# The Dynamic Analysis of the COVID-19 Spread Model in the SIHCR Population with Time Delay

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**Abstract.** This study discusses the dynamic analysis of the COVID-19 spread model in the SIHCR population with time delay to represent the behavior of the spread of COVID-19 with time delay. The SIHCR model divides the human population into five subpopulations, namely Susceptible ($S$), Infected ($I$), Hospitalized ($H$), Critical ($C$), and Recovered ($R$). The dynamic analysis is carried out by determining the equilibrium point, the basic reproduction number ($R_0$), and stability analysis of the equilibrium point. The result of this study is two equilibrium points, namely the disease-free equilibrium point ($E_0$) and the endemic equilibrium point ($E_1$). Then the basic reproduction number ($R_0$) was calculated using the given parameters and produce the value $R_0 > 1$. The stability analysis can be obtained by linearization around the equilibrium points. The disease-free equilibrium point is unstable and the endemic equilibrium point is locally asymptotically stable. Next, simulation of the SIHCR model with and without time delay was carried out under disease-free and endemic conditions. Simulations are carried out using variations in the value of the delay time to determine the dynamic behavior of the model. In disease-free and endemic conditions, it shows differences in the dynamic behavior of the model. The smaller the delay time, the condition is almost the same as the SIHCR model without time delay towards stability. Meanwhile, the greater the delay time, the longer the SIHCR model leads to stability. So it can be concluded that the time delay affects the stability of the SIHCR model.

**Keywords:** Mathematical Model of SIHCR · Dynamic Analysis · Basic Reproduction Number · Time Delay

## 1 Introduction

The spread of COVID-19 which continues to grow in various parts of the world, has an impact on the number of daily cases of COVID-19 which is increasing. This has an impact on the occupancy rate of inpatient and ICU beds in hospitals [1]. Research on the spread model of COVID-19 has been studied previously by [2–5]. The spread of COVID-19 can be represented by a mathematical model in the SIHCR population which divides the individual population into five compartments, namely: Susceptible ($S$) is a subpopulation of individuals who can be infected by COVID-19, Infected ($I$) is a subpopulation of individuals who are infected and can transmit COVID-19 but do


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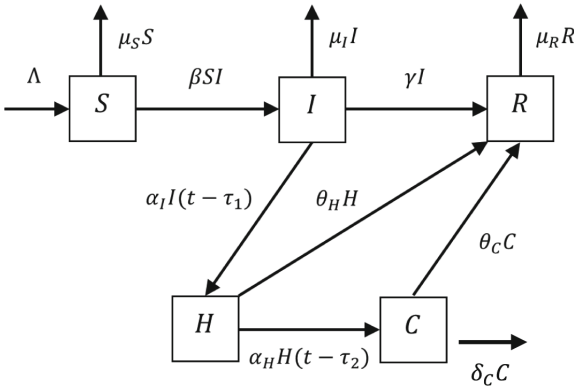


**Fig. 1.** The Compartment Diagram of SIHCR Model with Time Delay

not hospitalized, Hospitalized ($H$) is a subpopulation of individuals who is positive for COVID-19 and hospitalized, Critical ($C$) is a subpopulation of individuals who is positive for COVID-19 and is receiving intensive care in the ICU due to an increasingly critical condition, and Recovered ($R$) is a subpopulation of individuals who recover and will not be susceptible to COVID-19 infection [6].

The SIHCR model in this study uses a time delay ($\tau$). The time delay is used to determine how fast the rate of spread of the disease from Infected ($I$) to Hospitalized ($H$) and Hospitalized ($H$) to Critical ($C$). The use of time delay can consider the COVID-19 spread model where the rate of spread does not only depend on the present time ($t$) but also depends on the past time ($t-\tau$) [7]. The model for the spread of COVID-19 in the SIHCR population with time delay can be illustrated in Fig. 1.

Changes in the number of individuals in each compartment are influenced by several parameters, so that a system of differential equations is obtained as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \beta SI - \mu_S S \\
\frac{dI}{dt} &= \beta SI - \alpha_I I(t-\tau_1) - \gamma I - \mu_I I \\
\frac{dH}{dt} &= \alpha_I I(t-\tau_1) - \alpha_H H(t-\tau_2) - \theta_H H \\
\frac{dC}{dt} &= \alpha_H H(t-\tau_2) - \theta_C C - \delta_C C \\
\frac{dR}{dt} &= \gamma I + \theta_H H + \theta_C C - \mu_R R
\end{aligned} \tag{1}$$

The initial values of the variables and parameters used in the model of the spread of COVID-19 in the SIHCR population with time delay in Table 1 and 2.

Based on this explanation, we will study the dynamic analysis of the COVID-19 spread model in the SIHCR population with time delay assuming $\tau_1 = \tau_2 = \tau$.

