# Stability analysis and numerical simulation of SEIR model for pandemic COVID-19 spread in Indonesia

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## ARTICLE INFO

## ABSTRACT

The Aim of this research is construct the SEIR model for COVID-19, Stability Analysis and numerical simulation of the SEIR model on the spread of COVID-19. The method used to construct the model is the SEIR model by considering vaccination and isolation factors as model parameters, the analysis of the model uses the generation matrix method to obtain the basic reproduction numbers and the global stability of the COVID-19 distribution model. Numerical simulation models use secondary data on the number of COVID-19 cases in Indonesia. The results obtained are the SEIR model for COVID-19; model analysis yields global stability from the spread of COVID-19; The results of the analysis also provide information if no vaccine, Indonesia is endemic COVID-19. Then the simulation results provide a prediction picture of the number of COVID-19 in Indonesia in the following days, the simulation results also show that the vaccine can accelerate COVID-19 healing and maximum isolation can slow the spread of COVID-19. The results obtained can be used as a reference for early prevention of the spread of COVID-19 in Indonesia

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## 1. Introduction

According to the World Health Organization (WHO), COVID-19 is transmitted through people who have been infected with the corona virus. The virus can easily spread through small droplets from the nose or mouth compilation of someone infected with this virus to sneeze or cough. The drops then land on objects or surfaces which are touched and the healthy person adjusts their eyes, nose or mouth. How to spread the corona virus compilation of small droplets inhaled by someone compiling switch with the one supported by corona [1]. It's important to spend 1 m more distance than people who are sick. Until now there has been no research that states the COVID-19 corona virus can be transmitted through the air, "explained WHO as quoted from its website on March 23, 2020 [2].

The number of cases of corona virus infection that causes Covid-19 continues to increase in various parts of the world. The rate of increase, both for the number of cases of infection, death and cure, varies in each region. Each country also has its own policy to curb the spread of viruses that occur in its territory. According to data collected by John Hopkins University, as of March 23, 2020, the total number of Covid-19 cases worldwide had reached 331,273 cases, with 14,450 deaths, and 97,847 patients declared cured. The highest number of cases is still recorded in China, namely 81,397 cases, followed by Italy with 59,138 cases, and the United States as many as 33,073 cases. In terms of mortality, the largest number is in Italy, with 5476 cases. The number exceeds the death rate that occurred in China, which is 3265. Meanwhile, in terms of recovery, the largest number is in China, which is 72,362 patients. Both the progress of the number of infections, deaths, patients recovered until certain policies continue to be reported in various countries [2].

The number of COVID-19 cases in Indonesia continues to increase, until March 22, 2020 the number of positive cases of COVID-19 numbered 514 people with 29 people (5.64%) recovered and the number of deaths 48 people (9.34%) or the largest in Southeast Asia. The disease that has become a pandemic and causes a fairly high death in this world has not been found the cure [3]. Trend of the number of cases and spread map of COVID-19 in Indonesia is presented in Figs. 1 and 2.

Mathematical modeling of SIR, SIRS, SEIR and SEIRS on transmission of diseases such as dengue fever, tuberculosis, diabetes, HIV-AIDS has been done by [4–19], then mathematical modeling on the spread of COVID-19 has been carried out by [20] namely SEIRV mathematical modeling in the Wuhan, China taking into account environmental factors, while the analysis and simulation of the model used data of the number of COVID-19 cases in Wuhan.

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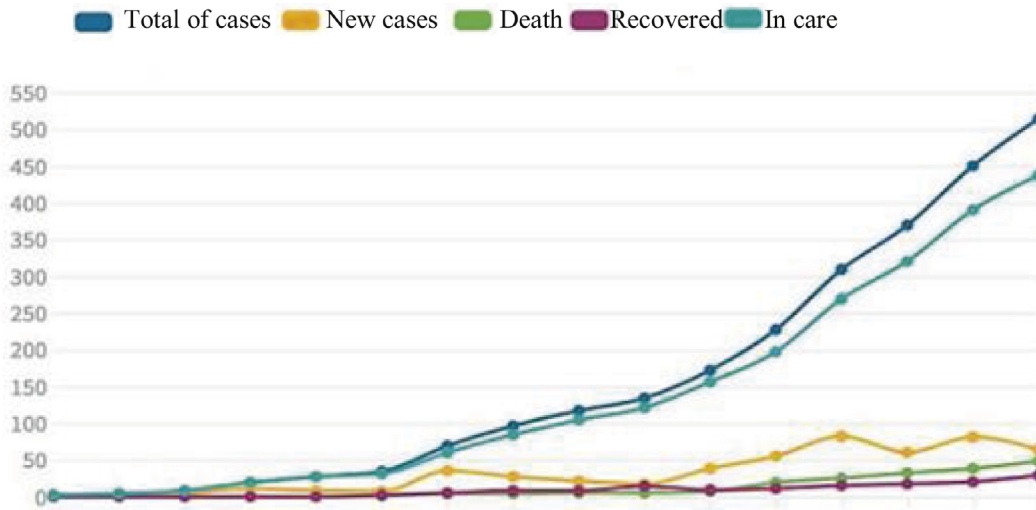
**Fig. 1.** Trend of the number of positive cases for COVID-19 in Indonesia on March 2020
Negative Positive.
*Source:* [2]



