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Stability Analysis and Numerical Simulation of the Transmission Dynamics of Covid-19 Infection

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Abstract

COVID-19 is an infectious disease caused by a new type of coronavirus, the model of transmission of which is currently from human to human. Many cities around the world have enacted follow-up policies, among others, to control the spread of COVID-19. The aim of this paper is to construct a dynamical model and carry out an analytical analysis of the stability of the dynamic behavior of coronavirus disease transmission. The form of the model is a non-linear system of differential equations with five state variables: susceptible individuals, exposed individuals, patients under surveillance in quarantine, infected individuals, and recovered individuals. Further, we discussed sensitivity Analysis of Parameters. Furthermore, the Routh–Hurwitz method is used to investigate the stability of the non-endemic equilibrium, and manifold center theory is used to analyze the stability of the endemic equilibrium. Finally, numerical simulation is demonstrated, in order to verify the proposed mathematical model and estimate the epidemic threshold parameters based on approximating the infection process. The infection parameters model was obtained by fitting the COVID-19 model to data from Indonesia.

Keywords: *Covid-19, SEQIR Model, Dynamical modelling, stability analysis.*

1. Introduction

Coronavirus disease 2019 (COVID-19) was first discovered in Wuhan city, Hubei Province, China, in December 2019. In early 2020, COVID-19 began to spread globally starting from the Asian region, resulting in a viral pandemic. Coronavirus is believed to be a zoonotic disease in origin, even though its current transmission mode is human to human, and it was quickly stated as a pandemic by the World Health Organization, due to the rapid manner in which it spread across the world: within 3 months (i.e., by early April 2020), it had spread to more than 200 countries. The first case in Indonesia was reported in March 2020, and the number of COVID-19 cases since then has stayed consistently high, standing at 463,007 as of 14 November 2020, explaining the importance of this research.

COVID-19 represents a global health emergency, having caused millions of infections and deaths. A 1902 model which divides the population into several subsets known as compartments (e.g., susceptible, infectious, and recovered) (Solís et al., 2021) called the SIR epidemic model, was devised in order to describe the spread of an epidemic in a given population (Arino and Portet, 2020) This model has been used to graph asymmetrical patterns in the modeling of the spread of coronavirus (Telles et al., 2021)

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and to design time-based data from the daily spread of new cases, in order to track the variables that cause COVID-19 transmission. Further, mathematical models have been modified to analyze the dynamics of infection transmission (Ala'raj et al,. 2021; Das and Samanta, 2021).

The spread of COVID-19 is influenced by the climate of an area, with those located in hotter and in colder areas in tropical climates being more vulnerable to exposure. High temperatures and humidity significantly reduce the likelihood of viral transmission, which means that they can also reduce the spread out of COVID-19 (Hattaf, and Yousfi, 2020; Zhao et al., 2020; Chen et al., 2020). The COVID-19 pandemic has placed a serious load on the global health system, putting medical practitioners under immense pressure (Afifi et al., 2021; López and Rodó, 2021). Humanitarian rescue is an important part of a government's emergency response management. This has forced mathematical scientists to focus on finding mathematical models that can be used for predictions, in order to help determine government policies (Deng and Kong, 2021).

Mathematical scientists began this process by conducting research in order to understand the characteristics of the pandemic before constructing a mathematical formulation. Next, the generalized logistic model have also been used to illustrate the outbreak of the COVID-19 pandemic (Wu et al., 2020). Mathematical models have a role in analyzing epidemic phenomena in the health field, in order to determine the level of viral spread for infectious diseases (Rosyada et al., 2019; Das and Shaikh, 2021; Sutimin, 2017; Sutimin, 2019; Alade, 2021). Mathematical equations can also be used to determine the effectiveness of treatments, when it comes to preventing outbreaks from developing and stopping the spread of a virus (Cullenbine et al,. 2021).

The local and global stability of the equilibrium point of the model have previously been discussed. Local, asymptotic stability of a non-endemic equilibrium is reached if the basic reproduction number is less than one. Global stability of an endemic equilibrium in the SLBS model can be achieved if the ratio is greater than one (Khasanah, 2019). The basic reproduction number is a sharp beginning parameter, which determines the global dynamics (Liu and Yang, 2012).

Then, mathematical models using a common susceptible–infectious–recovered (SIR) approach to analyze epidemics of COVID-19 transmission have been published by Bärwolff (2020) and Ajbar, et al (2021) have proposed the dynamical modeling of COVID-19 spread by using SIR model with linear incidence rate, nonlinear removal rate, and public awareness. Therefore, the environment has a role important in the spread and cure/death rate of a disease. Factors inhibiting the detection of a symptom include being vulnerable and asymptomatic, being without symptoms and infected, and being infected and recovering/dying (Signes-Pont, 2021). Studies investigating appropriate mathematical models using the model of Suspected, Infected, and Removed (SIR) and Suspected, Exposed, Infected and Removed (SEIR). The SEIR model is developed by modifying the SIR model that has been previously used (Erandi et al., 2020).

Further, Din and Algehyneb (2021) have published the local and global stability analysis of the SIR model with the convex incidence rate. The Lyapunov method is implemented to analysis of the global of the developed model, whereas the local stability is analysis by using Routh-Hurtwitz criteria. Martínez (Martínez, 2021) modified the SIR model by adding the "deceased" variable, thus creating the SIRD model (Zewdie and Gakkhar, 2020). This model is constructed by using a system of non-linear differential equations to detect trends in the pandemic and make appropriate predictions about the spread of COVID-19 infection. Developed compartments model for COVID-19 epidemic with SEIRV model (Yang and Wang, 2020) and SEIHR model (Rahman et al., 2021) and various studies on COVID-19 spread have been published by several researchers (Ndaïrou, 2020; Radha and Balamuralitharan, 2020; Serhan and Labbardi, 2021; Sugiyanto and Abrori, 2020). Mathematical modeling is used to estimate the reproduction number that can help to determine the potential and severity of the outbreak, as well as providing important information to identify the type of interventions and disease intensity (Tang et al., 2020).

Furthermore, a strategy is needed, in order to anticipate an increase in cases, to inhibit their growth, and slow or stop the spread of the virus. Thus, obtaining projections of future conditions is very important, as it can help to identify which policies are appropriate to implement. The dynamical system model approach is very important for predicting the future conditions of simulated results as well as selectable scenarios. Analyzing the interaction between variables and examining the most influential variables can help to determine the sensitivity of the related parameters. The goal of this paper is to develop a mathematical model which considers exposed persons and patients un-der surveillance in quarantine in the variables, also progression rate from quarantined individuals to infected individuals, the transmission of Covid-19 that can occur through exposed and infected individuals in the parameters, as well as to evaluate and analyze the stability of the proposed dynamical model. This analysis is conducted to investigate the behaviour of the system around non-endemic and endemic equilibrium points. We discuss the relationship between the basic reproduction number and stability, and the center manifold method is used to show that forward bifurcation occurs when the basic reproduction number equals unity.

