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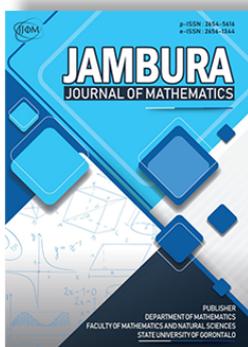
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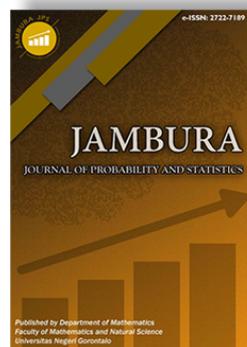
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Dynamic analysis of SEIR model for Covid-19 spread in Medan

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ABSTRACT. *In this study, a mathematical model was studied on the population of the spread of Covid-19 in Medan which the model use an epidemic mathematical model, SEIR (Susceptible, Exposed, Infected, and Recovered). Next, we determine the basic reproduction number R_0 using the next generation matrix and the equilibrium point which is analyzed using the Routh Hurwitz criteria. The disease-free equilibrium point is said to be locally asymptotically stable if $R_0 < 1$ and the endemic equilibrium point is said to be locally asymptotically stable if $R_0 > 1$. Numerical simulation of the model was carried out using real data on the number of Covid-19 cases in Medan and give insightful results to further explore the dynamics of the disease. Through the data obtained, the value of $R_0 > 1$ indicates that Covid-19 at the time of the study was still contagious to other individuals. Furthermore, based on the simulation formed from the SEIR model with the given initial and parameters, it was found that the greater the contact rate or the transmission rate, the more spread the disease would be and the smaller the cure rate, the more the disease would spread.*

1. Introduction

Covid-19 has high transmission rate and spread rapidly throughout the world. The World Health Organization (WHO) declared Covid-19 a global pandemic on March 8th, 2020 [1]. In Indonesia itself, the first case was recorded on March 2, 2020 and until now, the number of cases infected with Covid-19 continues to increase [2]. The spread of Covid-19 can be modeled using a mathematical model [3]. Mathematical model is a tool that can play a role in studying the spread of disease, which is commonly referred to as a mathematical model of epidemiology [4]. Mathematical modeling is useful for describing the state of a complex system into a simple one. Through the analysis of mathematical models also provide information about the behavior of the spread of Covid-19. One of the most important things in the analysis of mathematical models, especially in the study of disease spread systems, is in determining the function of the basic reproduction number (R_0) which is also called the threshold number. This threshold number will provide information on each parameter studied and its relationship with the spread of disease. The classic model of the spread of disease was formulated by Kermack in 1927, known as SIR (Susceptible, Infected and Recovered) model. In SIR model, the total population is divided into three subpopulations, namely Susceptible which states the number of healthy individuals but susceptible to infection, Infected which states the number of individuals who are infected and can transmit the disease, and Recovered which states the number of recovered individuals. Some diseases have a latent period (incubation period), which is the time between healthy individuals who become infected and can transmit the disease. This period resulted in the emergence of a new subpopulation,

namely Exposed. With these additions, the SIR model was developed and became the SEIR model. Thus, in this study, the spread of Covid-19 was studied using the SEIR model which refers to [5]. Here the population total size at time t is defined by $N(t)$, with $N(t) = S(t) + E(t) + I(t) + R(t)$ [6]. This system is portrayed by accompanying the nonlinear differential equations for the Medan current pandemic Covid-19. We assimilated real data of the number of deaths, the number of recovered cases, and the number of active cases. Numerical simulation of the model was carried out using real data on the number of Covid-19 cases in Medan and give insightful results to further explore the dynamics of the disease [7]. The goal is to compute the number of infected, recovered, and dead individuals on the basis of the number of contacts, probability of disease transmission, incubation period, recovery rate, and fatality rate. The epidemic disease model predicts a peak of infected and dead individuals per day as a function of time and assumes that births and natural deaths are balanced [8]. Recovered human individuals can enter into the susceptible class again at rate ρ and the population members solely decrease due to the disease as dictated by the fatality rate of the disease. This SEIR model does not consider vaccination and isolation factors as parameters in the model. Therefore, this research contains the determination of the equilibrium point, the basic reproduction number, stability analysis and simulation of the model.

