

## DYNAMICAL SYSTEM FOR COVID-19 OUTBREAK WITHIN VACCINATION TREATMENT

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### ABSTRACT

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COVID-19 is a deadly infectious disease that occurs throughout the world. Therefore, it is necessary to prevent the transmission of COVID-19 such as vaccination. The purpose of this research is to modify the model of the spread of the COVID-19 disease from the previous model. The equilibrium points and the basic reproduction number ( $\mathcal{R}_0$ ) of the modified model are determined. Then a stability analysis was carried out, and a numerical simulation was carried out to see the dynamics of the population that occurred. The analysis performed on the model obtained two equilibriums, namely the disease-free equilibrium and the endemic equilibrium. Disease-free equilibriums are locally asymptotically stable if  $\mathcal{R}_0 < 1$ . Meanwhile, the endemic equilibrium is locally asymptotically stable if  $\mathcal{R}_0 > 1$ . The numerical simulation results show the same results as the analytical results.



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## 1. INTRODUCTION

Coronavirus Disease is an infectious disease caused by a type of corona virus that was recently discovered in Wuhan, Hubei Province, China, in December 2019 [1]. In 2020, a new type of coronavirus (SARS-CoV-2) spread which was later named Coronavirus Disease 2019 (COVID-19) by the World Health Organization (WHO) [2]. In Wuhan, the capital city of Hubei Province, this virus has infected 90,308 people on March 2, 2020. The number of deaths reached 3,087 people or 6%, and the number of patients recovered was 45,726 people. Researchers at the Institute of Virology in Wuhan have carried out a metagenomics analysis to identify the new coronavirus as a potential etiology. They call it the 2019 novel coronavirus (nCoV-2019) [3]. Furthermore, the Centers for Disease Control and Prevention (CDC) in the United States mention the coronavirus 2019 as the 2019 novel coronavirus (2019-nCoV), and now the disease is popular with the term coronavirus disease-19 (COVID-19) [4].

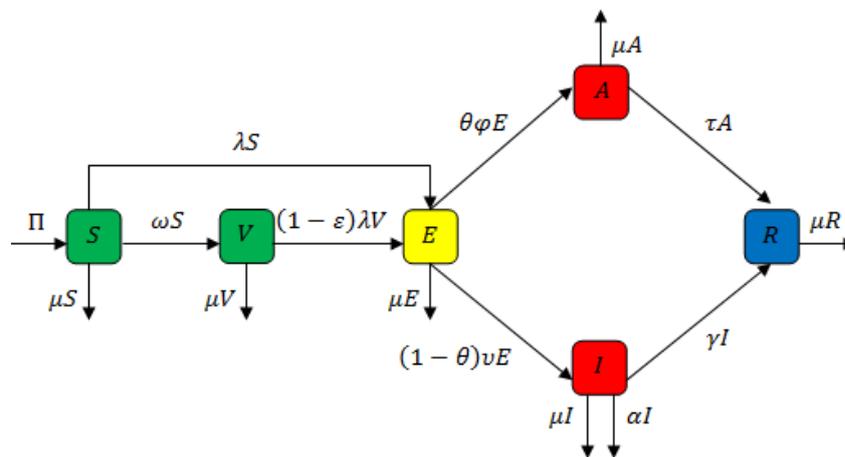
Based on data from WHO [5], on May 26, 2021, cases of COVID-19 worldwide reached 167,492,769 cases with 3,482,907 deaths. However, in Indonesia, the COVID-19 case on May 23, 2021, reached 1,775,220 cases with 1,633,045 recoveries and 49,328 deaths [6]. The data shows that the COVID-19 virus is a dangerous virus that must be dealt with immediately because it can have a negative impact on the economic sector.

Currently, the COVID-19 virus has disrupted the global economy [7]. According to Organization for Economic Co-operation and Development (OECD), the COVID-19 pandemic has an impact on the threat of a major economic crisis which is marked by the cessation of production activities in various countries, including Indonesia, the level of public consumption decreased, lost consumer confidence, and the fall of the stock market which ultimately led to uncertainty [8]. In Indonesia, it is not only the economic sector experiencing a downturn but also the education sector. The government of the Republic of Indonesia finally took a bold step by vaccinating [6]. This vaccination is expected to reduce or even eliminate pandemic outbreaks. So that all sectors of life can return to normal.

However, the effect of vaccination on the COVID-19 pandemic cannot be ascertained. It is not yet certain whether this vaccination is effective or not in reducing the number of COVID-19 cases. Therefore, the researchers modeled the dynamic system of the spread of the COVID-19 disease with the vaccination treatment to determine the effect of the vaccination rate and the effectiveness of the vaccine against the COVID-19 pandemic.

## 2. RESEARCH METHODS

The method used in this study is a literature study that aims to develop and modify a model for the spread of COVID-19. The model in this research is a modification of Cui et al. [9] and Resmawan et al. [10]. Modification of the model was carried out by removing the quarantine treatment and giving treatment in the form of vaccination and dividing infected individuals into two groups, namely people who are infected with clinical symptoms and people who are infected without clinical symptoms in a population  $N(t)$ , which can be seen in **Figure 1**. The model parameters used in the study are shown in **Table 1**. Furthermore, we will look for a disease-free equilibrium, endemic equilibrium, and the basic reproduction number of the system of **Equations (1)**. From the equilibriums obtained, the stability conditions will be determined, and a numerical simulation will be carried out to see the dynamics of the population in the form of the resulting solution curve.



