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## A Susceptible-Infected-Removed Epidemiological Model for COVID-19 Spreading in Indonesia

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### ABSTRACT

COVID-19 is a disease emerged from China in the late 2019 and still spreading to this date. Scientists worldwide are trying to give their contributions in many aspects, from searching for the vaccine to studying several policies in many aspects to deal with this disease. One of the important researches in COVID-19 is to study and predict the dynamic of the spreading by using epidemiological model. This research has been taken in many countries independently since the behavior of COVID-19 spreading might differ from one another. Each country has their own characteristics—e.g., the population density, geographic condition, health facilities and infrastructure, weather condition—which caused the different patterns of COVID-19 spreading. Therefore, each country probably has their own unique parameters which describe their own dynamicity of COVID-19 spreading even though the epidemiological models used in different countries are the same. Thus, in this paper, we estimate the parameters involved in our SIR epidemiological model for cases in Indonesia by using Least Square Method in Python. We use the daily cases released from Indonesian COVID-19 Response Acceleration Task Force. Several assumptions are made in this model, including the assumption that there is no vaccination to be released yet. The result shows that the COVID-19 will still exists in Indonesia for over 1.9 years from the first case emerged (until mid January 2022).

**Keywords:** COVID-19, epidemiological model, Indonesia, dynamical system

## **1. INTRODUCTION**

Coronavirus disease (COVID-19) is a disease sourced from Wuhan, China [1], [2]. It first appeared in December 2019 [3]. The disease quickly spread to other countries and caused several symptoms e.g., fever, cough, fatigue, muscle or body ache, sore throat, trouble breathing, and diarrhea. World Health Organization (WHO) declared COVID-19 as Public Health Emergency of International Concern (PHEIC) [4]. As 15 December 2020, WHO stated that there were more than 1.6 million deaths with total confirmed cases of more than 75 million cases.

COVID-19 has caused serious impact in many sectors e.g., business and economic, social welfare, education, and industry. All aspects in our daily lives are forced to be adapted in this particular condition. Schools, learning centers, offices, and many public places are temporary closed [5]–[8]. Furthermore, the global economy is also interrupted. Several restrictions among the countries worldwide slowed down economic activities [9]. Companies all over the world has started to experience contractions in production as there are several restrictions, worker illness, etc [10]. As the result, the unemployment rate worldwide is increased [11]. This conditions can led to the increasing poverty rate [12]–[14]. Therefore, we need several strategies to tackle the problems affected by the emergence of COVID-19.

Many scientists are currently working to give their studies and recommendations based on their expertise. Perdana et al., (2020) gives the study about three scenarios of food supply chain in the meantime of COVID-19 outbreak [15]. Rizou et al., (2020) discussed several measures on food safety of supply chain during this outbreak [16]. Charis M. Galanakis (2020) discussed the recommendation of several nutritions and bioactive ingredients which can help to promote immune system [17].

Furthermore, another important issue is to predict when and how the COVID-19 spread will end. Mathematical modeling, particularly epidemiological model, can assist us to give prediction of disease spread based on several conditions. There have been many researchers studying disease spread in Indonesia. Side & Noorani (2013) studied dengue fever disease spread in Sulawesi, Indonesia [18]. They used Susceptible-Infected-Removed (SIR) model in their study. Another study is also given by Kristiani et al., (2017). They discussed dengue disease spread by studying human and mosquito population [19]. Thus, they used SIR-SI model to perform their study.

Furthermore, in COVID-19 cases, there are also several studies discussing the disease spread. One of the studies is given by Annas et al., (2020). They studied the COVID-19 spread in Indonesia using SEIR model [20]. The parameters used in the model were obtained from other studies. However, it is important to use our own parameters since different countries may have different conditions and characteristics. In other words, the parameters involved in the model might be different from one another, even though the model used is the same.

