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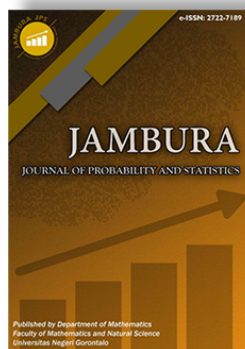
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Dynamics of Covid-19 model with public awareness, quarantine, and isolation

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ABSTRACT. This paper presents a new COVID-19 model that contains public awareness, quarantine, and isolation. The model includes eight compartments: susceptible aware (SA), susceptible unaware (SU), exposed (E), asymptomatic infected (A), symptomatic infected (I), recovered (R), quarantined (Q), and isolated (J). The introduction will be shown in the first section, followed by the model simulation. The equilibrium points, basic reproduction number, and stability of the equilibrium points are then determined. The model has two equilibrium points: disease-free equilibrium point and endemic equilibrium point. The next generation matrix is used to calculate the basic reproduction number R_0 . The disease-free equilibrium point always exists and is locally stable if $R_0 < 1$, whereas the endemic equilibrium point exists when $R_0 > 1$ and is locally stable if satisfying the Routh-Hurwitz criterion. Stability properties of the equilibrium confirmed by numerical simulation also show that quarantine rate and isolation rate have an impact in the transmission of COVID-19.



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1. Introduction

Corona Virus or we known as COVID-19 was an international concern, especially WHO. This disease that attacks the respiratory system affects various countries. In some severe cases, the infection can cause pneumonia, acute respiratory syndrome, kidney failure, and even death [1]. This disease was caused by coronavirus 2 (SARS-CoV-2), which originated in a wet market in Wuhan, China. Since 17 January 2020, the reported cases have increased significantly. The COVID-19 pandemic has caused a global crisis with 47,209,305 confirmed cases and 1,209,505 deaths worldwide as of 2 November 2020 [2]. Due to the large number of cases that have occurred, it is necessary to study the mechanism of COVID-19 transmission.

COVID-19 can be transmitted through liquid splashes when an infected individual coughs, sneezes, or talks [3]. COVID-19 poses a serious threat to the health and safety of people around the world. There are two actions to mitigate the virus. The first is to forecast daily confirmed cases so that the health system can efficiently manage the pandemic, such as testing and treating large numbers of confirmed patients. The next considered step is to understand the dynamics of disease spread so that public health professionals can effectively implement control estimates to slow the rapid growth of infection [4]. A mathematical model can be applied to find out the dynamics of the spread of the disease.

Mathematical modeling is a tool that can be applied to study dynamic phenomena [5]. In this case, mathematical modeling can help solve the COVID-19 problem. Through mathematical

modeling, the relationship between COVID-19 transmission and it is possible to identify a variety of epidemiological parameters that can aid in effective control [6]. The epidemic model commonly used in analyzing the spread of disease is the SIR model introduced by Kermack and Kedrick (1927), which divides the human population into several groups of individuals, namely susceptible individuals, infected individuals, and recovered individuals. Based on several previous studies, Fosu et al. [7] modeled the SIR implemented in Ghana and demonstrated that in an endemic state, it would take a maximum of 120 days for the entire cohort to transfer to the recovered compartment [7].

Efforts to reduce the rate of transmission of COVID-19 can be made by maintaining physical distance, using masks, washing hands, and limiting the entry of newcomers. Even so, the rate of spread of COVID-19 continues to increase. The current development of COVID-19 is the discovery of infected people who are not diagnosed but can transmit the infection to others [8]. Chen et al. [8] pointed out the need for several interventions to control the spread of COVID-19. Therefore a strategy is needed to stop interactions between individuals so that the transmission rate gets smaller, namely by carrying out quarantine. Memon et al. [9] demonstrate that the COVID-19 pandemic can be effectively managed through isolation and quarantine [9]. The goal of quarantine is to keep people who have been exposed to COVID-19 apart, even if they are still in the incubation period or have not yet manifested any symptoms. To lessen the risk of transmission, isolation involves keeping an infected person who needs COVID-19 treatment or someone who has been diagnosed with the disease apart from healthy individuals.