In this paper, significant novelties have been considered in this new work, which are explained as follows. The new model proposed in this article is a development of the SEIR model, i.e., accommodates a transfer from Q to I. This describes the reality more precisely since after self-isolating, some people became infected by covid-19, and hence in this case there is an additional parameter (transfer rate from quarantined individuals to infected individuals). In addition, the new proposed model also considers the transmission of Covid-19 that occurs through exposed individuals (individuals who have had contact with pathogen) and infected individual so that there are two more additional parameters i.e. the infection rate which was determined through infected individuals and the proportion of infected individuals who transmitted to susceptible individuals (S) so that they become exposed individuals. Therefore, from two points above, there are new information and parameters involved in our new proposed model so that it becomes the novelty in this study.

This paper is structured as follows: In the introduction, we describe the scientific background, importance, and objectives of this research. The mathematical model of coronavirus disease spread, positivity, the boundedness of solutions, and the basic reproduction number are discussed in the second section. In the third section, we calculate the equilibrium points and examine the existence and uniqueness of the endemic equilibrium. An analysis of the stability results is provided in the fourth section. In the fifth section, a numerical simulation based on data from Indonesia, is utilized to verify the proposed dynamical model. Finally, a summary of the main findings is given in the Conclusion section.

2. Methodology

The methods of the research can be separated into dynamical model formulation, sensitivity analysis of parameter, stability analysis of the model, laboratory experiment, and computational simulation. The research method steps can be described as follows

2.1 Developed Mathematical Model

The novel model was constructed by considering the role of exposed persons and patients under surveillance in quarantine in the COVID-19 infection spread model. In the model, virus transmission occurs through interaction between exposed and healthy individuals, as well as between infected individuals and healthy individuals. We assume that quarantined persons cannot transmit the virus to healthy persons. We divide the human population into five categories, based on their health status: susceptible individuals (S), exposed individuals (E), patients under surveillance in quarantine (Q), infected individuals (I), and recovered individuals I. Hence, the total human population at time t is represented by N(t) = S(t) + E(t) + Q(t) + I(t) + R(t). The notations and descriptions of the parameters for mathematical modelling are given in Table 1.

Table 1 Descriptions of parameters.

Symbol	Descriptions
λ	Recruitment rate of susceptible individuals
β_1	Infection rate determined through exposed individuals
β_2	Infection rate which determined through infected individuals
r	Proportion of susceptible individuals who become exposed individuals
κ	Progression rate from exposed individuals
ρ_1	Proportion of exposed individuals who become susceptible
ρ_2	Proportion of exposed individuals who become infected individuals
γ_1	Recovery rate of quarantined individuals
γ_2	Recovery rate of infected individuals
μ	Death rate due to infection
τ	Natural death rate
ω	Proportion of infected individuals who can transmit to susceptible
δ	Progression rate from quarantined individuals to infected individuals

The schematic model of COVID-19 infection in the community is given in Figure 1 where the notations used in the model are described in Table 1. The susceptible population is generated by recruitment through births, at a constant rate.

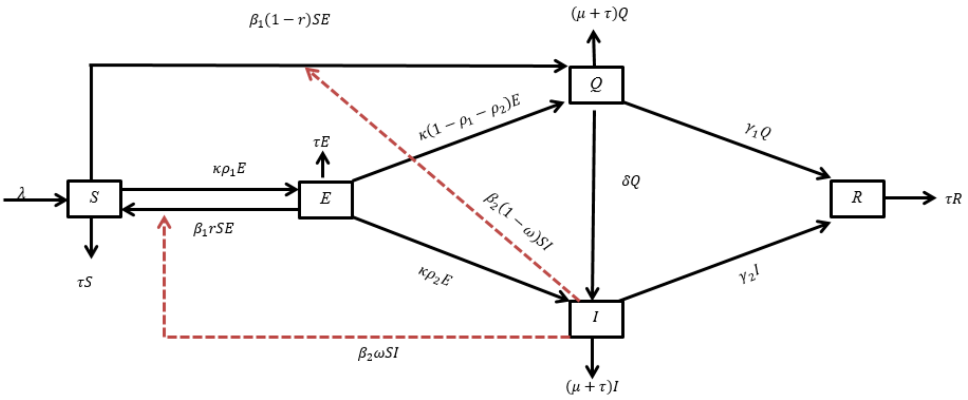

Figure 1. The Compartmental Model Of COVID-19 Infection Spread

The compartmental model is stratified, based on infection status, as the following categories: "Susceptible" represents an individual who is able to become infected; "exposed individuals" is an individual who has had contact with a pathogen, "quarantined" is an individual who is under surveillance in quarantine, and "infected" is an individual who is infected by a pathogen and is capable of transmitting the virus to others. Finally, "recovered" represents an individual who was previously infected and survived the virus with no long-term health effects. The dynamics of each compartment, which were used to formulate the differential equations describing the Covid-19 transmission, are described as follows:

1. Changes in the susceptible individuals (S) cover: (1) increment due to the natural birth rate of λ, (2) decrement due to infections from direct interactions between vulnerable individuals and COVID-19 carriers, and move to individuals E and Q with rates $\beta_1 r + \beta_2 \omega$ and $\beta_1(1 - r) + \beta_2(1 - \omega)$ respectively, (3) decrement due to natural death by τ. The dynamics of S are then formulated as the differential equation (1).

2. The number of individuals in the subpopulation E increased due to the interaction between susceptible individuals and COVID-19 carriers, causing an E and I with rate $\beta 1r$ and $\beta_2 \omega$ respectively. Individuals in E who returned to the individuals susceptible represented by the rate $\kappa\rho 1$, while those who entered the infected individuals represented by the rate $\kappa\rho 2$. Furthermore, it decreased due to the rate of development from E to Q of $(1-\rho 1-\rho 2)$. Finally, there is a natural death of τ. The dynamics of the exposed individuals E are then formulated as the differential equation (2).

3. Changes in the number of the quarantined individuals Q cover: (1) increment due to the rate of development of E and susceptible individuals to Q by the rate of $(1-\rho 1-\rho 2)$ and $\beta_1(1 - r)$respectively (2) decrement due to recovery with the rate of $\gamma 1$ (3) decrement due to deaths caused by COVID-19 with the rate of μ (4) decrement due to natural death with the rate of μ. This is modelled as the differential equation (3).

4. The number of individuals in the positive individuals infected by COVID-19 increased due to the rate of development from the E class to positive individuals at the rate of $\kappa\rho 2$. The infected individuals by COVID-19 decreased due to the rate of change of infected individuals to recover by $\gamma 2$, and the death rate due to COVID-19 and natural deaths with the rate of μ and τ respectively. This is modelled as the differential equation (4).

5. The number of the recovered individuals increased by population transmissions from Q and I with the rate of $\gamma 1$ and $\gamma 2$ respectively, and reduced due to natural deaths by τ. Hence, the rate of changes in the number of individuals in the recovered individuals is represented by the differential equation modelled as the equation (5).

