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SEIQR Model Analysis of COVID-19 Transmission Considering Vaccination Rate

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Abstract. COVID-19 is a disease caused by the Coronavirus. The disease can be transmitted, either directly or indirectly. Implementing quarantine and vaccinations can prevent the transmission of the virus. Therefore, this study focused on the quarantine and vaccination rate using the SEIQR epidemic mathematical model, where Q represents quarantine. The simulation in this study uses parameter values derived from journals and previous studies. It was found that the rate of population movement under quarantine and the rate of vaccinations affected the disease. If the population under quarantine is low but the vaccination rate is high, the disease will become an epidemic and can be transmitted ($R_0 > 1$). However, if the population undergoing quarantine is high and the vaccination rate is low, the disease will be controlled and will not become an epidemic ($R_0 < 1$).

INTRODUCTION

Coronavirus is a new type of virus (SARS-CoV-2) and the disease is called Coronavirus disease (COVID-19). This virus is an infectious disease where it can be transmitted through direct, indirect contact, or droplets in the air. To reduce the number of deaths due to COVID-19 transmission, the government is taking preventive measures by quarantining people who have been exposed to coronavirus.

Quarantine is an act of isolating or separating someone who has been exposed to the virus but has not shown any symptoms. The standard quarantine period for COVID-19 cases is conducted 14 days from the date of the positive case. An individual can complete their quarantine period if the test shows negative result of COVID-19. In addition, the government also urges the public to vaccinate as a way to reduce the spread of the coronavirus.

Vaccination is the process of introducing vaccines into the body to stimulate the body's immune system and ultimately become immune to certain infectious diseases. With vaccination, it is hoped that when an individual was exposed to the virus it can reduce the symptoms caused.

The development of the world of information and technology requires educators in the field of mathematics to be able to produce creative individuals who can create effective and efficient solutions to problems in the real world through the use of their mathematical abilities. Mathematical models can be used to analyze the dynamics of disease spread. Mathematical models are formulated based on the characteristics of the disease. In this study, the author used the development of the SEIR (Susceptible, Exposed, Infected, Recovered) model, namely SEIQR, where the population is divided into suspect (S) groups, which refers to any individuals who are susceptible to the disease, exposed (E) is any individuals who are infected with the disease but have not shown any symptoms and cannot transmit the disease, infected (I) is an individual who has been infected, quarantine (Q) is an infected individual who is then quarantined/isolated, recovered (R) is an individual who has recovered from the disease.

This study was conducted to determine the importance of the effect of quarantine and vaccination rate on the spread of COVID-19. Hence, the government and related parties can encourage the public to implement quarantine and vaccination.

METHODOLOGY

The method used in this research is an experiment by simulating parameter values obtained from previous studies. The model used is the SEIQR epidemic model (Susceptible, Exposed, Infected, Quarantine, Recovered). The assumption of forming a mathematical model of the spread of COVID-19 by implementing quarantine and vaccination rate can be arranged as follows:

1. The population is assumed to be closed, meaning that no individuals enter the population or leave the population (no migration). The total population is assumed to be constant.
2. The number of births and the number of deaths per unit of time are assumed to be the same.
3. The population is assumed to be homogeneously mixed, meaning that each individual has the same opportunity to make contact with other individuals.
4. Migration in Indonesia is not part of the migration.
5. Susceptible individuals (S) will be given a vaccine in order to become immune to the disease.
6. Latent individuals (E) who are quarantined cannot spread the disease.
7. Individuals who are implementing quarantine will not transmit the disease.
8. Individuals who have not been infected by the virus enter the compartment of susceptible individuals.
9. Infected individuals can recover from the disease.
10. Individuals can leave the infected group once they recovered from the disease. Once they recovered, the individual will be immune to the disease.
11. Viral infection occurred when there is close contact with an infected individual either directly or indirectly.
12. Each subpopulation experiences pure death.

Based on the assumptions above, a compartment diagram for the spread of COVID-19 can be seen in Fig. 1.

