# MATHEMATICAL MODELLING OF THE SPREAD OF COVID-19 WITH FIRST, SECOND AND THIRD DOSES OF VACCINATION IN SEMARANG CITY 

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#### Abstract

This research models the spread of Covid-19 by developing the $S V_{1} V_{2} V_{3} E I R$ model. In this model there are seven compartments, namely the susceptible subpopulation (S), the subpopulation that has received the first dose of vaccine $\left(V_{1}\right)$, the subpopulation that has received the second dose of vaccine $\left(V_{2}\right)$, the subpopulation that has received the third dose of vaccine $\left(V_{3}\right)$, the exposed subpopulation $(E)$, infected subpopulation ( $I$ ), and recovered subpopulation $(R)$. From the model that has been formed, a search for disease-free and endemic equilibrium points is carried out, then looking for the basic reproduction number $\left(R_{0}\right)$ as a benchmark for the presence or absence of the spread of Covid-19 in a population, then numerically simulating it using the Matlab R2017a software. The results of this numerical simulation are in accordance with the dynamic analysis carried out, namely if the condition is $R_{0}<1$ then Covid-19 cannot spread, whereas if the condition is $R_{0}>1$ then Covid-19 can spread in a certain area. In addition, the disease cannot spread quickly if the proportion of those who are vaccinated ( $\delta$ ) is increased, so that the use of vaccines can be used as an effort to prevent the spread of Covid-19.


Keywords: Covid-19, $S V_{1} V_{2} V_{3} E I R$ Model, Vaccination, Equilibrium Point, Basic Reproductive Number

## I. INTRODUCTION

Mathematics has an important role in analyzing and modelling various phenomena. One of the phenomena that can be modeled into a mathematical form is the spread of infectious diseases. Models that can be used to model this phenomenon include the SIR (Susceptible, Infected, Recovered) model and the SEIR (Susceptible, Exposed, Infected, Recovered) model. In the $S I R$ model there are 3 compartments, namely $S$ (Susceptible) or susceptible subpopulation, $I$ (Infected) or infected subpopulation, and $R$ (Recovered) or recovered subpopulation [1]. Meanwhile, the SEIR model has 4 compartments, namely $S$ (Susceptible) or susceptible subpopulation, $E$ (Exposed) or latent subpopulation, I (Infected) or infected subpopulation, and $R$ (Recovered) or recovered subpopulation [2].

Several previous studies have discussed modelling infectious diseases, one of which is research by Zulaikha et al [3] which discusses HFMD (Hand, Foot, and Mouth Disease) which attacks children in China by developing the SEIQR model (Susceptible, Exposed, Infected, Quarantine, Recovered). In addition, other infectious diseases that have been widely studied using mathematical models are Covid-19, including research from Alam dan Abadi [4]. In his research, the model developed was $S V_{1} V_{2} I R$ (Susceptible, Vaccinated 1,

Vaccinated 2, Infected, Recovered) with $V_{1}$ (Vaccinated 1) and $V_{2}$ (Vaccinated 2) being subpopulations that had received the first and second doses of the vaccine. As Med and A'yun [5] also researched the development of an infectious disease model, namely the model (Susceptible, Vaccinated, Not Vaccinated, Infected, Recovered), where $V_{1}$ is a subpopulation that has been vaccinated and $V_{2}$ is a subpopulation that has not been vaccinated. Other research regarding the analysis of the Covid-19 mathematical model has also been carried out by Fitriyah [6]. The model studied in this study is $S V_{1} V_{2} E I I_{v} R$ where $V_{1}$ is a subpopulation that has received the first dose of vaccine, $V_{2}$ is a subpopulation that has received a second dose of vaccine, $I$ is an infected subpopulation that has not carried out the first and second doses of vaccination, and $I_{v}$ is an infected subpopulation that has received the first and second doses of vaccination.

With the existence of this model, the dynamics of the spread of infectious diseases occurring in various regions of the world can be simply represented and can provide predictions of the dynamics of the spread of infectious diseases in the future, thus enabling the control of their spread by suppressing the rate of virus transmission of these infectious diseases. The infectious disease studied in this research is Covid-19, a disease transmitted from animals to humans or zoonosis [7]. With this disease, prevention measures need to be taken, one of which is through vaccination. Vaccines can help the body enhance immunity, so it can prevent the severe symptoms from occurring. In Indonesia, vaccination was carried out in early October 2021 with a total of two doses of vaccine, then due to the emergence of a new variant of Covid-19. In early January 2022, the government increased the vaccine dose to three doses. Due to efforts to prevent Covid-19, this study developed a mathematical model by adding additional variables, namely $V_{1}$ (subpopulation that had received the first dose of vaccination), $V_{2}$ (sub-population that had received the second dose of vaccination), and $V_{3}$ (sub-population that had received the third dose of vaccination). This study focuses on discussing the basic reproduction number $\left(R_{0}\right)$ or the threshold in determining the state of the disease virus in a specific area. This is because the variables used in this research have large dimensions.

## II. MATHEMATICS MODELS

In this study, the mathematical model for the spread of Covid-19 that was developed was the $S V_{1} V_{2} V_{3} E I R$ model with $V_{1}$ (subpopulation that had received the first dose of vaccination), $V_{2}$ (subpopulation that had received the second dose of vaccination), and $V_{3}$ (subpopulation that had received the third dose of vaccination). The model assumptions in determining the spread of Covid-19 in this study are
a. Covid-19 is a fatal disease.
b. The death rate for each subpopulation is assumed to be the same.
c. Each subpopulation has the same proportion infected with Covid-19.
d. Subpopulations that have had their first dose of vaccination have a higher level of immunity than those who have not been vaccinated.
e. The subpopulation that had received the second dose of vaccination had a higher level of immunity than those who had only received the first dose of vaccination.
f. The subpopulation that had received the third dose of vaccination had a higher level of immunity than those who had only received the first and second doses of vaccination.
g. The subpopulations that have received the first, second, and third doses of vaccination can be infected with Covid-19 because they interact with the infected subpopulation, so they enter the Exposed $(E)$ subpopulation.
h. The subpopulation that has not been vaccinated has a higher rate of development of the Covid-19 virus than the subpopulation that has been vaccinated.
i. The subpopulation that is not vaccinated has a lower recovery rate compared to the vaccinated subpopulation.
j. The subpopulation infected with Covid-19 can recover from the disease.
k. The subpopulation recovered has a good level of immune protection, making them less susceptible if they follow health protocols.

