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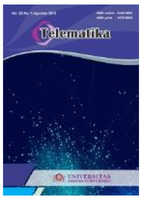

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SEIHR Model on Spread of COVID-19 and Its Simulation

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ABSTRACT

The modified SEIR model of the COVID-19 spread is divided into five compartments: susceptible, exposed, infected, isolated, and recovered. Discussion of the article includes equilibrium points, non-negativity of state variables, boundedness of state variables, stability analysis, sensitivity analysis, and numerical simulations. Based on the results, two equilibrium points were obtained: the disease-free equilibrium point and the endemic equilibrium point. The existence of an equilibrium point depends on the value of the basic reproduction number R_0 using the next-generation matrix, as well as on stability. The endemic equilibrium point exists if it is satisfied $R_0 > 1$. Then, the disease-free equilibrium point is said to be locally asymptotic stable if $R_0 < 1$, and the endemic equilibrium point is locally asymptotic stable if $R_0 > 1$. Sensitivity analysis was carried out to determine the most influential parameter in the spread of the virus, namely β. Finally, the numerical simulations determine the model's behavior and support the dynamic analysis results.

INTRODUCTION

SARS (Severe Acute Respiratory Syndrome) and MERS (Middle East Respiratory Syndrome) are two respiratory diseases caused by the coronavirus (WHO, 2020a). Additionally, a novel coronavirus known as 2019n-Cov was identified as the cause of COVID-19 illness. The World Health Organization (WHO) released several temporary guidelines for all nations on January 10, 2020. These temporary guidelines include monitoring individuals who may be COVID-19 carriers, gathering and testing samples (tracing), treating COVID-19 patients, and managing and reducing the burden of COVID infection in hospitals. The symptoms are typically minor and develop gradually. Humans, however, may contract the disease and exhibit mild or no symptoms, severe symptoms, fever, shortness of breath, or coughing coupled with chest pain and breathing difficulties. (WHO, 2020a).

Through measures including social isolation, tracking, home-based employment, and solid geographical limits, the government has attempted to regulate COVID-19. Therefore, isolation and quarantine are the most efficient methods of epidemic prevention without vaccines or treatments (Usaini et al., 2019). According to (WHO, 2020b), quarantine separates susceptible individuals and exposed individuals. Then, the definition of isolation is the separation of diseased people.

According to WHO, mathematical models are crucial for guiding policymakers and other decisionmakers in the field of health care to find solutions or make judgments (government) (Tang et al., 2020). Making mathematical models of actual situations is one method for discussing issues in the real world. A mathematical model can be created using the assumptions made about environmental problems. It can be theoretically resolved and then used once more to tackle actual issues. In light of the region explored with mathematical modeling, researchers are working together to investigate COVID-19 from all angles. Some solutions can be performed to decrease the number of infected numbers.

The SIR model is a simple mathematical representation of how disease spreads. The SIR model was first introduced by Kermack and McKendrick in 1927 and later developed into a reference tool and is very important in developing mathematical theories regarding disease transmission (Müller & Kuttler, 2015; Murray, 2002). Additionally, research has established the SIR model as a standard by which many scientists create more precise mathematical models of disease transmission. This mathematical model is employed as quantitative data in situations and offers advantages for disease outbreaks and policy-making. Several studies related to the disease spread of coronavirus are SARS (Feng, 2007) and MERS (Tahir et al., 2019; Usaini et al., 2019). In 2020 the coronavirus, so-called COVID-19, became a hot topic until now.

Youssef et al. (2020) constructed four compartments: S, E, I, and R, recovering individuals exposed and infected. In addition, Zeb et al. (2020) split the population into five groups: S, E, I, H, and R, isolating individuals exposed and infected. Furthermore, Labzai et al. (2020) constructed five compartments: S, E, I, H, and R. Recovering individuals exposed because of strong immunity and infected individuals need to be isolated.

Based on previous research, this paper constructs a new COVID-19 model by combining the study of Youssef et al., Zeb et al., and Labzai et al. Population in this model split population into five groups, named S, E, I, H, and R. The model that has been obtained is determined the point of equilibrium, finding the basic reproduction number R_0, sensitivity analysis, and analyze the stability of the model. The study obtained is simulated numerically as model validation in the final stage.

