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Sensitivity Analysis of SEIRS Model with Quarantine on the Spread of Covid-19

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ABSTRACT

Since the Covid-19 pandemic, various mathematical models have been developed to describe its spread using the compartment model. The purpose of this research was to construct a new model of Covid-19. This formulated model is an application of SEIRS epidemic model by Zhang & Teng (2007) and a modification of the Covid-19 model by Chatterjee et al. (2020) by adding variations of quarantine. The model is analyzed by determining the disease-free fixed point and basic reproduction number ($\mathcal{R}_0$) through the next generation matrix method. The next step is to analyze the sensitivity to find out the parameters that have the most influence on the spread of Covid-19. The disease will not spread in the population if the value of $\mathcal{R}_0 < 1$, while the disease will spread if the value of $\mathcal{R}_0 > 1$. The result of the sensitivity analysis stated the parameters that can be controlled and have the most significant effect, respectively, are the transmission rate from symptomatic infected individuals (β_2), transmission rates from asymptomatic infected individuals (β_1), quarantine rates for symptomatic infected individuals (θ_3), and quarantine rates for asymptomatic infected individuals (θ_2). Parameters β_2 and β_1 have a negative index, while θ_3 and θ_2 have a negative index. It means decreasing the transmission rate from infected individuals and increasing the quarantine rate for infected individuals can decrease the spread of Covid-19. Therefore there will not be an outbreak in the long term.

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A. INTRODUCTION

Coronavirus disease 2019 (COVID-19), the highly contagious infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has had a catastrophic effect on the world's demographics resulting in more than 6 million deaths worldwide as of March 2022, emerging as the most consequential global health crisis since the era of the influenza pandemic of 1918 (Cascella et al., 2022). It spread rapidly and risked becoming a continuing pandemic (Wang et al., 2020). Most of infected individuals have mild to moderate respiratory tract infections and can recover without special treatment (Kraemer et al., 2020). However, the condition can be an emergency for older adults and individuals with previous health problems such as hypertension and diabetes (Sanyaolu et al., 2020).

Transmission of Covid-19 generally occurs between humans through droplets from coughing or sneezing (Huang et al., 2020). Transmission can also occur in asymptomatic individuals, so it is difficult to know whether an individual whom infected or not (Sameni, 2020). There are some efforts to prevent the spread of Covid-19, those are frequent hand washing, wearing masks, and social distancing. Using masks is effective in preventing transmission from individuals who are not clinically detected (Chan & Yuen, 2020). They are very likely to accelerate transmission (Li et al., 2020). Social distancing is also an effective measure in decreasing Covid-19 cases, namely by maintaining a distance between individuals (Matrajt & Leung, 2020). Another effort is to quarantine, especially the individuals are declared infected. Asymptomatic infected individuals can self-isolation, while symptomatic infected individuals are advised to be hospitalized (Li et al., 2020).

Epidemiologically, infectious diseases can be studied using an epidemic model, namely by a compartmental model (Blackwood & Childs, 2018). There are several studies that discuss the epidemic model of the spread of Covid-19. Batista (2020) modeled the spread of Covid-19 using a deterministic differential equation by dividing the population into S (susceptible), I (infected), and R (recovered). The model has been extended by Carcione et al. (2020) and Khan & Atangana (2020) with E subpopulation (exposed). Okuonghae & Omame (2020) have developed SEIR deterministic model for Covid-19 with asymptomatic and symptomatic subpopulation variations. Furthermore, the SIQ deterministic model was developed by Bhadauria et al. (2021), where Q (quarantine) is a quarantine subpopulation of infected individuals. Individuals who recover from Covid-19 still have a chance to be re-infected (Wang et al., 2021), therefore the SEIRS epidemic model Zhang & Teng (2007) was applied in this study. This research is focused on determining the fixed point and calculating the basic reproduction number. Chatterjee et al. (2020) developed a stochastic SEIQR model for Covid-19 by assuming some parameters follow a certain distribution.

In this study, the model by Chatterjee et al. (2020) was modified by adding a quarantined subpopulation for susceptible individuals (Q_S) and exposed individuals (Q_E). In the study of Chatterjee et al. (2020), E is an individual infected with Covid-19 that cannot be transmitted. Still, in this study, E is an asymptomatic infected individual, and I is a symptomatic infected individual, because infected individuals with symptoms can already transmit the virus before symptoms appear. In addition, the sensitivity analysis of the parameters was not determined in previous research. This study will determine the sensitivity analysis of the model parameters by calculating the sensitivity index. It meant to see the effect of parameters on changes in the basic reproduction number. After getting the dominant parameters, it is expected to produce effective prevention strategies in everyday life to reduce the spread of Covid-19.