Sulaiman, (2020) performed a study of COVID-19 spread in Indonesia using SIR model [21]. He used Batista's code to obtain his own parameters involved in his model. Another study which obtained her own parameters is given by Aldila (2020). He studied COVID-19 spread in East Java, Indonesia using modified SEIR model [22]. In particular, he classified the susceptible into two compartments, i.e., aware and unaware susceptible. Furthermore, he also classified the infected into two compartment, i.e., detected and undetected infected. He used least square method to obtain several parameters used in his model. In this paper, we studied COVID-19 spread in Indonesia using SIR model. To obtain parameters involved in our model, we used

least square method. This study aims to simulate the COVID-19 spread in Indonesia without any act of vaccination. This can be used as an illustration of the possible condition if the vaccination is not given.

## 2. MATERIAL AND METHODS

The mathematical model used in this paper is deterministic SIR model. In constructing our SIR model, least square method is used to obtain parameters involved in our model by using Python.

### 2. 1. SIR Epidemiological Model

The SIR model used in this paper classified human population into three compartments, i.e., Susceptible ( $S$ ), Infected ( $I$ ), and Removed ( $R$ ). Susceptible individuals are those who are not infected and can be infected [23]. Susceptible individuals may remain susceptible throughout the time or could become infected. Infected individuals are those who are infected by the virus, and can infect susceptible individuals [24]. Infected individuals are then recovered or died, assigned as removed individuals. Removed individuals are those who are recovered or died [25].

To simplify the model, several assumptions are made. One of the assumptions is the total number of population ( $N(t)$ ). It is constant all the time ( $N(t) = S(t) + I(t) + R(t), \forall t$ ). Another assumption is that all of the population besides infected and removed, are considered as susceptible individuals. Thus, the increasing number of infected individuals will not cause that of the susceptible individuals increased since all of the population (besides infected and removed) are already considered as susceptible individuals. Furthermore, it is assumed that the vaccine has not yet been given to the population. This is in line with the the study which aims to simulate the COVID-19 spread in Indonesia without any act of vaccination. The scheme of SIR model is given in Figure 1.

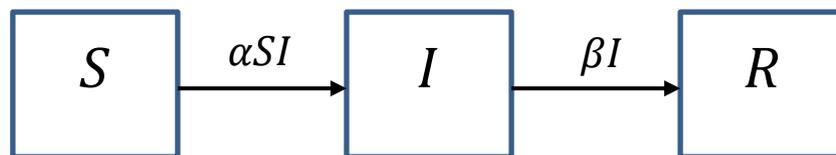


Figure 1. Scheme of SIR model

Based on the given assumptions, the SIR model which describes the rate of changes of the three compartments is given by the following system of Ordinary Differential Equations (ODEs):

$$\frac{d(S(t))}{dt} = -\alpha S(t)I(t),$$

$$\frac{d(I(t))}{dt} = \alpha S(t)I(t) - \beta I(t), \tag{1}$$

$$\frac{d(R(t))}{dt} = \beta I(t),$$

where  $\alpha$  represents the exponential growth factor of infected individuals and  $\beta$  represents the exponential decay factor of infected individuals. Both  $\alpha$  and  $\beta$  are positive real numbers ( $\alpha, \beta \in \mathbb{R}^+$ ). These parameters are then estimated by using least square method to fit the SIR model into the given data.

### 2. 2. Basic Effective Reproduction Rate

According to Cooper et al., (2020), the basic effective reproduction rate  $R_e$  is defined as:

$$R_e = \frac{\alpha S(t)}{\beta}.$$

The basic effective reproduction rate  $R_e$  can be used to determine whether a disease will vanish quickly or will be an epidemic [26]. If  $R_e < 1$ , then  $\frac{d(I(t))}{dt} < 0$  which implies that the number of infected individuals will decrease monotonically to zero. Otherwise, if  $R_e > 1$ , then  $\frac{d(I(t))}{dt} > 0$  which implies that the number of infected individuals will increase. The number of infected individuals will reach its peak if there is not any change. In other words, it will reach its peak when the rate of changes of the infected individuals is zero ( $\frac{d(I(t))}{dt} = 0$ ). This also implies that  $R_e = 1$ .