The variables and parameters used in the mathematical model of the spread of Covid19 are shown in Table 1 and Table 2 as follows:

Table 1. Variable Mathematical Model of the Spread of Covid-19 with the First, Second, and Third Doses of Vaccination

| Variable | Definition | Unit | Condition |
| :---: | :--- | :---: | :---: |
| $N(t)$ | Total population at time $t$ | Individual | $N(t) \geq 0$ |
| $S(t)$ | The subpopulation susceptible to Covid-19 at time $t$ | Individual | $S(t) \geq 0$ |
| $V_{1}(t)$ | The subpopulation that has had the first dose of vaccination <br> at time $t$ | Individual | $V_{1}(t) \geq 0$ |
| $V_{2}(t)$ | The subpopulation that has had the second dose of <br> vaccination at time $t$ | Individual | $V_{2}(t) \geq 0$ |
| $V_{3}(t)$ | The subpopulation that had received the third dose of <br> vaccination at time $t$ | Individual | $V_{3}(t) \geq 0$ |
| $E(t)$ | The subpopulation exposed to Covid-19 at time $t$ | Individual | $E(t) \geq 0$ |
| $I(t)$ | The subpopulation infected with Covid-19 at time $t$ | Individual | $I(t) \geq 0$ |
| $R(t)$ | The subpopulation recovered from Covid-19 at time $t$ | Individual | $R(t) \geq 0$ |

Illustratively the process of spreading Covid-19 with the first, second and third doses of vaccination is shown in Figure 1 as follows.


Figure 1. $S V_{1} V_{2} V_{3}$ EIR Compartmental Model Diagram

Table 4.2 Parameters of the Mathematical Model for the Spread of Covid-19 with the First, Second, and Third Doses of Vaccination

| Parameter | Definition | Unit | Condition |
| :---: | :---: | :---: | :---: |
| $\mu$ | Natural death rate | $\frac{1}{\text { time }}$ | $\mu \geq 0$ |
| $\pi$ | Birth rate | $\frac{\text { individual }}{\text { day }}$ | $\pi \geq 0$ |
| $\beta$ | Rate of infective interaction between subpopulations susceptible (Susceptible) and subpopulations infected with Covid19 (Infected) | $\frac{1}{\text { individual } \cdot \text { day }}$ | $\beta \geq 0$ |
| $\alpha$ | Virus growth rate | $\frac{1}{d a y}$ | $\alpha \geq 0$ |
| $\gamma$ | Recovery rate of the subpopulation infected with Covid-19 | $\frac{1}{d a y}$ | $\gamma \geq 0$ |
| $\omega_{1}$ | Rate of the Susceptible subpopulation receiving the first dose of vaccination | $\frac{1}{d a y}$ | $\omega_{1} \geq 0$ |
| $\omega_{2}$ | Rate of the Vaccinated 1 subpopulation receiving the second dose of vaccination | $\frac{1}{d a y}$ | $\omega_{2} \geq 0$ |
| $\omega_{3}$ | Rate of the Vaccinated 2 subpopulation receiving the third dose of vaccination | $\frac{1}{d a y}$ | $\omega_{3} \geq 0$ |
| $\sigma_{1}$ | Percentage decrease in the effectiveness of the first dose of the vaccine | Percent | $\sigma_{1} \geq 0$ |
| $\sigma_{2}$ | Percentage decrease in the effectiveness of the second dose of the vaccine | Percent | $\sigma_{2} \geq 0$ |
| $\sigma_{3}$ | Percentage decrease in the effectiveness of the third dose of the vaccine | Percent | $\sigma_{3} \geq 0$ |
| $\beta_{1}$ | Rate of infective interaction between the subpopulation that has received the first dose of vaccination and the infected subpopulation | $\frac{1}{\text { individual } \cdot \text { day }}$ | $\beta_{1} \geq 0$ |
| $\beta_{2}$ | Rate of infective interaction between the subpopulation that has received the second dose of vaccination and the infected subpopulation | $\frac{1}{\text { individual } \cdot \text { day }}$ | $\beta_{2} \geq 0$ |
| $\beta_{3}$ | Rate of infective interaction between the subpopulation that has received the third dose of vaccination and the infected subpopulation | $\frac{1}{\text { individual } \cdot \text { day }}$ | $\beta_{3} \geq 0$ |
| $\mu_{k}$ | Death rate due to Covid-19 | $\frac{1}{d a y}$ | $\mu_{k} \geq 0$ |
| $\delta$ | Proportion of the Susceptible subpopulation that has been vaccinated | - | $0 \leq \delta \leq 1$ |

Based on the diagram in Figure 1, it can be seen that the compartment is divided into seven subpopulations, namely subpopulations that are susceptible to Covid-19 (S), subpopulations that have carried out the first dose of vaccination $\left(V_{1}\right)$, subpopulations that have carried out the second dose of vaccination $\left(V_{2}\right)$, subpopulations that have administering the third dose of vaccination $\left(V_{3}\right)$, subpopulations exposed to Covid-19 $(E)$, subpopulations infected with Covid-19 (I), and subpopulations recovering from Covid-19 (R).