## 2 Method

The following are the stages of research in conducting a dynamic analysis of the COVID-19 spread model in the SIHCR population with time delay [10]:

1. Determine the disease-free equilibrium point

**Table 1.** The Initial Value of SIHCR Model with Time Delay (corona.jakarta.go.id, 2021)

| Variable | Description | Initial Value |
|---|---|---|
| $N(0)$ | The individual population in DKI Jakarta | 10609681 person |
| $S(0)$ | The initial subpopulation of susceptible individuals infected with COVID-19 | 8907422 person |
| $I(0)$ | The initial subpopulation of infected individuals with COVID-19 | 858198 person |
| $H(0)$ | The initial subpopulation of hospitalized individuals | 984 person |
| $C(0)$ | The initial subpopulation of critical individuals | 148 person |
| $R(0)$ | The initial subpopulation of individuals recovering from COVID-19 | 842929 person |

2. Determine the endemic equilibrium point
3. Determine the basic reproduction number
4. Analyze the local stability of the disease-free equilibrium point
5. Analyze the local stability of the endemic equilibrium point

The following are the stages of research in simulating the spread of COVID-19 in the SIHCR population:

1. Simulating the SIHCR model without time delay
2. Simulating the SIHCR model with time delay

## 3 Result and Discussion

### 3.1 The Dynamic Analysis of SIHCR Model with Time Delay

#### 3.1.1 The Disease-Free Equilibrium Point

The equilibrium point of a system is the point at which the system does not change with time or is stable [5]. This equilibrium point analysis assumes that the population change is constant, meaning that the system of Eqs. (1) must satisfy $\frac{dS}{dt} = 0$, $\frac{dI}{dt} = 0$, $\frac{dH}{dt} = 0$, $\frac{dC}{dt} = 0$, $\frac{dR}{dt} = 0$. To obtain a stable equilibrium point, it is assumed when the model is without time delay where $\tau_1 = \tau_2 = 0$ [11]. In the disease-free problem it is assumed $(I = 0)$ which means that there is no spread of disease in the population. So that the disease-free equilibrium point is obtained as follows Eq. 2:

$$E_0(S_0, I_0, H_0, C_0, R_0) = E_0\left(\frac{\Lambda}{\mu_S}, 0, 0, 0, 0\right) \tag{2}$$

#### 3.1.2 The Endemic Equilibrium Point

The endemic equilibrium point indicates the condition in which there is a spread of disease in the population, so in this condition it is assumed $(I \neq 0)$. T endemic equilibrium

**Table 2.** The Initial Parameters Value of SIHCR Model with Time Delay

| Parameter | Description | Value | Units | Source |
|---|---|---|---|---|
| $\Lambda$ | Natural birth rate | 0.001 | Individual per day | [8] |
| $\beta$ | Transmission rate from susceptible individuals to infected individuals | 0.17 | Individual per day | [2] |
| $\gamma$ | Recovery rate of infected individuals | 0.05 | Individual per day | [2] |
| $\mu_S$ | Natural death rate of susceptible individuals | 0.001 | Individual per day | [9] |
| $\mu_I$ | Natural death rate of infected individuals | 0.003 | Individual per day | [9] |
| $\mu_R$ | Natural death rate of recovered individuals | 0.002 | Individual per day | [9] |
| $\alpha_I$ | Probability of infected individuals to be hospitalized as the condition worsens | 0.01 | Percent | [3] |
| $\alpha_H$ | Probability of hospitalized individuals becomes critical individuals due to a worsening condition that requires intensive care in the ICU | $2 \times 10^{-5}$ | Percent | [3] |
| $\theta_H$ | Recovery rate of hospitalized individuals | 0.027 | Individual per day | [3] |
| $\theta_C$ | Recovery rate of critical individuals | 0.0009 | Individual per day | [3] |
| $\delta_C$ | Death rate of critical individuals | 0.003 | Individual per day | [3] |
| $t$ | Time | 90. | Day | [9] |
| $\tau_1$ | Time delay for infected individuals to hospitalized individuals | Varies | Day | Based on simulation |
| $\tau_2$ | Time delay for hospitalized individuals to critical individuals | Varies | Day | Based on simulation |

point $E_1(S^*, I^*, H^*, C^*, R^*)$ of the system in Eq. (3) is:

$$\begin{aligned} S^* &= \frac{\alpha_I+\gamma+\mu_I}{\beta} \\ I^* &= \frac{\Lambda\beta-\mu_S(\alpha_I+\gamma+\mu_I)}{\beta(\alpha_I+\gamma+\mu_I)} \end{aligned} \tag{3}$$