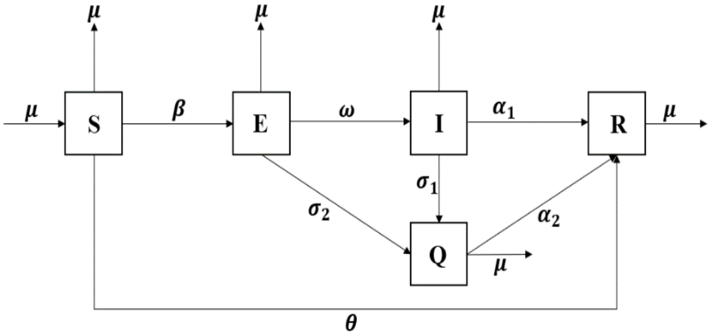


FIGURE 1. COVID-19 Transmission Compartment Flowchart

The variables and parameters used in the COVID-19 disease spread model by implementing quarantine and vaccination rate are presented in Table 1 and Table 2:

TABLE 1. List of model variables for the spread of COVID-19 disease

Variables	Definition	Unit
N(t)	Total population of individuals at time t	Individual
S(t)	Number of susceptible individuals infected at time t	Individual
E(t)	Number of exposed individuals at time t	Individual
I(t)	Number of infected individuals at time t	Individual
Q(t)	Number of individuals quarantined at time t	Individual
R(t)	Number of recovered individuals at time t	Individual

TABLE 2. List of model parameters for the spread of COVID-19 disease

Parameters	Definition	Unit
μ	The natural rate of birth and death	$\frac{1}{time}$
β	The rate at which an individual is susceptible to becoming an exposed individual after interacting with an infected individual	$\frac{1}{\text{day}}$
ω	The transfer rate from exposed individuals to infected individuals	$\frac{1}{\text{day}}$
σ_1	The rate at which individuals are exposed to quarantine/isolation	$\frac{1}{\text{day}}$
σ_2	The rate of infected individuals doing quarantine/isolation	$\frac{1}{\text{day}}$
α_1	The recovery rate of each infected individual	$\frac{1}{\text{day}}$

Parameters	Definition	Unit
α_2	The recovery rate of each individual who is in quarantine/isolation	$\frac{1}{\text{day}}$
θ	Vaccination rate in susceptible individuals	$\frac{individual}{population}$

RESULTS AND DISCUSSIONS

Based on Fig. 1, a mathematical model can be formed in the system of differential equations:

$$A \equiv \frac{dS}{dt} = \mu N - \beta SI - \theta S - \mu S$$

$$B \equiv \frac{dE}{dt} = \beta SI - \omega E - \sigma_2 E - \mu E$$

$$C \equiv \frac{dI}{dt} = \omega E - \alpha_1 I - \sigma_1 I - \mu I \qquad (1)$$

$$D \equiv \frac{dQ}{dt} = \sigma_1 I + \sigma_2 E - \alpha_2 Q - \mu Q$$

$$\mathrm{G} \equiv \frac{dR}{dt} = \alpha_1 I + \alpha_2 Q + \theta S - \mu R$$

with $N = S + E + I + Q + R$. It can show that $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dQ}{dt} + \frac{dR}{dt} = 0$, then $N(t)$ is constant. Thus equation (1) fulfills the assumption that the number of individuals in the population is constant and can be formed in the model to be:

$$A \equiv \frac{dS}{dt} = \mu - \beta SI - \theta S - \mu S \qquad (2)$$

$$B \equiv \frac{dE}{dt} = \beta SI - \omega E - \sigma_2 E - \mu E \qquad (3)$$

$$C \equiv \frac{dI}{dt} = \omega E - \alpha_1 I - \sigma_1 I - \mu I \qquad (4)$$

$$D \equiv \frac{dQ}{dt} = \sigma_1 I + \sigma_2 E - \alpha_2 Q - \mu Q \qquad (5)$$

$$G \equiv \frac{dR}{dt} = \alpha_1 I + \alpha_2 Q + \theta S - \mu R \qquad (6)$$

Equilibrium Points

The disease-free equilibrium point is obtained if $E = 0, I = 0,$ and $Q = 0$, so that no individual is infected with the disease. Substitution $E = 0$, $I = 0$ and $Q = 0$ into equation (2)-(6), it is found that the disease-free equilibrium point is:

$$E^0(S, E, I, Q, R) = \left(\frac{\mu}{\mu + \theta}, 0,0,0, \frac{\theta}{\mu + \theta}\right)$$

