Jurnal Matematika UNAND
Vol. **14** No. **2** Hal. 154 – 166
Edisi April 2025
ISSN : 2303–291X
e-ISSN : 2721–9410

https://doi.org/10.25077/jmua.14.2.154-166.2025

MATHEMATICAL MODEL OF COVID-19 WITH ASPECT OF COMMUNITY COMPLIANCE TO HEALTH PROTOCOLS

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Accepted August 9, 2024 Revised January 27, 2025 Published May 25, 2025

Abstract. *COVID-19 infection is still a health problem in various countries. Some people who recover from COVID-19 still experience some symptoms. Therefore, it is essential to implement health protocols to minimize transmission of the COVID-19 virus. Based on this, a mathematical model of COVID-19 with aspects of community compliance with health protocols is presented. The population is divided into three subpopulations: the susceptible subpopulation, the exposed subpopulation, and the infected subpopulation. The basic reproduction number, R_0, determines whether there are disease-free and endemic equilibrium points. When R_0 is less than 1, the disease-free equilibrium is locally asymptotically stable. Conversely, when R_0 is greater than 1, the endemic equilibrium point is locally stable. Numerical simulations will demonstrate how COVID-19 spreads, taking into account community adherence to health guidelines. The results of numerical simulations indicate that an increase in public adherence to health protocols leads to a decrease in the number of COVID-19 infections.*

Keywords: COVID-19, Health Protocols, Mathematical Models, Stability Analysis

1. Introduction

Since early 2020, Indonesia has been affected by the Coronavirus Disease 2019 (COVID-19). This disease is a respiratory condition triggered by the Severe Acute Respiratory Syndrome-Corona Virus (SARS-CoV), a specific type of coronavirus. This virus can spread through droplets (small droplets) when sneezing or coughing. The main clinical symptoms that appear when COVID-19 attacks the body are fever, dry cough, sneezing, and difficulty breathing [1]. The increasing spread of COVID-19 can be seen from October 31, 2020, when the government announced that the number of positive cases was 410,008 people, 337,801 people recovered, and 29,998 people died from COVID-19, exceeding the number of deaths in the city of

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Wuhan, China is where the virus emerged [2]. The number is increasing every day and there is a high increase during the year-end holidays leading up to the new year in January 2021. The number of positive people per day can reach 12,001 people who are positive for COVID-19. On January 31, 2021, 1,078,314 positive cases were announced, 873,221 people recovered, and 29,998 people died from COVID-19.

COVID-19 infection is still a health problem in various countries. Most people who recover from COVID-19 still experience some symptoms [3,4,5]. Therefore, prevention is carried out to reduce the spread of disease outbreaks. Most people have received the vaccine. Vaccines encourage the formation of specific immunity to COVID-19 disease to avoid infection or the possibility of serious illness or reduce the serious symptoms that appear [6,7,8,9]. Apart from that, the Indonesian government continues to educate other efforts to control the spread of COVID-19. In particular, following the health guidelines involves wearing masks, washing hands, and keeping a safe distance [10].

COVID-19 cases can be represented in a mathematical model. A mathematical model is a set of equations or inequalities that express the behavior of a problem that exists in the real world [11]. The resulting mathematical model can be an equation, inequality, or other. By using these mathematical principles, it can be seen that the resulting model is by the formula that has been formed [12].

Various studies have been carried out on mathematical models of the spread of COVID-19 in the field. Research by Kolebaje et al. [13] examines non-linear growth and mathematical models of COVID-19 in several African countries with the Atangana-Baleanu fractional derivative. In his research, actions or efforts to control the disease must concentrate on reducing the level of transmission through reducing contact, lockdown, and social distancing measures. Furthermore, Wangari et al. [14] examined a mathematical model of the spread of COVID-19 in Kenya with the mechanism for reinfection after the first infection. Numerical data shows that without non-pharmaceutical interventions, Kenya could see over 3,000 deaths. Wearing face masks and keeping physical distance has greatly delayed the peak of COVID-19 infections. This is strongly supported by simulations that vary parameters for consistent mask usage and social distancing while keeping other factors constant. Fu et al. [15] expanded the SIR model to optimize lockdown policies so that the economy and public health during the outbreak of COVID-19 continued to run well. [16] studied the impact of lockdown in India and revealed that if the lockdown policy was implemented the spread of COVID-19 could be limited. Implementing a partial lockdown can control the spread of COVID-19. Many other researchers also discuss mathematical models of the transmission of COVID-19 [17,18,19].

