BAREKENG: Journal of Mathematics and Its Applications
June 2024 Volume 18 Issue 2 Page 0903–0914
P-ISSN: 1978-7227 E-ISSN: 2615-3017
https://doi.org/10.30598/barekengvol18iss2pp0903-0914

MODELING THE SPREAD OF COVID-19 DISEASE WITH TIME DELAY IN PONTIANAK CITY

Fatma Arum Fatonah [1], Evi Noviani [2], Meliana Pasaribu [3*]

[1,2,3] *Department of Mathematics, Faculty of Mathematics and Natural Sciences, Universitas Tanjungpura*
Jln. Prof. Dr. H. Hadari Nawawi, Pontianak, 78124, Indonesia

Corresponding author's e-mail: * ***meliana.pasaribu@math.untan.ac.id***

Article History:

Received: 22nd November 2023
Revised: 8th January 2024
Accepted: 11th March 2024
Published: 1st June 2024

Keywords:

SIQR Model;
Equilibrium Point;
Quarantine;
Basic Reproduction

ABSTRACT

Coronavirus disease 2019 (COVID-19) is an infectious disease caused by a coronavirus originating from the city of Wuhan in 2019. This disease affects the respiratory system. The city of Pontianak has the highest population density in West Kalimantan. This density results in a higher spread of Covid-19. In this article, the spread of COVID-19 is formulated into a mathematical model, equilibrium points are sought, stability is analyzed, and a delay time is introduced to reduce the spread of COVID-19. The magnitude of the delay time given during quarantine complies with health protocols, which is between 2 – 14 days. This article aims to analyze the influence of the delay time in modeling the spread of Covid-19. The problem of COVID-19 spread is constructed into an SIQR model, with a sub-population of recovered individuals returning to the susceptible sub-population. The population is divided into four sub-populations: susceptible (S), Infected (I), Quarantined (Q), and Recovered (R). The parameters used include the natural birth rate (Λ), the rate of susceptibility to infection (β), the rate of infection under quarantine (δ), the recovery rate from infection (γ), the recovery rate from infection under quarantine (ε), the death rate from infection (α_1), the death rate under quarantine (α_2), the delay time from infection to quarantine process (τ), the natural death rate (μ), and the rate of recovered immunity returning to susceptibility (θ). The simulation results show that when the basic reproduction number is less than 1, the disease-free equilibrium is stable, and when the basic reproduction number is greater than 1, the endemic equilibrium point is stable. The addition of a time delay (τ) in the SIQR model affects the stability of the endemic equilibrium point but does not affect the stability of the disease-free equilibrium point.

How to cite this article:

F. A. Fatonah, E. Noviani and M. Pasaribu., "MODELING THE SPREAD OF COVID-19 DISEASE WITH TIME DELAY IN PONTIANAK CITY," *BAREKENG: J. Math. & App.*, vol. 18, iss. 2, pp. 0903-0914, June, 2024.

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

Coronavirus Disease 2019 (COVID-19), also known as the coronavirus, began to afflict population towards the end of 2019. According to local habits in the city of Wuhan, where bat consumption is common, it is believed that this disease outbreak was caused by bats [1]. COVID-19 was first detected in West Kalimantan on March 14, 2020, and in Indonesia on March 2, 2020. According to the Health Department in 2020, there were 196,759 positive cases in the city of Pontianak. Pontianak City has the highest population density in West Kalimantan, thus posing a higher risk of COVID-19 transmission. Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) is a new coronavirus responsible for this disease. The SARS-CoV-2 virus is more contagious than SARS-CoV and MERS-CoV, despite beingf from the same family. The high number of infections is due to the rapid spread of this disease [2]. Consequently, the World Health Organization (WHO) declared it a pandemic [2].

Real-world problems described mathematically are termed mathematical models. Mathematical models aim to understand real-world issues mathematically [3]. The spread of then COVID-19 virus can be modeled using various assumptions. The mathematical modeling used in the disease transmission mathematical model, with an example being the SIR (Susceptible, Infected, Recovered) model. The subpopulations are divided into Susceptible (S), Infected (I), and Recovered (R) [4]. The SIR model can be modified into the SIQR model, where the sub-population Q is quarantined. This article discusses individuals undergoing quarantine due to virus infection. Quarantine is a measure to prevent disease transmission by isolating individuals already exposed to COVID-19, and providing a delay time will reduce the spread [5]. The delay time is a period of immunity, and incubation period and provides an estimate of the delay for a stable system [6]. When faced with the same problem, the government implements quarantine or delay time to reduce the spread of COVID-19 in Pontianak City. Previous studies [7] and [5] did not explain the transition of recovered individuals to susceptible individuals. Therefore, this article added the assumption that recovered can return to being susceptible, thus the model used in SIQR. The form of differential equation system used is a nonlinear differential equation system with four sub-populations, including their Susceptible (S), Infected (I), Quarantined (Q), and Recovered (R) subpopulations.

The data used is the spread of COVID-19 in Pontianak city from October to December 2020. During this period, there was no vaccine available, and immigration and emigration factors were not considered, irrespective of age, gender, and being closed in nature, referring to a situation where the natural death rate and natural birth rate are the same. The parameters used were modified from previous research from Pasaribu and Helmi, et al., Manaqib, et al., Yulida, Hongfan Lu, et al., and Amir Khan, et al. [7] [8] [9] with subpopulations including susceptible, infected, quarantined, and recovered subpopulations. The aim of this study is to determine the equilibrium points of the COVID-19 spread modeling and analyze stability as well as the significant impact of delay time in the modeling.

