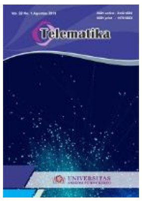

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Dynamical Analysis of the Spread of COVID-19 model and its Simulation with Vaccination and Social Distancing

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ABSTRACT

In this study, SEIRS on the impacts of vaccination and social isolation on the transmission of COVID-19, model development, and dynamical analysis were discussed. The four subpopulations that make up the human population in this model are the susceptible individual subpopulation (S), the exposed individual subpopulation (E), the infected individual subpopulation (I), and the recovered individual subpopulation (R). The premise behind this idea is that a person who has recovered from the sickness is nonetheless susceptible to reinfection. The fundamental reproduction number ($\mathcal{R}_0$) The fundamental reproduction number, and an assessment of the equilibrium point's local stability. The model has two equilibrium locations, according to the results of the dynamical study, one for a state with endemic disease and the other for a state without disease. Although there is always a disease-free equilibrium point, mathematical $\mathcal{R}_0$>1 suggests that there may also be an endemic equilibrium point. In the event where $\mathcal{R}_0$<1, the disease-free equilibrium point is locally asymptotically stable. However, if the Routh-Hurwitz conditions are met, the endemic equilibrium point is locally asymptotically stable. The outcomes of the numerical simulation support the analysis's conclusions.

INTRODUCTION

A severe case of acute respiratory syndrome Coronavirus 2 (SARS-CoV-2) is what causes infectious coronavirus sickness (COVID-19), which was discovered in the Chinese city of Wuhan in December 2019. SARS-CoV-2 is a virus that belongs to the same family as MERS and SARS. Despite having some similarities to the viruses that cause SARS and MERS, the virus is more infectious. On January 30, 2020, the World Health Organization (WHO) declared the COVID-19 outbreak a PHEIC (public health emergency of international concern). On March 11, 2020, the WHO subsequently formally proclaimed COVID-19 a global pandemic (Ministry of Health, 2020).

There are increasingly more instances of COVID-19 spreading over the world, especially in Indonesia. Indonesia has the most COVID-19 instances in Southeast Asia, according to World Meters data (2022), with 5,350,902 positive cases and 147,025 fatalities as of February 23, 2022. Up through March 30, 2022, there were 3,840 more positive cases in Indonesia, totaling 7,876 recoveries and 118 fatalities. Researchers are now interested in undertaking more extensive epidemiology investigations because of the COVID-19 epidemic. To comprehend the principles governing the prevention of COVID-19 disease

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transmission throughout the community, the researchers employed a range of techniques. One of them is to do mathematical modeling.

The classical theory of the first epidemic model, which consists of three subpopulations: susceptible (people who are not infected but can contract the disease), infected (persons who are ill and can spread diseases) and sick persons who have made a full recovery, was first presented by Kermack and McKendrick in 1927. According to Sihotang et al. (2019), several researchers add new subpopulations to their models, such as exposed persons (those who have been exposed to the disease but are not yet totally afflicted). Ilahi and Fadilaturrohmah (2021) used a model in earlier studies to examine how the treatment of chronically infected populations affected the propagation of the hepatitis C virus. Oktavia (2016) also employed a model to examine the stability of the dynamic system model of the transmission of the varicella virus, which causes chickenpox. Risky (2015) employed a population model in his study to examine the transmission of the T-disease TB, with a model that is as dissimilar as the two. Additionally, Zhafran et al. (2022) utilized a model to examine how immunization affected the spread of pneumonia in young children.

By assuming that the recovered subpopulation can re-infect the host, we extend the model of Annas et al. (2020) in this work. Annas et al. (2020) revealed the rate of change of individuals leaving susceptible subpopulations and changed to the rate of change of individuals entering other subpopulations due to the lack of social distance as a preventive measure against the spread of Coronavirus Disease. The dynamic analysis of the pattern used in this study is identical to the analysis carried out by Zhafran et al. in their study on the model of pneumonia illness transmission in toddlers under the influence of vaccination in 2022. Finding the equilibrium point and the base reproduction number, examining the model's equilibrium point's local stability, and interpreting numerical simulation results using the Order 4 Runge-Kutta method are all part of the analysis done on this model.

