DYNAMIC ANALYSIS OF THE COVID-19 MODEL WITH ISOLATION FACTORS

Atika Ratna Dewi[1*]**, Ridho Ananda**[2]**, Utti Marina Rifanti**[3]

[1] Data Science Study Program, Faculty of Informatics, Institut Teknologi Telkom Purwokerto
[2] Industrial Engineering Study Program, Faculty of Industrial Engineering and Design,
Institut Teknologi Telkom Purwokerto
[3] Telecommunication Engineering Study Program, Faculty of Telecommunication and Electrical Engineering,
Institut Teknologi Telkom Purwokerto
Jl. DI Panjaitan No. 128, Purwokerto, 53147, Indonesia

Corresponding author e-mail: ¹* atika@ittelkom-pwt.ac.id

Abstract. *Covid-19 is a type of infectious disease caused by SARS Cov-2. This virus has spread throughout the world to cause a pandemic. This study aimed to model and analyze the spread of Covid-19 with the isolation factor. The spread of Covid-19 can be made into an epidemic model by taking into account the population of susceptible humans (S), infected humans (I), isolated humans (L), and recovered humans (R). The method used in this research was to derive a non-linear system of differential equations model, complete the model qualitatively, find the primary reproduction ratio (R_0), see the model's behavior by analyzing the dynamics of the equilibrium point and make model simulations. This model has a disease-free equilibrium point that is asymptotically stable, while at the equilibrium point, the endemic is unstable. The results of the model simulation and analysis of the R_0 value indicate that the chance of successful Covid-19 spread and the isolation factor is a significant controlled parameter in reducing the R_0 value.*

Keywords: *covid-19, sir model, isolation, equilibrium point, basic reproduction ratio number*

https://ojs3.unpatti.ac.id/index.php/barekeng/   barekeng.math@yahoo.com

1. INTRODUCTION

The virus with the original name Novel Coronavirus (2019-nCov) is a new virus that causes human respiratory disease. Covid-19 is still in the same family as the viruses that cause SARS and MERS [1]. Starting from the Chinese city of Wuhan in early 2020, Covid-19 has become epidemic in Indonesia. On NBC News (2020), WHO has declared the disease spread caused by this coronavirus as a pandemic as of March 12, 2020 [2]. A pandemic is defined as an epidemic that occurs worldwide or over a vast area, crosses international boundaries, and usually affects many people [3]. This disease can spread through droplets of saliva from the nose or mouth of someone infected with Covid-19 when coughing or sneezing [4]. The number of confirmed cases of Covid-19 is still increasing day by day [5]. It shows the seriousness of handling positive cases of Covid-19 so that the pandemic ends soon. In addition to direct handling, all parties must also carry out prevention efforts. Consideration of a good strategy is very much needed in efforts to handle and prevent the Covid-19 pandemic.

Mathematical models for epidemics can be used to consider strategies to control the spread of disease. Mathematical models can also help predict future epidemic control to avoid a pandemic. Kermack and Mc Kendrick, in 1927, first introduced the epidemic model. The model is known as the SIR model, which divides the population into three classes, namely Susceptible (individuals susceptible to infection), Infected (infected individuals), and Recovered (individuals who have recovered) [6].

Many types of research on disease epidemic models have been developed. One of which is Wahyudi and Irma's research [7] using the SIR model to predict the condition of Covid-19 transmission in Indonesia. The SIR model was developed into various epidemic models by adding new sub-populations. Fanelli et al. [8] developed a SIR model used to predict the spread of Covid-19 in China, Italy, and France using the SIRD (Susceptible, Infected, Recovered, and Death) model. Putra and Abidin's research [9] also developed a SIR model with an Exposed (E) population to predict the number of Covid-19 cases as an effect of the lockdown in ASEAN countries. Studies on Covid-19 using various methods from several countries have also been widely studied, such as in Yousaf et al. [10] predicting Covid-19 cases in Pakistan using the ARIMA method. Another method used to predict Covid-19 cases is the RNN time series method. Shastri et al. [11] compared the number of positive cases in India and the USA.