2. Mathematical Model

2.1. Description of the Covid-19 Spread Model

The pattern of the spread of Covid-19 in this study was divided into four compartments: Suspectible, Exposed, Infected and Recovered which refers to [5]. The modeling among the four compartments is shown by the schematic diagram in Figure 1
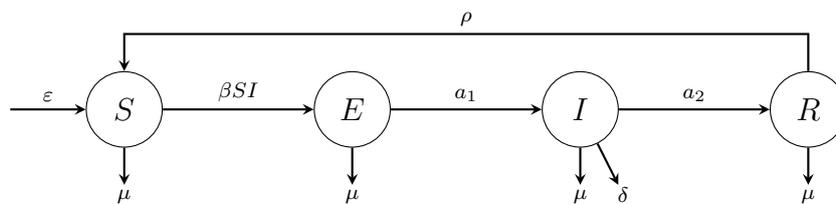
Figure 1. Covid-19 Disease Spread Scheme

which can be expressed in a nonlinear system of differential equations [9] as follows.

$$\frac{dS}{dt} = \mu N - (\alpha I + \mu + v)S,$$

$$\frac{dE}{dt} = \alpha IS - (\beta + \mu)E,$$

$$\frac{dI}{dt} = \beta E - (\gamma + \delta + \mu)I, \tag{1}$$

$$\frac{dR}{dt} = \delta I + vS - \mu R,$$

with initial conditions $S(0) = S_0$, $E(0) = E_0$, $I(0) = I_0$ and $R(0) = R_0$. Consider the following equation:

$$N(t) = S(t) + E(t) + I(t) + R(t).$$

Then, the derivative of $N(t)$ with respect to time is:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt}$$
$$= \epsilon - \mu N - \alpha_2 I - (\delta - \beta)I.$$

2.2. Basic Reproduction Number R_0

Next, we will discuss the basic reproduction number of the given system using the next generation matrix [8]. The reproduction number R_0 is defined as the expected value of the number of infections that occur every unit of time [10]. It can be seen that the system has a disease-free equilibrium point at $E_0 = \left(\frac{\epsilon}{\mu}, 0, 0, 0\right)$. Populations that can cause infection are Exposed and Infected populations. Then the system can be rewritten as vector F and vector V, namely [11]:

$$F = \begin{bmatrix} F_1 \\ F_2 \end{bmatrix} = \begin{bmatrix} \beta IS \\ 0 \end{bmatrix},$$

$$V = \begin{bmatrix} V_1 \\ V_2 \end{bmatrix} = \begin{bmatrix} (\alpha_1 + \mu)E \\ -\alpha_1 E + (\alpha_2 + \mu + \delta)I \end{bmatrix}.$$

The Jacobian matrices for F and V at disease-free equilibrium, E_0 are as follows:

$$F = \begin{bmatrix} 0 & \frac{\beta\epsilon}{\mu} \\ 0 & 0 \end{bmatrix}, V = \begin{bmatrix} (\alpha_1 + \mu) & 0 \\ -\alpha_1 & (\alpha_2 + \mu + \delta) \end{bmatrix}.$$

The reproduction number is obtained from the largest eigenvalue FV^{-1}, namely:

$$K = FV^{-1}$$
$$= \begin{bmatrix} 0 & \frac{\beta\epsilon}{\mu} \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{(\alpha_1 + \mu)} & 0 \\ \frac{\alpha_1}{(\alpha_1 + \mu)(\alpha_2 + \mu + \delta)} & \frac{1}{(\alpha_2 + \mu + \delta)} \end{bmatrix}.$$

The largest eigenvalue of the K matrix is $\frac{\alpha_1\beta\epsilon}{\mu(\alpha_1+\mu)(\alpha_2+\mu+\delta)}$ so obtained:

$$R_0 = \frac{\alpha_1\beta\epsilon}{\mu(\alpha_1 + \mu)(\alpha_2 + \mu + \delta)}.$$

The disease-free equilibrium point $E_0 = \left(\frac{\epsilon}{\mu}, 0, 0, 0\right)$ in the system is said to be asymptotically stable if $R_0 < 1$ and the endemic equilibrium point in the system is said to be asymptotically stable if $R_0 > 1$.