Based on this description, in this paper, we examine and study the dynamics that occur when people comply or do not with health protocols using mathematical models.

2. Methods

Model Formulation. In this section, a COVID-19 mathematical model with aspects of Community Compliance to Health Protocols is developed. The total human population at time t is denoted by $N(t)$ which consists of three subpopulations: (a) $S(t)$, a subpopulation of susceptible individuals who have the opportunity to be exposed to the virus, who will then become infected individuals, (b) $E(t)$, representing those who have been exposed to the virus but are not yet capable of passing it on to susceptible individuals, and (c) $I(t)$, a subpopulation of infected individuals who are able to transmit the virus to those who are still susceptible. Infected individuals can recover and become susceptible individuals. The total human population in the model discussed is:

$$N(t) = S(t) + E(t) + I(t). \tag{2.1}$$

Model Assumptions. The assumptions used to simplify the model are:

1. The total population is not constant.
2. The Recovered subpopulation was not included in this model.
3. The parameter Λ is the recruitment of individuals in the Susceptible subpopulation.
4. Infected people, whether they show symptoms or not, are categorized as an infected subpopulation.
5. Infected individuals will recover at rate π and die from infection at rate d.
6. The natural death rate of subpopulations $S(t)$, $E(t)$, and $I(t)$ is μ.

Model Equations. According to the provided description and assumptions, Figure 1 illustrates an appropriate compartment model to describe the dynamics of disease transmission.

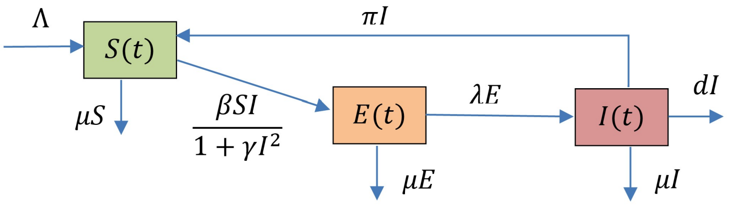

Figure 1. Transfer Diagram of the COVID-19 Mathematical Model with Aspects of Community Compliance to Health Protocols.

Based on Figure 1, a system of nonlinear differential equations is obtained which explains the mathematical model of COVID-19 with aspects of community compliance to health protocols as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - \frac{\beta S I}{1+\gamma I^2} - \mu S + \pi I,\\
\frac{dE}{dt} &= \frac{\beta S I}{1+\gamma I^2} - \lambda E - \mu E,\\
\frac{dI}{dt} &= \lambda E - \pi I - dI - \mu I.
\end{aligned} \tag{2.2}$$

with $t > 0$ and initial conditions $S(0) = S_0 \geq 0$, $S_P(0) = S_{P0} \geq 0$, $E(0) = E_0 \geq 0$, and $I(0) = I_0 \geq 0$. The parameters used in System 2.2 are given in Table 1.

Table 1. Description of parameters in the model

Parameter	**Description**
Λ	Rate of recruitment of susceptible individuals.
μ	Natural death rate.
β	Contact rate of susceptible individuals with infected individuals.
π	Individual recovery rate from being infected with COVID-19.
d	Individual death rate from COVID-19.
λ	The rate of change from exposed individuals to infected individuals.

In the next section, we will discuss the basic reproduction number, the existence of the balance point, the stability of the balance point, and numerical simulations to determine the influence of aspects of community compliance with health protocols on the spread of COVID-19.

