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Sensitivity analysis of SEIR epidemic model of Covid 19 spread in Indonesia

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Abstract. Epidemiological models may provide public health practitioners with some fundamental guidelines, allowing for the examination of issues that may influence disease prevention and treatment techniques. On establish the relative impact of the model parameters to disease transmission, a sensitivity analysis of the epidemiological model is undertaken. A sensitivity analysis of the Susceptible, Exposed, Infectious, and Recovered (SEIR) model of corona virus 2019 (COVID 19) was undertaken to determine the parameters' influence on the basic reproduction number and endemic equilibrium. The rate of contact between susceptible individual and exposed individuals and rate of exposed to infected individuals are the most impactful parameters on the basic reproduction number and the number of infectious individuals, according to our findings. Furthermore, the number of people who have been exposed is affected by the rate at which they proceed from exposed to infect. The findings show that if infectious people recover faster, the number of contagious people will decrease.

1. Introduction

COVID-19 is spread by people who have been infected with the corona virus, according to the World Health Organization (WHO). When someone infected with this virus sneezes or coughs, little droplets from their nose or mouth can easily spread the infection. The drips then settle on touched items or surfaces, and the healthy person adjusts their eyes, nose, or mouth accordingly. Compilation of small droplets breathed by someone compiling switch with the one supported by corona [1] is one way to propagate the corona virus. It is critical to travel 1 meter further than sick persons. "Until now, no research has shown that the COVID-19 corona virus can be spread through the air," revealed WHO on March 23, 2020 [2] as quoted from its website.

In various parts of the world, the number of instances of corona virus infection, which causes Covid-19, continues to rise. Each region has a different pace of increase in terms of infection, death, and cure. Each country has its own viral control policy to prevent the spread of viruses that develop on its soil. Mathematical modeling of SIR, SIRS, SEIR, and SEIRS on the transmission of diseases such as dengue fever, tuberculosis, diabetes, and HIV-AIDS has been done by [3–18], and then mathematical modeling on the spread of COVID-19 has been done by [19], namely SEIRV



mathematical modeling in Wuhan, China, taking environmental factors into account, while the analysis and simulation of the model used data.

Mathematical modeling has been widely utilized to discover and study the dynamics of disease propagation [20, 21], as well as to assess the efficacy of health interventions such as Wolbachia bacteria [22, 23] and immunization [24, 25]. The mathematical model of disease propagation is typically formulated as a deterministic [26] or stochastic mathematical model [27]. One of the challenges in analyzing the dynamics of disease spread or the effectiveness of a health intervention using a mathematical model is the sensitivity of the parameters to the results of the mathematical model. Sensitivity analysis is used to figure out which parameters and initial conditions (inputs) have an impact on the model's needed quantity (output). This has an impact on the accuracy of the mathematical model's predictions or outcomes. As a result, when using a mathematical model to analyze the dynamics or effectiveness of health interventions, sensitivity analysis is required to discover the most relevant parameter in the mathematical model [28, 29]. This information is crucial and beneficial throughout the parameter estimate stage, as well as the interpretation of research findings and the search for possible solutions if the parameter value changes. There are two forms of sensitivity analysis: local and global. The one-at-a-time (OAT) technique is used in the local sensitivity analysis, which is the most basic method with partial differentiation, in which various parameter values are taken one by one. Meanwhile, in global sensitivity analysis, all inputs are modified at the same time across the input space, typically utilizing a sampling-based approach that is frequently done with the Monte-Carlo method [29].

This research examines the epidemic model's locally sensitivity to the basic reproduction number (epidemic threshold) and infected fixed points. This research attempts to identify the parameters that have the most impact on the 2019 Covid epidemic model's basic reproduction number and infected fixed sites.

