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Stability Analysis And Numerical Simulation Of Covid-19 Transmission With Vaccination

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Abstract – This study reviews the epidemic model, that is SIRD (Susceptible, Infected, Recovered, Death) model of Covid-19 transmission with vaccination. The SIRD model contains four compartments in the population, namely the susceptible compartment, the infected compartment, the recovered compartment, and the death compartment. The model is analyzed for stability around the equilibrium point based on the eigenvalues of the Jacobian matrix. Furthermore, the basic reproduction number associated with the stability of the model is determined. The model is simulated with different parameter values for both equilibrium points. Numerical simulations are given to confirm the analytical results by showing the solutions and their phase portraits.

Keywords – Epidemic Model, Numerical Simulation, Stability System Stability, Threshold Number,

I. INTRODUCTION

Coronavirus Disease 2019 (Covid-19) is a new species of disease that has never been identified before in humans. Coronavirus is a virus that causes diseases ranging from mild to severe symptoms. There are two types of coronaviruses that can cause diseases with serious symptoms, namely Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS) [4]. The virus that causes Covid-19 is called Sars-CoV-2. One of the efforts to prevent Covid-19 transmission is vaccination. Starting from the beginning of 2021 until now the Covid-19 vaccine has been distributed to all Indonesian people. Given this vaccine is the most appropriate solution to reduce and break the chain of Covid-19 transmission.

Research on mathematical models of the spread of infectious diseases, especially Covid-19, has been carried out by many researchers such as Diagne in [1] discussing the mathematical model of Covid-19 with vaccination and treatment, Yundari et al in [5] discussing the analysis of the impact of vaccination on new cases of Covid-19 and recovery using the VAR model in Kalimantan, and Mu'tamar et al in [2] discussing the SIR model with vaccination and parameter estimation in Pekanbaru city. In this study, researchers reformulated the Mu'tammar et al model in [2] by adding a death compartment. Furthermore, at the end, numerical simulations were carried out with the help of Maple software.

II. MATHEMATICAL MODEL

The SIRD mathematical model of Covid-19 transmission contains four compartments in the population, namely the susceptible compartment, the infected compartment, the recovered compartment, and the death compartment. This model is the result of a reformulation of the SIR model by adding a compartment (death) with vaccination using the following assumptions:

1. Population is constant.
2. Population is closed, there is no population entry and exit.

3. Each individual has the same chance of being infected with Covid-19 disease.
4. Only Covid-19 disease exists in the population.
5. Covid-19 vaccine is given to each individual with vaccination rate θ.
6. Individuals in the susceptible population can migrate to the infected population due to contact between susceptible individuals and infected individuals with an infection rate β.
7. Individuals is recovery cannot turn back to susceptible.

   There is only death from Covid-19 with a death rate μ.
8. Infected individuals move to the recovered population with a recovery rate of γ.

Besed on the assumptions, the Covid-19 transmission model with vaccination consideration can be seen in the compartment diagram in Figure 1.

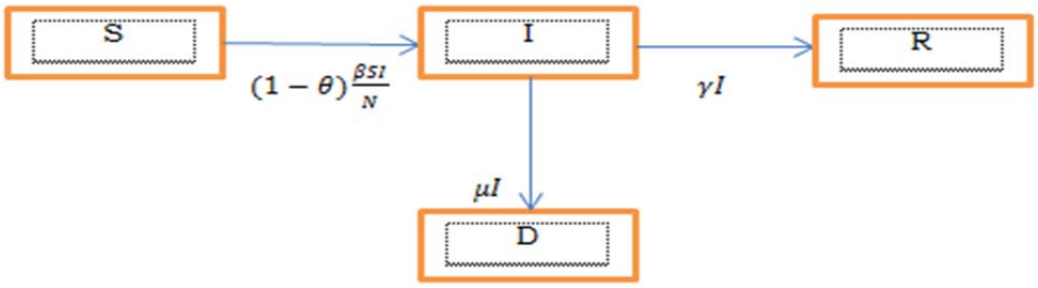

Fig. 1 Compartment Diagram of The SIRD Model

The SIRD model of Covid-19 transmission with vaccination is modeled in the following system of differential equations.

$$\begin{aligned}
\frac{dS}{dt} &= -(1-\theta)\frac{\beta SI}{N}, \\
\frac{dI}{dt} &= (1-\theta)\frac{\beta SI}{N} - \gamma I - \mu I, \\
\frac{dR}{dt} &= \gamma I, \\
\frac{dD}{dt} &= \mu I,
\end{aligned} \tag{1}$$

where *S(t)* denote the number of susceptible individuals in *t*, *I(t)* denote the number of infected individuals in *t*, *R(t)* denote the number of recovered individuals in *t*, and *D(t)* denote the number of dead individuals in *t*, with $S(t) + I(t) + R(t) + D(t) = N$.