3. Stability Analysis of Model

3.1. Disease-Free Equilibrium Point

Equilibrium points for disease-free are conditions where there is no spread of COVID-19 then, $E = I = 0$ [12]. To obtain the type of stability, the disease-free equilibrium point will be substituted $E_0 = \left(\frac{\epsilon}{\mu}, 0, 0, 0\right)$ by taking into account the linearization of the system of differential equations of the epidemic model, using the Jacobian matrix, we get:

$$J(S, E, I, R) =$$
$$\begin{bmatrix} -\beta - \mu & 0 & -\beta S & \rho \\ \beta I & -(\alpha_1 + \mu) & \beta S & 0 \\ 0 & \alpha_1 & -(\delta_1 + \mu + \alpha_2) & 0 \\ 0 & 0 & \alpha_2 & -(\mu + \rho) \end{bmatrix}.$$

The Jacobian matrix for the disease-free equilibrium point is given by:

$$J(E_0) = \begin{bmatrix} -\mu & 0 & -\frac{\beta\epsilon}{\mu} & \rho \\ 0 & -(\alpha_1 + \mu) & \frac{\beta\epsilon}{\mu} & 0 \\ 0 & \alpha_1 & -(\delta_1 + \mu + \alpha_2) & 0 \\ 0 & 0 & \alpha_2 & -(\mu + \rho) \end{bmatrix}.$$

Let $\frac{\beta\epsilon}{\mu} = a$. To obtain the eigenvalues of the matrix above, the determinant will be used, so that:

$$|J(E_0) - \lambda I| =$$
$$\begin{bmatrix} -\mu - \lambda & 0 & -a & \rho \\ 0 & -(\alpha_1 + \mu) - \lambda & a & 0 \\ 0 & \alpha_1 & -(\delta_1 + \mu + \alpha_2) - \lambda & 0 \\ 0 & 0 & \alpha_2 & -(\mu + \rho) - \lambda \end{bmatrix},$$

obtained

$$(-\mu - \lambda)(-\mu - \rho - \lambda)$$
$$(\lambda^2 + (\delta + 2\mu + \alpha_1 + \alpha_2)\lambda$$
$$+ \mu^2 + (\delta + \alpha_1 + \alpha_2)\mu + \alpha_1(a + \delta + \alpha_2)) = 0.$$

It is clear that, $\lambda_1 = -\mu$, $\lambda_2 = -(\mu + \rho)$ are both negative. To determine the other eigenvalues consider the equation K, then:

$$K = \lambda^2 + (\delta + 2\mu + \alpha_1 + \alpha_2)\lambda + \mu^2 \quad (2)$$
$$+ (\delta + \alpha_1 + \alpha_2)\mu + \alpha_1(a + \delta + \alpha_2)$$
$$l_1 = 1,$$
$$l_2 = \delta + 2\mu + \alpha_1 + \alpha_2,$$
$$l_3 = \mu^2 + (\delta + \alpha_1 + \alpha_2)\mu + \alpha_1(a + \delta + \alpha_2).$$

Using the Routh-Hurwitz criteria, it can be seen that all values $l_1 > 0, l_2 > 0$ and $l_3 > 0$. Thus, eq. (2) has negative real roots so that E_0 is local asymptotically stable for $R_0 < 1$.

3.2. Endemic Equilibrium Point

To obtain the type of stability, we define $E^* = (S^*, E^*, I^*, R^*)$ as the endemic equilibrium point of the system, we get:

$$
\begin{aligned}
S^* &= \frac{(\alpha_1 + \mu)(\delta + \mu + \alpha_2)}{\beta\alpha_1}, \\
E^* &= \frac{(\delta + \mu + \alpha_2)[\alpha_1\beta\epsilon(\mu + \rho) - \mu(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2)]}{\alpha_1\beta[(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2) - \alpha_1\alpha_2\rho]}, \\
I^* &= \frac{\alpha_1\beta\epsilon(\mu + \rho) - \mu(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2)}{\beta[(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2) - \alpha_1\alpha_2\rho]}, \\
R^* &= \frac{\alpha_1\alpha_2\beta\epsilon - \mu\alpha_2(\alpha_1 + \mu)(\delta + \mu + \alpha_2)}{\beta[(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2) - \alpha_1\alpha_2\rho]}.
\end{aligned}
$$

