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Vaccine Effectiveness Impact on the COVID-19 Dynamics Spread Outbreak Using Improved SEIR Mathematical Epidemic Model

Fadilah Akbar[1], **Ahmad Hanif Asyhar**[2,*], **Ahmad Lubab**[2], **Abdulloh Hamid**[2], **Moh. Hafiyusholeh**[2], **Dian Candra Rini Novitasari**[2], **Ahmad Zaenal Arifin**[3] **and Muhammad Fahrur Rozi**[4]

[1] *Department of Mathematics, Faculty of Science and Data Analytics, Institut Teknologi Sepuluh Nopember, Surabaya, Indonesia*
e-mail : fadilakbary123@gmail.com (F. Akbar)

[2] *Department of Mathematics, Faculty of Science and Technology, Universitas Islam Negeri Sunan Ampel, Surabaya, Indonesia*
e-mail : hanif@uinsby.ac.id (A.H. Asyhar); ahmadlubab@uinsby.ac.id (A. Lubab); doelhamid@uinsby.ac.id (A. Hamid); hafiyusholeh@uinsby.ac.id (M. Hafiyusholeh); diancrini@uinsby.ac.id (D.C.R. Novitasari)

[3] *Department of Mathematics, Faculty of Math and Science, Universitas PGRI Ronggolawe, Tuban, Indonesia*
e-mail : az_arifin@unirow.ac.id (A.Z. Arifin)

[4] *Department of Mathematics, Faculty of Mathematics and Natural Sciences, Universitas Brawijaya, Malang, Indonesia*
e-mail : m.f.rozi.mfr@gmail.com (M.F. Rozi)

Abstract The second wave of the COVID-19 outbreak in Surabaya resulted in significant casualties and losses across a range of sectors. The epidemic mathematical model is used as a mitigation strategy in controlling the spread of the COVID-19 infection outbreak, through the provision of control in the form of vaccination to the community. The objective of this study is to ascertain the impact of the efficacy of the COVID-19 vaccine through the utilization of the enhanced SEIR mathematical epidemic model. The COVID-19 data from Surabaya is employed as a case study, as this region of Indonesia has a significant impact on mortality rates. The model used has unstable characteristics at the disease-free equilibrium $\xi_0 = (10790.5498, 0, 0, 0)$, however, this model is stable at the endemic equilibrium point $\xi_1 = (1100.7897, 1.9526, 0.4642, 36.9607)$. It is known from the basic reproduction numbers $\mathcal{R}_0 = 9.79$, It is predicted that the outbreak will stop the epidemic on February 20, 2024. The government has taken control efforts by providing vaccines to the public. The simulation results with the addition of vaccine parameters produce the basic reproduction numbers with controlled treatment $\mathcal{R}_t < 5$ The outbreak stopped 533-592 days earlier. The simulation results from the model used have errors in the range of 16% to 40%.

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*Corresponding author.

1. Introduction

The disease caused by the SARS-CoV-2 virus, designated as "COVID-19", was first identified in Wuhan, Hubei Province, China, in December 2019 [1]. As of December 2021, the disease has been endemic throughout the world for approximately two years. In Indonesia, the disease has been endemic for one year and nine months. The COVID-19 outbreak in Indonesia has occurred in two waves. The first outbreak began in early March 2020 and continued until mid-May 2021. The second outbreak occurred starting from May 14 to the end of November 2021, with a total of 2,633 cases [2]. This number continued to increase, reaching 56,757 cases [3]. Upon the occurrence of the second outbreak, five provinces were identified as having the highest number of cases of the spread of COVID-19 in Indonesia. These provinces were DKI Jakarta, West Java, Central Java, East Java, and East Kalimantan [4].

In the initial phase of the COVID-19 outbreak in Indonesia, East Java Province held the highest number of cases in the country. This was largely due to the large number of individuals infected with COVID-19 in Surabaya. The high number of confirmed cases of infection led to the designation of Surabaya as a dangerous area or black zone. The transmission of this virus can occur through human contact, through the emission of droplets, and via airborne transmission, which can result in the rapid spread and increase in the number of infected individuals in multiple locations [5], [6]. One of the causes of the high number of cases is the lack of awareness among the Surabaya community regarding the importance of maintaining cleanliness and implementing health protocols set by the government. This behavior enables the virus that causes COVID-19 to become stronger, thus allowing it to fight antibodies and mutate into a new variant that is more dangerous [7], [8]. The mutated SARS-CoV-2 virus, which causes COVID-19, caused the second wave of COVID-19 infections in Indonesia. The previous SARS-CoV-2 virus variant that had spread in the community mutated and became more dangerous, resulting in the emergence of a new variant, the delta variant [9], [10].

As the capital city in East Java Province, Surabaya, which was also affected by the second wave of attacks, resulted in numerous residents becoming victims of COVID-19. On May 14, 2021, there were 6,110 cases of residents exposed to COVID-19 and 23,739 cases of Surabaya residents who were confirmed infected. The high number of recorded cases indicates that the spread is occurring at a rapid pace within the Surabaya community, particularly given that many individuals have not yet received the full dose of the COVID-19 vaccination [11], [12]. The impact of the COVID-19 pandemic has resulted in significant losses for Surabaya in various sectors, including health, the economy, tourism, education, and psychology.