2. Mathematical Modelling

The SEIR model was presented by Annas et al. in 2020 [30]. The dissemination of COVID-19 is separated into four divisions in the SEIR model, notably Suspected (**S**), Exposed (**E**), Infected (**I**), dan Recovered (**R**). Individuals in an infected class have the potential to infect others. The SEIR model can analyse changes in Covid-19 transmission in each human community as the following model:

$$\begin{aligned} \frac{dS}{dt} &= \mu N - (\alpha I + \mu + v)S, \\ \frac{dE}{dt} &= \alpha IS - (\beta + \mu)E, \\ \frac{dI}{dt} &= \beta E - (\sigma + \delta + \mu)I, \\ \frac{dR}{dt} &= \delta I + vS - \mu R, \end{aligned} \tag{1}$$

where N is the whole human population, S is Number of people who are susceptible, E is Total population at risk, I is infected people's numbers, R is the total population recovered, μ is Population birth/ death rate, α is probability of change from S to E populations, β is probability of change from E to I populations, σ is COVID-19's population mortality rate, δ is probability of change from I to R populations and v is Vaccines from Unknown Sources. From Annas et.al. (2020) [30] is obtained two equilibrium points, i.e. equilibrium points for Free disease, $E_0 = (S^*, I^*, R^*) = \left(\frac{\mu}{(\mu+v)}, 0, 0, \frac{v}{(\mu+v)}\right)$ and endemic point $E_e = (S^{**}, E^{**}, I^{**}, R^{**})$ where

$$S^{**} = \frac{(\mu_i + \delta + \mu)(\beta + \mu)}{\alpha\beta},$$

$$E^{**} = \frac{\alpha\beta\mu - (\mu_i + \delta + \mu)(\mu + v)}{\alpha\beta},$$

$$I^{**} = \frac{\alpha\beta\mu - (\mu_i + \delta + \mu)(\mu + v)(\beta + \mu)}{\alpha(\mu_i + \delta + \mu)(\beta + \mu)},$$

$$R^{**} = \frac{\delta\alpha\beta^2\mu - \beta(\mu_i + \delta + \mu)(\mu + v)(\beta + \mu) - v((\mu_i + \delta + \mu)(\beta + \mu))^2}{\beta\alpha^2(\mu_i + \delta + \mu)(\beta + \mu)}.$$

While the basic reproduction number (R_0) which determined by generation matrix method as

$$R_0 = \frac{\alpha\beta\mu}{(\mu + \beta)(\mu + v)(\mu_i + \delta + \mu)} \tag{2}$$

3. Sensitivity Analysis

It is vital to discover numerous aspects that contribute to the virus's transmission and prevalence in order to decide the best technique for minimizing the number of affected people. The first case of COVID-19 transmission was linked to R_0 and those who had been exposed to the virus.

Table 1. Estimation of parameter values in cases of COVID-19

Parameter	Value	References
μ	6.25×10^{-3}	[25]
α	0.62×10^{-8} / person / day	[11]
β	3 hari	[30]
σ	7.344×10^{-7}	[21]
δ	0.0006667 per day	[30]
v	1%	[30]

3.1. Sensitivity Analysis of Basic Reproduction (R_0)

The sensitivity index of each model parameter, which is connected with the basic reproduction number, R_0 , is calculated in this section. This index indicates the relative importance of each parameter in the model that depicts COVID-19 transmission. The index is used to find the parameter with the greatest impact on R_0 , which is subsequently utilized as the intervention's target. Parameters with a large impact on R_0 imply that they have a significant impact on COVID-19 endemicity. An technique similar to that outlined was used to derive the sensitivity index parameter to the basic reproduction number.

Definition 1 [31]: *The normalized sensitivity index is calculated using the normalized sensitivity index of the variable R_0 , which is differentiable on the parameter p :*

$$C_p^{R_0} = \frac{\partial R_0}{\partial p} \times \frac{p}{R_0} \tag{3}$$

where R_0 is the variable to be analyzed and is the parameter.

