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Analysis of SEIQV Epidemic Model on the Spread of Covid-19 in Jember Regency

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Abstract
Covid-19 is a disease that attacks the respiratory system caused by infection with SARSCoV-2. Efforts to prevent the spread of Covid-19 by vaccination. The spread of disease can be modeled into a mathematical equation. The model used in this study is the SEIQV Model. The disease spread model is analyzed by finding the equilibrium point and the stability of the equilibrium point as well as the basic reproduction number. In the Covid-19 distribution model, a bifurcation analysis is carried out which is needed to determine changes in stability and changes in the number of equilibrium points. Then perform a numerical solution using the fourth-order Runge-Kutta method which is simulated using MATLAB.

Keywords: *Covid-19, Vaccinate, SEIQV Model, Equilibrium Point, Basic Reproduction Number, Bifurcation, Fourth-order Runge-Kutta Method.*

1. Introduction

Coronavirus has been known since the 1930s which is known to infect humans to animals. At the beginning of 2020, the coronavirus (Covid-19) outbreak almost swept the entire country. The World Health Organization officially announced on February 11, 2020, that the new virus that causes pneumonia is called Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) and the disease it causes is called Coronavirus Disease 2019 (Covid-19) [7].

Covid-19 cases are increasing daily, and one of them can be found in Indonesia. The most effective prevention of disease is the use of vaccines because Covid-19 cases are increasing day by day and one of them can be found in Indonesia. Vaccines are the most effective prevention of disease because they contain substances that resemble disease-causing microorganisms, usually made from weakened or dead microbes. The Covid-19 vaccine is recommended to do two doses, namely the first dose and the second dose. The first dose of vaccination serves to introduce the Covid-19 vaccine and stimulate initial immunity in the recipient's body. The second dose of vaccination serves as a booster or enhancer of the ability of the vaccine [3].

Covid-19 spreading in a population can be modeled in mathematical modeling. Several studies have examined the spread of disease, including [6] by examining dengue fever in Surabaya using the SEIR model. In this study, four subpopulations were divided, namely

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susceptible (S), exposed (E), infected (I), and recovered (R). This study conducted a bifurcation analysis aimed at determining changes in stability and changes in the number of equilibrium points caused by changes in parameter values and conducted simulations using the fourth-order Runge-Kutta method to analyze the relationship between basic reproduction numbers and equilibrium point stability. The results obtained in this research occur advanced bifurcation means that the disease will spread and cannot be handled.

[5] This study used a mathematical model of SIR with vaccination. This study was divided into three subpopulations, namely susceptible (S), infected (I), and removed (R). The use of the term removed in this study is because the population consists of individuals who recover (Recovered) and die (Death). The simulation results obtained that the effectiveness of the vaccine affects suppressing the growth of infected populations. The number of infected populations can decrease as the effectiveness of vaccines increases so that healthy populations are maintained. [8] in his research conducted a mathematical model simulation of Covid-19 involving quarantine. The model used in this study is the SEAQIR model by separating individuals with clinical symptoms from individuals with no clinical symptoms. Based on the simulation results, increasing quarantine interventions can reduce the basic reproduction number, which means that it can prevent Covid-19 transmission. [2] In his research made modifications assuming the population grew logistically. The results obtained that the role of vaccines can reduce the number of infected individuals.

Based on previous research, the author will conduct a behavioral analysis of the spread of Covid-19 by testing the effectiveness of vaccines and investigating the presence of bifurcations. The mathematical model used is the SEIQV model which is divided into five subpopulations, namely healthy populations that are vulnerable to Covid-19 (S), populations that are infected but have not spread Covid-19 (E), populations infected with Covid-19 (I), populations that quarantine (Q), and populations that vaccinate (V) with vaccine variables divided into V_1 and V_2. The numerical solution of this model problem will be solved using the fourth-order Runge-Kutta method.

2. Methods

The study used data obtained from the Jember Regency Health Office from August 1, 2021 to November 30, 2021. The research steps in the Covid-19 spread model in Jember Regency are as follows:

a. Construction of the SEIQV model consists of six compartments: susceptible, exposed, infected, quarantined, vaccinated first, and vaccinated second.
b. Finding the equilibrium point in the SEIQV model is formed in equilibrium with the population rate of each compartment is zero so that a disease-free equilibrium point and an endemic equilibrium point and a basic reproduction number are obtained
c. Basic Reproduction Number (R_0) is used to determine the dynamics of disease transmission. The base reproduction number is determined using the Next Generation Matrix (NGM) method. The value of the base reproduction number is obtained from the largest eigenvalue of the Jacobian matrix.
d. Analyze the stability of the equilibrium point by finding the stability of the disease-free equilibrium point and endemic equilibrium point by entering the value of the equilibrium point into the Jacobian matrix, so that the characteristic roots of the Jacobian matrix are obtained to determine the stability of the two points.
e. Analysis of the occurrence of bifurcation by doing many settlements from populations I and (R_0) that affect bifurcation.
f. Parameter assumptions are used to simulate model results. The value of the parameter is obtained by making assumptions based on facts.
g. Numerical Solution analyzed the relationship between the basic reproduction number and equilibrium point stability with the fourth-order Runge-Kutta numerical method

using MATLAB and determined the effectiveness of the vaccine against infected populations.

h. Conclusions and suggestions are drawn conclusions from the results of the discussion that have been discussed earlier. Furthermore, suggestions are given for improvement in the next study who want to continue this research.

3. Results and Discussion

3.1. **Model Construction.** The assumptions of the mathematical model of the spread of Covid-19 as follows:

a. The population is closed, meaning that no individuals enter or exit the population, meaning that the total population is assumed to be constant.
b. The population is assumed to be homogeneous.
c. The birth rate is aimed only at the susceptible individual compartment (S), and natural death is aimed at all compartments.
d. The birth rate and death rate are assumed to be the same.
e. Vaccination is carried out in as many as 2 doses.
f. Covid-19 virus infection occurs when a susceptible individual (S) comes into contact with an infected individual (I).
g. Individuals who have had the first vaccination (V_1) can be infected, but the symptoms are not as severe as individuals who did not have the first vaccination.
h. Individuals infected with Covid-19 (I) must quarantine.
i. Individuals who have quarantined (Q) after recovery will have the first vaccination.
j. Individuals who have had a second vaccination (V_2) are assumed to be permanently immune to Covid-19 disease.