B. METHODS

The methods used in this research are literature study and mathematical approach. These are the stages of the research carried out:

a. Reconstruct the model of the spread of the Covid-19 disease by applying the SEIRS epidemic model by Zhang & Teng (2007) and modifying the SEIQR model for Covid-19 by Chatterjee et al. (2020).
b. Determine the disease fixed point in the model.
c. Determine the base reproduction number ($\mathcal{R}_0$) through the next generation matrix.
d. Determine parameter values from several kinds of literature and assumptions so that they are close to actual conditions.

e. Analyze the spread of Covid-19 based on parameter values where the initial value used is the case of Covid-19 DKI Jakarta September 1, 2020, from data.jakarta.go.id with Mathematica 11.0 software.

f. Look for the sensitivity index value of each parameter and describe the effect of parameter changes on the value of the basic reproduction number ($\mathcal{R}_0$) and population dynamics in the system.

1. The SEIRS Epidemic Model by Zhang & Teng (2007)

The SEIRS epidemic model consists of susceptible (S), exposed (E), infected (I), and recovered (R) subpopulations. The assumption used in this model is that individuals who recover can lose immunity and become susceptible again and do not consider the rate of death caused by the disease. Based on the above assumptions, the schematic of the SEIRS model by Zhang & Teng (2007) is shown in Figure 1.

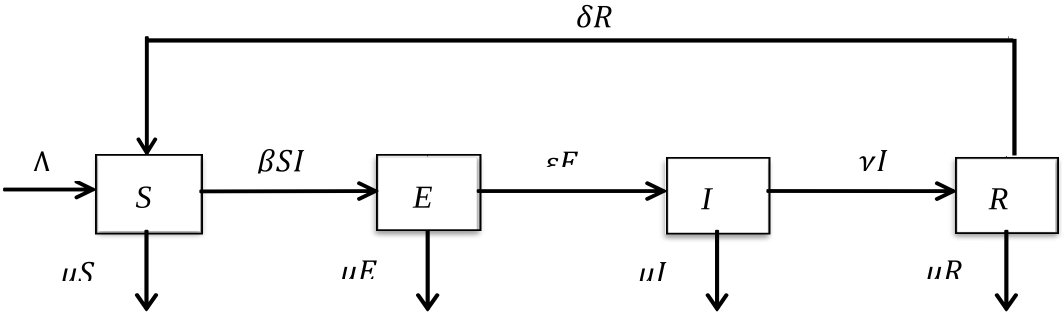

Figure 1. Compartment diagram of SEIRS model

Based on the SEIRS model scheme above, the following differential equation is obtained:

$$
\begin{aligned}
\frac{dS}{dt} &= -\beta SI + \Lambda - \mu S + \delta R \\
\frac{dE}{dt} &= \beta SI - (\varepsilon + \mu)E \\
\frac{dI}{dt} &= \varepsilon E - (\gamma + \mu)I \\
\frac{dR}{dt} &= \gamma I - (\delta + \mu)R
\end{aligned}
$$

where $\Lambda, \mu, \beta, \varepsilon, \gamma, \delta > 0$. A description of each parameter is:

N : total population (individual),
Λ : birth rate (individual/time),
μ : natural death rate (1/time),
β : transmission rate from I (1/individual.time),
ε : transition rate of E to I (1/time),
γ : recovery rate of I (1/time),
δ : transition rate of R to S (1/time).

2. The SEIQR model for Covid-19 by Chatterjee et al. (2020)

This SEIQR model consists of susceptible, exposed, infected, quarantined, recovered, and died individuals. Susceptible individuals are individuals who are not infected with Covid-19. Exposed individuals are individuals who have been infected with Covid-19 but have not been able to transmit it. Infected individuals are individuals who are infected with Covid-19, either asymptomatic or symptomatic, and can transmit. Quarantined individuals are infected with Covid-19 who are self-isolated or hospitalized. Recovered individuals are individuals who have recovered from Covid-19 infection. Died individuals are deaths due to Covid. The compartment diagram of the SEIQR model by Chatterjee et al. (2020) on the spread of Covid-19 is shown in Figure 2.