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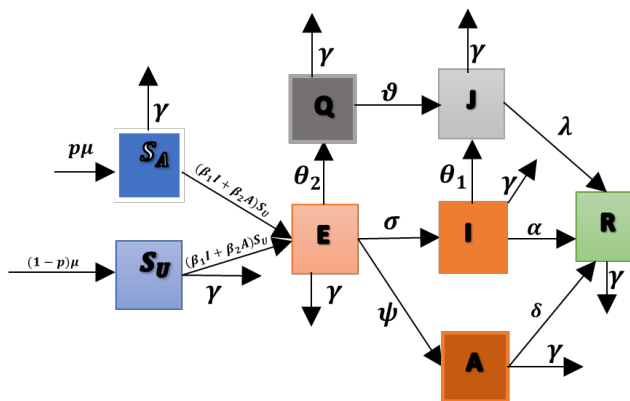


Figure 1. Diagram of COVID-19

COVID-19 also affects a nation’s economy, causing issues such as a shortage of jobs and difficulty supplying basic needs. Also, hospitals have trouble getting hold of necessities like test kits, ventilators, and personal protective equipment [10]. The model with implementation of the level of awareness for the Covid-19 disease shows that it can reduce the number of infected populations [11]. Yuan and Li [12] study the COVID-19 model by using susceptible individuals with protection awareness and susceptible individuals without protection awareness. Their research shows that awareness of human protection and willingness to take protective measures play an important role in controlling outbreaks [12]. Therefore, increasing awareness of self-protection is very important to prevent wider transmission. Thus, a COVID-19 model using public education, quarantine, and isolation is constructed in this paper.

We organize this paper as follows. In Section 2, we will show how to construct the COVID-19 model. Furthermore, the fixed point and local stability are investigated in Section 3. In Section 4, we calculate the sensitivity analysis of the basic reproduction number. Numerical simulations are carried out in Section 5 to validate analytical dynamics, and in the final section, we reach conclusions about our work.

2. Model Formulation

In this study, a COVID-19 model is constructed with public awareness, quarantine, and isolation. This model combines the research of Yuan and Li (2022) and Memon et al. (2021). Memon et al. (2021) constructed the COVID-19 model *SEIR* (Susceptible-Exposed-Infected-Recovered) by adding quarantine compartments (Q) and isolation (J). In this model, the quarantined individuals decrease from the exposed class, transferring individuals who are asymptomatic. The infected population occurs due to the development of COVID-19 by exposed individuals. The isolation group consists of infected individuals with symptoms and individuals who are quarantined but are getting worse. The isolation population is intended for medical treatment [8]. Memon et al. (2021) assume that individuals who have recovered tend to be vulnerable because there is no immunity to COVID-19 yet. Yuan and Li (2022) constructed the COVID-19 model *SEIR* (Susceptible-Exposed-Infected-Recovered) by dividing the infected population into infected with symptoms (I) and infected without symptoms (asymptomatic) (A).

The susceptible group (S) then divides into susceptible groups with protection awareness and those without protection awareness, becoming S_A and S_U . By raising public knowledge and implementing preventative measures, it is possible to successfully minimize contact with the disease’s cause and, in turn, indirectly control the disease’s occurrence [12].

This research contains the dependent variables $S_A(t)$, $S_U(t)$, $E(t)$, $I(t)$, $A(t)$, $Q(t)$, $J(t)$, and $R(t)$ respectively represent the size of the susceptible group with public awareness, the susceptible group without public awareness, the exposed group, the symptomatic infected, the asymptomatic infected, the quarantined group, the isolated group, and the recovered group. The parameters μ and γ are birth rates and death rates. The parameter p represents the proportion of susceptible groups with public awareness S_A and $1 - p$ without awareness. Susceptible groups with public awareness of S_A and S_U awareness can be infected with the virus at β_1 and β_2 rates, symptomatic infected and asymptomatic infected. Exposed individuals can quarantine at the rate of θ_2 . An exposed individual becomes an infected individual at σ for the symptomatic rate and ψ for the asymptomatic rate. The isolated group comes from quarantined individuals who are getting worse and symptomatic infected individuals. In this model, it is assumed that all individuals who have recovered will not return to susceptible individuals. The proposed model using eight compartments is shown in Figure 1.

The proposed model is expressed in a differential equations system (1).