2. RESEARCH METHODS

A differential equation is an equation that involves the derivatives of one or more variables with respect to one or several independent variables [10]. Differential equations include delay, which can be expressed in the form:

$$\sum_{k=0}^{n} a_k \frac{d^k}{dt^k} x(t) + \sum_{k=0}^{m} b_k \frac{d^k}{dt^k} x(t-\tau) = 0 \quad (1)$$

where $\boldsymbol{\tau}$ represents the delay time, and $\frac{\boldsymbol{d^0}}{\boldsymbol{dt^0}} \boldsymbol{x(t)} = \boldsymbol{x(t)}$. For example, $\boldsymbol{x(t) = e^{\lambda t}}$, then

$$\boldsymbol{\sum_{k=0}^{n} a_k \lambda^k e^{\lambda t} + \sum_{k=0}^{m} b_k \lambda^k e^{\lambda(t-\tau)} = 0}$$

$$\boldsymbol{e^{\lambda t}\left(\sum_{k=0}^{n} a_k \lambda^k + \sum_{k=0}^{m} b_k \lambda^k e^{-\lambda\tau}\right) = 0}.$$

Since $\boldsymbol{e^{\lambda t} \neq 0}$, we have

$$\boldsymbol{\sum_{k=0}^{n} a_k \lambda^k + \sum_{k=0}^{m} b_k \lambda^k e^{-\lambda\tau} = 0}.$$

$$\sum_{k=0}^{n} a_k \lambda^k + \sum_{k=0}^{m} b_k \lambda^k e^{-\lambda\tau} = 0. \quad (2)$$

Equation (2) is termed the characteristic equation of **Equation (1)**. For instance, if $\boldsymbol{P_1(\lambda) = \sum_{k=0}^{n} a_k \lambda^k}$ and $\boldsymbol{P_2(\lambda) = \sum_{k=0}^{m} b_k \lambda^k}$, then **Equation (2)** can be written as:

$$P_1(\lambda) + P_2(\lambda) e^{-\lambda\tau} = 0. \quad (3)$$

According to Forde **[11]**, a system of differential equations with delay can be expressed as follows.

$$\begin{aligned} x_1'(t) &= f_1(x(t), x(t-\tau)) \\ &\vdots \quad\quad \vdots \\ x_n'(t) &= f_n(x(t), x(t-\tau)). \end{aligned} \quad (4)$$

The article commences with an examination of the SIR model and the concept of time delay. Subsequently, several assumptions are formulated, and various parameters are defined. A flow diagram of COVID-19 spread is then constructed, and a model for its dissemination is developed. Equilibrium points are sought from the model, and stability is observed and analyzed. Following this, a delay time is introduced under the condition of $\boldsymbol{\tau > 0}$. A numerical simulation is conducted, and the results are interpreted concerning the stability analysis of the system using the mathematical model of COVID-19 spread incorporating time delay.

3. RESULTS AND DISCUSSION

The presentation of the results and discussion can be organized either separately or combined into a single subsection. The summary of findings can be effectively conveyed through graphs and figures. It's imperative that both the results and discussion sections avoid multiple interpretations. The discussion should directly address the research problems, substantiate and justify responses with the obtained results, compare them with relevant research findings, acknowledge the study's limitations, and highlight any novel insights discovered.

3.1 Mathematical Models

The population is divided into four subpopulations: susceptible subpopulation, infected subpopulation, quarantined subpopulation, and recovered subpopulation. The following are the basic assumptions used to model the spread of COVID-19:

1. The Population is assumed to be closed, with the natural death rate proportional to be natural birth rate. **[9]**
2. If the susceptible subpopulation comes into contact with the infected subpopulation, it will become the infected subpopulation. The population is assumed to be homogeneously mixed, meaning the transmission occurs equally for every individual. **[12]**
3. The quarantine process will be undergone by the infected subpopulation, either in hospitals or through self-quarantine at home. **[12]**
4. The infected subpopulation will decrease due to virus-related deaths and deaths during quarantine. **[13]**
5. Quarantine is conducted according to applicable health protocols. **[12]**
6. Both the subpopulation suffering from the disease and the subpopulation in quarantine can recover from the disease. **[8]**
7. Due to waning immunity, the recovered subpopulation can re-enter the susceptible subpopulation. **[14]**
8. The infected subpopulation undergoes the recovery process with critical care time obtained through the calculation of the time delay. **[7]**

From these assumptions, the following transition diagram is formed.

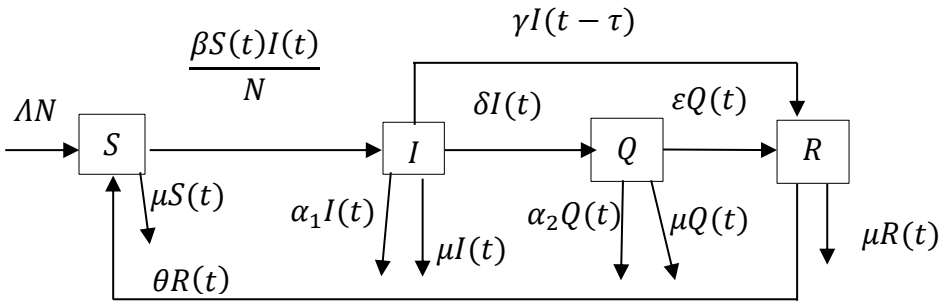

Figure 1. Transmission diagram of COVID-19 spread

Based on **Figure 1**, a system of differential equations can be employed to mathematically represent the spread of COVID-19 as follows:

$$\begin{cases} \dfrac{dS(t)}{dt} = \Lambda N - \mu S(t) - \dfrac{\beta S(t)I(t)}{N} + \theta R(t) \\ \dfrac{dI(t)}{dt} = \dfrac{\beta S(t)I(t)}{N} - \delta I(t) - \mu I(t) - \alpha_1 I(t) - \gamma I(t-\tau) \\ \dfrac{dQ(t)}{dt} = \delta I(t) - \varepsilon Q(t) - \mu Q(t) - \alpha_2 Q(t) \\ \dfrac{dR(t)}{dt} = \gamma I(t-\tau) + \varepsilon Q(t) - \mu R(t) - \theta R(t), \end{cases} \tag{5}$$

where $N = S + I + Q + R$ represents the total population.