The endemic equilibrium point is a condition where there are infected individuals in a population. So that we obtained the endemic equilibrium point $E_1(S^*, E^*, I^*, Q^*, R^*)$

$$S^* = \frac{\mu^2 + \mu\omega + \mu\alpha_1 + \mu\sigma_1 + \mu\sigma_2 + \omega\alpha_1 + \omega\sigma_1 + \alpha_1\sigma_2 + \sigma_1\sigma_2}{\beta\omega}$$

$$E^* = \frac{\begin{pmatrix} \beta\mu\omega - \mu^3 - \mu^2\omega - \mu^2\theta - \mu^2\alpha_1 - \mu^2\sigma_1 - \mu^2\sigma_2 - \mu\omega\theta - \mu\omega\alpha_1 - \mu\omega\sigma_1 \\ -\mu\theta\alpha_1 - \mu\theta\sigma_1 - \mu\theta\sigma_2 - \mu\alpha_1\sigma_2 - \mu\sigma_1\sigma_2 - \omega\theta\alpha_1 - \omega\theta\sigma_1 - \theta\alpha_1\sigma_2 - \theta\sigma_1\sigma_2 \end{pmatrix}}{(\mu + \sigma_2 + \omega)\beta\omega}$$

$$I^* = \frac{\begin{pmatrix} \beta\mu\omega - \mu^3 - \mu^2\omega - \mu^2\theta - \mu^2\alpha_1 - \mu^2\sigma_1 - \mu^2\sigma_2 - \mu\omega\theta - \mu\omega\alpha_1 - \mu\omega\sigma_1 \\ -\mu\theta\alpha_1 - \mu\theta\sigma_1 - \mu\theta\sigma_2 - \mu\alpha_1\sigma_2 - \mu\sigma_1\sigma_2 - \omega\theta\alpha_1 - \omega\theta\sigma_1 - \theta\alpha_1\sigma_2 - \theta\sigma_1\sigma_2 \end{pmatrix}}{\beta(\mu^2 + \mu\omega + \mu\alpha_1 + \mu\sigma_1 + \mu\sigma_2 + \omega\alpha_1 + \omega\sigma_1 + \alpha_1\sigma_2 + \sigma_1\sigma_2)}$$

$$Q^* = \frac{\begin{pmatrix} \beta\mu\omega - \mu^3 - \mu^2\omega - \mu^2\theta - \mu^2\alpha_1 - \mu^2\sigma_1 - \mu^2\sigma_2 - \mu\omega\theta - \mu\omega\alpha_1 - \mu\omega\sigma_1 \\ -\mu\theta\alpha_1 - \mu\theta\sigma_1 - \mu\theta\sigma_2 - \mu\alpha_1\sigma_2 - \mu\sigma_1\sigma_2 - \omega\theta\alpha_1 - \omega\theta\sigma_1 - \theta\alpha_1\sigma_2 - \theta\sigma_1\sigma_2 \end{pmatrix} (\mu\sigma_2 + \omega\sigma_1 + \alpha_1\sigma_2 + \sigma_1\sigma_2)}{\beta(\mu^2 + \mu\omega + \mu\alpha_1 + \mu\sigma_1 + \mu\sigma_2 + \omega\alpha_1 + \omega\sigma_1 + \alpha_1\sigma_2 + \sigma_1\sigma_2)\omega(\mu + \alpha_2)}$$