$$\begin{aligned}
 S'_A(t) &= p\mu - (\beta_1 I + \beta_2 A)S_A - \gamma S_A, \\
 S'_U(t) &= (1 - p)\mu - (\beta_1 I + \beta_2 A)S_U - \gamma S_U, \\
 E'(t) &= (\beta_1 I + \beta_2 A)S_A + (\beta_1 I + \beta_2 A)S_U \\
 &\quad - (\gamma + \theta_2 + \sigma + \psi)E, \\
 I'(t) &= \sigma E - (\gamma + \theta_1 + \alpha)I, \\
 A'(t) &= \psi E - (\gamma + \delta)A, \\
 Q'(t) &= \theta_2 E - (\gamma + \vartheta)Q, \\
 J'(t) &= \vartheta Q + \theta_1 I - (\gamma + \lambda)J, \\
 R'(t) &= \alpha I + \delta A + \lambda J - \gamma R,
 \end{aligned}
 \tag{1}$$

with initial conditions $S_A(0) \geq 0$, $S_U(0) \geq 0$, $E(0) \geq 0$, $I(0) \geq 0$, $A(0) \geq 0$, $Q(0) \geq 0$, $J(0) \geq 0$, and $R(0) \geq 0$ are positive. To simplify the model (1), we use new symbols as $e_1 = \gamma + \theta_2 + \sigma + \psi$,

$e_2 = \gamma + \theta_1 + \alpha, e_3 = \gamma + \delta, e_4 = \gamma + \vartheta$, dan $e_5 = \gamma + \lambda$. Since the first seven equations do not depend on $R(t)$, we can reduce the eight-equations model (1) to the seven-equation model as follows

$$\begin{aligned} S'_A(t) &= p\mu - (\beta_1 I + \beta_2 A)S_A - \gamma S_A, \\ S'_U(t) &= (1-p)\mu - (\beta_1 I + \beta_2 A)S_U - \gamma S_U, \\ E'(t) &= (\beta_1 I + \beta_2 A)S_A + (\beta_1 I + \beta_2 A)S_U - e_1 E, \\ I'(t) &= \sigma E - e_2 I, \\ A'(t) &= \psi E - e_3 A, \\ Q'(t) &= \theta_2 E - e_4 Q, \\ J'(t) &= \vartheta Q + \theta_1 I - e_5 J, \end{aligned} \tag{2}$$

with initial conditions $S_A(0) \geq 0, S_U(0) \geq 0, E(0) \geq 0, I(0) \geq 0, A(0) \geq 0, Q(0) \geq 0$, and $J(0) \geq 0$ are positive. Furthermore, we investigate the dynamics of model COVID-19, such as the existence of equilibrium points, basic reproduction number, local stability of equilibrium points, and numerical simulations.

3. Equilibrium Point and Basic Reproduction Number

In this section, we determine the equilibrium point and basic reproduction number. The equilibrium point is obtained by making the right-hand side of the equation in the model (2) equal to zero. Then the third equation of model (2) can be written as

$$E'(t) = \left(\beta_1 \frac{\sigma}{e_2} E + \beta_2 \frac{\psi}{e_3} E \right) S_A + \left(\beta_1 \frac{\sigma}{e_2} E + \beta_2 \frac{\psi}{e_3} E \right) S_U - e_1 E.$$

It is either $E = 0$ or

$$\left(\beta_1 \frac{\sigma}{e_2} + \beta_2 \frac{\psi}{e_3} \right) S_A + \left(\beta_1 \frac{\sigma}{e_2} + \beta_2 \frac{\psi}{e_3} \right) S_U = e_1.$$

Then it has two equilibrium points, a disease-free equilibrium point and an endemic equilibrium point. The disease-free equilibrium point is as follows

$$X_0 (S_A^0, S_U^0, E^0, I^0, A^0, Q^0, J^0) = \left(\frac{p\mu}{\gamma}, \frac{(1-p)\mu}{\gamma}, 0, 0, 0, 0, 0 \right).$$

The basic reproduction number (R_0) can be determined by using the next generation matrix technique. First, define $E(t), I(t), A(t), Q(t), J(t)$ as infected compartment. The next generation matrix denoted as $F(X_0)H^{-1}(X_0)$ where $F(X_0)$ is the Jacobian matrix of infected compartment and $H(X_0)$ respectively

$$F(X_0) = \begin{bmatrix} 0 & \frac{p\mu\beta_1}{\gamma} + \frac{(1-p)\mu\beta_1}{\gamma} & \frac{p\mu\beta_2}{\gamma} + \frac{(1-p)\mu\beta_2}{\gamma} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix},$$

and

$$H(X_0) = \begin{bmatrix} e_1 & 0 & 0 & 0 & 0 \\ -\sigma & e_2 & 0 & 0 & 0 \\ -\psi & 0 & e_3 & 0 & 0 \\ -\theta_2 & 0 & 0 & e_4 & 0 \\ 0 & -\theta_1 & 0 & 0 & e_5 \end{bmatrix}.$$

