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THE DYNAMICS OF COVID-19: THE EFFECT OF LARGE-SCALE SOCIAL RESTRICTIONS

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Abstract: Due to the global pandemic of Covid-19, Indonesian government released a large-scale social restriction policy to reduce the spread of the disease. It still allowed people to have activities outside. The government also had another policy to divide covid-19 patient into three categories, such as People under Monitoring (ODP), Patients under Surveillance (PDP), and Confirmed Patients. This study aimed to explore the Covid-19 model in which large scale social restriction had been involved. It was not only to figure out the stability analysis of the model but also to predict the spread of the disease through numerical simulation. We constructed model based on the characteristic of Covid-19. Human population have been divided into five sub population, such as Susceptible (0), Susceptible (1), Exposed, Infected, and Recovered. Three of them related to the Covid-19 patient's category. A disease-free equilibrium and endemic equilibrium have been determined. By using Next Generation Matrix, the basic reproduction number also had been obtained. Stability analysis have been done to explore the existence of the disease. A large scale-social restriction had a significant effect to the spread of the disease. The effectiveness of policy ranges from 80%-100% and it will reduce the number of people under monitoring.

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1. INTRODUCTION

Since the end of 2019, the disease caused by the corona virus has spread throughout the world. The disease, known as Covid-19 and first appeared in Wuhan China, has infected 6,535,354 patients as of early June 2020. Meanwhile, data obtained from the WHO site on June 5th, 2020, showed that 213 countries had been infected by Covid-19. Developed countries such as the United States, Brazil, Russia and Italy have been recorded as the countries with the most cases of Covid patients in the world [1-3]. Meanwhile, the number of patients who die in developing countries continues to increase every day. The number of death due to Covid-19 that occurred in Iran, Pakistan, India, Phillipine and Indonesia until the end of May 2020 were 7734, 1483, 5164, 950 and 1,573 people respectively [4-5].

Several countries issued new policies related to handling Covid-19. Countries such as Austria, Belgium, France, Ireland, Italy, Luxembourg, Portugal, Spain and the United Kingdom have implemented a full lockdown on their citizens to prevent the spread of the disease, while Korea and the United States had implemented a partial lockdown in several of its states [6-7]. Indonesia with an increasing number of corona patients had also issued new policies to reduce the movement of its citizens. Some big cities with a relatively large number of patients (known as red and black zones) were subject to large-scale social restrictions. This restriction did not apply to citizens who work in certain fields, such as: health, logistics, banking, and communications [8]. In addition to large-scale social restrictions, Indonesia had also implemented a naming system for cases of covid-19 patients, such as: People under Monitoring (ODP), Patients under Surveillance (PDP), and Confirmed Patients [9]. This form of labelling was done to classify the risk and appearance of symptoms from people who might or have been exposed to the corona virus.

In addition, based on the https://kawalcovid19.id site, the labelling system used by the Indonesian government was based on one of the characteristics of the Covid-19 or a person's travel history to areas that have local transmission. Following the differences between People in Monitoring (ODP), Patients in Oversight (PDP), and Confirmed Patients are shown in table 1.

Table 1. The Difference in labelling of Corona cases in Indonesia

People under Monitoring (ODP)	Patients under Surveillance (PDP)	Confirmed Patients
• If you have fever (body temperature is greater than 38^0C) or have fever history	• If you have fever or a history of fever and one of the symptoms of cough/cold/ shortness of breath without pneumonia	• Patients who were confirmed positive for SARS-CoV-2 through examination of clinical symptoms and microscopic laboratory with RT-PCR
• Cough or Cold	• Have a history of travel or traveling to a country that has local transmission of Covid-19	
• Have a history of travel to a country that has a local transmission of Covid-19	• Live in an area with local transmission in Indonesia in the last 14 days before the symptoms appear	
• Live in an area with local transmission in Indonesia in the last 14 days before symptoms appear, but has no history of contact with a positive person with Covid-19	• Have a history of fever or cough/cold without pneumonia and a history of contact with a positive case of Covid-19	

This study aimed to explore the dynamic behaviour of the spread of the Covid-19 which takes into account large-scale social restrictions in Surabaya, Indonesia. The mathematical model was built based on the characteristics of the Covid-19, while the division of the human population is based on the labelling system used by the Indonesian Government.