Various kinds of disease control strategies are carried out to minimize individuals affected by the disease and prevention efforts. One of them is the study of Balya et al. [12], which examines the impact of socialization and rapid tests on the Covid-19 spread model. The study of Utti et al. [13] developed an SEIR model to predict the number of confirmed positive cases in the presence of limited treatment. Another strategy in disease control is quarantine, as in the study of Mishra et al. [14] studying the SIR model by adding a population of quarantined individuals. Quarantined individuals are divided into 2, namely individuals who are quarantined at home and individuals who are quarantined in hospital.

Based on this explanation, this study examines the model of the spread of SIR (Susceptible, Infected, Recovered) disease by adding an isolated population. The addition of this isolation population is adjusted to the conditions of handling Covid-19, where individuals infected with Covid-19 are required to isolate themselves. The developed model consists of 4 populations, namely susceptible humans (S), infected humans (I), isolated humans (L), and humans who have recovered (R). The epidemic model for Covid-19 obtained will be completed qualitatively. The primary reproduction ratio number can determine the factors that influence the epidemic. Furthermore, the behaviour of the Covid-19 distribution model is determined based on the stability of the disease-free equilibrium point and the endemic equilibrium point.

2. RESEARCH METHOD

The method used in this research was as follows:
1. Reducing the spread of Covid-19 by isolation.
2. Completing the model qualitatively.
3. Finding the primary reproduction ratio (R_0)
4. Analyzing the results of R_0 is used to determine the factors that influence the epidemic.
5. Seeing the model's behavior by analyzing the dynamics of the equilibrium point.
6. Modeling simulation

3. RESULT AND DISCUSSION

The Covid-19 spread model with isolation was derived using a non-linear system of differential equations. Based on the spread of the Covid-19 model with the isolation, the equilibrium point analysis was carried out to determine the dynamic behavior of the model. Furthermore, the formula for the primary reproduction ratio (R_0) is reduced to determine the factors that influence a population to have a disease epidemic or not.

3.1. Covid-19 spread model with isolation

The isolation of the Covid-19 spread model was obtained by developing the initial SIR model, namely by adding an isolated human group (L). Several assumptions were used to facilitate the formation and discussion of the model, namely:

1. The human population is closed. It means that the increase or decrease in the number of people only occurs by birth or death, while the movement of people through immigration and emigration is ignored.
2. The human birth rate is fixed.
3. The human mortality rate is divided into natural deaths and due to Covid-19.
4. Every human being is born healthy.
5. Humans who are isolated do not spread disease.
6. Humans who have recovered cannot be reinfected.
7. Clean environmental factors, temperature, humidity, and seasonal variance are neglected.

Based on these assumptions, the Covid-19 spread model was obtained with isolation in the form of a first-order non-linear differential equation system, which is as follows :

$$
\begin{aligned}
\frac{dS}{dt} &= \delta - \frac{\alpha SI}{N} - \mu S \\
\frac{dI}{dt} &= \frac{\alpha SI}{N} - (\beta + \theta + \mu + \sigma)I \\
\frac{dL}{dt} &= \theta I - (\phi + \mu + \sigma)L \\
\frac{dR}{dt} &= \beta I + \phi L - \mu R
\end{aligned}
\tag{1}
$$

Where :

S	=	The number of susceptible humans in the population
I	=	The number of infected humans in the population
R	=	The number of healed humans in the population
L	=	The number of isolated humans in the population
δ	=	The rate of increase in susceptible humans
α	=	Chances of successful spread of Covid-19, susceptible humans become infected humans
μ	=	Human natural death rate
β	=	Infected human cure rate
σ	=	Death rate due to Covid-19
θ	=	Infected human isolation rate
ϕ	=	Human cure rate after isolation
N	=	Total human population

3.2 The Equilibrium Point of the Covid-19 Spread Model with Isolation

Based on system (1) if I = L = R = 0 then the disease-free equilibrium point is obtained as follows:

$$
W_0 = (\dot{S}, 0,0,0) = (\frac{\delta}{\mu}, 0,0,0)
\tag{2}
$$

Next, to determine the endemic equilibrium point, it is assumed that *I≠0, L≠0, R≠0*. Based on system (1), it is obtained that the endemic equilibrium point is

$$W_1 = (S^*, I^*, L^*, R^*) \tag{3}$$

by using Maple software, the values S^*, I^*, L^*, R^* is obtained, namely:

$$S^* = \frac{N(\beta + \theta + \mu + \sigma)}{\alpha}$$

$$I^* = \frac{-\delta\alpha + \beta\mu N + \mu\theta N + \mu^2 N + \mu\sigma N}{(\beta + \theta + \mu + \sigma)\alpha}$$

$$L^* = \frac{-(\theta(-\delta\alpha + \beta\mu N + \mu\theta N + \mu^2 N + \mu\sigma N))}{(\alpha(\beta\phi + \phi\theta + \phi\mu + \phi\sigma + \beta\mu + \mu\theta + \mu^2 + 2\mu\sigma + \beta\sigma + \sigma\theta + \sigma^2))}$$

$$R^* = \frac{-((-\delta\alpha + \beta\mu N + \mu\theta N + \mu^2 N + \mu\sigma N)(\beta\phi + \beta\mu + \beta\sigma + \phi\theta))}{(\alpha(\beta\phi + \phi\theta + \phi\mu + \phi\sigma + \beta\mu + \mu\theta + \mu^2 + 2\mu\sigma + \beta\sigma + \sigma\theta + \sigma^2)\mu)}$$

3.3 Basic Reproductive Ratio Figures (R_0)

By using the next-generation operator approach, the basic reproduction ratio for this case is

$$R_0 = \frac{\alpha}{\beta + \theta + \mu + \sigma} \tag{4}$$

If α value of is getting bigger and the value (β+θ+μ+σ) is getting smaller, then the value of R_0 will be bigger than one (R_0>1). It means that a disease epidemic has a greater possibility to occur. Conversely, if α value is getting smaller and the value of (β+θ+μ+σ) is getting bigger, then the value of R_0 will be less than one (R_0<1). It means that a disease epidemic has a smaller possibility to occur or no epidemic will occur.

3.4 Equilibrium Point Stability Analysis

Theorem 1 [15]

If the matrix A in the system $\dot{x} = A\mathbf{x}$ is a coefficient matrix with eigenvalues $\lambda_1, \lambda_2, \cdots, \lambda_n$, and $Re(\lambda_k)$ is the real part of the eigenvalues λ_k, then the stability of the equilibrium point $\mathbf{x}^* = \mathbf{0}$ of system solutions $\dot{x} = A\mathbf{x}$ is

     a. Stable, if $Re(\lambda_k) \leq 0, \forall k = 1, 2, \cdots, n$.
     b. Asymptotically stable, if $Re(\lambda_k) < 0, \forall k = 1, 2, \cdots, n$
     c. Unstable, if $Re(\lambda_k) > 0, for\ particular\ k$.

3.4.1 Behavioral Analysis of Models around the Disease-Free Equilibrium Point

The disease-free equilibrium point of the system of equations (1) is as in equation (2) so that the obtained Jacobian matrix around the disease-free equilibrium point is

$$J = \frac{\partial F}{\partial x}\left(\frac{\delta}{\mu}, 0, 0, 0\right) = \begin{pmatrix} -\mu & -\alpha\frac{\delta}{\mu} & 0 & 0 \\ 0 & \alpha\frac{\delta}{\mu} - (\beta + \theta + \mu + \sigma) & 0 & 0 \\ 0 & \theta & -(\phi + \mu + \sigma) & 0 \\ 0 & \beta & \phi & -\mu \end{pmatrix} \tag{5}$$

The eigenvalue of equation (5) is

$$\lambda_1 = -\mu, \ \lambda_2 = -\left(\frac{-\alpha\delta + \beta\mu + \theta\mu + \mu^2 + \sigma\mu}{\mu}\right),$$
$$\lambda_3 = -(\phi + \mu + \sigma), \lambda_4 = -\mu.$$

Based on the results obtained, it can be seen that the real part of the eigenvalues $\lambda_1, \lambda_2, \lambda_3, \lambda_4$ is negative. Then, according to Theorem 1, the equilibrium point $W_0 = (\dot{S}, 0, 0, 0) = (\frac{\delta}{\mu}, 0, 0, 0)$ is asymptotically stable.