Then the next generation matrix is

$$F(X_0)H^{-1}(X_0) = \begin{bmatrix} \frac{\mu(\beta_1\sigma e_3 + \beta_2\psi e_2)}{\gamma e_1 e_2 e_3} & \frac{\mu\beta_1}{\gamma e_2} & \frac{\mu\beta_2}{\gamma e_3} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}.$$

The spectral radius of $F(X_0)H^{-1}(X_0)$ is the basic reproduction number (R_0)

$$R_0 = \frac{\mu(\beta_1\sigma e_3 + \beta_2\psi e_2)}{\gamma e_1 e_2 e_3}.$$

The second equilibrium point

$$X^* = (S_A^*, S_U^*, E^*, I^*, A^*, Q^*, J^*),$$

where

$$\begin{aligned} S_A^* &= \frac{p\mu e_2 e_3}{(\beta_1\sigma e_3 + \beta_2\psi e_2)E^* + \gamma e_2 e_3}, \\ S_U^* &= \frac{(1-p)\mu e_2 e_3}{(\beta_1\sigma e_3 + \beta_2\psi e_2)E^* + \gamma e_2 e_3}, \\ E^* &= \frac{\mu(R_0 - 1)}{e_1 R_0}, \quad I^* = \frac{\sigma}{e_2} E^*, \\ A^* &= \frac{\psi}{e_3} E^*, \quad Q^* = \frac{\theta_2}{e_4} E^*, \\ J^* &= \frac{\sigma\theta_1 e_4 + \theta_2\vartheta e_2}{e_2 e_4 e_5} E^*, \end{aligned}$$

where $E^* = \frac{\mu(\beta_1\sigma e_3 + \beta_2\psi e_2) - \gamma e_1 e_2 e_3}{\beta_1\sigma e_1 e_3 + \beta_2\psi e_1 e_2}$. Then endemic equilibrium point X^* exist when $R_0 > 1$.

4. Stability Analysis

The system (2) is a nonlinear autonomous system. Local stability from disease-free and endemic equilibrium points can be analyzed by linearization.

Results linearization of model (2), the Jacobian matrix at disease-free equilibrium point is given by

$$J(X_0) = \begin{bmatrix} -\gamma & 0 & 0 & -\beta_1 S_A & -\beta_2 S_A & 0 & 0 \\ 0 & -\gamma & 0 & -\beta_1 S_U & -\beta_2 S_U & 0 & 0 \\ 0 & 0 & -e_1 & \beta_1(S_A + S_U) & \beta_2(S_A + S_U) & 0 & 0 \\ 0 & 0 & \sigma & -e_2 & 0 & 0 & 0 \\ 0 & 0 & \psi & 0 & -e_3 & 0 & 0 \\ 0 & 0 & \theta_2 & 0 & 0 & -e_4 & 0 \\ 0 & 0 & 0 & \theta_1 & 0 & \vartheta & -e_5 \end{bmatrix}, \tag{3}$$

The eigenvalues of the Jacobian matrix $J(X_0)$ are $\lambda_{1,2} = -\gamma, \lambda_3 = -e_4, \lambda_4 = -e_5$, snf $\lambda_5, \lambda_6, \lambda_7$ are characteristic equation that can be written as

$$\lambda^3 + c_1\lambda^2 + c_2\lambda + c_3, \tag{4}$$

with $c_1 = e_1 + e_2 + e_3, c_2 = e_2 e_3 + e_1 e_2 (1 - R_1) + e_1 e_3 (1 - R_A), c_3 = e_1 e_2 e_3 (1 - R_0)$. Based on Routh-Hurwitz criteria, the real part of the root of the characteristic eq. (4) is negative if and only if all three conditions are met, yield $c_1 > 0, c_3 > 0$ and $c_1 c_2 - c_3 > 0$.

- $c_1 > 0$ because e_1, e_2, e_3 is positive.
- Since $R_0 < 1$, so that $e_1 e_2 e_3 (1 - R_0) > 0$.
- Since $R_0 < 1$, we get $R_1 < 1$ and $R_A < 1$. The result $c_1 c_2 - c_3 = (e_1 + e_2 + e_3)(e_2 e_3 + e_1 e_2 (1 - R_1) + e_1 e_3 (1 - R_A)) - e_1 e_2 e_3 (1 - R_0) > 0$.

If $R_0 < 1$, then each λ of the characteristic equation (4) has a negative real part which causes a locally asymptotically stable disease-free equilibrium point.