2. MATERIALS AND METHOD

This modelling is constructed from the basic model of SIR disease spread which was first developed by Kermack-Mckendrik in 1927 [10]. We propose a mathematical model with the compartments shown in Figure 1. The human population is divided into five sub-populations, namely Susceptible ($S_0(t)$), Susceptible ($S_1(t)$), Exposed ($E(t)$), Infected ($I(t)$), and Recovered ($R(t)$). $S_0(t)$ represents humans who are at risk of being infection, $S_1(t)$ represents people under monitoring (ODP), $E(t)$ represents patients under surveillance (PDP), $I(t)$ represents patients who have been confirmed positive for the corona virus, and $R(t)$ represents patients who have recovered from Covid-19. Meanwhile, large-scale social restrictions is included in the model as a parameter that limits the spread of the disease from the population of $S_0(t)$ and $S_1(t)$ to the population of $E(t)$ (with parameter p). Some assumptions are used to simplify the phenomenon and to provide the limitation of the modelling, such as a) the population is closed (no-migration), b) there are natural death and death by the disease, c) patients under surveillance and confirmed patients can recover on its own without treatment of drugs (recovery occurs due to an increase in the immune system), and d) patients who have recovered can be re-infected by the corona virus.

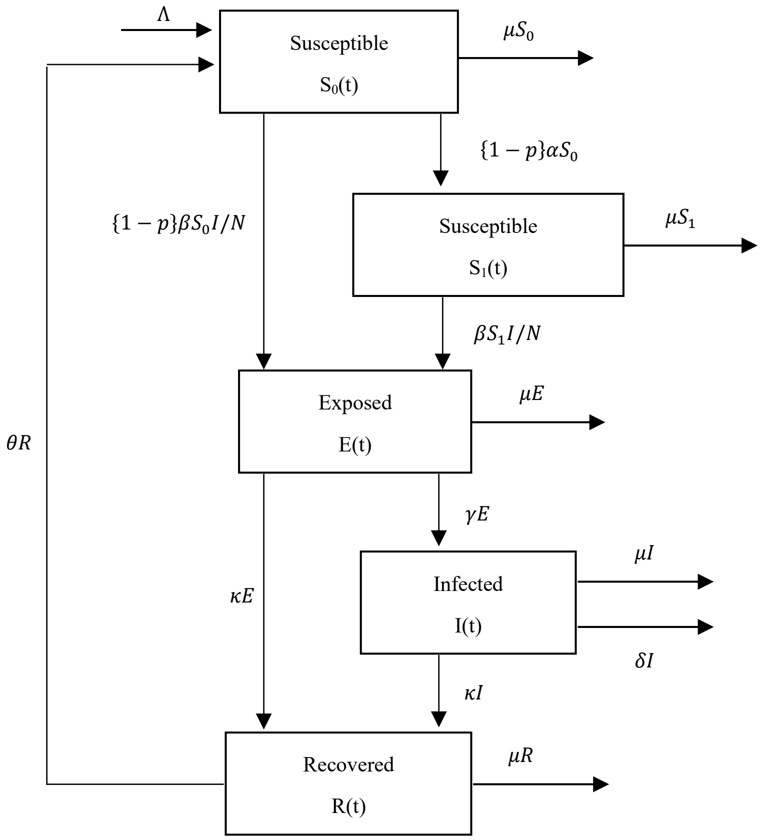


Figure 1. Compartment Model of Covid-19 in Surabaya, Indonesia

Regard to the compartment diagram, mathematical model is described as follows

$$\dot{S_0} = \Lambda - \{1-p\}\beta S_0 \frac{I}{N} - \{1-p\}\alpha S_0 - \mu S_0 + \theta R \tag{1}$$

$$\dot{S_1} = \{1-p\}\alpha S_0 - \beta S_1 \frac{I}{N} - \mu S_1 \tag{2}$$

$$\dot{E} = \{1-p\}\beta S_0 \frac{I}{N} - \beta S_1 \frac{I}{N} - \gamma E - \kappa E - \mu E \tag{3}$$

$$\dot{I} = \gamma E - \mu I - \delta I - \kappa I \tag{4}$$

$$\dot{R} = \kappa E + \kappa I - \mu R - \theta R \tag{5}$$

with

$N = S_0 + S_1 + E + I + R$ and $S_0(0), S_1(0), E(0), I(0), R(0)$ are given

Λ : quantifying the recruitment rate

p : quantifying the efficiency large-scale social restriction $(0 \leq p \leq 1)$

β : quantifying the human-to-human transmission coefficient per unit time (days) per person

α : quantifying the rate of human movements per unit time (days) per person

γ : quantifying the incubation rate per unit time (days) per person

θ : quantifying the rate of re-infection per unit time (days) per person

μ : quantifying the natural death rate per unit time (days) per person

κ : quantifying the recovery rate per unit time (days) per person

δ : quantifying the rate of death-by infection per unit time (days) per person

All parameters are assumed to be positive.