**Fig. 2.** Spread map of COVID-19 in Indonesia on March 2020
*Source:* [2].

This SEIRV model does not consider vaccination and isolation factors as parameters in the model. Therefore, this research build, analyze using generation matrices method and simulate the SEIR model through isolation and vaccination on the spread of COVID-19 in Indonesia using Matlab software.

## 2. Method

The SEIR mathematical modeling on the spread of COVID-19 is a theoretical study. The method used to construct the model is the SEIR model [12] by considering vaccination and isolation factors as model parameters, the model analysis uses the generation matrix method [9] to obtain the basic reproduction number and the global stability for COVID-19 spreading. Numerical simulation of model use secondary data on the number of COVID-19 cases in Indonesia [21] by using Matlab software to predict the number of COVID-19 cases in Indonesia as a measure to prevent the number of COVID-19 cases in Indonesia.

## 3. Results and discussion

### 3.1. SEIR model formulation for COVID-19

The SEIR model on the spread of COVID-19 is divided into four compartments namely Suspected (S), Exposed (E), Infected (I), and
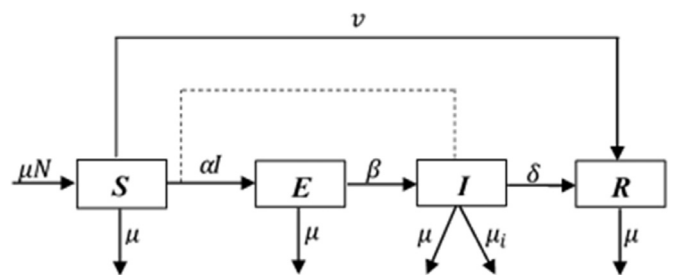


**Fig. 3.** Scheme of the Model SEIR transmission for COVID-19.

Recovered (R). Individuals in an infected class can cause other individuals to become infected. The changes that occur in each human population in Covid-19 transmission for the SEIR model can be interpreted by Fig. 3

Definition of variables and parameters of model SEIR for COVID-19 presented in Table 1.

Based on the population scheme in Fig. 3, the rate of change in the number of people Suspected, Exposed, Infected and Recovered over time in the SEIR mathematical model of the spread of Covid-19 can be interpreted as follows:

$$\frac{dS}{dt} = \mu N - (\alpha I + \mu + v)S \tag{1}$$

**Table 1**
Defintion of variable/parameter.

| Variable/Parameter | Definition |
|---|---|
| $N$ | Number of human population |
| $S$ | Number of Suspected population |
| $E$ | Number of Exposed population |
| $I$ | Number of Infected Population |
| $R$ | Number of Recovered Population |
| $\mu$ | The rate of birth/death population |
| $\alpha$ | Probably of changing from $S$ to $E$ |
| $\beta$ | Probably of changing from $E$ to $I$ |
| $\mu_i$ | The rate of death population by COVID-19 |
| $\delta$ | Probably of changing from $I$ to $R$ |
| $v$ | Vaccine of Suspected Population |

$$\frac{dE}{dt} = \alpha IS - (\beta + \mu)E \tag{2}$$

$$\frac{dI}{dt} = \beta E - (\mu_i + \delta + \mu)I \tag{3}$$

$$\frac{dR}{dt} = \delta I + vS - \mu R \tag{4}$$

Let $S = \frac{S}{N}$; $E = \frac{E}{N}$; $I = \frac{I}{N}$; and $R = \frac{R}{N}$, simplified model becomes:

$$\frac{dS}{dt} = \mu - (\alpha I + \mu + v)S \tag{5}$$

$$\frac{dE}{dt} = \alpha IS - (\beta + \mu)E \tag{6}$$

$$\frac{dI}{dt} = \beta E - (\mu_i + \delta + \mu)I \tag{7}$$

$$\frac{dR}{dt} = \delta I + vS - \mu R \tag{8}$$

### 3.2. Analysis of SEIR model for COVID-19

#### 3.2.1. Equilbrium analysis

Based on Eqs. (5)–(8), stability analysis is carried out to determine the disease free equilibrium point and endemic equilibrium point. To determine the two equilibrium points, each equation in Eqs. (5)–(8), must be equal to zero, or $\frac{dS}{dt} = 0$, $\frac{dE}{dt} = 0$, $\frac{dI}{dt} = 0$, and $\frac{dR}{dt} = 0$, thus obtained:

$$\mu - (\alpha I + \mu + v)S = 0 \tag{9}$$

$$\alpha IS - (\beta + \mu)E = 0 \tag{10}$$

$$\beta E - (\mu_i + \delta + \mu)I = 0 \tag{11}$$

$$\delta I + vS - \mu R = 0 \tag{12}$$

Then, we found the equilibrium point of $S$, $E$, $I$, and $R$.

#### 3.2.2. Free-disease equilibrium for COVID-19

Equilibrium points for disease-free are conditions where there is no spread of COVID-19 then, $E = I = 0$
From Eq. (9):
$\mu - (\alpha I + \mu + v)S = 0$ thus obtained

$$S = \frac{\mu}{(\mu + v)}$$

From Eq. (12):

$\delta I + vS - \mu R = 0$ thus obtained:

$$R = \frac{v}{(\mu + v)}$$

Then, the Equilibrium points of disease-free for COVID-19 are:

$$K_0 = (S, E, I, R) = \left( \frac{\mu}{(\mu + v)}, 0, 0, \frac{v}{(\mu + v)} \right) \tag{13}$$

#### 3.2.3. Endemic equilibrium for COVID-19

Endemic equilibrium points are used to indicate the possibility of disease spread. Because in endemic conditions and disease spread, the population $S \neq 0, E \neq 0, I \neq 0$, and $R \neq 0$. From Eqs. (9)–(12) obtained endemic equilibrium points from COVID-19 are:

$$S = \frac{(\mu_i + \delta + \mu)(\beta + \mu)}{\alpha \beta}$$

$$E = \frac{\alpha \beta \mu - (\mu_i + \delta + \mu)(\mu + v)}{\alpha \beta}$$

$$I = \frac{\alpha \beta \mu - (\mu_i + \delta + \mu)(\mu + v)(\beta + \mu)}{\alpha(\mu_i + \delta + \mu)(\beta + \mu)}$$

$$R = \frac{\delta \alpha \beta^2 \mu - \beta(\mu_i + \delta + \mu)(\mu + v)(\beta + \mu) - v((\mu_i + \delta + \mu)(\beta + \mu))^2}{\beta \alpha^2 (\mu_i + \delta + \mu)(\beta + \mu)}$$

Then, the Equilibrium points of endemic for COVID-19 are:

$$K_e = (S, E, I, R) = \begin{pmatrix} \frac{(\mu_i + \delta + \mu)(\beta + \mu)}{\alpha \beta}, \frac{\alpha \beta \mu - (\mu_i + \delta + \mu)(\mu + v)}{\alpha \beta}, \\ \frac{\alpha \beta \mu - (\mu_i + \delta + \mu)(\mu + v)(\beta + \mu)}{\alpha(\mu_i + \delta + \mu)(\beta + \mu)}, \\ \frac{\delta \alpha \beta^2 \mu - \beta(\mu_i + \delta + \mu)(\mu + v)(\beta + \mu) - v((\mu_i + \delta + \mu)(\beta + \mu))^2}{\beta \alpha^2 (\mu_i + \delta + \mu)(\beta + \mu)} \end{pmatrix} \tag{14}$$

Base on the Eqs. (5)–(8), found the Jacobian matrices

$$J = \begin{matrix} -(\alpha I + \mu + v) & 0 & \alpha S & 0 \\ \alpha I & -(\mu + \beta) & \alpha S & 0 \\ 0 & \beta & -(\mu_i + \delta + \mu) & 0 \\ v & 0 & \delta & -\mu \end{matrix} \tag{15}$$

Then find the eigenvalue of the Jacobian matrix in Eq. (15)

$$\det(\lambda I - J) = \begin{matrix} \lambda + (\alpha I + \mu + v) & 0 & -\alpha S & 0 \\ -\alpha I & \lambda + (\mu + \beta) & -\alpha S & 0 \\ 0 & -\beta & \lambda + (\mu_i + \delta + \mu) & 0 \\ -v & 0 & -\delta & \lambda + \mu \end{matrix} = 0$$

