BAREKENG: Journal of Mathematics and Its Applications
December 2023 Volume 17 Issue 4 Page 2147–2160
P-ISSN: 1978-7227 E-ISSN: 2615-3017
https://doi.org/10.30598/barekengvol17iss4pp2147-2160

ANALYSIS OF THE COVID-19 EPIDEMIC MODEL WITH SELF-ISOLATION AND HOSPITAL ISOLATION

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ABSTRACT

Article History:

Received: 3rd July 2023
Revised: 2nd October 2023
Accepted: 2nd November 2023

Keywords:

Basic Reproduction Number;
COVID-19;
Disease-Free Equilibrium Point;
Ecemic Equilibrium Point.

This research developed the SIR model with self-isolation and hospital isolation. The analysis is carried out through the disease-free and endemic equilibrium point analysis and the sensitivity analysis of the basic reproduction number. Based on the disease-free equilibrium point analysis, for a certain period of time the population will be free from COVID-19 if the basic reproduction number is less than 1. If the basic reproduction number is more than 1, the disease will persist in the population, this will lead to an endemic equilibrium point. Based on the sensitivity analysis of parameter values on the basic reproduction number, the parameter for the isolation rate of individually infected individuals in hospitals is -0.4615166040, and the self-isolation rate at home is -0.01853667767. This indicates that isolation in hospitals is more effective than self-isolation in suppressing the spread of COVID-19.

How to cite this article:

M. Manaqib, T. N. Padilah and I. Maulana., "ANALYSIS OF THE COVID-19 EPIDEMIC MODEL WITH SELF-ISOLATION AND HOSPITAL ISOLATION," *BAREKENG: J. Math. & App.*, vol. 17, iss. 4, pp. 2147-2160, December, 2023.

Journal homepage: *https://ojs3.unpatti.ac.id/index.php/barekeng/*
Journal e-mail: *barekeng.math@yahoo.com ; barekeng.journal@mail.unpatti.ac.id*

Research Article· Open Access

1. INTRODUCTION

A coronavirus is a group of viruses that can cause disease in animals or humans. Several types of coronaviruses are known to cause respiratory infections in humans ranging from cold coughs to more serious ones such as Middle East Respiratory Syndrome (MERS) and *Severe Acute Respiratory Syndrome* [1]. A new type of coronavirus has been discovered to cause COVID-19 disease. The new virus and the disease it caused became known in December 2019 in Wuhan, China and caused an outbreak in the area. COVID-19 is now a pandemic that occurs in many countries around the world [2]. People can get COVID-19 from others infected with this virus. COVID-19 can spread primarily from person to person through splashes from the nose or mouth that come out when an infected person coughs, sneezes or talks [3]. Many people infected with COVID-19 experience only mild symptoms, especially in the early stages. Therefore, COVID-19 can be transmitted from people who only have mild symptoms, such as a mild cough, but feel healthy. Some reports suggest that asymptomatic people can transmit the virus but it is not yet known how often transmission in that way occurs [4]. Based on the Circular Letter of the Minister of Health of the Republic of Indonesia Number HK.02.01/MENKES/202/2020 concerning Self-Isolation Protocol in Handling Coronavirus Disease (COVID-19), Indonesia has declared COVID-19 as a non- natural disaster in the form of a disease outbreak that must be countermeasures so that there is no increase in cases [5].

Government spokesperson for handling the coronavirus, Achmad Yurianto said, not all positive patients must be isolated in hospitals. There are some asymptomatic cases who can self-isolate at home. Isolation means separating people who are sick with COVID-19 symptoms and may be contagious to prevent transmission. Self-isolation is an important measure taken by people who have symptoms of COVID-19 to prevent transmission to others in the community, including family members. Self-isolation is done when someone who has a fever, cough, or other COVID-19 symptoms stays at home and does not go to work, school, or to public places. This is done voluntarily or on the recommendation of a health care provider [6].

Mathematical modeling is an approach that can be used to explain problems that occur in the real world and find solutions [7], [8]. The problem of the spread of infectious diseases can also be modeled into mathematical modeling called epidemic models. In 1926, Kermack and McKendrick formulated the SIR model to study the Black Death in London during the period 1665-1666 and the bubonic plague in Mumbai in 1906 [9]. In this SIR model, the population is divided into three compartments: the susceptible compartment labeled S, the infected compartment labeled I, and the removed compartment labeled R. The number of new infections an individual infection during the overall infection period when individuals are in the initial population are all susceptible is referred to as the basic reproduction ratio number (R_0). Value ofR_0 states the threshold for disease transmission. The number of infections decreases if $\mathrm{R}_0 < 1$and increases if $\mathrm{R}_0 > 1$. Therefore, to control the spread of the disease, one of the main factors is to estimate the value and then reduce it to less than one R_0[10]. Value R_0used to describe the transmission of infectious agents. Further values R_0 is modeled depends on the structure of the model and the assumptions used [11].

Mathematical models of the spread of respiratory diseases have been developed by several researchers, including TBC [12] and MERS- Cov [13], [14]. Similarly, the COVID-19 disease began to be developed from the basic model of the SIR disease epidemic [15]–[19]. In Indonesia, the beginning of research related to mathematical modeling of COVID-19 includes the prediction of COVID-19 cases in Indonesia using the Richard curve, analysis [20] of COVID-19 clusters in Jakarta using the SIR model [21]and modeling the spread of COVID-19 in South Kalimantan Province using the SIR model [22].