3. Result and Discussion

Existence of Equilibrium Points and Basic Reproduction Numbers. The equilibrium point of System 2.2 can be determined by equating System 2.2 to zero, i.e.

$$\begin{aligned}\frac{dS}{dt} &= \Lambda - \frac{\beta SI}{1+\gamma I^2} - \mu S + \pi I = 0,\\ \frac{dE}{dt} &= \frac{\beta SI}{1+\gamma I^2} - \lambda E - \mu E = 0,\\ \frac{dI}{dt} &= \lambda E - \pi I - dI - \mu I = 0.\end{aligned}$$

When there are no subpopulations that are either susceptible or infected ($E = 0$ and $I = 0$), the disease-free equilibrium point is $E_0 = (S, E, I) = \left(\frac{\Lambda}{\mu}, 0, 0\right)$. Following this, the basic reproduction number (R_0) will be calculated using the Next Generation Matrix method. The basic reproduction number, also referred to as the epidemic threshold value, estimates the number of new infection cases generated by a single initial infection in a susceptible subpopulation. R_0 can be determined using the theory proposed by [20].

The infected compartments in System 2.2 are E and I. Let F_i be the rate of new infections entering compartment i and V_i be the movement of individuals leaving compartment i, then:

$$\begin{aligned}\frac{dE}{dt} &= F_E - V_E = \frac{\beta SI}{1+\gamma I^2} - (\lambda E + \mu E),\\ \frac{dI}{dt} &= F_I - V_I = 0 - (-\lambda E + \pi I + dI + \mu I).\end{aligned}$$

The Jacobian matrices of F and V at the disease-free equilibrium point $E_0 = (S, E, I) = \left(\frac{\Lambda}{\mu}, 0, 0\right)$ are:

$$DF(E_0) = F = \begin{pmatrix} \frac{\partial F_E(E_0)}{\partial E} & \frac{\partial F_E(E_0)}{\partial I} \\ \frac{\partial F_I(E_0)}{\partial E} & \frac{\partial F_I(E_0)}{\partial I} \end{pmatrix} = \begin{pmatrix} 0 & \frac{\beta\Lambda}{\mu} \\ 0 & 0 \end{pmatrix},$$

$$DV(E_0) = V = \begin{pmatrix} \frac{\partial V_E(E_0)}{\partial E} & \frac{\partial V_E(E_0)}{\partial I} \\ \frac{\partial V_I(E_0)}{\partial E} & \frac{\partial V_I(E_0)}{\partial I} \end{pmatrix} = \begin{pmatrix} \lambda + \mu & 0 \\ -\lambda & d + \mu + \pi \end{pmatrix}.$$

Next, we determine $\mathbf{FV}^{-1}$:

$$\mathbf{FV}^{-1} = \begin{pmatrix} \frac{\Lambda\gamma\alpha\beta}{(\gamma+\mu)\mu} + \frac{\Lambda\beta}{\gamma+\mu} & \frac{\lambda\theta}{(\lambda\theta+\mu)(d+\mu+\pi)} & \\ \frac{\frac{\Lambda\gamma\alpha\beta}{(\gamma+\mu)\mu} + \frac{\Lambda\beta}{\gamma+\mu}}{d+\mu+\pi} & 0 & 0 \end{pmatrix}.$$

The basic reproduction number is obtained by determining the largest eigenvalue of the matrix $\mathbf{FV}^{-1}$.

$$\begin{vmatrix} \frac{\beta\Lambda\lambda}{\mu(\lambda+\mu)(d+\mu+\pi)} & \frac{\beta\Lambda}{\mu(d+\mu+\pi)} \\ 0 & 0 \end{vmatrix} = 0$$

It is obtained that the eigenvalues are $q_1 = 0$ and $q_2 = \frac{\beta\Lambda\lambda}{\mu(\lambda+\mu)(d+\mu+\pi)}$. It can be seen that $q_1 < q_2$ because all parameter values are positive. Therefore, the basic reproduction number for System 2.2 is:

$$R_0 = \frac{\beta\Lambda\lambda}{\mu(\lambda + \mu)(d + \mu + \pi)}.$$

The basic reproduction number indicates that a person infected with the COVID-19 virus can spread it to other susceptible people during the infectious period at an average rate of:

$$\frac{\beta\Lambda\lambda}{\mu(\lambda + \mu)(d + \mu + \pi)}.$$

The following discussion focuses on the theorem about the existence of the equilibrium point for System 2.2, which is based on R_0.