3.4.2 Analysis of Model Behavior around Endemic Equilibrium Points

The endemic equilibrium point of the system of equations (1) is as in equation (3). The obtained Jacobian matrix around the endemic equilibrium point is

$$J = \frac{\partial F}{\partial x}(S^*, I^*, L^*, R^*) = \begin{pmatrix} \frac{\alpha\delta + \beta\mu N + \mu\theta N + \mu^2 N + \mu\sigma N}{(\beta + \theta + \mu + \sigma)N} - \mu & -\beta - \theta - \mu - \sigma & 0 & 0 \\ -\frac{\alpha\delta + \beta\mu N + \mu\theta N + \mu^2 N + \mu\sigma N}{(\beta + \theta + \mu + \sigma)N} & 0 & 0 & 0 \\ 0 & \theta & -(\phi + \mu + \sigma) & 0 \\ 0 & \beta & \phi & -\mu \end{pmatrix} \quad (6)$$

By using Maple software, the eigenvalue of equation (6) is

$$\lambda_1 = \frac{1}{2}\frac{1}{A}(\sqrt{B}),$$
$$\lambda_2 = -\frac{1}{2}\frac{1}{A}(\sqrt{C}),$$
$$\lambda_3 = -(\phi + \mu + \sigma),$$
$$\lambda_4 = -\mu$$

Where:
$A = (\beta + \theta + \mu + \sigma)N$

$B = \delta\alpha + (24\beta N^2\mu\theta\sigma + 8\beta N\delta\alpha\mu + 8\beta N\delta\alpha\sigma + 8\beta N\delta\theta\alpha + 8\theta N\delta\alpha\mu + 8\theta N\delta\alpha\sigma + 8N\mu\delta\alpha\sigma$
$\quad + 24\beta N^2\mu^2\sigma + 24\beta N^2\mu^2\theta + 12\beta^2 N^2\mu\theta + 12\beta^2 N^2\mu\sigma + 12\beta N^2\mu\sigma^2 + 12\beta N^2\mu\theta^2$
$\quad + 4\beta^2 N\delta\alpha + 24\theta N^2\mu^2\sigma + 12\theta^2 N^2\mu\sigma + 12\theta N^2\mu\sigma^2 + 4\theta^2 N\delta\alpha + 4N\mu^2\delta\alpha + 4N\sigma^2\delta\alpha$
$\quad + 12\beta N^2\mu^3 + 12\beta^2 N^2\mu^2 + 4\beta^3 N^2\mu + 12\theta^2 N^2\mu^2 + 4\theta^3 N^2\mu + 12N^2\mu^3\sigma + 12N^2\mu^2\sigma^2$
$\quad + 4N^2\sigma^3\mu + 4N^2\mu^4 + \delta^2\alpha^2 + 12\mu^3\theta N^2)^{1/2}$

$C = -\delta\alpha + (24\beta N^2\mu\theta\sigma + 8\beta N\delta\alpha\mu + 8\beta N\delta\alpha\sigma + 8\beta N\delta\theta\alpha + 8\theta N\delta\alpha\mu + 8\theta N\delta\alpha\sigma + 8N\mu\delta\alpha\sigma$
$\quad + 24\beta N^2\mu^2\sigma + 24\beta N^2\mu^2\theta + 12\beta^2 N^2\mu\theta + 12\beta^2 N^2\mu\sigma + 12\beta N^2\mu\sigma^2 + 12\beta N^2\mu\theta^2$
$\quad + 4\beta^2 N\delta\alpha + 24\theta N^2\mu^2\sigma + 12\theta^2 N^2\mu\sigma + 12\theta N^2\mu\sigma^2 + 4\theta^2 N\delta\alpha + 4N\mu^2\delta\alpha + 4N\sigma^2\delta\alpha$
$\quad + 12\beta N^2\mu^3 + 12\beta^2 N^2\mu^2 + 4\beta^3 N^2\mu + 12\theta^2 N^2\mu^2 + 4\theta^3 N^2\mu + 12N^2\mu^3\sigma + 12N^2\mu^2\sigma^2$
$\quad + 4N^2\sigma^3\mu + 4N^2\mu^4 + \delta^2\alpha^2 + 12\mu^3\theta N^2)^{1/2}$

Based on the results obtained, it can be seen that the real part of the eigenvalues $\lambda_2, \lambda_3, \lambda_4$ is negative while the real part of the eigenvalue λ_1 is positive. Then, according to Theorem 1, the equilibrium point $W_1 = (S^*, I^*, L^*, R^*)$ is not stable.