This study developed a model of the spread of COVID-19 with quarantine or isolation factors added. SIR Model [9] Two isolation subpopulations were added, namely individuals isolated in hospitals and individuals isolated at home (self-isolation). Next, the model is analyzed by finding the basic reproduction number, equilibrium point and stability. The disease-free equilibrium point was found for stability using the eigenvalue analysis of the Jacobian matrix and using the Routh-Hurwitz criterion. The model is simulated using Maple 2018 software to provide a geometric picture of the solution and to support the theorem obtained. Finally, a sensitivity analysis was carried out to determine the parameters that most influence the spread of COVID-19.

2. RESEARCH METHODOLOGY

In general, the steps carried out in this study:

1. Model Formulation
   At this stage, a mathematical model of the spread of COVID-19 is carried out by adding isolation factors in hospitals and self-isolation.
2. Equilibrium Point

   The model obtained then looks for the equilibrium point and the basic reproduction number. The basic reproduction number is needed to find the boundaries of the parameters of the disease will be endemic or endemic using the next generation matrix method.
3. Stability Analysis

   Furthermore, the equilibrium point is found for stability using the eigenvalue analysis of the Jacobian matrix mathematical model.
4. Numerical Simulation

   The model is simulated using Maple 2018 software to provide a geometric picture of the solution and to support the theorem obtained.
5. Sensitivity Index Base reproduction number

   This provides information about the importance of each parameter in the model that represents the spread of COVID-19 disease. The index is used to identify the parameters that have the most significant influence on which are then used as intervention targets.

3. RESULTS AND DISCUSSION

3.1 Mathematical Models

The group of individuals of the COVID-19 epidemic model with isolation is divided into five groups, namely sub-populations of susceptible individuals S (susceptible), infected and infectious individuals I (infective), isolated individuals in Hospital Q1, isolated individuals at home (self-isolation) Q2, and recovered individuals R (recovery). The assumptions used in the COVID-19 epidemic reduction model with isolation are as follows.

1. Any newborn individual will be a vulnerable individual.
2. The increase in the number of vulnerable individuals comes only from the number of births, no immigration. There was also no emigration.
3. Infected and contagious individuals are considered to be individuals infected with a clinically asymptomatic disease called asymptomatic people and can transmit the disease to susceptible individuals.
4. There is no incubation period. If a susceptible individual interacts with an infected individual and transmits it, then the susceptible individual can become infected and can directly transmit to another susceptible individual.
5. Infected and infectious individuals with clinical symptoms are directly divided into two sub-populations, namely the sub-population of individuals isolated in hospitals and the sub-population of individuals isolated at home (self-isolation).
6. Every vulnerable individual, infected and contagious individuals, and recovered individuals can meet each other.
7. Any individual isolated in a hospital or an individual isolated at home (self-isolation) is considered unable to transmit the disease because they do not interact with individuals who are not isolated. This means that medical personnel caring for isolated individuals in hospitals are considered unable to become infected by isolated individuals. Medical personnel can only be infected by infected and contagious individuals or asymptomatic people.

8. Recovered individuals are considered immune and cannot be reinfected.

The variables used to derive the COVID-19 epidemic model with isolation are nonnegative, while the parameters are positive. The variables and parameters of the COVID-19 epidemic model with isolation are presented in **Table 1** and **Table 2**.

Table 1. Variables of the COVID-19 Epidemic Model with Isolation

Symbol	Definition	Unit
S	number of susceptible individuals	individuals
I	number of infected and infectious individuals	individuals
$Q1$	number of individuals isolated in Hospital	individuals
$Q2$	number of individuals isolated at home (self-isolation)	individuals
R	number of individuals recovered	individuals
N	total number of individuals	individuals

Table 2. COVID-19 Epidemic Model Parameters with Isolation

Symbol	Definition	Unit
A	birth rate	individu per time
μ	natural death rate	per time
β	the level of interaction of susceptible individuals with infected individuals	per time
α	death rate due to disease for infected individuals	per time
α_1	death rate due to disease for individuals isolated in Hospital	per time
α_2	disease mortality rates for individuals isolated at home	per time
δ_1	level of isolation in Hospital for infected individuals	per time
δ_2	level of self-isolation at home for infected individuals	per time
γ	recovery rate of infected individuals without isolation/asymptomatic people	per time
ε_1	recovery rate of individuals isolated in hospital	per time
ε_2	recovery rate of individuals isolated at home	per time

Susceptible individuals can become infected individuals due to direct contact with infected individuals at a rate of β. Infected individuals will undergo isolation in hospitals or self-isolate at a rate of $\delta_1$and δ_2. Each compartment will experience natural death and birth at a rate equal to $\mu$and A. Deaths that occurred due to COVID-19 occurred in hospital isolation compartments and self-isolation respectively amounting to $\alpha_1$and α_2. Individuals who isolate themselves in hospitals or self-isolate can recover from COVID-19 by $\varepsilon_1$and ε_2. So the scheme for spreading the COVID-19 disease by isolating in hospitals and self-isolating is as follows.