The creation of a mathematical model for COVID-19 transmission is still very much in progress and is still being done today. The spread of COVID-19 is hampered, particularly in the present, by the advent of preventive measures such immunization and social seclusion. Therefore, this study uses a model with parameters for social distance and vaccination to analyze the transmission of COVID-19.

RESEARCH METHODS

These are the steps involved in doing the research, shown in Figure 1.

1. Construct a mathematical model.
   According to a revised study by Annas et al. (2020), a mathematical model for the propagation of COVID-19 has been developed, which includes the presumption that recovered subpopulations can be reinfected. The four subpopulations in this model are susceptible (S), exposed (E), infected (I), and recovered (R).
2. Determine the equilibrium points of the model.
   Using the notion of an autonomous equilibrium point, the model equilibrium point may be found. Endemic equilibrium points and free-disease equilibrium points are the two main types of equilibrium points. To derive these, we follow Alligood et al. (2000), Murray (2002), Boyce and DiPrima (2012), and Brauer and Chavez (2012).
3. Establish the fundamental reproduction number.

This fundamental reproduction number can be calculated using the Next Generation Matrix approach starting from the equilibrium point of the created model. Researched by us is Driessche and Watmough (2002).

4. Investigate the stability of the equilibrium points locally.

   To obtain the Jacobian matrix, the nonlinear model must first be linearized. The characteristic equation's eigenvalues are then obtained by adding the equilibrium points to the Jacobian matrix. Therefore, when all the real portions' eigenvalues are negative, locally asymptotically stability is attained. Additionally, when there is at least one positive number, unstable is obtained. To investigate these, we check Robinson (2012).

5. Computational simulation.

   Numerical simulations are performed to demonstrate the analytical findings by selecting a small number of parameters that completely satisfy the stability requirements. The 4th-order Runge-Kutta approach is used to numerically solve the model (Chapra and Canale, 2010).

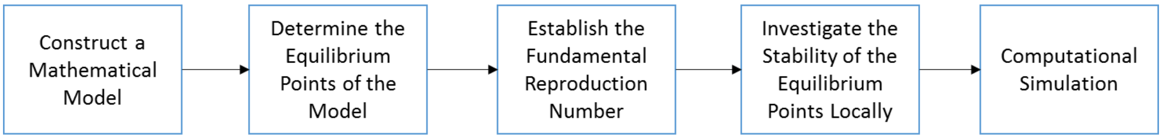

Figure 1. Research Design

RESULTS AND DISCUSSION

1. Model Formulation

The recovered subpopulation can be reinfected, according to the study changes outlined by Annas et al. (2020), which are reflected in this mathematical model of COVID-19 transmission. With the addition of this supposition, the dynamic analysis conducted in this study is identical to the analysis conducted by Zhafran et al. in their study on the model of pneumonia in toddlers with the influence of vaccination in 2022. Four subpopulations of the population are distinguished: susceptible persons, who are not infected but are at risk of developing the disease, exposed refers to people who have been exposed to the disease but are not yet entirely ill; Infected people are those who have the disease and are able to spread it, while recovered people are those who have recovered from the illness. The population total in this model is $N(t) = S(t) + E(t) + I(t) + R(t)$.

The COVID-19 spread model's compartment diagram is depicted in Figure 2, and its parameters are listed in Table 1.

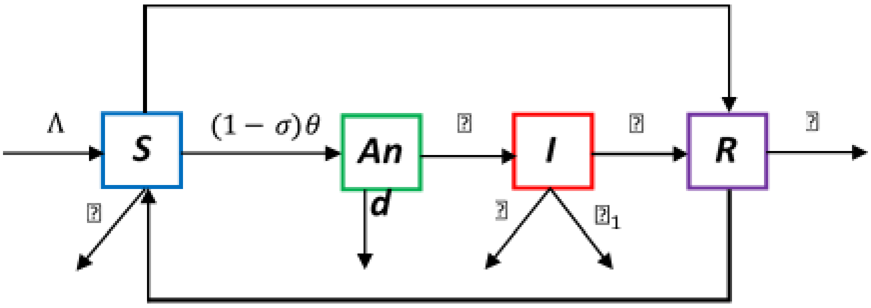

Figure 2 shows the COVID-19 spread model's compartment diagram.