$$\begin{aligned}
R^* = {} & \frac{1}{\beta(\mu^2 + \mu\omega + \mu\alpha_1 + \mu\sigma_1 + \mu\sigma_2 + \omega\alpha_1 + \omega\sigma_1 + \alpha_1\sigma_2 + \sigma_1\sigma_2)\omega(\mu + \alpha_2)}(\beta\mu\omega^2\alpha_1 \\
& +\beta\mu\omega\alpha_2\sigma_2 + \beta\omega^2\alpha_1\alpha_2 + \beta\omega^2\alpha_2\sigma_1 + \beta\omega\alpha_1\alpha_2\sigma_2 + \beta\omega\alpha_2\sigma_1\sigma_2 + \mu^4\theta + 2\mu^3\omega\theta \\
& -\mu^3\omega\alpha_1 + 2\mu^3\theta\alpha_1 + \mu^3\theta\alpha_2 + 2\mu^3\theta\sigma_1 + 2\mu^3\theta\sigma_2 - \mu^3\alpha_2\sigma_2 + \mu^2\omega^2\theta - \mu^2\omega^2\alpha_1 \\
& +3\mu^2\omega\theta\alpha_1 + 2\mu\omega\theta\alpha_2 + 4\mu^2\omega\theta\sigma_1 + 2\mu^2\omega\theta\sigma_2 - \mu^2\omega\alpha_1^2 - \mu^2\omega\alpha_1\alpha_2 - \mu^2\omega\alpha_1\sigma_1 \\
& -\mu^2\omega\alpha_1\sigma_2 - \mu^2\omega\alpha_2\sigma_1 - \mu^2\omega\alpha_2\sigma_2 + \mu^2\theta\alpha_1^2 + 2\mu^2\theta\alpha_1\alpha_2 + 2\mu^2\theta\alpha_1\sigma_1 + 4\mu^2\theta\alpha_1\sigma_2 \\
& +2\mu^2\theta\alpha_2\sigma_1 + \mu^2\theta\alpha_2\sigma_2 + \mu^2\theta\sigma_1^2 + 4\mu^2\theta\sigma_1\sigma_2 + \mu^2\theta\sigma_2^2 - 2\mu^2\alpha_1\alpha_2\sigma_2 - 2\mu^2\alpha_2\sigma_1\sigma_2 \\
& -\mu^2\alpha_2\sigma_2^2 + \mu\omega^2\theta\alpha_1 + \mu\omega^2\theta\alpha_2 + 2\mu\omega^2\theta\sigma_1 - \mu\omega^2\alpha_1^2 - \mu\omega^2\alpha_1\alpha_2 - \mu\omega^2\alpha_1\sigma_1 \\
& -\mu\omega^2\alpha_2\sigma_1 + \mu\omega\theta\alpha_1^2 + 3\mu\omega\theta\alpha_1\alpha_2 + 3\mu\omega\theta\alpha_1\sigma_1 + 3\mu\omega\theta\alpha_1\sigma_2 + 3\mu\omega\theta\alpha_2\sigma_1 \\
& +\mu\omega\theta\alpha_2\sigma_2 + 2\mu\omega\theta\sigma_1^2 + 4\mu\omega\theta\sigma_1\sigma_2 - \mu\omega\alpha_1^2\alpha_2 - \mu\omega\alpha_1^2\sigma_2 - 2\mu\omega\alpha_1\alpha_2\sigma_1 \\
& -3\mu\omega\alpha_1\alpha_2\sigma_2 - \mu\omega\alpha_1\sigma_1\sigma_2 - \mu\omega\alpha_2\sigma_1^2 - 3\mu\alpha_2\sigma_1\sigma_2 + \mu\theta\alpha_1^2\alpha_2 + 2\mu\theta\alpha_1^2\sigma_2 \\
& +2\mu\theta\alpha_1\alpha_2\sigma_1 + 2\mu\theta\alpha_1\alpha_2\sigma_2 + 4\mu\theta\alpha_1\sigma_1\sigma_2 + 2\mu\theta\alpha_1\sigma_2^2 + \mu\theta\alpha_2\sigma_1^2 + 2\mu\theta\alpha_2\sigma_1\sigma_2 \\
& +2\mu\theta\sigma_1^2\sigma_2 + 2\mu\theta\sigma_1\sigma_2^2 - \mu\alpha_1^2\alpha_2\sigma_2 - 2\mu\alpha_1\alpha_2\sigma_1\sigma_2 - 2\mu\alpha_1\alpha_2\sigma_2^2 - \mu\alpha_2\sigma_1^2\sigma_2 \\
& -2\mu\alpha_2\sigma_1\sigma_2^2 + \omega^2\theta\alpha_1\alpha_2 + \omega^2\theta\alpha_1\sigma_1 + \omega^2\theta\alpha_2\sigma_1 + \omega^2\theta\sigma_1^2 - \omega^2\alpha_1^2\alpha_2 - 2\omega^2\alpha_1\alpha_2\sigma_1 \\
& -\omega^2\alpha_2\sigma_1^2 + \omega\theta\alpha_1^2\alpha_2 + \omega\theta\alpha_1^2\sigma_2 + 2\omega\theta\alpha_1\alpha_2\sigma_1 + \omega\theta\alpha_1\alpha_2\sigma_2 + 3\omega\theta\alpha_1\sigma_1\sigma_2 + \omega\alpha_2\sigma_1^2 \\
& +\omega\theta\alpha_1\sigma_1\sigma_2 + 2\omega\theta\sigma_1^2\sigma_2 - 2\omega\alpha_1^2\alpha_2\sigma_2 - 4\omega\alpha_1\alpha_2\sigma_1\sigma_2 - 2\omega\alpha_2\sigma_1^2\sigma_2 + \theta\alpha_1^2\alpha_2\sigma_2 \\
& +\theta\alpha_1^2\sigma_2^2 + 2\theta\alpha_1\alpha_2\sigma_1\sigma_2 + 2\theta\alpha_1\sigma_1\sigma_2^2 + \theta\alpha_2\sigma_1^2\sigma_2 + \theta\sigma_1^2\sigma_2^2 - \alpha_1^2\alpha_2\sigma_2^2 - 2\alpha_1\alpha_2\sigma_1\sigma_2^2 \\
& -\alpha_2\sigma_1^2\sigma_2^2)
\end{aligned}$$