The following is a model of the spread of Covid-19 involving the first to third doses of vaccination:

$$
\begin{align*}
& \left\{\begin{array}{l}
\frac{d S}{d t}=\pi-(1-\delta) \beta S I-\delta \omega_{1} S-\mu S \\
\frac{d V_{1}}{d t}=\delta \omega_{1} S-\sigma_{1} \beta_{1} I V_{1}-\omega_{2} V_{1}-\mu V_{1} \\
\frac{d V_{2}}{d t}=\omega_{2} V_{1}-\sigma_{2} \beta_{2} I V_{2}-\omega_{3} V_{2}-\mu V_{2} \\
\frac{d V_{3}}{d t}=\omega_{3} V_{2}-\sigma_{3} \beta_{3} I V_{3}-\mu V_{3} \\
\frac{d E}{d t}=(1-\delta) \beta S I-\alpha E+\sigma_{1} \beta_{1} I V_{1}+\sigma_{2} \beta_{2} I V_{2}+\sigma_{3} \beta_{3} I V_{3}-\mu E \\
\frac{d I}{d t}=\alpha E-\left(\mu+\mu_{k}\right) I-\gamma I \\
\frac{d R}{d t}=\gamma I-\mu R \\
\text { with } N=S+V_{1}+V_{2}+V_{3}+E+I+R
\end{array}\right. \\
&
\end{align*}
$$

In the system of equation (1), a simplification process is carried out by changing the system into a proportion form between the number of subpopulations and the total population. The system of equations (1) can be simplified by assuming
$s=\frac{S}{N}, v_{1}=\frac{V_{1}}{N}, v_{2}=\frac{V_{2}}{N}, v_{3}=\frac{V_{3}}{N}, e=\frac{E}{N}, i=\frac{I}{N}, r=\frac{R}{N}$
$b=\beta N, b_{1}=\beta_{1} N, b_{2}=\beta_{2} N, b_{3}=\beta_{3} N, \Pi=\frac{\pi}{N}$
Obtained $s+v_{1}+v_{2}+v_{3}+e+i+r=\frac{S}{N}+\frac{V_{1}}{N}+\frac{V_{2}}{N}+\frac{V_{3}}{N}+\frac{E}{N}+\frac{I}{N}+\frac{R}{N}=1$
So that the system of equations (1) can be simplified by substituting equation (2) into the system of equations (1). In addition, the system of equation (1) does not contain the variable $r$, so the variable $r$ is temporarily ignored from the system because it has no effect on other equations, then the recovered subpopulation $(r)$ can be calculated using the formula $r=1-\left(s+v_{1}+v_{2}+v_{3}+e+i\right)$. Therefore, the system of equations (1) can be written as follows:

$$
\left\{\begin{array}{l}
\frac{d s}{d t}=\Pi-(1-\delta) b s i-\delta \omega_{1} s-\mu s  \tag{3}\\
\frac{d v_{1}}{d t}=\delta \omega_{1} s-\sigma_{1} b_{1} i v_{1}-\omega_{2} v_{1}-\mu v_{1} \\
\frac{d v_{2}}{d t}=\omega_{2} v_{1}-\sigma_{2} b_{2} i v_{2}-\omega_{3} v_{2}-\mu v_{2} \\
\frac{d v_{3}}{d t}=\omega_{3} v_{2}-\sigma_{3} b_{3} i v_{3}-\mu v_{3} \\
\frac{d e}{d t}=(1-\delta) b s i-\alpha e+\sigma_{1} b_{1} i v_{1}+\sigma_{2} b_{2} i v_{2}+\sigma_{3} b_{3} i v_{3}-\mu e \\
\frac{d i}{d t}=\alpha e-\left(\mu+\mu_{k}\right) i-\gamma i
\end{array}\right.
$$

Because each variable of the system of differential equations (3) is a human subpopulation, it is necessary to show that all variables $s(t), v_{1}(t), v_{2}(t), v_{3}(t), e(t), i(t), r(t)$ positive and boundness for each $t>0$.

Teorema 1 If $s(0) \geq 0, v_{1} \geq 0, v_{2} \geq 0, v_{3} \geq 0, e(0) \geq 0, i(0) \geq 0$, and $r \geq 0$ then the set of solutions $\left\{s(t), v_{1}(t), v_{2}(t), v_{3}(t), e(t), i(t), r(t)\right\}$ of the system of equations (3) consists of positive elements for each $t>0$.
Proof: Suppose $N(t)=s(t)+v_{1}(t)+v_{2}(t)+v_{3}(t)+e(t)+i(t)+r(t)$, it will be shown that the solution of the system of equations (3) positive. Proof of a positive solution is given from points a$)-\mathrm{g}$ ).
a) From the first equation in the system of equations (3) is obtained

$$
\begin{aligned}
& \Leftrightarrow \frac{d s}{d t}=\Pi-(1-\delta) b s i-\delta \omega_{1} s-\mu s \geq-\left((1-\delta) b i+\delta \omega_{1}+\mu\right) s \\
& \Leftrightarrow \frac{d s}{s} \geq-\left((1-\delta) b i+\delta \omega_{1}+\mu\right) d t
\end{aligned}
$$

From the equation above, the two sides are integrated to obtain

$$
\begin{aligned}
& \Leftrightarrow \int \frac{d s}{s} \geq \int-\left((1-\delta) b i+\delta \omega_{1}+\mu\right) d t \\
& \Leftrightarrow \ln |s| \geq\left(-\int((1-\delta) b i) d t\right)-\left(\delta \omega_{1}+\mu\right) t+C \\
& \Leftrightarrow s(t) \geq A e^{\left.-\int((1-\delta) i) i\right) d t} e^{-\left(\delta \omega_{1}+\mu\right) t}, \text { dengan } e^{C}=A
\end{aligned}
$$

When $t=0$ then

$$
\Leftrightarrow s(t) \geq 0
$$

b) From the second equation in the system of equations (3) is obtained

$$
\begin{aligned}
& \Leftrightarrow \frac{d v_{1}}{d t}=\omega_{1} s-\sigma_{1} b_{1} i v_{1}-\omega_{2} v_{1}-\mu v_{1} \geq-\left(\sigma_{1} b_{1} i+\omega_{2}+\mu\right) v_{1} \\
& \Leftrightarrow \frac{d v_{1}}{v_{1}} \geq-\left(\sigma_{1} b_{1} i+\omega_{2}+\mu\right) d t
\end{aligned}
$$