RESEARCH METHODS

Combining the literature review, theory, and experiment. Action research carried out consists of the following:

1. Model construction.

   The COVID-19 epidemic model was built on the assumptions of previous studies (Youssef et al., Zeb et al., and Labzai et al.). Five compartments are used to describe the process of spreading disease from one to another.
2. Determine the equilibrium points

   The differential equation's right side is set to zero to determine the equilibrium point. There are often two equilibrium points: disease-free $(I = 0)$ and endemic $(I \neq 0)$.
3. Determine the basic reproduction number

   The basic reproduction number is determined using the next-generation matrix. A value of less than one indicates that each infected individual will infect less than one susceptible, so there is no epidemic. However, if the number is greater than one, it indicates that each infected individual will transmit from one susceptible so that an outbreak will occur.
4. Determine non-negativity and boundedness of state variables
5. Determining the stability of the equilibrium points

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The linearization of the model to create the Jacobian matrix is the first step in determining stability. Additionally, it was established based on the sign of the eigenvalues at each produced equilibrium point of the characteristic equation based on the Jacobian matrix. The equilibrium point is locally asymptotically stable when all of the real part's eigenvalues are negative.

6. Sensitivity analysis

   Sensitivity analysis was carried out to determine the most influential parameters in the spread of the virus, with the aim that later, it can be controlled for the most influential parameters.
7. Numerical simulation

   Numerical simulations are carried out by choosing parameter values that satisfy the stability requirements to illustrate the analytical results and use the Runge-Kutta 4th-order method.

RESULTS AND DISCUSSION

A. Model Formulation

This study discusses the COVID-19 model with an isolation compartment. We divide the total human population into five compartments: the susceptible (*S*), the exposed (*E*), the infected (*I*), the isolation (*H*), and the recovered (*R*). In simple terms, the dynamics of the spread of COVID-19 are shown in Figure 1.

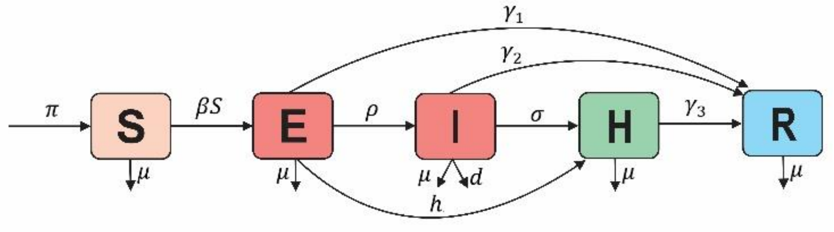

Figure 1. SEIHR Model to COVID-19 Spread

Based on Figure 1, the model takes the following form:

$$\begin{aligned}
\frac{dS}{dt} &= \pi - \beta SI - \mu S,\\
\frac{dE}{dt} &= \beta SI - \rho E - \gamma_1 E - hE - \mu E,\\
\frac{dI}{dt} &= \rho E - dI - \gamma_2 I - \mu I - \sigma I,\\
\frac{dH}{dt} &= hE - \gamma_3 H - \mu H + \sigma I,\\
\frac{dR}{dt} &= \gamma_1 E + \gamma_2 I + \gamma_3 H - \mu R,
\end{aligned} \tag{1}$$

where the parameter π new birth rate in susceptible human population, β is represents the contact coefficient of transmission, μ is the natural death rate of a human, d is the death rate due to COVID-19, γ_1 is the rate of recovery from exposed due to the strong immunity of these individuals, γ_2 is the rate of recovery from infection, γ_3 is the rate of recovery from isolation, ρ is the transmission rate of infected, h is the rate of isolation from exposed, and σ is the rate of isolation from infection.

B. Equilibrium Point and Basic Reproduction (R_0)

Equation (1) can be simplified to

$$\begin{aligned} \frac{dS}{dt} &= \pi - \beta SI - \mu S, \\ \frac{dE}{dt} &= \beta SI - k_1 E, \\ \frac{dI}{dt} &= \rho E - k_2 I, \\ \frac{dH}{dt} &= hE - k_3 H + \sigma I, \\ \frac{dR}{dt} &= \gamma_1 E + \gamma_2 I + \gamma_3 H - \mu R, \end{aligned} \tag{2}$$

where $k_1 = \rho + \gamma_1 + h + \mu$, $k_2 = d + \gamma_2 + \mu + \sigma$, $k_3 = \gamma_3 + \mu$.