Basic Reproduction Number

The basic reproduction number (R_0) is found using the Next Generation Matrix (NGM) method from equations (3) until (5). The steps in determining the basic reproduction number:

1. Retrieve equations to describe new infected cases and changes in the infection compartment of the system. Furthermore, this system is called the infected subsystem. The infected subsystems are E, I and Q.
2. Linearize the infected system at the disease-free equilibrium point. This linear system is carried out using the Jacobian Matrix (J).

3. Decomposition of the Jacobian matrix becomes $J = (\mathcal{F}i + \mathcal{V}i)x$, $\mathcal{F}i$ is the matrix of infection/disease transmission and $\mathcal{V}i$ is the transition matrix.

$$\mathcal{F} = \begin{bmatrix} 0 & \dfrac{\beta\mu}{\mu+\theta} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \text{and } \mathcal{V} = \begin{bmatrix} -\omega - \sigma_2 - \mu & 0 & 0 \\ \omega & -\alpha_1 - \sigma_1 - \mu & 0 \\ \sigma_2 & \sigma_1 & -\mu - \alpha_2 \end{bmatrix}$$

Then the NGM with a large domain denoted by K is $K = -\mathcal{F}\mathcal{V}^{-1}$

$$K = \begin{bmatrix} \dfrac{\beta\mu\omega}{(\omega + \sigma_2 + \mu)(\alpha_1 + \sigma_1 + \mu)(\mu + \theta)} & \dfrac{\beta\mu}{(\alpha_1 + \sigma_1 + \mu)(\mu + \theta)} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

Using equation $det\ (\lambda I - K) = 0$, then the basic reproduction number (R_0) from the largest eigenvalue of the K . matrix is obtained

$$R_0 = \frac{\beta\mu\omega}{(\omega + \sigma_2 + \mu)(\alpha_1 + \sigma_1 + \mu)(\mu + \theta)}$$

Stability Analysis

$$J = \begin{bmatrix} -\mu - \theta & 0 & \dfrac{-\beta\mu}{\mu+\theta} & 0 & 0 \\ 0 & -\omega - \sigma_2 - \mu & \dfrac{\beta\mu}{\mu+\theta} & 0 & 0 \\ 0 & \omega & -\sigma_1 - \alpha_1 - \mu & 0 & 0 \\ 0 & \sigma_2 & \sigma_1 & -\alpha_2 - \mu & 0 \\ \theta & 0 & \alpha_1 & \alpha_2 & -\mu \end{bmatrix}$$

The eigenvalues are obtained as follows:

$$\lambda_1 = -\mu - \theta$$

$$\lambda_2 = -\alpha_2 - \mu$$

$$\lambda_3 = -\mu$$

$$\lambda_4 = \frac{1}{2}\frac{1}{\mu + \theta}\left(\begin{array}{c} -2\mu^2 - \omega\mu - 2\mu\theta - \mu\alpha_1 - \mu\sigma_1 - \sigma_2\mu - \omega\theta - \theta\alpha_1 \\ -\theta\sigma_1 - \theta\sigma_2 + (4\beta\mu^2\omega + 4\beta\mu\omega\theta + \mu^2\omega^2 - 2\mu^2\omega\alpha_1 \\ -2\mu^2\omega\sigma_1 + 2\mu^2\omega\sigma_2 + \mu^2\sigma_1^2 + 2\mu^2\alpha_1\sigma_1 - 2\mu^2\alpha_1\sigma_2 \\ +\mu^2\sigma_1^2 - 2\mu^2\sigma_1\sigma_2 + \mu^2\sigma_2^2 + 2\mu\omega^2\theta - 4\mu\omega\theta\alpha_1 \\ -4\mu\omega\theta\sigma_1 + 4\mu\omega\theta\sigma_2 + 2\mu\theta\alpha_1^2 + 4\mu\theta\alpha_1\sigma_1 - 4\mu\theta\alpha_1\sigma_2 \\ +2\mu\theta\sigma_1^2 - 4\mu\theta\sigma_1\sigma_2 + 2\mu\theta\sigma_2^2 + \omega^2\theta^2 - 2\omega\theta^2\alpha_1 \\ -2\omega\theta^2\sigma_1 + 2\omega\theta^2\sigma_2 + \theta^2\alpha_1^2 + 2\theta^2\alpha_1\sigma_1 - 2\theta^2\alpha_1\sigma_2 \\ +\theta^2\sigma_1^2 - 2\theta^2\sigma_1\sigma_2 + \theta^2\sigma_2^2)^{\frac{1}{2}} \end{array}\right)$$