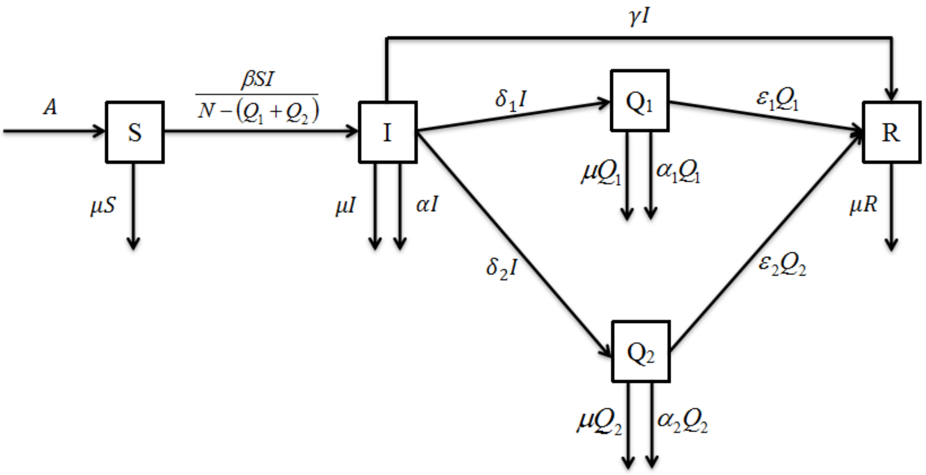


Figure 1. COVID-19 Epidemic Model Diagram with Isolation

Based on **Figure 1**, the spread of COVID-19 with isolation can be modeled into the following system of nonlinear ordinary differential equations:

$$\frac{dS}{dt} = A - \frac{\beta SI}{S+I+R} - \mu S$$
$$\frac{dI}{dt} = \frac{\beta SI}{S+I+R} - (\gamma + \delta_1 + \delta_2 + \mu + \alpha)I$$

$$\begin{aligned}\frac{dQ_1}{dt} &= \delta_1 I - (\varepsilon_1 + \mu + \alpha_1)Q_1 \\ \frac{dQ_2}{dt} &= \delta_2 I - (\varepsilon_2 + \mu + \alpha_2)Q_2 \\ \frac{dR}{dt} &= \gamma I + \varepsilon_1 Q_1 + \varepsilon_2 Q_2 - \mu R\end{aligned} \tag{1}$$

with $N = S + I + R + Q_1 + Q_2$the variables and parameters used explained in **Table 1** and **Table 2**. The rate of change in the total number of individuals is obtained by adding up the five equations in System (1) that is.

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dQ_1}{dt} + \frac{dQ_2}{dt} + \frac{dR}{dt}$$
$$\Leftrightarrow \frac{dN}{dt} = A - \mu N - \alpha I - \alpha_1 Q_1 - \alpha_2 Q_2.$$

Next, a positive invariant region is defined that satisfies System (1), namely

$$\Omega = \left\{(S, I, Q_1, Q_2, R) \in \Re_+^5 : S + I + Q_1 + Q_2 + R \leq \frac{A}{\mu}\right\}.$$

is a closed set of domains of System (1).

3.2 Model Analysis

Model analysis is carried out by analyzing the stability of the model equilibrium point. The equilibrium point is reached when$\frac{dS}{dt} = 0, \frac{dI}{dt} = 0, \frac{dQ_1}{dt} = 0, \frac{dQ_2}{dt} = 0,$ dan $\frac{dR}{dt} = 0$ [23].

$$A - \frac{\beta SI}{S + I + R} - \mu S = 0 \tag{2}$$

$$\frac{\beta SI}{S + I + R} - (\gamma + \delta_1 + \delta_2 + \mu + \alpha)I = 0 \tag{3}$$

$$\delta_1 I - (\varepsilon_1 + \mu + \alpha_1)Q_1 = 0 \tag{4}$$

$$\delta_2 I - (\varepsilon_2 + \mu + \alpha_2)Q_2 = 0 \tag{5}$$

$$\gamma I + \varepsilon_1 Q_1 + \varepsilon_2 Q_2 - \mu R = 0 \tag{6}$$

The disease-free equilibrium point is the equilibrium point when there is no disease in the population. This means that the number of infected and infectious individuals, the number of individuals isolated in hospitals, the number of individuals isolated at home, and the number of recovered individuals are zero ( ) $I = 0, Q_1 = 0, Q_2 = 0,$ dan $R = 0$.

Theorem 1. Disease-free equilibrium points System (1) viz$E_0 = \left(\frac{A}{\mu}, 0,0,0,0\right)$.

Proof. If the values $I = 0, Q_1 = 0, Q_2 = 0,$ dan $R = 0$are substituted into Equation (2) then it is obtained $A - \mu S = 0 \Leftrightarrow S = \frac{A}{\mu}$that a disease-free equilibrium point is obtained E_0, namely$E_0 = \left(\frac{A}{\mu}, 0,0,0,0\right)$

■

Theorem 2. System (1) has a basic reproduction number

$$R_0 = \frac{\beta}{\gamma + \delta_1 + \delta_2 + \mu + \alpha}.$$

Proof. The basic reproduction number (R 0) is determined using *the next generation matrix method* . [24], [25]Given the model in **System (1)** . Derivation of the basic reproduction ratio number is carried out by first grouping subpopulations into compartments $\boldsymbol{x}=\begin{pmatrix} I \\ Q_1 \\ Q_2 \end{pmatrix}$so that $\boldsymbol{y}=\begin{pmatrix} S \\ R \end{pmatrix}$a $\frac{dy}{dt}=\begin{bmatrix} A-\frac{\beta SI}{S+I+R}-\mu S \\ \gamma I+\varepsilon_1 L_1+\varepsilon_2 L_2-\mu R \end{bmatrix}$.compartment model can be formed$\frac{dx}{dt}=\begin{bmatrix} \frac{\beta SI}{S+I+R}-(\gamma+\delta_1+\delta_2+\mu+\alpha)I \\ \delta_1 I-(\varepsilon_1+\mu+\alpha_1)L_1 \\ \delta_2 I-(\varepsilon_2+\mu+\alpha_2)L_2 \end{bmatrix}$