From the linearization of the system of differential equations we get:

$$
J(S, E, I, R) =
\begin{bmatrix}
-\beta I - \mu & 0 & -\beta S & \rho \\
\beta I & -(\alpha_1 + \mu) & \beta S & 0 \\
0 & \alpha_1 & -(\delta_1 + \mu + \alpha_2) & 0 \\
0 & 0 & \alpha_2 & -(\mu + \rho)
\end{bmatrix}.
$$

Then the endemic equilibrium point is given by:

$$
J(S, E, I, R) =
\begin{bmatrix}
\xi_1 & 0 & \xi_{13} & \rho \\
\xi_{21} & -(\alpha_1 + \mu) & \xi_{23} & 0 \\
0 & \alpha_1 & -(\delta_1 + \mu + \alpha_2) & 0 \\
0 & 0 & \alpha_2 & -(\mu + \rho)
\end{bmatrix},
$$

where

$$\xi_{11} = -\left[\frac{\alpha_1\beta\epsilon(\mu + \rho) - \mu(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2)}{[(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2) - \alpha_1\alpha_2\rho]}\right]$$
$$- \mu,$$

$$\xi_{13} = -\left[\frac{(\alpha_1 + \mu)(\delta + \mu + \alpha_2)}{\alpha_1}\right],$$

$$\xi_{21} = \frac{\alpha_1\beta\epsilon(\mu + \rho) - \mu(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2)}{[(\mu + \rho)(\alpha_1 + \mu)(\delta + \mu + \alpha_2) - \alpha_1\alpha_2\rho]},$$

$$\xi_{23} = \frac{(\alpha_1 + \mu)(\delta + \mu + \alpha_2)}{\alpha_1}.$$

We will determine the local stability of the equilibrium point E^*.

$$
|J(E^*) - \lambda I| =
\begin{bmatrix}
-\beta I - \mu - \lambda & 0 & -\beta S & \rho \\
\beta I & -(\alpha_1 + \mu) - \lambda & -\beta S & 0 \\
0 & \alpha_1 & -(\delta_1 + \mu + \alpha_2) - \lambda & 0 \\
0 & 0 & \alpha_2 & -(\mu + \rho) - \lambda
\end{bmatrix}
$$

$$= 0.$$

The equilibrium point E^* of the system is said to be locally asymptotically stable if $R_0 > 1$. The determinants are obtained as follows:

$$l_1 = 1,$$
$$l_2 = \beta i + \delta + 4\mu + \rho + \alpha_1 + \alpha_2,$$
$$
\begin{aligned}
l_3 &= 6\mu^2 + (3\beta i + 3\delta + 3\rho + 3\alpha_1 + 3\alpha_2)\mu \\
&+ ((i + s)\beta + \rho + \delta + \alpha_2)\alpha_1 \\
&+ i(\delta + \rho + \alpha_2)\beta + \rho(\delta + \alpha_2),
\end{aligned}
$$
$$
\begin{aligned}
l_4 &= 4\mu^3 + (3\beta i + 3\delta + 3\rho + 3\alpha_1 + 3\alpha_2)\mu^2 \\
&+ (((2i + 2s)\beta + 2\rho + 2\delta + 2\alpha_2)\alpha_1 \\
&+ 2i(\delta + \rho + \alpha_2)\beta + 2\rho(\delta + \alpha_2))\mu \\
&+ (((i + s)\rho + i(\delta + \alpha_2))\beta + \rho(\delta + \alpha_2))\alpha_1 \\
&+ i\rho\beta(\delta + \alpha_2),
\end{aligned}
$$
$$
\begin{aligned}
l_5 &= \mu^4 + (\beta i + \delta + \rho + \alpha_1 + \alpha_2)\mu^3 \\
&+ (((i + s)\beta + \rho + \delta + \alpha_2)\alpha_1 + i(\delta + \rho + \alpha_2)\beta \\
&+ \rho(\delta + \alpha_2))\mu^2 + ((((i + s)\rho + i(\delta + \alpha_2))\beta \\
&+ \rho(\delta + \alpha_2))\alpha_1 + i\rho\beta(\delta + \alpha_2))\mu + i\rho\beta\alpha_1(\delta + 2\alpha_2).
\end{aligned}
$$

Using the Routh Hurwitz criteria, it can be seen that all values $l_1 > 0, l_2 > 0, l_3 > 0, l_4 > 0$ and $l_5 > 0$. Since all determinant values are greater than 0, they have negative real roots so that E_1 is locally asymptotically stable for $R_0 > 1$ [12].