3.5 Simulation of the Stability of the Endemic Equilibrium Point of the Covid-19 Spread Model with Isolation

The parameter values given to make a simulation of the endemic equilibrium point of the Covid-19 spread model with isolation are presented in Table 1 as follows:

Table 1. Endemic Equilibrium Point Simulation Parameter Value

Parameter	Scores
(S(0), I(0), L(0), R(0))	(29639, 1446, 1257, 645)
N	S+I+L+R
δ	1000
α	0.8
μ	0.01
β	0.2
θ	0.3
σ	0.01
ϕ	0.6
R_0	1.54

By using the assistance of the MATLAB GUI, a simulation of the endemic equilibrium point of the Covid-19 spread model with isolation can be obtained, which is presented in Figure 1 below:
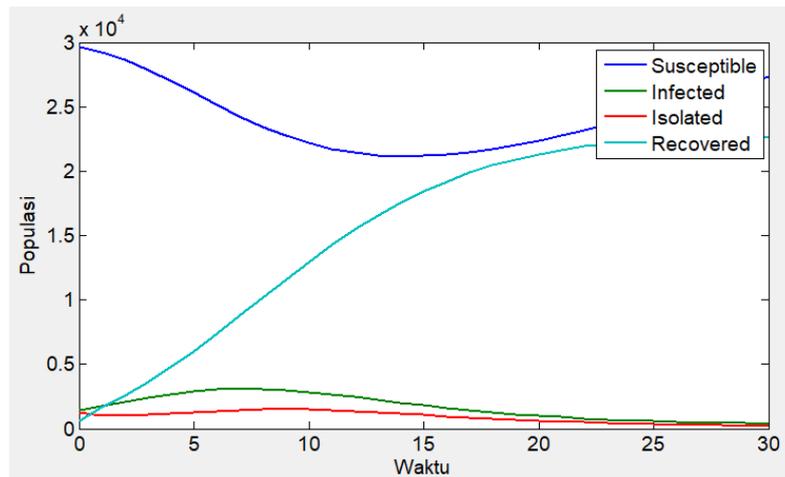
Figure 1. Graph of S(t), I(t), L(t), R(t) against Time for Endemic Equilibrium Point

Based on Figure 1, it can be seen that the number of susceptible humans has decreased from time to time. Furthermore, after the 15th time, it will increase again. The number of infected humans has increased until the 10th time, then it decreased. In proportion to the number of isolated humans, it increased until the 10th time and decreased to 0. Meanwhile, the number of recovered humans continued to increase. The following will present a graph with a different parameter value of (Probability of successfully spreading Covid-19, susceptible humans become infected humans), namely:
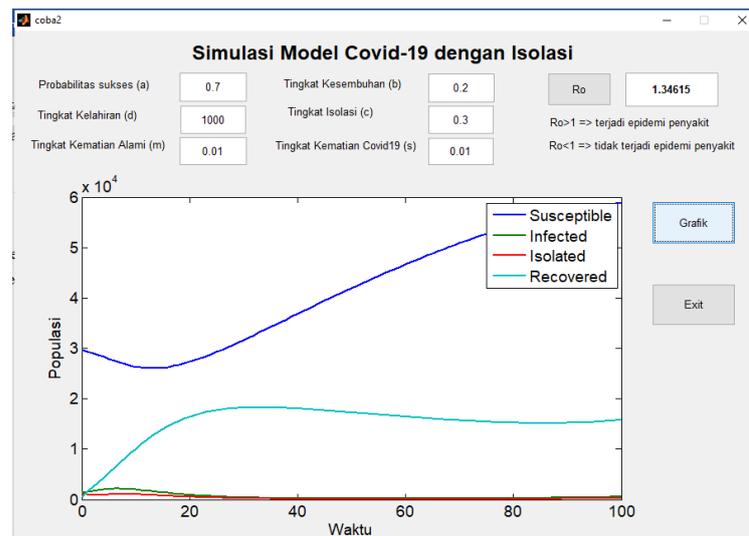