**Figure 1.** Compartment Diagram of the COVID-19 Disease Spread Model

The model above is given by the following system of non-linear differential equations:

$$\begin{aligned}
 \frac{dS}{dt} &= \Pi - \lambda S - \omega S - \mu S \\
 \frac{dV}{dt} &= \omega S - (1 - \varepsilon)\lambda V - \mu V \\
 \frac{dE}{dt} &= \lambda S + (1 - \varepsilon)\lambda V - \theta\phi E - (1 - \theta)vE - \mu E \\
 \frac{dA}{dt} &= \theta\phi E - \tau A - \mu A \\
 \frac{dI}{dt} &= (1 - \theta)vE - \gamma I - \alpha I - \mu I \\
 \frac{dR}{dt} &= \tau A + \gamma I - \mu R
 \end{aligned}
 \tag{1}$$

where  $\lambda = \frac{\beta(\sigma E + \varepsilon I + \zeta A)}{N}$ .

**Table 1.** Parameter Value

Parameter	Description	Value	Unit	Source
$\Pi$	Birth rate	13,330	People/day	Estimation
$\beta$	Possibility of transmission upon contact	0.25	–	Estimation
$\sigma$	The contact rate of susceptible people with exposed people	0.12	1/day	Estimation
$\varepsilon$	The rate of contact of susceptible people with infected people accompanied by clinical symptoms	0.05	1/day	[11]
$\zeta$	The rate of contact of susceptible people with infected people without clinical symptoms	0.08	1/day	Estimation
$\omega$	Vaccination rates	0.1 – 1	1/day	Estimation
$\varepsilon$	Vaccine effectiveness	0.1 – 0.9	–	Estimation
$\theta$	Proportion of infected persons without clinical symptoms	0.15	–	Estimation
$\phi$	Transmission rate after completing the incubation period and moving to the infected class without clinical symptoms	0.00048	1/day	[11]
$v$	Transmission rate after completing the incubation period and transition to the infected class accompanied by clinical symptoms	0.005	1/day	[11]
$\tau$	Recovery rate of infected people without clinical symptoms	0.854302	1/day	[11]
$\gamma$	The rate of recovery of infected people accompanied by clinical symptoms	0.33029	1/day	[12]
$\alpha$	The death rate caused by COVID-19 in the class of people who are infected with clinical symptoms	$1.78 \times 10^{-5}$	1/day	[12]
$\mu$	Human natural death rate	$4.36 \times 10^{-5}$	1/day	[13]

### 3. RESULTS AND DISCUSSION

#### 3.1. Fixed Point

The fixed point of system of **Equation (1)** obtained by solving  $\frac{dS}{dt} = \frac{dV}{dt} = \frac{dE}{dt} = \frac{dA}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$  as follows:

$$\begin{aligned}\Pi - \lambda S - \omega S - \mu S &= 0 \\ \omega S - (1 - \varepsilon)\lambda V - \mu V &= 0 \\ \lambda S + (1 - \varepsilon)\lambda V - \theta\varphi E - (1 - \theta)vE - \mu E &= 0 \\ \theta\varphi E - \tau A - \mu A &= 0 \\ (1 - \theta)vE - \gamma I - \alpha I - \mu I &= 0 \\ \tau A + \gamma I - \mu R &= 0\end{aligned}\quad (2)$$

where  $\lambda = \lambda = \frac{\beta(\sigma E + \varepsilon I + \zeta A)}{N}$ .

Based on the system of **Equation (2)**, two types of equilibriums are obtained, namely disease-free equilibrium and endemic equilibrium. The disease-free equilibrium fulfill  $E = A = I = 0$ , while the endemic equilibrium has  $E \neq 0, A \neq 0$  dan  $I \neq 0$ .

The disease-free equilibrium is a condition when everyone is healthy or it can be said that there is no disease in a certain population. From the system of **Equation (2)** a disease-free equilibrium is obtained

$$T^0(S, V, E, A, I, R) = (S^0, V^0, 0, 0, 0, 0).$$

with

$$S^0 = \frac{\Pi}{\omega + \mu} \text{ and } V^0 = \frac{\omega\Pi}{\mu(\omega + \mu)}.$$

The endemic equilibrium is a condition when in a certain population there are still sick people or the disease has not disappeared. From the system of **Equation (2)** the endemic equilibrium is obtained

$$T^*(S, V, E, A, I, R) = (S^*, V^*, E^*, A^*, I^*, R^*)$$

with

$$\begin{aligned}S^* &= \frac{\Pi}{\lambda + \omega + \mu}, & A^* &= \frac{\theta\varphi E}{\tau + \mu}, \\ V^* &= \frac{\omega S}{(1 - \varepsilon)\lambda + \mu}, & I^* &= \frac{(1 - \theta)vE}{\gamma + \alpha + \mu}, \\ E^* &= \frac{\lambda S + (1 - \varepsilon)\lambda V}{\theta\varphi + (1 - \theta)v + \mu}, & R^* &= \frac{\tau A + \gamma I}{\mu}.\end{aligned}$$

#### 3.2. Basic Reproduction Number

The approach to determining the basic reproduction number ( $\mathcal{R}_0$ ) using the next generation matrix follows Driessche and Watmough [14]. Determination of the basic reproduction number is based on the order of subpopulations causing infection only [15], i.e.  $E, A$  and  $I$  as follows:

$$\begin{aligned}\frac{dE}{dt} &= \lambda S + (1 - \varepsilon)\lambda V - \theta\varphi E - (1 - \theta)vE - \mu E, \\ \frac{dA}{dt} &= \theta\varphi E - \tau A - \mu A, \\ \frac{dI}{dt} &= (1 - \theta)vE - \gamma I - \alpha I - \mu I.\end{aligned}\quad (3)$$