Determining the equilibrium point of this model, we set all derivatives equal to zero. One of these is the disease-free equilibrium point (y^0):

$$y^0 = (S^0, E^0, I^0, H^0, R^0) = \left(\frac{\pi}{\mu}, 0,0,0,0\right).$$

Next, calculate R_0 of equation (2). The second point of equilibrium will then be covered, and the Next Generation Matrix technique will be used to get R_0.

Let $x = (E, I)$ and may be stated as

$$\frac{dx}{dt} = f - v,$$

where

$$f = \begin{bmatrix} \beta SI \\ \rho E \end{bmatrix}, v = \begin{bmatrix} k_1 E \\ k_2 I \end{bmatrix}.$$

Then, at the point y^0, the partial derivatives of the matrices f and v.

$$F(y^0) = \begin{bmatrix} 0 & \frac{\beta\pi}{\mu} \\ \rho & 0 \end{bmatrix}, V(y^0) = \begin{bmatrix} k_1 & 0 \\ 0 & k_2 \end{bmatrix}.$$

The Next Generation Matrix by calculating $M = FV^{-1}$. Additionally, because all parameters are positive, the reproduction number may be calculated from the M matrix's spectral radius as follows.

$$M = \begin{bmatrix} 0 & \frac{\beta\pi}{\mu k_2} \\ \frac{\rho}{k_1} & 0 \end{bmatrix},$$

$$R_0 = \frac{\rho\beta\pi}{\mu k_1 k_2}.$$

Theorem 1. There exists a positive endemic equilibrium point y^* for model (4) if $R_0 > 1$.

Proof. The second point of equilibrium of model (6) is obtained

$$S^* = \frac{k_1 k_2}{\rho\beta},$$

$$E^* = \frac{\pi\rho\beta - k_1 k_2 \mu}{\beta k_1 \rho} = \frac{k_2 \mu}{\beta\rho}(R_0 - 1),$$

$$I^* = \frac{\pi\rho\beta - k_1 k_2 \mu}{\beta k_1 k_2} = \frac{\mu}{\beta}(R_0 - 1),$$

$$H^* = \frac{(\pi\rho\beta - k_1k_2\mu)Y}{\beta k_1k_2\rho k_3} = \frac{\mu Y}{\beta k_3\rho}(R_0 - 1),$$

$$R^* = \frac{(\pi\rho\beta - k_1k_2\mu)Z}{\beta k_1k_2\rho k_3\mu} = \frac{Z}{\beta k_3\rho}(R_0 - 1),$$

where $Z = \rho\gamma_2k_3 + \rho\gamma_3\sigma + \gamma_1k_2k_3 + \gamma_3hk_2$, and $Y = (\alpha\sigma + hk_2)$.

The values of S^*, E^*, I^*, H^*, and R^* make it obvious that if $R_0 > 1$, there exists a positive endemic equilibrium point called y^*.

C. Non-negativity of State Variables

Then we present the non-negativity of the solution for the state variables $S(t), E(t), I(t), H(t)$ and $R(t)$ of equation (2) for all $t > 0$.

Theorem 2. All the state variables $S(t), E(t), I(t), H(t)$ and $R(t)$ of equation (2) with non-negative initial values have the non-negative solution for all the time $t > 0$.

Proof. It follows from the first equation of equation (2) that one has

$$\frac{dS}{dt} = \pi - G(t)S(t),$$

where $G(t) = \beta I + \mu$. Then, we multiply the equation above by

$$e^{\int_0^t G(r)\,dr},$$

to get

$$\frac{dS}{dt}e^{\int_0^t G(r)\,dr} = \big(\pi - G(t)S(t)\big)e^{\int_0^t G(r)\,dr},$$

which implies

$$\frac{dS}{dt}e^{\int_0^t G(r)\,dr} + G(t)S(t)\frac{dS}{dt}e^{\int_0^t G(r)\,dr} = \pi e^{\int_0^t G(r)\,dr}.$$

Then, we can rewrite it into the following equation

$$\frac{d}{dt}\left(S(t)e^{\int_0^t G(r)\,dr}\right) = \pi e^{\int_0^t G(r)\,dr}.$$