Theorem 3.1. *Given* $R_0 = \dfrac{\beta\Lambda\lambda}{\mu(\lambda + \mu)(d + \mu + \pi)}$.

(1) If $R_0 \leq 1$ *then System 2.2 has a disease-free equilibrium point* $E_0 = \left(\frac{\Lambda}{\mu}, 0, 0\right)$.
(2) If $R_0 > 1$ *then System 2.2 has an endemic equilibrium point* $E^* = (S^*, E^*, I^*)$.

Proof. By equating the right side of System 2.2 to zero, we obtain:

$$\frac{dS}{dt} = \Lambda - \frac{\beta SI}{1 + \gamma I^2} - \mu S + \pi I = 0, \tag{3.1}$$

$$\frac{dE}{dt} = \frac{\beta SI}{1 + \gamma I^2} - \lambda E - \mu E = 0, \tag{3.2}$$

$$\frac{dI}{dt} = \lambda E - \pi I - dI - \mu I = 0. \tag{3.3}$$

Based on Equation 3.1, it is obtained:

$$\begin{aligned} &\Lambda - \frac{\beta SI}{1+\gamma I^2} - \mu S + \pi I = 0, \\ \iff\; &S = \frac{(\pi I + \Lambda)(\gamma I^2 + 1)}{I^2\gamma\mu + \beta I + \mu}. \end{aligned} \tag{3.4}$$

From Equation 3.3:

$$\begin{aligned} &\frac{dI}{dt} = \lambda E - \pi I - dI - \mu I = 0, \\ \iff\; &E = \frac{I(d+\mu+\pi)}{\lambda}. \end{aligned} \tag{3.5}$$

Note that $k_1 = \lambda + \mu$ and $k_2 = d + \mu + \pi$. Substitute Equation 3.4 and Equation 3.5 into Equation 3.2, and we get:

$$\begin{aligned} &\frac{\beta(\pi I + \Lambda)I}{I^2\gamma\mu + \beta I + \mu} - \frac{(Ik_1k_2)}{\lambda} = 0, \\ \iff\; &\frac{I(-I^2\gamma k_1k_2\mu - I\beta k_1k_2 + I\beta\lambda\pi + \Lambda\beta\lambda - k_1k_2\mu)}{(I^2\gamma\mu + \beta I + \mu)\lambda} = 0, \\ \iff\; &I(-I^2\gamma k_1k_2\mu - I\beta k_1k_2 + I\beta\lambda\pi + \Lambda\beta\lambda - k_1k_2\mu) = 0. \end{aligned} \tag{3.6}$$

Equation 3.6 produces $I = 0$ or $(-I^2\gamma k_1k_2\mu - I\beta k_1k_2 + I\beta\lambda\pi + \Lambda\beta\lambda - k_1k_2\mu) = 0$. For $I = 0$, we get $S = \frac{\Lambda}{\mu}$ and $E = 0$. Given $R_0 = \dfrac{\beta\Lambda\lambda}{\mu k_1k_2}$, substituting $R_0\mu k_1k_2 = \beta\Lambda\lambda$ into $(-I^2\gamma k_1k_2\mu - I\beta k_1k_2 + I\beta\lambda\pi + \Lambda\beta\lambda - k_1k_2\mu) = 0$, we get:

$$\begin{aligned} -I^2\gamma k_1k_2\mu - I\beta k_1k_2 + I\beta\lambda\pi + R_0\mu k_1k_2 - k_1k_2\mu = 0, \\ I^2\gamma k_1k_2\mu + (\beta k_1k_2 - \beta\lambda\pi)I - k_1k_2\mu(R_0 - 1) = 0. \end{aligned} \tag{3.7}$$