The SEIRS model of COVID-19 spread is represented by the following system of nonlinear differential equations:

$$
\begin{aligned}
\frac{dS}{dt} &= \Lambda + \gamma R - \nu S - (1-\sigma)\theta S I - \mu S, \\
\frac{dE}{dt} &= (1-\sigma)\theta S I - \beta E - \mu E, \\
\frac{dI}{dt} &= \beta E - (\mu + \mu_1) I - \delta I, \\
\frac{dR}{dt} &= \nu S + \delta I - \gamma R - \mu R,
\end{aligned} \tag{1}
$$

with $0 < \sigma < 1$ is the number of people socially isolating themselves as a preventative step against the spread of COVID-19, and $0 < \nu < 1$ is the rate of vaccination.

Table 1. An explanation of the model's parameters

Symbol	Description
Λ	birth rate
β	the rate of change of individuals from subpopulation E to I
γ	the rate of change of individuals from subpopulation R to S
δ	recovery rate of individuals infected with COVID-19
θ	the rate of transmission of the disease from subpopulation S to E
μ	natural mortality rate
μ_1	death rate due to being infected with COVID-19
ν	rate of administration of the vaccine
σ	the rate of change of individuals who take precautions to prevent the spread of COVID-19 in the form of *social distancing*,

2. Basic Reproduction Number and Equilibrium Points

Equation of State and the Fundamental Reproduction Number ($\mathcal{R}_0$)

The rule (1)'s equilibrium point can be found using the methods listed below.

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0,$$

so that we obtain disease-free equilibrium point

$$Q_0 = (S_0, E_0, I_0, R_0) = \left(\frac{d_4\Lambda}{\mu^2 + (\nu+\gamma)\mu}, 0, 0, \frac{\Lambda\nu}{\mu^2 + (\nu+\gamma)\mu}\right).$$

where

$$d_4 = \gamma + \mu.$$

According to this equilibrium point condition, there are no people in either the exposed subpopulation or the sick subpopulation. Since there are no members of the exposed group, there are likewise no members of the infected subpopulation when equilibrium is reached. Because every parameter is positive, it may be assumed that the disease-free equilibrium point exists in every situation.

The SEIRS model is the one that is examined in this study as it relates to COVID-19 diffusion. The average number of newly infected people brought on by one infected person during the spread of COVID-19 in a sensitive population is represented by the basic reproduction numbers ($\mathcal{R}_0$) in this instance. The fundamental reproduction number is determined using the Next Generation Matrix.

$$\mathcal{R}_0 = \rho(K) = max\{\lambda_1, \lambda_2\} = \frac{d_4\Lambda\beta(1-\sigma)\theta}{d_2 d_3(\mu^2 + (\nu+\gamma)\mu)}.$$

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Furthermore, we get the point of endemic equilibrium.

$$Q^* = (S^*, E^*, I^*, R^*),$$

with

$$S^* = \frac{d_2 d_3}{(1-\sigma)\theta\beta},$$

$$E^* = \frac{d_3 d_4 \Lambda}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right),$$

$$I^* = \frac{d_4 \Lambda\beta}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right),$$

$$R^* = \frac{d_2 d_3 \nu}{d_4(1-\sigma)\theta\beta} + \frac{\Lambda\beta\delta}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right).$$

where

$d_2 = \beta + \mu,$
$d_3 = \mu + \mu_1 + \delta,$
$w_1 = \beta + \gamma + \delta + \mu_1,$

$w_2 = \beta\gamma + \beta\delta + \beta\mu_1 + \gamma\delta + \gamma\mu_1,$

$w_3 = \beta\gamma\mu_1.$

Because of the parameter $0 < \sigma < 1$, we have the value S^* is positive, while E^*, I^*, and R^* are positive when $\mathcal{R}_0 > 1$. Thus, we conclude that the equilibrium point exists Q^* when $\mathcal{R}_0 > 1$.