By taking the integration of the equation above with respect to t, one has

$$S(t)e^{\int_0^t G(r)\,dr} - S(0) = \int_0^t \pi e^{\int_0^t G(r)\,dr}\,dp.$$

We further assume that $S(0) = S_0 > 0$ and multiply the equation above by $e^{-\int_0^t G(r)\,dr}$. One can derive

$$S(t) = S_0e^{-\int_0^t G(r)\,dr} + \pi e^{-\int_0^t G(r)\,dr}\left(\int_0^t e^{\int_0^t G(r)\,dr}\,dp\right) \geq 0,$$

which means that the solution of $S(t)$ is positive for all the time $t > 0$.

Employing a similar way for the states $E(t), I(t), H(t)$, and $R(t)$, then assuming $E(0) = E_0 > 0$, $I(0) = I_0 > 0, H(0) = H_0 > 0, R(0) = R_0 > 0$, so obtained

$$E(t) = E_0e^{-k_1t} + \beta e^{-k_1t}\left(\int_0^t S(p)I(p)e^{k_1t}\,dp\right) \geq 0,$$

$$I(t) = I_0e^{-k_2t} + \rho e^{-k_2t}\left(\int_0^t E(p)e^{k_2t}\,dp\right) \geq 0,$$

$$H(t) = H_0 e^{-k_3 t} + e^{-k_3 t}\left(\int_0^t \big(hE(p) + \sigma I(p)\big)e^{k_3 t}\, dp\right) \geq 0,$$

$$R(t) = R_0 e^{-\mu t} + e^{-\mu t}\left(\int_0^t (\gamma_1 E(p) + \gamma_2 I(p) + \gamma_3 H(p))e^{\mu t}\, dp\right) \geq 0.$$

Finally, we can conclude that the non-negativity of the solution for the state variables $S(t), E(t), I(t), H(t)$, and $R(t)$ are obtained for all the time $t > 0$.

D. Boundedness of State Variables

Now, we state the following theorem for the boundedness of the solution for the state variables $S(t), E(t), I(t), H(t)$, and $R(t)$.

Theorem 3. All the state variables $S(t), E(t), I(t), H(t)$, and $R(t)$ are bounded in a region $\Omega = \left\{N(t) \in \mathbb{R}^5 : N(t) \leq \frac{\pi}{\mu}\right\}$.

Proof. Let $N(t)$ be the total population of the dynamical system (2). Then we derive $N(t)$ with respect to t and employ all the state variables in (2) to get

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dH}{dt} + \frac{dR}{dt},$$
$$= \pi - \mu N(t) - dI(t) \leq \pi - \mu N(t),$$

which gives

$$N(t) \leq \frac{\pi}{\mu} + N(0)e^{-\mu t},$$

where $N(0)$ is the initial value of the total population. Then by taking the limit $t \longrightarrow \infty$, one has

$$\lim_{t \longrightarrow \infty} \sup N(t) \leq \frac{\pi}{\mu},$$

which implies that

$$S(t) + E(t) + I(t) + H(t) + R(t) \leq \frac{\pi}{\mu}.$$

It follows from Theorem 2, and we can conclude that all state variables $S(t), E(t), I(t), H(t)$, and $R(t)$ are positive in the bounded region Ω.

E. Stability Analysis

The Jacobi matrix is created using the linearization procedure in equation (2) as follows:

$$J_1 = \begin{bmatrix} -\beta I - \mu & 0 & -\beta S & 0 & 0 \\ \beta I & -k_1 & \beta S & 0 & 0 \\ 0 & \rho & -k_2 & 0 & 0 \\ 0 & h & \sigma & -k_3 & 0 \\ 0 & \gamma_1 & \gamma_2 & \gamma_3 & -\mu \end{bmatrix}. \tag{3}$$

First, for y^0 then the Jacobi matrix equation (3) is

$$J_1 = \begin{bmatrix} -\mu & 0 & -\beta\pi/\mu & 0 & 0 \\ 0 & -k_1 & \beta\pi/\mu & 0 & 0 \\ 0 & \rho & -k_2 & 0 & 0 \\ 0 & h & \sigma & -k_3 & 0 \\ 0 & \gamma_1 & \gamma_2 & \gamma_3 & -\mu \end{bmatrix}. \tag{4}$$

