vaccination after infection	0,84314
ψ	The rate of Individual vaccination before the infection	0,00404
μ	The rate of individual natural mortality	0,00126
μ_c	The rate of death due to Covid-19 infection	0,01471

According to data from the Central Bureau of Statistics of Maluku Province, the life expectancy of the people of Maluku Province in 2022 is 66.09 years. Thus, the natural mortality rate of individuals in Maluku Province is

$$\mu = \frac{1}{Life\ Expectancy} = \frac{1}{66{,}09\ years} = 0{,}00126\ month^{-1}$$

The mortality rate, recovery rate due to Covid-19 infection, vaccination rate after Covid-19 infection, and vaccination rate before Covid-19 infection are calculated respectively based on data on patients who died and patients who recovered after Covid-19 infection and data on vaccinated individuals. Based on the data obtained, it is known that the average number of patients who die from Covid-19 infection is 3 per month. The average number of patients who recover is 172 per month, while the total number of infected patients per month is 204. Meanwhile, the average number of people vaccinated is 7,693 per month. Thus, the death rate, individual recovery rate, vaccination rate after infection, and vaccination rate after infection in Maluku Province due to Covid-19 are as follows:

$$\alpha(t) = \frac{The\ average\ number\ of\ infected\ patients}{number\ of\ population} = \frac{204}{1.862.626} = 0{,}00011$$

$$\beta(t) = \frac{The\ average\ number\ of\ patients\ cured}{The\ average\ number\ of\ infected\ patients} = \frac{172}{204} = 0{,}84314$$

$$\gamma(t) = \frac{Average\ number\ of\ patients\ vaccinated\ after\ infection}{average\ number\ of\ infected\ patients} = \frac{172}{204} = 0{,}84314$$

$$\psi(t) = \frac{Average\ number\ of\ patients\ vaccinated\ before\ infection}{number\ of\ population} = \frac{7.520}{1.862.626} = 0{,}00404$$

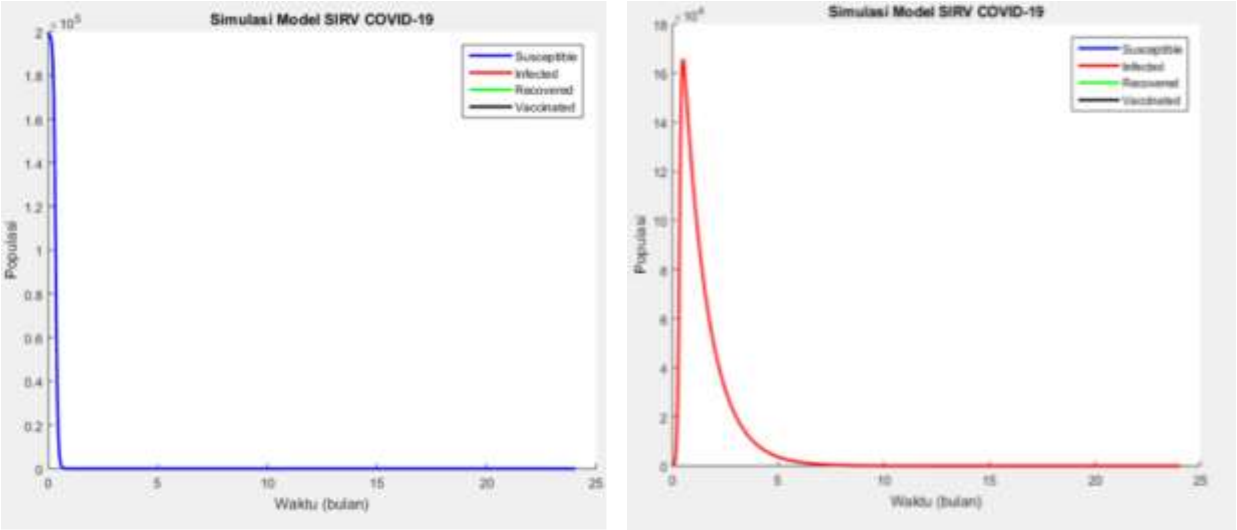
The individual birth rate was calculated based on data on babies born in Maluku Province in 2022. Based on data obtained from the Maluku Provincial Health Office [25], it is known that the number of babies born in Maluku Province in 2022 is 31,217. Thus, the individual birth rate in Maluku Province is

$$k(t) = \frac{Number\ of\ babies\ born}{Total\ resident\ population} = \frac{31.217}{1.862.626} = 0{,}01676$$