Subtitution the value $S = \frac{\mu}{(\mu + v)}$ and $I = 0$, obtained:

$$\begin{matrix} \lambda + (\mu + v) & 0 & -\alpha \mu(\mu + v)^{-1} & 0 \\ 0 & \lambda + (\mu + \beta) & -\alpha \mu(\mu + v)^{-1} & 0 \\ 0 & -\beta & \lambda + (\mu_i + \delta + \mu) & 0 \\ -v & 0 & -\delta & \lambda + \mu \end{matrix} = 0$$

$$(\lambda + \mu)(\lambda + (\mu + v)) \left( (\lambda + (\mu + \beta))(\lambda + (\mu_i + \delta + \mu)) - \frac{\alpha \beta \mu}{(\mu + v)} \right) = 0$$

$$(\lambda + A)(\lambda + B)((\lambda + C)(\lambda + D) - E) = 0 \tag{16}$$

with

$A = \mu$; $B = (\mu + v)$; $C = (\mu + \beta)$; $D = (\mu_i + \delta + \mu)$ and $E = \frac{\alpha \beta \mu}{(\mu + v)}$

If Eq. (16) is resolved, then:

$$\lambda^4 + (A + B + C + D)\lambda^3 + (AB + (A + B)(C + D) + CD - E)\lambda^2 + ((A + B)(CD - E) + AB(C + D))\lambda + ABCD - ABE = 0 \tag{17}$$

Based on Descartes' rule [14] the number of negative roots of the characteristic Eq. (17) is equal to the number of variations in

the change in the coefficient sign, so Eq. (17) has four negative values if it is in the form of:

$$K = L_1 \lambda^4 - L_2 \lambda^3 + L_3 \lambda^2 - L_4 \lambda + L_5$$

with

$$L_1 = 1$$

$$L_2 = A + B + C + D$$

$$L_3 = AB + (A + B)(C + D) + CD - E$$

$$L_4 = (A + B)(CD - E) + AB(C + D)$$

$$L_5 = ABCD - ABE$$

With condition $L_1, L_2, L_3, L_4, L_5 > 0$

This concludes that if $CD > E$ and $L_1, L_2, L_3, L_4, L_5 > 0$, then:

$$\lambda_1, \lambda_2, \lambda_3, \lambda_4 < 0$$

Because the characteristic values of the equation system in the COVID-19 model are negative, the equilibrium point is stable global asymptotic.

### 3.2.4. The basic reproduction number ($R_0$) of SEIR model for COVID-19

The basic reproduction number ($R_0$) is determined using the matrices generation method, Based on Eqs. (5)–(8), to determine ($R_0$).

$$Let \; F = \begin{pmatrix} 0 & \alpha S \\ \beta & 0 \end{pmatrix} and \; V = \begin{pmatrix} (\beta + \mu) & 0 \\ 0 & \mu_i + \delta + \mu \end{pmatrix}$$

Then, we found:

$$V^{-1} = \frac{1}{(\beta + \mu)(\mu_i + \delta + \mu)} \begin{pmatrix} \mu_i + \delta + \mu & 0 \\ 0 & (\beta + \mu) \end{pmatrix}$$

$$V^{-1} = \begin{pmatrix} \frac{1}{(\beta + \mu)} & 0 \\ 0 & \frac{1}{\mu_i + \delta + \mu} \end{pmatrix}$$

and then,

$$P = FV^{-1} = \begin{pmatrix} 0 & \alpha S \\ \beta & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{(\beta + \mu)} & 0 \\ 0 & \frac{1}{\mu_i + \delta + \mu} \end{pmatrix}$$

$$P = \begin{pmatrix} 0 & \frac{\alpha S}{(\mu_i + \delta + \mu)} \\ \frac{\beta}{(\beta + \mu)} & 0 \end{pmatrix}$$

Then, by the matrices generation method [9], we found:

$$R_0 = \frac{\alpha \beta \mu}{(\mu + \beta)(\mu + \nu)(\mu_i + \delta + \mu)} \tag{18}$$

### 3.2.5. Stability analysis of SEIR model for COVID-19

Theorem 1

1 If $R_0 \leq 1$ then system in Eqs. (5)–(8) of the model is global asymptotic stable.
2 If $R_0 > 1$, then system in Eqs. (5)–(8) is unstable in $D = \{(S, E, I, R) \in R_+^4, \; S + E + I + R \leq S_0\}$.

Proof

Let $X = (E, I)^T$, it can be stated that $\frac{dX}{dt} \leq (F - V)X$, with F and V are matrices on search $R_0$. then, let **u** is a eigen vector of F.