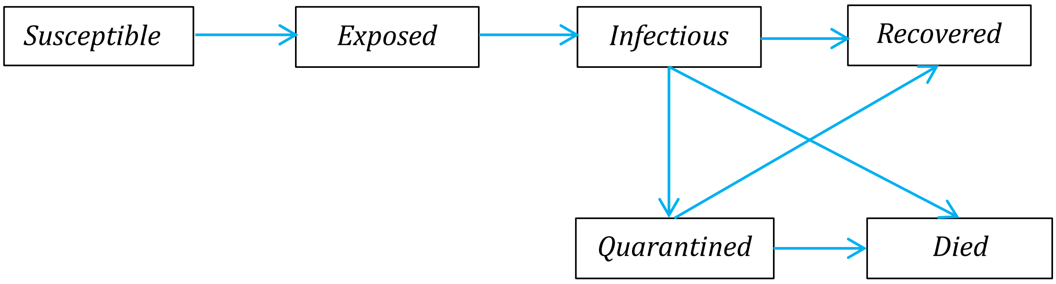

Figure 2. Compartment diagram of the Covid-19 spread model (redrawn from Chatterjee et al. (2020)

The research of Chatterjee et al. (2020) was studied with a stochastic approach using a Monte Carlo simulation with the assumption that several parameters follow the Gamma distribution. In his journal, if the number of quarantined individuals is more than 50%, then Covid-19 cases in India would result in a 62% decrease in cumulative positive cases.

C. RESULT AND DISCUSSION

1. Mathematical Model

The formulated model is an application of the SEIRS epidemic model by Zhang & Teng (2007) because individuals who recover from Covid-19 can be re-infected. This model is also a modification of Chatterjee et al. (2020) because the susceptible individuals (S) can quarantine, so the quarantine subpopulation is added for susceptible individuals (Q_S). Furthermore, symptomatic infected individuals can already transmit the virus before the onset of symptoms, so the exposed individuals (E) is assumed to be asymptomatic infected individuals, and infected individuals (I) is assumed to be symptomatic infected individuals. E can transmit the virus, so Q_E is assumed to be an infected individual who is self-isolated, while Q_I is assumed to be an infected individual who is hospitalized. The limitations in formulating a mathematical model of the spread of COVID-19 are detailed as follows:

a. Newborn individuals are classified as susceptible individuals to Covid-19, so births in subpopulation S are births with a rate of λ.
b. Individuals in subpopulation S can be infected with Covid-19 from individuals in a subpopulation E at a rate of β_1 and individuals in subpopulation I at a rate of β_2.
c. Individuals in subpopulation S will transition to subpopulation Q_S at a rate of θ_1 if individuals with symptoms similar to Covid-19 are quarantined.
d. Individuals in subpopulation Q_S will transition to subpopulation S if they have finished quarantine at the rate σ_1.

e. Individuals in subpopulation E will transition to subpopulation Q_E if they self-isolate at a rate θ_2 and individuals in subpopulation I will transition to subpopulation Q_I if hospitalized at a rate θ_3.
f. Individuals in each subpopulation can experience natural death at a rate of μ, and individuals in subpopulations E, Q_E, I, and Q_I can experience death from Covid-19 at a rate of η_1, η_2, η_3, and η_4, respectively.
g. Individuals from subpopulations E and Q_E will transition to subpopulation I after symptoms appear with rates ε and σ_2, respectively.
h. Individuals from subpopulations E, Q_E, I, and Q_I will transition to subpopulation R after being declared recovered at the rates of ω,σ_3, γ, and σ_4, respectively.
i. Individuals from the subpopulation R can lose immunity to the disease to transition to the subpopulation S at a rate of δ.

The compartment diagram is shown in Figure 3, where (→) represents the movement between individuals in the model of Zhang & Teng (2007), (→) represents the movement between individuals in the model of Chatterjee et al. (2020) and (→) is a modification of the model, as shown in Figure 3.

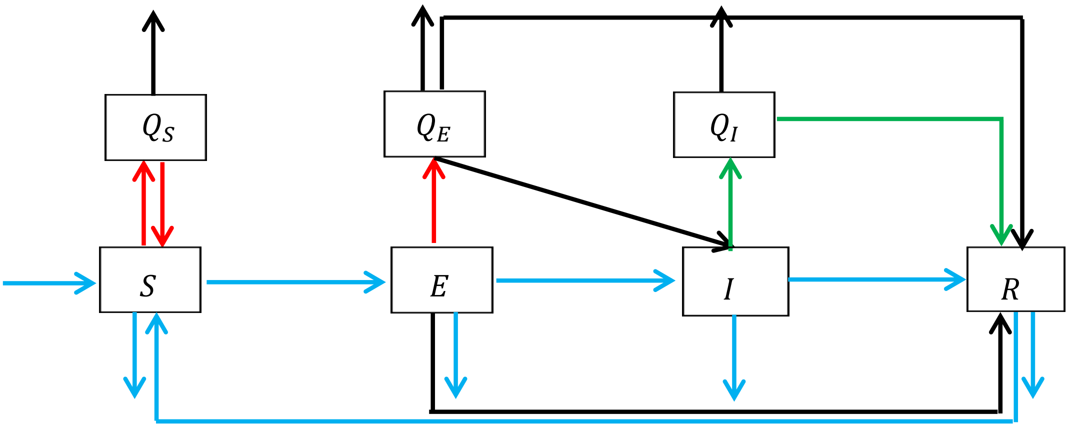

Figure 3. Compartment diagram of the Covid-19 spread model

Based on the diagram above, the following differential equations are obtained:

$$\begin{aligned}
\frac{dS}{dt} &= \lambda N + \sigma_1 Q_s + \delta R - \mu_0 S - \beta_1 \frac{SE}{N} - \beta_2 \frac{SI}{N} - \theta_1 S \\
\frac{dQ_S}{dt} &= \theta_1 S - \sigma_1 Q_s - \mu_0 Q_S \\
\frac{dE}{dt} &= \beta_1 \frac{SE}{N} + \beta_2 \frac{SI}{N} - (\varepsilon + \omega + \theta_2 + \mu_0 + \eta_1) E \\
\frac{dQ_E}{dt} &= \theta_2 E - (\sigma_2 + \sigma_3 + \mu_0 + \eta_2) Q_E \qquad (1) \\
\frac{dI}{dt} &= \varepsilon E + \sigma_2 Q_E - (\gamma + \theta_3 + \mu_0 + \eta_3) I \\
\frac{dQ_I}{dt} &= \theta_3 I - (\mu_0 + \sigma_4 + \eta_4) Q_I
\end{aligned}$$

$$\frac{dR}{dt} \quad = \omega E + \sigma_3 Q_E + \sigma_4 Q_I + \gamma I - (\delta + \mu_0) R$$

where $\lambda, \eta_1, \eta_2, \eta_3, \eta_4, \mu, \beta_1, \beta_2, \theta_1, \theta_2, \theta_3, \sigma_1, \sigma_2, \varepsilon, \omega, \sigma_3, \sigma_4, \delta > 0$, and $N = S(t) + E(t) + I(t) + Q_S(t) + Q_E(t) + Q_I(t) + R(t), \forall t \geq 0$. The parameters are described as follows:

λ : birth rate,
η_1 : disease-related death rate in E
η_2 : disease-related death rate in Q_E,
η_3 : disease-related death rate in I,
η_4 : disease-related death rate in Q_I,
β_1 : transmission rate from E,
β_2 : transmission rate from I,
θ_1 : quarantine rate of S,
θ_2 : quarantine rate of E,
θ_3 : quarantine rate of I,
σ_1 : transition rate of Q_S to S,
σ_2 : transition rate of Q_E to I,
ω : recovery rate of E,
σ_3 : recovery rate of Q_E,
σ_4 : recovery rate of Q_I,

2. Fixed Point Model

Determining the fixed point is conducted by solving those equation (1) and satisfy the condition

$$\frac{dS}{dt} = \frac{dQ_S}{dt} = \frac{dE}{dt} = \frac{dQ_E}{dt} = \frac{dI}{dt} = \frac{dQ_I}{dt} = \frac{dR}{dt} = 0 \tag{2}$$

On the equation (2), a disease-free fixed point and an endemic fixed point are obtained. The disease-free fixed point is a fixed point when there is not any infected individual ($E = I = 0$). It means that,

$$T_0 = (\bar{S}, \bar{Q}_S, \bar{E}, \bar{Q}_E, \bar{I}, \bar{Q}_I, \bar{R}) \tag{3}$$

with

$$\bar{S} = \frac{N\lambda(\mu_0 + \sigma_1)}{\mu_0(\theta_1 + \mu_0 + \sigma_1)}$$

$$\bar{Q}_S = \frac{N\theta_1\lambda}{\mu_0(\theta_1 + \mu_0 + \sigma_1)}$$

$$\bar{E} = 0$$

$$\bar{Q}_E = 0$$

$$\bar{I} = 0$$

$$\bar{Q}_I = 0$$

$$\bar{R} = 0.$$

The endemic fixed point is a fixed point when there are any infected individuals ($E \neq 0$ and $I \neq 0$). Hence,

$$T_1 = (S^*, Q_S^*, E^*, Q_E^*, I^*, Q_I^*, R^*) \tag{4}$$

with

$$S^* = \frac{N(\delta R + \lambda N + \sigma_1 Q_S)}{\beta_1 E + \beta_2 I + N(\theta_1 + \mu)}$$