From the equation above, the two sides are integrated to obtain
$\Leftrightarrow \int \frac{d v_{1}}{v_{1}} \geq \int-\left(\sigma_{1} b_{1} i+\omega_{2}+\mu\right) d t$
$\Leftrightarrow \ln \left|v_{1}\right| \geq\left(-\int\left(\sigma_{1} b_{1} i\right) d t\right)-\left(\omega_{2}+\mu\right) t+C$
$\Leftrightarrow v_{1}(t) \geq A e^{-\int\left(\sigma_{1} b_{1} i\right) d t} e^{-\left(\omega_{2}+\mu\right) t}$, dengan $e^{C}=A$
When $t=0$ then
$\Leftrightarrow v_{1}(t) \geq 0$
c) From the third equation in the system of equations (3) is obtained
$\Leftrightarrow \frac{d v_{2}}{d t}=\omega_{2} v_{1}-\sigma_{2} b_{2} i v_{2}-\omega_{3} v_{2}-\mu v_{2} \geq-\left(\sigma_{2} b_{2} i+\omega_{3}+\mu\right) v_{2}$
$\Leftrightarrow \frac{d v_{2}}{v_{2}} \geq-\left(\sigma_{2} b_{2} i+\omega_{3}+\mu\right) d t$
From the equation above, the two sides are integrated to obtain
$\Leftrightarrow \int \frac{d v_{2}}{v_{2}} \geq \int-\left(\sigma_{2} b_{2} i+\omega_{3}+\mu\right) d t$
$\Leftrightarrow \ln \left|v_{2}\right| \geq\left(-\int\left(\sigma_{2} b_{2} i\right) d t\right)-\left(\omega_{3}+\mu\right) t+C$
$\Leftrightarrow v_{2}(t) \geq A e^{-\int\left(\sigma_{2} b_{2} i\right) d t} e^{-\left(\omega_{3}+\mu\right) t}$, dengan $e^{C}=A$
When $t=0$ then
$\Leftrightarrow v_{2}(t) \geq 0$
d) From the fourth equation in the system of equations (3) is obtained
$\Leftrightarrow \frac{d v_{3}}{d t}=\omega_{3} v_{2}-\sigma_{3} b_{3} v_{3}-\mu v_{3} \geq-\left(\sigma_{3} b_{3} i+\mu\right) v_{3}$
$\Leftrightarrow \frac{d v_{3}}{v_{3}} \geq-\left(\sigma_{3} b_{3} i+\mu\right) d t$
From the equation above, the two sides are integrated to obtain
$\Leftrightarrow \int \frac{d v_{3}}{v_{3}} \geq \int-\left(\sigma_{3} b_{3} i+\mu\right) d t$
$\Leftrightarrow \ln \left|v_{3}\right| \geq\left(-\int\left(\sigma_{3} b_{3} i\right) d t\right)-\mu t+C$
$\Leftrightarrow v_{3}(t) \geq A e^{-\int\left(\sigma_{3} b_{3}\right) d t} e^{-\mu t}$, dengan $e^{C}=A$
When $t=0$ then
$\Leftrightarrow v_{3}(t) \geq 0$
e) From the fifth equation in the system of equations (3) is obtained
$\Leftrightarrow \frac{d e}{d t}=(1-\delta) b s i-\alpha e+\sigma_{1} b_{1} i v_{1}+\sigma_{2} b_{2} i v_{2}+\sigma_{3} b_{3} i v_{3}-\mu e \geq-(\alpha+\mu) e$
$\Leftrightarrow \frac{d e}{e} \geq-(\alpha+\mu) d t$
From the equation above, the two sides are integrated to obtain
$\Leftrightarrow \int \frac{d e}{e} \geq \int-(\alpha+\mu) d t$
$\Leftrightarrow \ln |e| \geq-(\alpha+\mu) t+C$
$\Leftrightarrow e(t) \geq A e^{-(\alpha+\mu) t}$, dengan $e^{C}=A$
When $t=0$ then

$$
\Leftrightarrow e(t) \geq 0
$$

f) From the sixth equation in the system of equations (3) is obtained
$\Leftrightarrow \frac{d i}{d t}=\alpha e-\left(\mu+\mu_{k}\right) i-\gamma i \geq-\left(\left(\mu+\mu_{k}\right)+\gamma\right) i$
$\Leftrightarrow \frac{d i}{i} \geq-\left(\left(\mu+\mu_{k}\right)+\gamma\right) d t$
From the equation above, the two sides are integrated to obtain
$\Leftrightarrow \int \frac{d i}{i} \geq \int-\left(\left(\mu+\mu_{k}\right)+\gamma\right) d t$
$\Leftrightarrow \ln |i| \geq-\left(\left(\mu+\mu_{k}\right)+\gamma\right) t+C$
$\Leftrightarrow i(t) \geq A e^{-\left(\left(\mu+\mu_{k}\right)+\gamma\right) t}$, dengan $e^{C}=A$
When $t=0$ then
$\Leftrightarrow i(t) \geq 0$
g) From the seventh equation in the system of equations (3) is obtained $h$
$\Leftrightarrow \frac{d r}{d t}=\gamma i-\mu r \geq-\mu r$
$\Leftrightarrow \frac{d r}{r} \geq-\mu d t$
From the equation above, the two sides are integrated to obtain
$\Leftrightarrow \int \frac{d r}{r} \geq \int-\mu d t$
$\Leftrightarrow \ln |r| \geq-\mu t+C$
$\Leftrightarrow r(t) \geq A e^{-\mu t}$, dengan $e^{C}=A$
When $t=0$ then
$\Leftrightarrow r(t) \geq 0$
Therefore, it is proven that equation a$)$-g) is a positive solution.
Teorema 2 The set of solutions $\left\{s(t), v_{1}(t), v_{2}(t), v_{3}(t), e(t), i(t), r(t)\right\}$ of the system of equations (3) with initial conditions is limited to the region $\Omega=$ $\left\{\left(s(t), v_{1}(t), v_{2}(t), v_{3}(t), e(t), i(t), r(t)\right) \in \mathbb{R}_{+}^{7}: 0 \leq N \leq \frac{\Pi}{\mu}\right\}$
Proof: The total population of the system of equation (3) is $N(t)=s(t)+v_{1}(t)+v_{2}(t)+$ $v_{3}(t)+e(t)+i(t)+r(t) . N$ differentiable with respect to $t$ is obtained
$\frac{d N}{d t}=\frac{d s}{d t}+\frac{d v_{1}}{d t}+\frac{d v_{2}}{d t}+\frac{d v_{3}}{d t}+\frac{d e}{d t}+\frac{d i}{d t}+\frac{d r}{d t}$

$$
\begin{aligned}
& \Leftrightarrow \frac{d N}{d t}=\Pi-\mu\left(s+v_{1}+v_{2}+v_{3}+e+i+r\right)-\mu_{k} i \\
& \Leftrightarrow \frac{d N}{d t}=\Pi-\mu N-\mu_{k} i
\end{aligned}
$$