The variables used in the SIQR model to mathematically represent the spread of COVID-19 are defined as follows:

N	:	Total compartments (individuals)
$S(t)$	:	Total susceptible compartments at time t (individuals)
$I(t)$	:	Total infected compartments at time t (individuals)
$Q(t)$	:	Total quarantined compartments at time t (individuals)
$R(t)$	:	Total recovered compartments at time t (people)
Λ	:	The natural birth rate ($\frac{1}{day}$)
β	:	the rate of susceptibility to infection ($\frac{1}{day}$)
δ	:	The rate of infection under quarantine ($\frac{1}{day}$)
γ	:	The recovery rate from infection. ($\frac{1}{day}$)
ε	:	The recovery rate from infection under quarantine ($\frac{1}{day}$)
α_1	:	The death rate from infection ($\frac{1}{day}$)
α_2	:	The death rate under quarantine ($\frac{1}{day}$)
τ	:	The delay time from infection to quarantine process ($2-14$ day)
μ	:	the natural death rate ($\frac{1}{day}$)
θ	:	The rate of recovered immunity returning to susceptibility ($\frac{1}{day}$)

The equilibrium point, which remains constant over time, is the point of equilibrium or balance point **[15]**. From the system, there are two equilibrium points, namely $E_1 = (S_1, I_1, Q_1, R_1)$ and $E_2 = (S_2, I_2, Q_2, R_2)$. The stability of the system is then analyzed where: $S_1 = N, I_1 = 0, Q_1 = 0, R_1 = 0, S_2 = \frac{(\delta+\mu+\alpha_2+\gamma)N}{\beta}$,

$$I_2 = \frac{\beta\mu N - \mu((\delta+\mu+a_1+\gamma)N) + \beta\theta R}{\beta(\delta+\mu+a_1+\gamma)}, Q_2 = \frac{\delta\mu N}{(\delta+\mu+a_1+\gamma)(\varepsilon+\mu+a_2)} - \frac{\delta\mu N}{\beta(\varepsilon+\mu+a_2)} + \frac{\delta\theta R}{(\delta+\mu+a_1+\gamma)(\varepsilon+\mu+a_2)}, \; R_2 = \frac{\beta\gamma\mu N(\varepsilon+\mu+a_2) + \beta\varepsilon\delta\mu N - \gamma\mu N(\varepsilon+\mu+a_2)(\delta+\mu+a_1+\gamma) - \varepsilon\delta\mu N(\delta+\mu+a_1+\gamma)}{\gamma\theta(\varepsilon+\mu+a_2) - \varepsilon\delta\theta + (\mu+\theta)(\delta+\mu+a_1+\gamma)(\varepsilon+\mu+a_2)}.$$

3.2. Stability Analysis Without Time Delay

The basic reproduction numbers are determined by identifying the largest eigenvalue in the Next Generation Matrix method. In deriving the basic reproduction numbers for the observed sub-population *I*, which represents the source of disease spread. The following differential equations are considered

$$\frac{dI(t)}{dt} = \frac{\beta S(t) I(t)}{N} - \delta I(t) - \mu I(t) - \alpha_1 I(t) - \gamma I(t-\tau) \quad (6)$$

$$\frac{dQ(t)}{dt} = \delta I(t) - \epsilon Q(t) - \mu Q(t) - \alpha_2 Q(t). \quad (7)$$

Based on **Equation (6)** and **Equation (7)**, involving infected and quarantined individuals, respectively, we derive two matrices, F and V, by substituting the disease-free equilibrium point into the matrix. This yield

$$J(I,Q) = \begin{pmatrix} \frac{\partial}{\partial I}\left(\frac{\beta SI}{N} - \delta I - \mu I - a_1 I - \gamma I\right) & \frac{\partial}{\partial Q}\left(\frac{\beta SI}{N} - \delta I - \mu I - a_1 I - \gamma I\right) \\ \frac{\partial}{\partial I}(\delta I - \varepsilon Q - \mu Q - \alpha_2 Q) & \frac{\partial}{\partial Q}(\delta I - \varepsilon Q - \mu Q - \alpha_2 Q) \end{pmatrix}$$

$$J(I,Q) = \begin{pmatrix} \frac{\beta S}{N} - \delta - \mu - a_1 - \gamma & 0 \\ \delta & \varepsilon - \mu - a_2 \end{pmatrix}$$

$$F = \begin{pmatrix} \beta & 0 \\ 0 & 0 \end{pmatrix}, V = \begin{pmatrix} \delta + \mu + a_1 + \gamma & 0 \\ -\delta & \varepsilon + \mu + a_2 \end{pmatrix}.$$

This leads to the formulation of the next-generation matrix as follows:

$$FV^{-1} = \begin{pmatrix} \frac{\beta(\varepsilon+\mu+a_2)}{(\delta+\mu+a_1+\gamma)(\varepsilon+\mu+a_2)} & 0 \\ 0 & 0 \end{pmatrix}.$$