The second equilibrium using linearization of model (2) at the endemic equilibrium point is as follows.

$$J(X^*) = \begin{bmatrix} a_{11} & 0 & 0 & -\beta_1 S_A^* & -\beta_2 S_A^* & 0 & 0 \\ 0 & a_{22} & 0 & -\beta_1 S_U^* & -\beta_2 S_U^* & 0 & 0 \\ a_{31} & a_{32} & -e_1 & a_{33} & a_{34} & 0 & 0 \\ 0 & 0 & \sigma & -e_2 & 0 & 0 & 0 \\ 0 & 0 & \psi & 0 & -e_3 & 0 & 0 \\ 0 & 0 & \theta_2 & 0 & 0 & -e_4 & 0 \\ 0 & 0 & 0 & \theta_1 & 0 & \vartheta & -e_5 \end{bmatrix},$$

where $a_{11} = -\beta_1 I^* - \beta_2 A^* - \gamma$, $a_{22} = -\beta_1 I^* - \beta_2 A^* - \gamma$, $a_{31} = \beta_1 I^* + \beta_2 A^*$, $a_{32} = \beta_1 I^* + \beta_2 A^*$, $a_{33} = \beta_1 (S_A^* + S_U^*)$, and $a_{34} = \beta_2 (S_A^* + S_U^*)$. Then, the eigenvalues of the Jacobian matrix $J(X^*)$ are obtained, which are $\lambda_1 = -e_4$, $\lambda_2 = -e_5$, and $\lambda_3, \lambda_4, \lambda_5, \lambda_6, \lambda_7$ are the eigenvalues in the characteristic equation of $J(X^*)$ can be written as

$$\lambda^5 + c_1 \lambda^4 + c_2 \lambda^3 + c_3 \lambda^2 + c_4 \lambda + c_5, \tag{5}$$

with

$$\begin{aligned} c_1 &= 2\gamma R_0 + e_1 + e_2 + e_3, \\ c_2 &= 2\gamma R_0(e_1 + e_2 + e_3) + d + e_2 e_3 + e_1 e_2(1 - R_A) \\ &\quad + e_1 e_3(1 - R_A), \\ c_3 &= 2\gamma R_0(e_1 e_2 + e_2 e_3 + e_1 e_3) + d(e_1 + e_2 + e_3) \\ &\quad + e_1 e_2 e_3(1 - R_0 - \gamma R_0) - \gamma e_1 R_0(e_2 R_A + e_3 R_A), \\ c_4 &= 2\gamma R_0 e_1 e_2 e_3 + d(e_1 e_2 + e_1 e_3 + e_2 e_3) \\ &\quad - (\gamma e_1 + \gamma^2 e_1 R_0)(e_2 R_A + e_3 R_A) - \gamma e_1 e_2 e_3 R_0^2, \\ c_5 &= \gamma^2 e_1 e_2 e_3 R_0 (R_0 - 1), \end{aligned}$$

with

$$d = \frac{\gamma^2 R_0^2}{\mu} = \frac{\mu(\beta_1 \sigma e_3 + \beta_2 \psi e_2)^2}{e_1^2 e_2^2 e_3^2}.$$

According to the Routh-Hurwitz criterion, real values for each characteristic (5) are negative or only for $c_1 > 0$, $c_5 > 0$, $c_1 c_2 - c_3 > 0$, $c_3(c_1 c_2 - c_3) + c_1(c_5 - c_1 c_4) > 0$, and $(c_1 c_2 - c_3)(c_3 c_4 - c_2 c_5) - (c_5 - c_1 c_4)^2 > 0$. If $R_0 > 1$ and γ, e_1, e_2, e_3 positive, then $c_1 > 0$ also $c_5 > 0$. Then when the criteria are met, the endemic equilibrium point is locally asymptotically stable.

5. Sensitivity Analysis

Sensitivity analysis was carried out to determine the parameters that influence the epidemic model [13]. This analysis is focused on the parameters of the basic reproduction number R_0 . This aims to determine the effect of changes in parameter values on the basic reproduction number R_0 [14]. The normalized sensitivity index is obtained by the normalized sensitivity index of R_0 , differentiable on the parameter q , defined as follows.

$$I_q^{R_0} = \frac{\partial R_0}{\partial q_i} \times \frac{q}{R_0}. \tag{6}$$

If the parameter value is positive, the R_0 value will increase. Conversely, if the parameter value is negative, the R_0 value will decrease. Analysis for each parameter is as follows.