Furthermore,

$$\frac{dx}{dt}=F(\boldsymbol{x},\boldsymbol{y})-V(\boldsymbol{x},\boldsymbol{y}) \Leftrightarrow \frac{dx}{dt}=\begin{bmatrix} \frac{\beta SI}{S+I+R} \\ \delta_1 I \\ \delta_2 I \end{bmatrix}-\begin{bmatrix} (\gamma+\delta_1+\delta_2+\mu+\alpha)I \\ (\varepsilon_1+\mu+\alpha_1)L_1 \\ (\varepsilon_2+\mu+\alpha_2)L_2 \end{bmatrix}$$

by Fstating new infections that occur and Vstating disease progression, death, isolation, and recovery. So, obtained $F(\boldsymbol{x},\boldsymbol{y})=\begin{bmatrix} F_1(\boldsymbol{x},\boldsymbol{y}) \\ F_2(\boldsymbol{x},\boldsymbol{y}) \\ F_3(\boldsymbol{x},\boldsymbol{y}) \end{bmatrix}=\begin{bmatrix} \frac{\beta SI}{S+I+R} \\ \delta_1 I \\ \delta_2 I \end{bmatrix}$and $V(\boldsymbol{x},\boldsymbol{y})=\begin{bmatrix} V_1(\boldsymbol{x},\boldsymbol{y}) \\ V_2(\boldsymbol{x},\boldsymbol{y}) \\ V_3(\boldsymbol{x},\boldsymbol{y}) \end{bmatrix}=\begin{bmatrix} (\gamma+\delta_1+\delta_2+\mu+\alpha)I \\ (\varepsilon_1+\mu+\alpha_1)L_1 \\ (\varepsilon_2+\mu+\alpha_2)L_2 \end{bmatrix}$so

$$J_{1_{(x,y)}}=\begin{bmatrix} \frac{\beta S(S+I+R)-\beta SI}{(S+I+R)^2} & 0 & 0 \\ \delta_1 & 0 & 0 \\ \delta_2 & 0 & 0 \end{bmatrix}$$

And

$$J_{2_{(x,y)}}=\begin{bmatrix} \gamma+\delta_1+\delta_2+\mu+\alpha & 0 & 0 \\ 0 & \varepsilon_1+\mu+\alpha_1 & 0 \\ 0 & 0 & \varepsilon_2+\mu+\alpha_2 \end{bmatrix}.$$

Disease-free equilibrium point System (1) is $E_0=(S^*,I^*,Q_1{}^*,Q_2{}^*,R^*)=\left(\frac{A}{\mu},0,0,0,0\right)$so that the matrix $F$and V:

$$F=J_{1_{(E_0)}}=\begin{bmatrix} \beta & 0 & 0 \\ \delta_1 & 0 & 0 \\ \delta_2 & 0 & 0 \end{bmatrix}$$

And

$$V=J_{2_{(E_0)}}=\begin{bmatrix} \gamma+\delta_1+\delta_2+\mu+\alpha & 0 & 0 \\ 0 & \varepsilon_1+\mu+\alpha_1 & 0 \\ 0 & 0 & \varepsilon_2+\mu+\alpha_2 \end{bmatrix}.$$

The next generation matrix of System (1) is

$$M=FV^{-1}=\begin{bmatrix} \frac{\beta}{\gamma+\delta_1+\delta_2+\mu+\alpha} & 0 & 0 \\ \frac{\delta_1}{\gamma+\delta_1+\delta_2+\mu+\alpha} & 0 & 0 \\ \frac{\delta_2}{\gamma+\delta_1+\delta_2+\mu+\alpha} & 0 & 0 \end{bmatrix}.$$

The eigenvalues of the matrix $M$are obtained from the following Equation.

$$det(M-\lambda I)=0$$

$$\Leftrightarrow \left(\frac{\beta}{\gamma+\delta_1+\delta_2+\mu+\alpha}-\lambda\right)\lambda^2=0$$

So that the eigenvalues of the matrix are obtained, Mnamely $\lambda_1=0$, $\lambda_2=0$, and $\lambda_3=\frac{\beta}{\gamma+\delta_1+\delta_2+\mu+\alpha}$. The basic reproduction number value is obtained from the matrix spectral radius$M$, $\rho(M)$that is

$\rho(M) = maks\,\{\lambda_1, \lambda_2, \lambda_3\} = maks\,\left\{0{,}0, \frac{\beta}{\gamma+\delta_1+\delta_2+\mu+\alpha}\right\} = \frac{\beta}{\gamma+\delta_1+\delta_2+\mu+\alpha}$.Thus, the value of the basic reproduction ratio number for System (1) is obtained, namely

$$R_0 = \frac{\beta}{\gamma + \delta_1 + \delta_2 + \mu + \alpha}.$$

■

Theorem 3. If $R_0 > 1$ then System (1) has an endemic equilibrium point$E_1 = (S^*, I^*, {Q_1}^*, {Q_2}^*, R^*)$

$$S^* = \frac{A}{\mu} - \frac{\gamma + \delta_1 + \delta_2 + \mu + \alpha}{\mu} I^*$$

$$I^* = \frac{(\beta - m)Ar}{m[(\mu + \gamma + (1-m))r + \varepsilon_1\delta_1(\varepsilon_2 + \mu + \alpha_2) + \varepsilon_2\delta_2(\varepsilon_1 + \mu + \alpha_1)]}.$$

$$Q_1^* = \frac{\delta_1}{\varepsilon_1 + \mu + \alpha_1} I^*$$

$$Q_2^* = \frac{\delta_2}{\varepsilon_2 + \mu + \alpha_2} I^*$$

$$R^* = \left(\frac{\gamma}{\mu} + \frac{\varepsilon_1\delta_1}{\mu(\varepsilon_1 + \mu + \alpha_1)} + \frac{\varepsilon_2\delta_2}{\mu(\varepsilon_2 + \mu + \alpha_2)}\right) I^*$$

with $m = \gamma + \delta_1 + \delta_2 + \mu + \alpha$and $r = (\varepsilon_1 + \mu + \alpha_1)(\varepsilon_2 + \mu + \alpha_2)$.