Based on the dynamics described above, the proposed mathematical model for the spread of COVID-19 infection in the community consists of five-variable non-linear differential equations (comprising the SEQIR model), as follows:

$$\frac{dS}{dt} = \lambda + \kappa\rho_1 SE - \tau S - \left(\beta_1 E + \beta_2 I\right) S \tag{1}$$

$$\frac{dE}{dt} = \beta_1 rSE + \beta_2 \omega SI - A_1 E \tag{2}$$

$$\frac{dQ}{dt} = \beta_1\left(1 - r\right) SE + \beta_2\left(1 - \omega\right) SI + \kappa\left(1 - \rho_1 - \rho_2\right) E - A_2 Q \tag{3}$$

$$\frac{dI}{dt} = \kappa\rho_2 E + \delta Q - A_3 I \tag{4}$$

$$\frac{dR}{dt} = \gamma_1 Q + \gamma_1 I - \tau R \tag{5}$$

where

$$A_1 = \tau + \kappa$$
$$A_2 = \mu + \tau + \delta + \gamma_1$$
$$A_3 = \mu + \tau + \gamma_2$$

with the initial condition $S(0) > 0, E(0) > 0, Q(0) > 0, I(0) \geq 0, R \geq 0$.

2.2 Sensitivity analysis of parameter and stability analysis of the model

In this step, we investigated a sensitivity analysis was carried out to determine the parameters that most influence changes in the basic reproduction number. Next, the stability analysis at the equilibrium point. it will be analyzed using the Routh–Hurwitz method to analyze the stability of the non-endemic equilibrium, and manifold center theory is used to analyze the stability of the endemic equilibrium.

2.3 Laboratory experiment and numerical simulations

The data for the simulations is obtained from https://covid19.go.id, on 12 July to 16 August 2021. The parameters are estimated from laboratory experiment analysis by using the nonlinear least-square method with MAPLE software. While, Solving the system equation, numerically using a 4th order Runge-Kutta method is studied numerically with MATLAB software.

3. Results and Discussion.

In this section, we proposed results and discussion of this research. First, we describe the investigation of several analytical properties to the dynamics of COVID-19 spread. The properties of the dynamical model such as Positivity and Boundedness of Solutions, a uniqueness endemic equilibrium, and stability analysis that are given in the following theorem.

3.1 Positivity and Boundedness of Solutions

This model is a transmission model of COVID-19 in a closed population (N), divided into five categories: susceptible (S), exposed (E), quarantined (Q), infected (I), and recovered (R). Thus, it is very important to prove that all the variables are positive at all times, $t > 0$

Theorem 1. Suppose initial conditions S (0) ≥ 0, E(0) ≥ 0, Q(0) ≥ 0, I(0) ≥ 0, R(0) ≥ 0, then the solutions for model (1)-(5) are positive for all time $t > 0$:

Proof of Theorem 1Consider the initial condition, For $t > 0$, from $\frac{dS}{dt}$ in equation (1), we have

$$\frac{dS}{dt} = \lambda + \kappa\rho_1 SE - \tau S - \left(\beta_1 E + \beta_2 I\right) S$$
$$\frac{dS}{dt} = \lambda - \left(\tau + \beta_1 E + \beta_2 I - \kappa\rho_1 E\right) S$$
$$\frac{dS}{dt} + \left(\tau + \beta_1 E + \beta_2 I - \kappa\rho_1 E\right) S = \lambda$$

The above equation can be written as follows

$\frac{dS(t)}{dt} + qS(t) = \lambda$, where $q = \tau + \beta_1 E + \beta_2 I - \kappa\rho_1 E$

By using integrating factor method, we find

$$\frac{dS(t)}{dt} \cdot e^{\int_0^t q\, d\eta} + qS(t) \cdot e^{\int_0^t q\, d\eta} = \lambda e^{\int_0^t q\, d\eta}$$

$$\Leftrightarrow \frac{d}{dt}\left(S(t) \cdot e^{\int_0^t q\, d\eta} \right) = \lambda e^{\int_0^t q\, d\eta}$$

Hence, we obtain

$$S(t) e^{\int_0^t q\, d\eta} - S(0) = \int_0^t \lambda e^{\int_0^t q\, d\eta} dt$$

$$S(t) = S(0) e^{-\int_0^t q\, d\eta} + e^{-\int_0^t q\, d\eta} \left\{ \int_0^t \lambda e^{\int_0^t q\, d\eta} dt \right\} \geq 0,$$

$\forall t > 0$

In a similar way, it can be proved that E(t) ≥ 0, Q(t) ≥ 0, I(t) ≥ 0, and R(t) ≥ 0. Thus, the solution of S (t), E(t), Q(t), I(t), and R(t) of model (1)-(5) are positive for all time

t > 0. ■

Theorem 2. The feasible region defined by $\Omega = \{ (\mathrm{S(t), E(t), Q(t), I\,(t), R(t)}) \in \mathbb{R}^5_+ : 0 \leq \mathrm{N(t)} \leq \mathrm{U} \}$ with $\mathrm{U} = \max\{ \mathrm{N(0)}, \frac{\lambda}{\tau} \}$, is positively invariant for models (1)-(5).

Proof. Let $N(t) = S(t) + E(t) + Q(t) + I(t) + R(t)$

From models (1)-(5), we have

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dQ}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \tag{6}$$

$$= \lambda - \tau N - (Q-1)\mu \leq \lambda - \tau N \tag{7}$$

That is,

$$\frac{dN}{dt} \leq \lambda - \tau N \tag{8}$$

By integrating inequality (8) using initial condition $N(0)$ representing the total population at $t = 0$ we find

$$N(t) \leq N(0) e^{-\tau t} - \frac{\lambda}{\tau} e^{-\tau t} + \frac{\lambda}{\tau} \tag{9}$$

Letting t tend to infinity, we obtain. $N(t) \leq \frac{\lambda}{\tau}$

Therefore, Ω is positively invariant for models (1)-(5), it indicates that all feasible solutions of models (1)-(5) belong to the region Ω. ■

3.2 Basic Reproduction Number

In this subsection, we derive a basic reproduction number $\Re_0$. The number $\Re_0$ is a measure to determine the rate of spread of COVID-19 in a population. $\Re_0$ is defined as the average number of new cases of infection caused by an infected individual in a susceptible sub-population. As we know the basic reproduction number $\Re_0$ in the epidemic model, if $\Re_0 < 1$, then the disease does not proliferate in the population. Conversely, if $\Re_0 > 1$, then infection will spread among the population (Yang and Wang, 2020).