3. Local Stability Analysis of Eqilibrium Points

A group of nonlinear differential equations make up System (1). The system (1) is linearized by circling the equilibrium point, it is feasible to assess the stability of the equilibrium point. The system linearization result's (1) Jacobi matrix is.

$$J = \begin{pmatrix} -\big((1-\sigma)\theta I + d_1\big) & 0 & -(1-\sigma)\theta S & \gamma \\ (1-\sigma)\theta I & -d_2 & (1-\sigma)\theta S & 0 \\ 0 & \beta & -d_3 & 0 \\ \nu & 0 & \delta & -d_4 \end{pmatrix}.$$

Local stability of disease-free equilibrium points ($\boldsymbol{Q_0}$)

The Jacobian matrix for equilibrium points without disease $Q_0 = \left(\frac{d_4\Lambda}{\mu^2+(\nu+\gamma)\mu}, 0, 0, \frac{\Lambda\nu}{\mu^2+(\nu+\gamma)\mu}\right)$ is

$$J(Q_0) = \begin{pmatrix} -d_1 & 0 & -\dfrac{d_4\Lambda(1-\sigma)\theta}{\mu^2+(\nu+\gamma)\mu} & \gamma \\ 0 & -d_2 & \dfrac{d_4\Lambda(1-\sigma)\theta}{\mu^2+(\nu+\gamma)\mu} & 0 \\ 0 & \beta & -d_3 & 0 \\ \nu & 0 & \delta & -d_4 \end{pmatrix}.$$

One can solve the equation, i.e., to get the characteristic equation of the matrix.

$$J(Q_0)|\lambda I - J(Q_0)| = 0$$

$$\begin{vmatrix} \lambda + d_1 & 0 & \dfrac{d_4\Lambda(1-\sigma)\theta}{\mu^2+(\nu+\gamma)\mu} & -\gamma \\ 0 & \lambda + d_2 & -\dfrac{d_4\Lambda(1-\sigma)\theta}{\mu^2+(\nu+\gamma)\mu} & 0 \\ 0 & -\beta & \lambda + d_3 & 0 \\ -\nu & 0 & -\delta & \lambda + d_4 \end{vmatrix} = 0.$$

By expanding the first column, it can be shown.

$$\big((\lambda+d_1)(\lambda+d_4)-\nu\gamma\big)\left((\lambda+d_2)(\lambda+d_3)-\frac{d_4\Lambda\beta(1-\sigma)\theta}{\mu^2+(\nu+\gamma)\mu}\right)=0,$$

with

$$(\lambda+d_1)(\lambda+d_4)-\nu\gamma=0, \tag{2}$$

or

$$(\lambda+d_2)(\lambda+d_3)-\frac{d_4\Lambda\beta(1-\sigma)\theta}{\mu^2+(\nu+\gamma)\mu}=0. \tag{3}$$

Equation (2) can be expressed in the form of quadric equation as following.

$$\lambda^2 + a_1\lambda + a_2 = 0, \tag{4}$$

with

$a_1 = d_1 + d_4 > 0$ and $a_2 = \mu^2 + (\nu+\gamma)\mu > 0$.

Because $a_1 > 0$ and $a_2 > 0$, equation (4) has real negative eigenvalues λ_1 and λ_2 when $\mathcal{R}_0 > 1$.

Furthermore, the same as before, equation (3) can be expressed in the form of the quadratic equation below.

$$\lambda^2 + a_3\lambda + a_4 = 0, \tag{5}$$

with

$a_3 = d_2 + d_3 > 0$, and $a_4 = d_2 d_3(1-\mathcal{R}_0) > 0$ when $\mathcal{R}_0 < 1$. Equation (5) has real negative eigenvalues λ_3 and λ_4 when $\mathcal{R}_0 < 1$.