$$Q_S^* = \frac{\theta_1 S}{\mu + \sigma_1}$$

$$E^* = \frac{\beta_2 SI}{\beta_1 S - N(\varepsilon + \eta_1 + \theta_2 + \mu + \omega)}$$

$$Q_E^* = \frac{\theta_2 E}{\eta_2 + \mu + \sigma_2 + \sigma_3}$$

$$I^* = \frac{\varepsilon E + \sigma_2 Q_E}{\gamma + \eta_3 + \theta_3 + \mu}.$$

3. Basic Reproduction Number

Basic reproduction number ($\mathcal{R}_0$) expresses the average number of infections caused by one infected individual that occurs in a susceptible subpopulation. The population system will experience disease outbreak if $\mathcal{R}_0 > 1$, whereas an outbreak will not occur (a disease-free condition) in the population system if $\mathcal{R}_0 \leq 1$ (Allen & Lahodny, 2012). The value of $\mathcal{R}_0$ is obtained from the dominant eigenvalues of the next generation matrix $\boldsymbol{R} = FV^{-1}$, which is evaluated at a fixed point (T_0) (Driessche & Watmough, 2002). The next generation matrix $\boldsymbol{R}$ is based on the order of the subpopulations that caused the infection only. The infected subpopulations undergoing treatment (self-isolated and hospitalized) are assumed not to consider as new infections, so the subpopulations used in determining the basic reproduction number are E and I (Allen & Lahodny, 2012). Based on the equation (1) obtained:

$$\begin{aligned} \frac{dE}{dt} &= \beta_1 \frac{SE}{N} + \beta_2 \frac{SI}{N} - (\varepsilon + \omega + \theta_2 + \mu_0 + \eta_1)E \\ \frac{dI}{dt} &= \varepsilon E + \sigma_2 Q_E - (\gamma + \theta_3 + \mu_0 + \eta_3)I. \end{aligned} \tag{5}$$

After that, defined matrix $\mathcal{F}$ and $\mathcal{V}$ from the equation (5):

$$\mathcal{F} = \begin{pmatrix} \beta_1 \frac{SE}{N} + \beta_2 \frac{SI}{N} \\ 0 \end{pmatrix}, \mathcal{V} = \begin{pmatrix} \varepsilon E + \omega E + \theta_2 E + \mu_0 E + \eta_1 E \\ \gamma I + \theta_3 I + \mu_0 I + \eta_3 I - \varepsilon E - \sigma_2 Q_E \end{pmatrix}. \tag{6}$$

Furthermore, matrix F is formed which represents the matrix of increasing rate on infection and matrix V represents the matrix of movement rate on disease:

$$F = \begin{pmatrix} \frac{\partial \mathcal{F}_1}{\partial E} & \frac{\partial \mathcal{F}_1}{\partial I} \\ \frac{\partial \mathcal{F}_2}{\partial E} & \frac{\partial \mathcal{F}_2}{\partial I} \end{pmatrix}, V = \begin{pmatrix} \frac{\partial \mathcal{V}_1}{\partial E} & \frac{\partial \mathcal{V}_1}{\partial I} \\ \frac{\partial \mathcal{V}_2}{\partial E} & \frac{\partial \mathcal{V}_2}{\partial I} \end{pmatrix}$$

$$F = \begin{pmatrix} \beta_1 \frac{S}{N} & \beta_2 \frac{S}{N} \\ 0 & 0 \end{pmatrix}, V = \begin{pmatrix} \varepsilon + \omega + \theta_2 + \mu_0 + \eta_1 & 0 \\ -\varepsilon & \gamma + \theta_3 + \mu_0 + \eta_3 \end{pmatrix}. \tag{7}$$

The next generation matrix $\boldsymbol{R}$ is

$$\begin{aligned} \boldsymbol{R} &= FV^{-1} \\ &= \begin{pmatrix} \beta_1 \frac{S}{N} & \beta_2 \frac{S}{N} \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \varepsilon + \omega + \theta_2 + \mu_0 + \eta_1 & 0 \\ -\varepsilon & \gamma + \theta_3 + \mu_0 + \eta_3 \end{pmatrix}^{-1} \end{aligned}$$

with

$$S = \frac{N\lambda(\mu_0 + \sigma_1)}{\mu_0(\theta_1 + \mu_0 + \sigma_1)}.$$

Hence, $\mathcal{R}_0$ is the dominant eigenvalue of matrix $\boldsymbol{R}$, which is

$$\mathcal{R}_0 = \frac{\lambda(\varepsilon\beta_2 + \beta_1 d)(\mu_0 + \sigma_1)}{\mu_0 c d(\theta_1 + \mu_0 + \sigma_1)} \tag{8}$$

with

$$c = \varepsilon + \omega + \eta_1 + \theta_2 + \mu_0$$
$$d = \gamma + \eta_3 + \theta_3 + \mu_0.$$