The prolonged and intensive loss of human resources due to the COVID-19 pandemic has resulted in Surabaya experiencing a decline in the quality of its human resources, increased community inequality, and the imposition of restrictions on community activities (PPKM) to prevent the further spread of the outbreak [13]. An analysis of the growth pattern of COVID-19 cases in Surabaya based on the available confirmed data can be employed as a countermeasure or mitigation strategy. The analysis method that can be employed is the use of a mathematical model, which will then be simulated using a numerical approach [14]. The mathematical model was then adjusted to reflect the conditions and circumstances of the second wave of the COVID-19 outbreak in Surabaya. The

numerical simulation generated from the mathematical model provides a visual representation of the conditions and situations that occur when the second wave of the COVID-19 pandemic attacks in Surabaya.

The utilization of mathematical models for epidemics is, in fact, flexible, contingent upon the researchers themselves to employ the desired model equation. Furthermore, mathematical models can be combined or modified according to the needs and data obtained [15]. The objective is to rectify inappropriate parameters, unforeseen parameters, or errors that arise from the use of a simple model, thereby yielding invalid and less precise results or visualizations. The SEIR epidemic model is a commonly employed mathematical model for analyzing the dynamics of disease spread. The SEIR acronym stands for the four main variables that comprise the model: susceptible, exposed, infected, and recovered.

One of the studies that discusses the mathematical epidemic model of the spread of COVID-19 infection [16] case study in Tuban which focused on parameter estimation. The mathematical model used is the SEIR epidemic model, where the model used is assumed to be exposed to individuals who are still likely not to be infected, so there are new parameters added to the model, the MAPE value obtained makes the mathematical model used quite good. Research with the same focus and using assumptions similar to the previous one in the model used was also carried out [17], the difference in the model used is that exposed individuals are still likely to be uninfected, considered cured immediately, and not susceptible again. In the SEIR epidemic model used, there are additional parameters with the assumption that individuals who recover from COVID-19 can still be re-infected so that recovered individuals become susceptible individuals. The next study which also discusses the mathematical epidemic model of the spread of COVID-19 infection, was carried out [18] with a case study in the Province of Lambordia which focused on deterministic analysis of epidemic models and numerical simulations, with the epidemic model used was SEIR.

In this study, the SEIR epidemic mathematical model will be used, with modifications made to the mortality rates in each variable. It is assumed that individuals who have recovered can still be susceptible to infection. As the epidemic model is expressed in the form of a mathematical equation, a simulation method employing a numerical approach is required to visualize the condition of the outbreak. One such method is the 5th-order Runge-Kutta method, which is still relatively underutilized. The fourth-order Runge-Kutta method is demonstrably superior to the Euler and Heun methods in terms of accuracy and precision [19].

2. Mathematical Model and Parameters

2.1. SEIR Epidemic Model

The basic epidemic model used is the SIR (Susceptible, Infected, and Recovery) model, in this study the model was developed by adding a delay factor for infection, namely Exposed so that the epidemic model was modified to SEIR (Susceptible, Exposed, Infected, and Recovery) [20], [21]. In the case of COVID-19, individuals who are included in the exposed population are individuals who are suspected of being infected with COVID-19, have the status of a person under surveillance, and have the possibility of not being infected so that they are again vulnerable and enter the susceptible population [16], [22].

The condition of the cases in Indonesia, individuals who have recovered can still be infected with COVID-19 again, so that individuals from the recovery population can become vulnerable again so that they enter the susceptible population [23], [24]. Based on the conditions and situations described previously, the epidemic model can be formulated mathematically into the following form:

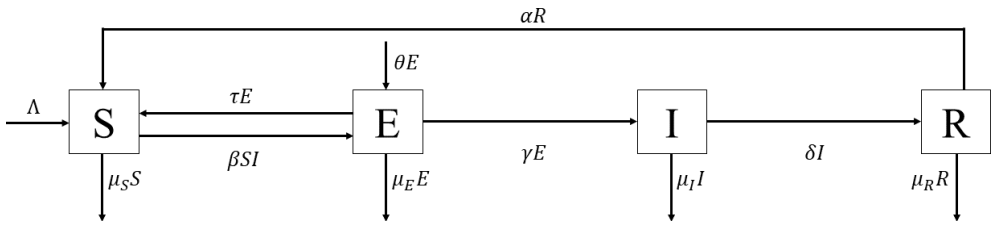


FIGURE 1. SEIR epidemic model compartment

Based on the compartment diagram in Figure 1, the SEIR COVID-19 epidemic model in the Surabaya can be compiled into a mathematical form as follows:

$$\frac{dS(t)}{dt} = \Lambda + \tau E(t) + \alpha R(t) - (\beta I(t) + \mu_S)\, S(t) \tag{2.1}$$

$$\frac{dE(t)}{dt} = \beta S(t) I(t) - (\gamma + \tau + \mu_E - \theta)\, E(t) \tag{2.2}$$

$$\frac{dI(t)}{dt} = \gamma E(t) - (\delta + \mu_I)\, I(t) \tag{2.3}$$

$$\frac{dR(t)}{dt} = \delta I(t) - (\alpha + \mu_R)\, R(t) \tag{2.4}$$

In equations (2.1), (2.2), (2.3), and (2.4) there are several parameters that are used as a reference in analyzing the model used. To get parameter values, probability, mortality, and epidemiology can be used based on the data we have. In general, the description of the mathematical model can be described as follows:

TABLE 1. Model parameter estimation

Parameters	Description	Value
Λ	Natural birth rate	0.267605634
α	The rate of individuals who have recovered is vulnerable	0.008685
β	The rate at which susceptible individuals become exposed	0.0021215
τ	The rate at which individuals are re-exposed vulnerable	0.26776
θ	Rate of increase in exposed individuals migrating into cities	0.000812
γ	The rate at which an exposed individual becomes sick from infection	0.2245
δ	Rate of recovered infected individuals	0.9192

μ_S	Mortality rate in susceptible individual population	0.0000248
μ_E	Death rate in the population of exposed individuals	0.06376
μ_I	Death rate in the population of infected individuals due to COVID-19	0.025189
μ_R	Death rate in a population of recovered individuals	0.00286

2.2. SEIR Epidemic Model with Control Treatment

In the SEIR epidemic model used in equation (2.1) to equation (2.4), it will show the dynamics of the spread of the COVID-19 outbreak without any treatment given to the community. In order to control the spread of the outbreak, the population rate of infected individuals should be reduced as much as possible. One method that can be used to control the outbreak is to give vaccines to the community so that they have immunity to prevent viral infections due to COVID-19 [25]. Based on the description previously, the SEIR epidemic model will be mathematically developed by modifying the parameters used in equation (2.1) and equation (2.2) [26]. The reason for modifying the two equations is, to reduce the rate of population increase which is directly related to the infected population in the compartment diagram, the development of the modified mathematical model of the SEIR epidemic model can be written as follows [27]:

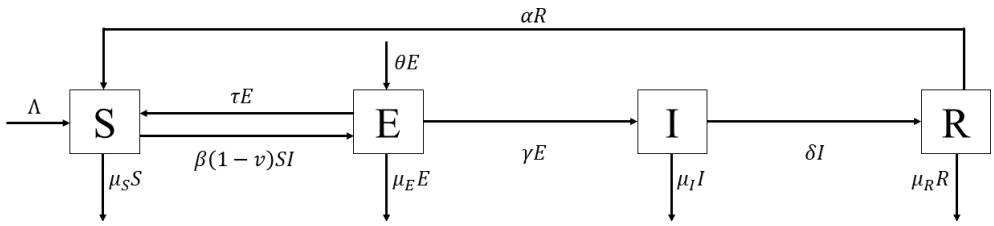


Figure 2. SEIR epidemic model compartment with vaccine effectiveness

Based on the compartment diagram in Figure 2, the SEIR epidemic model can be compiled into a mathematical form as follows:

$$\frac{dS(t)}{dt} = \Lambda + \tau E(t) + \alpha R(t) - (\beta(1-v)I(t) + \mu_S)S(t) \tag{2.5}$$

$$\frac{dE(t)}{dt} = \beta(1-v)S(t)I(t) - (\gamma + \tau + \mu_E - \theta)E(t) \tag{2.6}$$

It is presumed that all residents of Surabaya have received a complete vaccination regimen against the COVID-19, comprising two doses of vaccine. The incorporation of the parameter v into equations (2.6) and (2.6) represents the effectiveness of the vaccine. The majority of vaccines administered to the residents of Surabaya were Sinovac and AstraZeneca vaccines. The efficacy of the vaccine will be determined by the Sinovac and AstraZeneca vaccines in accordance with the regulations of the Indonesian Food and Drug Supervisory Agency (BPOM). The efficacy of the Sinovac and AstraZeneca vaccines is presented in Table 2 as follows [28], [29]:

Table 2. Control parameters with vaccine

Parameters	Description	Value	Percentage of Vaccine Ability
v_S	The effectiveness of the Sinovac vaccine	0.501	50.1%
v_A	The effectiveness of the AstraZeneca vaccine	0.621	62.1%

3. System Equilibrium Point

3.1. Global Equilibrium Point

In the epidemic model to analyze the dynamics of the spread of epidemic diseases in an area, there are at least two local equilibrium points, namely the equilibrium point in disease free conditions, and the equilibrium point in endemic conditions. Before starting the process of looking for a local equilibrium point, the first thing that needs to be done is to find the global equilibrium point, so that by using the global equilibrium point, it is easier to enter assumptions under various conditions given to the model [30]. In finding the equilibrium point of each main variable, equations (2.1) to (2.4) are used, assuming $\frac{dS(t)}{dt} = \frac{dE(t)}{dt} = \frac{dI(t)}{dt} = \frac{dR(t)}{dt} = 0$ so that so that the global equilibrium point $\xi_t = (S_t, E_t, I_t, R_t)$ is obtained from this epidemic model as follows:

$$S_t = \frac{\Lambda + \tau E_t + \alpha R_t}{\beta I_t + \mu_S} \tag{3.1}$$

$$E_t = \frac{\beta S_t I_t}{\gamma + \tau + \mu_E - \theta} \tag{3.2}$$

$$I_t = \frac{\gamma E_t}{\delta + \mu_I} \tag{3.3}$$

$$R_t = \frac{\delta I_t}{\alpha + \mu_R} \tag{3.4}$$

Armed with equations (3.1), (3.2), (3.3), and (3.4), it will then be used to find the equilibrium point for each condition, namely disease free conditions and endemic conditions.