$$\begin{aligned} I_\mu^{R_0} &= 1, \\ I_{\beta_1}^{R_0} &= \frac{\beta_1 \sigma (\gamma + \delta)}{\gamma \beta_1 \sigma + \gamma \beta_2 \psi + \beta_1 \delta \sigma + \beta_2 \theta_1 \psi + \beta_2 \psi \alpha}, \\ I_{\beta_2}^{R_0} &= \frac{\beta_2 \psi (\gamma + \alpha + \theta_1)}{\gamma \beta_1 \sigma + \gamma \beta_2 \psi + \beta_1 \delta \sigma + \beta_2 \theta_1 \psi + \beta_2 \psi \alpha}, \end{aligned}$$

$$\begin{aligned} I_p^{R_0} &= 0, \\ I_{\theta_1}^{R_0} &= -\frac{\sigma \beta_1 \theta_1 (\gamma + \delta)}{(\gamma + \alpha + \theta_1)(\gamma \beta_1 \sigma + \gamma \beta_2 \psi + \beta_1 \delta \sigma + \beta_2 \theta_1 \psi + \beta_2 \psi \alpha)}, \\ I_{\theta_2}^{R_0} &= -\frac{\theta_2}{\gamma + \sigma + \psi + \theta_2}, \\ I_\vartheta^{R_0} &= 0, \\ I_\sigma^{R_0} &= \frac{\left(\gamma^2 \beta_1 + \gamma \beta_1 \psi + \gamma \beta_1 \theta_2 + \gamma \beta_1 \delta - \gamma \beta_2 \psi \right) \sigma}{(\gamma + \sigma + \psi + \theta_2)(\gamma \beta_1 \sigma + \gamma \beta_2 \psi + \beta_1 \delta \sigma + \beta_2 \theta_1 \psi + \beta_2 \psi \alpha)}, \\ I_\psi^{R_0} &= \frac{\left(\gamma^2 \beta_2 - \gamma \beta_1 \sigma + \gamma \beta_2 \theta_1 + \gamma \beta_2 \theta_2 + \gamma \beta_2 \alpha + \gamma \beta_2 \sigma \right) \psi}{(\gamma + \sigma + \psi + \theta_2)(\gamma \beta_1 \sigma + \gamma \beta_2 \psi + \beta_1 \delta \sigma + \beta_2 \theta_1 \psi + \beta_2 \psi \alpha)}, \\ I_\lambda^{R_0} &= 0, \\ I_\alpha^{R_0} &= -\frac{\sigma \beta_1 \alpha (\gamma + \delta)}{(\gamma + \alpha + \theta_1)(\gamma \beta_1 \sigma + \gamma \beta_2 \psi + \beta_1 \delta \sigma + \beta_2 \theta_1 \psi + \beta_2 \psi \alpha)}, \\ I_\delta^{R_0} &= -\frac{\psi \beta_2 \delta \alpha (\gamma + \alpha + \theta_1)}{(\gamma + \delta)(\gamma \beta_1 \sigma + \gamma \beta_2 \psi + \beta_1 \delta \sigma + \beta_2 \theta_1 \psi + \beta_2 \psi \alpha)}. \end{aligned}$$

To show the sensitivity index of R_0 , substitute the parameter value in Table 1. The results of the sensitivity index can be seen in Table 2. It can be seen that θ_1 and θ_2 can decrease the value of R_0 . Because θ_1 and θ_2 are negative, the larger the value, the smaller R_0 . The results show that the parameter θ_1 and θ_2 have an effect on reducing R_0 and have an impact on the stability of the equilibrium point.

Table 1. The parameter of COVID-19 model

Parameter	Definition	Value	Source
μ	Recruitment rate	1.943	[12]
γ	Natural death rate	0.3933	[12]
β_1	Transmission rate $S(t)$ from symptomatic infection	0.976	[12]
β_2	Transmission rate $S(t)$ from asymptomatic infection	1.638	[12]
p	Public awareness rate	0.4	[12]
$1 - p$	Rate of carelessness in public awareness	1 - 0.4	[12]
θ_1	Isolation rate of $I(t)$	1.0715	[9]
θ_2	Quarantine rate of $E(t)$	1.1973	[9]
ϑ	Transmission rate from $Q(t)$ to $J(t)$	0.68	[8]
σ	Symptomatic proportion	0.86834	[8]
ψ	Asymptomatic proportion	0.132	[8]
λ	Recovery rate of $J(t)$	1.7039	[9]
α	Recovery rate of $I(t)$	0.13029	[8]
δ	Recovery rate of $A(t)$	0.1	[8]

Table 2. The value of sensitivity index of R_0

Parameter	Value of Sensitivity Index
μ	1
β_1	0.6028
β_2	0.3971
p	0
θ_1	-0.4049
θ_2	-0.4621
ϑ	0
σ	0.2676
ψ	0.3462
λ	0
α	-0.0492
δ	-0.0805

6. Numerical Simulation

In this section, we will illustrate the spread of the COVID-19 model with public awareness, quarantine, and isolation through

numerical simulations. We use Matlab as the application and use fourth-order Runge-Kutta to solve the model with step size $h = 0.1$. The parameter values of the model are given by Table 1. The first simulation is carried out using parameter values in Table 1. Then, simulate with parameter values in Table 1, except parameter value $\beta_1 = 0.476$. This simulation aims to determine the effect of infected individuals in the model of the spread of COVID-19. Then a simulation was carried out with an intervention strategy, with the aim of knowing its effect on the spread of COVID-19.