with $\Lambda\beta - \mu_S(\alpha_I + \gamma + \mu_I) > 0$ and $\Lambda\beta > \mu_S(\alpha_I + \gamma + \mu_I)$

$$H^* = \frac{\alpha_I(\Lambda\beta - \mu_S(\alpha_I + \gamma + \mu_I))}{\beta(\alpha_I + \gamma + \mu_I)(\alpha_H + \theta_H)}$$

$$C^* = \frac{\alpha_H\alpha_I(\Lambda\beta - \mu_S(\alpha_I + \gamma + \mu_I))}{\beta(\theta_C + \delta_C)(\alpha_I + \gamma + \mu_I)(\alpha_H + \theta_H)}$$

$$R^* = \frac{(\Lambda\beta - \mu_S(\alpha_I + \gamma + \mu_I))(\gamma(\theta_C + \delta_C)(\alpha_H + \theta_H) + \theta_H\alpha_I(\theta_C + \delta_C) + \theta_C\alpha_H\alpha_I)}{\mu_R\beta(\theta_C + \delta_C)(\alpha_I + \gamma + \mu_I)(\alpha_H + \theta_H)}$$

### 3.1.3 Basic Reproductive Number

T basic reproduction number can be obtained from the maximum eigenvalues by constructing the Next Generation Matrix [10]. Then the matrix $\boldsymbol{F}$ is obtained, namely the transmission matrix and the matrix $\boldsymbol{V}$, namely the transition matrix [12] as follows:

$$\boldsymbol{F} = \begin{bmatrix} \frac{\beta\Lambda}{\mu_S} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

and

$$\boldsymbol{V} = \begin{bmatrix} \alpha_I + \gamma + \mu_I & 0 & 0 \\ -\alpha_I & \alpha_H + \theta_H & 0 \\ 0 & -\alpha_H & \theta_C + \delta_C \end{bmatrix}$$

From matrix $\boldsymbol{F}$ and matrix $\boldsymbol{V}$, the Next Generation Matrix is obtained as follows:

$$\boldsymbol{K} = \boldsymbol{F}\boldsymbol{V}^{-1} = \begin{bmatrix} \frac{\beta\Lambda}{\mu_S(\alpha_I+\gamma+\mu_I)} & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

The value used as the basic reproduction number is the spectral radius or the dominant absolute eigenvalue [13], so that is obtained

$$R_0 = \frac{\beta\Lambda}{\mu_S(\alpha_I + \gamma + \mu_I)} \tag{4}$$

### 3.1.4 The Local Stability Analysis of Disease-Free Equilibrium Point

Analysis of the stability of the equilibrium point in the system of nonlinear Eqs. (1) can be obtained by linearization using the Taylor series around the equilibrium point [10]. First, the nonlinear system of Eqs. (1) is linearized around the disease-free equilibrium point, so that is obtained

$$\boldsymbol{J}_{\boldsymbol{E}_0} = \begin{vmatrix} \lambda + \beta I_0 + \mu_S & \beta S_0 & 0 & 0 & 0 \\ -\beta I_0 & \lambda - \beta S_0 + \gamma + \mu_I + \alpha_I e^{-\lambda\tau} & 0 & 0 & 0 \\ 0 & -\alpha_I e^{-\lambda\tau} & \lambda + \theta_H + \alpha_H e^{-\lambda\tau} & 0 & 0 \\ 0 & 0 & -\alpha_H e^{-\lambda\tau} & \lambda + \theta_C + \delta_C & 0 \\ 0 & -\gamma & -\theta_H & -\theta_C & \lambda + \mu_R \end{vmatrix} = 0$$

Suppose $\tau = 0$, with the help of Maple software, the characteristic equation of the matrix $\boldsymbol{J}_{\boldsymbol{E}_0}$ is obtained as follows:

$$a_0\lambda^5 + a_1\lambda^4 + a_2\lambda^3 + a_3\lambda^2 + a_4\lambda + a_5 = 0 \tag{5}$$

Note that the values of the roots of the characteristic Eq. (5) can be analyzed for stability if they meet the stability requirements based on the Routh-Hurwitz criteria for $n = 5$, as follows

$$a_0.a_1.a_2.a_3.a_4.a_5 > 0$$

Next, substitute the parameter values in Table 2 to see the stability of the disease-free equilibrium point specifically, so that is obtained

$$\begin{aligned} a_0 &= 1 > 0 \\ a_1 &= -0.07308 < 0 \\ a_2 &= -0.003429302 < 0 \\ a_3 &= -0.000021036792 < 0 \\ a_4 &= -4.0232462 \times 10^{-8} < 0 \\ a_5 &= -2.2550892 \times 10^{-11} < 0 \end{aligned}$$