Based on the system of **Equation (3)**, obtained matrices  $F$  and  $V$  which are then evaluated at the disease-free equilibrium  $T^0$ , i.e.:

$$F = \begin{pmatrix} \sigma\beta\Omega & \zeta\beta\Omega & \varepsilon\beta\Omega \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

with

$$\Omega = \left( \frac{\mu}{\omega + \mu} + (1 - \varepsilon) \left( \frac{\omega}{(\omega + \mu)} \right) \right)$$

and

$$V = \begin{pmatrix} k_1 & 0 & 0 \\ -\theta\varphi & k_2 & 0 \\ -(1 - \theta)v & 0 & k_3 \end{pmatrix}$$

while

$$\begin{aligned} k_1 &= \theta\varphi + (1 - \theta)v + \mu & k_3 &= \gamma + \alpha + \mu \\ k_2 &= \tau + \mu \end{aligned}$$

Thus, the  $G$  matrix is obtained, with  $G = FV^{-1}$  as follows:

$$G = \begin{pmatrix} \sigma\beta\Omega & \zeta\beta\Omega & \varepsilon\beta\Omega \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \cdot \begin{pmatrix} \frac{1}{k_1} & 0 & 0 \\ \frac{\theta\varphi}{k_1 k_2} & \frac{1}{k_2} & 0 \\ \frac{(v - \theta v)}{k_1 k_3} & 0 & \frac{1}{k_3} \end{pmatrix} = \begin{pmatrix} G_{11} & G_{12} & G_{13} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

Thus

$$G_{11} = \frac{\varepsilon\beta\Omega(k_2 v - k_2 \theta v)}{k_1 k_2 k_3} + \frac{\sigma\beta\Omega}{k_1} + \frac{\zeta\theta\varphi\beta\Omega}{k_1 k_2}, \quad G_{12} = \frac{\zeta\beta\Omega}{k_2}, \quad \text{and} \quad G_{13} = \frac{\varepsilon\beta\Omega}{k_3}.$$

Based on the  $G$  matrix, the dominant eigenvalue is obtained, namely:

$$\mathcal{R}_0 = \frac{\Omega\beta(k_2\varepsilon(v - \theta v) + k_2 k_3 \sigma + k_3 \zeta\theta\varphi)}{k_1 k_2 k_3} = \mathcal{R}_0^1 + \mathcal{R}_0^2 + \mathcal{R}_0^3 \quad (4)$$

with

$$\mathcal{R}_0^1 = \Omega\beta \left( \frac{k_2\varepsilon(v - \theta v)}{k_1 k_2 k_3} \right), \quad \mathcal{R}_0^2 = \Omega\beta \left( \frac{k_2 k_3 \sigma}{k_1 k_2 k_3} \right), \quad \text{and} \quad \mathcal{R}_0^3 = \Omega\beta \left( \frac{k_3 \zeta\theta\varphi}{k_1 k_2 k_3} \right).$$

### 3.3. Equilibrium Stability Analysis

This section will describe the stability properties for disease-free equilibrium  $T^0$  and endemic equilibrium  $T^*$ .

**Theorem 1.** If  $\mathcal{R}_0 < 1$  then the disease-free equilibrium  $T^0$  for the system of **Equation (1)** is locally asymptotically stable.

**Proof.** Stability properties  $T^0(S, V, E, A, I, R) = \left( \frac{\Pi}{\omega + \mu}, \frac{\omega\Pi}{\mu(\omega + \mu)}, 0, 0, 0, 0 \right)$  can be known by linearizing the system (1) around  $T^0$ , so that the Jacobi matrix for the disease-free equilibrium  $T^0$  is obtained as follows:

$$J_{T^0} = \begin{pmatrix} J_{11} & 0 & J_{13} & J_{14} & J_{15} & 0 \\ J_{21} & J_{22} & J_{23} & J_{24} & J_{25} & 0 \\ J_{31} & J_{32} & J_{33} & J_{34} & J_{35} & 0 \\ 0 & 0 & J_{43} & J_{44} & 0 & 0 \\ 0 & 0 & J_{53} & 0 & J_{55} & 0 \\ 0 & 0 & 0 & J_{64} & J_{65} & J_{66} \end{pmatrix}$$

with

$$\begin{aligned} J_{11} &= -(\omega + \mu), & J_{34} &= \frac{\beta\zeta\mu}{\omega + \mu} + (1 - \varepsilon) \left( \frac{\beta\zeta\omega}{(\omega + \mu)} \right), \\ J_{13} &= -\frac{\beta\sigma\mu}{\omega + \mu}, & J_{35} &= \frac{\beta\varepsilon\mu}{\omega + \mu} + (1 - \varepsilon) \left( \frac{\beta\varepsilon\omega}{(\omega + \mu)} \right), \\ J_{14} &= -\frac{\beta\zeta\mu}{\omega + \mu}, & J_{43} &= \theta\varphi, \\ J_{15} &= -\frac{\beta\varepsilon\mu}{\omega + \mu}, & J_{44} &= -(\tau + \mu), \\ J_{21} &= \omega, & J_{53} &= (1 - \theta)v, \end{aligned}$$