Next, the number $\Re_0$ is derived from the next-generation matrix (NGM), in order to find the dominant eigenvalues of the Jacobian matrix calculated at the non-endemic equilibrium point. The infected compartments are E and I. Suppose $x = [E, I]^T$, such that we can write

$$\frac{dx}{dt} = F(x) - V(x) \tag{10}$$

$$F(x) = \begin{bmatrix} F_1 \\ F_2 \end{bmatrix} = \begin{bmatrix} \beta_1 rSE + \beta_2 \omega SI \\ 0 \end{bmatrix} \tag{11}$$

$$V(x) = \begin{bmatrix} V_1 \\ V_2 \end{bmatrix} = \begin{bmatrix} A_1 E \\ -\kappa \rho_2 E - \delta Q + A_3 I \end{bmatrix} \tag{12}$$

$$F = \begin{pmatrix} \frac{\partial F_1}{\partial E} & \frac{\partial F_1}{\partial I} \\ \frac{\partial F_2}{\partial E} & \frac{\partial F_2}{\partial I} \end{pmatrix} = \begin{pmatrix} \beta_1 rS & \beta_2 \omega S \\ 0 & 0 \end{pmatrix} \tag{13}$$

$$V = \begin{pmatrix} \frac{\partial V_1}{\partial E} & \frac{\partial V_1}{\partial I} \\ \frac{\partial V_2}{\partial E} & \frac{\partial V_2}{\partial I} \end{pmatrix} = \begin{pmatrix} A_1 & 0 \\ -\kappa \rho_2 & A_3 \end{pmatrix} \tag{14}$$

F and V are Jacobian matrices of $F(x)$ and $V(x)$ at the non-endemic equilibrium point. By substituting the non-endemic equilibrium value, $\varepsilon_0(S_0, E_0, Q_0, I_0, R_0) = \left(\frac{\lambda}{\tau}, 0, 0, 0, 0\right)$ at F and V matrices, we obtain

$$F = \begin{pmatrix} \beta_1 r\left(\frac{\lambda}{\tau}\right) & \beta_2 \omega\left(\frac{\lambda}{\tau}\right) \\ 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} \frac{1}{A_1} & 0 \\ \frac{-\kappa \rho_2}{A_1 A_3} & \frac{1}{A_3} \end{pmatrix} \tag{15}$$

The reproduction number $\Re_0$ for the COVID-19 dynamical models (1)-(5) can be calculated from the spectral radius of $\left(FV^{-1}\right), \rho\left(NGM\right) = \rho\left(FV^{-1}\right)$ (FV^(-1)),ρ(NGM) = ρ(FV^(-1)), obtained as follows:

$$\Re_0 = \frac{\lambda r \beta_1}{\tau A_1} + \frac{\lambda \omega \beta_2 \kappa \rho_1}{A_1 A_3} \tag{16}$$

3.3 Sensitivity Analysis of Parameters

The idea of sensitivity can be applied to infectious disease models to decide which variable or parameter is sensitive to a particular situation. The effects of changing parameter values on the functional value of the reproduction number $\Re_0$ are obtainable in this section. The essential parameter must be found, which could be an important threshold for disease management. The sensitivity index of $\Re_0$ with respect to the given parameters is given by

$$\xi_{\alpha}^{R_0} = \frac{\alpha}{R_0}\frac{\partial R_0}{\alpha}$$

The normalized sensitivity indices for 16 parameters are obtained as

$$\frac{\alpha}{R_0}\frac{\partial R_0}{\alpha} = \frac{\frac{\lambda r\beta_1}{\tau A_1}+\frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}}{\frac{\lambda r\beta_1}{\tau A_1}+\frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}}$$
$$=1$$

$$\frac{r}{R_0}\frac{\partial R_0}{r} = \frac{\lambda r\beta_1}{\left(\frac{\lambda r\beta_1}{\tau A_1}+\frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}\right)\tau A_1}$$
$$= \frac{\beta_1A_3}{\omega\beta_2\kappa\rho_1\tau + r\beta_1A_3}$$

$$\frac{\beta_1}{R_0}\frac{\partial R_0}{\beta_1} = \frac{\lambda r\beta_1}{\left(\frac{\lambda r\beta_1}{\tau A_1}+\frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}\right)\tau A_1}$$
$$= \frac{\beta_1 rA_3}{\tau\omega\beta_2\kappa\rho_1 + \beta_1 rA_3}$$

$$\frac{\omega}{R_0}\frac{\partial R_0}{\omega} = \frac{\lambda\omega\beta_2\kappa\rho_1}{\left(\frac{\lambda r\beta_1}{\tau A_1}+\frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}\right)A_1A_3}$$
$$= \frac{\lambda\omega\beta_2\kappa\rho_1}{\tau\omega\beta_2\kappa\rho_1 + r\beta_1A_3}$$

$$\frac{\beta_2}{R_0}\frac{\partial R_0}{\beta_2} = \frac{\lambda\omega\beta_2\kappa\rho_1}{\left(\frac{\lambda r\beta_1}{\tau A_1}+\frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}\right)A_1A_3}$$
$$= \frac{\tau\omega\beta_2\kappa\rho_1}{\omega\beta_2\kappa\rho_1 + r\beta_1A_3}$$

$$\frac{\rho_1}{R_0}\frac{\partial R_0}{\rho_1} = \frac{\lambda\omega\beta_2\kappa\rho_1}{\left(\frac{\lambda r\beta_1}{\tau A_1}+\frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}\right)A_1A_3}$$
$$= \frac{\tau\omega\beta_2\kappa\rho_1}{\omega\beta_2\kappa\rho_1 + r\beta_1A_3}$$

$$\frac{\kappa}{R_0}\frac{\partial R_0}{\kappa} = -\frac{\kappa\left(-\omega\beta_2\rho_1\tau^2 + r\beta_1A_3\right)}{A_1\left(\omega\beta_2\kappa\rho_1\tau + r\beta_1A_3\right)}$$

$$\frac{\gamma_2}{R_0}\frac{\partial R_0}{\gamma_2} = -\frac{\gamma_2\kappa\omega\beta_2\rho_1}{\left(\frac{\lambda r\beta_1}{\tau A_1} + \frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}\right)A_1\left(A_3\right)^2}$$

$$= -\frac{\tau\gamma_2\kappa\omega\beta_2\rho_1}{A_3\left(\omega\beta_2\kappa\rho_1 + r\beta_1A_3\right)}$$

$$\frac{\mu}{R_0}\frac{\partial R_0}{\mu} = -\frac{\lambda\mu\kappa\omega\beta_2\rho_1}{\left(\frac{\lambda r\beta_1}{\tau A_1} + \frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}\right)A_1\left(A_3\right)^2}$$

$$= -\frac{\tau\mu\kappa\omega\beta_2\rho_1}{A_3\left(\omega\beta_2\kappa\rho_1 + r\beta_1A_3\right)}$$

$$\frac{\tau}{R_0}\frac{\partial R_0}{\tau} = \frac{\tau\left(-\frac{\lambda r\beta_1}{\tau^2A_1} - \frac{\lambda r\beta_1}{\tau\left(A_1\right)^2} - \frac{\lambda\omega\beta_2\kappa\rho_1}{\left(A_1\right)^2A_3} - \frac{\lambda\omega\beta_2\kappa\rho_1}{A_1\left(A_3\right)^2}\right)\lambda\mu\kappa\omega\beta_2\rho_1}{\frac{\lambda r\beta_1}{\tau A_1} + \frac{\lambda\omega\beta_2\kappa\rho_1}{A_1A_3}}$$

$$= -\frac{A_1\tau^2\kappa\omega\beta_2\rho_1 + A_3\kappa\omega\beta_2\rho_1 + A_1\left(A_3\right)^2r\beta_1 + \left(A_3\right)^2r\tau\beta_1}{A_1A_3\left(\tau\omega\beta_2\kappa\rho_1 + r\beta_1A_3\right)}$$