Based on these results, it can be seen that the disease-free equilibrium point is unstable, because there are Routh-Hurwitz criteria that are not met, namely $a_1, a_2, a_3, a_4, a_5 < 0$. Next, calculate the eigenvalues of the characteristic Eq. (5). Using the parameter values in Table 2, which are as follows

$$\begin{aligned} \lambda_1 &= -0.001 \\ \lambda_2 &= -0.002 \\ \lambda_3 &= -0.0039 \\ \lambda_4 &= -0.02702 \\ \lambda_5 &= 0.107 \end{aligned}$$

Based on these results, it can be seen that there is one positive eigenvalue, namely $\lambda_5 > 0$ and four negative eigenvalues, namely $\lambda_1, \lambda_2, \lambda_3, \lambda_4 < 0$. Thus, the stability property of the disease-free equilibrium point in the SIHCR population is unstable.

### 3.1.5 The Local Stability Analysis of Endemic Equilibrium Point

Next, an analysis of the local stability of the endemic equilibrium point is carried out by linearizing the system of nonlinear Eqs. (1) around the endemic equilibrium point, so that is obtained

$$\boldsymbol{J}_{\boldsymbol{E}_1} = \begin{vmatrix} \lambda+\beta I^*+\mu_S & \beta S^* & 0 & 0 & 0 \\ -\beta I^* & \lambda-\beta S^*+\gamma+\mu_I+\alpha_I e^{-\lambda\tau} & 0 & 0 & 0 \\ 0 & -\alpha_I e^{-\lambda\tau} & \lambda+\theta_H+\alpha_H e^{-\lambda\tau} & 0 & 0 \\ 0 & 0 & -\alpha_H e^{-\lambda\tau} & \lambda+\theta_C+\delta_C & 0 \\ 0 & -\gamma & -\theta_H & -\theta_C & \lambda+\mu_R \end{vmatrix} = 0$$

First, find the local stability of the endemic equilibrium point when $\tau = 0$. The characteristic equation obtained from the matrix $\boldsymbol{J}_{\boldsymbol{E}_1}$ is

$$b_0\lambda^5 + b_1\lambda^4 + b_2\lambda^3 + b_3\lambda^2 + b_4\lambda + b_5 = 0 \tag{6}$$

Note that the values of the roots of the characteristic Eq. (6) can be analyzed for stability if they meet the stability requirements based on the Routh-Hurwitz criteria for $n = 5$, as follows

i. $b_0 > 0$
ii. $b_1 > 0$
iii. $b_1b_2 - b_0b_3 > 0$
iv. $c_1 > 0$
v. $d_1 > 0$

where

$$c_1 = \frac{(b_1b_2-b_0b_3)b_3-(b_1b_4-b_0b_5)b_1}{b_1b_2-b_0b_3}$$
$$d_1 = \frac{(b_1b_4-b_0b_5)c_1-\frac{(b_1b_2-b_0b_3)b_5}{b_1b_2-b_0b_3}}{c_1}$$

Next, substitute the parameter values in Table 2 to see the stability of the endemic equilibrium point specifically, so that is obtained

$$b_0 = 1 > 0$$
$$b_1 = 0.0356184127 > 0$$
$$b_1b_2 - b_0b_3 = 0.000008746836505 > 0$$
$$c_1 = 0.000001598597917 > 0$$
$$d_1 = 5.116130591 \times 10^{-10} > 0$$

Based on these results, it can be seen that the endemic equilibrium point is stable, because it meets the Routh-Hurwitz criteria. Furthermore, the eigenvalues from the characteristic Eq. (6) will be calculated using the parameter values in Table 2, so that is obtained

$$\lambda_1 = -0.002$$
$$\lambda_2 = -0.0039$$
$$\lambda_3 = -0.02702$$
$$\lambda_4 = -0.001349206349 + 0.0102557126618201\ I$$
$$\lambda_5 = -0.001349206349 - 0.0102557126618201\ I$$

Based on these results, it can be seen that all eigenvalues have a negative real part. Thus it can be concluded that the stability property of the endemic equilibrium point in the SIHCR population when $\tau = 0$ is locally asymptotically stable.