Let that:

$$R_0 = \rho(FV^{-1}) = \rho(V^{-1}F)$$

If $V^{-1}F = R_0$, then $uV^{-1}F = R_0u$

Let Lyapunov function:

$$\mathcal{L}_0 = uV^{-1}X$$

$$\frac{d\mathcal{L}_0}{dt} = uV^{-1}\frac{dX}{dt}$$

$$\frac{d\mathcal{L}_0}{dt} = uV^{-1}(F - V)X$$

$$\frac{d\mathcal{L}_0}{dt} = (uV^{-1}F - u)X$$

$$\frac{d\mathcal{L}_0}{dt} = u(R_0 - 1)X$$

If $R_0 \leq 1$, then $\frac{d\mathcal{L}_0}{dt} = 0$, so that $uX = 0$, as a result $E = I = 0$ with $u > 0$

If $R_0 < 1$ then the Equation $\frac{dE}{dt} + \frac{dI}{dt} = 0$ and we found:

$$\alpha IS - (\beta + \mu)E + \beta E - (\mu_i + \delta + \mu)I = 0$$

$$\alpha IS - (\mu_i + \delta + \mu)I = 0 \; with \; E = 0$$

$$R_0 \left[ \frac{(\mu + \beta)(\mu + \nu)(\mu_i + \delta + \mu)}{\beta \mu} \right] IS - (\mu_i + \delta + \mu)I = 0$$

$$(\mu_i + \delta + \mu) \left[ R_0 \frac{(\mu + \beta)(\mu + \nu)}{\beta \mu} S - 1 \right] = 0$$

$$(\mu_i + \delta + \mu) \left[ R_0 \frac{(\mu + \beta)}{\beta} - 1 \right] = 0$$

It means, $(\mu_i + \delta + \mu)[R_0 - 1] \approx 0$

Then it can be seen that, if $R_0 < 1$, then $\frac{d\mathcal{L}_0}{dt} < 0$

This proves that the system is global asymptotic stable.

In contrast, if $R_0 < 1$, then it follows from the continuity of the vector fields that $\frac{d\mathcal{L}_0}{dt} > 0$ in a neighborhood of the system in D. Thus the system in Eqs. (5)–(8) is unstable by the Lyapunov stability theory. The last part of the theorem can be proved by the persistent theory [22] which is similar to the proof of Theorem 2.5 in [23].

### 3.3. Numerical simulation of the SEIR model of COVID-19 in Indonesia

Model simulations are performed using Mathematica software. The initial values $S(0)$, $E(0)$, $I(0)$, $R(0)$ and parameter values of the models used in this simulation are presented in Tables 2 –4, with the basic reproduction number values $R_0$ obtained based on Eq. (18), is $R_0 = \frac{\alpha \beta \mu}{(\mu + \beta)(\mu + \nu)(\mu_i + \delta + \mu)}$

**Table 2**
Initial Value of SEIR Model for COVID-19 in Indonesia.

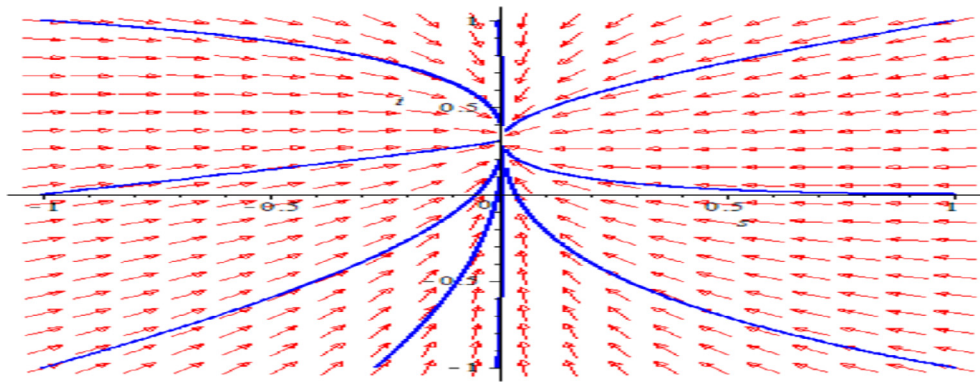| Variable | Estimated value | Source |
|---|---|---|
| $N(0)$ | 269.6 juta | [24] |
| $S(0)$ | 37,538 | [21] |
| $E$ | 13,923 | [21] |
| $I$ | 23,191 | [21] |
| $R$ | 13,213 | [21] |

**Fig. 4.** Stability phase portrait of the SEIR Model for COVID-19 in Indonesia .

**Table 3**
Parameter value of SEIR Model for COVID-19 in Indonesia.

| Parameter | Estimated value | Source |
|-----------|-----------------|--------|
| $\mu$ | $6.25\times10^{-3}$ | [25] |
| $\alpha$ | $0.62\times10^{-8}$ /person/day | [11] |
| $\delta$ | 0.0006667 per day | [11] |
| $\mu_i$ | $7.344\times10^{-7}$ | [21] |