4. Analysis of the Spread of Covid-19 Based on Parameter Values

The simulated population is 10,558,781 with initial values, based on DKI Jakarta Covid-19 data on September 1, 2020, and obtained from data.jakarta.go.id. The initial value of $S(0) = 10{,}500{,}477$; $E(0) = 2{,}423$; $I(0) = 1{,}500$; $Q_S(0) = 18{,}273$; $Q_E(0) = 3{,}000$; $Q_I(0) = 1{,}841$; and $R(0) = 31{,}267$. The following parameter values used are shown in Table 1.

Table 1. Parameter values

Parameter	Value	Unit	Source
λ	3.6×10^{-5}	1/day	Assumed
μ	3.91×10^{-5}	1/ day	(Amaku et al., 2021)
η_1	0.0035	1/day	(Chowdhury et al., 2022)
η_2	0.0021	1/day	Assumed
η_3	0.0097	1/day	(Chowdhury et al., 2022)
η_4	0.00425	1/day	Assumed
β_1	0.2516	1/day	(Chowdhury et al., 2022)
β_2	0.3110	1/day	(Worldometer, 2021)
θ_1	0.005	1/day	Assumed
θ_2	0.1	1/day	(Riyapan et al., 2021)
ε	0.1961	1/day	(WHO, 2020)
θ_3	0.2	1/day	(Riyapan et al., 2021)
σ_1	0.045	1/day	Assumed
σ_2	0.2857	1/day	Assumed
ω	0.07	1/day	(Chowdhury et al., 2022)
γ	0.022855	1/day	Assumed
σ_3	0.0875	1/day	Assumed
σ_4	0.04571	1/day	(Mayorga et al., 2020)
δ	0.210487	1/day	(Bezabih et al., 2020)

Next, population dynamics in the system presented in Figure 4.

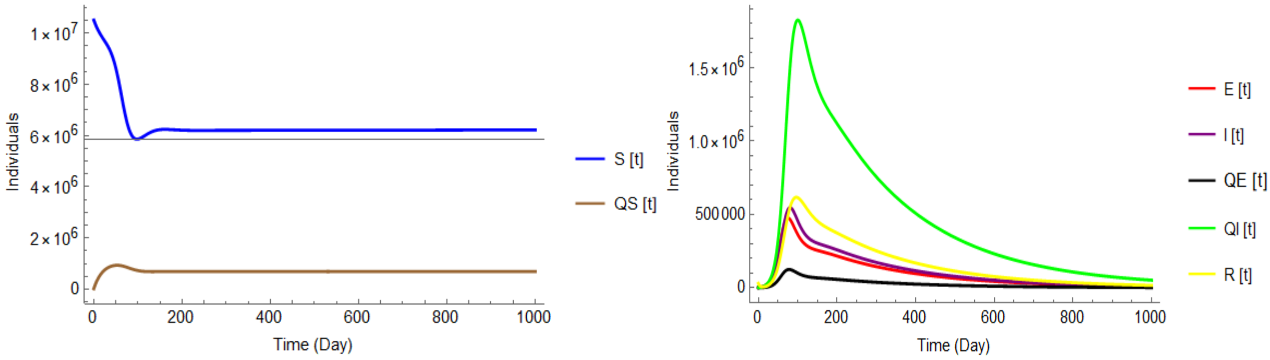

Figure 4. Population dynamics for Covid-19

Figure 4 shows that the number of susceptible individuals (S) decreases significantly and then increases until it stabilizes to a certain value, according to the endemic fixed point. The number of quarantined susceptible individuals (Q_S) increases and then moves until it stabilizes to a value, according to the endemic fixed point . The number of individuals who recovered (R), asymptomatic (E), symptomatic (I), self-isolated (Q_E), and hospitalized (Q_I) increased to a peak, then decreased and moved toward a value. Based on equation (8), the basic reproduction number ($\mathcal{R}_0$) that obtained in this condition, is 1.15193. It means that each infected individual allows for transmit the virus to at least 1 individual.

The number of infected individuals, i.e., asymptomatic, with symptoms, self-isolated, and hospitalized, has decreased but has not reached zero. It means that the disease will not disappear within 1000 days, with the start time of the analysis being September 1, 2020. It follows the $\mathcal{R}_0$ results obtained, which are more than 1. As a result, Covid-19 will still exist/spread in the population.