Next, analyze the local stability of the endemic equilibrium point when $\tau \neq 0$ or $(\tau > 0)$. The first step is to find the determinant of the matrix $\boldsymbol{J}_{\boldsymbol{E}_1}$ using the cofactor expansion method, so that the eigenvalues are obtained

$$\lambda_1 = -A_1 - \mu_S, \lambda_2 = -\mu_R, \lambda_3 = -\theta_C - \delta_C$$

If substitute the parameter values in Table 2, so that is obtained

$$\begin{aligned}\lambda_1 &= -0.002698412698\\ \lambda_2 &= -0.002\\ \lambda_3 &= -0.0039\end{aligned}$$

it can be seen that the eigenvalues $\lambda_1$, $\lambda_2$ and $\lambda_3$ have negative real parts. The other two eigenvalues are found using the following equation

$$\lambda^2 + 0.01702\lambda + 0.01e^{-\lambda\tau}\lambda - 0.0003 + 0.0002702e^{-\lambda\tau} = 0 \tag{7}$$

The solution of characteristic Eq. (7) is in pure imaginary form, namely $\lambda = i\omega$ with $\omega > 0$ [14, 15]. Substituting $\lambda = i\omega$ into Eq. (7), so that is obtained

$$(i\omega)^2 + 0.01702i\omega + 0.01i\omega e^{-(i\omega)\tau} - 0.0003 + 0.0002702e^{-(i\omega)\tau} = 0$$

$$\begin{aligned}\Big(-\omega^2 + 0.01\omega\sin(\omega\tau) - 0.0003 + 0.0002702\cos(\omega\tau)\Big) + i(0.01702\omega\\ + 0.01\omega\cos(\omega\tau) - 0.0002702\sin(\omega\tau)) = 0\end{aligned} \tag{8}$$

Then separate the real and imaginary parts of Eq. (8), so that is obtained

$$-\omega^2 - 0.0003 = -0.01\omega\sin(\omega\tau) - 0.0002702\cos(\omega\tau) \tag{9}$$

$$0.01702\omega = -0.01\omega\cos(\omega\tau) + 0.0002702\sin(\omega\tau) \tag{10}$$

Eliminate Eqs. (9) and (10) to $\tau$ by squaring each side of the equation, then add up the results of the square so that is obtained

$$\begin{aligned}\omega^4 + \Big(0.01702^2 + 0.0006\Big)\omega^2 + 0.0003^2 &= 0.01^2\omega^2\Big(\sin^2(\omega\tau) + \cos^2(\omega\tau)\Big)\\ &\quad + 0.0002702^2\Big(\sin^2(\omega\tau) + \cos^2(\omega\tau)\Big)\\ \omega^4 + \Big(0.01702^2 - 0.01^2 + 0.0006\Big)\omega^2 + 0.0003^2 - 0.0002702^2 &= 0\\ \omega^4 + 0.00079\omega^2 + 1.699 \times 10^{-8} &= 0\end{aligned} \tag{11}$$

The next step is to find the root of Eq. (11) using Maple software so that the value of is obtained as follows:

$$\begin{aligned}\omega_1 &= 0.02770455301\\ \omega_2 &= -0.02770455301\\ \omega_3 &= 0.004705118773\\ \omega_4 &= -0.004705118773\end{aligned}$$

Note that the root of the characteristic equation is purely imaginary, namely $\lambda = i\omega$, so that the value of $\lambda$ is obtained as follows:

$$\lambda_1 = 0.02770455301\ I$$
$$\lambda_2 = -0.02770455301\ I$$
$$\lambda_3 = 0.004705118773\ I$$
$$\lambda_4 = -0.004705118773\ I$$

Then look for the value of the time delay $\tau$. by substituting each value of $\omega$ that has been obtained into Eqs. (9) and (10). First, substitute each value of $\omega$ into Eq. (9) as follows:

Substituting $\omega_1 = 0.02770455301$ into Eq. (9), so that is obtained

$$0.0004675422575 = -0.0002770455301 \sin(0.02770455301\tau) - 0.0002702 \cos(0.02770455301\tau) \quad (12)$$

Substituting $\omega_2 = -0.02770455301$ into Eq. (9), so that is obtained

$$0.0004675422575 = 0.0002770455301 \sin(-0.02770455301\tau) - 0.0002702 \cos(-0.02770455301\tau) \quad (13)$$

Substituting $\omega_3 = 0.004705118773$ into Eq. (9), so that is obtained

$$0.0002778618573 = -0.00004705118773 \sin(0.004705118773\tau) - 0.0002702 \cos(0.004705118773\tau) \quad (14)$$

Substituting $\omega_4 = -0.004705118773$ into Eq. (9), so that is obtained

$$0.0002778618573 = 0.00004705118773 \sin(-0.004705118773\tau) - 0.0002702 \cos(-0.004705118773\tau) \quad (15)$$

Then substitute each value of $\omega$ into Eq. (10) as follows:

Substituting $\omega_1 = 0.02770455301$ into Eq. (10), so that is obtained

$$0.0004715314922 = -0.0002770455301 \cos(0.02770455301\tau) + 0.0002702 \sin(0.02770455301\tau) \quad (16)$$

Substituting $\omega_2 = -0.02770455301$ into Eq. (10), so that is obtained

$$-0.0004715314922 = 0.0002770455301 \cos(-0.02770455301\tau) + 0.0002702 \sin(-0.02770455301\tau) \quad (17)$$