The assumptions above can be described schematically in the process of spreading Covid-19 which can be presented in the transfer diagram in Figure 1 as follows:

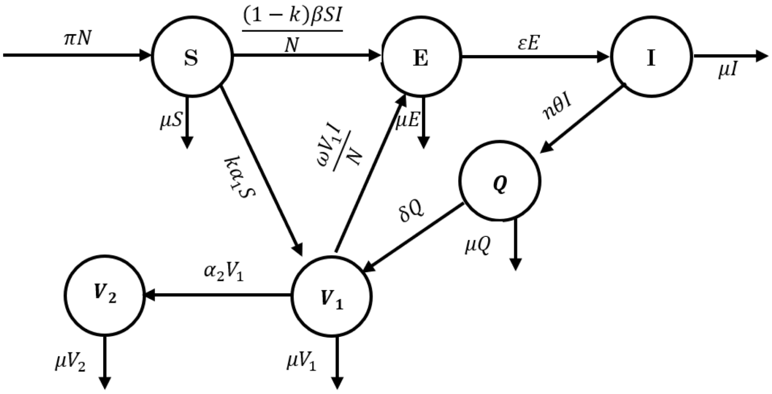


Figure 1. Transfer diagram of SEIQV model

Based on the compartment Figure 1 obtained a system of nonlinear differential equations of the SEIQV model:

$$
\begin{aligned}
\frac{dS}{dt} &= \pi N - \left(k\alpha_1 + \mu + \frac{(1-k)\beta I}{N}\right) S,\\
\frac{dE}{dt} &= \frac{(1-k)\beta SI}{N} + \frac{\omega V_1 I}{N} - (\mu+\varepsilon)E,\\
\frac{dI}{dt} &= \varepsilon E - (n\theta+\mu)I,\\
\frac{dQ}{dt} &= n\theta I - (\delta+\mu)Q,\\
\frac{dV_1}{dt} &= k\alpha_1 S + \delta Q - \left(\mu + \alpha + \frac{\omega I}{N}\right) V_1,\\
\frac{dV_2}{dt} &= \alpha_2 V_1 - \mu V_2.
\end{aligned}
\tag{1}
$$

The system of equations (1) can be simplified into a non-dimensional form which can be expressed as follows:

$$
\begin{aligned}
\frac{ds}{dt} &= \pi - (k\alpha_1 + \mu + (1-k)\beta i)s,\\
\frac{de}{dt} &= (1-k)\beta si + \omega v_1 i - (\mu+\varepsilon)e,\\
\frac{di}{dt} &= \varepsilon e - (n\theta+\mu)i,\\
\frac{dq}{dt} &= n\theta i - (\delta+\mu)q,\\
\frac{dv_1}{dt} &= k\alpha_1 s + \delta q - (\mu+\alpha+\omega i)v_1,\\
\frac{dv_2}{dt} &= \alpha_2 v_1 - (\mu+\rho)v_2.
\end{aligned}
\tag{2}
$$

3.2. **Equilibrium Point.** The equilibrium point is obtained when the equation system (2) satisfies $\frac{ds}{dt} =, \frac{de}{dt} =, \frac{di}{dt} =, \frac{dq}{dt} =,$ and $\frac{dv_1}{dt} = 0$. So that two equilibrium points are obtained, namely disease-free equilibrium points and endemic equilibrium points and basic reproduction numbers.

3.2.1. *Disease-free Equilibrium Point.* The disease-free equilibrium point is obtained as follows $(E^0 = (s,e,i,q,v_1,v_2) = \left(\frac{\pi}{(k\alpha_1+\mu)}, 0, 0, 0, \frac{k\alpha_1\pi}{(k\alpha_1+\mu)(\mu+\alpha_2)}, 0\right)$.

3.2.2. *Basic Reproduction Number.* The basic reproduction number is used to see the possibility of spreading Covid-19. The base reproduction number is obtained from the largest eigenvalue in the Next Generation Matrix. The Next Generation Matrix of the equation system (2) is as follows

$$K = FV^{-1}$$

with

$$
F = \begin{bmatrix} 0 & \frac{(1-k)\beta\pi(\mu+\alpha_2)+\omega k\alpha_1\pi}{(k\alpha_1+\mu)(\mu+\alpha_2)} & 0\\ 0 & 0 & 0\\ 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} (\varepsilon+\mu) & 0 & 0\\ -\varepsilon & (n\theta+\mu) & 0\\ 0 & -n\theta & (\delta+\mu) \end{bmatrix}
$$

Obtained R_0 values of the matrix K are as follows

$$R_0 = \frac{(1-k)\beta\pi\varepsilon(\mu+\alpha_2) + \varepsilon\omega k\alpha_1\pi}{(k\alpha_1+\mu)(\mu+\alpha_2)(\varepsilon+\mu)(n\theta+\mu)}.$$

