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SEIR Model Analysis of Coronavirus Disease 2019 (Covid-19) Transmission Considering Vaccination Rates

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Abstract. Coronavirus disease 2019 (Covid-19) is a disease that attacks the respiratory system from mild to severe symptoms. This disease can attack someone who has a weak immune system. Vaccination is an effort to build a person's immune system to fight disease. This study aims to determine the spread of the Covid-19 disease by paying attention to the rate of vaccination. The data used is the data in September 2021 for the spread of the Covid-19 disease by focusing on the second dose of vaccination. In this study, the experimental method was used by performing numerical simulations using parameter values obtained from previous studies. The results show that the rate of vaccination affects the Covid-19 disease. If no individual is vaccinated ($\theta = 0$) obtained $R_0 > 1$ which means the disease will spread. But when the vaccination rate is increased to 0.2 it is obtained $R_0 < 1$ which means the disease will disappear.

INTRODUCTION

Viruses, bacteria, and fungi are some of the factors that cause infectious diseases. This disease can attack when a person has weak antibodies. Transmission of this disease can be through direct contact, sneezing, and droplets in the air. One of the infectious diseases that are endemic and caused by a virus is the coronavirus [1]. Since the Covid-19 pandemic entered Indonesia, the government has begun to implement various policies to suppress the rate of transmission. One of the efforts to reduce the rate of transmission is by giving vaccines to people who are susceptible to exposure to the disease. This vaccination program is expected to form herd immunity. Vaccination is the administration of a vaccine to an individual who is susceptible to being exposed to a disease to increase or create immunity to a disease so that when exposed to the disease it will not experience a severe impact and will not infect others [2].

Mathematical modeling is the application of mathematics by modeling a problem into mathematical language. One example of a problem that can be made into a mathematical model is the spread of disease, a mathematical model can help to predict the spread of disease in a population both for diseases that cause death and those that do not cause death [3]. The SIR model is a disease spread model that can be developed into an epidemic model of SEIR, SIS, SVIR, and others. The SIR epidemic model is divided into three subpopulations susceptible, infected, and recovered (removed from the possibility of re-infecting or transmitting the disease after infection) [4].

In this study, an SEIR epidemic model of the spread of Covid-19 disease will be formed with the rate of vaccination. From the model formed, we will find the equilibrium point free of disease and endemic, the basic reproduction number, and model simulation using parameter values.

METHODOLOGY

This study uses data on the spread of the Covid-19 disease in Indonesia in September 2021. The method used in this research is an experiment that simulates parameter values obtained from previous studies. The model used is the SEIR epidemic model (Susceptible, Exposed, Infected, Recovered). The assumption of forming a mathematical model of the spread of the Covid-19 disease with the vaccination rate can be arranged as follows:

1. The population is assumed to be closed, meaning that no individuals enter the population or leave the population (no migration). The total population is assumed to be constant.
2. The number of births and the number of deaths per unit of time is assumed to be the same.
3. The population is assumed to be homogeneously mixed, meaning that each individual has the same opportunity to make contact with other individuals.
4. Migration in Indonesia is not part of the migration.

5. Susceptible individuals will be given a vaccine so that it can cause individuals who are given the vaccine to become immune to the disease.
6. The individual has received 2 doses of the vaccine.
7. Individuals can leave the infected group because they are recovering from the disease. Once recovered, the individual will be immune to the disease.
8. Viral infection occurs when contact with an infected individual is either direct or indirect.
9. Each subpopulation experiences pure death.

Based on the assumptions above, a compartment diagram for the spread of COVID-19 can be seen in Fig.1.

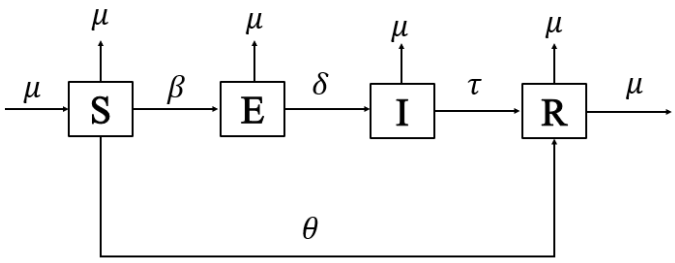


FIGURE 1. COVID-19 Transmission Compartment Flowchart

Variables and Parameters

The variables and parameters used in the Covid-19 disease spread model with vaccination rates are presented in Table 1 and Table 2:

TABLE 1. List of model variables for the spread of Covid-19 disease

Variables	Definition	Unit
N(t)	Total population of individuals at time t	Individual
S(t)	Number of susceptible individuals infected at time t	Individual
E(t)	Number of exposed individuals at time t	Individual
I(t)	Number of infected individuals at time t	Individual
R(t)	Number of recovered individuals at time t	Individual

TABLE 2. List of model parameters for the spread of Covid-19 disease

Parameters	Definition	Unit
μ	The natural rate of birth and death	$\frac{1}{time}$
β	The rate at which an individual is susceptible to becoming an exposed individual after interacting with an infected individual	$\frac{1}{\text{day}}$
δ	The rate of transfer from exposed individuals to infected individuals	$\frac{1}{\text{day}}$
τ	The recovery rates of each individual	$\frac{1}{\text{day}}$
θ	Vaccination rates for susceptible individuals	$\frac{individual}{population}$

RESULTS AND DISCUSSIONS

Based on Fig. 1, a mathematical model can be formed in the system of differential equations:

$$\begin{aligned}\frac{dS}{dt} &= \mu N - \beta SI - \mu S - \theta S \\ \frac{dE}{dt} &= \beta SI - \delta E - \mu E \\ \frac{dI}{dt} &= \delta E - \tau I - \mu I \\ \frac{dR}{dt} &= \tau I + \theta S - \mu R\end{aligned} \tag{1}$$

with $N = S + E + I + R$. It can show that $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$, then $N(t)$ is constant. Thus equation (1) fulfills the assumption that the number of individuals in the population is constant and can be formed in the model to be:

$$\frac{dS}{dt} = \mu - \beta SI - \mu S - \theta S \tag{2}$$

$$\frac{dE}{dt} = \beta SI - \delta E - \mu E \tag{3}$$

$$\frac{dI}{dt} = \delta E - \tau I - \mu I \tag{4}$$

$$\frac{dR}{dt} = \tau I + \theta S - \mu R \tag{5}$$

Equilibrium Point

The disease-free equilibrium point is obtained if $E = 0$ and $I = 0$, so that no individual is infected with the disease. Substitution $E = 0$ and $I = 0$ into equation (2)-(5), it is found that the disease-free equilibrium point is:

$$E^0(S, E, I, R) = \left(\frac{\mu}{\mu + \theta}, 0, 0, \frac{\theta}{\mu + \theta}\right) \tag{6}$$

The endemic equilibrium point is a condition where there are infected individuals in a population. So that the endemic equilibrium point is obtained $E_1(S^*, E^*, I^*, R^*)$

$$\begin{aligned}S^* &= \frac{\delta\mu + \delta\tau + \mu^2 + \mu\tau}{\beta\delta} \\ I^* &= \frac{\beta\delta\mu - \delta\mu^2 - \delta\mu\tau - \delta\mu\theta - \delta\tau\theta - \mu^3 - \mu^2\tau - \mu^2\theta - \mu\tau\theta}{\beta(\delta\mu + \delta\tau + \mu^2 + \mu\tau)} \\ E^* &= \frac{\beta\delta\mu - \delta\mu^2 - \delta\mu\tau - \delta\mu\theta - \delta\tau\theta - \mu^3 - \mu^2\tau - \mu^2\theta - \mu\tau\theta}{\delta(\delta + \mu)\beta} \\ R^* &= \frac{\begin{pmatrix}\beta\delta^2\tau - \delta^2\mu\tau + \delta^2\mu\theta - \delta^2\tau^2 + \delta^2\tau\theta - \delta\mu^2\tau + 2\delta\mu^2\theta \\ -\delta\mu\tau^2 + 3\delta\mu\tau\theta + \delta\tau^2\theta + \mu^3\theta + 2\mu^2\tau\theta + \mu\tau^2\theta\end{pmatrix}}{\beta(\delta\mu + \delta\tau + \mu^2 + \mu\tau)\delta}\end{aligned} \tag{7}$$

Basic Reproduction Number

The basic reproduction number (R_0) is found using the Next Generation Matrix (NGM) method from equations (3) and (4). The steps in determining the basic reproduction number:

1. Retrieve an equation that describes a new infected case and a change in the infection compartment of the system. Furthermore, this system is called the infected subsystem. The infected subsystems are E and I.