Finally, the disease-free equilibrium point is locally asymptotically stable if $\mathcal{R}_0 < 1$.

Local stability of endemic equilibrium points($\boldsymbol{Q^*}$)

The Jacobian matrix of the endemic equilibrium point $Q^* = (S^*, E^*, I^*, R^*)$ is

$$J(Q^*) = \begin{pmatrix} -\left(\dfrac{d_4\Lambda\beta(1-\sigma)\theta}{(\mu^3+w_1\mu^2+w_2\mu+w_3)}\left(1-\dfrac{1}{\mathcal{R}_0}\right)+d_1\right) & 0 & -\dfrac{d_2d_3}{\beta} & \gamma \\ \dfrac{d_4\Lambda\beta(1-\sigma)\theta}{(\mu^3+w_1\mu^2+w_2\mu+w_3)}\left(1-\dfrac{1}{\mathcal{R}_0}\right) & -d_2 & \dfrac{d_2d_3}{\beta} & 0 \\ 0 & \beta & -d_3 & 0 \\ \nu & 0 & \delta & -d_4 \end{pmatrix}.$$

By way of

$$m = \frac{d_4\Lambda\beta(1-\sigma)\theta}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right),$$

the matrix of characteristic equation $J(Q^*)$ can be obtained by solving the equation $|\lambda I - J(Q^*)| = 0$, i.e.

$$\begin{vmatrix} \lambda + m + d_1 & 0 & \frac{d_2 d_3}{\beta} & -\gamma \\ -m & \lambda + d_2 & -\frac{d_2 d_3}{\beta} & 0 \\ 0 & -\beta & \lambda + d_3 & 0 \\ -\nu & 0 & -\delta & \lambda + d_4 \end{vmatrix} = 0.$$

so that we have characteristic equation as follows

$$\lambda^4 + b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_4 = 0, \qquad (6)$$

with

$$b_1 = d_1 + d_2 + d_3 + d_4 + \frac{d_4\Lambda\beta(1-\sigma)\theta}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right) > 0,$$

$$b_2 = d_2 d_4 + d_3 d_4 + (d_2 + d_3)\left(\frac{d_4\Lambda\beta(1-\sigma)\theta}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right) + d_1\right)$$

$$+ \frac{{d_4}^2\Lambda\beta(1-\sigma)\theta}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right) + \mu^2 + (\nu + \gamma)\mu > 0,$$

$$b_3 = \frac{d_2 d_3 d_4\Lambda\beta(1-\sigma)\theta}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right) + (d_2 + d_3) \times$$

$$\left(\frac{{d_4}^2\Lambda\beta(1-\sigma)\theta}{(\mu^3 + w_1\mu^2 + w_2\mu + w_3)}\left(1 - \frac{1}{\mathcal{R}_0}\right) + \mu^2 + (\nu + \gamma)\mu\right) > 0,$$

$$b_4 = d_4\Lambda\beta(1-\sigma)\theta\left(1 - \frac{1}{\mathcal{R}_0}\right) > 0.$$

Because it is difficult to locate the root of the characteristic equation, the Routh-Hurwitz criterion is employed to establish the stability characteristics of the equilibrium point Q^*. The characteristic equation (6)'s roots are locally asymptotically stable according to this criterion if $b_1 > 0, b_4 > 0, b_1 b_2 - b_3 > 0$, and $b_1 b_2 b_3 - {b_1}^2 b_4 - {b_3}^2 > 0$. It will be shown with numerical simulations.

4. Numerical Simulation

To demonstrate the conclusions reached by the analysis, numerical simulations are run. MATLAB software was used to do numerical simulations using the Runge-Kutta Order 4 technique. There are three kinds of simulations carried out, namely simulations for $\mathcal{R}_0$, simulations for the influence of vaccination, and simulations to test the impact of social distance on COVID-19 dissemination. Table 2 lists the parameter values for simulations with parameter $\mathcal{R}_0$.