**Table 4**
Assumption parameter values    of the SEIR Model for COVID-19 in Indonesia.

| Parameter | Simulation 1 | Simulation 2 | Simulation 3 |
|-----------|--------------|--------------|--------------|
| $\nu$ | 1% | 50% | 100% |
| $\beta$ | 3 days | 7 days | 14 days |

*3.3.1. Numerical simulation results of the SEIR model of COVID-19 in Indonesia*

The value of the equilibrium points of the SEIR model is determined by substituting the parameter values    (simulation 1) in Tables 3 and 4 in Eqs. (5)–(8) which are equated with zero, then the following Eqs. (5)–(8) system is obtained:

$$\begin{cases} 548.60625 - \left(7.0634x10^{-4}I(t) + 0.5063\right)S = 0 \\ \left(7.0634x10^{-4}I(t) + 0.5063\right)S - 0.07777E = 0 \\ 0.0714\,E - 0.00692I = 0 \\ 0.00692I + 0.5S - 0.00625R = 0 \end{cases} \quad (19)$$

The equation system (19) provides the equilibrium points of the endemic SEIR model of the spread of COVID-19, namely:

$$(S^*,\ E^*,\ I^*, R^*) = (0.00982, 0.01793,\ 0, 01, 811, 0.89008)$$

These equilibrium points explain that the number of COVID-19 suspected populations was 982 people, exposed to 1793 people, infected 1811 people and those recovered were 89,008 people from the total 100,000 human population.

The eigenvalues based on Eq. (17) with the parameter values in Tables 2 and 3 for the Covid-19 transmission SEIR model are:

$$\lambda_1 = -0.13875,\ \lambda_2 = -0.00625,\ \lambda_3 = -0.07292,\ \lambda_4 = -0.33625$$

In the same way, the equilibrium values    and eigenvalue for simulation 2 and simulation 3 are written in Table 5. The eigenvalues obtained are real and negative, based on [17], the type of stability at this equilibrium point is asymptotic stable . The stability phase of the system can be illustrated in Fig. 4 and the fitting data of the SEIR model using Runge Kutta method versus the real data for covid 19 in Indonesia can be illustrated in Fig. 5.
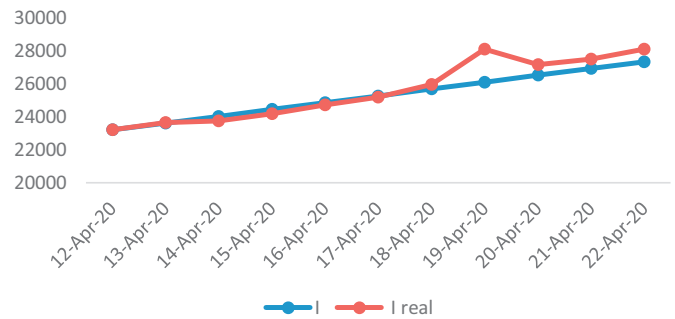


**Fig. 5.** Fitting infected data of SEIR model for covid19 versus real data in Indonesia.

According to Fig. 5, The fitting data of SEIR Model and the real data of covid 19 in Indonesia is a similar, this shown that the SEIR model on the spread of covid 19 can be used to predict the number cases of covid 19 in Indonesia, so that the government can take strategic steps to prevent this pandemic.

The basic reproduction number $R_0$ for the endemic case of Covid-19 from Eq. (18) with only 1% vaccination is $R_0$= 3.2094. This means that, if a person is infected with Covid-19 it will infect 3 other people. Whereas the $R_0$ value for simulation 2 and simulation 3 presented in Table 5 explains that 50% vaccine will reduce transmission of COVID-19 and 100% does not couse spreading of Covid-19 in Indonesia.

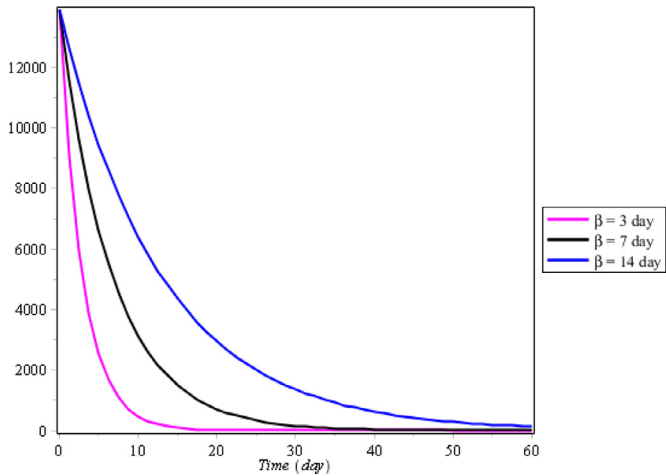*3.3.1.1. Simulation 1 of the SEIR model for COVID-19 in Indonesia.*
Numerical simulation to determine the effect of variations in population isolation time on the dynamics of the number of Exposed and Infected Covid-19. The simulation uses the initial values    in Table 2 and the parameters in Table 3 with vaccination $\nu = 50\%$. The numerical simulation results of the Covid-19 spreading model are presented in Figs. 6 and 7