Substituting $\omega_3 = 0.004705118773$ into Eq. (10), so that is obtained

$$0.00008008112152 = -0.00004705118773 \cos(0.004705118773\tau) + 0.0002702 \sin(0.004705118773\tau) \quad (18)$$

Substituting $\omega_4 = -0.004705118773$ into Eq. (10), so that is obtained

$$\begin{aligned} -0.00008008112152 =& 0.00004705118773\cos(-0.004705118773\tau) \\ &+ 0.0002702\sin(-0.004705118773\tau) \end{aligned} \tag{19}$$

Then by using Maple software, the time delay value $\tau$ is obtained as follows: The time delay value from Eq. (12), (13), (16) and (17) is

$$\tau_1 = 177$$

The time delay value from Eq. (14), (15), (18) and (19)

$$\tau_2 = 100$$

The time delay value that has been obtained is not used when simulating the model because it has a value that is too large, so it requires high Matlab software specifications. Therefore, when the simulation will use a small value of the time delay which will be explained in the next discussion.

### 3.2 The Simulation on SIHCR Model Without and With Time Delay

#### 3.2.1 The Simulation on the SIHCR Model in Disease-Free Condition

Simulation on the SIHCR model in disease-free conditions was carried out when $R_0 < 1$. The parameter values used are approximately the parameter values in Table 2. This is because the stability of the disease-free equilibrium point using the parameter values in Table 2 will result in an unstable disease-free equilibrium point. Thus, the parameter values used are as follows:

$$\begin{aligned} &\Lambda = 0.001;\ \beta = 0.1;\ \gamma = 0.07;\ \mu_S = 0.001;\ \mu_I = 0.003;\ \mu_R = 0.002; \\ &\alpha_I = 0.036;\ \alpha_H = 0.000083;\ \theta_H = 0.054;\ \theta_C = 0.0015;\ \delta_C = 0.003 \end{aligned}$$

Based on these parameters, the value of $R_0 = 0.92$ is obtained which indicates the population is in a disease-free condition. Furthermore, simulations were carried out in disease-free conditions using the SIHCR model without and with time delay. First, a simulation on the SIHCR model without time delay will be carried out in disease-free conditions.

Based on Fig. 2, it can be seen that the Susceptible, Infected, Hospitalized, Critical, and Recovered populations experienced a decrease in the number of populations towards the equilibrium point within 90 days. Note that the graph shows that the spread of COVID-19 in the population continued to decrease over time until COVID-19 disappeared.

Furthermore, simulation of the SIHCR model with time delay in disease-free conditions was carried out. In this section, three simulations are carried out using variations of the time delay parameter values presented in Table 3.

The following is a graph of the results of each simulation of the SIHCR model with time delay in disease-free conditions (Figs. 3, 4 and 5).

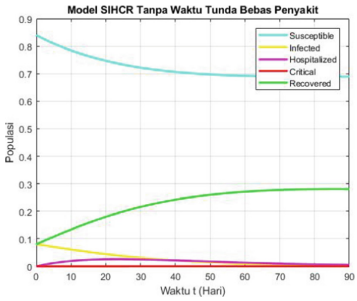


**Fig. 2.** Graph of SIHCR Model Without Time Delay When $R_0 < 1$

**Table 3.** Parameter Value of Time Delay $\tau$

| Parameter | Simulation 1 | Simulation 2 | Simulation 3 |
|---|---|---|---|
| $\tau$ | 0.01 | 0.05 | 0.1 |

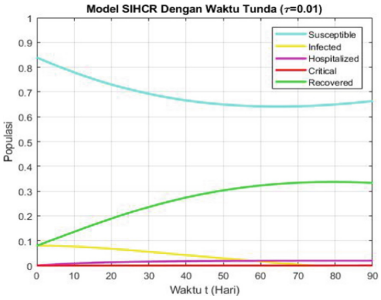


**Fig. 3.** Graph of SIHCR Model With Time Delay When $R_0 < 1$ with $\tau = 0.01$

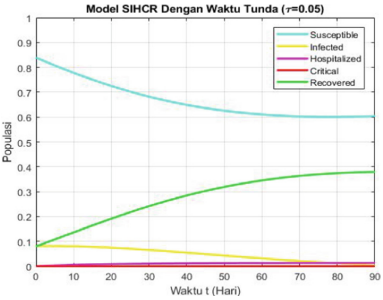


**Fig. 4.** Graph of SIHCR Model With Time Delay When $R_0 < 1$ with $\tau = 0.05$

Based on simulation 1, simulation 2, and simulation 3 for the SIHCR model with time delay in disease-free conditions, it shows that there are differences in the behavior