The sensitivity index will be used to determine the impact of each parameter on a disease's epidemic, allowing measures to be made to control its spread. The sensitivity index of each parameter is derived from R_0 using definition 1 above. The sensitivity index of each parameter is calculated at the basic reproduction number R_0 , shown in Table 2, by referring to the formulation of equation (3) and the parameter values in Table 1. The sensitivity index R_0 to the parameters, for instance, is

$$\begin{aligned} C_\mu^{R_0} &= \frac{\partial R_0}{\partial \mu} \times \frac{\mu}{R_0} \\ &= \left(\frac{R_0}{\alpha}\right) \times \frac{\alpha}{R_0} \\ &= 1 \end{aligned}$$

and

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

$$= R_0 \left(-\frac{1}{(\beta + \mu)} + \frac{1}{\beta} \right) \times \frac{\beta}{R_0}$$

$$= 0.0021$$

where $R_0 = \frac{\alpha\beta\mu}{(\mu+\beta)(\mu+v)(\sigma+\delta+\mu)}$.

The findings can be found in the following table.

Table 2. Index of model parameters related to basic reproduction number

Parameter	Parameter value	Sensitivity Index
μ	6.25×10^{-3}	-0.2902
α	0.62×10^{-8} / person / day	1
β	3 day	0.0021
σ	7.344×10^{-7}	-0.0001
δ	0.0006667 per day	-0.0964
v	1%	-0.6154

The sensitivity index of each parameter in the basic reproductive number, R_0 , provided in Table 2, is calculated using the formulation of equation (3) and parameter values from Table 1. The sensitivity index in Table 2 sequentially shows the parameter with the highest sensitivity to the lowest sensitivity. The parameter α and β has a positive sensitivity index, while the parameter μ, σ, δ and v have a negative sensitivity index. Positive sensitivity indexes indicate that the increase in basic reproductive numbers is significant. As a result, increasing (or decreasing) the value of the parameter while maintaining the value of the other parameters will lead to increases (or decreases) in the basic reproductive numbers. Negative sensitivity indexes indicate that the rise in basic reproductive numbers has a negative significance. In other words, increasing (or reducing) the value of the parameter while the values of the other parameters remain constant will result in decreases (or rises) in the basic reproductive numbers.

3.2. Sensitivity analysis to infected points (I^{**})

Sensitivity analysis of I^{**} was conducted to determine which parameters have the most effect on I^{**} . The parameters to be analyzed are $\alpha, \beta, \sigma, \delta, v$. The results of the sensitivity index of the parameters to the infected fixed point are determined using the same approach as defined in definition 1, and the following table 3 summarizes the findings.

Table 3. Sensitivity Index of Parameter to Infected Point.

Parameter	Parameter value	Sensitivity Index
μ	6.25×10^{-3}	-1.613×10^8
α	0.62×10^{-8} / person / day	4.227×10^{14}
β	3 day	0.0006
σ	7.344×10^{-7}	-130.343
δ	0.0006667 per day	-130.343
v	1%	-1.613×10^8

Table 3 shows the value of the sensitivity index of the model parameters. Positive values for the parameters α and β illustrate that the prevalence of the disease increases with increasing parameter

values while the sensitivity index of the parameters μ , σ , δ and ν are negative indicating the opposite. Thus, the parameters μ , σ , δ and ν contributed to the decrease in the value of the infected number and thus, contributed to the decrease in the prevalence of the disease. Moreover, the table shows that the most positive sensitive parameter is the spread rate of the COVID19 virus and the most negative sensitive model parameters are the decrease in infections due to the COVID19 virus.

4. Conclusions

In this work, we have discussed the SEIR model of Covid 19 disease. We carried out a sensitivity analysis to determine the important model parameters that significantly affect the dynamics of Covid 19 disease transmission in Indonesia. We observed that the most important sensitive parameters were and (positive) and other rates (negative). Increased rates of exposure and infection increase disease transmission and increased mortality reduces disease transmission significantly. Thus, increasing the mortality rate and reducing the rate of spread of the virus can reduce the prevalence of the COVID-19 disease. Very sensitive parameters must be estimated carefully, as small variations in these parameters will lead to large quantitative changes. An insensitive parameter, on the other hand, does not require much effort to estimate, because a small variation in that parameter will not result in a large change in the desired quantity.

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