The Next Generation Matrix is typically constructed from the coefficients of the differential equations governing the spread of the disease. In this case, there are two subpopulations spreading the disease, subpopulations I and Q, and the resulting matrix V is square. Additionally, knowing that $\delta > 0$ and $\varepsilon > 0$, it follows that the determinant of the matrix V is not equal to zero. Thus, because the matrix is square and nonsingular, it has an inverse. The basic reproduction number (R_0) is obtained by finding the spectral radius (largest eigenvalue) of the Next Generation Matrix. Subsequently, the transitivity and transmission mathematical formulas are applied, followed by employing Jacobian mathematical formulas to determine the mathematical expressions. The calculation yield:

$$R_0 = \frac{\beta}{(\delta+\mu+a_1+\gamma)}. \quad (8)$$

Theorem 1. *If $R_0 < 1$, then the disease-free equilibrium point in the SIQR model is asymptotically locally stable and if $R_0 > 1$, then it is unstable.*

Proof. Given $R_0 < 1$, we have $\beta(\delta + \mu + a_1 + \gamma)$. The stability of the disease-free equilibrium point of system (1) is investigated by linearizing the system (1) using the Jacobian matrix, followed by employing the disease-free equilibrium points. The eigenvalues of the Jacobian matrix for disease-free state are obtained with $|J - \lambda I|$, and the characteristic equation is derived. The next step is to find the determinants of the equation and obtain the proper values $\lambda_1 = -\mu, \lambda_2 = \beta - (\delta + \mu + a_1 + \gamma), \lambda_3 = -(\varepsilon + \mu + a_2)$ and $\lambda_4 = -(\mu + \theta)$. Thus, it is proven that $R_0 < 1$, then the disease-free equilibrium point is stable asymptotically locally. Knowing $R_0 > 1$, thus $\beta > (\delta + \mu + a_1 + \gamma)$, with the same analysis, it can be seen that λ_2 is a positive value; consequently, $\lambda_1 < 0$, $\lambda_2 > 0, \lambda_3 < 0$, and $\lambda_4 < 0$. Then, the disease-free equilibrium point is unstable, thus proving that $R_0 > 1$ has a point of equilibrium free of disease of unstable nature.

Theorem 2. *If $R_0 > 1$, then the endemic equilibrium point in the SIQR model is asymptomatically locally stable, and if $R_0 < 1$, then it is unstable.*

Proof. Given $R_0 > 1$, thus $\beta > (\delta + \mu + a_1 + \gamma)$. To investigate the stability of the disease-free equilibrium point of (1), we linearize the system (1) using the Jacobian matrix and then examine the endemic equilibrium points obtained with $|\lambda I - J|$. Thus, we obtain eigenvalue $\lambda_1 > 0, \lambda_2 > 0, \lambda_3 > 0$, and $\lambda_4 > 0$. Therefore, it is proven that when $R_0 > 1$, the endemic equilibrium point is locally asymptotically stable. Knowing $R_0 < 1$, thus $\beta > (\delta + \mu + a_1 + \gamma)$. With the same analysis, it can be seen that λ is a negative value. Consequently $\lambda_1 > 0, \lambda_2 > 0, \lambda_3 > 0$, and $\lambda_4 < 0$. Then the endemic equilibrium point is unstable thus proving that $R_0 < 1$ has an endemic equilibrium point is unstable nature.

3.3. Stability Analysis with Time Delay (τ)

In System (1), its stability is further analyzed by considering the delay time (τ) with the condition $\tau > 0$.

$$\begin{cases} \dfrac{dS(t)}{dt} = \Lambda N - \mu S(t) - \dfrac{\beta S(t) I(t)}{N} + \theta R(t) \\ \dfrac{dI(t)}{dt} = \dfrac{\beta S(t) I(t)}{N} - \delta I - \mu I - \alpha_1 I - \gamma I(t-\tau) \\ \dfrac{dQ(t)}{dt} = \delta I(t) - \varepsilon Q(t) - \mu Q(t) - \alpha_2 Q(t) \\ \dfrac{dR(t)}{dt} = \gamma I(t-\tau) + \varepsilon Q(t) - \mu R(t) - \theta R(t). \end{cases}$$

To evaluate the disease-free equilibrium point, the system is linearized using the Jacobian matrix. The growth rate of the sub-population is then analyzed with a delay time, assuming $I(t-\tau) = e^{\lambda\tau}$.

$$J = \begin{pmatrix} -\mu - \frac{\beta I}{N} & -\frac{\beta S}{N} & 0 & \theta \\ \frac{\beta I}{N} & \frac{\beta S}{N} - \delta - \mu - a_1 - \gamma e^{-\lambda\tau} & 0 & 0 \\ 0 & \delta & -(\varepsilon + \mu + a_2) & 0 \\ 0 & \gamma e^{-\lambda\tau} & \varepsilon & -(\mu + \theta) \end{pmatrix}$$

Substituting the disease-free equilibrium point and finding the characteristic equation of Jacobian matrix for the disease-free state.

$$\left| \begin{pmatrix} -\mu - \lambda & -\beta & 0 & \theta \\ 0 & \beta - \delta - \mu - a_1 - \gamma e^{-\lambda\tau} - \lambda & 0 & 0 \\ 0 & \delta & -(\varepsilon + \mu + a_2) - \lambda & 0 \\ 0 & \gamma e^{-\lambda\tau} & \varepsilon & -(\mu + \theta) - \lambda \end{pmatrix} \right| = 0$$

The resulting characteristic equation is.

$$(-\mu - \lambda)(\beta - \delta - \mu - a_1 - \gamma e^{-\lambda\tau} - \lambda)(-(\varepsilon + \mu + a_2) - \lambda)(-(\mu + \theta) - \lambda) = 0.$$

The eigenvalues are obtained as follows:

$$\lambda_1 = -\mu,\ \lambda_2 = \beta - \delta - \mu - a_1 - \gamma e^{-\lambda\tau},\ \lambda_3 = -(\varepsilon + \mu + a_2), \lambda_4 = -(\mu + \theta)$$

For $\tau = 0$, because μ, θ, ε, and $a_2 > 0$ then λ_1, λ_3 and $\lambda_4 < 0$. For $\lambda_2 = \beta - \delta - \mu - a_1 - \gamma e - \lambda\tau$ has some of the following possibilities.