$$\lambda_5 = -\frac{1}{2}\frac{1}{\mu + \theta}\left(\begin{array}{c} 2\mu^2 + \omega\mu + 2\mu\theta + \mu\alpha_1 + \mu\sigma_1 + \sigma_2\mu + \omega\theta \\ +\theta\alpha_1 + \theta\sigma_1 + \theta\sigma_2 + (4\beta\mu^2\omega + 4\beta\mu\omega\theta + \mu^2\omega^2 \\ -2\mu^2\omega\alpha_1 - 2\mu^2\omega\sigma_1 + 2\mu^2\omega\sigma_2 + \mu^2\alpha_1^2 + 2\mu^2\alpha_1\sigma_1 \\ -2\mu^2\alpha_1\sigma_2 + \mu^2\sigma_1^2 - 2\mu^2\sigma_1\sigma_2 + \mu^2\sigma_2^2 + 2\mu\omega^2\theta \\ -4\mu\omega\theta\alpha_1 - 4\mu\omega\theta\sigma_1 + 4\mu\omega\theta\sigma_2 + 2\mu\theta\alpha_1^2 + 4\mu\theta\alpha_1\sigma_1 \\ -4\mu\theta\alpha_1\sigma_2 + 2\mu\theta\sigma_1^2 - 4\mu\theta\sigma_1\sigma_2 + 2\mu\theta\sigma_2^2 + \omega^2\theta^2 \\ -2\omega\theta^2\alpha_1 - 2\omega\theta^2\sigma_1 + 2\omega\theta^2\sigma_2 + \theta^2\alpha_1^2 + 2\theta\alpha_1\sigma_1 \\ -2\theta^2\alpha_1\sigma_2 + \theta^2\sigma_1^2 - 2\theta^2\sigma_1\sigma_2 + \theta^2\sigma_2^2)^{\frac{1}{2}} \end{array}\right)$$

Numerical Calculation and Simulation

- For the parameter value obtained from the data on the rate of population growth in Indonesia
- For the parameter value of it is assumed that it takes 10 contacts to produce 1 infected individual.
- The value of the parameter is obtained from the number of individuals who have been vaccinated with the 2nd dose until September 30, 2021 divided by the population.
- This simulation data cannot be used as a benchmark with real conditions in Indonesia at this time because in the model many assumptions are used, meaning that many conditions are different from the actual conditions.

TABLE 3. Disease-free equilibrium point parameter values for equations (2) to (6)

Parameters	Value	Unit	Reference
μ	0.0125	$\frac{1}{time}$	[1]
β	0.1	$\frac{1}{\text{day}}$	[2]
ω	0.0007142857143	$\frac{1}{\text{day}}$	[2]
σ_1	0.084	$\frac{1}{\text{day}}$	[3]
σ_2	0.0039798	$\frac{1}{\text{day}}$	[4]
α_1	0.099087	$\frac{1}{\text{day}}$	[5]
α_2	0.11624	$\frac{1}{\text{day}}$	[5]
θ	0.01891695041	$\frac{individual}{population}$	[6]

Based on the parameter values, the basic reproduction number from the system (2) to (6) is $R_0 = 0.002193844058 < 1$. Because $R_0 < 1$ then the disease will not spread. The disease-free equilibrium point is $E_0(S, E, I, Q, R) = (0.3978743906, 0, 0, 0, 0.6021256094)$. The simulation results at the disease-free equilibrium point using the Maple18 program based on the parameters in Table 3 with the initial value distribution of S(0)=0.38, E(0)=0.4, I(0)=0.25, Q(0)=0.17, R(0)=0.27 which is shown in Fig. 2