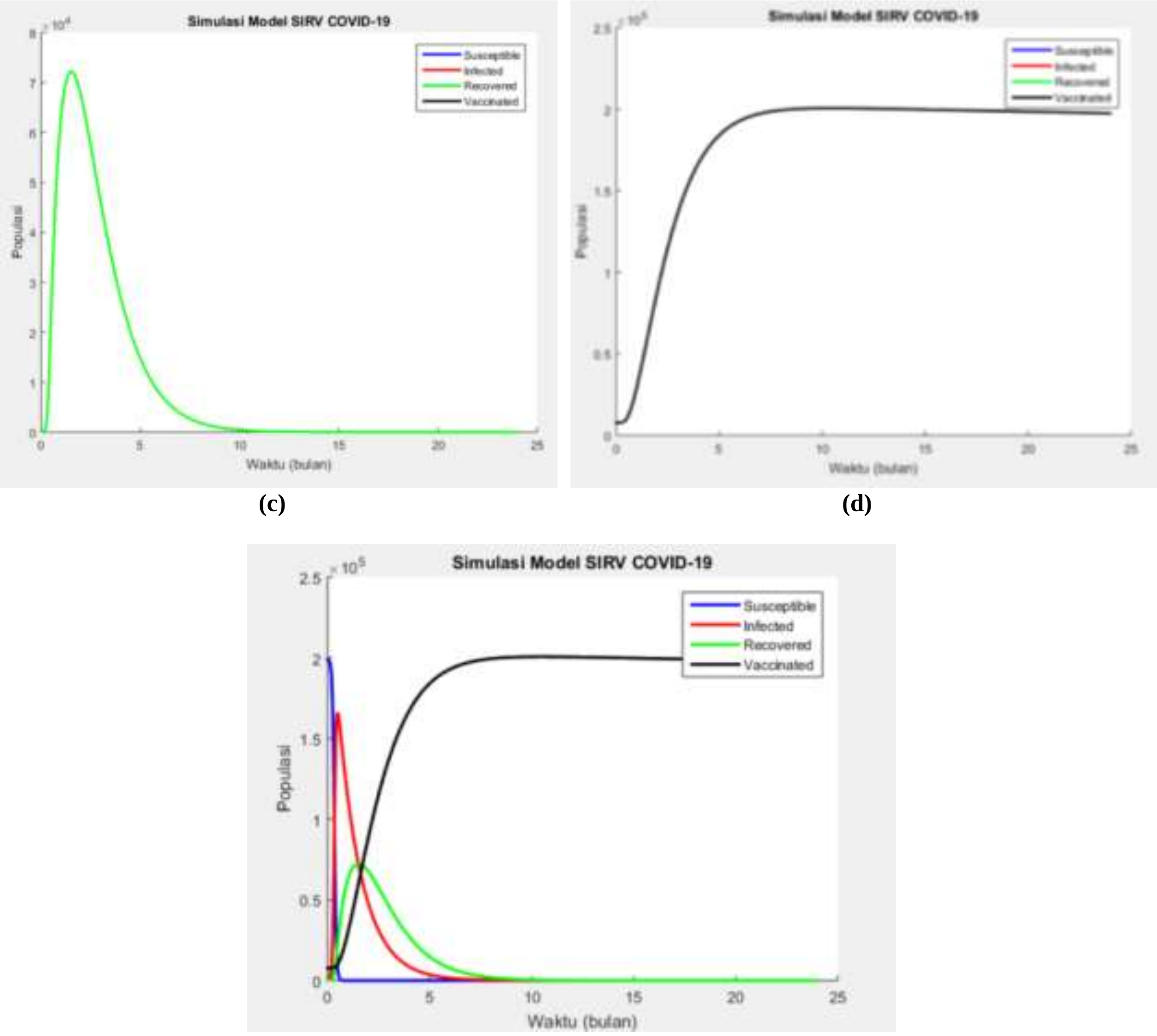
Based on the data obtained, the average number of infected patients each month is 204, so the parameter value of the vulnerable individuals' rate of becoming infected can be obtained.

$$\alpha(t) = \frac{The\ average\ number\ of\ infected\ patients}{number\ of\ population} = \frac{204}{1.862.626} = 0{,}00011$$

The simulation process was performed with an initial time $t_0 = 0$ and end time $t_{24} = 24$, with the initial condition of each state variable is $S_0^* = 198.890,\quad I_0^* = 204,\quad R_0^* = 172,\quad V_0^* = 7.693$



(a) **(b)**



(c) (d)

(e)

Figure 3. Simulation Graph of SIRV Model
(a) Graph of the number of vulnerable individuals, (b) Graph of the number of infected individuals,
(c) Graph of the number of cured individuals, (d) Graph of the number of vaccinated individuals,
(e) SIRV graph

Figure 3 is a simulation result to show the inter-compartmental linkage graph of the four subpopulations. It can be seen that the number of susceptible, infected, and cured individuals decreases drastically as the number of vaccinated individuals increases.

4. CONCLUSIONS

Based on the stability analysis of the SIRV model, the spread of Covid-19 in Maluku Province has two equilibrium points, namely

$E_0(S(t),I(t),R(t),V(t)) = (\frac{k}{\mu+\psi,}, 0,0,\frac{\psi k}{\mu(\mu+\psi)})$ as the disease-free equilibrium point and

$$E_1(S(t), I(t), R(t), V(t)$$
$$= \left\{ \begin{matrix} \left(\frac{\mu_c+\mu+\beta}{\alpha}\right), \left(\frac{k\alpha-\mu\mu_c-\mu^2-\mu\beta-\psi\mu_c-\psi\mu-\psi\beta}{\alpha(\mu_c+\mu+\beta)}\right), \left(\frac{\beta(k\alpha-\mu^2-\mu\mu_c-\beta\mu-\psi\mu_c-\psi\mu-\psi\beta)}{\alpha(\mu_c+\mu+\beta)(\mu+\gamma)}\right), \\ \left(\frac{\gamma\left(\frac{k\alpha\beta-\mu^2\beta-\mu\mu_c\beta-\beta^2\mu-\psi\mu_c\beta-\psi\mu\beta-\psi\beta^2}{\alpha(\mu_c+\mu+\beta)(\mu+\gamma)}\right)+\psi\left(\frac{\mu_c+\mu+\beta}{a}\right)}{\mu}\right) \end{matrix} \right\}$$

with a basic reproduction number is $R_0 = 0{,}00040$. Based on the data and simulation results, it can be concluded that the Covid-19 virus will disappear (stable of equilibrium point) due to the increasing number of vaccinations. $R_0 < 1$, which is due to the increasing number of vaccinations. Therefore, it can be concluded that vaccination can reduce the spread of Covid-19 in Maluku Province.

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