## 3. RESULT AND DISCUSSION

### 3. 1. Parameter Estimation

Parameters used in this model are obtained by fitting the model with least square method in Python based on the given COVID-19 daily cases data in Indonesia. The COVID-19 daily cases data are obtained from Indonesian COVID-19 Response Acceleration Task Force. We used the data from 2 March 2020 until 1 November 2020 (245 days). Accordingly, parameters estimated by using least square method is given in Table 1.

**Table 1.** Estimated parameters using least square method

Parameters	Value
$\alpha$	0.450551
$\beta$	0.407695

Another parameters used in this model (not fitted) is  $N(t_0)$ ,  $S(t_0)$ ,  $I(t_0)$ , and  $R(t_0)$ . We assume that the time  $t_0$  is set when the first COVID-19 case emerged in Indonesia. Thus,  $I(t_0)$  and  $R(t_0)$  are set based on the given data from Indonesian COVID-19 Response Acceleration Task Force. The total population  $N(t_0)$  is set based on the Indonesia's total population in 2020 which given by Indonesian Directorate General of Population and Civil Registration. Furthermore, based on the assumption discussed in the preceeding section,  $S(t_0)$  can be calculated as:

$$S(t_0) = N(t_0) - (I(t_0) + R(t_0)).$$

The value of  $N(t_0)$ ,  $S(t_0)$ ,  $I(t_0)$ , and  $R(t_0)$  are given in Table 2.

**Table 2.** Value of  $N(t_0)$ ,  $S(t_0)$ ,  $I(t_0)$ , and  $R(t_0)$  parameter

Parameters	Value
$N(t_0)$	268,583,016
$S(t_0)$	268,583,014
$I(t_0)$	2
$R(t_0)$	0

One may considered using the ratio value instead of the real value for the parameters to keep the computational cost as low as possible.

### 3. 2. Numerical Results

As the parameters value are set, ODEs system of SIR model is constructed and further solved numerically. The comparison between numerical result and given data for susceptible, infected, and removed individuals are given in Figure 2, Figure 3, and Figure 4, respectively. The X-axis represents the number of individuals and Y-axis represents the days.

The number of infected individuals are fluctuative during the early 245 days. Nevertheless, the model have tried to fit the given data of the three compartments. The long-term simulation of the infected individuals is given in Figure 5.

Based on the long-term result, it is predicted that the COVID-19 spread in Indonesia without any vaccination will reach its peak between 343<sup>rd</sup>-349<sup>th</sup> days from the first emerged case (7 February 2021-13 February 2021). The number of infected individuals are since then will continuously decreased and will reach its end in 694<sup>th</sup> days (24<sup>th</sup> January 2022).

As the susceptibles individuals become infected, the number of infected individuals is increasing while the number of susceptibles is decreasing as shown in Figure 6. The increasing infected individuals caused the removed individuals increased until the number of infected individuals reach its peak. Since then, the infected individuals are gradually decreased as they become removed individuals. As the number of infected individuals approaches zero, the

shifting between susceptible to infected and infected to removed are also getting smaller until there is no infected individuals left.