Table 2. Parameter values for simulations $\mathcal{R}_0$

Parameter	Simulation I	Simulation II
Λ	1.25	1.25
β	0.15	0.15
μ	0.06	0.06
μ_1	0.04	0.04
δ	0.7	0.7
ν	0.5	0.5
γ	0.05	0.15
σ	0.75	0.25
θ	0.8	0.8

Numerical simulation I$(\boldsymbol{\mathcal{R}_0 < 1})$

Simulation I was done to show how stable the disease-free equilibrium point (Q_0) is. If the parameter values in Table 2's second column are used and then are substituted into $\mathcal{R}_0$, then, we obtain $\mathcal{R}_0 = 0.670 < 1$. Based on the values of these parameters, there is just one point of balance, that is, the point of equilibrium without illness

$$Q_0 = (3.756, 0, 0, 17.076),$$

and it can be checked that the above numerical results are defined on

$$\Omega = \left\{(S, E, I, R) \in \mathbb{R}^4 \,\middle|\, 0 \leq S + E + I + R \leq \frac{\Lambda}{\mu}\right\}.$$

Numerical simulations performed with initial values $(0) = 7, E(0) = 4, I(0) = 3, R(0) = 6$, toward the equilibrium of disease-free conditions Q_0. The simulation results in Figure 2 reflect the results of the analysis obtained. If $\mathcal{R}_0 < 1$ then the disease-free equilibrium point is locally asymptotically stable. Figure 2 shows that over time, exposed (E) and infected (I) subpopulations will further decline towards 0 which means there is no spread of COVID-19.

Numerical simulation II$(\boldsymbol{\mathcal{R}_0 > 1})$

Simulation II was performed to illustrate the stability of the disease-free equilibrium point (Q_0) and the endemic equilibrium point(Q^*). Substitute parameter values in the third column of Table 2 result in $\mathcal{R}_0 = 3.301 > 1$. There are two equilibrium points based on the values of these parameters: the endemic equilibrium point and the disease-free equilibrium point. $Q_0 = (6.162, 0, 0, 14.671\,)$ $Q^* = (1.867, 7.494, 1.405, 9.128)$ It can be checked that both numerical results are defined on Ω, are presented in Figure 3.

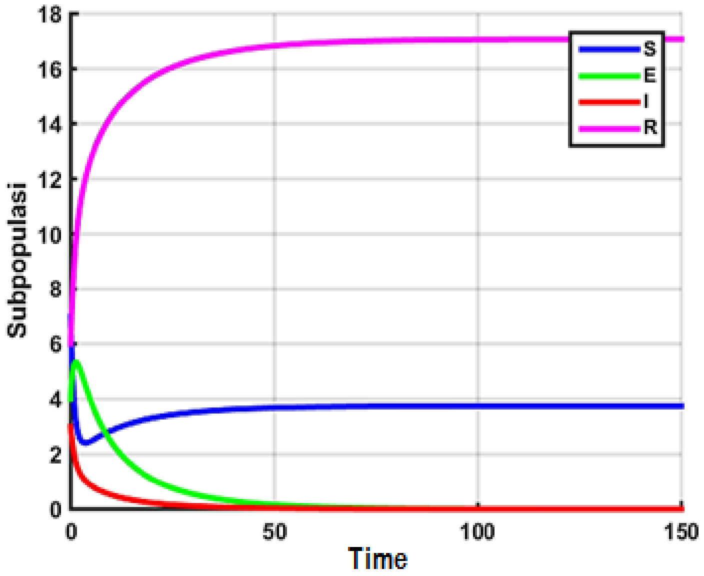

Figure 3. Solution graph for $\mathcal{R}_0 < 1$

When the equilibrium point Q* satisfies the Routh-Hurwitz criterion, it is locally asymptotically stable, i.e.$b_1 > 0, b_4 > 0, b_1 b_2 - b_3 > 0$, and $b_1 b_2 b_3 - {b_1}^2 b_4 - {b_3}^2 > 0$. Numerical simulations are performed with initial values$S(0) = 7, E(0) = 4, I(0) = 3, R(0) = 6$. Over time (t), the number of individuals in the subpopulations S, E, I, and R goes towards the point of endemic equilibrium Q^*. The results of the numerical simulations obtained show that if $\mathcal{R}_0 > 1$, then the equilibrium point Q^* is locally asymptotically stable. By using the parameters in Table 2, we end up.