3.2.3. *Endemic Equilibrium Point.* The endemic equilibrium point is obtained as follows

$$\begin{aligned}
s^* &= \frac{\pi}{(k\alpha_1 + \mu + (1-k)\,\beta i^*)},\\
e^* &= \left(\frac{(1-k)\,\beta\pi\,(\delta+\mu)\,(\mu+\alpha_2+\omega i) + \omega k\alpha_1\pi\,(\delta+\mu) + \omega\delta n\theta i\,(k\alpha_1+\mu+(1-k)\,\beta i)}{(k\alpha_1+\mu+(1-k)\,\beta i)\,(\delta+\mu)\,(\mu+\alpha_2+\omega i)\,(\mu+\varepsilon)}\right) i^*,\\
q^* &= \frac{n\theta i^*}{(\delta+\mu)},\\
v_1^* &= \frac{k\alpha_1\pi\,(\delta+\mu) + \delta n\theta i^*\,(k\alpha_1+\mu+(1-k)\,\beta i^*)}{(k\alpha_1+\mu+(1-k)\,\beta i^*)\,(\delta+\mu)\,(\mu+\alpha_2+\omega i^*)},\\
v_2^* &= \frac{k\alpha_1\alpha_2\pi + \delta q^*\,(k\alpha_1+\mu+(1-k)\,\beta i^*)}{(k\alpha_1+\mu+(1-k)\,\beta i^*)\,(\mu+\alpha_2+\omega i^*)\,(\mu)},\\
i^* &= \frac{-b \pm \sqrt{b^2-4ac}}{2a},
\end{aligned}$$

with

$$\begin{aligned}
a =& \left[(\delta+\mu)\,(\mu+\varepsilon)\,(n\theta+\mu)\,(1-k)\,\beta\omega - (1-k)\,\beta\varepsilon\omega\delta n\theta\right],\\
b =& (k\alpha_1+\mu)\,(\delta+\mu)\,(\mu+\varepsilon)\,(n\theta+\mu)\,\omega + (\mu+\varepsilon)\,(n\theta+\mu)\,(\mu+\alpha_2)\,(\delta+\mu)\,(1-k)\,\beta\\
&- ((1-k)\,\beta\pi\varepsilon\omega\,(\delta+\mu) + \omega\varepsilon\delta n\theta\,(k\alpha_1+\mu)),\\
c =& (1-R_0)\,(k\alpha_1+\mu)\,(\delta+\mu)\,(\mu+\varepsilon)\,(n\theta+\mu)\,(\mu+\alpha_2)\,.
\end{aligned}$$

3.3. **Equilibrium Point Stability Analysis.** Analysis of the stability of the two equilibrium points is carried out after obtaining the equilibrium points. The system of equations (2) is a system of equations that are nonlinear, so linearization is needed using Jacobian matrices, including the following:

$$J = \begin{bmatrix}
-(k\alpha_1+\mu+(1-k)\,\beta i) & 0 & -(1-k)\,\beta s & 0 & 0 & 0\\
(1-k)\,\beta i & -(\mu+\varepsilon) & (1-k)\,\beta s & 0 & \omega i & 0\\
0 & \varepsilon & -(n\theta+\mu) & 0 & 0 & 0\\
0 & 0 & n\theta & -(\delta+\mu) & 0 & 0\\
k\alpha_1 & 0 & \omega v_1 & \delta & -(\mu+\alpha_2+\omega i) & 0\\
0 & 0 & 0 & 0 & \alpha_2 & -\mu
\end{bmatrix}.$$

3.3.1. *Local Stability Analysis of Disease-Free Equilibrium Point.* Analysis of the stability of the disease-free equilibrium point is performed by substituting $E^0 = (s, 0, 0, q, v_1, v_2)$ into the Jacobian matrix so that the Jacobian matrix of disease-free equilibrium point $J\left(E^0\right)$ is as follows,

$$J\left(E^0\right) = \begin{bmatrix}
a & 0 & b & 0 & 0 & 0\\
0 & c & d & 0 & 0 & 0\\
0 & e & f & 0 & 0 & 0\\
0 & 0 & g & h & 0 & 0\\
z & 0 & j & k & l & 0\\
0 & 0 & 0 & 0 & m & n
\end{bmatrix},$$

with $a = -(k\alpha_1+\mu)$, $b = \frac{-(1-k)\beta\pi}{(ka_1+\mu)}$, $c = -(\mu+\varepsilon)$, $d = \frac{(1-k)\beta\pi}{(ka_1+\mu)}$, $e = \varepsilon$, $f = -(n\theta+\mu)$, $g = n\theta$, $h = -(\delta+\mu)$, $z = k\alpha_1$, $j = \frac{k\alpha_1\pi\omega}{(ka_1+\mu)(\mu+\alpha_2)}$, $k = \delta$, $l = -(\mu+\alpha_2)$, $m = \alpha_2$, and $n = -\mu$. From the Jacobian matrix $J\left(E^0\right)$ obtained the characteristic equation is

$$(n-\lambda)\,(l-\lambda)\,[(h-\lambda)\,(a-\lambda)\,\{(c-\lambda)\,(f-\lambda)-de\} = 0,$$

by suppose $p = (h-\lambda)\,(a-\lambda)\,\{(c-\lambda)\,(f-\lambda)-de\}$ then it can simplified to

$$
\begin{aligned}
(n-\lambda)\,(l-\lambda)\,p &= 0,\\
(-\mu-\lambda)\,(-\mu-\alpha_2-\lambda)\,p &= 0,
\end{aligned}
$$

obtained $\lambda_1 = -\mu,\ \lambda_2 = -\mu-\alpha_2$, because a_2 and μ are positive, the real value part of both eigenvalues is $\lambda_1 < 0$ dan $\lambda_2 < 0$ or negative real values. Next, find the other eigenvalues by looking at the equation

$$
\begin{aligned}
p =& (h-\lambda)\,(a-\lambda)\,\{(c-\lambda)\,(f-\lambda)-de\} = 0,\\
p =& \lambda^4 + \ \lambda^{3}\,(-a-c-f-h)\,\lambda^3 + (ac+af+ah+cf+ch+fh-ed)\,\lambda^2\\
&+ (-acf-ach-afh-cfh+ead+edh)\,\lambda + acfh - eadh = 0.
\end{aligned} \tag{3}
$$

Equation (3) can be written as follows:

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0,$$

with each a_1, a_2, a_3 is

$$
\begin{aligned}
a_1 &= -a-c-f-h,\\
a_2 &= ac+af+ah+cf+ch+fh-ed,\\
a_3 &= -acf-ach-afh-cfh+ead+edh,\\
a_4 &= acfh-eadh,
\end{aligned}
$$

because the eigenvalue of equation (3) is difficult to determine, it uses the Routh-Hurwitz criterion to find out the roots of the equation. The Routh-Hurwitz formula can be written in Table 1 below:

TABLE 1. Routh-Hurwitz criteria disease-free equilibrium points

Variable	Coefficient		
λ^4	a_0	a_2	a_4
λ^3	a_1	a_3	$a_5 = 0$
λ^2	b_1	$b_2 = 0$	
λ^1	c_1		
λ^0	$d_1 = a_4$		

with coefficients – coefficients:

$$
\begin{aligned}
a_0 &= 1, & b_1 &= \frac{a_1a_2 - \ a_0a_3}{a_1},\\
a_1 &= -a-c-f-h, & b_2 &= \frac{a_1a_4 - \ a_0\,(0)}{a_1} = a_4,\\
a_2 &= ac+af+ah+cf+ch+fh-ed, & c_1 &= \frac{b_1a_3 - \ a_1\,(0)}{b_1} = a_3,\\
a_3 &= -acf-ach-afh-cfh+ead+edh, & d_1 &= \frac{c_1b_2-(0)\,b_1}{c_1} = a_4,\\
a_4 &= acfh-eadh. & & .
\end{aligned}
$$

The Routh-Hurwitz criterion of a system is said to be asymptotic stable if the variables in the primary column are positive, which means that the disease-free equilibrium point for the SEIQV model proves to be asymptotic stable if it meets $a_1 > 0,\ a_1a_2 > a_0a_3,\ c_1 > 0$, and $d_1 > 0$.

3.3.2. *Local Stability Analysis of Endemic Equilibrium Points.* Analysis of the stability of the endemic equilibrium point is carried out by entering $E^1 = (s^*, e^*, i^*, q^*, v_1^*, v_2^*)$ into the Jacobian matrix then obtaining the Jacobian matrix $J\left(E^1\right)$:

$$J\left(E^1\right) = \begin{bmatrix} a & 0 & b & 0 & 0 & 0 \\ 0 & c & d & 0 & e & 0 \\ 0 & 0 & f & 0 & g & 0 \\ 0 & 0 & 0 & h & i & 0 \\ 0 & 0 & 0 & 0 & j & 0 \\ 0 & 0 & 0 & 0 & 0 & k \end{bmatrix},$$

with

$$\begin{aligned}
a &= -\left(k\alpha_1 + \mu + (1-k)\,\beta i^*\right), \\
b &= -\left(1-k\right)\beta\ s^*, \\
c &= -\left(\mu + \varepsilon\right), \\
d &= (1-k)\,\beta\ s^* - \frac{(1-k)^2\,\beta s^*}{(k\alpha_1 + \mu + (1-k))}, \\
e &= \omega i^*, \\
f &= -\left(n\theta + \mu\right) - \frac{\varepsilon\left((1-k)\,\beta s^* - \frac{(1-k)^2\beta s^*}{(k\alpha_1+\mu+(1-k))}\right)}{-\left(\mu+\varepsilon\right)}, \\
g &= \frac{\varepsilon\omega i^*}{(\mu+\varepsilon)}, \\
h &= -\left(\delta + \mu\right), \\
z &= \frac{n\theta\varepsilon\omega i^*}{\left(-\left(n\theta+\mu\right) - \frac{\varepsilon\left((1-k)\beta s^* - \frac{(1-k)^2\beta s^*}{(k\alpha_1+\mu+(1-k))}\right)}{-(\mu+\varepsilon)}\right) - \left(\mu+\varepsilon\right)}, \\
j &= -\left(\mu + \alpha_2 + \omega i^*\right) - \frac{k\alpha_1\omega}{(1-k)\,\beta} \\
&\quad - \left(\delta - \frac{\frac{\left(\omega v_1^* - \frac{k\alpha_1 s^*}{i^*} + \frac{k\alpha_1(-\mu-\varepsilon)(-n\theta-\mu)}{(1-k)\beta\varepsilon i^*}(-\delta-\mu)\right)}{n\theta} n\theta\varepsilon\omega i^*}{-\left(\delta+\mu\right)\left(-\left(n\theta+\mu\right) - \frac{\varepsilon\left((1-k)\beta s^* - \frac{(1-k)^2\beta s^*}{(k\alpha_1+\mu+(1-k))}\right)}{-(\mu+\varepsilon)}\right) - \left(\mu+\varepsilon\right)}\right), \\
k &= -\,\mu.
\end{aligned}$$

Thus obtained the similarity of its characteristics, namely:

$$\left(a-\lambda\right)\left(c-\lambda\right)\left(f-\lambda\right)\left(h-\lambda\right)\left(j-\lambda\right)\left(j-\lambda\right)\left(k-\lambda\right) = 0. \tag{4}$$

So that equation (4) obtained the eigenvalue of its characteristic root as follows:
$\lambda_1 = a = -\left(k\alpha_1 + \mu + (1-k)\,\beta i^*\right)$,
then it is clear the value $\lambda_1 = a < 0$.
$\lambda_2 = c = -\left(\mu+\varepsilon\right)$,
then it is clear the value $\lambda_2 = c < 0$.
$\lambda_3 = f = -\left(\frac{(n\theta+\mu)(-\mu-\varepsilon)+\varepsilon\left((1-k)\beta s^* - \frac{(1-k)^2\beta s^*}{(k\alpha_1+\mu+(1-k))}\right)}{(-\mu-\varepsilon)}\right)$,
with $\frac{(n\theta+\mu)(-\mu-\varepsilon)}{(-\mu-\varepsilon)} > \frac{\varepsilon\left((1-k)\beta s^* - \frac{(1-k)^2\beta s^*}{(k\alpha_1+\mu+(1-k))}\right)}{(-\mu-\varepsilon)}$,
then $\lambda_3 = f < 0$.