4. Numerical Analysis of SEIR Model Of COVID-19 Spread

In this section, it will be observed how the distribution of each population using the parameters that will be shown in Table 1 for both $R_0 < 1$ and $R_0 > 1$. Based on the number of Covid-19 disease data in Medan City, the initial values were obtained for $s(t) = 0.936347, e(t) = 0.034512, i(t) = 0.000122$ and $r(t) = 0.029019$. The number of deaths caused by Covid-19 is 512 people in 1 year, so $\delta = \frac{512}{(299 \times 12)} = 0.0143$. Furthermore, the value of the natural death rate parameter has been determined, namely from the inverse of the life expectancy of Medan City, that is, according to the Medan City Health Office, the average life expectancy in Medan City is 72.54 years so that the natural death rate is obtained $\mu = \frac{1}{(72.54 \times 12)} = 0.00115$.

The next step is simulating the model using the best estimated parameters numerically to predict the new cases and cumulative cases for upcoming days [13].

4.1. Disease-Free Equilibrium Point Simulation

Simulation of the disease-free equilibrium point E_0 can be determined by providing an initial value and parameters that meet the conditions $R_0 < 1$. The parameter values are presented in Table 1. Simulations at the E_0 disease-free equilibrium point can be seen in Figure 2. From Figure 2 it can be seen that the Susceptible population has decreased until it reaches the equilibrium point. The Exposed population at the beginning of time has increased, but at a certain time it has decreased until it reaches the equilibrium point, namely $E = 0$, meaning that there is no longer an Exposed population in the spread of Covid-19. The Infected population at the beginning of time has increased, but at

Table 1. Parameter Values

Parameter	Parameter Name	$R_0 < 1$	$R_0 > 1$	Source
μ	Natural death rate	0.00115	0.00115	sumut.bps.go.id
ϵ	Birth rate	0.00115	0.00115	sumut.bps.go.id
δ	Death rate due to Covid-19	0.0143	0.0143	[1]
β	Rate of individuals becoming asymptomatically infected	0.00061	0.68	Assumed
α_1	The rate of individuals becoming infected with symptoms	0.0003	0.06	Assumed
α_2	The recovery rate of individuals infected with Covid-19	0.099	0.029	Assumed
ρ	The rate of individuals returning to being vulnerable	0.00017	0.00017	[5]
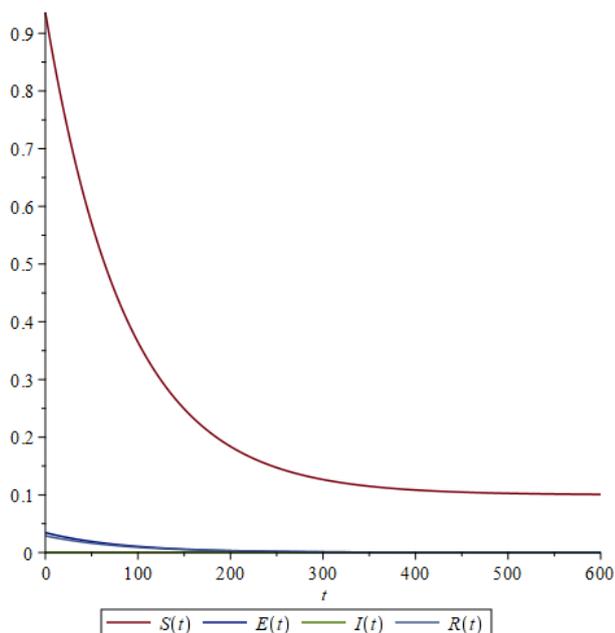
Figure 2. The dynamics of Covid-19 Spread when $R_0 < 1$
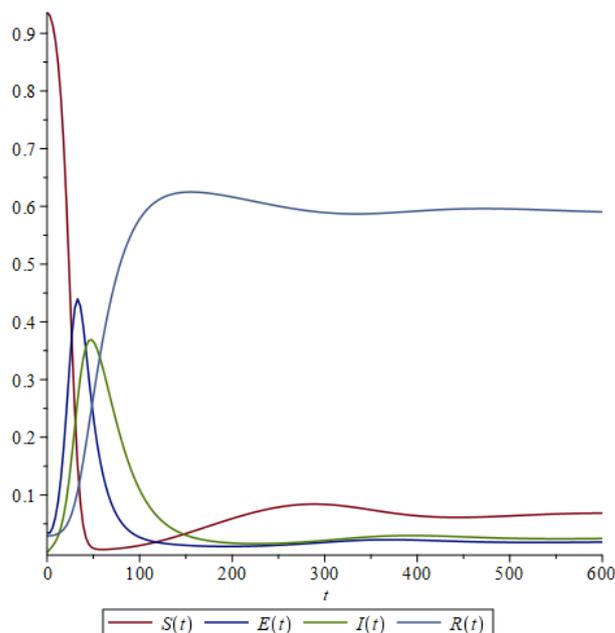
Figure 3. The dynamics of Covid-19 Spread when $R_0 > 1$