.

Proof. The endemic equilibrium point is the equilibrium point when there is a disease and the disease causes an epidemic in the population, so that $I$the disease endemic equilibrium point is obtained, namely $I^* > 0$. Based on **Equation (2)**, it is obtained

$$\frac{\beta SI}{S + I + R} = A - \mu S. \tag{7}$$

From **Equation (3)** it is obtained

$$\frac{\beta SI}{S + I + R} = (\gamma + \delta_1 + \delta_2 + \mu + \alpha)I. \tag{8}$$

From **Equation (7)** and **Equation (8)** obtained

$$S = \frac{A}{\mu} - \frac{\gamma + \delta_1 + \delta_2 + \mu + \alpha}{\mu} I. \tag{9}$$

From **Equation (4)** obtained

$$Q_1 = \frac{\delta_1}{\varepsilon_1 + \mu + \alpha_1} I. \tag{10}$$

From **Equation (5)** obtained

$$Q_2 = \frac{\delta_2}{\varepsilon_2 + \mu + \alpha_2} I. \tag{11}$$

Substitution of **Equation (10)** and **Equation (11)** to **Equation (6)** obtained

$$R = \left(\frac{\gamma}{\mu} + \frac{\varepsilon_1\delta_1}{\mu(\varepsilon_1 + \mu + \alpha_1)} + \frac{\varepsilon_2\delta_2}{\mu(\varepsilon_2 + \mu + \alpha_2)}\right) I. \tag{12}$$

Substitution of **Equation (9)** and **Equation (12)** to **Equation (8)** obtained

$$\frac{\beta\left(\frac{A}{\mu} - \frac{\gamma + \delta_1 + \delta_2 + \mu + \alpha}{\mu} I\right) I}{\left(\frac{A}{\mu} - \frac{\gamma + \delta_1 + \delta_2 + \mu + \alpha}{\mu} I\right) + I + \left(\frac{\gamma}{\mu} + \frac{\varepsilon_1\delta_1}{\mu(\varepsilon_1 + \mu + \alpha_1)} + \frac{\varepsilon_2\delta_2}{\mu(\varepsilon_2 + \mu + \alpha_2)}\right) I} = (\gamma + \delta_1 + \delta_2 + \mu + \alpha)I.$$

For example $m = \gamma + \delta_1 + \delta_2 + \mu + \alpha$so

$$\frac{\beta\left(\frac{A}{\mu} - \frac{m}{\mu} I\right) I}{\left(\frac{A}{\mu} - \frac{m}{\mu} I\right) + I + \left(\frac{\gamma}{\mu} + \frac{\varepsilon_1\delta_1}{\mu(\varepsilon_1 + \mu + \alpha_1)} + \frac{\varepsilon_2\delta_2}{\mu(\varepsilon_2 + \mu + \alpha_2)}\right) I} = mI$$

$$\Leftrightarrow I = (\beta - m)\frac{A}{m}\left[\frac{r}{\mu r + \gamma r + \varepsilon_1\delta_1(\varepsilon_2 + \mu + \alpha_2) + \varepsilon_2\delta_2(\varepsilon_1 + \mu + \alpha_1) + (1 - m)r}\right]$$

with $r = (\varepsilon_1 + \mu + \alpha_1)(\varepsilon_2 + \mu + \alpha_2)$so

$$I = (\beta - m)\frac{A}{m}\left[\frac{r}{\mu r + \gamma r + \varepsilon_1\delta_1(\varepsilon_2 + \mu + \alpha_2) + \varepsilon_2\delta_2(\varepsilon_1 + \mu + \alpha_1) + (1 - m)r}\right]$$

$$\Leftrightarrow I = \frac{(\beta - m)Ar}{m\left[\big(\mu + \gamma + (1 - m)\big)r + \varepsilon_1\delta_1(\varepsilon_2 + \mu + \alpha_2) + \varepsilon_2\delta_2(\varepsilon_1 + \mu + \alpha_1)\right]}. \quad (13)$$

Based on **Equation (9)**, **Equation (10)**, **Equation (11)**, **Equation (12)**, and **Equation (13)** The endemic equilibrium point is obtained E_1, namely $E_1 = (S^*, I^*, {Q_1}^*, {Q_2}^*, R^*)$with

$$S^* = \frac{A}{\mu} - \frac{\gamma + \delta_1 + \delta_2 + \mu + \alpha}{\mu} I^*$$

$$I^* = \frac{(\beta - m)Ar}{m\left[(\mu + \gamma + (1 - m))r + \varepsilon_1\delta_1(\varepsilon_2 + \mu + \alpha_2) + \varepsilon_2\delta_2(\varepsilon_1 + \mu + \alpha_1)\right]}.$$

$$Q_1^* = \frac{\delta_1}{\varepsilon_1 + \mu + \alpha_1} I^* \quad (14)$$

$$Q_2^* = \frac{\delta_2}{\varepsilon_2 + \mu + \alpha_2} I^*$$

$$R^* = \left(\frac{\gamma}{\mu} + \frac{\varepsilon_1\delta_1}{\mu(\varepsilon_1 + \mu + \alpha_1)} + \frac{\varepsilon_2\delta_2}{\mu(\varepsilon_2 + \mu + \alpha_2)}\right) I^*$$