Let

$$s = \frac{S}{N}, i = \frac{I}{N}, r = \frac{R}{N}, d = \frac{D}{N},$$

Thus, the system (1) can be writen in the following form

$$\frac{ds}{dt} = -(1-\theta)\beta si,$$

$$\frac{di}{dt} = (1-\theta)\beta si - \gamma i - \mu \text{i}, \quad (2)$$
$$\frac{dr}{dt} = \gamma i,$$
$$\frac{dd}{dt} = \mu i.$$

III. Results And Discussion

3.1. Stability Analysis

There are two equilibrium points that describe the state of the model (2), the first one is the disease-free equilibrium point ($i = 0$), which is a condition where the population is free from disease and the second one is the endemic equilibrium point ($i > 0$), which is a condition where there are still individuals infected with the disease in the population. The disease-free equilibrium point of system (2) is

$$E^0 = (S^0, 0, 0, 0),$$

and the disease endemic equilibrium point of system (2) is

$$E^* = S^*, I^*, R^*, D^* = \left(\frac{\gamma+\mu}{(1-\theta)\beta}, I^*, R^*, D^*\right).$$

Stability of the equilibrium points depend on the Jacobian matrix. Jacobian matrix for the disease-free equilibrium is

$$J^0 = \begin{bmatrix} 0 - & \beta s^0(1-\theta) & 0 & 0 \\ 0 & \beta s^0(1-\theta) - \gamma - \mu & 0 & 0 \\ 0 & \gamma & 0 & 0 \\ 0 & \mu & 0 & 0 \end{bmatrix} \quad (3)$$

The eigenvalues for disease-free are obtained as follows, $\lambda_{1,2,3} = 0$ and $\lambda_4 = (\beta s^0 - \beta s^0\theta - \gamma - \mu)$. Since $\lambda_{1,2,3} = 0$, the stability of the disease-free equilibrium point depends on λ_4. If $\lambda_4 < 0$ then the equilibrium point $E^0$is stable, otherwise if $\lambda_4 > 0$ then the equilibrium point E^0 is unstable.

Jacobian matrix for the endemic disease equilibrium point is

$$J^* = \begin{bmatrix} \beta s^*(-1+\theta) & -\gamma - \mu & 0 & 0 \\ -\beta s^*(-1+\theta) & 0 & 0 & 0 \\ 0 & \gamma & 0 & 0 \\ 0 & \mu & 0 & 0 \end{bmatrix} \quad (4)$$

The eigenvalues for the endemic disease are obtained as follows $\lambda_{1,2} = 0$, $\lambda_{3,4} = \frac{1}{2}(-\beta i^*(1-\theta) \pm \sqrt{D}$ where $D = (\beta^2 i^{*2} - 2\beta^2 i^{*2}\theta + \beta^2 i^{*2}\theta^2 - 4\beta i^*\mu + 4\beta i^*\theta\gamma + 4\beta i^*\theta\mu - 4\beta i^*\gamma)$. Since $\lambda_{1,2} = 0$,, the stability of the endemic equilibrium point depends on the value of $\lambda_{3,4}$.

a. If $D < 0$ then $\lambda_{3,4}$ is complex, because $-\beta i^*(1-\theta)$ is negative, then the real part of $\lambda_{3,4}$ is negative, it means that the equilibrium point E^* is stable.

b. If $D > 0$ then $\lambda_{3,4}$ is real number of different sign, it means that the equilibrium point E^* is unstable.

c. If $D = 0$ then $\lambda_{3,4}$ is repeated negative numbers, it means that the equilibrium point E^* is stable.