3.4 Equilibrium Points of The Model

By solving the system of equations $\left\{\frac{dS}{dt} = 0, \frac{dE}{dt} = 0, \frac{dQ}{dt} = 0, \frac{dI}{dt} = 0\,\frac{dR}{dt} = 0\right\}$, we derive non-endemic and endemic equilibrium points for system (1)-(5). The non-endemic equilibrium points can be written as $\varepsilon_0\left(S_0, E_0, Q_0, I_0, R_0\right) = \left(\frac{\lambda}{\tau}, 0, 0, 0, 0\right)$, and the endemic equilibrium points are $\varepsilon_1 = \left\{S^*, E^*, Q^*, I^*\right\}$ where

$$E^* = \frac{\omega\left(S\tau - \lambda\right)}{\left(\omega - r\right)S^*\beta_1 + \left(1 - \kappa\omega\rho_1\right) + A_1}, \tag{17}$$

$$Q^* = \frac{\left(S^*\tau - \lambda\right)\left(-S^*\tau\omega\beta_2\rho_2 - A_3S^*r\beta_1 + A_1A_3\right)}{\left(S^*\omega\beta_1 - S^*\tau\beta_1 - \kappa\omega\rho_1 + A_1\right)S^*\beta_2} \tag{18}$$

$$I^* = \frac{\left(S\tau - \lambda\right)\left(S^*r\beta_1 - A_1\right)}{\left(\left(\omega - r\right)S^*\beta_1 - \kappa\omega\rho_1 + A_1\right)S^*\beta_2} \tag{19}$$

The solution of S* satisfies the polynomial equation

$$a_2\left(S^*\right)^2 + a_1S^* + a_0 = 0 \tag{20}$$

with

$$a_2 = \delta\beta_1\beta_2\left(\omega - r\right), \omega > r \tag{21}$$

$$a_1 = A_2A_3\beta_1r + \left(\left(\left(1 - \omega\right)\delta + \rho_2\kappa\omega\right)\tau + \left(\left(1 - \omega\ \rho_1\right)\delta + \rho_2\omega\left(\gamma_1 + \mu\right)\right)\kappa\right)\beta_2 \tag{22}$$

$$a_0 = A_1A_2A_3$$

$$= \frac{A_1^2A_2A_3^2\tau}{\beta_2\omega\lambda\kappa\rho_2 + A_3\left(\beta_1r\lambda - \tau A_1\right)}\left(1 - \Re_0\right) \tag{23}$$

Based on Descartes's rule of signs $a_2 > 0$, $a_1 < 0$ must be satisfied for positive S^*. The existence and uniqueness of the endemic equilibrium is given in the following theorem.

Theorem 3. If $\Re_0 > 1$, with $\Re_0 = \frac{\lambda r \beta_1}{\tau A_1} + \frac{\lambda \omega \beta_2 \kappa \rho_1}{A_1 A_3}$, then there is a unique endemic equilibrium $\varepsilon_1 = \{S^*, E^*, Q^*, I^*\}$ for equations (1)-(5).

Proof of Theorem 3. From Equations (21), (22), and (23), we can find that the value $a_2 > 0$, based on Descartes' rule of signs: it must satisfy $a_0 < 0$ for S* to be conditional. As is well-known,

$$\begin{aligned} a_0 &= A_1 A_2 A_3 \\ &= k(1 - \Re_0) \end{aligned}$$

where $k = \frac{A_1^2 A_2 A_3^2 \tau}{\beta_2 \omega \lambda \kappa \rho_2 + A_3(\beta_1 r \lambda - \tau A_1)}$

If $k > 0$, then $(1 - \Re_0 < 0 \Leftrightarrow \Re_0 > 1)$ such that there is a unique endemic equilibrium. ■

3.5 Stability Analysis Results

Next, we analyze the stability of the equilibrium points. Stability analysis is used to determine the behavior of the population around the equilibrium point. The local stability of the non-endemic equilibrium point is given in Theorem 4.

Theorem 4. Let $\Re_0 = \frac{\lambda r \beta_1}{\tau A_1} + \frac{\lambda \omega \beta_2 \kappa \rho_1}{A_1 A_3}$.

i.) If $\Re_0 < 1$ then the non-endemic equilibrium point will be locally asymptotically stable; and

ii.) If $\Re_0 > 1$, then the non-endemic equilibrium point will be unstable.

Proof. The Jacobian matrix associated to the non-endemic equilibrium point Ɛ₀, J(Ɛ₀), is represented as

$$J(\varepsilon_0) = \begin{bmatrix} -\tau & \kappa\rho_1 - \frac{\beta_1 \lambda}{\tau} & 0 & -\frac{\beta_2 \lambda}{\tau} \\ 0 & \frac{\beta_1 \lambda}{\tau} - A_1 & 0 & \frac{\beta_2 \omega \lambda}{\tau} \\ 0 & \frac{\beta_1 (1-r)\lambda}{\tau} + \kappa(1 - \rho_1 - \rho_2) & -A_2 & \frac{\beta_2 (1-r)\lambda}{\tau} \\ 0 & \kappa\rho_2 & \delta & -A_3 \end{bmatrix} \tag{24}$$

The stability at the non-endemic equilibrium point for COVID-19 can be analyzed using the eigenvalues obtained from the Jacobian matrix (J(Ɛ₀)). According to the Routh–Hurwitz criterion, if all real parts of the eigenvalues are negative, then Ɛ₀ is locally asymptotically stable. Next, we find the eigenvalues of the Jacobian matrix, by calculating

$$\begin{bmatrix} X+\tau & -\kappa\rho_1+\dfrac{\beta_1\lambda}{\tau} & 0 & \dfrac{\beta_2\lambda}{\tau} \\ 0 & X-\left(\dfrac{\beta_1\lambda}{\tau}-A_1\right) & 0 & -\dfrac{\beta_2\omega\lambda}{\tau} \\ 0 & -\left(\dfrac{\beta_1(1-r)\lambda}{\tau}+\kappa(1-\rho_1-\rho_2)\right) & X+A_2 & -\dfrac{\beta_2(1-r)\lambda}{\tau} \\ 0 & -\kappa\rho_2 & -\delta & X+A_3 \end{bmatrix} \tag{25}$$