1. If $\lambda_2 < 0$, the system (1) is stable asymptotic at the disease-free equilibrium point.
2. If $\lambda_2 = 0$, the system (1) is stable at the disease-free equilibrium point.
3. If $\lambda_2 > 0$, the system (1) becomes unstable at the disease-free equilibrium point, resulting in $I > 0$ and endemic occurs in system (1).

For $\tau > 0$ and $w > 0$, If $\lambda_2 = iw$ is obtained,

$$-\beta + \delta + \mu + a_1 + \cos(w\tau) + i(w + \sin(w\tau)) \qquad = 0.$$

Then the real and imaginary parts are separated, squared, and added to obtained.

$$W = -\beta + \delta + \mu + a_1 + \cos(w\tau) - \sin(w\tau).$$

Consequently, the system (1) becomes unstable at the disease-free equilibrium point if $w > 0$ when $\tau > 0$, then resulting in $\beta\mu N - \mu((\delta + \mu + a_1 + \gamma)N) + \beta\theta R > \beta(\delta + \mu + a_1 + \gamma)$, thus leading to endemicity in the system (1). The Jacobian matrix J *is expressed as*

$$J = \begin{pmatrix} -\mu - \left(\frac{\beta\mu N - \mu((\delta+\mu+a_1+\gamma)N) + \beta\theta R}{(\delta+\mu+a_1+\gamma)}\right) & -\delta - \mu - a_2 - \gamma & 0 & \theta \\ \left(\frac{\beta\mu N - \mu((\delta+\mu+a_1+\gamma)N) + \beta\theta R}{(\delta+\mu+a_1+\gamma)}\right) & \gamma - \gamma e^{-\lambda\tau} & 0 & 0 \\ 0 & \delta & -(\varepsilon + \mu + a_2) & 0 \\ 0 & \gamma e^{-\lambda\tau} & \varepsilon & -(\mu + \theta) \end{pmatrix}.$$

Let's assume:

$$\begin{aligned} k_1 &= -\mu - \left(\frac{\beta\mu N - \mu\big((\delta + \mu + a_1 + \gamma)N\big) + \beta\theta R}{(\delta + \mu + a_1 + \gamma)}\right) \\ h &= (\varepsilon + \mu + a_2\ ) \\ g &= (\varepsilon + \mu + a_2\ )(\mu + \theta) \end{aligned} \tag{9}$$

Then, the characteristic equation of the Jacobian matrix is obtained as follows:

$$\begin{aligned} -\lambda^4 + \lambda^3(h - \gamma - k_1) + \lambda^2(-g - \gamma h - k_1 h + k_1\gamma) + \lambda(-\gamma g - k_1 g + k_1\gamma h) + \\ k_1\gamma g + (\lambda^3\gamma + \lambda^2\gamma h - \lambda^2 k_1\gamma - \lambda k_1\gamma h - k_1\gamma g)e^{-\lambda\tau} = 0. \end{aligned} \tag{10}$$

Let's assume:

$$\begin{aligned} a &= -1 \\ b &= h - \gamma - k_1 \\ c &= (-g - \gamma h - k_1 h + k_1\gamma) \\ d &= (-\gamma g - k_1 g + k_1\gamma h) \\ e &= k_1\gamma g + (\lambda^3\gamma + \lambda^2\gamma h - \lambda^2 k_1\gamma - \lambda k_1\gamma h - k_1\gamma g). \end{aligned} \tag{11}$$

When $\tau = 0$, the roots of **Equation (9)** are obtained as follows.

$$\lambda = \frac{-(h-\gamma-k_1) \pm \sqrt{(h-\gamma-k_1)^2 - 4(h-\gamma-k_1)(-g-\gamma h-k_1 h+k_1\gamma)}}{-2} \tag{12}$$

According to the Routh-Hurwitz criterion, when $b > 0$ and $-2c > 0$, there are no positive real roots if $b > 0$ and $c > 0$. For $b > 0$, the following applies:

$$W_{1,2} = \frac{-b \pm \sqrt{(b)^2 - 4(-1^2 - c^2)}}{-2}.$$

Thus, λ in the characteristic **Equation (11)** is a negative value. If $b > 0$ and $(-1^2 - c^2) > 0$, there is no positive real root W. Then, considering $(-1^2 - c^2)$,

1. If $(-1^2 - c^2) < 0$, it is unlikely to occur because it results in $I < 0$ when $\tau > 0$.
2. If $(-1^2 - c^2) = 0$, there are two characteristics roots of W_2, namely the positive characteristic W_+^2 resulting in $\lambda = 0$ and the negative characteristics W_-^2 resulting in a negative value of λ, indicating that the system (1) is stable at the equilibrium point for $\tau > 0$
3. If $(-1^2 - c^2) > 0$, λ has no positive root. Thus, the system (1) is asymptomatically stable at the endemic equilibrium point at $\tau > 0$

By substituting **Equation (11)** to obtain $-2c > 0$.

3.4. Numerical Simulations

The simulation was conducted using a mathematical application by providing each parameter value can be seen in **Table 1**. And there are 3 cases as well as numerical simulation, namely disease-free, endemic, and endemic with delay time.