$$\begin{aligned}
J_{22} &= -\mu, & J_{55} &= -(\gamma + \alpha + \mu), \\
J_{23} &= -(1 - \varepsilon) \left( \frac{\beta\sigma\omega}{(\omega + \mu)} \right), & J_{64} &= \tau, \\
J_{24} &= -(1 - \varepsilon) \left( \frac{\beta\zeta\omega}{(\omega + \mu)} \right), & J_{65} &= \gamma, \\
J_{25} &= -(1 - \varepsilon) \left( \frac{\beta\varepsilon\omega}{(\omega + \mu)} \right), & J_{66} &= -\mu. \\
J_{31} &= 0, \\
J_{32} &= 0, \\
J_{33} &= \frac{\beta\sigma\mu}{\omega + \mu} + (1 - \varepsilon) \left( \frac{\beta\sigma\omega}{(\omega + \mu)} \right) - (\theta\varphi + (1 - \theta)v + \mu),
\end{aligned}$$

Eigenvalues for disease-free equilibrium  $T^0$  obtained by  $|J_{T_0} - \lambda I| = 0$ , or

$$\begin{vmatrix}
J_{11} - \lambda & 0 & J_{13} & J_{14} & J_{15} & 0 \\
J_{21} & J_{22} - \lambda & J_{23} & J_{24} & J_{25} & 0 \\
0 & 0 & J_{33} - \lambda & J_{34} & J_{35} & 0 \\
0 & 0 & J_{43} & J_{44} - \lambda & 0 & 0 \\
0 & 0 & J_{53} & 0 & J_{55} - \lambda & 0 \\
0 & 0 & 0 & J_{64} & J_{65} & J_{66} - \lambda
\end{vmatrix} = 0,$$

so that the characteristic equation is obtained as follows:

$$(J_{11} - \lambda)(J_{22} - \lambda)(J_{66} - \lambda)(\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3) = 0 \quad (5)$$

with

$$\begin{aligned}
a_1 &= (1 - \mathcal{R}_0^2)k_1 + k_2 + k_3 \\
a_2 &= (1 - (\mathcal{R}_0^2 + \mathcal{R}_0^3))k_1k_2 + (1 - (\mathcal{R}_0^1 + \mathcal{R}_0^2))k_1k_3 + k_2k_3 \\
a_3 &= (1 - \mathcal{R}_0)k_1k_2k_3
\end{aligned}$$

Based on **Equation (5)**, six eigenvalues are obtained with three negative eigenvalues, namely

$$\lambda_1 = J_{11} = -(\omega + \mu), \quad \lambda_2 = J_{22} = -\mu, \quad \lambda_3 = J_{66} = -\mu.$$

while the other three eigenvalues are obtained by solving the following equation

$$(\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3) = 0 \quad (6)$$

Based on criteria Routh-Hurwitz [16], **Equation (6)** at the disease-free equilibrium  $T^0$  is stable if it satisfies the following stability conditions:

$$a_1 > 0, a_3 > 0, \text{ and } a_1a_2 > a_3 \quad (7)$$

Since all parameters are positive, the coefficient  $a_3$  will be positive when  $\mathcal{R}_0 < 1$ . Furthermore, for the coefficient  $a_1$  will be positive if  $\mathcal{R}_0^2 < 1$ . Hence  $\mathcal{R}_0 < 1$ , we also have  $\mathcal{R}_0^2 < 1$ . Then, to prove  $a_1a_2 > a_3$  it takes parameter values at the time of the condition  $\mathcal{R}_0 < 1$ . The parameters used are presented in **Table 1** and **Table 2**. So that for  $\mathcal{R}_0 < 1$  condition (6) is fulfilled. So, it is proved that the disease-free equilibrium  $T^0$  for system (1) is locally asymptotically stable if  $\mathcal{R}_0 < 1$ .

**Theorem 2.** If  $\mathcal{R}_0 > 1$  then the endemic equilibrium  $T^*$  for the system of **Equation (1)** is locally asymptotically stable.

**Proof.** Let  $\phi = \beta$  is the bifurcation parameter. Based on the condition  $\mathcal{R}_0 = 1$  resulted in

$$\phi = \phi^* = \frac{k_1k_2k_3}{\Omega(k_2\varepsilon(v - \theta v) + k_2k_3\sigma + k_3\zeta\theta\varphi)}.$$

The equilibrium  $T^0$  has one zero eigenvalue and five negative eigenvalues if  $\mathcal{R}_0 = 1$  or  $\phi = \phi^*$ . The zero eigenvalue has a right eigenvector  $(u_1, u_2, u_3, u_4, u_5, u_6)$  and left eigenvector  $(v_1, v_2, v_3, v_4, v_5, v_6)$ .

$$\begin{aligned}
\text{Let } u_3 > 0, \text{ hence } u_4 &= \frac{\theta\varphi}{k_2}u_3 > 0, u_5 = \frac{(1-\theta)v}{k_3}u_3 > 0, u_6 = -\left(\frac{\tau\theta\varphi}{\mu k_2} + \frac{\gamma(1-\theta)v}{\mu k_3}\right)u_3 < 0, \\
u_1 &= -\left(\frac{\beta\sigma\mu}{(\omega + \mu)^2} + \frac{\beta\zeta\mu}{(\omega + \mu)^2} \frac{\theta\varphi}{k_2} + \frac{\beta\varepsilon\mu}{(\omega + \mu)^2} \frac{(1-\theta)v}{k_3}\right)u_3 < 0,
\end{aligned}$$