The characteristic equation of the Jacobian matrix at J(Ɛ$_0$) is an equation in the form of polynomial factors:

$$p(X)=\frac{1}{\mu}(X+\tau)\left(a_0X^3+a_1X^2+a_2X+a_3\right) \tag{26}$$

where

$$a_0=\tau^2>0, \tag{27}$$

$$a_1=-\lambda r\tau\beta_1+\left(A_1+A_2+A_3\right)\tau^2, \tag{28}$$

$$a_2=\tau^2A_1\left(1-\Re_0\right)+\frac{\tau\left(\beta_2\kappa\lambda\rho_2\omega+A_2A_3\tau+\left(A_3\right)^2\tau\right)}{A_3}, \tag{29}$$

$$\begin{aligned} a_3 &= \left(\left(r-\omega\right)\lambda^2\beta_1\beta_2+\left(\tau\rho_1\omega\beta_2\kappa+\tau\left(\omega\tau-A_1\right)\beta_2\right)\lambda\right)\delta \\ &+\left(-\tau rA_2A_3\beta_1-\beta_2\kappa\tau\left(\mu+\tau+\gamma_1\right)\omega\rho_2\right)\lambda+\tau^2A_3A_2A_1 \end{aligned} \tag{30}$$

Note that Hurwitz's matrix is as follows:

$$H(p)=\begin{pmatrix} a_1 & a_3 & 0 \\ a_0 & a_2 & 0 \\ 0 & a_1 & a_3 \end{pmatrix}$$

From the matrix $H(p)$, we obtain Hurwitz's determinant

$$\Delta_1(p)=\left|a_1\right|=a_1$$

$$\Delta_2(p)=\begin{vmatrix} a_1 & a_3 \\ a_0 & a_2 \end{vmatrix}=a_1a_2-a_3a_0$$

$$\begin{aligned} \Delta_3(p) &= \begin{vmatrix} a_1 & a_3 & 0 \\ a_0 & a_2 & 0 \\ 0 & a_1 & a_3 \end{vmatrix} \\ &= a_1a_2a_3-a_3a_3a_0=a_3\left(a_1a_2-a_3a_0\right) \\ &= a_3\Delta_2(p) \end{aligned}$$

In order for all polynomial roots to have a negative real root part, the following must be satisfied

$$
\begin{aligned}
&\Delta_1(p) > 0 \Leftrightarrow a_1 > 0,\\
&\Delta_2(p) > 0 \Leftrightarrow a_1 a_2 - a_3 a_0 > 0, \qquad (31)\\
&\Delta_3(p) > 0 \Leftrightarrow a_3\left(a_1 a_2 - a_3 a_0\right) > 0,
\end{aligned}
$$

From equation (27), $a_1 > 0$ so we have

$$
\frac{a_2}{a_0} > 0 \Leftrightarrow a_2 > 0
$$

$$
\frac{a_3}{a_0} > 0 \Leftrightarrow a_3 > 0
$$

From Equation (26), we obtain the eigenvalue $X_1 = -\tau$. Based on the Routh–Hurwitz criterion, if the cubic degree polynomial satisfies $a_1 > 0, a_2 > 0$ and $a_1 a_2 > a_3 a_0$, then the polynomial has roots with negative real part. From Equation (29), it can be seen that $a_2 > 0$ is fulfilled if $\left(1-\Re_0\right) > 0$, such that $\Re_0 < 1$. This proves that the non-endemic equilibrium point, $\varepsilon_0 = \left(S^0, E^0, Q^0, I^0, H^0\right)$ is locally asymptotically stable if $\Re_0 < 1$ and unstable if $\Re_0 > 1$. ■

An infectious disease analysis in the epidemiological model use basic reproduction number $\left(\Re_0\right)$ (Ajbar et al., 2021; Martínez, 2021; Zewdie and Gakkhar, 2020). This number is important to determine whether the disease will disappear or remain in the

population as time increases. If $\Re_0 > 1$, it indicates that one infected individual can infect more than one susceptible individual. This implies that the non-endemic equilibrium is unstable which results in an epidemic breaks out.

Theorem 5. Let $\Re_0 = \dfrac{\lambda r \beta_1}{\tau A_1} + \dfrac{\lambda \omega \beta_2 \kappa \rho_1}{A_1 A_3}$. The endemic equilibrium state $\varepsilon_1 = \left\{S^*, E^*, Q^*, I^*\right\}$ is stable if $\Re_0 > 1$ and unstable if $\Re_0 < 1$.

Proof. Stability analysis of the endemic equilibrium point for the case $\Re_0 > 1$ can be carried out using center manifold theory. We suppose that the equilibrium point of the system is around the bifurcation point when $\Re_0 = 1$. Selecting β_2 as the bifurcation parameter from the formula of $\Re_0$, as $\beta_2 = \beta_2^*$, it can be found that

$$
\beta_2^* = \frac{\left(-\lambda r \beta_1 + A_1 \tau\right) A_3}{\lambda \omega \kappa \rho_2}
$$

The Jacobian matrix for the system at the non-endemic equilibrium point when $\beta_2 = \beta_2^*$ is given as follows:

$$
J\left(\varepsilon_0, \beta_2^*\right) = \begin{bmatrix}
-\tau & \kappa\rho_1 - \dfrac{\beta_1 \lambda}{\tau} & 0 & -\dfrac{\left(-\lambda r \beta_1 + A_1 \tau\right) A_3}{\omega \kappa \rho_2 \tau} \\
0 & \dfrac{\beta_1 \lambda}{\tau} - A_1 & 0 & \dfrac{\left(-\lambda r \beta_1 + A_1 \tau\right) A_3}{\kappa \rho_2 \tau} \\
0 & \dfrac{\beta_1 (1-r) \lambda}{\tau} + \kappa\left(1 - \rho_1 - \rho_2\right) & -A_2 & \dfrac{\left(-\lambda r \beta_1 + A_1 \tau\right) A_3 (1-\omega)}{\omega \kappa \rho_2 \tau} \\
0 & \kappa \rho_2 & \delta & -A_3
\end{bmatrix}
$$