Based on Fig. 6, the number of Exposed populations immediately decreases if they are isolated for 3 days, but the number of COVID-19 infected populations in Indonesia has increased dramatically and only takes three days to reach a peak of 34,000 people. Then, if isolation of Suspected COVID-19 is carried out for 7 days, the number of Exposed populations decreases after the fourth day with the population infected with COVID-19 in Indonesia experiencing a not very high increase and reaching a peak on the sixth day with the number sufferers of COVID-19 around 32,000 people. Furthermore, if isolation of Suspected COVID-19 is carried out for 14 days, the number of Exposed populations decreases after the seventh day with the population infected with COVID-19 in Indonesia experiencing a smaller increase and reaching a peak on the
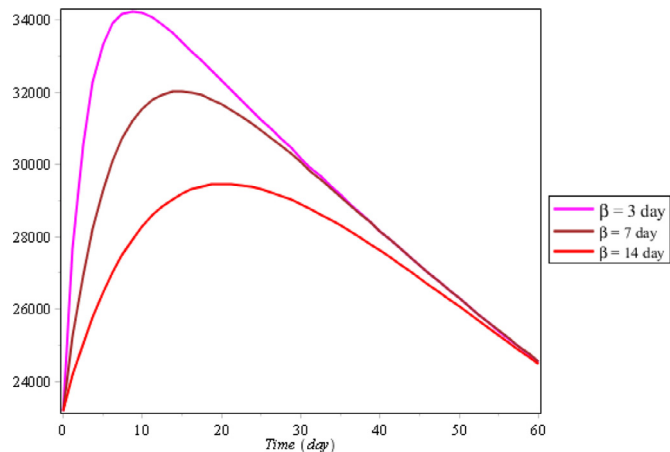
**Table 5**
The Values of equilibrium point, eigen value and $R_0$.

| Simulation | $\lambda_1$ | $\lambda_2$ | $\lambda_3$ | $\lambda_4$ | $S^*$ | $E^*$ | $I^*$ | $R^*$ | $R_0$ |
|---|---|---|---|---|---|---|---|---|---|
| 1 | −0.13875 | −0.00625 | −0.07292 | −0.33625 | 0.00982 | 0.01793 | 0,01,811 | 0.89008 | 3.20949 |
| 2 | −0.07292 | −0.00625 | −0.14911 | −0.50387 | 0.00555 | 0.02307 | 0.04521 | 0.92616 | 0.10057 |
| 3 | −0.07292 | −0.00625 | −0.07768 | −0.98387 | 0.00389 | 0.03106 | 0.03042 | 0.93463 | 0.04955 |



**Fig. 6.** Variation in the number of population Exposed (E) for different values of $\beta$.



**Fig. 7.** Variation in the number of population Infected (I) for different values of $\beta$.



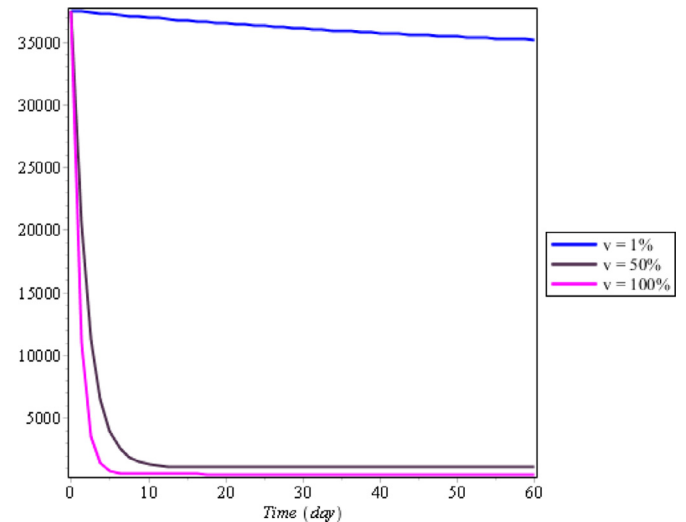**Fig. 8.** Variation in the number of population Suspected (S) for different values of $v$.