In Equation 3.7, it can be seen that if $R_0 = 1$, then we obtain $I^2\gamma k_1k_2\mu + (\beta k_1k_2 - \beta\lambda\pi)I = 0$. So, $I = 0$ or $I\gamma k_1k_2\mu + (\beta k_1k_2 - \beta\lambda\pi) = 0$. Next, it can be noted that:

$$\begin{aligned} &I\gamma k_1k_2\mu + (\beta k_1k_2 - \beta\lambda\pi) = 0, \\ \iff\; &I = \frac{\beta(\lambda\pi - k_1k_2)}{\gamma k_1k_2\mu}, \\ \iff\; &I = \frac{\beta(-d\lambda - d\mu - \lambda\mu - \mu^2 - \mu\pi)}{\gamma k_1k_2\mu}. \end{aligned}$$

It can be seen that I is negative. So for $R_0 = 1$, we obtain the disease-free equilibrium point $S = \frac{\Lambda}{\mu}$, $E = 0$, and $I = 0$. For $R_0 < 1$, in equation (8) it can be seen that the coefficient I^2, namely $a = \gamma k_1k_2\mu$, is positive, the coefficient I, namely $b = (\beta k_1k_2 - \beta\lambda\pi)$, is positive, and the constant $c = -k_1k_2\mu(R_0 - 1)$ is positive. There are two cases in determining the roots of I, namely:

(1) If $D \geq 0$ and the sum of the roots is negative, then both roots are negative; it can be concluded that negative values for I are ignored.
(2) If $D < 0$, then the roots obtained are complex numbers, so that I, which has a complex value, is also ignored.

So for $R_0 \leq 1$, we obtain a disease-free equilibrium point $E_0 = \left(\frac{\Lambda}{\mu}, 0, 0\right)$. Furthermore, for $R_0 > 1$, from equation (8), we obtain that a is positive, b is positive, and c is negative. The discriminant will be positive, and the real and distinct roots will be obtained. Since $a > 0$ means the curve opens upwards, and $c < 0$ means the curve cuts the negative y-axis, the roots of the quadratic equation obtained are two and have different signs. Therefore, there will be an endemic equilibrium point for $I > 0$ while $I < 0$ is ignored. So for $R_0 > 1$, we will get the endemic equilibrium point $E^* = (S^*, E^*, I^*)$. $\square$

Local Stability of Equilibrium Point. Next, we will discuss the local stability of disease-free and endemic equilibrium points.

Theorem 3.2. *Given* $R_0 = \dfrac{\Lambda\beta\lambda}{\mu k_1 k_2}$, *with* $k_1 = \lambda + \mu$ *and* $k_2 = d + \mu + \pi$.

(1) The disease-free equilibrium point $E_0 = (S^0, E^0, I^0) = \left(\frac{\Lambda}{\mu}, 0, 0\right)$ *is locally asymptotically stable if* $R_0 < 1$.

(2) The disease-free equilibrium point $E_0 = (S, E, I) = \left(\frac{\Lambda}{\mu}, 0, 0\right)$ *becomes unstable when* R_0 *exceeds 1.*

(3) The endemic equilibrium point $E_1 = (S^*, E^*, I^*)$ *is locally asymptotically stable if* $R_0 > 1$.

Proof. System 2.2 has a disease-free equilibrium point $E_0 = (S, E, I) = \left(\frac{\Lambda}{\mu}, 0, 0\right)$. The Jacobian matrix of System 2.2 is:

$$J(S,E,I) = \begin{pmatrix} -\frac{\beta I}{I^2\gamma+1} - \mu & 0 & \pi - \frac{\beta S}{I^2\gamma+1} + \frac{2\beta S I^2\gamma}{(I^2\gamma+1)^2} \\ \frac{\beta I}{I^2\gamma+1} & -(\lambda+\mu) & \frac{\beta S}{I^2\gamma+1} - \frac{2\beta S I^2\gamma}{(I^2\gamma+1)^2} \\ 0 & \lambda & -(d+\mu+\pi) \end{pmatrix}.$$