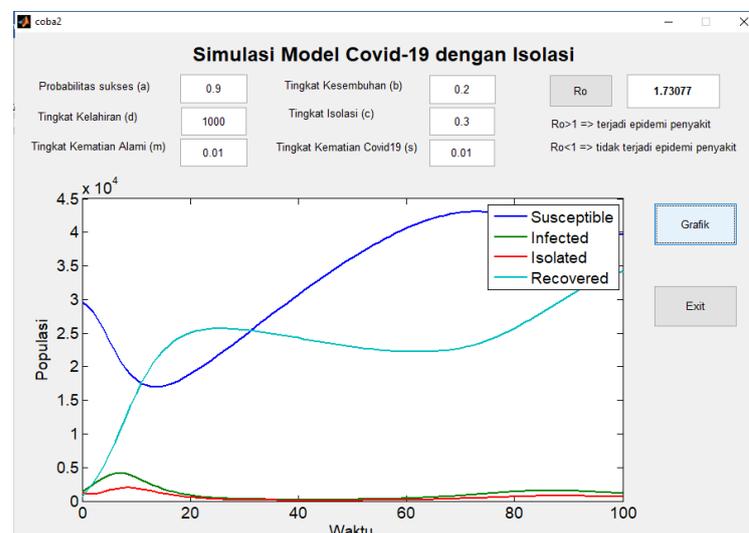**Figure 2.** Graph of S(t), I(t), L(t), R(t) against Time for Endemic Equilibrium Point with α=0.7

Figure 3. Graph of S(t), I(t), L(t), R(t) against Time for Endemic Equilibrium Point with α=0.9

Based on Figure 1-3, it can be seen that the greater the value of α parameter or the chance of successful spread of Covid-19 of susceptible humans become infected humans (if the other parameter values remain), the greater value of R_0 will be. As a result, the number of susceptible humans is decreasing rapidly. It means that the parameter's value is very influential on the population. Thus, there is a need for prevention efforts. The chances of successful spread of Covid-19 are getting smaller, namely by implementing the 5M health protocol (Wearing masks, washing hands with soap, keeping a distance, staying away from crowds, and Reducing Mobility).

Several simulations of the Covid-19 model are presented to determine the isolation effect on the system, as shown in Figures 4, 5, and 6 below:
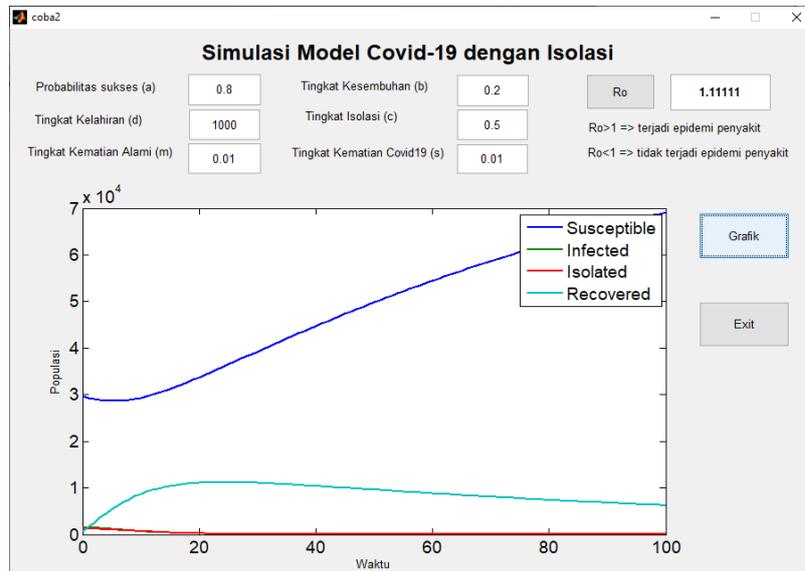

Figure 4. Graph of S(t), I(t), L(t), R(t) against Time for Endemic Equilibrium Point with σ=0.5