3.2. Disease Free Equilibrium Point

This disease free equilibrium point can occur if it is assumed that in a population there is no epidemic of infectious disease. In simple terms it can be said that there are no exposed or infected individuals, meaning the population is at $E = 0$ and the population is at $I = 0$ [31]. By substituting this example into equations (3.1) and (3.4), we get a disease free equilibrium point $\xi_0 = (S_0, E_0, I_0, R_0)$ as follows:

$$R_0 = \frac{\delta I_0}{\alpha + \mu_R} = \frac{\delta \cdot 0}{\alpha + \mu_R} = 0$$

$$S_0 = \frac{\Lambda + \tau E_0 + \alpha R_0}{\beta I_0 + \mu_S} = \frac{\Lambda + (\tau \cdot 0) + (\alpha \cdot 0)}{(\beta \cdot 0) + \mu_S} = \frac{\Lambda}{\mu_S}$$

Based on the above solution, the equilibrium point at the disease free condition is $\xi_0 = (10790.5498, 0, 0, 0)$.

3.3. Endemic Equilibrium Point

The equilibrium point in this endemic condition can occur if it is assumed that there is an epidemic of infectious disease. Simply put, it can be said that there are individuals who are exposed or infected, meaning the population is at $E \neq 0$ and the population is at $I \neq 0$ [31]. With this example equations (3.2) and (3.4) will be used by substituting into equations (2.1) and (2.3) to get the points S_1 and I_1, after that S_1 and I_1 will be used by substituting them into equations (3.2) and (3.4), the disease free equilibrium point is obtained $\xi_1 = (S_1, E_1, I_1, R_1)$ as follows:

$$S_1 = \frac{(\delta + \mu_I)(\gamma + \tau + \mu_E - \theta)}{\gamma\beta}$$

$$I_1 = \frac{(\mu_S S_1 - \Lambda)(\alpha + \mu_R)(\gamma + \tau + \mu_E - \theta)}{\tau\beta S_1(\alpha + \mu_R) + \alpha\delta(\gamma + \tau + \mu_E - \theta) - \beta S_1(\alpha + \mu_R)(\gamma + \tau + \mu_E - \theta)}$$

$$E_1 = \frac{(\delta + \mu_I)(\mu_S S_1 - \Lambda)(\alpha + \mu_R)(\gamma + \tau + \mu_E - \theta)}{\gamma(\tau\beta S_1(\alpha + \mu_R) + \alpha\delta(\gamma + \tau + \mu_E - \theta) - \beta S_1(\alpha + \mu_R)(\gamma + \tau + \mu_E - \theta))}$$

$$R_1 = \frac{\delta(\mu_S S_1 - \Lambda)(\alpha + \mu_R)(\gamma + \tau + \mu_E - \theta)}{\tau\beta S_1(\alpha + \mu_R)\alpha\delta(\gamma + \tau + \mu_E - \theta) - \beta S_1(\alpha + \mu_R)(\gamma + \tau + \mu_E - \theta)}$$

Based on the above solution, the equilibrium point at the disease free condition is $\xi_1 = (1100.7897, 1.9526, 0.4642, 36.9607)$.

4. Basic Reproduction Number

$\mathcal{R}_0$ or commonly known as the notation of the basic reproduction number, is the average number of susceptible individuals population that can be directly infected by other infected individuals, this is caused by the presence of infected individuals who enter the population of susceptible individuals [30]. To get the basic reproduction number, you can use the Driessche and Watmough method, by finding the largest eigenvalue of the next generation matrix obtained from the population sample in which there are infected individuals. The next generation matrix can be formed from the equations for the exposed and infected populations (E and I), each of which is linearized using the Jacobian matrix method, then substituted with the equilibrium point in disease free conditions [16].

4.1. Natural Basic Reproduction Number ($\mathcal{R}_0$)

The natural basic reproduction number is obtained by using equations (2.2) and (2.3) which are entered into the next generation matrix which will then look for the eigenvalues. Based on the analysis and calculations performed, the matrix F is obtained which is the rate of emergence of new infections in population I, and matrix V is also obtained which is the rate of movement of individuals out of population I minus the rate of movement of individuals into population I, as follows:

$$\varphi = \begin{bmatrix} \beta SI + \theta E \\ 0 \end{bmatrix}, \quad \psi = \begin{bmatrix} (\gamma + \tau + \mu_E) E \\ -\gamma E + (\delta + \mu_I) I \end{bmatrix}$$

$$J(\varphi) = \begin{bmatrix} \frac{\partial(\beta SI + \theta E)}{dE} & \frac{\partial(\beta SI + \theta E)}{dI} \\ \frac{\partial(0)}{dE} & \frac{\partial(0)}{dI} \end{bmatrix}, \quad J(\psi) = \begin{bmatrix} \frac{\partial((\gamma+\tau+\mu_E)E)}{dE} & \frac{\partial((\gamma+\tau+\mu_E)E)}{dI} \\ \frac{\partial(-\gamma E+(\delta+\mu_I)I)}{dE} & \frac{\partial(-\gamma E+(\delta+\mu_I)I)}{dI} \end{bmatrix}$$

$$F = \begin{bmatrix} \theta & \beta S_0 \\ 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} \gamma + \tau + \mu_E & 0 \\ -\gamma & \delta + \mu_I \end{bmatrix}$$

Then look for the next generation matrix $\left(K = FV^{-1}\right)$, where V^{-1} is the inverse matrix of the V matrix.

$$V^{-1} = \begin{bmatrix} \frac{1}{\gamma+\tau+\mu_E} & 0 \\ \frac{\gamma}{(\gamma+\tau+\mu_E)(\delta+\mu_I)} & \frac{1}{\delta+\mu_I} \end{bmatrix}$$