Based on (4), Thus, the eigenvalues are obtained $\lambda_1 = -\mu < 0$, $\lambda_2 = -\mu < 0$, and $\lambda_3 = -k_3 < 0$. Therefore, the stability of the point y^0 depends on

$$M_1 = \begin{vmatrix} -k_1 - \lambda & \dfrac{\beta\pi}{\mu} \\ \rho & -k_2 - \lambda \end{vmatrix}.$$

So that it is obtained

$$\lambda^2 + a_1\lambda + a_2, \tag{5}$$

where

$a_1 = k_1 + k_2,$

$a_2 = \dfrac{-\beta\pi\rho + k_1k_2\mu}{\mu} = k_1k_2(1 - R_0).$

Its real roots are negative if the characteristic equation (5) satisfies the Routh-Hurwitz requirements. If $R_0 < 1$, then $a_1 > 0$ and $a_2 > 0$. According to Theorem 1, the point K^0 is determined to be locally asymptotically stable if $R_0 < 1$. The Routh-Hurwitz criterion is not met if $R_0 > 1$ because the value of $a_2 < 0$. As a result, the point K^0 is locally unstable if $R_0 > 1$.

Second, the Jacobi matrix equation (3) at the point y^* is

$$J_2 = \begin{bmatrix} -\mu R_0 & 0 & -k_1k_2/\rho & 0 & 0 \\ \mu(R_0 - 1) & -k_1 & k_1k_2/\rho & 0 & 0 \\ 0 & \rho & -k_2 & 0 & 0 \\ 0 & h & \sigma & -k_3 & 0 \\ 0 & \gamma_1 & \gamma_2 & \gamma_3 & -\mu \end{bmatrix}.$$

So that the eigenvalues are obtained $\lambda_1 = -\mu < 0$ and $\lambda_2 = -k_3 < 0$. Therefore, the stability of the point y^* depends on

$$M_2 = \begin{vmatrix} -\mu R_0 & 0 & -k_1k_2/\rho \\ \mu(R_0 - 1) & -k_1 & k_1k_2/\rho \\ 0 & \rho & -k_2 \end{vmatrix}.$$

So that it is obtained

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3, \tag{6}$$

where

$a_1 = R_0\mu + k_1 + k_2,$

$a_2 = R_0k_1\mu + R_0k_2\mu,$

$a_3 = R_0k_1k_2\mu - k_1k_2\mu = k_1k_2\mu(R_0 - 1).$

From these results, it can be concluded that if $R_0 > 1$ then $a_1 > 0$, $a_2 > 0$, $a_3 > 0$, and if $R_0 < 1$ then $a_3 < 0$. Finding the root value based on the characteristic equation (6) is difficult. Therefore, determine the stability of the point y^* using the Routh-Hurwitz criterion. In addition, the point y^* is asymptotically stable if and only if it satisfies the conditions listed below:

1) $a_1 > 0,$
2) $a_2 > 0,$
3) $a_1a_2 - a_3 > 0.$

If both requirements (1) and (2) are satisfied, then point y^* is locally asymptotically stable: $a_1a_2 - a_3 = (\mu(k_1 + k_2)R_0^2 + k_1k_2 + (k_1^2 + k_1k_2 + k_2^2)R_0)\mu > 0.$

It is clear that the endemic equilibrium point y^* satisfies all the criteria. Therefore, the endemic equilibrium point y^* is locally asymptotically stable when $R_0 > 1$.

F. Sensitivity Analysis

Sensitivity analysis of the basic reproduction numbers that have been obtained using the parameter values in Table 1.

Table 1. Parameter Values of The Model

Parameter	Value	Source
π	1.685	[(Rois et al., 2021a), (Rois et al., 2021b)]
β	1.2203×10^{-4}	Assumption
μ	3.9139×10^{-5}	Assumption
ρ	0.0714	(Annas et al., 2020)
d	0.087	(Sasmita et al., 2020)
γ_1	0.1	Assumption
γ_2	0.1	Assumption
γ_3	0.1	(Aldila et al., 2020)
σ	0.083	(Aldila et al., 2020)
h	0.2435	(Aldila et al., 2020)

This sensitivity index can be used to determine how important certain factors are for the spread of disease. As a result, this method is used to identify the parameters that need to be controlled and those that have a substantial impact on R_0. Parameter sensitivity analysis using the method introduced by Chitnis et al. (Rois et al., 2021c).