$$u_2 = -\left(\frac{\omega}{\mu} \left(\frac{\beta\sigma\mu}{(\omega + \mu)^2} + \frac{\beta\zeta\mu}{(\omega + \mu)^2} \frac{\theta\varphi}{k_2} + \frac{\beta\epsilon\mu}{(\omega + \mu)^2} \frac{(1 - \theta)v}{k_3}\right) + (1 - \epsilon) \left(\frac{\beta\sigma\omega}{(\omega + \mu)}\right) \frac{1}{\mu} + (1 - \epsilon) \left(\frac{\beta\zeta\omega}{(\omega + \mu)}\right) \frac{1}{\mu} \frac{\theta\varphi}{k_2} + (1 - \epsilon) \left(\frac{\beta\epsilon\omega}{(\omega + \mu)}\right) \frac{1}{\mu} \frac{(1 - \theta)v}{k_3}\right) u_3 < 0.$$

Furthermore,  $v_2 = 0, v_1 = 0, v_6 = 0$ . Let  $v_3 > 0$ , then  $v_4 = \frac{\Omega\beta\zeta}{k_2} v_3 > 0, v_5 = \frac{\Omega\beta\epsilon}{k_3} v_3 > 0$ .

Based on the Castillo-Chaves and Song equation [16] defined

$$a = \sum_{k,i,j=1}^6 v_k u_i u_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(T^0, \phi^*), \quad b = \sum_{k,i,j=1}^6 v_k u_i \frac{\partial^2 f_k}{\partial x_i \partial \phi}(T^0, \phi^*) \tag{8}$$

with

$$\begin{aligned} x_1 &= S, & x_2 &= V, & x_3 &= E, \\ x_4 &= A, & x_5 &= I, & x_6 &= R. \end{aligned}$$

$$\begin{aligned} f_1 &= \frac{dx_1}{dt} = \Pi - \frac{\phi(\sigma x_3 + \epsilon x_5 + \zeta x_4)}{N} x_1 - \omega x_1 - \mu x_1, \\ f_2 &= \frac{dx_2}{dt} = \omega x_1 - (1 - \epsilon) \frac{\phi(\sigma x_3 + \epsilon x_5 + \zeta x_4)}{N} x_2 - \mu x_2, \\ f_3 &= \frac{dx_3}{dt} = \frac{\phi(\sigma x_3 + \epsilon x_5 + \zeta x_4)}{N} x_1 + (1 - \epsilon) \frac{\phi(\sigma x_3 + \epsilon x_5 + \zeta x_4)}{N} x_2 - \theta\varphi x_3 - (1 - \theta)v x_3 - \mu x_3, \\ f_4 &= \frac{dx_4}{dt} = \theta\varphi x_3 - \tau x_4 - \mu x_4, \\ f_5 &= \frac{dx_5}{dt} = (1 - \theta)v x_3 - \gamma x_5 - \alpha x_5 - \mu x_5, \\ f_6 &= \frac{dx_6}{dt} = \tau x_4 + \gamma x_5 - \mu x_6. \end{aligned}$$

Based on the system of Equation (1), the following partial derivatives for Equation (8) are obtained

$$\begin{aligned} \frac{\partial^2 f_3}{\partial x_1 \partial x_3}(T^0, \phi^*) &= \frac{\sigma\phi^*}{N} = \frac{\mu\sigma\phi^*}{\Pi}, & \frac{\partial^2 f_3}{\partial x_1 \partial x_4}(T^0, \phi^*) &= \frac{\zeta\phi^*}{N} = \frac{\mu\zeta\phi^*}{\Pi}, \\ \frac{\partial^2 f_3}{\partial x_1 \partial x_5}(T^0, \phi^*) &= \frac{\epsilon\phi^*}{N} = \frac{\mu\epsilon\phi^*}{\Pi}, & \frac{\partial^2 f_3}{\partial x_2 \partial x_3}(T^0, \phi^*) &= \frac{(1 - \epsilon)\mu\sigma\phi^*}{\Pi}, \\ \frac{\partial^2 f_3}{\partial x_2 \partial x_4}(T^0, \phi^*) &= \frac{(1 - \epsilon)\mu\zeta\phi^*}{\Pi}, & \frac{\partial^2 f_3}{\partial x_2 \partial x_5}(T^0, \phi^*) &= \frac{(1 - \epsilon)\mu\epsilon\phi^*}{\Pi}, \\ \frac{\partial^2 f_3}{\partial x_3 \partial \phi}(T^0, \phi^*) &= \sigma\Omega, & \frac{\partial^2 f_3}{\partial x_4 \partial \phi}(T^0, \phi^*) &= \zeta\Omega, \\ \frac{\partial^2 f_3}{\partial x_5 \partial \phi}(T^0, \phi^*) &= \epsilon\Omega. \end{aligned}$$