a certain time it has decreased until it reaches the equilibrium point, namely $I = 0$, meaning that there is no Infected population in the spread of Covid-19 and the Recovered population at the beginning of time has increased, but at a certain time t the Recovered population decreased until it reached the equilibrium point, namely $R = 0$, so that the disease-free equilibrium point with $R_0 < 1$ condition is stable, meaning that there is no spread of Covid-19 or does not infect other individuals R.

4.2. Endemic Equilibrium Point Simulation

The simulation of the endemic equilibrium point E^* can be determined by providing an initial value and several parameters that meet the conditions $R_0 > 1$. The parameter values are presented in Table 1. The simulation for the equilibrium point E^* can be seen in Figure 3 below. From Figure 3, it can be seen that the Susceptible population has decreased until it reaches the equilibrium point. The Exposed population increased at the beginning of time due to interactions with the Susceptible population, but at a certain time the Exposed population decreased until it reached the equilibrium point. This decrease is due to the displacement of the Exposed population into the Infected population, so that the Infected population increases at the beginning of time, but at a certain time it decreases until it reaches the equilibrium point. This is because some of the Infected population have recovered from Covid-19, so the recovered population has increased to a point of equilibrium. The endemic equilib-

rium point is locally asymptotically stable [14], this shows that each population is heading to a point of equilibrium and stability, meaning that in this condition the spread of Covid-19 is still happening and is still transmitting to other individuals. Based on the simulation formed from the SEIR model with the initial values and parameters given, it is found that the greater the contact rate or the transmission rate, the more spread the disease will be and the smaller the cure rate, the more the disease will spread. The parameters that affect the size of the value of R0 are α_2 and β, which means that if the value of α_2 increases, the reproduction number will decrease, while if the β value increases, the reproduction number will increase. So, if one parameter increases, the other parameters must be of small value for reproduction numbers greater than one.

5. Conclusions and Suggestions

5.1. Conclusions

Based on the simulation results of numerical analysis of Covid-19 sufferers in Medan City, with the initial values and parameters given, it is obtained that the greater the rate of contact or the rate of transmission with the same healing rate, the more the disease will spread. The smaller the healing rate with the same contact rate, the more the disease will spread. In the condition $R_0 < 1$, the number of reproduction numbers $R_0 = 0.000032$ is obtained so that the disease-free equilib-

rium point is locally asymptotically stable. This shows that for a long period of time, the population with Covid-19 will disappear. The number of reproduction numbers when $R_0 > 1$ is obtained $R_0 = 15.0104$ so that the endemic equilibrium point is locally asymptotically stable. This shows that for a certain period of time, the population with Covid-19 is still transmitting to other individuals.

5.2. Suggestions

In this study, numerical simulations on the Covid-19 disease spread model are only limited to the Medan City area in 2021. Therefore, for further research, data collection can be carried out in other areas in order to determine the spread of the Covid-19 disease in the area. In the mathematical model formed, new compartments can be added or involve types of patient care such as quarantine for Covid-19.

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