Definition 1. The normalized forward sensitivity index of R_0 that depends differentiably on a parameter τ is defined by

$$C_\tau^{R_0} = \frac{\partial R_0}{\partial \tau}\frac{\tau}{R_0}.$$

Some of the parameters obtained are as follows:

$$C_\pi^{R_0} = \frac{\partial R_0}{\partial \pi} \times \frac{\pi}{R_0} = 1,$$

$$C_\beta^{R_0} = \frac{\partial R_0}{\partial \beta} \times \frac{\beta}{R_0} = 1,$$

$$C_\rho^{R_0} = \frac{\partial R_0}{\partial \rho} \times \frac{\rho}{R_0} = \frac{\gamma_1 + h + \mu}{\rho + \gamma_1 + h + \mu} = 0.828,$$

$$C_\mu^{R_0} = \frac{\partial R_0}{\partial \mu} \times \frac{\mu}{R_0} = -\frac{-3\mu^2 - X_1\mu - X_2}{k_1 k_2} = -1.0002,$$

with $X_1 = 2d + 2h + 2\rho + 2\sigma + 2\gamma_1 + 2\gamma_2$, and $X_2 = (h + \rho + \gamma_1)(d + \sigma + \gamma_2)$.

$$C_{\gamma_1}^{R_0} = \frac{\partial R_0}{\partial \gamma_1} \times \frac{\gamma_1}{R_0} = -\frac{\gamma_1}{\rho + \gamma_1 + h + \mu} = -0.241,$$

$$C_{\gamma_2}^{R_0} = \frac{\partial R_0}{\partial \gamma_2} \times \frac{\gamma_2}{R_0} = -\frac{\gamma_2}{d + \gamma_2 + \mu + \sigma} = -0.370,$$

$$C_h^{R_0} = \frac{\partial R_0}{\partial h} \times \frac{h}{R_0} = -\frac{h}{\rho + \gamma_1 + h + \mu} = -0.587,$$

$$C_d^{R_0} = \frac{\partial R_0}{\partial d} \times \frac{d}{R_0} = -\frac{d}{d + \gamma_2 + \mu + \sigma} = -0.322,$$

$$C_{\sigma}^{R_0} = \frac{\partial R_0}{\partial \sigma} \times \frac{\sigma}{R_0} = -\frac{\sigma}{d + \gamma_2 + \mu + \sigma} = -0.307.$$

$R_0 = 3.348$ is generated using the parameter values in Table 1, and the parameter sensitivity index is shown in Figure 2.

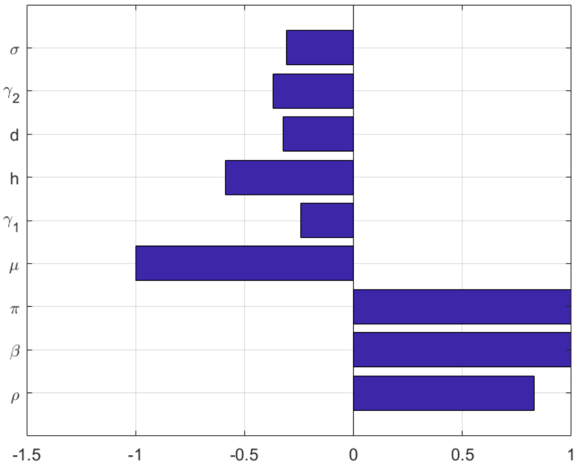

Figure 2. Sensitivity Index of R_0

The parameter indices with positive and negative values are displayed in Figure 2. Those parameters with positive indices are $\pi, \beta,$ and ρ. R_0 will increase (decrease) if the value of one of the parameters increases (decrease). Because of this, COVID-19 is spreading to increase (decrease). Furthermore, for parameters with negative indexes such as $\mu, \gamma_1, \gamma_2, h, d,$ and σ. The distribution of COVID-19 will decrease (increase) if the value of one of these parameters is increased (decreased).

G. Numerical Simulations

To illustrate the analysis findings, a numerical simulation of solution (2) is as follows. These were conducted using the Runge-Kutta 4th order method (Trisilowati et al., 2021) to show the transmission of the COVID-19 model. Table 1 displays the parameter values utilized in this simulation.