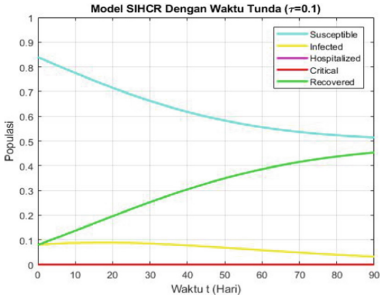


**Fig. 5.** Graph of SIHCR Model With Time Delay When $R_0 < 1$ with $\tau = 0.1$

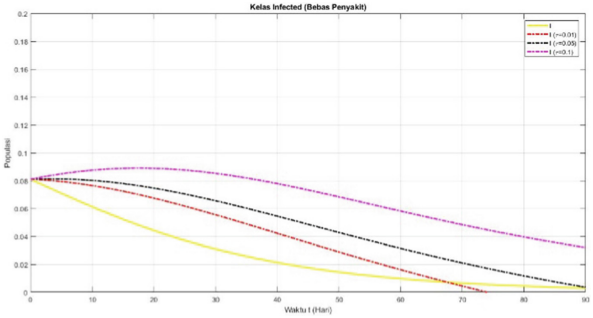


**Fig. 6.** Graph of Infected Class With and Without Time Delay When $R_0 < 1$

of each population with respect to time when using variations in the time delay value. The smaller the time delay given, the faster the SIHCR model leads to stability. On the other hand, the greater the time delay given, the longer the SIHCR model leads to stability.

Furthermore, simulations were carried out in the Infected class with and without time delay in disease-free conditions. In this section, the value of the time delay parameter is used as shown in Table 3. The following is a graph of the results of each simulation of the Infected class with and without delay in disease-free conditions.

Based on Fig. 6, there are differences in the behavior of the Infected class with and without time delay in disease-free conditions. The Infected class with time delay shows that it takes longer to reach stability than the Infected class without time delay.

### 3.2.2 The Simulation on the SIHCR Model in Endemic Condition

The simulation on the SIHCR model in endemic conditions was carried out when $R_0 > 1$. The parameter values used are the parameter values in Table 2. Based on the parameter values in Table 2, the $R_0 = 2.69$ value is obtained which indicates the population is in endemic conditions, so that the endemic equilibrium point is locally asymptotically stable. Furthermore, simulations in endemic conditions were carried out using the SIHCR model without and with time delay. First, a simulation of the SIHCR model without time delay will be carried out in endemic conditions.

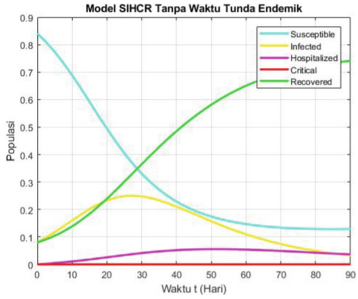


**Fig. 7.** Graph of SIHCR Model Without Time Delay When $R_0 > 1$

Based on Fig. 7, it can be seen that the Infected and Hospitalized populations have increased in population. This shows that there is a spread of COVID-19 in a population. Thus, if $R_0 > 1$ then the endemic equilibrium point is locally asymptotically stable.

Furthermore, simulation of the SIHCR model with time delay in endemic conditions was carried out. In this section, three simulations are carried out using variations in the value of the time delay parameter which are presented in Table 3. The following is a graph of the results of each simulation of the SIHCR model with time delays in endemic conditions (Figs. 8, 9 and 10).