The next generation matrix K is obtained as follows:

$$\begin{aligned} K &= FV^{-1} \\ &= \begin{bmatrix} \frac{\theta\mu_S(\delta+\mu_I)+\beta\Lambda\gamma}{\mu_S(\gamma+\tau+\mu_E)(\delta+\mu_I)} & \frac{\beta\Lambda}{\mu_S(\delta+\mu_I)} \\ 0 & 0 \end{bmatrix} \end{aligned} \tag{4.1}$$

The next generation K matrix that has been obtained is then searched for its eigenvalues such that it obtains the characteristic equation that is used to obtain the basic reproduction number value as follows:

$$\begin{aligned} \mathcal{R}_0 &= \frac{\theta\mu_S\left(\delta+\mu_I\right)+\beta\Lambda\gamma}{\mu_S\left(\gamma+\tau+\mu_E\right)\left(\delta+\mu_I\right)} \\ &= 9.79 \end{aligned} \tag{4.2}$$

4.2. Basic Reproduction Numbers with Controlled Treatment ($\mathcal{R}_t$)

The basic reproduction number in this condition can be obtained in the same way as before, except that the equations used are not equations (2.2) and (2.3), but using equations (2.3) and (2.6). The value of the basic reproduction number by giving Sinovac vaccine ($\mathcal{R}_t$) to the community, is obtained from the characteristic equation with the following form:

$$\begin{aligned} \mathcal{R}_t &= \frac{\theta\mu_S\left(\delta+\mu_I\right)+\beta\left(1-v_S\right)\Lambda\gamma}{\mu_S\left(\gamma+\tau+\mu_E\right)\left(\delta+\mu_I\right)} \\ &= 4.88 \end{aligned} \tag{4.3}$$

As for the value of the basic reproduction number by administering the AstraZeneca vaccine ($\mathcal{R}_t^*$) to the community, it is obtained from the characteristic equation with the following form:

$$\begin{aligned} \mathcal{R}_t^* &= \frac{\theta\mu_S\left(\delta+\mu_I\right)+\beta\left(1-v_A\right)\Lambda\gamma}{\mu_S\left(\gamma+\tau+\mu_E\right)\left(\delta+\mu_I\right)} \\ &= 3.71 \end{aligned} \tag{4.4}$$

5. Stability Analysis of Equilibrium Points

The purpose of doing a stability analysis on an epidemic model is to determine the rate of spread of a disease that is endemic in an area. One method that can be used to perform stability analysis is to use the Routh-Hurwitz criterion, this criterion uses a special table to obtain stable conditions and eigenvalues in fairly complex and long equations such as polynomials. Under this criterion, the model is said to be stable when all the first columns in the table are positive. The table used in the Routh-Hurwitz criteria is presented as follows [11]:

TABLE 3. Arrangement of polynomials in the Routh-Hurwitz table

λ^n	a_0	a_2	a_4	$\cdots$	a_{2n}
λ^{n-1}	a_1	a_3	a_5	$\cdots$	a_{2n+1}
λ^{n-2}	b_1	b_2	b_3	$\cdots$	b_n
λ^{n-3}	c_1	c_2	b_3	$\cdots$	c_n
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\ddots$	$\vdots$
λ^0	q	$\cdots$	$\cdots$	$\cdots$	q_n

From the table above, we will get b_1, b_2, c_1, c_2, and q in the following way:

$$b_1 = \frac{a_1a_2 - a_0a_3}{a_1}, b_2 = \frac{a_1a_4 - a_0a_5}{a_1}, \cdots, b_n = \frac{a_1a_{2n} - a_0a_{2n+1}}{a_1}$$

and

$$c_1 = \frac{b_1a_3 - a_1b_2}{b_1}, c_2 = \frac{b_1a_5 - a_1a_3}{b_1}, \cdots, c_n = \frac{b_1a_{2n+1} - a_1b_n}{b_1}$$

In this study, local stability analysis was carried out at the disease free equilibrium point (ξ_0), as well as at the endemic equilibrium point (ξ_1). Equations (2.1) to (2.4) are used to analyze by first linearizing the equation using the Jacobian matrix as follows:

$$J(\xi_t) = \begin{bmatrix} -(\beta I_t + \mu_S) & \tau & -\beta S_t & \alpha \\ \beta I_t & -(\gamma + \tau + \mu_E - \theta) & \beta S_t & 0 \\ 0 & \gamma & -(\delta + \mu_I) & 0 \\ 0 & 0 & \delta & -(\alpha + \mu_R) \end{bmatrix} \tag{5.1}$$

Matrix (5.1) will be used to perform a stability analysis around the disease free equilibrium point. By substituting the disease free equilibrium point $\xi_0 = (S_0, E_0, I_0, R_0)$ into the matrix (5.1), we get the Jacobian matrix for the disease free equilibrium point ($J(\xi_0)$) as follows:

$$J(\xi_0) = \begin{bmatrix} -\mu_S & \tau & -\frac{\beta\Lambda}{\mu_S} & \alpha \\ 0 & -(\gamma + \tau + \mu_E - \theta) & \frac{\beta\Lambda}{\mu_S} & 0 \\ 0 & \gamma & -(\delta + \mu_I) & 0 \\ 0 & 0 & \delta & -(\alpha + \mu_R) \end{bmatrix} \tag{5.2}$$