The existence of an equilibrium point is indicated by each element being positive according to the conditions for establishing this model. It is noticed that Q_1^*, Q_2^*,and R^* at the equilibrium point$E_1 = (S^*, I^*, {Q_1}^*, {Q_2}^*, R^*)$ System (14) is positive if and only if it I^* is positive, so it needs to be shown $I^* > 0$. Noticed

$$\begin{aligned} I^* &= \frac{(\beta - m)Ar}{m\left[\big(\mu + \gamma + (1 - m)\big)r + \varepsilon_1\delta_1(\varepsilon_2 + \mu + \alpha_2) + \varepsilon_2\delta_2(\varepsilon_1 + \mu + \alpha_1)\right]} \\ &= \frac{\left(\frac{\beta}{m} - 1\right)Ar}{\big(\mu + \gamma + (1 - m)\big)r + \varepsilon_1\delta_1(\varepsilon_2 + \mu + \alpha_2) + \varepsilon_2\delta_2(\varepsilon_1 + \mu + \alpha_1)} \\ &= \frac{(R_0 - 1)Ar}{\big(\mu + \gamma + (1 - m)\big)r + \varepsilon_1\delta_1(\varepsilon_2 + \mu + \alpha_2) + \varepsilon_2\delta_2(\varepsilon_1 + \mu + \alpha_1)} \end{aligned}$$

Note that all parameters used are positive and $R_0 > 1$hence $I^* > 0$. It is proven that if $R_0 > 1$then $I^* > 0$.

■

Theorem 4 . If $R_0 < 1$then the equilibrium point $E_0$is locally asymptotically stable.

Proof. The COVID-19 epidemic model with isolation in System (1) is a nonlinear system. Analysis of model behavior is carried out by first forming the Jacobian matrix resulting from the linearization of System (1) around the equilibrium point [23]. The Jacobian matrix is the result of linearizing the model around the equilibrium point $E_0 = \left(\frac{A}{\mu}, 0,0,0,0\right)$, namely

$$J_{\left(\frac{A}{\mu},0,0,0,0\right)} = \begin{bmatrix} -\mu & -\beta & 0 & 0 & 0 \\ 0 & \beta - (\gamma + \delta_1 + \delta_2 + \mu + \alpha) & 0 & 0 & 0 \\ 0 & \delta_1 & -(\varepsilon_1 + \mu + \alpha_1) & 0 & 0 \\ 0 & \delta_2 & 0 & -(\varepsilon_2 + \mu + \alpha_2) & 0 \\ 0 & \gamma & \varepsilon_1 & \varepsilon_2 & -\mu \end{bmatrix} \quad (15)$$

The characteristic equation for $J_{\left(\frac{A}{\mu},0,0,0,0\right)}$is

$$(-\mu-\lambda)(-\mu-\lambda)(-(\varepsilon_2+\mu+\alpha_2)-\lambda)(\beta-(\gamma+\delta_1+\delta_2+\mu+\alpha)-\lambda)(-(\varepsilon_1+\mu+\alpha_1)-\lambda)=0.$$

So we get the eigenvalues $\lambda_1=-\mu$, $\lambda_2=-\mu$, $\lambda_3=-(\varepsilon_2+\mu+\alpha_2)$, $\lambda_4=\beta-(\gamma+\delta_1+\delta_2+\mu+\alpha)$, and $\lambda_3=-(\varepsilon_1+\mu+\alpha_1)$.

Note that the parameter values $\mu,\varepsilon_2,\alpha_2,\beta,\gamma,\delta_1,\delta_2,\alpha,\varepsilon_1,\alpha_1>0$are so clear $\lambda_1<0,\lambda_2<0,\lambda_3<0$,and $\lambda_5<0$.Next

$$\lambda_4=\beta-(\gamma+\delta_1+\delta_2+\mu+\alpha)=\frac{\beta}{\gamma+\delta_1+\delta_2+\mu+\alpha}-1=R_0-1,$$

value is obtained $\lambda_4<0$if $R_0<1$.Because the sign of the five eigenvalues of Characteristic Equation **(15)** is negative then the disease-free equilibrium point $E_0$is locally asymptotically stable if$R_0<1$. ■

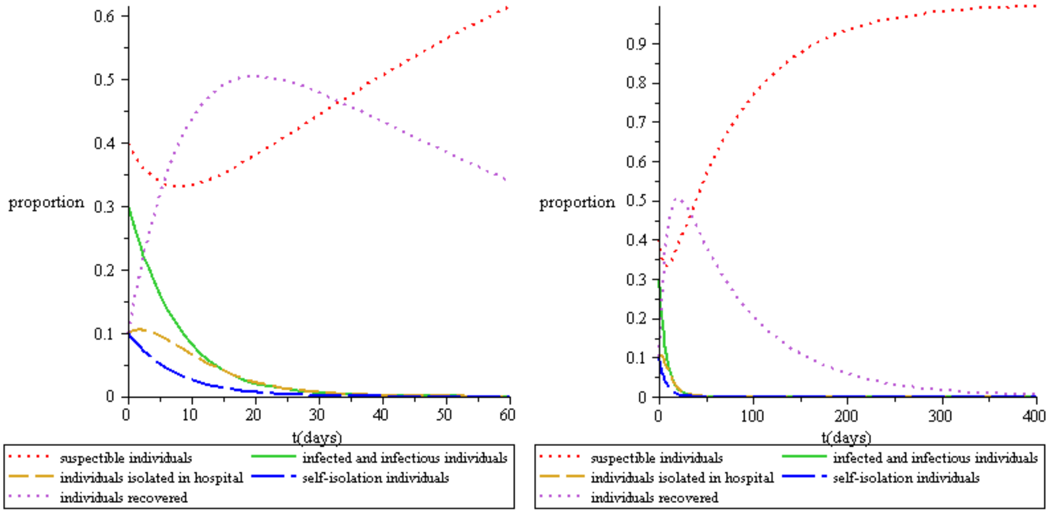
3.3 Model Simulation

The simulation model for the spread of Covid-19 disease with isolation was carried out using parameters from several studies which are presented in **Table 3**.