$\lambda_4 = h = -\left(\delta + \mu\right),$
then it is clear the value $\lambda_4 = h < 0$.

$$\lambda_5 = j = -\left(\mu + \alpha_2 + \omega i^*\right) - \frac{k\alpha_1\omega}{\left(1-k\right)\beta} - \left(\delta - \frac{\frac{\left(\omega v_1^* - \frac{k\alpha_1 s^*}{i^*} + \frac{k\alpha_1(-\mu-\varepsilon)(-n\theta-\mu)}{(1-k)\beta\varepsilon i^*}(-\delta-\mu)\right)}{n\theta} n\theta\varepsilon\omega i^*}{-\left(\delta+\mu\right)\left(-\left(n\theta+\mu\right) - \frac{\varepsilon\left((1-k)\beta s^* - \frac{(1-k)^2\beta s^*}{(k\alpha_1+\mu+(1-k))}\right)}{-(\mu+\varepsilon)}\right) - \left(\mu+\varepsilon\right)}\right),$$

then it is clear the value $\lambda_5 = j < 0$.
$\lambda_6 = k = -\mu,$
then it is clear the value $\lambda_6 = k < 0$.
Since it is proved that all eigenvalues are negative reals, the endemic equilibrium point is asymptotic stable.

3.4. **Bifurcation Analysis.** This subchapter will discuss the existence of bifurcations using endemic equilibrium points in order to obtain the function of infected populations or $f\left(i^*\right)$. As for the calculation to search $f\left(i^*\right)$ as follows:

$$f\left(i^*\right) = \left(a{i^*}^2 + bi^* + c\right) = 0,$$

with

$$\begin{aligned} a &= \left(\delta+\mu\right)\left(\mu+\varepsilon\right)\left(n\theta+\mu\right)\left(1-k\right)\beta\omega - \left(1-k\right)\beta\varepsilon\omega\delta n\theta, \\ b &= \left(k\alpha_1+\mu\right)\left(\delta+\mu\right)\left(\mu+\varepsilon\right)\left(n\theta+\mu\right)\omega + \left(\mu+\varepsilon\right)\left(n\theta+\mu\right)\left(\mu+\alpha_2\right)\left(\delta+\mu\right)\left(1-k\right)\beta \\ &\quad - \left(\left(1-k\right)\beta\pi\varepsilon\omega\left(\delta+\mu\right) + \omega\varepsilon\delta n\theta\left(k\alpha_1+\mu\right)\right), \\ c &= \left(1-R_0\right)k_1, \end{aligned}$$

with $k1 = \left(k\alpha_1+\mu\right)\left(\delta+\mu\right)\left(\mu+\varepsilon\right)\left(n\theta+\mu\right)\left(\mu+\alpha_2\right)$.

It will then be simulated to produce a bifurcation curve $\left(R_0, i\right)$. Figure 2 is the result of a bifurcation curve with several parameters, namely $\pi = \mu = 0.0098,\ \delta = 0.071, \beta = 0.4,\ \varepsilon = 0.01,\ k = 0.0848,\ \alpha_1 = 0.0653, \alpha_2 = 0.0033,\ \theta = 0.0624,\ n = 0.40,\ \omega = 0.20$

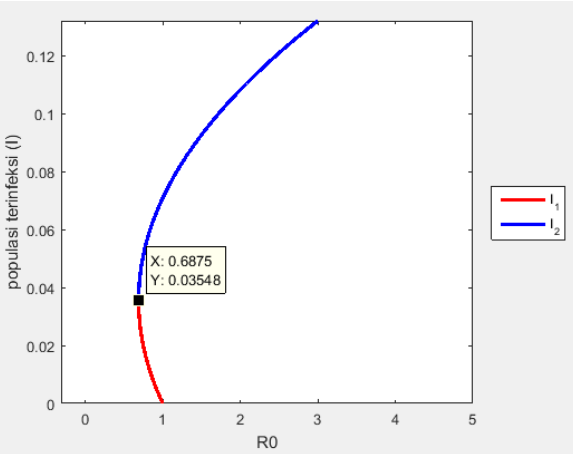


FIGURE 2. Bifurcation curve

Figure 2 shows that backward bifurcation has occurred in the SEIQV Model characterized by the emergence of an endemic equilibrium point when the value of the base reproduction number is less than one.

3.5. **Numerical and Simulation Solutions.**

The numerical settlement used in this case is the fourth-order Runge-Kutta method. The parameter values are as follows

3.5.1. *Disease-Free Equilibrium Point.*

Table 2. Disease-free equilibrium point parameter values

No.	Parameters	Parameters Value	Unit	Reference
1	N	2536729	$individu$	[1]
2	π	0.0098	$\frac{1}{hari}$	[1]
3	μ	0.0098	$\frac{1}{hari}$	[1]
4	δ	0.071	$\frac{1}{hari}$	[2]
5	β	0.1	$\frac{1}{hari}$	[4]
6	ε	0.071	$\frac{1}{hari}$	[2]
7	k	0.0848	$\frac{1}{hari}$	Assumption
8	α_1	0.00219	$\frac{1}{hari}$	Assumption
9	α_1	0.033	$\frac{1}{hari}$	[3]
10	θ	0.11624	$\frac{1}{hari}$	[9]
11	n	0.90		Assumption
12	ω	0.011	$\frac{1}{hari}$	[3]

Table 3. The initial value of each population on the spread of Covid-19

No.	Population when $t = 0$	Initial value
1	$s(0)$	0.862
2	$e(0)$	0.0017
3	$i(0)$	0.0046
4	$q(0)$	0.00081
5	$v_1(0)$	0.084
6	$v_2(0)$	0.0451

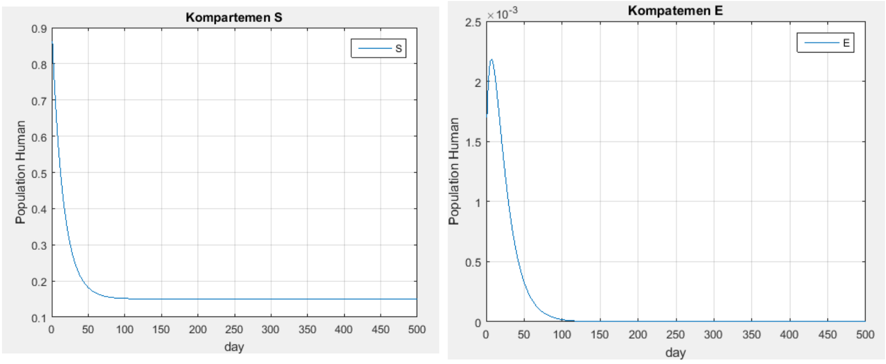
The simulation results of the population stability diagram using the parameter values in Table 2 and the initial values in Table 3 are expected to produce in accordance with the value of $R_0 = 0.122$ can be seen in Figure 3 as follows:

Figure 3 Population graph of Jember Regency at $R_0 < 1$ when $0 \leq t \leq 500$ Figure 3 shows the compartment S, E, I, Q, V_1, and V_2 at the time $0 \leq t \leq 500$ The graph of the growth rate of each compartment will be explained as follows:

a. Population growth rate S
The growth rate of compartment S decreases every time. The decline in the population of susceptible individuals is influenced by the large number of individuals who have the first vaccination, the movement to the latent population due to contact with infected individuals and the presence of natural death. From Figure 3(A) it can be seen that this population will continue to decline to 0.1504 and stabilize on the 145th day (December 24, 2022).

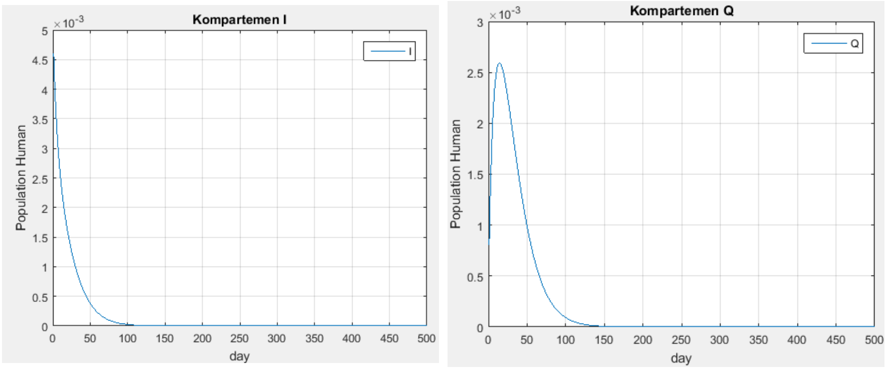
b. Population growth rate E
The growth rate of compartment E initially increased until day 7 (August 8, 2021) and will decrease because the rate of movement to the infected compartment is greater than the increase. From Figure 3(B) it can be seen that this population will continue to decline until the 210th day (February 27, 2021) and stabilize.

c. Population growth rate I
The growth rate of compartment I will decrease. This decrease in rate is due to the large number of individuals quarantined due to Covid-19 infection and natural death.



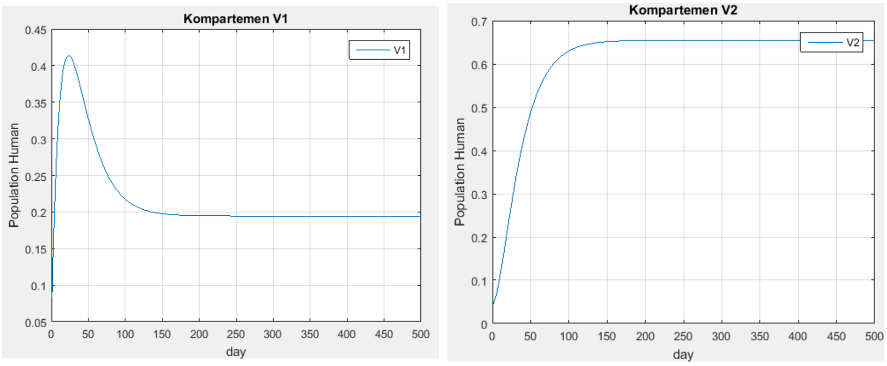
(A) Simulation of compartement S

(B) Simulation of compartement E



(C) Simulation of compartement I

(D) Simulation of compartement Q



(E) Simulation of compartement V_1

(F) Simulation of compartement V_2

FIGURE 3. Population graph of Jember Regency at $R_0 < 1$ when $0 \leq t \leq 500$

From Figure 3(C) it can be seen that this population will experience a decline until the 284th day (May 12, 2022) and stabilize.

d. Population growth rate Q
The growth rate of compartment Q initially rose until the 14th day (August 15, 2021), this increase in population was due to the large number of individuals quarantined. After that, the rate of population growth decreased due to the large number of individuals who had the first vaccination, and the presence of natural deaths. From Figure 3(D) it can be seen that this population continued to decline until the 289th day (May 17, 2022) and stabilized.

e. Population growth rate V_1
The growth rate of compartment V_1 initially increased until the 23rd day (August 24, 2021), this population increase was due to the large number of vulnerable displacements

to carry out the first vaccination. After that, it decreases because the rate of increase is smaller than the rate of movement to compartment E due to loss of immunity from the vaccine and the move to compartment V_2 due to the second vaccine. From Figure 3(E) it can be seen that this population continued to decline until it reached 0.1945 and stabilized on the 295th day (May 23, 2022).

f. Population growth rate V_2
The growth rate of compartment V_2 continues to increase due to the population taking the second vaccine immune to the Corona-19 virus, this population increases to 0.6551 and stabilizes on the 303rd day (May 31, 2022).