2. Linearize the infected system at the disease-free equilibrium point. This linear system is carried out using the Jacobian Matrix (J)

3. Decomposition of the Jacobian matrix becomes $J = (\mathcal{F}i + \mathcal{V}i)x$, $\mathcal{F}i$ is the matrix of infection/disease transmission and $\mathcal{V}i$ is the transition matrix.

$$\mathcal{F} = \begin{bmatrix} 0 & \frac{\beta\mu}{\mu+\theta} \\ 0 & 0 \end{bmatrix} \text{ and } \mathcal{V} = \begin{bmatrix} -\delta-\mu & 0 \\ \delta & -\tau-\mu \end{bmatrix}$$

Then the NGM with a large domain denoted by K is $K = -\mathcal{F}\mathcal{V}^{-1}$

$$K = \begin{bmatrix} \frac{\beta\mu\delta}{(\delta+\mu)(\tau+\mu)(\mu+\theta)} & \frac{\beta\mu}{(\tau+\mu)(\mu+\theta)} \\ 0 & 0 \end{bmatrix}$$

Using equation $det\ (\lambda I - K) = 0$, then the basic reproduction number (R_0) from the largest eigenvalue of the K . matrix is obtained

$$R_0 = \frac{\beta\mu\delta}{(\delta+\mu)(\tau+\mu)(\mu+\theta)} \tag{8}$$

Stability Analysis

$$J = \begin{bmatrix} -\mu-\theta & 0 & \frac{-\beta\mu}{\mu+\theta} & 0 \\ 0 & -\delta-\mu & \frac{\beta\mu}{\mu+\theta} & 0 \\ 0 & \delta & -\tau-\mu & 0 \\ \theta & 0 & \tau & -\mu \end{bmatrix} \tag{9}$$

The eigenvalues are obtained as follows:

$\lambda_1 = -\mu - \theta$

$\lambda_2 = -\mu$

$$\lambda_3 = \frac{1}{2}\frac{\left(-\delta\mu - \delta\theta - 2\mu^2 - \mu\tau - 2\mu\theta - \tau\theta + \begin{pmatrix} 4\beta\delta\mu^2 + 4\beta\delta\mu\theta + \delta^2\mu^2 + 2\delta^2\mu\theta + \delta^2\theta^2 \\ -2\delta\mu^2\tau - 4\delta\mu\tau\theta - 2\delta\tau\theta^2 + \mu^2\tau^2 + 2\mu\tau^2\theta + \tau^2\theta^2 \end{pmatrix}^{\frac{1}{2}}\right)}{\mu+\theta} \tag{10}$$

$$\lambda_4 = -\frac{1}{2}\frac{\left(\delta\mu + \delta\theta + 2\mu^2 + \mu\tau + 2\mu\theta + \tau\theta + \begin{pmatrix} 4\beta\delta\mu^2 + 4\beta\delta\mu\theta + \delta^2\mu^2 + 2\delta^2\mu\theta + \delta^2\theta^2 \\ -2\delta\mu^2\tau - 4\delta\tau\theta - 2\delta\tau\theta^2 + \mu^2\tau^2 + 2\mu\tau^2\theta + \tau^2\theta^2 \end{pmatrix}^{\frac{1}{2}}\right)}{\mu+\theta}$$

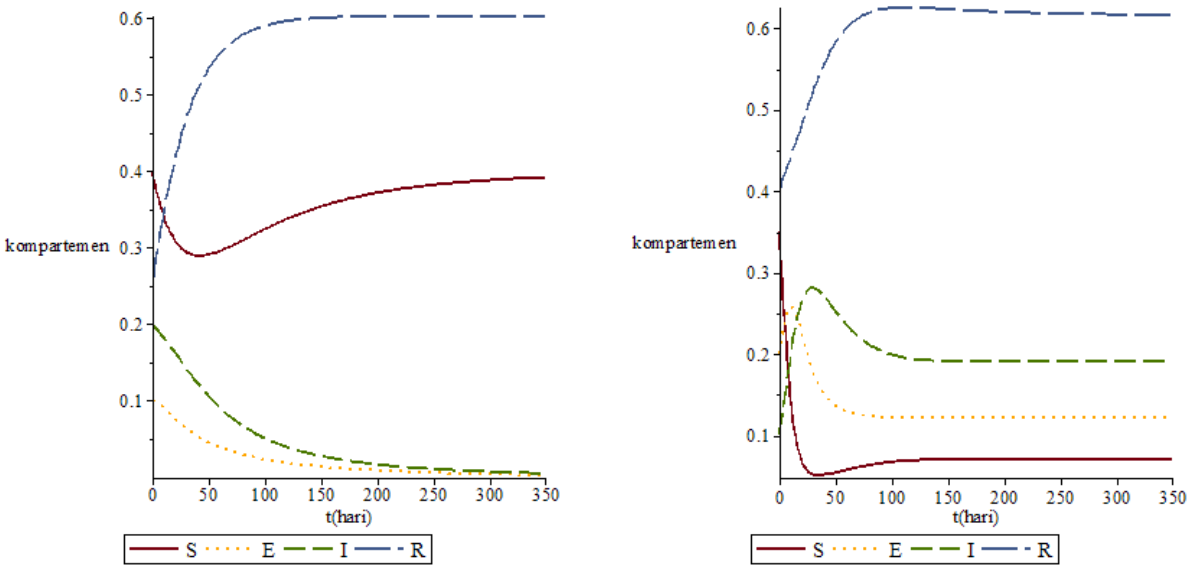
- Parameter value μ is obtained from data on population growth rate in Indonesia
- For parameter values δ it is assumed that the incubation period for Covid-19 disease is 14 days and will attack a person's body.
- Parameter value τ assumes a person infected with Covid-19 can recover within 30 days.
- Parameter value θ is obtained from the number of individuals who have been vaccinated with the 2nd dose up to September 30, 2021 divided by the population.