6.1. Endemic Equilibrium Simulation

Using the parameter values in Table 1, we get $R_0 = 1.3386 > 1$. The basic reproduction number shows that the spread of the COVID-19 virus always exists.

Then implementing the parameter values in the model (2) obtained, the disease-free equilibrium point $X_0 = (1.9760, 2.9641, 0, 0, 0, 0, 0)$ and the endemic equilibrium point $X^* = (1.4762, 2.2143, 0.1896, 0.1032, 0.0507, 0.2116, 0.1275)$. To show the stability of the equilibrium point, this simulation produces successive Routh-Hurwitz criterion values $c_3(c_1c_2 - c_3) + c_1(c_5 - c_1c_4) = 20.9675 > 0$ and $(c_1c_2 - c_3)(c_3c_4 - c_2c_5) - (c_5 - c_1c_4)^2 = 6250.4588 > 0$. Therefore, the endemic equilibrium points are asymptotically locally stable. The simulation results are represented by Figure 2.

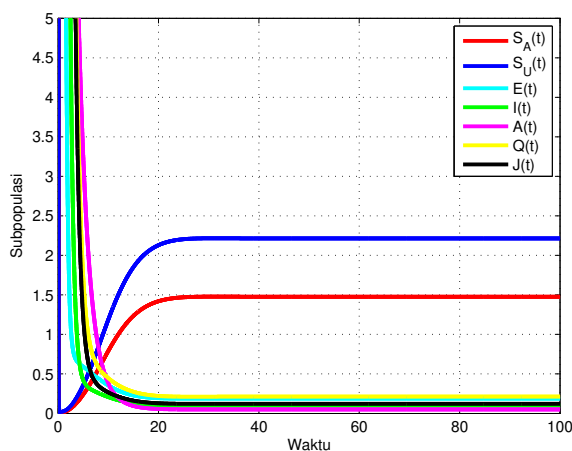


Figure 2. Solution model (2) of COVID-19 using parameter in Table 1.

Based on Figure 2, the numerical solution converges to the endemic equilibrium point. One of the causes is an infection that can cause disease again in the future. A simulation is performed with parameter values Table 1, except $\beta_1 = 0.476$, to verify this condition. Obtained basic reproduction numbers $R_0 = 0.8196 < 1$. The basic reproduction number shows that the endemic equilibrium point does not exist. The simulation results are shown in Figure 3. When the infection does not exist, the disease will not appear in the future. Therefore, the infection has a role in the dynamics of the COVID-19 spread model at R_0 and the stability of the equilibrium point.

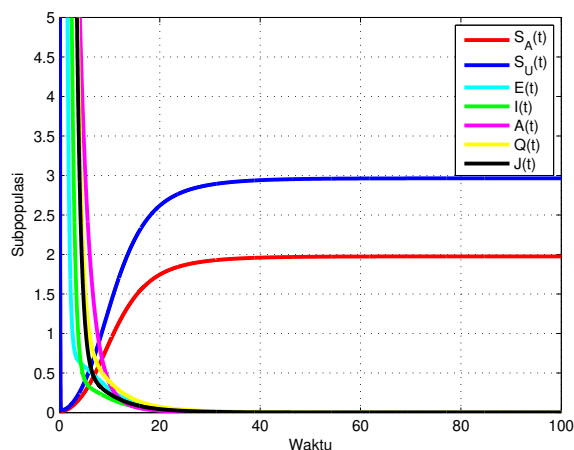


Figure 3. Solution model (2) of COVID-19 using parameter in Table 1, except $\beta_1 = 0.476$.

6.2. The Impact of Quarantine

This numerical simulation was carried out to determine the effect of quarantine on the spread of COVID-19. The value of the quarantine rate parameter acts to lower the previous baseline reproduction number ($R_0 = 1.33$). Quarantine rate value in Table 1, doubled from the previous value to $\theta_2 = 2.2$. This simulation obtained $R_0 = 0.95 < 1$ with a disease-free equilibrium point $X_0 = (1.9760, 2.9641, 0, 0, 0, 0, 0)$. The simulation results are shown in Figure 4. Increased quarantine rates can avoid endemic conditions.