So, based on Equation (8) we get

$$\begin{aligned} a &= v_3 u_1 u_3 \frac{\partial^2 f_3}{\partial x_1 \partial x_3}(T^0, \phi^*) + v_3 u_1 u_4 \frac{\partial^2 f_3}{\partial x_1 \partial x_4}(T^0, \phi^*) + v_3 u_1 u_5 \frac{\partial^2 f_3}{\partial x_1 \partial x_5}(T^0, \phi^*) \\ &\quad + v_3 u_2 u_3 \frac{\partial^2 f_3}{\partial x_2 \partial x_3}(T^0, \phi^*) + v_3 u_2 u_4 \frac{\partial^2 f_3}{\partial x_2 \partial x_4}(T^0, \phi^*) + v_3 u_2 u_5 \frac{\partial^2 f_3}{\partial x_2 \partial x_5}(T^0, \phi^*) \\ &= v_3 \left( u_1 u_3 \frac{\mu\sigma\phi^*}{\Pi} + u_1 u_4 \frac{\mu\zeta\phi^*}{\Pi} + u_1 u_5 \frac{\mu\epsilon\phi^*}{\Pi} + u_2 u_3 \frac{(1 - \epsilon)\mu\sigma\phi^*}{\Pi} + u_2 u_4 \frac{(1 - \epsilon)\mu\zeta\phi^*}{\Pi} \right. \\ &\quad \left. + u_2 u_5 \frac{(1 - \epsilon)\mu\epsilon\phi^*}{\Pi} \right), \end{aligned}$$

Since  $v_3, u_3, u_4, u_5 > 0$  and  $u_1, u_2 < 0$ , then  $a < 0$  and then we get

$$\begin{aligned} b &= v_3 u_3 \frac{\partial^2 f_3}{\partial x_3 \partial \phi}(T^0, \phi^*) + v_3 u_4 \frac{\partial^2 f_3}{\partial x_4 \partial \phi}(T^0, \phi^*) + v_3 u_5 \frac{\partial^2 f_3}{\partial x_5 \partial \phi}(T^0, \phi^*) \\ &= v_3 u_3 \sigma\Omega + v_3 u_4 \zeta\Omega + v_3 u_5 \epsilon\Omega, \end{aligned}$$

Hence  $v_3, u_3, u_4, u_5 > 0$ , so that  $b > 0$ .

The value of  $a$  and  $b$  obtained meets the criteria for case 4 of the Castillo-Chavez and Song Theorem [16]. As a result, when  $\varphi$  changed from  $\varphi < \varphi^*$  ( $\mathcal{R}_0 < 1$ ) into  $\varphi > \varphi^*$  ( $\mathcal{R}_0 > 1$ ), the endemic equilibrium  $T^*$  which is unstable turns from negative to positive and locally asymptotically stable. Hence, we have proved if  $\mathcal{R}_0 > 1$  then the endemic equilibrium  $T^*$  is locally asymptotically stable.

### 3.4. Numerical Simulation

Numerical simulations on the modified model are carried out to show stability and show the stability properties of each fixed point by entering the parameter values in Table 2. Then, numerical simulations are carried out to study things in dynamical systems. In this case, the dynamics of the human population and varying parameter values, namely parameters that are still possible for humans to control in an effort to suppress the spread of COVID-19, among them are the parameters of the rate of vaccination ( $\omega$ ) and vaccine efficacy ( $\varepsilon$ ).

**Table 2. Parameter Value of Research on the Spread of COVID-19**

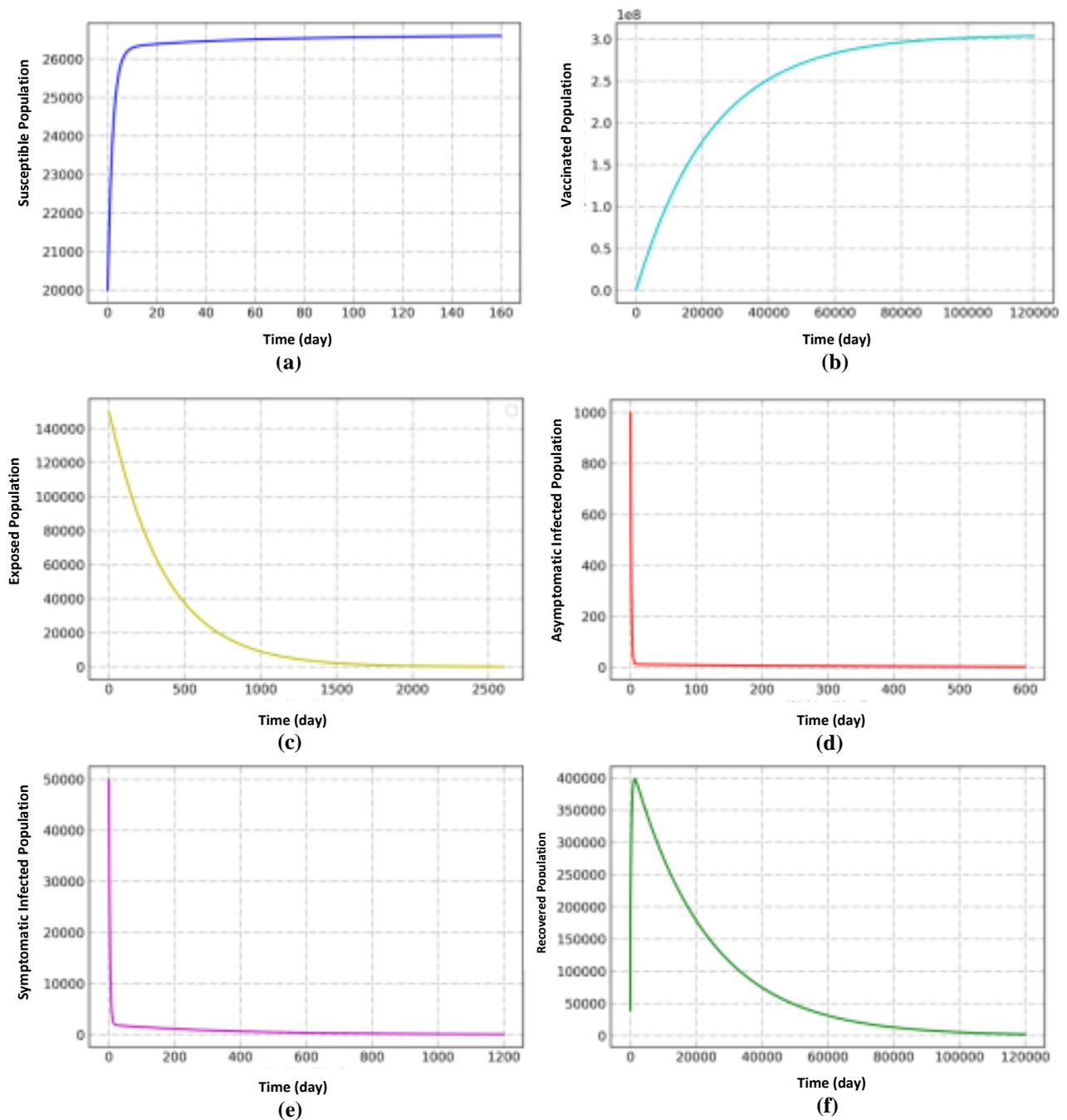
Parameter	$\mathcal{R}_0 < 1$		$\mathcal{R}_0 > 1$	
	Value	Source	Value	Source
$\omega$	0.5	Assumption	0.8	Assumption
$\varepsilon$	0.95	Assumption	0.5	Assumption