The matrix $J\left(\varepsilon_0,\beta_2^*\right)$ has eigenvalues such that right eigenvector corresponding to these eigenvalues can be denoted by $w=\left[w_1 \quad w_2 \quad w_3 \quad w_4\right]^T$, satisfying $J\left(\varepsilon_0,\beta_2^*\right)\cdot w=0$, where

$$w_1=\frac{\left(-\kappa\omega\tau\rho_1+\lambda\omega\beta_1-\lambda r\beta_1+A1\tau\right)}{\omega\tau^2},$$

$$w_2=1,$$

$$w_3=\frac{\left(\kappa\omega\tau\left(\rho_1+\rho_2\right)+\omega\tau\left(A1-\kappa\right)-\lambda\beta_1\left(\omega-r\right)-A1\tau\right)}{A2\omega\tau},$$

$$w_4=\frac{\left(-\lambda r\beta_1+A1\tau\right)}{\lambda\omega\beta_2}.$$

Then, v , which is the left eigenvector, is denoted by $v=\left[v_1 \quad v_2 \quad v_3 \quad v_4\right]^T$, satisfying $v\cdot J\left(\varepsilon_0,\beta_2^*\right)=0$ with

$$v_1=0,$$

$$v_2=\frac{\left(A2\kappa\tau\rho_2-\delta\kappa\tau(\rho_2+\rho_1-1)-\delta\lambda\beta_1\left(r-1\right)\right)}{\delta\left(-\lambda r\beta_1+A1\tau\right)},$$

$$v_3=1,$$

$$v_4=\frac{A_2}{\delta}.$$

Let $S=h_1, E=h_2, Q=h_3, I=h_4$, and we obtain

$$a=\sum_{k,i,j=1}^{4} v_k w_i w_j \frac{\partial^2 f_k}{\partial h_i \partial h_j}\left(\varepsilon_0\right),$$

$$a=2\left(v_2 w_1 w_2 \frac{\partial^2 f_2}{\partial h_1 \partial h_2}\left(\varepsilon_0\right)+v_2 w_1 w_4 \frac{\partial^2 f_2}{\partial h_1 \partial h_4}\left(\varepsilon_0\right)\right.$$
$$\left.+v_3 w_1 w_2 \frac{\partial^2 f_3}{\partial h_1 \partial h_2}\left(\varepsilon_0\right)+v_3 w_1 w_4 \frac{\partial^2 f_3}{\partial h_1 \partial h_4}\left(\varepsilon_0\right)\right)$$

We have

$$a=-\frac{\left(2\left(\beta_1\lambda\left(\omega-r\right)+\tau\left(\tau+\kappa\left(1-\omega\rho_1\right)\right)\right)\right)\left(\left(1-\omega\right)\delta\tau^2A_1^2+A_1A_2\kappa\omega\tau^2\rho_2+\left(1-\rho_1-\rho_2\right)\kappa A_1\tau\omega\delta+\left(\omega-r\right)\lambda\delta\beta_1\left(2A_1\tau-r\lambda\beta_1\right)\right)\right)}{\omega^2\delta\tau^2\lambda\left(A_1\tau-\lambda r\beta_1\right)},$$

with $\omega>r$

Furthermore, we find

$$b=\sum_{k,i,j=1}^{4} v_k w_i \frac{\partial^2 f_k}{\partial h_i \partial \beta_2^*}\left(\varepsilon_0\right),$$

$$b=v_2 w_1 \frac{\partial^2 f_2}{\partial h_1 \partial \beta_2^*}\left(\varepsilon_0\right)+v_2 w_4 \frac{\partial^2 f_2}{\partial h_4 \partial \beta_2^*}\left(\varepsilon_0\right)+v_3 w_1 \frac{\partial^2 f_3}{\partial h_1 \partial \beta_2^*}\left(\varepsilon_0\right)+v_3 w_4 \frac{\partial^2 f_3}{\partial h_4 \partial \beta_2^*}\left(\varepsilon_0\right)$$

$$b = \frac{\left(\left(1 - \rho_1 - \rho_2 \right) \tau\delta + A_2 \tau \rho_2 \right) \kappa}{\delta \beta_2 \tau} + \frac{\left(1 - \omega \right) A_1}{\beta_2 \omega} + \frac{\beta_1 \lambda \left(\omega - r \right)}{\beta_2 \tau \omega}$$

We find that $a < 0$ and $b > 0$. This indicates that the dynamical model will have a forward bifurcation (Wang et al., 2021) at $\Re_0 = 1$, that is, there is a change in stability where the non-endemic equilibrium point becomes unstable. The endemic equilibrium point is thus stable when $\Re_0 > 1$, and the endemic equilibrium point is unstable if $\Re_0 < 1$. ■

So that, the proposed model has an endemic equilibrium point and the forward bifurcation occurs. From Theorem 4, it can be seen that, if the basic reproduction number is more than one, then the endemic equilibrium point is stable, meaning that infected individuals will transmit the disease to more than one individual, and the virus will persist in the population

3.6 Simulation Results

In this section, we demonstrate a numerical experiment to verify the proposed dynamical COVID-19 transmission model with case study di Indonesia. We estimated important model parameters based on data from Indonesia, on 12 July to 16 August 2021. To estimate the parameters involved in the model, we used the nonlinear least-square method, which is a well-known method (see e.g. (Cao et al., 2012) for more detailed basic theory). This works by fitting the parameters from the solution of models (1) – (5) to the observation data, and the estimated parameters derived by minimizing the least-square error, which are shown in Table 2.

Table 2 Parameter estimation for Indonesia

Parameters	Value	Unit
λ	3.94	day^{-1}
β_1	3.604×10^{-8}	day^{-1}
β_2	0.195	day^{-1}
r	6.5×10^{-3}	-
κ	0.5944	day^{-1}
ρ_1	0.622×10^{-6}	-
ρ_2	1.3822×10^{-18}	-
γ_1	1.0541×10^{-5}	day^{-1}
γ_2	1.969×10^{-1}	day^{-1}
μ	0.0999	day^{-1}
τ	3.849×10^{-10}	day^{-1}
ω	0.8192	-
δ	1.835×10^{-2}	day^{-1}

To illustrate endemic simulations, we used this parameter values and initial conditions as follows: $S(0) = 170101; E(0) = 123317; Q(0) = 4782; I(0) = 40427; R(0) = 34754$

The value of $\Re_0$ is determined using the parameters that are estimated in Table 1, we find $\Re_0 = 4.0438 > 1$. Numerical simulation of the SEQIR model for COVID-19 spread to determine the effect of variation in infection rate of the dynamical behavior of the number Exposed, Quarantined, and Infected individuals are demonstrated by using MATLAB R2019b package as in Figure 3-6.