Disease Free equilibrium and endemic equilibrium are determined by setting the right-hand side of the equation (1) - (5) equal to zero, such that the following form is obtained

1. Disease-Free Equilibrium

$$DFE := \left(S_0 = -\frac{\Lambda}{\alpha p - \alpha - \mu}, S_1 = \frac{(-1+p)\Lambda\alpha}{(\alpha p - \alpha - \mu)\mu}, E = 0, I = 0, R = 0\right)$$

2. Endemic Equilibrium

$$EE := (S_0 = S_0^*, S_1 = S_1^*, E = E^*, I = I^*, R = R^*)$$

It is not easy to determine the endemic equilibrium due to the complexity of equations (1) - (5), however it is still possible to show the result numerically. At the disease-free equilibrium, it can be seen that if the value of $p = 0$ (large-scale social restriction is not efficient to implement) then a population of people under monitoring will be obtained. Meanwhile, if the value of $p = 1$ (large-scale social restriction is efficient to reduce the spread of the Covid-19) then there will be no population of people under monitoring.

3. RESULTS AND DISCUSSION

Furthermore, one of the most significant thresholds in studying disease transmission models is knowing the position where the disease will remain in a population or will extinct for a long time. This threshold is known as the basic reproduction number. In this section we show the basic reproduction numbers generated by next generation matrix, stability analysis, sensitivity analysis, and numerical simulation.

a. Basic Reproduction Number

By using the next generation matrix approach, the determination of the basic reproduction number can be determined using a matrix F and V which is the Jacobian matrix associated with the incidence rate of new infections [11].

$$J_{\mathcal{F}} = \begin{bmatrix} 0 & \dfrac{\beta(\alpha p - \mu p - \alpha + \mu)}{\alpha p - \alpha - \mu} \\ 0 & 0 \end{bmatrix}$$

$$J_V = \begin{bmatrix} \gamma + \kappa + \mu & 0 \\ -\gamma & \delta + \kappa + \mu \end{bmatrix}$$

The basic reproduction number R_0 is determined using a spectral radius $F.V^{-1}$ so that the following form is obtained

$$R_0 = \frac{n\gamma}{klm}$$

with

$k \ = \alpha p - \alpha - \mu$

$l \ \ = \gamma + \kappa + \mu$

$m = \delta + \kappa + \mu$

$n \ = \beta(\alpha p - \mu p - \alpha + \mu)$

b. Local Stability

From equations (1) - (5) and the disease-free equilibrium point, the Jacobian matrix is obtained as follows

$$J = \begin{bmatrix} \alpha p - \alpha - \mu & 0 & 0 & \dfrac{-\beta p\mu + \beta\mu}{\alpha p - \alpha - \mu} & \theta \\ -\alpha p + \alpha & -\mu & 0 & \dfrac{-(p-1)\alpha\beta}{\alpha p - \alpha - \mu} & 0 \\ 0 & 0 & -\gamma - \kappa - \mu & \dfrac{\beta(\alpha p - \mu p - \alpha + \mu)}{\alpha p - \alpha - \mu} & 0 \\ 0 & 0 & \gamma & -\delta - \kappa - \mu & 0 \\ 0 & 0 & \kappa & \kappa & -\mu - \theta \end{bmatrix}$$

Furthermore, the stability analysis is carried out by analyzing the eigenvalues at the disease-free equilibrium [12]. From the Jacobian matrix above, five eigenvalues are obtained as follows:

a. $\lambda_1 = k = \alpha p - \alpha - \mu$. The value of p lies between 0 and 1 so that the eigenvalue λ_1 is always negative. It means that the disease-free equilibrium will be stable when the value of λ_1 is satisfied.

b. $\lambda_2 = -\mu$. All parameter are assumed to be positive so that the eigenvalue of λ_2 is always negative. It means that the disease-free equilibrium will be stable when the value of λ_2 is satisfied.

c. $\lambda_3 = -\mu - \theta$. All parameter are assumed to be positive so that the eigenvalue of λ_3 is always negative. It means that the disease-free equilibrium will be stable when the value of λ_3 is satisfied.