Because the state variable of equation $i$ is positive for every $t \geq 0$ is obtained $\frac{d N}{d t} \leq \Pi-\mu N$
Because $N(t) \geq 0$ then $\frac{d N}{d t} \geq 0$ so we get $0 \leq \Pi-\mu N$ or $(t) \leq \frac{\Pi}{\mu}$. So it is evident that the solution to the system of equations (3) is boundness.

## III. ANALYSIS OF THE MODEL

The system of equations (3) has an equilibrium point. The equilibrium point is obtained when the sixth equations of the system of equations (3) equal zero or $\frac{d s}{d t}=\frac{d v_{1}}{d t}=\frac{d v_{2}}{d t}=\frac{d v_{3}}{d t}=$ $\frac{d e}{d t}=\frac{d i}{d t}=0$. So the system of equation (3) becomes

$$
\begin{align*}
& \Pi-(1-\delta) b s i-\delta \omega_{1} s-\mu s=0  \tag{4}\\
& \delta \omega_{1} s-\sigma_{1} b_{1} i v_{1}-\omega_{2} v_{1}-\mu v_{1}=0  \tag{5}\\
& \omega_{2} v_{1}-\sigma_{2} b_{2} i v_{2}-\omega_{3} v_{2}-\mu v_{2}=0  \tag{6}\\
& \omega_{3} v_{2}-\sigma_{3} b_{3} i v_{3}-\mu v_{3}=0  \tag{7}\\
& (1-\delta) b s i-\alpha e+\sigma_{1} b_{1} v_{1}+\sigma_{2} b_{2} i v_{2}+\sigma_{3} b_{3} i v_{3}-\mu e=0  \tag{8}\\
& \alpha e-\left(\mu+\mu_{k}\right) i-\gamma i=0 \tag{9}
\end{align*}
$$

The equilibrium point in the system of equations (4) to (9) is divided into two, namely disease-free and endemic equilibrium points. From the disease-free equilibrium point, the basic reproduction number $\left(R_{0}\right)$ can be obtained in the system of equation (3). The following is the disease-free equilibrium point, the basic reproduction number ( $R_{0}$ ), and the endemic equilibrium point of the system of equations (3).

### 3.1 Disease-Free Equilibrium Point

The disease-free equilibrium point is obtained when there is no disease in a population, so $i=0$. So, the disease-free equilibrium point is obtained from the system of equation (3), namely

$$
\begin{aligned}
& T K_{1}=\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) \\
& T K_{1}=\left(\frac{\Pi}{\left(\delta \omega_{1}+\mu\right)}, \frac{\delta \omega_{1} \Pi}{\left(\delta \omega_{1}+\mu\right)\left(\omega_{2}+\mu\right)}, \frac{\delta \omega_{1} \omega_{2} \Pi}{\left(\delta \omega_{1}+\mu\right)\left(\omega_{2}+\mu\right)\left(\omega_{3}+\mu\right)}, \frac{\delta \omega_{1} \omega_{2} \omega_{3} \Pi}{\left(\delta \omega_{1}+\mu\right)\left(\omega_{2}+\mu\right)\left(\omega_{3}+\mu\right) \mu}, 0,0\right)
\end{aligned}
$$

### 3.2 Basic Reproduction Number

The basic reproduction number is obtained using the next generation matrix method. The step in obtaining the results of the basic reproduction number in the system of equations (3),
namely taking the equations of the infected class subpopulations in the equation system, including the disease-exposed subpopulation (e) and the disease-infected subpopulation (i), is then formed into a matrix. Then, decompose the matrix formed in the second step into the following matrix form $\dot{\mathbf{x}}=\boldsymbol{F}-\boldsymbol{V}$ as following
$F=\left[\begin{array}{c}(1-\delta) b s i+\sigma_{1} b_{1} i v_{1}+\sigma_{2} b_{2} i v_{2}+\sigma_{3} b_{3} i v_{3} \\ 0\end{array}\right]$
$F=\left[\begin{array}{c}u s i+k i v_{1}+x i v_{2}+y i v_{3} \\ 0\end{array}\right]$
and
$V=\left[\begin{array}{c}(\alpha+\mu) e \\ -\alpha e+\left(\mu+\mu_{k}+\gamma\right) i\end{array}\right]$
$V=\left[\begin{array}{c}m e \\ -\alpha e+n i\end{array}\right]$
with
$m=(\alpha+\mu), n=\left(\mu+\mu_{k}+\gamma\right), u=(1-\delta) b, k=\sigma_{1} b_{1}$
$x=\sigma_{2} b_{2}$, and $y=\sigma_{3} b_{3}$
Furthermore linearize the transmission matrix ( F ) and transition matrix $(\mathrm{V})$ into the form of matrix F and matrix V as follows:

$$
\begin{align*}
\mathbb{F} & =\frac{\partial F_{i}}{\partial e, i}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) \\
& =\left[\begin{array}{ll}
\frac{d e}{d e}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) & \frac{d e}{d i}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) \\
\frac{d i}{d e}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) & \frac{d i}{d i}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right)
\end{array}\right] \\
& =\left[\begin{array}{ll}
0 & u\left(\frac{\Pi}{p}\right)+k\left(\frac{\delta \omega_{1} \Pi}{p q}\right)+x\left(\frac{\delta \omega_{1} \omega_{2} \Pi}{p q r}\right)+y\left(\frac{\delta \omega_{1} \omega_{2} \omega_{3} \Pi}{p q r \mu}\right) \\
0 & 0
\end{array}\right] \tag{10}
\end{align*}
$$