Table 3 . Parameter Values for Numerical Simulation of the Spread of COVID-19

No	Parameter	Mark	Reference
1.	A	0.0126	[26]
2.	μ	0.0126	[26]
3.	β	0.2	[27]
4.	α	0.015	[28]
5.	α_1	0.025	[28]
6.	α_2	0.015	[28]
7.	δ_1	0.084	[27]
8.	δ_2	0.0039798	[29]
9.	γ	0.099087	[30]
10.	ε_1	0.155	[28]
11.	ε_2	0.11624	[28]

Simulation results using Maple 2018 software and based on the parameters in **Table 3** as well as the initial values $S(0)=0{,}4$; $I(0)=0{,}3$; $Q_1(0)=0{,}1$; $Q_2(0)=0{,}1$; $R(0)=0{,}1$obtained $\mathcal{R}_0=0.9315381513$ and presented in the following image.

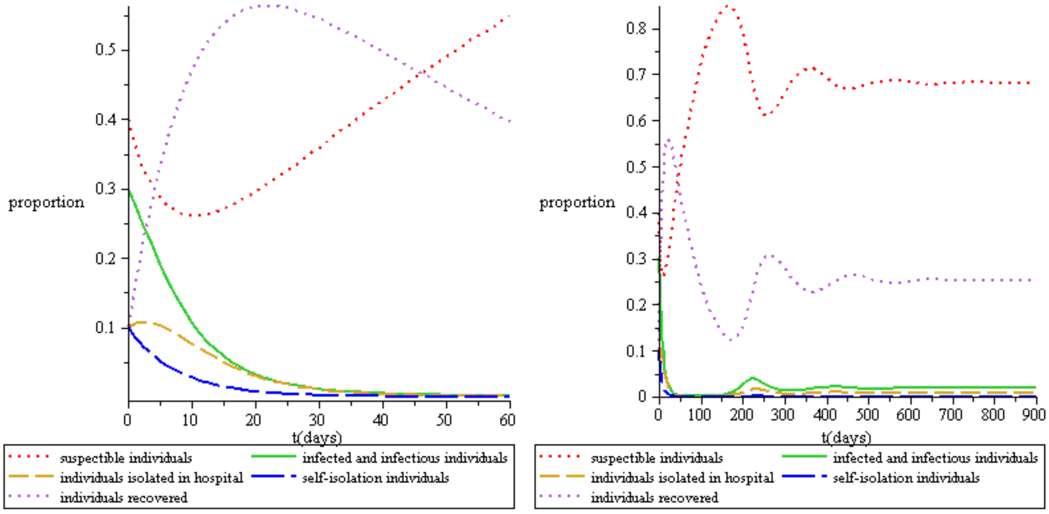


(a) **(b)**

Figure 2 . System Simulation (1) Disease-Free Equilibrium Point E_0,(a)t = 1-60 days, (b) t = 1-400 days

Based on **Figure 2** , the number of susceptible individuals initially decreased but after the 10th day it increased until on the 400th day it reached point 1 and stabilized at that point. The number of infected individuals, hospital isolated individuals and self-isolated individuals decreased, until on the 60th day together they reached point 0 and stabilized at that point. The number of individuals recovering from COVID-19 in the first 15 days increased but thereafter decreased until on the 100th day it reached point 0 and stabilized at that point. The conclusion that can be obtained from this simulation is that the disease will disappear from the population after the 60th day and if $R_0 < 1$, this result is in accordance with **Theorem 4** which was previously established.

Next, a simulation is carried out for ($R_0 > 1$). If the parameters in **Table 3** are used and the parameters $\beta$are enlarged to 0,3, then the initial reproduction number of System (1) is $R_0 = 1.397307227$. If the initial value $S(0) = 0{,}4$; $I(0) = 0{,}3$; $Q_1(0) = 0{,}1$; $Q_2(0) = 0{,}1$; $R(0) = 0{,}1$is obtained, a numerical simulation is obtained, **Figure 3** following.



(a) **(b)**

Figure 3. System Simulation (1) Endemic Equilibrium Point E_1, (a)t = 1-60 days, (b) t = 1-900 days

Based on **Figure 3** , the number of susceptible individuals initially increased in the first 150 days but then fluctuated up and down until it reached a stable point at 0.7 on the 600th day. The number of infected individuals, hospital isolated individuals and self-isolated individuals decreased, until on the 60th day together they reached point 0, but there was an increase again and reached a peak on the 225th and 400th days. After that, the number of infected individuals, hospital isolated individuals and self-isolated individuals decreased and stabilized on the 600th consecutive day, stable at 0.005; 0.002; and 0.0001. The conclusion that can be obtained from this simulation is that the disease will persist in the population if $R_0 > 1$. This result is in accordance with Theorem 2 that if $R_0 > 1$an endemic equilibrium point appears.