Based on the characteristic equation obtained from the Jacobian matrix in equation (5.2) in the form of a polynomial, the criteria table obtained from the results of the polynomial arrangement is as follows:

TABLE 4. Routh-Hurwitz table disease free equilibrium points

λ^4	1.0000	−4.5980	0.0000
λ^3	1.5111	−0.0534	0
λ^2	−4.5627	0.0000	0
λ^1	−0.0534	0	0
λ^0	0.0000	0	0

From the criteria in Table 4, there are four eigenvalues, each of which is $\lambda_1 = -0.00002$,

$\lambda_2 = -0.0115$, $\lambda_3 = -3.0252$, and $\lambda_4 = 1.5256$. The next step using the same method, to perform a stability analysis around the endemic equilibrium point, the endemic equilibrium point $\xi_1 = (S_1, E_1, I_1, R_1)$ is substituted. We get the Jacobian matrix for the disease free equilibrium point $(J(\xi_1))$ as follows:

$$J(\xi_1) = \begin{bmatrix} -(\beta I_1 + \mu_S) & \tau & -\beta S_1 & \alpha \\ \beta I_1 & -(\gamma + \tau + \mu_E - \theta) & \beta S_1 & 0 \\ 0 & \gamma & -(\delta + \mu_I) & 0 \\ 0 & 0 & \delta & -(\alpha + \mu_R) \end{bmatrix} \tag{5.3}$$

Based on the characteristic equation obtained from the jacobian matrix in equation (5.3) in polynomial form, the criteria table obtained from the results of the polynomial arrangement is as follows:

TABLE 5. Routh-Hurwitz table of endemic equilibrium points

λ_4	1.0000	1.0680	0.0000
λ_3	1.5121	0.0124	0
λ_2	1.0597	0.0000	0
λ_1	0.0124	0	0
λ_0	0.0000	0	0

Based on the criteria in Table 5, there are four eigenvalues, each of which is $\lambda_1 = -1.4999 + 0.0000i$, $\lambda_2 = -0.0026 + 0.0117i$, $\lambda_3 = -0.0026 - 0.0117i$, and $\lambda_4 = -0.0061 + 0.0000i$.

6. Numerical Simulation

To visualize the conditions in the mathematical model formed from the equations of the epidemic model used, one way that can be utilized is simulation with numerical methods [32]. The numerical method that is often used is 4th Order Runge-Kutta, to improve the simulation results so that the visualization is closer to actual conditions, 4th Order Runge-Kutta is developed to 5th order [19]. All parameter values listed in Table 1, along with the vaccine effectiveness values contained in Table 2, are substituted into all equations from (2.1) to (2.6) which will be processed and then simulated. As the basis of the 5th order Runge-Kutta method, there are at least seven basic processes that must be carried out from the general form, the general form of 5th order Runge-Kutta can be described as in equation (6.1) as follows [33]:

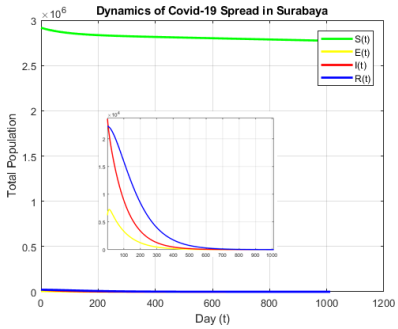
$$y_{i+1} = y_i + \frac{1}{90}(7k_1 + 32k_3 + 12k_4 + 32k_5 + 7k_6) \tag{6.1}$$

By following the rules of the steps as follows:

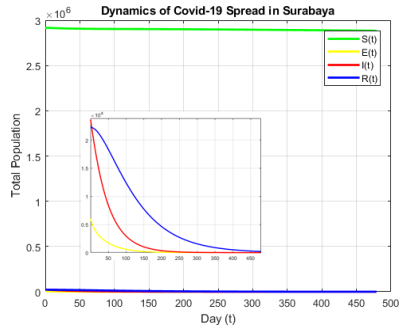
$$\begin{aligned} k_1 &= hf(t_i, y_i) \\ k_2 &= hf\left(t_i + \frac{h}{2}, y_i + \frac{k_1}{2}\right) \\ k_3 &= hf\left(t_i + \frac{h}{4}, y_i + \frac{3k_1 + k_2}{16}\right) \end{aligned} \tag{6.2}$$

$$k_4 = hf\left(t_i + \frac{h}{2}, y_i + \frac{k_3}{2}\right)$$
$$k_5 = hf\left(t_i + \frac{3h}{4}, y_i + \frac{-3k_2 + 6k_3 + 9k_4}{16}\right)$$
$$k_6 = hf\left(t_i + h, y_i + \frac{k_1 + 4k_2 + 6k_3 - 12k_4 + 8k_5}{7}\right)$$

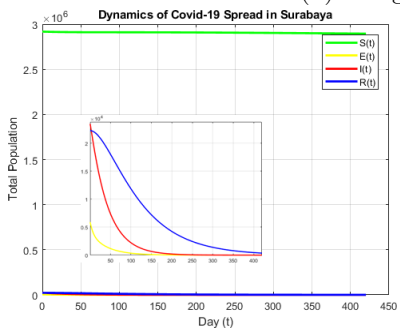
If equations (6.1) and (6.2) are used for simulations in equations (2.1) to (2.4), it will produce a visualization of the dynamic state of the spread of the second wave of COVID-19 infection in Surabaya without any mitigation measures to control the outbreak. Then equations (6.1) and (6.2) can also be used to visualize the dynamics of the spread of the second wave of COVID-19 infection in Surabaya with the existence of mitigation measures for epidemic control with vaccines, if used to simulate equations (2.6), (2.6), (2.3) , and (2.4). The simulation results are obtained as follows:



(A) Not using vaccine



(B) Using Sinovac vaccine



(C) Using AstraZeneca vaccine

FIGURE 3. Model numerical simulation results

Figures 3a, 3b, and 3c are comparisons obtained from the three conditions given to the model. In the first condition, the COVID-19 outbreak was not given any treatment in its handling, so the second wave of the COVID-19 outbreak will last for 1013 days, it is predicted that the outbreak will stop on February 20, 2024. This condition is compared to when all Surabaya people were given the Sinovac vaccine, the outbreak will lasts 480

days, and will be completed on September 5, 2022. The next condition is when compared to when all Surabaya people were given the AstraZeneca vaccine, the outbreak will last 421 days and will end on July 8, 2022.

7. Error Analysis

In this study, the accuracy of the model will be analyzed based on the magnitude of the error obtained from the simulation results, so it is hoped that the model used can be used to predict the rate of spread dynamics. The smaller the resulting error, the closer the simulation results to the actual, so that the model can be said to be more accurate and has good predictive results. To find the resulting error value, the Means Absolute Percentage Error (MAPE) method is used. MAPE reviews errors based on the difference from the average value of the data, the standard measurement accuracy of MAPE can be grouped into four categories. Each category can be presented in Table 6 as follows [34]:

Table 6. MAPE value interpretation

MAPE Value (%)	Interpretation
$0-10$	Very Accurate Prediction Results
$10-20$	Good Prediction Results
$20-50$	Prediction Results Quite Accurate / Decent
>50	Less Accurate Prediction Results

This method has a general mathematical form as follows:

$$MAPE = \left(\frac{1}{n}\sum_{1}^{n}\left|\frac{y_i - \hat{y}_i}{y_i}\right|\right) \times 100 \tag{7.1}$$

where:

n : Amount of data
y_i : Actual data at time to $i, i = 1, 2, 3, \ldots$
$\hat{y}_i$: Prediction data at time to $i, i = 1, 2, 3, \ldots$

If equations (6.2) are substituted by the actual data and the simulation results, the error for each variable presented in Table 6 will be as follows:

Table 7. Error values from simulation results of the model without vaccination compared with actual data

Value	S	E	I	R
$MAPE$	16.68%	23.20%	30.79%	16.11%

Judging from the error value in Table 7, it is known that the variables S and R have model simulations with good predictive results. The model simulation on variables E and I shows that the prediction results are quite accurate, in other words the overall model has quite accurate results, so the model can be used as one of the mitigation methods that can be done.

8. Discussion

Based on the local stability conditions analyzed around the two equilibrium points, it was found that the SEIR epidemic mathematical model used was unstable at the disease free equilibrium point. In contrast to the endemic equilibrium point from the SEIR epidemic mathematical model used, the mathematical model at the endemic equilibrium point can be said to be asymptotically stable. Stability conditions in this model are also experienced by research conducted by Arifin and Achamyelesh, where the model point is unstable at the disease free equilibrium point, but stable at the endemic equilibrium point [16], [20]. The next review after the stable condition of the model is known, namely reviewing the analysis of the basic reproduction number, it is obtained the value of the basic reproduction number of each which indicates the condition of one individual's ability to infect other individuals.

When people don't get the vaccine, every individual infected with COVID-19 can infect 9-10 people. Meanwhile, when the public is given the Sinovac vaccine, the ability of one individual infected with COVID-19 to be able to infect other individuals will decrease to 4-5 people. When the public is given the AstraZeneca vaccine, the ability of one individual infected with COVID-19 to be able to infect other individuals will decrease to 3-4 people. Simply put, $\mathcal{R}_0 > \mathcal{R}_t > \mathcal{R}_t^* > 1$, which indicates that COVID-19 will still exist in Surabaya with or without giving vaccines to the public. Although COVID-19 will still exist, but the outbreak can be controlled more so that the spread of transmission does not occur, so that there is no situation that is very dangerous to the community, the government's decision is right by giving vaccines to the community as a form of mitigation, even though it is not optimal.

The situation is very dangerous with this kind of transmission capability in the capital city of a province with a population of close to three million, as well as a city with the second largest industrial and corporate center in Indonesia. As a form of mitigation to control the outbreak, giving vaccines to the community has proven to be quite effective, where the $\mathcal{R}_0$ value has been reduced to three to five. The use of vaccines with the parameters used is still not said to be optimal, because $\mathcal{R}_0 \geq 1$ which indicates there is still transmission that causes the spread of infection, so it is necessary to use more optimal parameters so that the spread of COVID-19 transmission can be overcome. As a suggestion for future research, optimal vaccine parameters can be searched using the Phontryargin Minimum Principle (PMP) or Linear Quadratic Regulator (LQR).