and

$$
\begin{align*}
\mathbb{V} & =\frac{\partial V_{i}}{\partial e, i}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) \\
& =\left[\begin{array}{ll}
\frac{d e}{d e}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) & \frac{d e}{d i}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) \\
\frac{d i}{d e}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right) & \frac{d i}{d i}\left(\hat{s}, \hat{v}_{1}, \hat{v}_{2}, \hat{v}_{3}, \hat{e}, \hat{i}\right)
\end{array}\right] \\
& =\left[\begin{array}{cc}
\alpha+\mu & 0 \\
-\alpha & \mu+\mu_{k}+\gamma
\end{array}\right] \\
& =\left[\begin{array}{cc}
m & 0 \\
-\alpha & n
\end{array}\right] \tag{11}
\end{align*}
$$

with

$$
\begin{aligned}
& m=(\alpha+\mu), n=\left(\mu+\mu_{k}+\gamma\right), u=(1-\delta) b, k=\sigma_{1} b_{1} \\
& x=\sigma_{2} b_{2}, y=\sigma_{3} b_{3}, p=\delta \omega_{1}+\mu, q=\omega_{2}+\mu, \text { and } r=\omega_{3}+\mu
\end{aligned}
$$

The equation V is inverted, so it is obtained as follows

$$
\begin{align*}
\mathbb{V}^{-1} & =\frac{1}{m n}\left[\begin{array}{cc}
n & 0 \\
\alpha & m
\end{array}\right] \\
\mathbb{V}^{-1} & =\left[\begin{array}{ll}
\frac{1}{m} & 0 \\
\frac{\alpha}{m n} & \frac{1}{n}
\end{array}\right] \tag{12}
\end{align*}
$$

Furthermore, determining the next generation matrix by looking for the value of $K=\mathbb{F V}^{-1}$ to obtain two different eigenvalues, namely

$$
\begin{aligned}
& \lambda_{1}=0 \\
& \lambda_{2}=\left(\frac{\alpha u \Pi \mu q r+\alpha k \delta \omega_{1} \Pi \mu r+\alpha x \delta \omega_{1} \omega_{2} \Pi \mu+\alpha y \delta \omega_{1} \omega_{2} \omega_{3} \Pi}{m n \mu p q r}\right)
\end{aligned}
$$

So

$$
R_{0}=\left(\frac{\alpha u \Pi \mu q r+\alpha k \delta \omega_{1} \Pi \mu r+\alpha x \delta \omega_{1} \omega_{2} \Pi \mu+\alpha y \delta \omega_{1} \omega_{2} \omega_{3} \Pi}{m n \mu p q r}\right)
$$

with

$$
\begin{aligned}
& m=(\alpha+\mu) \\
& n=\left(\mu+\mu_{k}+\gamma\right) \\
& u=(1-\delta) b \\
& k=\sigma_{1} b_{1} \\
& x=\sigma_{2} b_{2} \\
& y=\sigma_{3} b_{3} \\
& p=\delta \omega_{1}+\mu \\
& q=\omega_{2}+\mu \\
& r=\omega_{3}+\mu
\end{aligned}
$$

### 3.3 Endemic Equilibrium Point

Furthermore, the endemic equilibrium point of the Covid-19 distribution model is in the system of equation (2), then the equilibrium point is obtained when the spread of disease occurs in a population $\left(i^{*}>0\right)$. The endemic equilibrium point is obtained $T K_{2}=\left(s^{*}, v_{1}^{*}, v_{2}^{*}\right.$ $\left.v_{3}^{*}, e^{*}, i^{*}\right)$ with

$$
\begin{aligned}
& s^{*}=\frac{\Pi}{u i^{*}+p} \\
& v_{1}^{*}=\frac{\delta \omega_{1} \Pi}{\left(u i^{*}+p\right)\left(k i^{*}+q\right)} \\
& v_{2}^{*}=\frac{\delta \omega_{1} \omega_{2} \Pi}{\left(u i^{*}+p\right)\left(k i^{*}+q\right)\left(x i^{*}+r\right)} \\
& v_{3}^{*}=\frac{\delta \omega_{1} \omega_{2} \omega_{3} \Pi}{\left(u i^{*}+p\right)\left(k i^{*}+q\right)\left(x i^{*}+r\right)\left(y i^{*}+\mu\right)} \\
& e^{*}=\frac{i^{*}}{m}\left[u\left(\frac{\Pi}{u i^{*}+p}\right)+k\left(\frac{\delta \omega_{1} \Pi}{\left(u i^{*}+p\right)\left(k i^{*}+q\right)}\right)+x\left(\frac{\delta \omega_{1} \omega_{\omega^{*}} \Pi}{\left(u i^{*}+p\right)\left(k i^{*}+q\right)\left(x i^{*}+r\right)}\right)+y\left(\frac{\delta \omega_{1} \omega_{2} \omega_{\Pi} \Pi}{\left(u i^{*}+p\right)\left(k i^{*}+q\right)\left(x i^{*}+r\right)\left(y i^{*}+\mu\right)}\right)\right]
\end{aligned}
$$

and $i^{*}>0$ if $R_{0}>1$ and satisfy several possibilities that $i^{*}$ has exactly one positive real root by using Descartes' sign rule.

## IV. NUMERICAL SIMULATION

The parameter values used in the Covid-19 spread model were obtained from previous research, while the total population and each sub-population were obtained from BPS data [15] and Covid-19 cases in Semarang City in 2022. The data provided have been obtained including $S$ (Susceptible) $=989.150, V_{1}($ Vaccinated 1$)=236.408, V_{2}($ Vaccinated 2$)=$ 168.919, $V_{3}($ Vaccinated 3) $=108.709, E \quad($ Exposed $)=25.127, I \quad($ Infected $)=27.741, R$ $($ Recovered $)=100.510, N($ total population in Semarang City $)=1.656 .564$.