Furthermore, the basic reproduction number is determined by assuming $\frac{dI}{dt} > 0$ in model (2) as follows

$$\beta si(1-\theta) - \gamma i - \mu i > 0$$

$$i(\beta s(1-\theta)-\gamma-\mu)>0$$
$$\beta s(1-\theta)-\gamma-\mu>0$$
$$\beta s(1-\theta)>\gamma+\mu$$
$$\frac{\beta s(1-\theta)}{(\gamma+\mu)}>1 \quad (5)$$

It can be concluded that the basic reproduction number is

$$R_0=\frac{\beta s(1-\theta)}{(\gamma+\mu)}.$$

3.2. Numerical Simulation

This section discusses the numerical simulation as an implementation of the SIRD model. The initial values are given $s(0)=0{,}9;\ i(0)=0{,}0125; r(0)=0{,}01; d(0)=0{,}0775$. Furthermore, the parameter values for disease-free are assumed to be $\beta=0{,}07;\ \gamma=0{,}27;\ \theta=0{,}001;\ \mu=0{,}001$, while the parameter values for endemic disease are assumed to be $\beta=0{,}07;\ \gamma=0{,}0027;\ \theta=0{,}001;\ \mu=0{,}001$ [3]. Based on the numerical simulation results, the graphic of solutions is shown in Figure 2 and Figure 3.

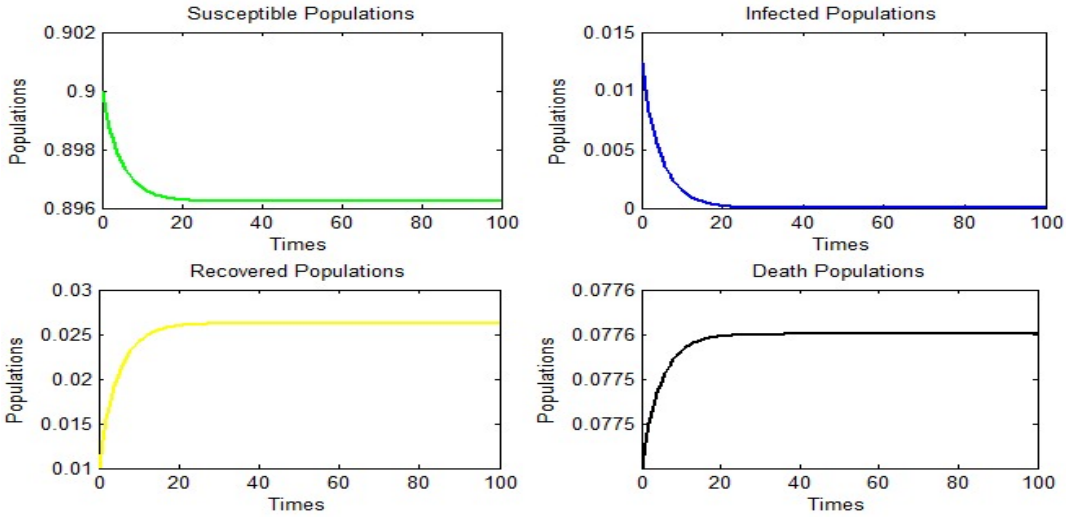

Fig. 2 Graph of the disease-free equilibrium point of the *SIRD* model.

Figure 2 shows that the susceptible population and infected population also decreased due to the death caused by Covid-19 and the recovery from Covid-19. Then, the recovered population and the death population increased.