Other parameter values can be seen in Table 1. Since the parameters that can be changed in this study are the parameters  $\omega$  and  $\varepsilon$ , then the parameter values that are changed in the study are the parameter values  $\omega$  and  $\varepsilon$ . Population dynamics were observed when  $\mathcal{R}_0 < 1$  and  $\mathcal{R}_0 > 1$ . In this case,  $\mathcal{R}_0$  is the basic reproduction number defined in Equation (4). The initial value used is  $S(0) = 20,000, V(0) = 250,000, E(0) = 150,000, A(0) = 1,000, I(0) = 50,000$ , and  $R(0) = 40,000$ .

The system of Equation (1) when  $\mathcal{R}_0 < 1$  has one disease-free equilibrium can be represented by a numerical solution. The equilibrium is obtained using the parameter values in Table 2, with  $\mathcal{R}_0 = 0.346029 < 1$  and disease-free equilibrium  $T^0(S = 26,657.7, V = 3.05707 \times 10^8, E = 0, A = 0, I = 0, R = 0)$ . By linearizing and calculating the system of Equation (1) around the equilibrium, the Jacobian matrix and eigenvalues for the disease-free equilibrium are obtained. It can be concluded that the disease-free equilibrium is stable because all eigenvalues are negative, namely  $\lambda_1 = -0.854346, \lambda_2 = -0.500044, \lambda_3 = -0.33036, \lambda_4 = -0.00285491, \lambda_5 = -0.0000436$ , and  $\lambda_6 = -0.0000436$ .

Dynamics of subpopulations with vulnerable populations ( $S$ ), vaccinated population ( $V$ ), exposed population ( $E$ ), asymptomatic infected population ( $A$ ), symptomatic infected population ( $I$ ), population that has recovered from the disease ( $R$ ), to a disease-free equilibrium  $T^0$  as can be seen in Figure 2. The number of susceptible populations and vaccinated populations increases continuously until they reach stability around their respective equilibrium, that is  $S = 26,657.7$  and  $V = 3.05707 \times 10^8$ . The exposed population, the asymptomatic infected population and the symptomatic infected population decreased steadily until they stabilized around a equilibrium  $E = A = I = 0$ . Meanwhile, the population that recovered from the disease initially increased, then decreased continuously until it reached stability around a equilibrium  $R = 0$ . The simulation results are in accordance with Theorem 1 that if  $\mathcal{R}_0 < 1$ , disease-free equilibrium  $T^0$  is locally asymptotically stable.