Furthermore, numerical simulations will be carried out to determine the effectiveness of the use of vaccination in suppressing the rate of spread of Covid-19 by varying the parameters $k,\ a_1, and \omega$ shown in Table 4 as follows:

Table 4. Parameter value variations

Variations	k	a_1	ω	R_0	The disease disappears day to day-
1	0.044	0.253	0.5	0.8113	665
2	0.064	0.453	0.1	0.3130	390
3	0.0848	0.653	0.011	0.1221	284
4	0.1	0.853	0.006	0.0806	136

Furthermore, the simulation results obtained on the effectiveness of vaccine use against Covid-19 infection are as follows:

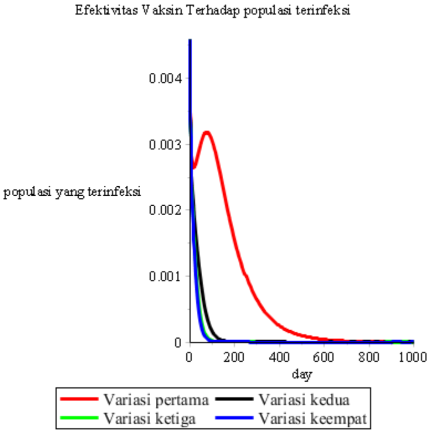


Figure 4. The effectiveness of the vaccine against infected populations

Based on Figure 4, it is found that the infected population in the first variation obtained a value $R_0 = 0,8113$, graph of compartments $I(t)$ initially fell to day 17 (August 18, 2021), then rose to day 75 (October 24, 2021) and down to day 665 indicated by a curve in red. The infected population on the second variation obtained values $R_0 = 0.3130$ and the disease will decrease until the 390th day (August 26, 2022) and stabilize at that point indicated by a black curve. The third variation was obtained values $R_0 = 0.1221$ and the disease will slowly descend until the 284th day (May 12, 2022) indicated by a green curve. The fourth variety was obtained values $R_0 = 0.0806$ and the disease will slowly descend until the 136th day (December 15, 2021) indicated by a blue curve. It can be concluded that increasing the value of k, a_1, and reducing the value of ω can reduce the rate of spread of Covid-19 in Jember Regency. This can be seen from the blue curve in compartment $I(t)$ indicating that the spread of Covid-19 will disappear faster.

3.5.2. *Endemic Equilibrium Point.*

TABLE 5. Endemic equilibrium point parameter values

No.	Parameters	Parameters Value	Unit	Reference
1	N	2536729	*individu*	[1]
2	π	0.0098	$\frac{1}{hari}$	[1]
3	μ	0.0098	$\frac{1}{hari}$	[1]
4	δ	0.071	$\frac{1}{hari}$	[7]
5	β	0.4	$\frac{1}{hari}$	Assumption
6	ε	0.01	$\frac{1}{hari}$	Assumption
7	k	0.00848	$\frac{1}{hari}$	Assumption
8	α_1	0.00219	$\frac{1}{hari}$	Assumption
9	α_1	0.0033	$\frac{1}{hari}$	Assumption
10	θ	0.0624	$\frac{1}{hari}$	Assumption
11	n	0.40		Assumption
12	ω	0.2	$\frac{1}{hari}$	Assumption

Next, simulate the endemic equilibrium point by entering the parameter values of Table 5 and the initial values of Table 3 which are expected to produce values $R_0 > 1$ can be seen in Figure 5 as follows:

Figure 5 shows the compartments S, E, I, Q, V_1, and V_2 to the time $0 \leq t \leq 500$ The graph of the growth rate of each compartment will be explained as follows:

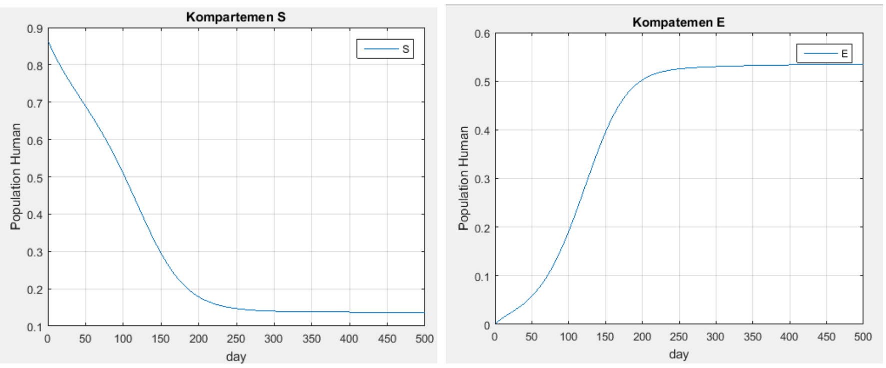
a. Population growth rate S
The growth rate of compartment S has decreased. The decrease in the number of susceptible individuals is due to the large number of infected individuals so that they move to the latent population and move to the first vaccine to vaccinate and natural death. From Figure 5(A) it can be seen that the population of this compartment will continue to decline until it reaches 0.1338 and stabilizes at that point.

b. Population growth rate E
The growth rate of compartment E has increased. This factor in population increase is due to the displacement of vulnerable populations and the first vaccine individuals to lose immunity due to Covid-19. From Figure 5(B) it can be seen that this population will continue to increase to the point of 0.5380 and stabilize.

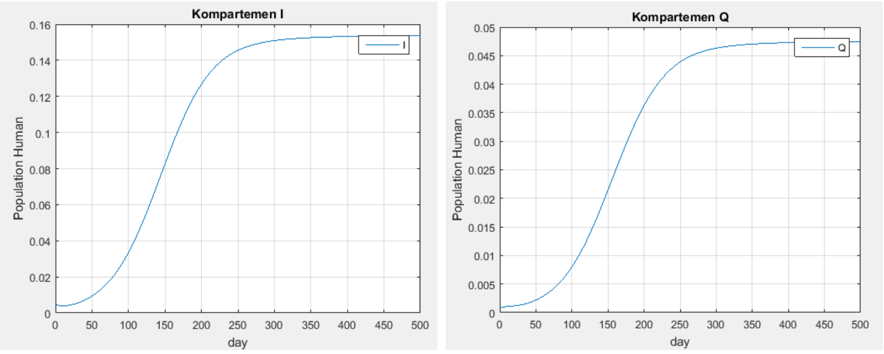
c. Population growth rate I
The growth rate of compartment I will increase. This factor in population increase is due to the movement of latent populations to infected populations due to confirmed exposure to Covid-19. From Figure 5(C) it can be seen that this population will continue to increase to 0.1547 and stabilize.

d. Population growth rate Q
The growth rate of compartment Q is constantly increasing. This increasing population factor is due to the movement of individuals infected with Covid-19 must quarantine so as not to infect other individuals. From Figure 5(D) it can be seen that this population will continue to increase to 0.0478 and stabilize.