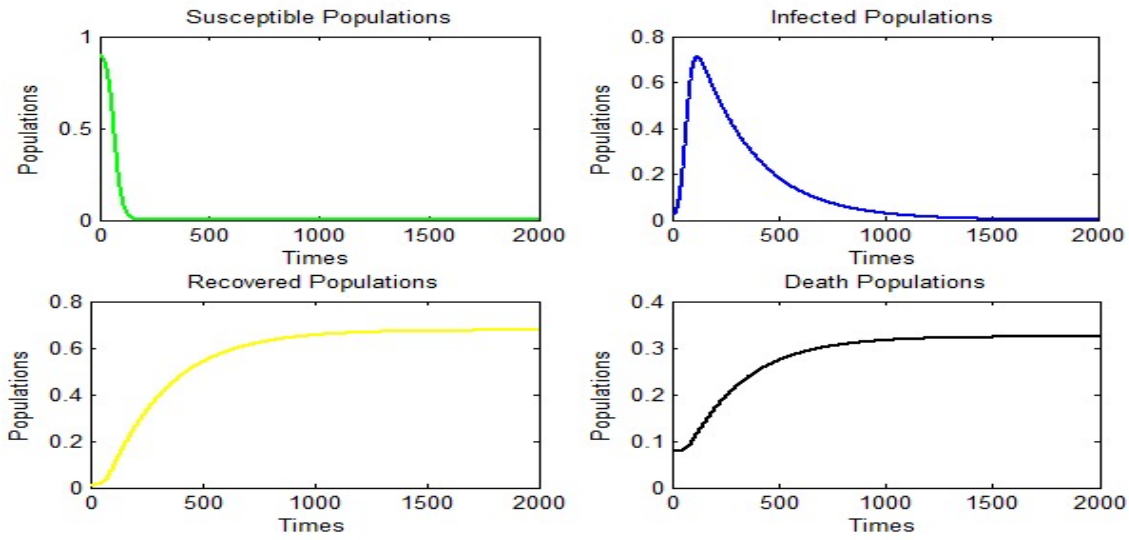

Fig. 3 Graph of the endemic disease equilibrium point of the *SIRD* model.

Figure 3 shows that the susceptible population has decreased because of the infected individuals, so it makes the infected population has increased, while the recovered and death population has increased.

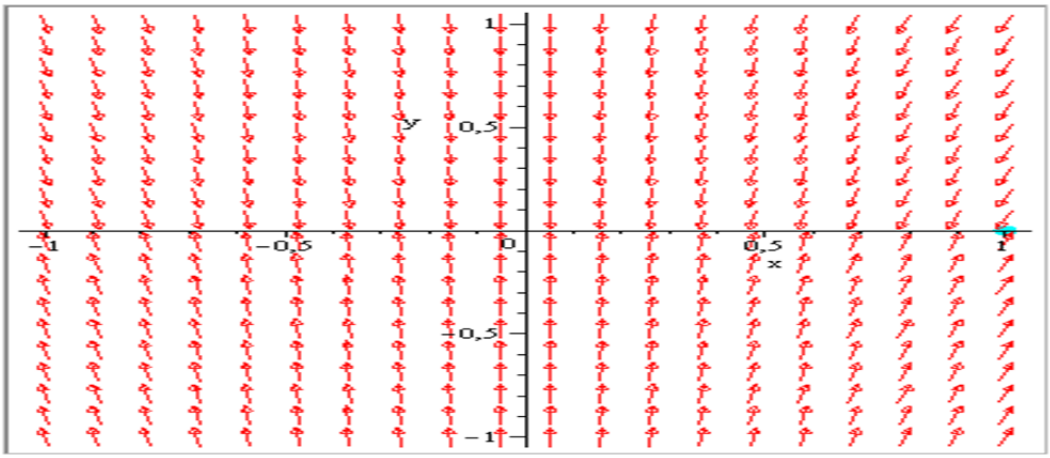

Fig. 4 Phaseportrait the disease-free equilibrium point

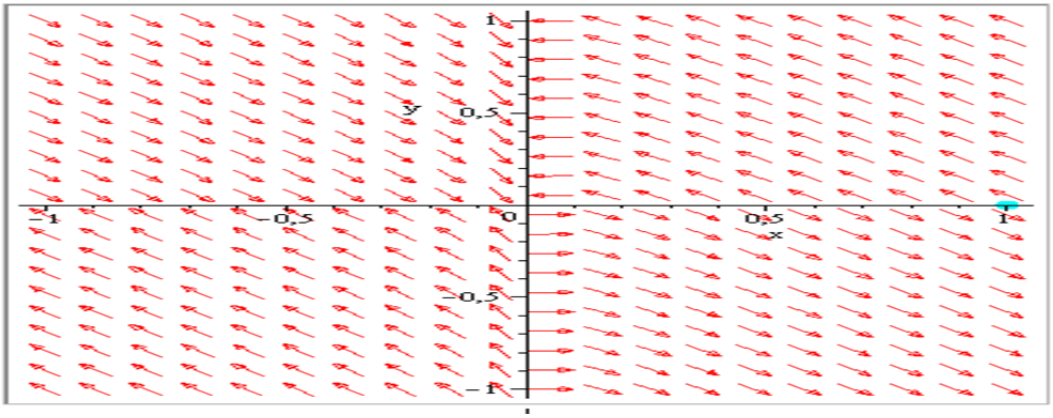

Fig. 5 Phaseportrait the disease-endemic equilibrium point

From figure (4) can be seen that the traject tory from phaseportrait of system (2) is stable node.

IV. CONCLUSIONS

Based on the discussion, it can be concluded that that the disease-free equilibrium point and the disease-endemic equilibrium point are asymptotically stable associated with value of R_0.

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