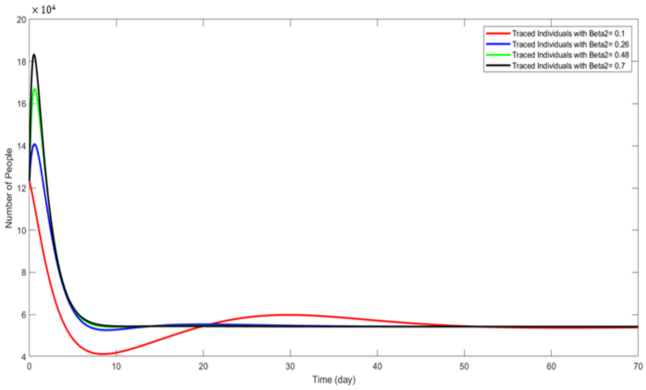

Figure 3 Effect of the variations in β_2 values on the number of Exposed Individuals

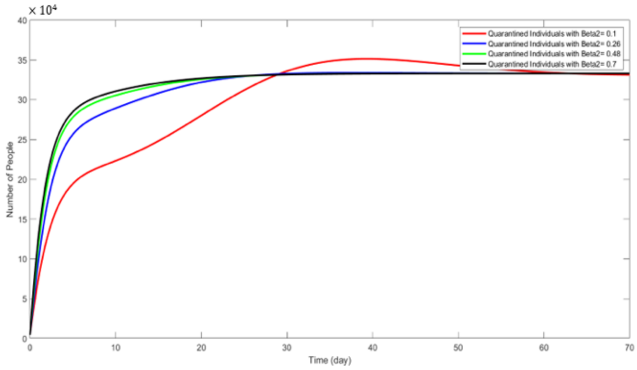

Figure 4 Effect of the variations in β_2 values on the number of Quarantined individuals

According to Figure 3, the number of Exposed individuals decreases for $\beta_2 = 0.7$ on the seven days, it decreased to 55600 people, meanwhile for $\beta_2 = 0.1$, it decreased to 41500 people. At Figure 4, the number of Quarantined individuals increases and only takes nine days to reach a peak of 308.700 people for $\beta_2 = 0.7$, but for $\beta_2 = 0.1$ just reach 219.400 people.

Corresponding to this, it can be seen that from Figure 5, the number of Infected individuals decreased on the nine days reaching 190.800 people for $\beta_2 = 0.7$ and for $\beta_2 = 0.1$ just reach 140.600 people so that if the β_2 value is higher, then the number of Infected individuals will also be higher, as well as Exposed individuals.

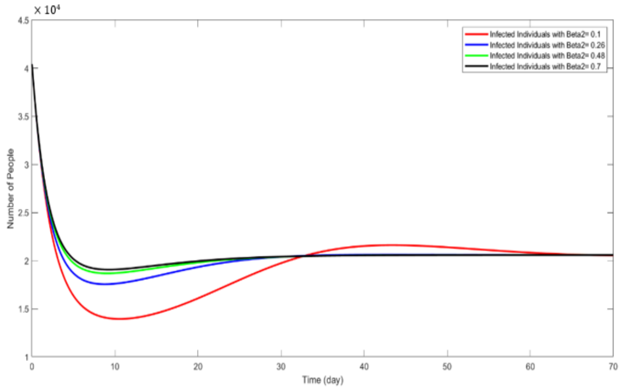

Figure 5 Effect of the variations in β_2 values on the number of Infected individuals

Based on figure 3-5 with variation of rate infection, the number of Quarantined individuals increases, but the number of Traced and Infected individuals have decreases. So that quarantine is very necessary to reduce COVID-19 transmission. Furthermore, we depicted the model of the transmission of COVID-19 as shown in Figure 6.

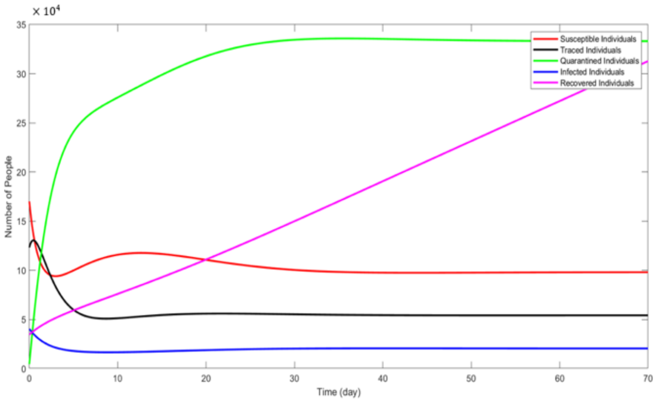

Figure 6 Endemic model simulation $(\Re_0 > 1)$

From Figure 6, it can be seen that the outbreak will disappear if the sizes of the T, and I compartment decrease, while Q compartment increases. The size of the recovered category increases. We know that the susceptible category is growing smaller with time, which means there are many people who have come into contact with infected individuals and, thus, become exposed individuals, meaning that the expose and quarantine category is growing. This indicates that there are infected people who transmit the virus to more than one other person in the given period. Therefore, there is a large number of infected people over time, which can lead to an outbreak in a very short time, $\Re_0 = 4.0438$.

Next, we will analyze the parameters that have the most influence on the rate of spread of the COVID-19 disease. We evaluated the sensitivity index of the basic reproduction number on the values of the basic parameters given in Table 2. The results of the sensitivity index $\Re_0$ for the estimated parameters are given in Table 3.

Table 3. The sensitivity index of parameter

Parameter	Sensitivity indices of $\Re_0$
λ	1
r	0.999
β_1	0.999

β_2	3.269×10^{-7}
ω	3.269×10^{-7}
ρ_1	3.269×10^{-7}
κ	-0.999
γ_2	-2.169×10^{-7}
μ	-1.1×10^{-7}
τ	-0.999

The parameters $\lambda, r, \beta_1, \beta_2, \omega, \rho_1$ are parameters with positive indices that contribute to endemic dispersion, because they increase $\Re_0$. Vice versa, a parameter with a negative index contributes to controlling the disease because they have reduced reproduction number.

4. Conclusions

We have modified dynamical model for the COVID-19 outbreak. The proposed model was constructed by dividing the human population into susceptible, exposed, quarantined, infected and recovered compartments with considering progression rates from quarantined to infected individuals and the transmission of Covid-19 that can occur through exposed and infected individuals in the population. Results showed that the related basic reproduction number became the unique threshold to guarantee the existence of COVID-19. Analytically, it was proven that the spread of COVID-19 infection depends on the basic reproduction number, which can be used to investigate the stability of the model at the equilibrium point. Further, the center manifold theorem has been implemented to analyze the forward bifurcation at the reproduction number equals to unity. If the basic reproduction number is less than unity, the situation is thought to be under control and COVID-19 cannot persist in the population. Thus, we can reduce the spread of COVID-19 by reducing the basic reproduction number to less than one. From the formula of reproduction number, it shows that the infection rate, which was determined through infected individuals and the proportion of infected individuals who can transmit to susceptible individuals, was directly proportional to the reproduction number. Hence, decreasing these parameters will reduce the reproduction number.

Furthermore, we estimated the parameter values based on data from Indonesia, and a numerical simulation was conducted. We found $\Re_0 = 4.0438$ for an endemic situation. This indicates that mathematical modelling is an efficient method to estimate this kind of pandemic situation, if the parameters can be properly estimated. From the simulation results, we also derived that with the variation of infection rate parameters, the number of traced and infected individuals decreased, while the number of quarantined individuals increased. Hence, quarantine is one effective strategy to reduce the COVID-19 spread.

In future research, the dynamical model needs to be further developed. Modification of the mathematical model can be carried out by considering the optimal COVID-19 spread control model and assessing the impact of control strategies that can reduce the number of exposed individuals, patients under surveillance in quarantine, and infected individuals in the population.

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