$b_1 b_2 - b_3 = 4.89952 > 0$, and $b_1 b_2 b_3 - {b_1}^2 b_4 - {b_3}^2 = 1.65972 > 0$.

Figure 4 shows that the spread of COVID-19 will last for a considerable period.

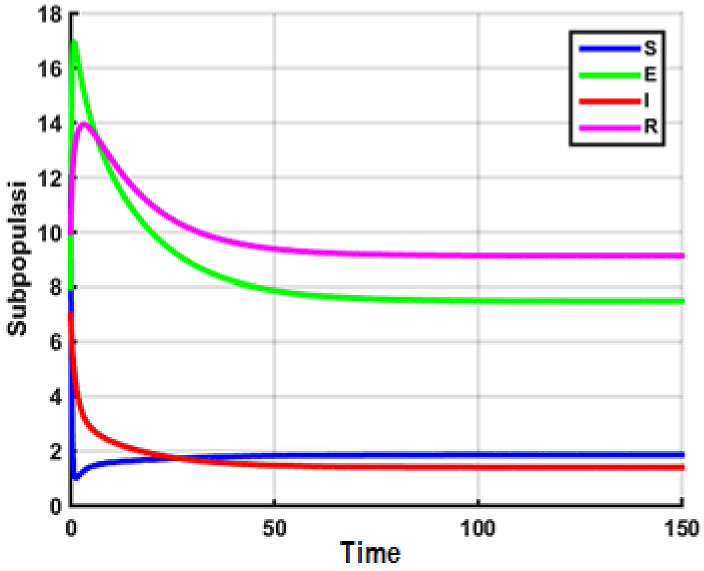

Figure 4. Graph of the $\mathcal{R}_0 > 1$ Solution

Numerical simulation of the effect of vaccination corona disease

In this subsection, we discussed the effect of vaccination (ν) on infected subpopulations (I). The parameter values used in this simulation, i.e. $\Lambda = 1.25, \beta = 0.15, \gamma = 0.15, \delta = 0.7, \mu = 0.06, \mu_1 = 0.04, \theta =$

$0.8, \sigma = 0.5, \nu_1 = 0.05, \nu_2 = 0.25, \nu_3 = 0.75,$ and $\nu_4 = 0.90$. The initial value used is $(7,4,3,6)$. The results of numerical simulations for the effect of vaccination on the spread of COVID-19 are presented in Figure 5.

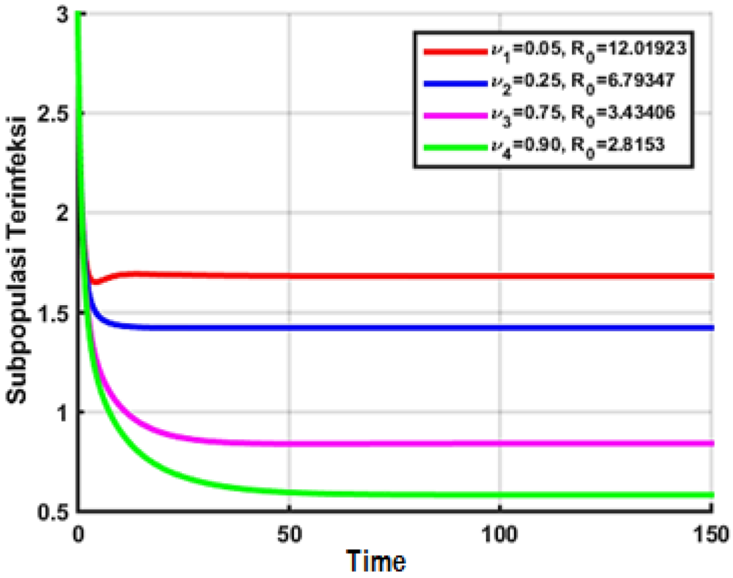

Figure 5. Effect of vaccination on the spread of COVID-19

According to Figure 5, the lower the number of people who have COVID-19 infection, the higher the proportion of immunizations administered. Therefore, it can be claimed that immunization can slow the rate at which COVID-19 spreads.