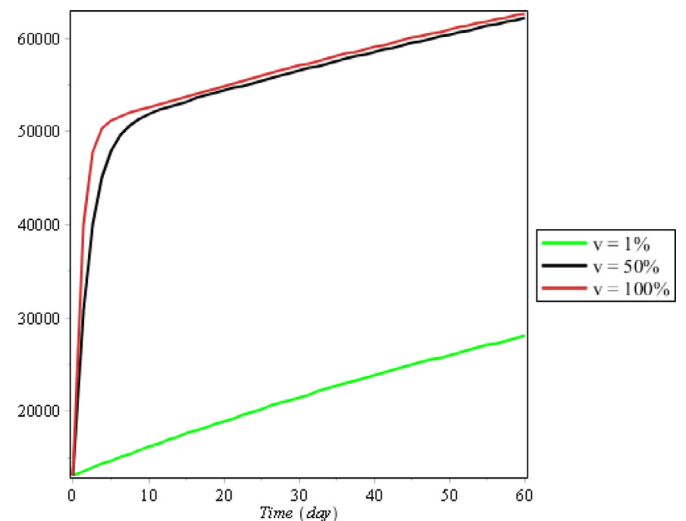**Fig. 9.** Variation in the number of population Recovered (R) for different values of $v$.

eighth day with the number of patients COVID-19 around 29,000 people. This shows that isolation is very influential in increasing the number of population infected with COVID-19, so isolation is very necessary to do with Suspected COVID-19 population in Indonesia.

*3.3.1.2. Simulation 2 of the SEIR model for COVID-19 in Indonesia.* Numerical simulation to determine the effect of variations in population isolation time on the dynamics of the number of Suspected and Recovered Covid-19 in Indonesia. The simulation uses the initial values in Table 2 and the parameters in Table 3 with the value $\beta = 14$ days. The numerical simulation results of the Covid-19 spreading model are presented in Figs. 8 and 9.

Based on Fig. 8, by giving 3% vaccine, the number of Suspected populations requires a long time to decrease, as well as the number of populations recovered from COVID-19 in Indonesia, the number is very small and the duration is quite long as shown in Fig. 9. Then, if the vaccine is 50%, then the number of Suspected populations requires a short amount of time to decrease, with the

number of people recovered of COVID-19 in Indonesia being large, around 60,000 people with a short duration of time as shown in Fig. 8. Furthermore, if by giving a vaccine of 100%, then the number of Suspected populations decreases in a very short time and the number of people recovering of COVID-19 in Indonesia is becoming more that around 6200 people with a very short duration of time as in Fig. 8. This shows that the giving of vaccines in the Suspected group is very influential in increasing the total population of Recovered COVID-19 is so necessary to provide vaccines conducted on Suspended COVID-19 populations in Indonesia.

### 3.4. Discussion

The SIR and SEIR models [8,10,17] developed a tuberculosis (TB) transmission model, conducted analyzes and predicted the number of TB cases in South Sulawesi. Then [18,19] built a Dengue Fever (DHF) transmission model, conducted an analysis and predicted the number of Dengue Fever cases in South Sulawesi. The COVID-19 spreading model conducted by [20] is a SEIRV model in the Wuhan, China by considering environmental factors, analysis and simulation models using data on the number of COVID-19 cases in Wuhan. This SEIRV model does not consider vaccination and isolation factors as parameters in the model, while the results of this study build the COVID-19 spreading model by considering vaccination and isolation periods in the COVID-19 population in Indonesia. Analysis of the model also uses the method [9] to obtain the basic reproduction numbers. In contrast to [17,18,19] who used Maple to predict the number of TB and DHF cases, the results of this study use Mathematica to predict the number of patients with COVID-19 in Indonesia in the form of numerical simulation. Results of the simulation of the SEIR model for COVID-19 spreading provided information and predictions on the number of COVID-19 cases in Indonesia. The results of this simulation is very helpful in improving the ability of the strategy in guarding the number of COVID-19 cases in Indonesia.

## 4. Conclusion

Based on the results of the study, it was concluded that the SEIR model could be a reference model for the spread of COVID-19 in Indonesia. Analysis of the model provides an overview of global stability in the spread of COVID-19 and also provides information if Indonesia is in COVID-19 endemic status. Then the simulation results provide a predictive picture of the number of COVID-19 cases in Indonesia and also show that vaccines can accelerate COVID-19 healing and the isolation period can slow the spread of COVID-19 in Indonesia. The results obtained can be used as a reference for early prevention of the spread of COVID-19 in Indonesia.

### Declaration of Competing Interest

All authors declare no conflicts of interest in this paper.

### CRediT authorship contribution statement

**Suwardi Annas:** Conceptualization, Methodology. **Muh. Isbar Pratama:** Software, Writing - review & editing. **Muh. Rifandi:** Data curation. **Wahidah Sanusi:** Supervision, Validation. **Syafruddin Side:** Conceptualization, Writing - original draft.

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