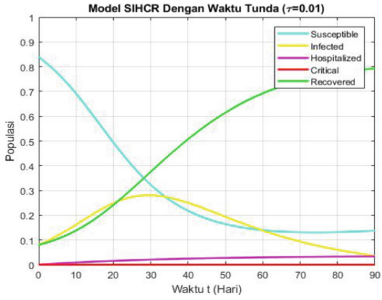


**Fig. 8.** Graph of SIHCR Model With Time Delay When $R_0 > 1$ with $\tau = 0.01$

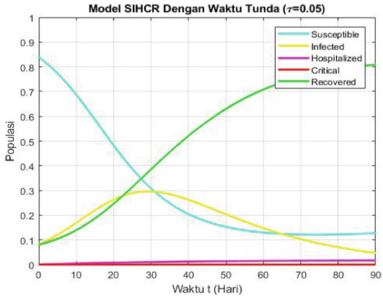


**Fig. 9.** Graph of SIHCR Model With Time Delay When $R_0 > 1$ with $\tau = 0.05$

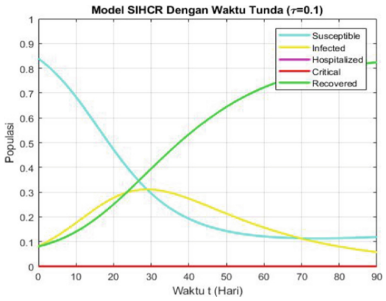


**Fig. 10.** Graph of SIHCR Model With Time Delay When $R_0 > 1$ with $\tau = 0.1$

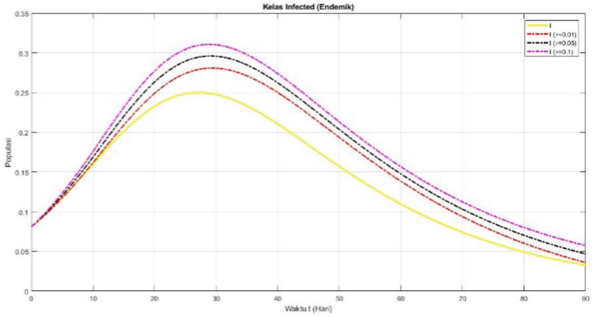


**Fig. 11.** Graph of Infected Class With and Without Time Delay When $R_0 > 1$

Based on simulation 1, simulation 2, and simulation 3 for the SIHCR model with time delay in endemic conditions, it shows that there are differences in the behavior of each population with respect to time when using variations in the time delay value. The smaller the time delay given, the faster the SIHCR model leads to stability. On the other hand, the greater the time delay given, the longer the SIHCR model leads to stability.

Furthermore, simulations were carried out in the Infected class with and without time delay in endemic conditions. In this section, the value of the time delay parameter is used as shown in Table 3. The following is a graph of the results of each simulation of the Infected class with and without delay in endemic conditions.

Based on Fig. 11, there are differences in the behaviour of the Infected class with and without time delay in endemic conditions. The Infected class with time delay showed longer peak days of infection and stability than the Infected class without time delay.

## 4 Conclusion

Based on the dynamic analysis of the model of the spread of COVID-19 in the SIHCR population with and without time delay, it was obtained:

a. The disease-free equilibrium point is $E_0(S_0, I_0, H_0, C_0, R_0) = E_0\left(\frac{\Lambda}{\mu_S}, 0, 0, 0, 0\right)$. The stability analysis at the disease-free equilibrium point is unstable based on the Routh-Hurwitz criteria and their eigenvalues.

b. The endemic equilibrium point is $E_1(S^*, I^*, H^*, C^*, R^*)$, where

$$S^* = \frac{\alpha_I + \gamma + \mu_I}{\beta}$$

$$I^* = \frac{\Lambda\beta - \mu_S(\alpha_I + \gamma + \mu_I)}{\beta(\alpha_I + \gamma + \mu_I)}$$

$$H^* = \frac{\alpha_I(\Lambda\beta - \mu_S(\alpha_I + \gamma + \mu_I))}{\beta(\alpha_I + \gamma + \mu_I)(\alpha_H + \theta_H)}$$

$$C^* = \frac{\alpha_H\alpha_I(\Lambda\beta - \mu_S(\alpha_I + \gamma + \mu_I))}{\beta(\theta_C + \delta_C)(\alpha_I + \gamma + \mu_I)(\alpha_H + \theta_H)}$$

$$R^* = \frac{(\Lambda\beta - \mu_S(\alpha_I + \gamma + \mu_I))(\gamma(\theta_C + \delta_C)(\alpha_H + \theta_H) + \theta_H\alpha_I(\theta_C + \delta_C) + \theta_C\alpha_H\alpha_I)}{\mu_R\beta(\theta_C + \delta_C)(\alpha_I + \gamma + \mu_I)(\alpha_H + \theta_H)}$$

The stability analysis at the endemic equilibrium point when $\tau = 0$ and $\tau \neq 0$ are locally asymptotically stable based on the Routh-Hurwitz criteria and their eigenvalues.

c. The basic reproduction number obtained is $R_0 = 2.69 > 1$ (corona.jakarta.go.id, 2021), thus causing the COVID-19 disease to become endemic.

Based on the results of the numerical simulation of the SIHCR model with and without time delay, it is obtained:

a. In disease free condition

Based on the simulation results when $R_0 < 1$, it shows the difference in the dynamic behavior of the SIHCR model with and without time delay. The smaller the delay time, the condition is almost the same as the SIHCR model without time delay towards stability. Meanwhile, the greater the delay time, the longer the SIHCR model leads to stability.

b. In endemic condition

Based on the simulation results when $R_0 > 1$, it shows the difference in the dynamic behavior of the SIHCR model with and without time delay. The smaller the delay time, the condition is almost the same as the SIHCR model without time delay towards stability. Meanwhile, the greater the delay time, the longer the SIHCR model leads to stability.

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