Table 1. The Parameter Values of the Mathematical Model for the Spread of COVID-19

Parameter	Value
δ	0.00032
Λ	0.00006
μ	0.00006
γ	0.00077
β	0.00329
ε	0.00077
a_1	0.00002
a_2	0.00009
θ	0.02

These parameter values were derived from COVID-19 data in Pontianak City. Graphs for disease-free, endemic, and endemic were obtained with the given delay time.

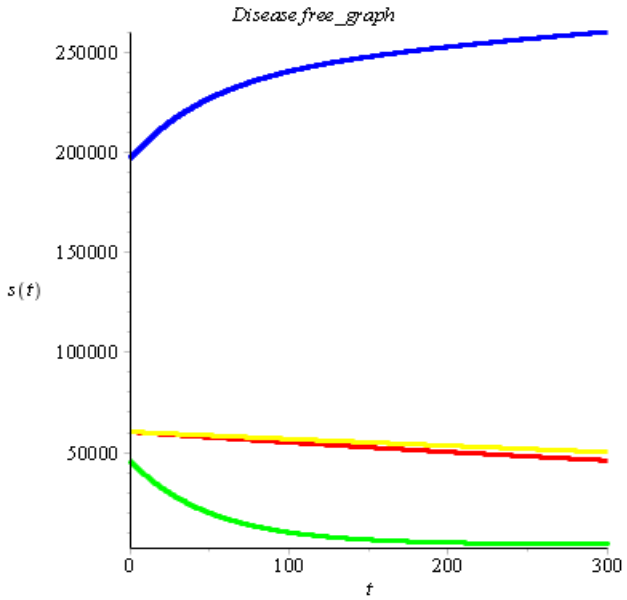

Figure 2. Disease-free

In **Figure 2**, the blue line represents the growth rate of the susceptible subpopulation, which is moving upwards. This is because the recovered subpopulations transition back to the susceptible state due to the loss of the immune system and natural births. On the red line, it can be observed that the growth rate of the infected subpopulation has decreased. This is because the susceptible subpopulation does not have direct contact with an infected subpopulation. Then, the yellow line represents the growth rate of the quarantined subpopulation. The number of infected subpopulations equals the number of subpopulations in quarantine because every infected compartment must undergo quarantine. This line does not experience any upward or downward movements because the susceptible populations do not have direct contact, thus the quarantined subpopulations do not increase. The green line indicates that the growth rate of the treated subpopulation has slowed down. This is because the sub-population transitions back to the susceptible state due to the loss of the human immune system. Additionally, the recovered subpopulation decreases due to natural deaths.

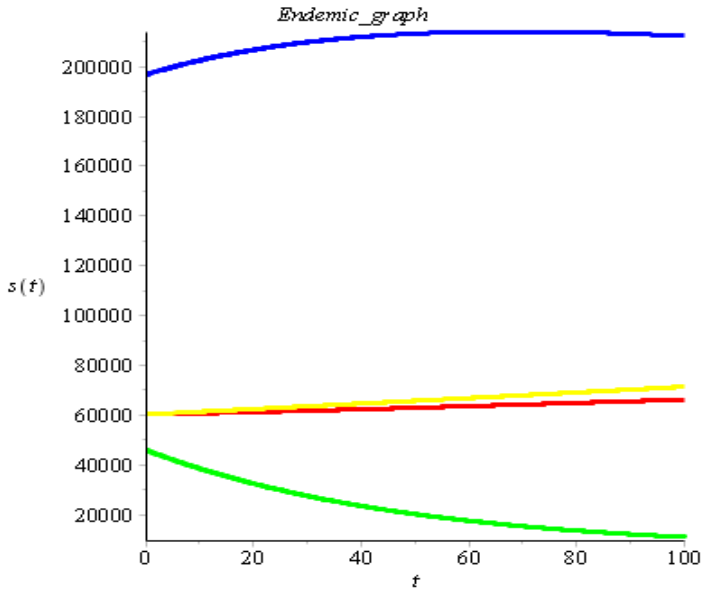

Figure 3. **Endemic**

Figure 3 illustrates that the blue line represents the growth rate of the susceptible subpopulation, which is increasing. This is because the susceptible individuals transition into the susceptible state due to loss of the immune system and natural births. On the red line, it can be observed that the growth rate of the infected subpopulation has slightly increased. This is attributed to the susceptibility of the subpopulations to infection due to direct contact with infected individuals. Moreover, the yellow line depicts an increasing growth rate of the subpopulation in quarantine. This is due to the rising number of infected subpopulations, resulting in an increase in the quarantined subpopulation.

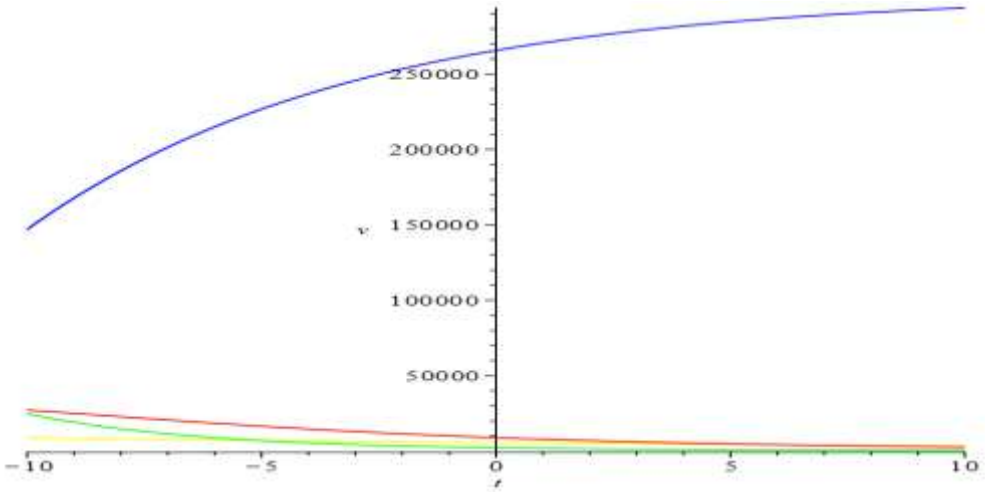

Figure 4. **Endemic Delay Time**

From **Figure 4**, it is evident that the initial parameters do not result in an increase or decrease when no delay time is applied, indicating that the endemic equilibrium point reaches stability within a value less than $t = 90$. Therefore, the introduction of a delay in endemics, specifically when $\tau = 12$, impacts the spread of COVID-19, consequently reducing the number of infected sub-population.