d. $\lambda_4 = \frac{1}{2} . \frac{-kl-km+\sqrt{(kl+km)^2-(4k^2lm-4\gamma kn)}}{k}$. The value of k is always negative while the value of l and m are always positive so that the real part of this eigenvalue λ_4 is always positive. It means that the disease-free equilibrium will not be stable when $(kl + km)^2 - (4k^2lm - 4\gamma kn) < 0$. This condition will be satisfied when the of value $R_0 > 1$.

e. $\lambda_5 = -\frac{1}{2} . \frac{kl+km+\sqrt{(kl+km)^2-4k^2lm+4\gamma kn}}{k}$. The value of k is always negative while the value of l and m are always positive so that the real part of this eigenvalue λ_4 is always positive. It means that the disease-free equilibrium will not be stable when $(kl + km)^2 - (4k^2lm - 4\gamma kn) < 0$. This condition will be satisfied when the of value $R_0 > 1$.

Regard to the eigenvalues (a) - (e), it can be concluded that the disease-free equilibrium of the equations (1) – (5) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

c. Sensitivity Analysis

Sensitivity analysis on the predetermined threshold value, R_0, needs to be done to find out which parameter has the most influence on the spread of the disease. This analysis is not only for experimental design but also for data assimilation and simplification of complex models [13]. This analysis is used to determine the robustness of the model's predictions to parameter values so that the parameter which has the highest effect on the threshold value can be determined. The following is the definition for determining the sensitivity of a parameter value [14].

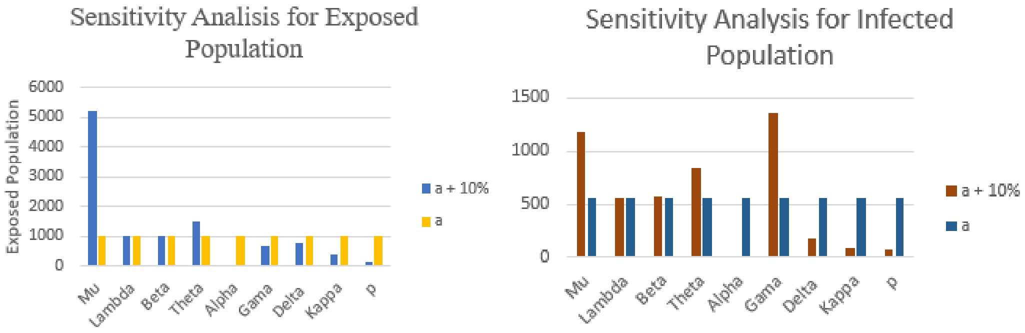
$$e_a = \left(\frac{a}{\lambda}\right) \cdot \left(\frac{d\lambda}{da}\right)$$

with

$a =$ parameter tested

$\lambda =$ the change of variable value based on the selection parameter

In this study, the sensitivity analysis of parameter values use the $a \pm 10\%$ rule which is the result can be seen in the change of exposed and infected populations. The elasticity of parameters can be seen in Figure 2.