3.4 Basic Reproduction Number Sensitivity Analysis

Based on **Theorem 4** and the results of numerical simulations, it is concluded that the disease will disappear from the population if the value $R_0 < 1$, in addition, based on **Theorem 1** and the numerical results shows that the condition is endemic or the disease is endemic if $R_0 > 1$. This shows that value $R_0$is very influential in the spread of the COVID-19 disease, therefore it is necessary to analyze which parameters influence the value R_0. So in this section, the sensitivity index for each model parameter is calculated which is correlated with the basic reproduction number R_0. This index provides information about the importance of each parameter in the model representing the spread of the COVID-19 disease. The index is used to identify parameters that have the most significant influence on R_0those that are then used as intervention targets. Parameters with a high impact R_0indicate that these parameters have a dominant influence on the spread of the COVID-19 disease. Sensitivity analysis of the basic reproduction number was calculated using the approach by **[31]**. The sensitivity index $R_0$for the parameters in this study will be looked for, namely in **Table 1**.

The following is an example of calculating the sensitivity index $R_0$for parameters γ, for other parameters it is analogous

$$C_{\gamma}^{R_0} = \frac{\partial R_0}{\partial \gamma} \times \frac{\gamma}{R_0} = -\frac{\beta}{(\gamma+\delta_1+\delta_2+\mu+\alpha)^2} \times \frac{\gamma(\gamma+\delta_1+\delta_2+\mu+\alpha)}{\beta} = -\frac{\gamma}{\gamma+\delta_1+\delta_2+\mu+\alpha}.$$

The following table shows the sensitivity of the parameter index to the basic reproduction number.

Table 4. Sensitivity of Parameter Index toR_0

No.	Parameter	Sensitivity Index
1.	β	+1.000000000
2.	γ	-0.4615166040
3.	δ_1	-0.3912460236
4.	α	-0.06986536136
5.	μ	-0.05883533343
6.	δ_2	-0.01853667767

Table 4 shows the sensitivity of the parameter index to the spread of disease (R_0) from the most influential to the least influential. In general, there are three parameters that have a dominant influence R_0, namely the level of interaction between susceptible individuals and infected individuals (β), the recovery rate for infected individuals without isolation/people without symptoms (γ), and the level of isolation in hospitals for infected individuals (δ_1). Furthermore, there are three parameters whose influence is not very significant, namely the death rate due to disease for infected individuals (α), the natural death rate (μ), and the level of self-isolation at home for infected individuals (δ_2).

A parameter βhas a positive sensitivity index, which means that an increase in the parameter value βcontributes to an increase in the value R_0or vice versa, provided that the other parameters are constant. Index sensitivity $C_{\beta}^{R_0} = +1$means that an increase (or decrease) in the parameter value, $\beta$for example 10%, results in an increase (or decrease) in the value $R_0$of 10%. The other five parameters , namely , δ_1, α, μ, and $\delta_2$have negative sensitivity, meaning that an increase in the parameter value contributes to a decrease in value R_0or vice versa, provided that the other parameters are constant. Index sensitivity $C_{\gamma}^{\mathcal{R}_0} = -0.461516604$means that an increase (or decrease) in the parameter value, $\gamma$for example 10%, results in a decrease (or increase) in the value $R_0$of 4.61%.

Based on the model analysis and sensitivity analysis in this research, recommendations can be prepared so that the COVID-19 disease disappears or does not become an epidemic, namely:

1. Reducing the level of contact between infected individuals and susceptible individuals (β). For example, by avoiding crowds, wearing a mask when leaving the house, maintaining distance, and limiting people's mobility.
2. Increasing the recovery rate of infected individuals without isolation/asymptomatic people (γ). For example, by carrying out massive tracing of people who have contact with positive COVID-19 patients so that people without symptoms can be identified and isolated and their recovery accelerated.
3. Increase the level of isolation of COVID-19 patients, either self-isolation (δ_2) or treatment in hospital (δ_1). This needs to be done so that the patient does not infect people around him.

4. CONCLUSIONS

Based on the research results, the following conclusions were obtained:

1. The mathematical model of the spread of COVID-19 disease with self-isolation and isolation in hospitals is a system of nonlinear differential equations that has one equilibrium point free disease $E_0 = \left(\frac{A}{\mu}, 0,0,0,0\right)$. Point equilibrium it has local asymptotic stability when $R_0 < 1$. This model also has one point equilibrium endemic $E_1 = \left(S^*, I^*, Q_1^*, Q_2^*, R^*\right)$existing _ If $R_0 > 1$.

2. Based on the sensitivity analysis of the basic reproduction number, it was found that the influencing parameters were the level of interaction between susceptible individuals and infected individuals, the recovery rate for infected individuals without isolation/people without symptoms, and the level of isolation in hospitals for infected individuals. The value of sensitivity analysis for the isolation rate of individually infected individuals in hospitals is -0.4615166040, and the self-isolation rate at home is -0.01853667767. This indicates that isolation in hospitals is more effective than self-isolation in suppressing the spread of COVID-19.
3. Based on analysis of the stability of the equilibrium point and numerical simulations, it is concluded that the disease will disappear from the population if$R_0 < 1$ and will persist in the population if $R_0 > 1$. Recommendations so that the COVID-19 disease disappears or does not become an epidemic, namely reducing the level of contact between infected individuals and susceptible individuals by avoiding crowds, wearing masks when leaving the house, maintaining distance, and limiting community mobility; increasing the recovery rate for infected individuals without isolation/people without symptoms by carrying out massive tracing of people who have contact with positive COVID-19 patients so that people without symptoms can be identified and can be isolated and their recovery accelerated; as well as increasing the level of isolation of COVID-19 patients, whether self-isolating or being treated in hospital so that these patients do not infect people around them.

ACKNOWLEDGMENT

We would like to express our gratitude to the Research and Publishing Center (Puslitpen) of UIN Syarif Hidayatullah Jakarta and University of Singaperbangsa Karawang for their support in this research.

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