Numerical simulation of the effect of *social distancing* on the spread of COVID-19

In this subsection, the effect of *social distancing* (parameter σ) on infected subpopulations (I) is discussed. In this simulation, parameter values are used i.e $\Lambda = 1.25, \beta = 0.15, \gamma = 0.15, \delta = 0.7, \mu = 0.06, \mu_1 = 0.04, \theta = 0.8, v = 0.5, \sigma_1 = 0.2, \sigma_2 = 0.5, \sigma_3 = 0.7,$ and $\sigma_4 = 0.9$. The initial value provided is $(7,4,3,6)$. Figure 6 shows the outcomes of numerical simulations showing how social distance affects the transmission of the coronavirus disease. Figure 6 shows that the more people who practice social distance, the faster the number of infected people declines and, over time, the COVID-19 epidemic can be stopped. Therefore, it can be claimed that putting social distance into practice will hasten the end of COVID-19's expansion.

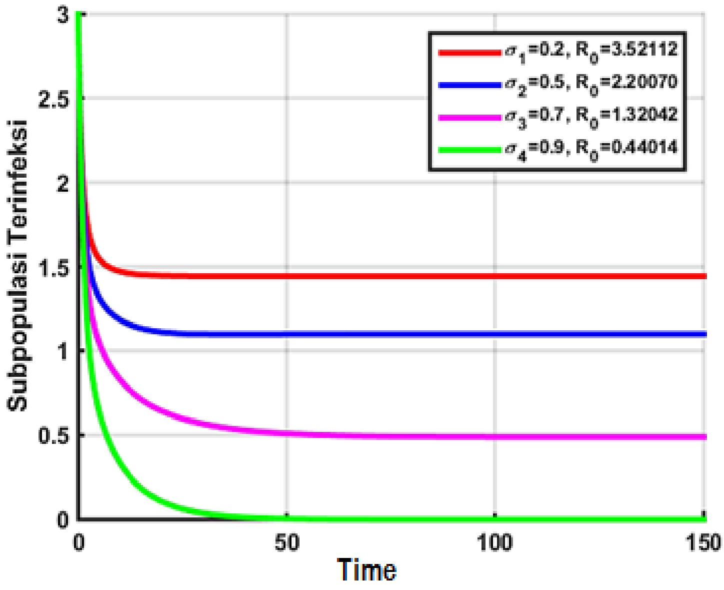

Figure 6. The effect of *social distancing* on the spread of COVID-19

CONCLUSIONS

Following conclusions can be drawn from the findings and discussion: The human population is divided into four subpopulations by the nonlinear SEIRS differential equation system known as the COVID-19 spread model, namely (S) subpopulations that are not infected but are susceptible to contracting the disease, (E) subpopulations that have been exposed to the disease but have not been fully infected, (I) subpopulations that are infected and can transmit diseases, and (R) subpopulations that have recovered from the disease and assumed that the recovered subpopulation can be reinfected. The endemic equilibrium point and the disease-free equilibrium point are both equilibrium points in the COVID-19 dissemination model. The endemic equilibrium point has a mathematical condition of $\mathcal{R}_0 > 1$, whereas the disease-free equilibrium point is stable. SEIRS. The stability analysis of the equilibrium point demonstrates that if $\mathcal{R}_0 < 1$, the disease-free equilibrium point is asymptotically stable. If the Routh-Hurwitz requirements are satisfied, the endemic equilibrium point is an internal asymptotic firm. The outcomes of mathematical simulations performed on $\mathcal{R}_0$ support the analysis's conclusions. The simulation results on how social distance and vaccine administration affect COVID-19 outbreak demonstrate that social distance and vaccine administration can hasten the pandemic's end.

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