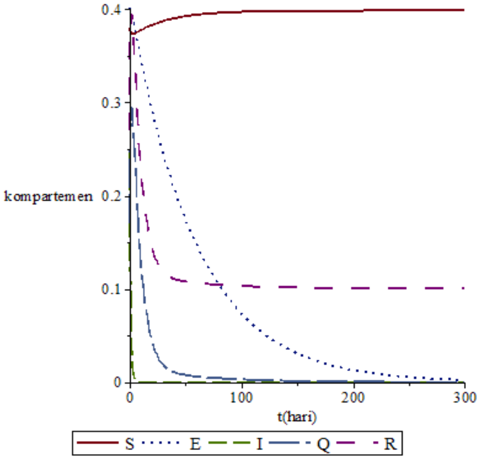


FIGURE 1. Simulation Towards a Disease-Free Equilibrium Point

Based on Fig. 2 the suspectable population increased to the point of 0.3978743906 on the 10th day after previously experiencing a decline and was stable at that point. The exposed population continued to decline until the 95th day towards the zero point and then stabilized at that point. The infected population stabilized at zero on day 30, as well as the population that decreased slowly and then stabilized at zero on day 90. The recovered population has decreased towards to the stable point.

Based on Fig. 2, it is also found that the exposed population and the infected population will go to zero. This is in accordance with the basic reproduction's theory that less than zero so the disease will disappear or mark with $R_0 < 1$.

TABLE 4. Endemic equilibrium points parameter values for equations (2) to (6)

Parameters	Value	Unit	Reference
μ	0.0125	$\frac{1}{time}$	[1]
β	0.7	$\frac{1}{\text{day}}$	[2]
ω	0.5	$\frac{1}{\text{day}}$	[7]
σ_1	0.06	$\frac{1}{\text{day}}$	Assumption
σ_2	0.05	$\frac{1}{\text{day}}$	Assumption
α_1	0.099087	$\frac{1}{\text{day}}$	[4]
α_2	0.11624	$\frac{1}{\text{day}}$	[4]
θ	0.01891695041	$\frac{individual}{population}$	[6]

Based on the parameter values, the basic reproduction number from the system of equations (2) to (6) is $R_0 = 1.442803286 > 1$ which means 1 individual can transmit the disease to 1 other individual. The simulation results at the disease-free equilibrium point using the Maple18 program based on the parameters in table 4 with any initial value s(0)=0.38, e(0)=0.4, i(0)=0.25, q(0)=0.17, r(0)=0.27 which is shown in Fig. 3.

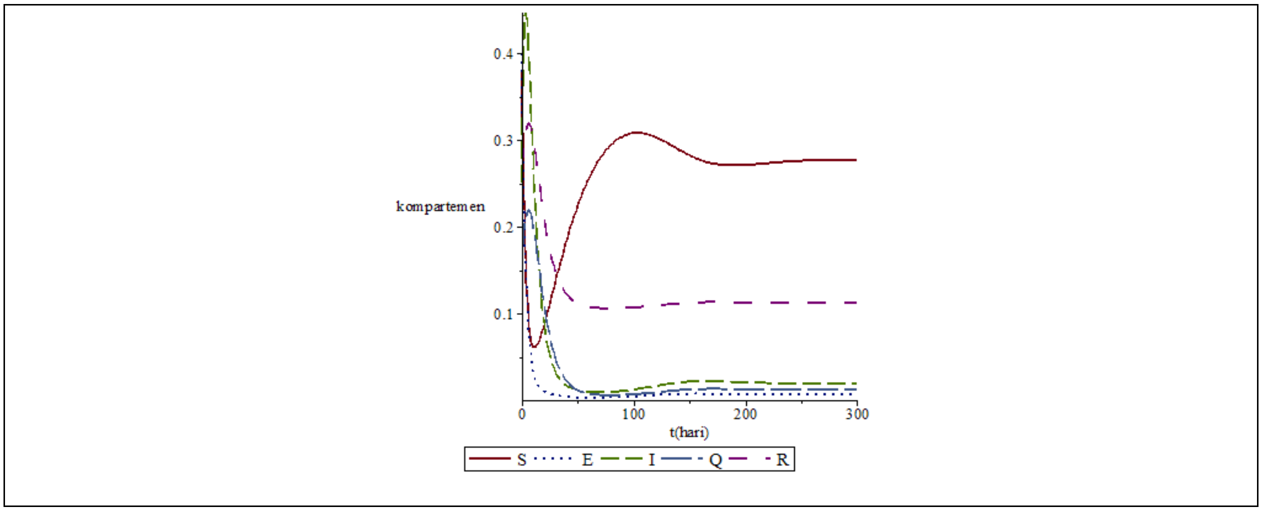
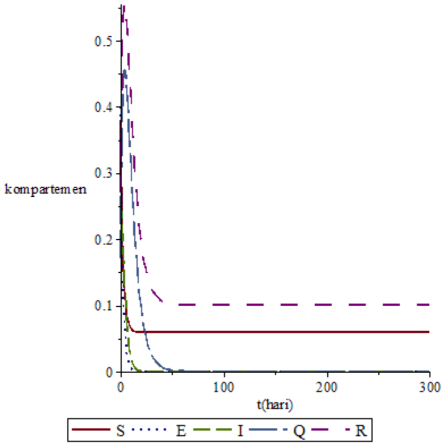