The Jacobian matrix evaluated at the disease-free equilibrium point $E_0 = (S, E, I) = \left(\frac{\Lambda}{\mu}, 0, 0\right)$ is:

$$J(E_0) = \begin{vmatrix} -\mu & 0 & \pi - \frac{\beta\Lambda}{\mu} \\ 0 & -k_1 & \frac{\beta\Lambda}{\mu} \\ 0 & \lambda & -k_2 \end{vmatrix}.$$

Next, we determine the roots of the characteristics.

$$|J(E_0) - pI| = 0,$$

$$\iff \begin{vmatrix} -\mu - p & 0 & \pi - \frac{\beta\Lambda}{\mu} \\ 0 & -k_1 - p & \frac{\beta\Lambda}{\mu} \\ 0 & \lambda & -k_2 - p \end{vmatrix} = 0,$$

$$\iff p^3 - (-k_2 - k_1 - \mu)p^2 - \frac{(\lambda\beta\Lambda - k_2\mu k_1 - k_1\mu^2)p}{\mu} - \lambda\beta\Lambda + k_2\mu k_1 = 0. \tag{3.8}$$

Based on Equation 3.8, the eigenvalues are obtained as follows:

(1) $p_1 = -\mu$,

(2) $p_2 = \dfrac{\sqrt{(k_1-k_2)^2\mu + 4\lambda\beta\Lambda\mu} - (k_1+k_2)\mu}{2\mu}$,

(3) $p_3 = \dfrac{-\sqrt{(k_1-k_2)^2\mu + 4\lambda\beta\Lambda\mu} - (k_1+k_2)\mu}{2\mu}$.

The equilibrium point E_0 is asymptotically stable if p_1, p_2, p_3, and p_4 are negative. Because $\mu > 0$, the value of p_1 is negative. Then it can be seen that p_2 and p_3 are negative if:

$$\begin{aligned}
\sqrt{[((k_1-k_2)^2\mu + 4\lambda\beta\Lambda)\mu]} - (k_1+k_2)\mu &< 0,\\
\iff \sqrt{[((k_1-k_2)^2\mu + 4\lambda\beta\Lambda)\mu]} &< (k_1+k_2)\mu,\\
\iff \left[((k_1-k_2)^2\mu + 4\lambda\beta\Lambda)\mu\right] &< [(k_1+k_2)\mu]^2,\\
\iff (k_1-k_2)^2\mu^2 + 4\lambda\beta\Lambda\mu &< [(k_1+k_2)\mu]^{,}\, 2\\
\iff 4\lambda\beta\Lambda\mu &< (k_1+k_2)^2\mu^2 - (k_1-k_2)^2\mu^2,\\
\iff 4\lambda\beta\Lambda &< 4\mu k_1 k_2,\\
\iff \frac{\lambda\beta\Lambda\mu}{\mu k_1 k_2} &< 1,\\
\iff R_0 &< 1.
\end{aligned}$$

If $R_0 > 1$, it will result in p_2 being non-negative, so the equilibrium point E_0 is unstable. The Jacobian matrix for the endemic equilibrium point $E_1 = (S^*, E^*, I^*)$ is as follows:

$$J(E_1) = \begin{pmatrix} -\frac{\beta I}{I^2\gamma+1} & 0 & \frac{\pi-\beta(\pi I+\Lambda)}{I^2\gamma\mu+\beta I+\mu} + \frac{2\beta(\pi I+\Lambda)I^2\gamma}{(I^2\gamma+1)(I^2\gamma\mu+\beta I+\mu)} \\ \frac{\beta I}{I^2\gamma+1} & -k_1 & \frac{\beta(\pi I+\Lambda)}{I^2\gamma\mu+\beta I+\mu} - \frac{2\beta(\pi I+\Lambda)I^2\gamma}{(I^2\gamma+1)(I^2\gamma\mu+\beta I+\mu)} \\ 0 & \lambda & -k_2 \end{pmatrix}.$$