5. Sensitivity Analysis

Sensitivity analysis is used to examine the effect of changes in parameter values on the model. Sensitivity analysis is carried out on the basic reproduction number and the disease-free fixed point. The sensitivity index $\gamma_p^{\mathcal{R}_0}$ can be defined as follows:

$$\gamma_p^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial p} \times \frac{p}{\mathcal{R}_0} \tag{9}$$

With p is the value of model parameter. The Sensitivity index is used to show the relative change in the basic reproduction number ($\mathcal{R}_0$) when the value of the parameter p is changed (Chitnis et al., 2008). Example of the calculation in determining the sensitivity index value of the parameters β_1 and θ_2:

$$\begin{aligned}
\gamma_{\beta_1}^{\mathcal{R}_0} &= \frac{\partial \mathcal{R}_0}{\partial \beta_1} \times \frac{\beta_1}{\mathcal{R}_0} \\
&= \frac{\lambda(\mu + \sigma_1)}{\mu(\varepsilon + \omega + \eta_1 + \theta_2 + \mu)(\theta_1 + \mu + \sigma_1)} \times \frac{\beta_1}{\mathcal{R}_0} \\
&= 0.489681 \\
\gamma_{\theta_2}^{\mathcal{R}_0} &= \frac{\partial \mathcal{R}_0}{\partial \theta_2} \times \frac{\theta_2}{\mathcal{R}_0} \\
&= -\frac{\lambda(\varepsilon\beta_2 + \beta_1(\gamma + \eta_3 + \theta_3 + \mu))(\mu + \sigma_1)}{\mu(\varepsilon + \omega + \eta_1 + \theta_2 + \mu)^2(\gamma + \eta_3 + \theta_3 + \mu)(\theta_1 + \mu + \sigma_1)} \times \frac{\theta_2}{\mathcal{R}_0} \\
&= -0.270534
\end{aligned}$$

The sensitivity index for each parameter is shown in Table 2.

Table 2. Parameter sensitivity index

Parameter	**Sensitivity index**
β_1	0.489681
β_2	0.510319
ε	-0.0201984
γ	-0.0501446
θ_1	-0.0999219
θ_2	-0.270534
θ_3	-0.438807
η_1	-0.0094687
η_3	-0.0212821
ω	-0.189374
λ	1
μ	-1.0001
σ_1	0.0998351
σ_1	0.0998351

Table 2 shows that each parameter has a different effect on the basic reproduction number ($\mathcal{R}_0$). Sensitivity index value $\beta_1, \beta_2, \lambda$, and σ_1 are positive, so increasing these parameters will contribute to the increases in $\mathcal{R}_0$. While the value of the sensitivity index $\varepsilon, \gamma, \theta_1, \theta_2, \theta_3, \eta_1, \eta_3, \omega$, and μ are negative. It means that increasing these parameters will contribute to the decreases in $\mathcal{R}_0$. Based on the sensitivity index, the parameters that have the greatest influence are natural death rate(μ) and birth rate (λ), but these two parameters are external factors beyond the control of the epidemiological field, so they are not discussed in this paper. Parameters that can be controlled are transmission rate from symptomatic individuals (β_2), transmission rate from asymptomatic individuals (β_1), quarantine rate of symptomatic individuals (θ_3), and quarantine rate of asymptomatic individuals (θ_2).

Parameters β_2 and β_1 have sensitivity index values of 0.510319 and 0.489681 respectively. It means if β_2 is decreased by 10%, then the value of $\mathcal{R}_0$ will decrease by 5.10319% ($\mathcal{R}_0 = 1.09314$). If β_1 is decreased by 10%, then the value of $\mathcal{R}_0$ will decrease by 4.89681% ($\mathcal{R}_0 = 1.09552$). The sensitivity index values for θ_3 and θ_2 are -0.438807 and -0.270534 respectively. It means if θ_3 increased by 10%, then the value of $\mathcal{R}_0$ will decrease by 4.38807% ($\mathcal{R}_0 = 1.10138$). If θ_2 increased by 10%, then the value of $\mathcal{R}_0$ will decrease by 2.70534% ($\mathcal{R}_0 = 1.12076$). Furthermore, an illustration is given to determine the population dynamics when there is a change in the parameter value. The changed parameters are β_2 and θ_3, because they are easy to control. The population dynamics when the parameter value of β_2 is decreased by 50% ($\beta_2 = 0.1555$) and the value of θ_3 increased by 50% ($\theta_3 = 0.3$) are shown in Figure 5.