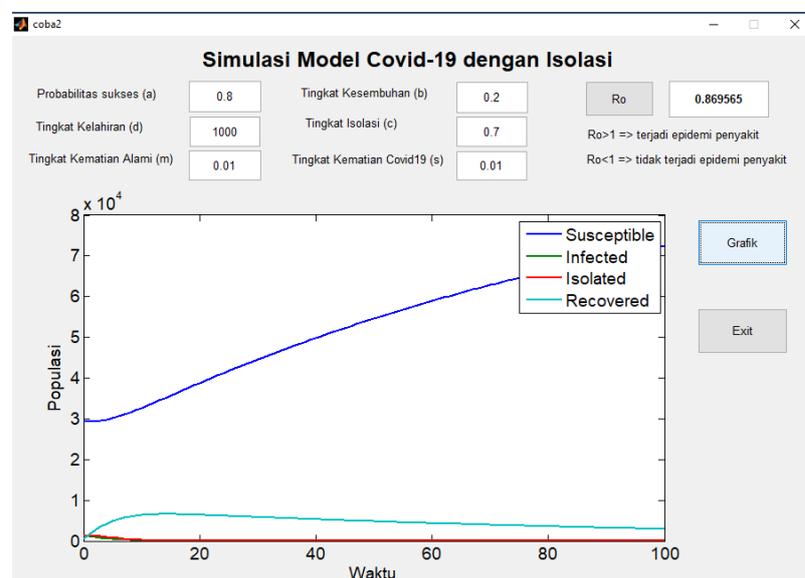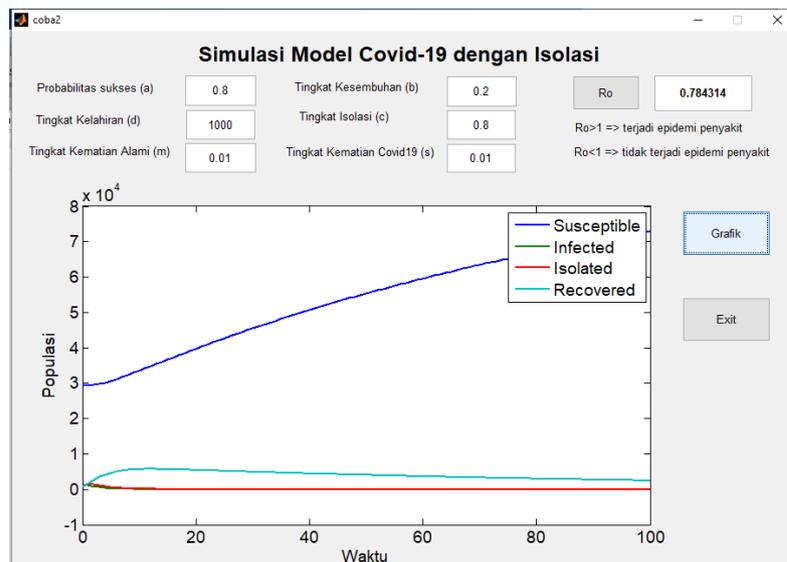**Figure 5.** Graph of S(t), I(t), L(t), R(t) against Time for Endemic Equilibrium Point with σ=0.7

Figure 6. Graph of S(t), I(t), L(t), R(t) against Time for Endemic Equilibrium Point with σ=0.8

Based on Figure 4-6, it can be seen that the greater parameter value θ or the isolation level of infected humans (if the other parameter values remain), the value of R_0 will be smaller. As a result, the number of susceptible humans grows continually, while the value of infected human's declines continually. It means that the parameter value θ is very influential on the population. Thus, there is a need for strict isolation efforts for people who are confirmed positive for Covid-19. The form of isolation for people who are confirmed positive for Covid-19 can be in the form of isolation in hospitals, independent isolation in their respective homes, or isolation in places that have been provided by the government while still complying with existing health protocols.

4. CONCLUSIONS

Based on the results of research on the Covid-19 spread model with isolation, it can be concluded that:
1. The spread of Covid-19 by isolation can be made into a model in the form of a system of non-linear differential equations.
2. The model of the spread of Covid-19 with Isolation has a disease-free equilibrium point $W_0 = (\frac{\delta}{\mu}, 0,0,0)$ which is asymptotically stable and the endemic equilibrium point $W_1 = (S^*, I^*, L^*, R^*)$ is unstable.
3. The basic reproduction ratio formula for the Covid-19 spread model with isolation is