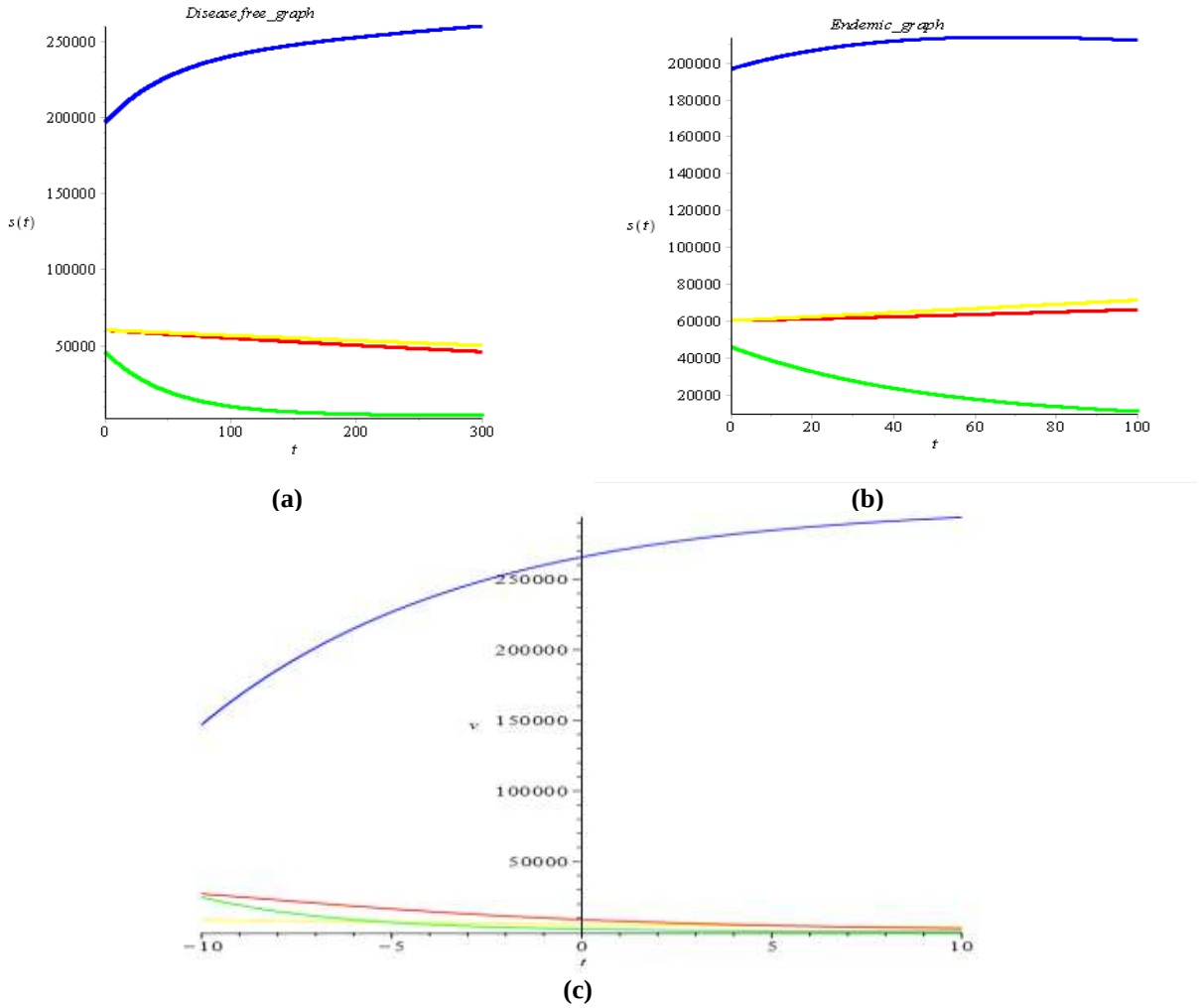

Figure 5. Graphic Differences (a) Disease-free, (b) Endemic, (c) Endemic Delay Time

In **Figure 5** (a), **Figure 5** (b), and **Figure 5** (c), the blue line represents the growth rate of the susceptible subpopulation, which rises due to natural births. in **Figure 5** (a) and **Figure 5** (c), the yellow lines represent the growth rate of the infected sub-population, which decreases due to natural deaths, deaths from infection, the recovery process with delayed calculations, and the presence of quarantined subpopulations. However, **Figure 5** (b) shows an increase due to the increase in the infected Sub-population. Furthermore, in **Figure 5** (a) and **Figure 5** (c), the red lines represent the growth rate of the quarantined sub-population, which remains stable due to natural deaths, deaths from infection, and the recovery rate of the quarantined subpopulations, while **Figure 5** (b) shows an increase due to the increase in the quarantined infected subpopulations. In **Figure 5** (a), **Figure 5** (b), and **Figure 5** (c), the green lines represent the growth rate represents the growth rate of the recovered subpopulations, which decreases due to natural deaths and a decline in the immune system. In **Figure 5** (c), with the inclusion of a delay, the yellow line representing the infected sub-populations, and the green line representing the recovered compartments can reduce or delay the spread of the disease for a period of 2-14 days.