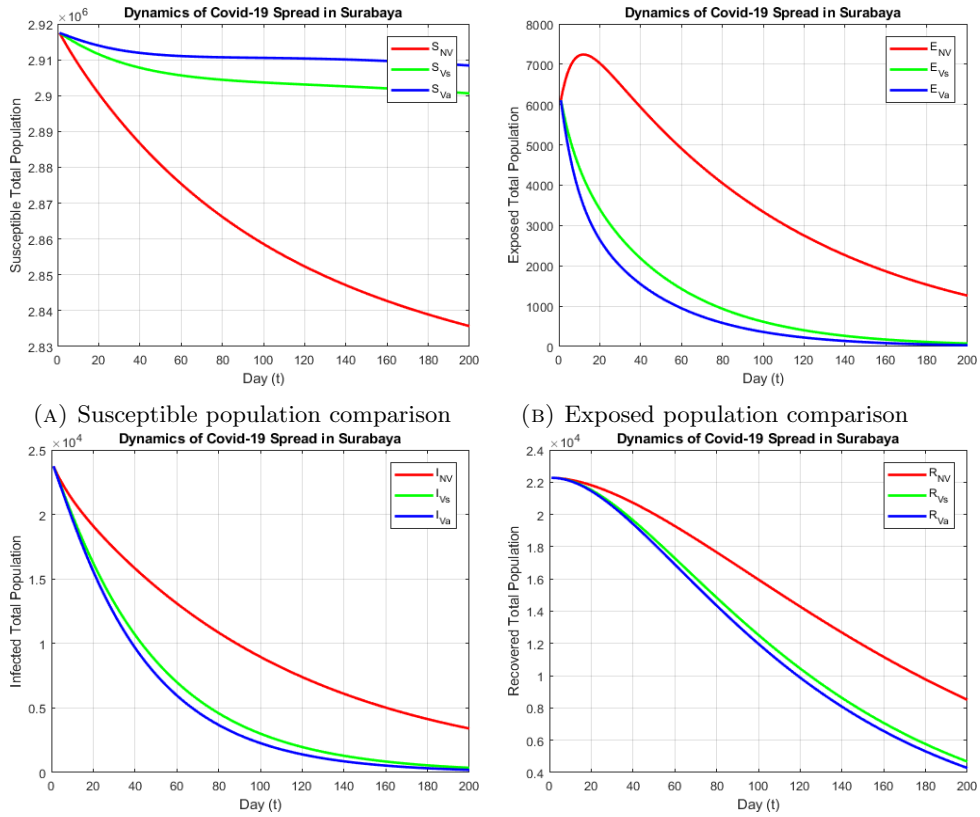
For comparison, the total population of each variable is presented in Table 8 as follows:

Table 8. Total population of each variable comparison

Variables	Day(t)	Condition of the Vaccine Given		
		No vaccine	Sinovac	AstraZeneca
S	50	2880752	2906552	2911377
	100	2858613	2903658	2910528
	150	2844818	2902302	2909887
	200	2835688	2900620	2908386
E	50	5401	1766	1209
	100	3340	614	361
	150	2055	213	108
	200	1261	74	32

I	50	14399	8648	7603
	100	8963	3012	2276
	150	5540	1048	681
	200	3409	365	204
R	50	20034	18493	18183
	100	15965	12533	11981
	150	11905	7815	7290
	200	8508	4677	4280

If the total population is represented in a graph, it will look as follows:



(A) Susceptible population comparison (B) Exposed population comparison

(C) Infected population comparison (D) Recovery population comparison

FIGURE 4. Each variable population comparison

Based on the simulations obtained in Figures 4a to 4d, it appears that giving vaccines to the community has a significant enough effect in reducing the rate of increase in the infected population. The outbreak would be that if all residents were given the Sinovac vaccine, the outbreak would be over 533 days faster than if all the people of Surabaya were not vaccinated at all. The COVID-19 outbreak will also be finished 592 days faster if all residents are given the AstraZeneca vaccine, compared to if the entire Surabaya

community is not given the vaccine at all. These results indicate that the vaccine is proven to help reduce the spread of the COVID-19 disease outbreak circulating in the community, this is in accordance with research conducted by Shadabfar et al [35].

After the simulation results are obtained, there are errors that occur as a result of the use of numerical methods that use the actual approach. When viewed from Table 7 which refers to Table 6, the error obtained is still below the tolerance standard, in such a way that the error obtained from the simulation results of the SEIR epidemic mathematical model can be categorized as quite accurate. The error obtained from the model is still large enough to be used as a prediction, one way to minimize the error is to estimate parameters on S, E, I, and R. There are many gaps that make the SEIR epidemic model used can still be improved and refined In other words, the government can still add treatments to control the outbreak, such as adding quarantine (Q), administering anti-virus drugs (M), or reducing the number of transmigrations. Other methods that can be used are optimization to minimize errors using Multiple Object Particle Swarm Optimization (MOPSO), Multiple Object Firefly Optimization (MOFO), and Red Fox Optimization [36]-[38].

9. Conclusion

Based on the results of the research discussed previously, by utilizing the SEIR epidemic model that has been developed with a conditional approach, with a spread rate of one person can infect 9-10 other people, the second wave of COVID-19 outbreak in Surabaya will last for 1013 days and will stop spreading. on February 20, 2024. The use of vaccines as an effort to repeat the rate of spread of COVID-19 infection has proven to be quite effective by decreasing the level of a person's ability to transmit, from initially one person can infect 10 people to 3-5 people, this can also seen from the simulation results which show that the outbreak stopped 533-592 days earlier, which is estimated to fall on September 5 or July 8, 2022. Based on the results of the simulation model, it can be said that the outbreak has been handled quite well, the government's action by giving Vaccines as mitigation are appropriate, although not optimal for stop the entire spread of infection.

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