$$R_0 = \frac{\alpha}{\beta + \theta + \mu + \sigma}$$

The factors that affect the spread of Covid-19 per unit time are
- Chances of successful spread of Covid-19, susceptible humans to become infected humans (α),
- Natural human mortality rate (μ),
- The cure rate of infected humans (β),
- The isolation rate of infected humans (θ),
- Death rate due to Covid-19 (σ).
4. The results of the model simulation and analysis of R_0 by taking several different parameter values indicate that the probability of a successful spread of Covid-19 (α) is the most significant controlled parameter to reduce R_0. Thus, there is a need for prevention efforts. The chances of successful spread of Covid-19 are getting smaller, namely by implementing the 5M health protocol (Wearing masks, washing hands with soap, keeping a distance, staying away from crowds, and Reducing Mobility). It is followed by the effectiveness of the isolation level of infected humans (θ). The form of isolation can be in the form of isolation in hospitals, self-isolation in their respective homes, or isolation in places that the government has provided to increase the chances of eradicating Covid-19 from the community

ACKNOWLEDGEMENT

REFERENCES

[1]   T. Hu, Y. Liu, M. Zhao, Q. Zhuang, L. Xu, and Q. He, "A comparison of COVID-19, SARS and MERS," *PeerJ*, vol. 8, pp. 1–30, 2020.

[2]   C. Siemaszko, "Coronavirus outbreak labeled a pandemic by World Health Organization," 2020. [Online]. Available: https://www.nbcnews.com/health/health-news/coronavirus-outbreak-labeledpandemic-world-health-organization-n1155741. [Accessed: 27-Mar-2020].

[3]   J. M. Last, "A dictionary of epidemiology," *Int. J. Epidemiol.*, vol. 15, no. 2, p. 277, 1986.

[4]   W. H. Organization, "QA for Public," 2020. [Online]. Available: https://www.who.int/indonesia/news/novel-coronavirus/qa-for-public. [Accessed: 05-Sep-2020].

[5]   W. H. Organization, "WHO Coronavirus Disease (Covid-19) Dashboard," 2020. [Online]. Available: https://covid19.who.int/table. [Accessed: 10-Sep-2020].

[6]   W. O. M. Kermack, "A contribution to the mathematical theory of epidemics," in *Proceedings of the Royal Society A, Mathematical, Physical and Engineering Sciences*, 1927, pp. 700–721.

[7]   B. A. Wahyudi and I. Palupi, "Prediction of the peak Covid-19 pandemic in Indonesia using SIR model," *J. Teknol. dan Sist. Komput.*, vol. 9, no. 1, pp. 49–55, 2021.

[8]   D. Fanelli and F. Piazza, "Analysis and forecast of COVID-19 spreading in China, Italy and France," *Chaos, Solitons and Fractals*, vol. 134, p. 109761, 2020.

[9]   A. P. Putra and S. A. Z. Abidin, "Aplication of SEIR Model in Covid-19 and the Effect of Lockdown on Reducing The Number of Active Cases," vol. 5, no. 2, pp. 185–192, 2020.

[10]   M. Yousaf, S. Zahir, M. Riaz, S. M. Hussain, and K. Shah, "Statistical analysis of forecasting COVID-19 for upcoming month in Pakistan," *Chaos, Solitons and Fractals*, vol. 138, 2020.

[11]   S. Shastri, K. Singh, S. Kumar, P. Kour, and V. Mansotra, "Time series forecasting of Covid-19 using deep learning models: India-USA comparative case study," *Chaos, Solitons and Fractals*, vol. 140, p. 110227, 2020.

[12]   M. A. Balya *et al.*, "Investigating the Impact of Social Awareness and Rapid Test on A COVID-19 Transmission Model," vol. 4, no. 1, pp. 46–64, 2021.

[13]   U. M. Rifanti, A. R. Dewi, N. Nurlaili, and S. T. Hapsari, "Model Matematika COVID-19 dengan Sumber Daya Pengobatan yang Terbatas," *Limits J. Math. Its Appl.*, vol. 18, no. 1, p. 23, 2021.

[14]   B. K. Mishra *et al.*, "COVID-19 created chaos across the globe: Three novel quarantine epidemic models," *Chaos, Solitons and Fractals*, vol. 138, p. 109928, 2020.

[15]   W. . Boyce and R. . DiPrima, *Elementary Differential Equations with Boundary Value Problems*, 10th ed. New Jersey : Prentice-Hall, 2012.