Numerical Calculation and Simulation

TABLE 3. List of model parameters for the spread of Covid-19 disease

Parameters	Value	Unit	Reference
μ	0.0125	$\frac{1}{time}$	[5]
β	0.1	$\frac{1}{\text{day}}$	[6]
δ	0.07142857143	$\frac{1}{\text{day}}$	[7]
τ	0.0333333	$\frac{1}{\text{day}}$	[8]
θ	0.01891695041	$\frac{individual}{population}$	[9]

Based on the parameter values, the basic reproduction number is $R_0 = 0.7387996421 < 1$. Because $R_0 < 1$ then the disease will not spread. Furthermore, if the value of parameter β is enlarged from the previous value to 0.76. Using the parameter values in table 3, the basic reproduction number is obtained $R_0 = 5.614877281 > 1$, which means that 1 individual can infect 6 other individuals. The simulation results at the disease-free and endemic equilibrium point using software are based on the parameter values in Table 3 as shown in Fig. 2.



(a) (b)

FIGURE 2. (a) simulation to a disease-free equilibrium point, (b) simulation to the endemic equilibrium point

Based on Fig. 2(a) the vulnerable population decreased until the 40th day, then rose to the point of 0.3978743906 and was stable at that point. The exposed population decreased until the 300th day towards point 0 and became stable at that point. The infected population decreases slowly towards point 0 and stabilizes at that point. The recovery population will increase until the 140th day to the point of 0.6021250694 and become stable at that point which is influenced by the rate of vaccination and individuals who have recovered.

Meanwhile, Fig. 2(b) for the simulation towards the endemic equilibrium point. The vulnerable population will decrease until the 30th day then increase to the 110th day to the point of 0.07086074562 and stable at that point. The exposed population increased until the 10th day and then decreased to the 80th day to 0.1224108941 and was stable at that point. The infected population will increase until the 30th day, then decrease until the 140th day to the point of 0.1907702246 and become stable at that point. The recovery population increased until the 80th day to the point of 0.6159581356 which was influenced by the rate of vaccination and the population that had recovered and left the population.

TABLE 4. Effectiveness of Vaccination Rate on Population

Vaccination Rate ($\boldsymbol{\theta}$)	Basic Reproduction Number ($\boldsymbol{R_0}$)
0	14.11218569
0.2	0.83012857
0.4	0.42764199
0.6	0.28800379
0.8	0.21711054
1	0.17422451

Using the parameter values in Table 3 by changing the $\boldsymbol{\theta}$ value as in table 4. The results obtained are the rate of vaccination affects the spread of Covid-19 which is indicated by the basic value of reproduction. At $\boldsymbol{\theta = 0}$ the value of $\boldsymbol{R_0 > 1}$, but at $\boldsymbol{\theta = 0.2}$ the value of $\boldsymbol{R_0 < 1}$.

CONCLUSION

Based on the existing results, the rate of vaccination affects the spread of the Covid-19 disease which is indicated by the basic reproduction number. When $\theta = 0$ the basic reproduction number obtained $R_0 = 14.11218569$ which means 1 individual can transmit the disease to 14 other individuals. However, when the vaccination rate was increased to 0.2, the basic reproduction number was 0.8301285699 which indicated that the disease would disappear and be under control.

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