The obtained value of $R_0 = 0{,}281196$, indicating that $R_0 < 1$. Therefore, $R_0 < 1$ the disease will not spread; in other words, the group will be free from the disease for a certain period. However, with $R_0 = 3{,}046413$ indicating $R_0 > 1$, the disease will spread, resulting in an epidemic. All three simulations showed a decrease in the infected sub-populations. Without a delay, the spread of COVID-19 continues to increase, resulting in a decrease in the recovered sub-population. However, with a delay, the spread of COVID-19 is hindered for a certain period, reducing the spread and increasing the recovered sub-populations.

4. CONCLUSIONS

1. There are two equilibrium points: the disease-free equilibrium $(S_1, I_1, Q_1, R_1) = (N, 0,0,0)$ and the endemic equilibrium point $(S_2, I_2, Q_2, R_2) = \left(\frac{(\delta+\mu+a_2+\gamma)N}{\beta} = S_2, \frac{\beta\mu N-\mu\left((\delta+\mu+a_1+\gamma)N\right)+\beta\theta R}{\beta(\delta+\mu+a_1+\gamma)} = I_2, \frac{\delta\mu N}{(\delta+\mu+a_1+\gamma)(\varepsilon+\mu+a_2)} - \frac{\delta\mu N}{\beta(\varepsilon+\mu+a_2)} + \frac{\delta\theta R}{(\delta+\mu+a_1+\gamma)(\varepsilon+\mu+a_2)} = Q_2, \frac{\beta\gamma\mu N(\varepsilon+\mu+a_2)+\beta\varepsilon\delta\mu N-\gamma\mu N(\varepsilon+\mu+a_2)(\delta+\mu+a_1+\gamma)-\varepsilon\delta\mu N(\delta+\mu+a_1+\gamma)}{\gamma\theta(\varepsilon+\mu+a_2)-\varepsilon\delta\theta+(\mu+\theta)(\delta+\mu+a_1+\gamma)(\varepsilon+\mu+a_2)} = R_2\right)$
2. If $R_0 < 1$, then the disease-free balance point is locally asymptotically stable. This indicates that the spread of COVID-19 will decrease within a few days, leading to a decrease in the sub-population infected with COVID-19, or it can be said that the disease is absent altogether. However, if $R_0 > 1$, then the endemic equilibrium point is local asymptotically stable.
3. The sub-population infected with the COVID-19 virus will increase and remain endemic with a locally asymptotically stable spread rate.

REFERENCES

[1] Rauf Eka Ubaya Taruna, Sahrudin. Analisis Tugas Polisi Pamong Praja Dalam Pencegahan Dan Pengendalian COVID-19. *Jurnal Progres Administrasi Publik* 2022; 2: 12–19.

[2] Afwan MI, Helma. Pemodelan Matematika Penyebaran Penyakit COVID-19 Dengan Menggunakan Model SIRS. *UNPjoMath* 2021; 4: 34–40.

[3] Widowati, Sutimin. *PEMODELAN MATEMATIKA*. Semarang.

[4] Huo Hai-Feng, Feng Li-Xiang. Global Stability of an Epidemic Model with Incomplete Treatment and Vaccination. *Hindawi Publishing Corporation* 2012; 2012: 1–14.

[5] Xu Jie, Zhang Tiansi. Dynamic Analysis for a SIQR Epidemic Model with Specific Nonlinear Incidence Rate. *Journal of Applied Mathematics and Physics* 2019; 1840–1860.

[6] Mukherjee D. Stability Analysis of an S-I Eoidemic Model with Time Delay. *Mathl Comput* 1995; 24: 63–68.

[7] Lu H, Ding Y, Gong S, et al. Mathmetatical Modeling and Dynamic analysis of SIQR With Delay for Pandemic Covid-19. *Mathematical Biosciences and Engineering* 2021; 18: 3197–3214.

[8] Manaqib M, Azizah M, S EH, et al. Analisis Model Matematika Penyebaran Penyakit COVID-19 Dengan Lockdown dan Karantina. *Barekeng: Jurnal Ilmu Matematika dan Terapan* 2021; 15: 479–492.

[9] Pasaribu M, Helmi. Aplikasi Persamaan Diferensial Stokastik Pada Masalah Kontrol Optimum Berkendala. *Barekeng: Jurnal Ilmu Matematika dan Terapan* 2021; 15: 257–266.

[10] Bronson R, Costa GB. Persamaan Diferensial. In: Simarmata L, Prasetyo T (eds). Ciracas, Jakarta, 2007.

[11] Kuang Y. Delay Differential Equations with Applications in Population Dynamic. 1993.

[12] Masita, Darmawati, Fardinah. Pemodelan Matematika SEIqInqR Pada Penyebaran COVID-19. *Journal of Mathematics: Theory and Applications* 2021; 3: 31–37.

[13] Suryani I, Wartono, Aprijon, et al. Kestabilan Model Sird Penyebaran Penyakit Ebola Dengan Pengaruh Adanya Migrasi. *Seminar Nasional Teknologi Informasi, Komunikasi dan Industri* 2019; 11: 494–504.

[14] Yulida Y, Karim MA. Pemodelan Matematika Penyebaran COVID-19 Di Provinsi Kalimantan Selatan. *Open Jurnal Systems* 2020; 14: 3257–3264.

[15] Perco Lawrence. *Differential Equations and Dynamical System*. New York: Springer-Verlag.