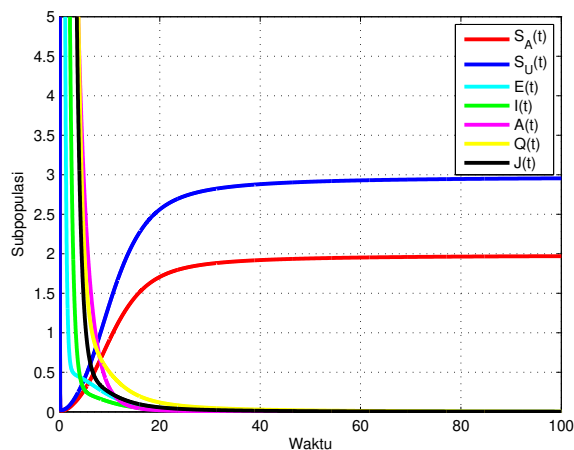


Figure 4. Solution model (2) of COVID-19 using parameter in Table 1, except $\theta_2 = 2.2$.

6.3. The Impact of Isolation

This numerical simulation was carried out to determine the effect of isolation on the spread of COVID-19. The value of the isolation rate parameter serves to lower the previous baseline reproduction number ($R_0 = 1.33$). Parameters related to the effect of isolation in the COVID-19 model are ϑ and θ_1 , which are quarantined individuals that get worse and the isolation rate from symptomatic infection. This simulation uses $\vartheta = 1.2$ and $\theta_1 = 2$ as new parameter values to show the effect of isola-

tion. The result from the simulation is a basic reproduction number of $R_0 = 0.96 < 1$ and a disease-free equilibrium point of $X_0 = (1.9760, 2.9641, 0, 0, 0, 0, 0)$. From R_0 , it can be concluded that isolation affects the spread of COVID-19. Simulation results are shown in Figure 5.

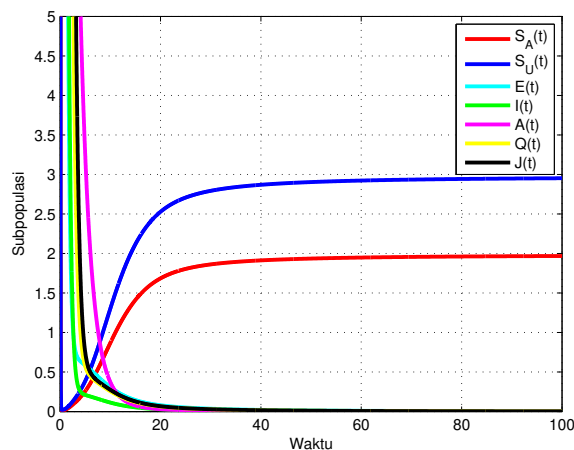


Figure 5. Solution model (2) of COVID-19 using parameter in Table 1, except $\vartheta = 1.2$ and $\theta_1 = 2$.

7. Conclusions

We introduce the new model of COVID-19 with quarantine, isolation, and public awareness. The quarantine for exposed individuals so that they be apart of other individuals and isolation purpose to keep infected symptomatic individuals for treatment and aside from individuals. Susceptible is divided into two compartments, namely susceptible with public awareness and without public awareness. In this model, we found two equilibrium points, the disease-free equilibrium point and the endemic equilibrium point. After we find the equilibrium point using the spectral radius of the next generation matrix, we can determine for basic reproduction number, R_0 . The disease-free equilibrium point (X_0) always exists, and the equilibrium point (X^*) exist when $R_0 > 1$. Linearization and Jacobian matrix to approximate local stability of equilibrium points. If $R_0 < 1$, the disease-free equilibrium point is locally stable. Based on the Routh-Hurwitz criteria, the endemic equilibrium point will be locally asymptotically stable if $R_0 > 1$ and satisfy the Routh-Hurwitz criterion. Sensitivity analysis shows that the parameter θ_1 and θ_2 have an effect on reducing R_0 and have an impact on the stability of the equilibrium point. Numerical simulations confirm both equilibrium points using fourth-order Runge-Kutta and Matlab as simulations. The simulation also shows that θ_1 and θ_2 , which isolation rate and quarantine rate have an impact on the transmission of COVID-19.

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Data availability. Several parameter values are cited from some references. See Table 1.

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