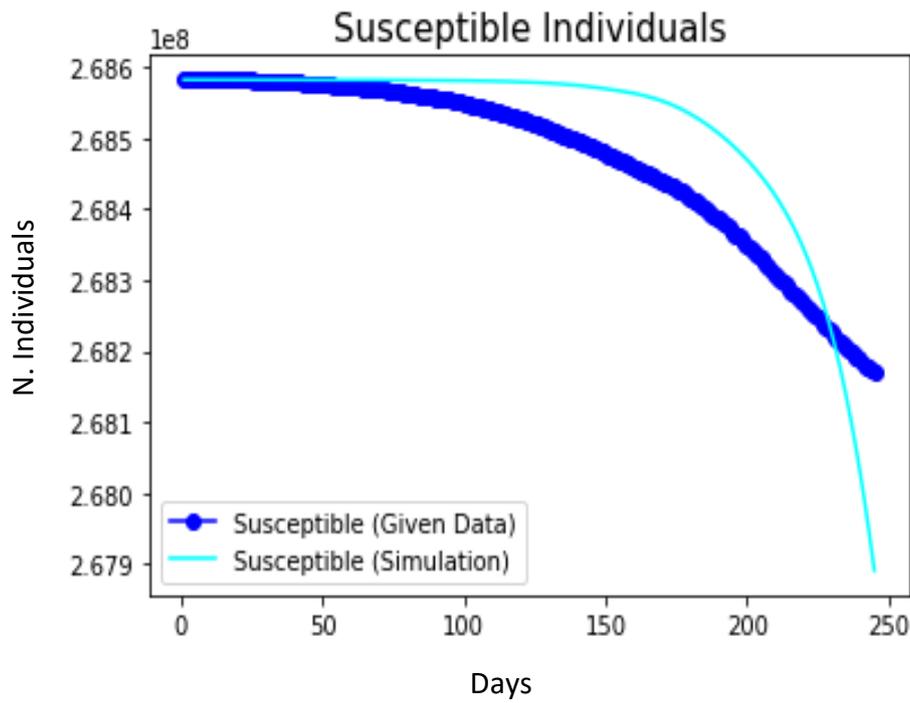


Figure 2. Comparison between numerical results and given data for susceptible individuals

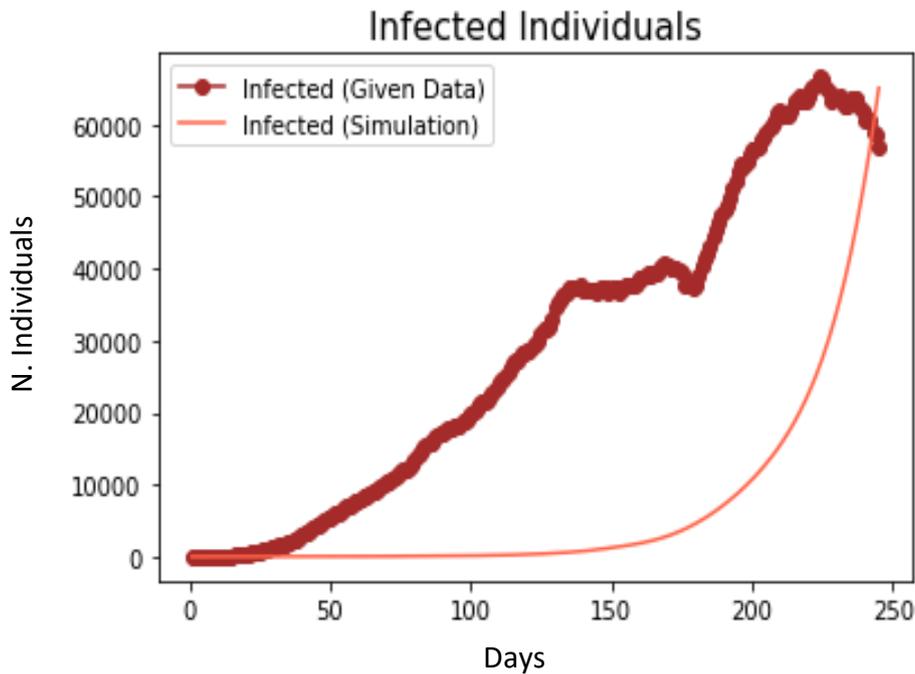


Figure 3. Comparison between numerical results and given data for infected individuals