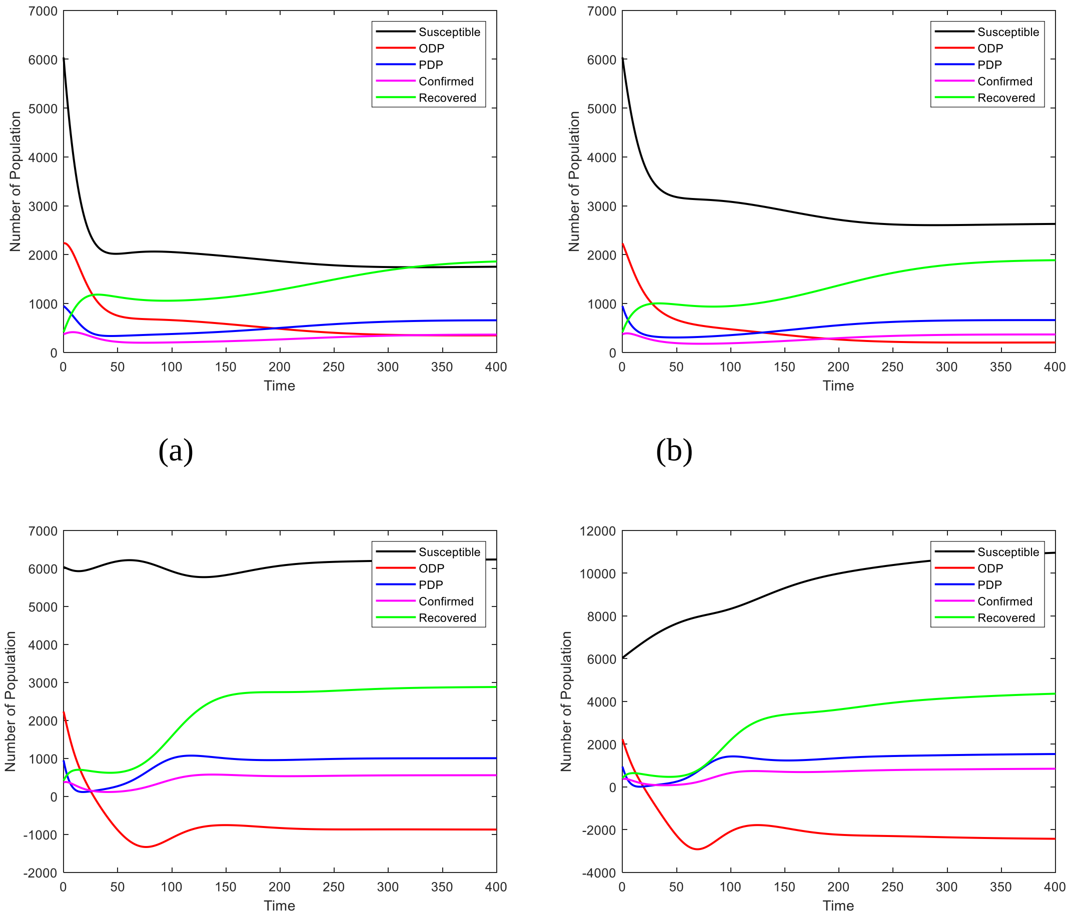
(a) (b)

Figure 2. Sensitivity analysis for exposed population (a) and infected population (b)

Regard to the results of the sensitivity analysis, there are two parameter values that are interesting to explore, such as μ and p parameters. Furthermore, by using numerical simulation, the behaviour of the developed model will be seen using several values μ and p. The stability of the endemic equilibrium is also explored with respect to the threshold value of R_0.

d. Numerical Simulation

Numerical simulation is used to see the behavior of the model that has been developed with the initial conditions $(S_0(0) = 6037, S_1(0) = 2232, E(0) = 948, I(0) = 368, R(0) = 415)$. The parameters used in this simulation produce a value of $R_0 > 1$, which means that the endemic equilibrium point is stable. The results of numerical simulations on the effect of large-scale social restrictions on the developed model can be seen in Figure 3.



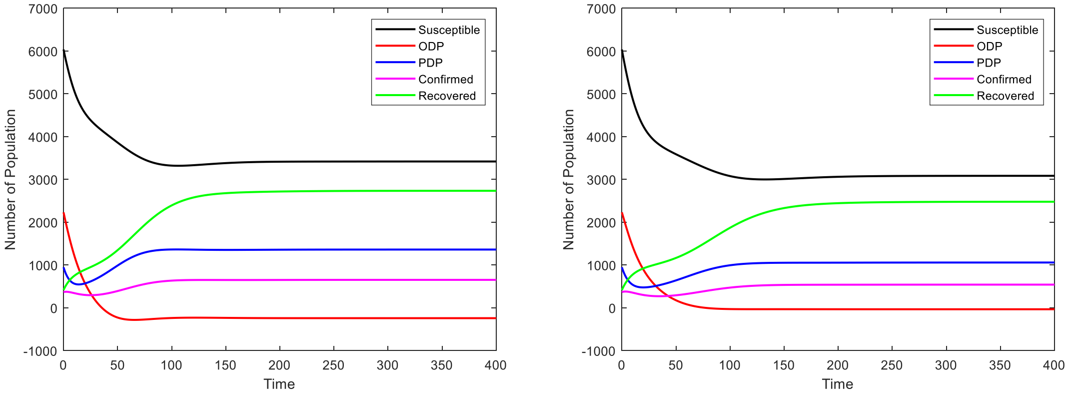
(a) (b)

(c) (d)