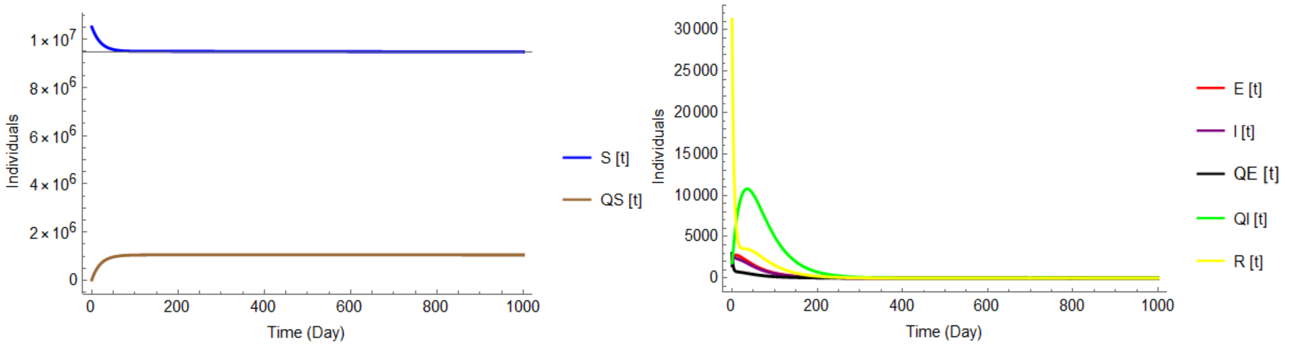

Figure 5. Population dynamics when $\beta_2 = 0.1555$ and $\theta_3 = 0.3$

Figure 5 shows the population dynamics due to changes in parameter values β_2 and θ_3. The value of $\mathcal{R}_0$ obtained is $0.769629 < 1$, so that the population will reach a disease-free condition. The number of S decreases and then stabilizes to a value, while the number of Q_S increases until it stabilizes to a certain value according to the disease-free fixed point. The number of E, I, Q_E, Q_I and R will go to 0, according to the value of $\mathcal{R}_0$ obtained. The given illustration shows that decreasing of β_2 and increasing of θ_3 can decrease the value of $\mathcal{R}_0$ according to the sensitivity index value in Table 2. Namely, β_2 has a positive index, while θ_3 has a negative index.

In line with this study, the research of Chatterjee et al. (2020) conducted a simulation stating the effectiveness of quarantine in reducing Covid-19 cases, but no sensitivity analysis was carried out previously. As a result, we cannot know the magnitude of the influence of each model parameter on the spread of Covid-19. In this study, a sensitivity analysis was carried out to show how the effect of increasing and decreasing each parameter was carried out. The results of this study indicate that it is not only the quarantine rate parameter that has a large effect but also the transmission rate parameter. Therefore, the strategy to suppress the spread of Covid-19 is to reduce the transmission rate of infected individuals (with symptoms and asymptomatic) and increase the quarantine of infected individuals. However, in actual conditions, of course, encounter obstacles such as detecting how many contacts occur between individuals who carry the virus and individuals who do not carry the virus thoroughly. As a result, we can take action to prevent its spread by complying with health protocols such as social distancing, wearing masks, frequently washing hands, and reducing mobility.

D. CONCLUSION AND SUGGESTIONS

The SEIRS model with variations quarantine (Q_S, Q_E, Q_I) can be used to determine the characteristics of the spread of Covid-19. With the initial value obtained from the Covid-19 case in DKI Jakarta on September 1, 2020, the $\mathcal{R}_0$ value is greater than 1 and there will still be infected individuals on the 1000th day. Therefore, a parameter sensitivity analysis was conducted to determine an effective control strategy to achieve a disease-free condition. The results of the sensitivity analysis show that the major influential and controllable parameters are transmission rate from symptomatic individuals (β_2), transmission rate from asymptomatic individuals (β_1), quarantine rate of symptomatic individuals (θ_3), and quarantine rate of asymptomatic individuals (θ_2). Transmission rate from symptomatic individuals (β_2) and transmission rate from asymptomatic individuals (β_1) have a positive relation to the basic reproduction number $(\mathcal{R}_0)$. On the other hand, quarantine rate of symptomatic individuals (θ_3) and quarantine rate of asymptomatic individuals (θ_2) have a negative relation with $\mathcal{R}_0$. Based on these results, to achieve a disease-free condition or make a value of $\mathcal{R}_0 < 1$, efforts that can be made daily is decreasing the transmission rate by reducing contact between individuals. Another effort that can be made is increasing quarantine for infected individuals, either self-isolated or hospitalized. The suggestion from this research is to add a vaccination compartment to the model. In this study, to determine the parameters still refers to previous studies. Future research is expected to obtain parameter values from data with actual conditions.

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