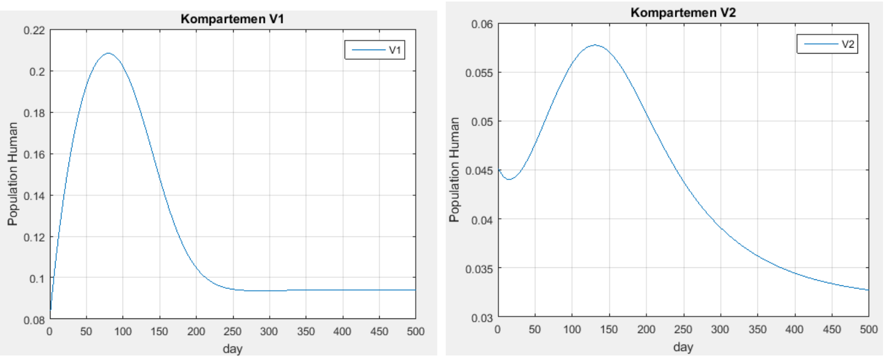
e. Population growth rate V_1
The growth rate of the V_1 compartment initially increased until the 81st day, this population increase was due to the large number of individuals who had the first vaccination, but over time the number of this population decreased to 0.0938 and stabilized at that point. The growth rate of the V_1 compartment initially increased until the 81st day, this population increase was due to the large number of individuals who had the first vaccination, but over time the number of this population decreased to 0.0938 and stabilized at that point.



(A) Simulation of compartement S (B) Simulation of compartement E



(C) Simulation of compartement I (D) Simulation of compartement Q



(E) Simulation of compartement V_1 (F) Simulation of compartement V_2

Figure 5. Current human population stability graph $R_0 > 1$ then $0 \leq t \leq 500$

f. Population growth rate V_2
The growth rate of compartment V_2 initially increased until the 133rd day, the increase in this compartment was due to the move from the first vaccine and over time decreased to 0.0316.

4. Conclusion

Based on the results of the analysis and discussion in writing this final project, it can be concluded that by comparing the results of the program simulation with Covid-19 data obtained from the Jember Regency Health Office, it can be stated that there are similarities to the pattern of Covid-19 spread in Jember Regency which is predicted that the infected population will decrease and disappear until May 2022. The equilibrium point obtained, which is an asymptotic stable disease-free equilibrium point with a reproduction number of less than one and an asymptotic stable endemic equilibrium point with more than one reproduction number. The model formed shows backward bifurcation characterized by the appearance of two endemic equilibrium points when the value of the reproduction number is less than one. The effectiveness of the vaccine is influenced by several parameters, namely: k, a_1, and ω. The results of the simulation of vaccine effectiveness in reducing the spread of Covid-19 show that the greater the value of k, a_1, and the smaller the value of ω, the smaller the value of the reproduction number. This shows that the vaccine is considered effective in efforts to prevent the spread of Covid-19 in Jember Regency.

References

[1] Badan Pusat Statistik Kabupaten Jember, 2021, *Jumlah Penduduk Menurut Tempat Lahir di Jember*, $https://jemberkab.bps.go.id/statictable/2021/11/03/315/jumlah - penduduk - menurut - tempat - lahir - dikabupaten - jember - 2020.html\ on\ August\ 10, 2022$

[2] Harianto, J., I. P. Sari, 2022, Analisis Kestabilan Titik Ekuilibrium Model Epidemik SEIV dengan Pertumbuhan Logistik, *Majalah Ilmiah Matematika dan Statistika*, Volume 22, Issue 1, Pages 59 – 68.

[3] Info-Kesehatan, 2021, *Apa Perbedaan Vaksin Dosis Pertama dan Kedua*, $http://www.pramita.co.id/id/inspirasi/info - kesehatan/apa - perbedaan - vaksin - dosis - pertama - dan - kedua\ on\ November\ 16, 2021$

[4] Manaqib, M., Irma, F. Mujiyanti, 2019, Mathematical Model for Mers-CoV Disease Transmission with Medical Mask Usage and Vaccination, *Indonesia Journal of Pure and Applied Mathematic*, Volume 1, Pages 30 – 42.

[5] Mu'tamar, K., S. Putra., S. A. Perdana, 2021, Analisis Penyebaran Covid-19 Dengan Menggunakan Model SIR dan Vaksin Serta Estimasi Parameter. *Jurnal Ilmu Matematika dan Terapan*, Volume 15, Issue 2, Pages 323 – 324.

[6] Ningsih, D. K., Hariyanto, S. Winarko, 2016, Analisis Bifurkasi Pada Model Epidemiologi SEIR Demam Berdarah di Surabaya, *Jurnal Sains dan Seni ITS*, Volume 5, Issue 1, Pages 2337-3520.

[7] Sutaryo., N. Yang, L. Sagoro, dan D. S. Sabrina, 2020, *Buku praktis penyakit corona 19 (corona-19)*, Gadjah Mada University Press, Yogyakarta.

[8] Resmawan, A., R. Nuha, dan L. Yahya, 2021, Analisis Model Transmisi Covid-19 dengan melibatkan Intervensi Karantina, *Jambura Journal of Mathematics*, Volume 3, Issue 1, Pages 66-79.

[9] 9. Wu, Z., Hu, Y., Xu, M., Chen, Z., Yang, W., Jiang, Z., Li, M., Jin, H., Cui, G., Chen, P., Wang, L., Zhao, G., Ding, Y., Zhao, Y., dan Yin, W, 2021, *Safety, tolerability, and immunogenicity of an inactivated SARS-CoV-2 vaccine (CoronaVac) in healthy adults aged 60 years and older: A randomised, double-blind, placebo-controlled, phase 1/2 clinical trial. The Lancet Infectious*