The characteristic polynomial of the matrix $J(E_1)$ is as follows.

$$a_0p^3 + a_1p^2 + a_2p + a_3 = 0, \tag{3.9}$$

with:

$$\begin{aligned}
a_0 &= 1,\\
a_1 &= \frac{\gamma(k_1+k_2+\mu)I^2 + \beta I + k_1 + k_2 + \mu}{I^2\gamma+1},\\
a_2 &= \frac{1}{((I^2\gamma+1)(I^2\gamma\mu+\beta I+\mu))}\Bigg(((k_1+k_2)\mu + k_1k_2)\,\gamma^2\mu I^4\\
&\quad + ((2k_1+2k_2)\mu + \lambda\pi + k_1k_2)\,\gamma\beta I^3\\
&\quad + \left(2\gamma(k_1+k_2)\mu^2 + 2k_1k_2\gamma\mu + (\lambda\gamma\Lambda + \beta(k_1+k_2)\beta)\right) I^2\\
&\quad + \beta\left((2k_1+2k_2)\mu + k_1k_2 - \lambda\pi\right) I\\
&\quad + (k_1+k_2)\mu^2 + k_1k_2\mu - \Lambda\beta\lambda\Bigg),
\end{aligned}$$

$$a_3 = \frac{I^4\gamma^2 k_1 k_2 \mu^2 + 2I^3\beta\gamma k_1 k_2 \mu + (2k_1 k_2 \mu^2\gamma + \lambda\mu\beta\gamma\Lambda + \beta^2(k_1k_2 - \lambda\pi))I^2}{(I^2\gamma + 1)(I^2\gamma\mu + \beta I + \mu)} + \frac{2\mu\beta(k_1k_2 - \lambda\pi)I + \mu(-\Lambda\beta\lambda + k_1k_2\mu)}{(I^2\gamma + 1)(I^2\gamma\mu + \beta I + \mu)}.$$

For $R_0 > 1$, the values $a_0, a_1, a_2, a_3 > 0$ are obtained. All roots of the polynomial in Equation 3.8 have a negative part if and only if $|a_1| > 0$, $\begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} > 0$, and $\begin{vmatrix} a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 \\ 0 & 0 & a_3 \end{vmatrix} > 0$. In other words, all roots of the polynomial 3.9 have a negative part if and only if $a_1a_2 > a_3$ if and only if $R_0 > 1$. □

4. Numerical Simulation

The numerical simulation in this study shows explicitly how the level of health protocol compliance (γ) affects the infected population.

Table 2. Model parameter values

Parameter	**Unit**	**Source**
Λ	552	[21]
μ	5.258×10^{-5}	[16]
β	0.99102	[21]
π	0.012122	[21]
d	0.18169	[21]
λ	0.0083116	[21]

Several selected γ parameter values are $\frac{20\%}{30 \text{ days}}, \frac{40\%}{30 \text{ days}}, \frac{60\%}{30 \text{ days}}$, and $\frac{80\%}{30 \text{ days}}$, then the obtained results are given in Figure 2 and Figure 3.

Figure 2 and 3 illustrates that as public adherence to health protocols increases, the number of COVID-19 infections decreases. Community compliance is demonstrated by the extent to which people follow health measures such as mask-wearing, handwashing, and adhering to government rules to prevent the spread of COVID-19. Increased adherence to health protocols leads to reduced exposure to the COVID-19 virus.

The relationship between susceptible individuals and various values of γ over time is shown. The number of susceptible individuals is affected by how well health protocols are followed. The more adherence to health protocols, the lower the rate of infected individuals. The conclusion is that there is a correlation between compliance with health protocols and the level of spread of the COVID-19 virus. This indicates that the stricter people implement and follow health protocols, the lower the possibility of transmitting COVID-19.