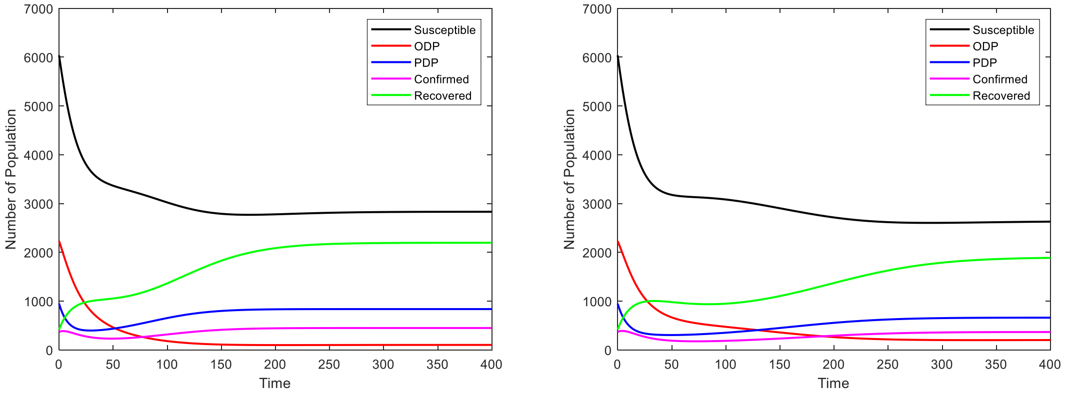
Figure 4. The effect of large-scale social restriction when (a) the value of $p = 0$, (b) the value of $p = 0.25$, (c) the value of $p = 0.835$, and (d) the value of $p = 0.95$

Based on the numerical simulation results in Figure 3, it can be stated that the decline in the number of people under monitoring (ODP) occurs very quickly, namely in the time range $t = 0 - 50$ days. These results indicate that the implementation of large-scale social restrictions can be said to be successful if the effectiveness of the implementation ranges from 80% to 100%. It means that the government can strictly control everyone to remain at home during times of large-scale social distancing. However, from the numerical simulation results, it can also be said that the success of this policy will only reduce the number of people under monitoring (ODP), while from the number of patients under surveillance (PDP) and patients with positive confirmation (Confirmed), there is no significant change. With a high infection rate, Covid-19 will remain in the population for a long time. If we look at the numerical simulation results, for a relatively long time ($t \to \infty$) the exposed and infected population will remain.

Furthermore, the results of numerical simulations on the effect of natural mortality on the developed model by taking the value of $p = 0.5$ can be seen in Figure 4. Based on the numerical simulation results in Figure 4, the population of people under monitoring (ODP) decreases in the range of time $t = 50 - 100$ days. It was also followed by a transient decrease in the number of patients under surveillance (PDP) at $t = 0 - 25$ days and patients who were confirmed positive for Covid-19 (Confirmed) at $t = 0 - 25$ days. The number of patient under surveillance (PDP) has indeed increased, but it is for a long time period ($t \to \infty$). The decreasing of population has been influenced by the change of natural death rate. This is more clearly shown in Figure 4. (a), (b), (c), and (d), the number of patient under surveillance populations has decreased according to the change of the natural death rate, 1361, 1058, 836, and 660 respectively. Likewise, the number of positive Covid-19 confirmed patients who experienced a decrease in the number also correspond to the change of the natural death rate. This natural reduction in mortality can occur if the human immune system is enhanced [15]. It means that a good immune system in a population can reduce the spread of Covid-19, although for a long time period ($t \to \infty$), the disease will remain in a population.



(a) (b)



(c) (d)

Figure 4. The effect of natural death rate when (a) the value of $\mu = 0.025$, (b) the value of $\mu = 0.02$, (c) the value of $\mu = 0.016$, and (d) the value of $\mu = 0.014$

4. CONCLUSION

In this study, a mathematical model of the spread of the Covid-19 has been produced that takes into account large-scale social restriction policies and the labelling of people under monitoring (ODP), patients under surveillance (PDP) and patient confirmation (Confirmed patients). In addition, this research has also produced a disease-free equilibrium point obtained analytically, the threshold requirement, namely R_0, the critical point stability requirements through the threshold value, sensitivity analysis to determine the most influential parameters in the model, and numerical simulation in around the endemic equilibrium point.

From the results of this study, it can be concluded that large-scale social restriction policies will be successful if the effectiveness of their implementation ranges from 80% -100%. This policy will reduce the number of people under monitoring. In addition, this study can also conclude that the change of the death rate in a population will also reduce the spread of the Covid-19. This changing in mortality can be done by increasing the immune system in a population.

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CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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