FIGURE 2. Simulation Towards the Endemic Equilibrium Point

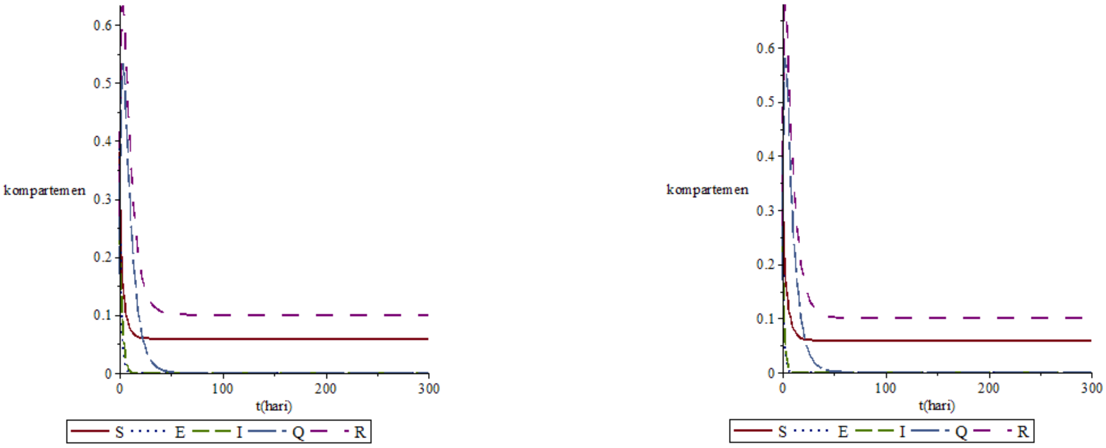
Based on Fig. 3, the suspect population decreased until the 10th day and then increased to a stable point. The exposed population reached a stable point on the 105th day. The infected population increased until the 4th day and then decreased to a stable point on the 225th day. The population that was quarantined increased until the 6th day then drop and became stable. The recovered population increased until the 6th day and then decreased to its stable point.

TABLE 5. The Effectiveness of Vaccination and Quarantine Rate After Being Infected or Exposed to COVID-19 Disease

Vaccination Rate (θ)	**Quarantine after infection (σ_1)**	**Quarantine after exposed (σ_2)**	**Rate of the exposed population becoming infected (ω)**	**Basic Reproduction Number (R_0)**
0.2	0.3	0.3	0.3	4.630623693
0.2	0.5	0.5	0.3	0.140613594
0.2	0.7	0.7	0.3	0.048819513
0.5	0.3	0.3	0.3	1.920014702
0.5	0.5	0.5	0.3	0.058303198
0.5	0.7	0.7	0.3	0.020242237
0.7	0.3	0.3	0.3	1.381063207
0.7	0.5	0.5	0.3	0.041937388
90.7	0.7	0.7	0.3	50.014560206



(a) $\sigma_1 = \sigma_2 = 0.3$



(b). $\sigma_1 = \sigma_2 = 0.5$ $\sigma_1 = \sigma_2 = 0.7$

FIGURE 4. Numerical simulation

Based on Table 5, it is found that quarantine affects the spread of COVID-19. It can be seen that when the exposed population commit quarantine at 0.7 point although the vaccination rate is still low (only 0.2), the spread of the disease is controlled with a basic reproduction number of 0.04881951322. If 70% of the population have been vaccinated, but when exposed population commit quarantine is in a small-scale or 30%, the disease will become an epidemic with a basic reproduction number of 1.381063207.

CONCLUSION

Based on the existing results, the value of the basic reproduction number R_0 is influenced by the parameters of the transmission rate and the vaccination rate and the quarantined population σ_1 and σ_2. If the vaccination rate is large but the quarantined population is small, then the transmission will be in a larger scale. When the vaccination rate are small, but the exposed and infected population implemented the quarantine, the spread of the disease will be controlled, obtaining the basic reproduction number less than one or marked as ($R_0 < 1$).

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