### 4.1 Simulation when Disease-Free

The initial values used to carry out the simulation when disease free are $S(0)=0,598, V_{1}(0)=$ $0,143, V_{2}(0)=0,102, V_{3}(0)=0,066, E(0)=0,015, I(0)=0,017$. Parameter values used to obtain the simulation results of the spread of Covid-19 are shown in Table 3:

Table 3. Parameter Value when $R_{0}<1$

| Parameter | Value | References |
| :---: | :---: | :---: |
| $\mu$ | 0,013 | Assumption |
| $\Pi$ | 0,67 | Assumption |
| $\beta$ | 0,007 | $[6]$ |
| $\alpha$ | 0,001 | $[8]$ |
| $\gamma$ | 0,09 | $[9]$ |
| $\omega_{1}$ | 0,022 | $[6]$ |
| $\omega_{2}$ | 0,0071 | $[6]$ |
| $\omega_{3}$ | 0,0056 | $[10]$ |
| $\sigma_{1}$ | 0,447 | $[6]$ |
| $\sigma_{2}$ | 0,22 | $[11]$ |
| $\sigma_{3}$ | 0,8 | $[12]$ |
| $\beta_{1}$ | 0,005 | $[6]$ |
| $\beta_{2}$ | 0,002 | $[6]$ |
| $\beta_{3}$ | 0,01 | $[13]$ |
| $\mu_{k}$ | 0,002 | $[14]$ |
| $\delta$ | 0,31 | $[15]$ and $[16]$ |

Furthermore, plots are displayed with different values of the basic reproduction number ( $R_{0}$ ) namely when $R_{0}=0,14 ; R_{0}=0,201$; and $R_{0}=0,22$ to see the condition of the disease-free equilibrium point. These different basic reproduction numbers are obtained by changing the value of the parameter $\delta$ which is presented in Table 4 below:

Table 4. Parameter Value $\delta$ for $R_{0}=0,14 ; R_{0}=0,201$; and $R_{0}=0,22$

| Parameter | Parameter Value <br> for $\boldsymbol{R}_{\mathbf{0}}=\mathbf{0}, \mathbf{1 4}$ | Parameter Value for <br> $\boldsymbol{R}_{\mathbf{0}}=\mathbf{0 , 2 0 1}$ | Parameter Value <br> for $\boldsymbol{R}_{\mathbf{0}}=\mathbf{0 , 2 2}$ |
| :---: | :---: | :---: | :---: |
| $\delta$ | 0,31 | 0,1 | 0,05 |

Based on Table 4, the following simulation results are obtained:


Figure 2. Simulation when $R_{0}=0,14$


Figure 3. Simulation when $R_{0}=0,201$


Figure 4. Simulation when $R_{0}=0,22$

Based on Figure 2 when $R_{0}=0,14$ the solution for each subpopulation $S, V_{1}, V_{2}, V_{3}, E$, and $I$ was obtained sequentially to 33,$804 ; 11,47 ; 4,378 ; 1,88 ; 0 ; 0$, then in Figure 3 when $R_{0}=$ 0,201 the solution for each subpopulation $S, V_{1}, V_{2}, V_{3}, E$, and $I$ was obtained sequentially to 44,$079 ; 4,824 ; 1,842 ; 0,793 ; 0 ; 0$, then in Figure 4 when $R_{0}=0,22$ the solution for each subpopulation $S, V_{1}, V_{2}, V_{3}, E$, and $I$ was obtained sequentially to 47,$518 ; 2,6 ; 0,993$; 0,$428 ; 0 ; 0$. These values are disease-free equilibrium points in each state of $R_{0}$. Thus, when $R_{0}<1$, the solution for each subpopulation tends to reach a disease-free equilibrium point.

### 4.2 Simulation when Endemic

The initial values used to carry out the simulation when endemic are $S(0)=0,598$, $V_{1}(0)=0,143, V_{2}(0)=0,102, V_{3}(0)=0,066, E(0)=0,015, I(0)=0,017$. Parameter values used to obtain the simulation results of the spread of Covid-19 are shown in Table 5:

Table 5. Parameter Value when $R_{0}>1$

| Parameter | Value | References |
| :---: | :---: | :---: |
| $\mu$ | 0,013 | Assumption |
| $\Pi$ | 0,67 | Assumption |
| $\beta$ | 0,05 | Assumption |
| $\alpha$ | 0,036 | $[14]$ |
| $\gamma$ | 0,09 | $[9]$ |
| $\omega_{1}$ | 0,022 | $[6]$ |
| $\omega_{2}$ | 0,0071 | $[6]$ |
| $\omega_{3}$ | 0,0056 | $[10]$ |
| $\sigma_{1}$ | 0,447 | $[6]$ |
| $\sigma_{2}$ | 0,22 | $[11]$ |
| $\sigma_{3}$ | 0,8 | $[12]$ |
| $\beta_{1}$ | 0,03 | Assumption |
| $\beta_{2}$ | 0,02 | Assumption |
| $\beta_{3}$ | 0,06 | Assumption |
| $\mu_{k}$ | 0,002 | $[14]$ |
| $\delta$ | 0,11 | Assumption |
|  |  |  |

Furthermore, plots are shown with different basic reproduction number values $\left(R_{0}\right)$ namely when $R_{0}=14,37 ; R_{0}=15,098$; and $R_{0}=16,28$ to see the condition of the endemic equilibrium point. These different basic reproduction numbers are obtained by changing the value of the parameter $\delta$ which is presented in Table 6 below:

| Parameter | Parameter Value for $R_{0}=$ 14,37 | Parameter Value for $R_{0}=15,098$ | Parameter Value for $R_{0}=16,28$ |
| :---: | :---: | :---: | :---: |
| $\delta$ | 0,11 | 0,085 | 0,048 |

Based on Table 6, the simulation results are obtained as follows:


Figure 5. Simulation when $R_{0}=14,37$


Figure 6. Simulation when $R_{0}=15,098$


Figure 7. Simulation when $R_{0}=16,28$
Based on Figure 5 when $R_{0}=14,37$ the solution for each subpopulation $S, V_{1}, V_{2}, V_{3}, E$, and $I$ was obtained sequentially to 3,$1799 ; 0,097 ; 0,0183 ; 0,00046 ; 12,799 ; 4,388223836$, then in Figure 6 when $R_{0}=15,098$ the solution for each subpopulation $S, V_{1}, V_{2}, V_{3}, E$, and $I$ was obtained sequentially to 3,$1 ; 0,073 ; 0,014 ; 0,00034 ; 12,828 ; 4,398$, then in Figure 7 when $R_{0}=16,28$ the solution for each subpopulation $S, V_{1}, V_{2}, V_{3}, E$, and $I$ was obtained sequentially to 2,$99 ; 0,04 ; 0,0074 ; 0,000185 ; 12,868 ; 4,412$. These values are endemic equilibrium points in each state of $R_{0}$. Thus, when $R_{0}>1$, then the solution for each subpopulation tends to reach the endemic equilibrium point.

### 4.3 Vaccine Success Simulation

In the next simulation, a numerical test was carried out to evaluate the success of using the vaccine using the assumption that the parameter value for the rate of development of the Covid-19 virus ( $\alpha$ ) was 0,002 and changing the parameter value for the proportion of Susceptible subpopulations ( $S$ ) who had been vaccinated ( $\delta$ ) which is shown in Table 7 below:

Table 7. Successful Use of Vaccines

| Parameter Value <br> $\boldsymbol{\delta}$ | Basic Reproduction Number <br> $\left(\boldsymbol{R}_{\mathbf{0}}\right)$ | Condition Variable $\boldsymbol{i}$ |
| :---: | :---: | :---: |
| 0,9 | 0,716932511 | Free from Covid-19 <br> $\left(R_{0}<1\right)$ |
| 0,8 | 0,837555459 | Free from Covid-19 <br> $\left(R_{0}<1\right)$ |
| 0,5 | 1,332109546 | Covid-19 is spreading <br> $\left(R_{0}>1\right)$ |
| 0,3 | 1,846849514 | Covid-19 is spreading <br> $\left(R_{0}>1\right)$ |

Meanwhile, the values of parameters other than $\delta$ and $\alpha$ have the same values as the parameters when conditions are endemic $\left(R_{0}>1\right)$ as shown in Table 5. Next, a graph of the numerical test using MATLAB R2017a is shown in Figure 7-Figure 10 and presented with daily timeframes up to 300 days and 4000 days as follows:


Figure 7. Simulation of variable $i$ when $\delta=0,9$


Figure 8. Simulation of variable $i$ when $\delta=0,8$


Figure 9. Simulation of variable $i$ when $\delta=0,5$


Figure 10. Simulation of variable $i$ when $\delta=0,3$
Based on Figure 7, the infected subpopulation (I) with a proportion of $\delta=0,9$ decreased until 200 days to point 0 and produced a basic reproduction number $\left(R_{0}\right)$ of 0,716932511 which means that Covid-19 has not spread or is disease free. Furthermore, in Figure 8 the infected subpopulation ( $I$ ) with a proportion of $\delta=0,8$ decreased until 250 days to point 0 and produced a basic reproduction number $\left(R_{0}\right)$ of 0,976866469 which means that Covid-19 has not spread or is disease free. In Figure 9 the infected subpopulation (I) with the proportion $\delta=0,5$ experienced an increase until 3000 days of 0,206 and produced a basic reproduction number of 1,332109546 which means that Covid-19 is spreading or endemic in a certain area, then in Figure 10 the infected subpopulation ( $I$ ) with a proportion of $\delta=0,3$ increased until 1200 days of 0,4 and produced a basic reproduction number of 1,846849514 which means that Covid-19 is spreading or endemic in a certain area. Thus, it can be concluded that if the proportion of the Susceptible ( $S$ ) subpopulation that is vaccinated ( $\delta$ ) increases, then the disease cannot spread quickly.

## V. CONCLUSION

The mathematical model for the spread of Covid-19 involving the first to third doses of vaccination can be arranged in a system of non-linear differential equations. The disease-free equilibrium point of the Covid-19 spread model involving the first to third doses of vaccination is $K_{1}=\left(\frac{\Pi}{\left(\delta \omega_{1}+\mu\right)}, \frac{\delta \omega_{1} \Pi}{\left(\delta \omega_{1}+\mu\right)\left(\omega_{2}+\mu\right)}, \frac{\delta \omega_{1} \omega_{2} \Pi}{\left(\delta \omega_{1}+\mu\right)\left(\omega_{2}+\mu\right)\left(\omega_{3}+\mu\right)}, \frac{\delta \omega_{1} \omega_{2} \omega_{3} \Pi}{\left(\delta \omega_{1}+\mu\right)\left(\omega_{2}+\mu\right)\left(\omega_{3}+\mu\right) \mu^{\prime}}\right.$, $0,0)$. Meanwhile, the endemic equilibrium point of the model is $T K_{2}=\left(s^{*}, v_{1}^{*}, v_{2}^{*}, v_{3}^{*}, e^{*}, i^{*}\right)$. The basic reproduction number of the model has been formed in this study is

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$R_{0}=\left(\frac{\alpha u \Pi \mu q r+\alpha k \delta \omega_{1} \Pi \mu r+\alpha x \delta \omega_{\omega_{2}} \Pi \mu+\alpha y \delta \omega_{1} \omega_{2} \omega_{\square} \Pi}{m n \mu p q r}\right)$. Based on the numerical simulation results it is
known that if the condition is $R_{0}<1$ hen Covid-19 cannot spread or is free from the disease, whereas if the condition is $R_{0}>1$, then Covid-19 can spread or become endemic in a certain area. In addition, the disease cannot spread quickly if the proportion of the Susceptible ( $S$ ) subpopulation that is vaccinated $(\delta)$ is increased.

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