In line with the Indonesian government's regulations, the number of COVID-19 infections can be reduced by continuing to comply with health protocols. Even

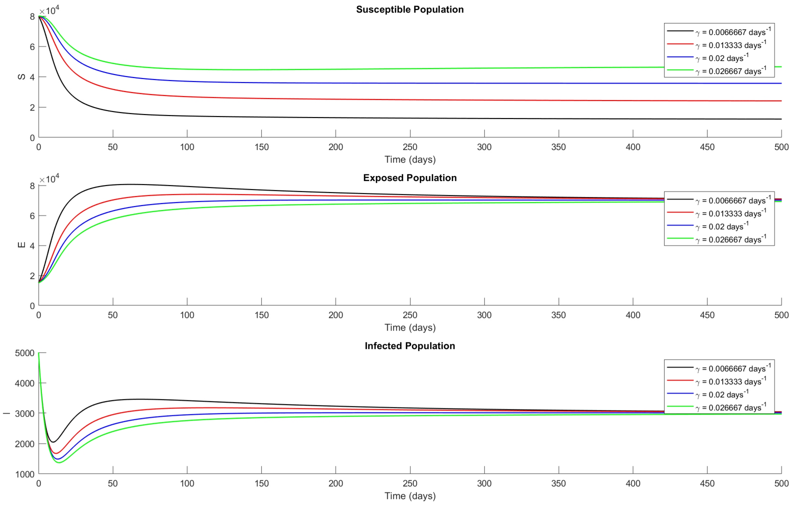

Figure 2. Graphs of $S(t)$, $E(t)$, $I(t)$ against t with several γ values.

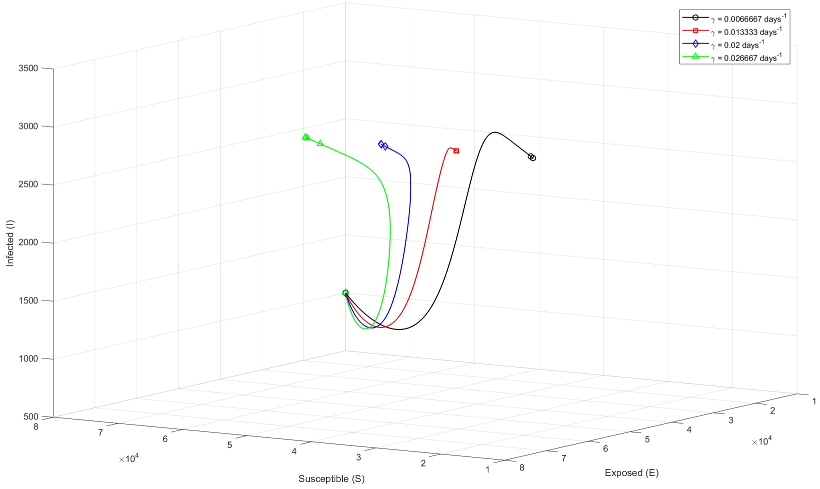

Figure 3. Solution of system 2.2 for several parameter values γ

though COVID-19 cases in 2023 may not be as severe as when COVID-19 first appeared, people should still maintain their health by adhering to health protocols for the common good and avoiding infection with the COVID-19 virus.

5. Conclusion and Suggestions

This paper presents a mathematical model of COVID-19 with aspects of community compliance to health protocols. Based on the R_0 value, two equilibrium points are obtained, namely the disease-free equilibrium point ($R_0 \leq 1$) and the endemic equilibrium point ($R_0 > 1$). Local stability analysis is carried out to determine the behavior of the system 2.2 solution around the two stability points. If R_0 is less than 1, the disease-free equilibrium point is locally asymptotically stable, whereas if R_0 is greater than 1, the endemic equilibrium point is locally asymptotically stable. The last numerical simulation session examined how community adherence to health protocols influences the spread of COVID-19.

There are several simplifications in forming the model in this paper. For future studies, we can consider subpopulations of infected humans who show symptoms and those who do not.

6. Acknowledgement

We are grateful for the financial support from the Institute for Research and Community Service of Udayana University for this research.

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