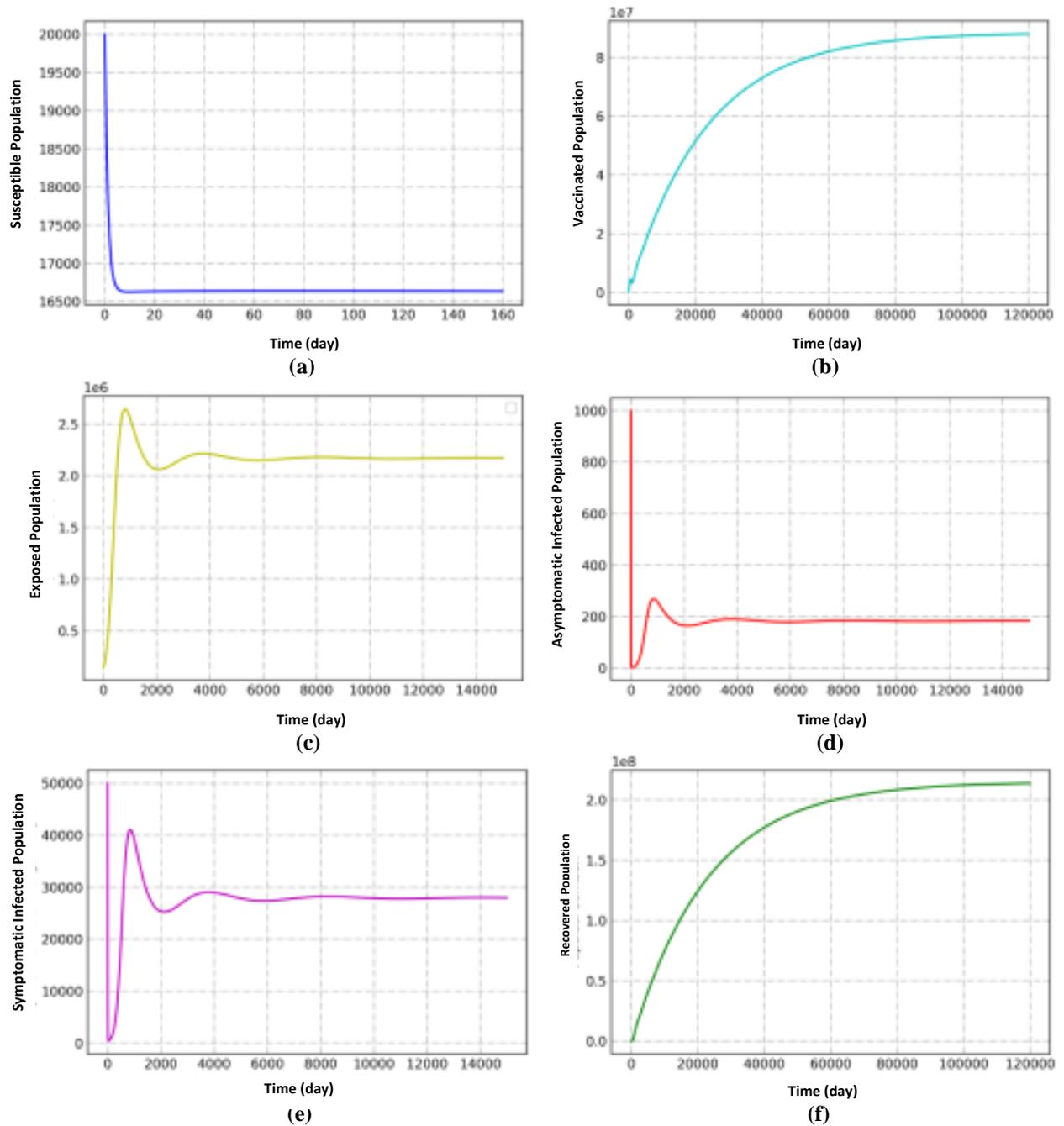
A dynamical system also has one endemic equilibrium which can be represented by a numerical solution. The equilibrium is obtained using the parameter values in Table 2, with  $\mathcal{R}_0 = 3.45475$ . The endemic equilibrium  $T^*(S = 16,657.1, V = 8.84648 \times 10^7, E = 2.16974 \times 10^6, A = 182,855, I = 27,913.9, R = 2.15043 \times 10^8)$ . By linearization and calculation of the system of Equation (1) around a equilibrium, the Jacobian matrix and eigenvalues for endemic equilibrium are obtained. Furthermore, it can be concluded that the endemic fixed point is stable because there are four negative eigenvalues and two eigenvalues whose real part is negative. They are  $\lambda_1 = -0.854346, \lambda_2 = -0.800258, \lambda_3 = -0.330375, \lambda_4 = 0.0000436, \lambda_5 = -0.0000753128 - 0.0006794i$ , and  $\lambda_6 = -0.0000753128 + 0.0006794i$ .



**Figure 2.** Population Dynamics for  $\mathcal{R}_0 < 1$

(a) Susceptible Population, (b) Vaccinated Population, (c) Exposed Population, (d) Asymptomatic Infected Population, (e) Symptomatic Infected Population, and (f) Recovered Population

The dynamics of the subpopulation for  $\mathcal{R}_0 > 1$  is shown in **Figure 3**. Population dynamics indicate that a subpopulation is moving towards an endemic equilibrium or is stable around an endemic equilibrium. The vulnerable population declines continuously until it stabilizes around a equilibrium, specifically  $S = 16,657.1$ . The vaccinated population increases steadily until it stabilizes around a fixed point  $V = 8.84648 \times 10^7$ . The exposed population, asymptomatic infected population and symptomatic infected population initially fluctuated, then stabilized around their respective fixed points, namely  $E = 2.16974 \times 10^6$ ,  $A = 182,855$ , and  $I = 27,913.9$ . Meanwhile, the recovered population experienced a continuous increase until it reached stability around a fixed point  $R = 2.15043 \times 10^8$ . This simulation result is in accordance with Theorem 2 that if  $\mathcal{R}_0 > 1$ , the endemic equilibrium  $T^*$  is locally asymptotically stable.



**Figure 3.** Population Dynamics for  $R_0 > 1$

(a) Susceptible Population, (b) Vaccinated Population, (c) Exposed Population, (d) Asymptomatic Infected Population, (e) Symptomatic Infected Population, and (f) Recovered Population

#### 4. CONCLUSIONS

This research is a modification of the mathematical model of the spread of the COVID-19 disease. The model considers vaccination of susceptible individuals. The resulting model is able to describe the spread of the COVID-19 virus. The results of the analysis performed on the modified model obtained two equilibriums, namely disease-free equilibrium and endemic equilibrium. The disease-free equilibrium is locally asymptotically stable if the basic reproduction number is less than one, while the endemic equilibrium is locally asymptotically stable if the basic reproduction number is greater than one. Numerical simulations of population dynamics show that the results are consistent with the stability of the disease-free equilibrium and endemic equilibrium.

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