1) Numeric simulation for $R_0 < 1$

Shows the stability of the point y^0. Except for $\mu = 3.9139 \times 10^{-4}$ and the parameter values in the preceding table are used so that it is obtained $R_0 = 0.334 < 1$.

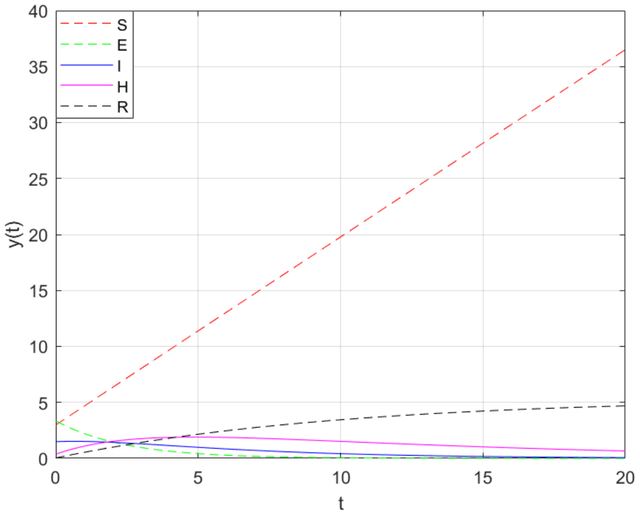

Figure 3. Simulation Results of The System (2) for $R_0 < 1$

The simulation's findings demonstrate that the solution graphs to y^0. This indicates that no one has contracted COVID-19 after a considerable amount of time. The analysis findings are supported by the numerical simulation results, which show that y^0 is locally asymptotically stable if $R_0 < 1$.

2) Numeric simulation for $R_0 > 1$

This simulation demonstrates the stability of the y^* point gave the parameter values listed in Table 1, with $R_0 = 3.348 < 1$.

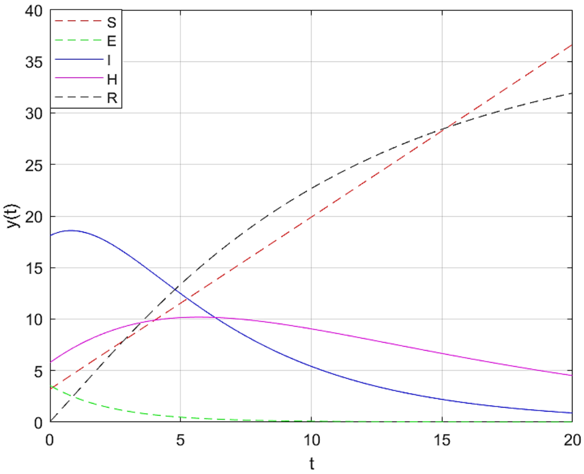

Figure 4. Simulation Results of The System (2) for $R_0 > 1$

The simulation's results reveal the graph solution of the point y^*, and this indicates that COVID-19 is to control the disease's spread. The analysis's findings are supported by the numerical simulation results, which show that the point of y^* is locally stable and asymptomatic if $R_0 > 1$. $R_0 > 1$ is obtained from the parameter values that are provided. It denotes that COVID-19 has caused a disease outbreak. Therefore, it is necessary to take control measures to reduce the epidemic.

CONCLUSIONS AND RECOMMENDATIONS

There are two equilibrium points in the modified SEIR model of the spread of COVID-19: the disease-free equilibrium (y^0) and the endemic equilibrium (y^*). The point y^0 exists regardless of whether $R_0 > 1$ is true, whereas the point y^* only occurs if $R_0 > 1$. Each parameter in R_0 has its sensitivity analysis described. The findings indicated that the variables $\pi, \beta,$ and ρ, and have a positive index. The spread of COVID-19 increases (decreases) if the value of one of the parameters is increased (decreased), which causes R_0 to increase (decrease). Negative index parameters, including $\mu, \gamma_1, \gamma_2, h, d,$ and σ. The distribution of COVID-19 will decrease (increase) if the value of one of these parameters is increased (decreased). The point y^* is asymptotically stable with the criteria, but the point y^0 is asymptotically stable if it meets $R_0 < 1$.

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