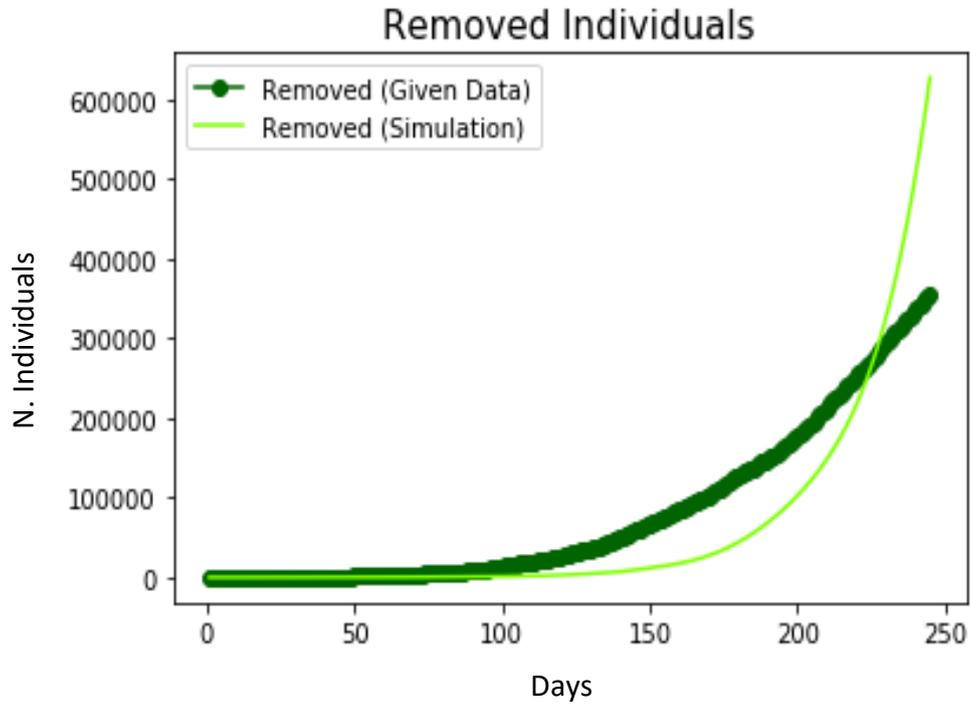


Figure 4. Comparison between numerical results and given data for removed individuals

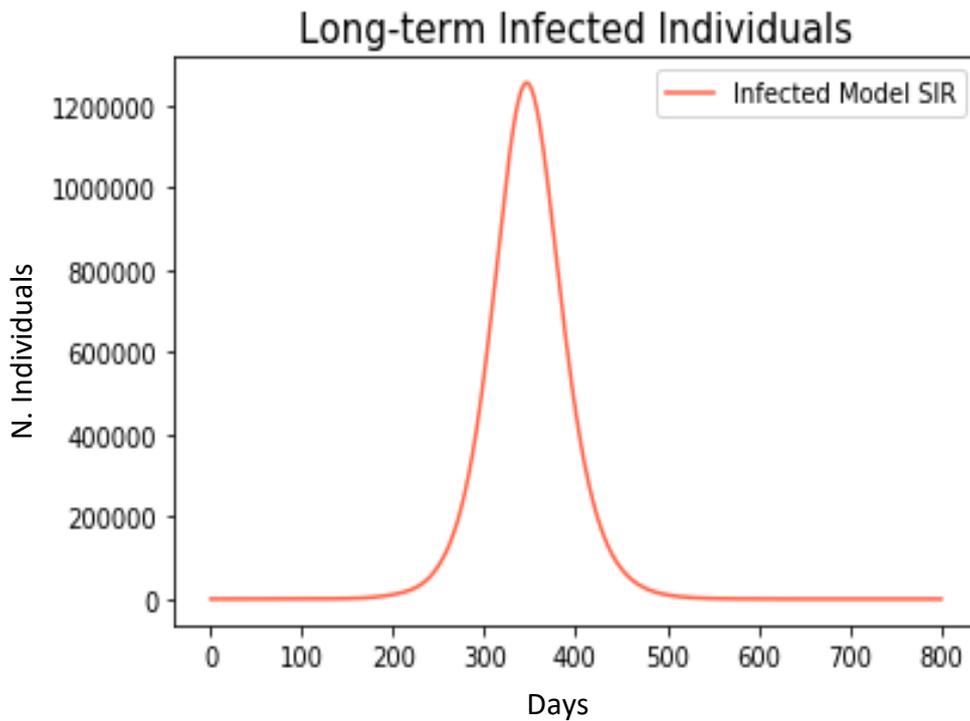


Figure 5. Long-term simulation of infected individuals

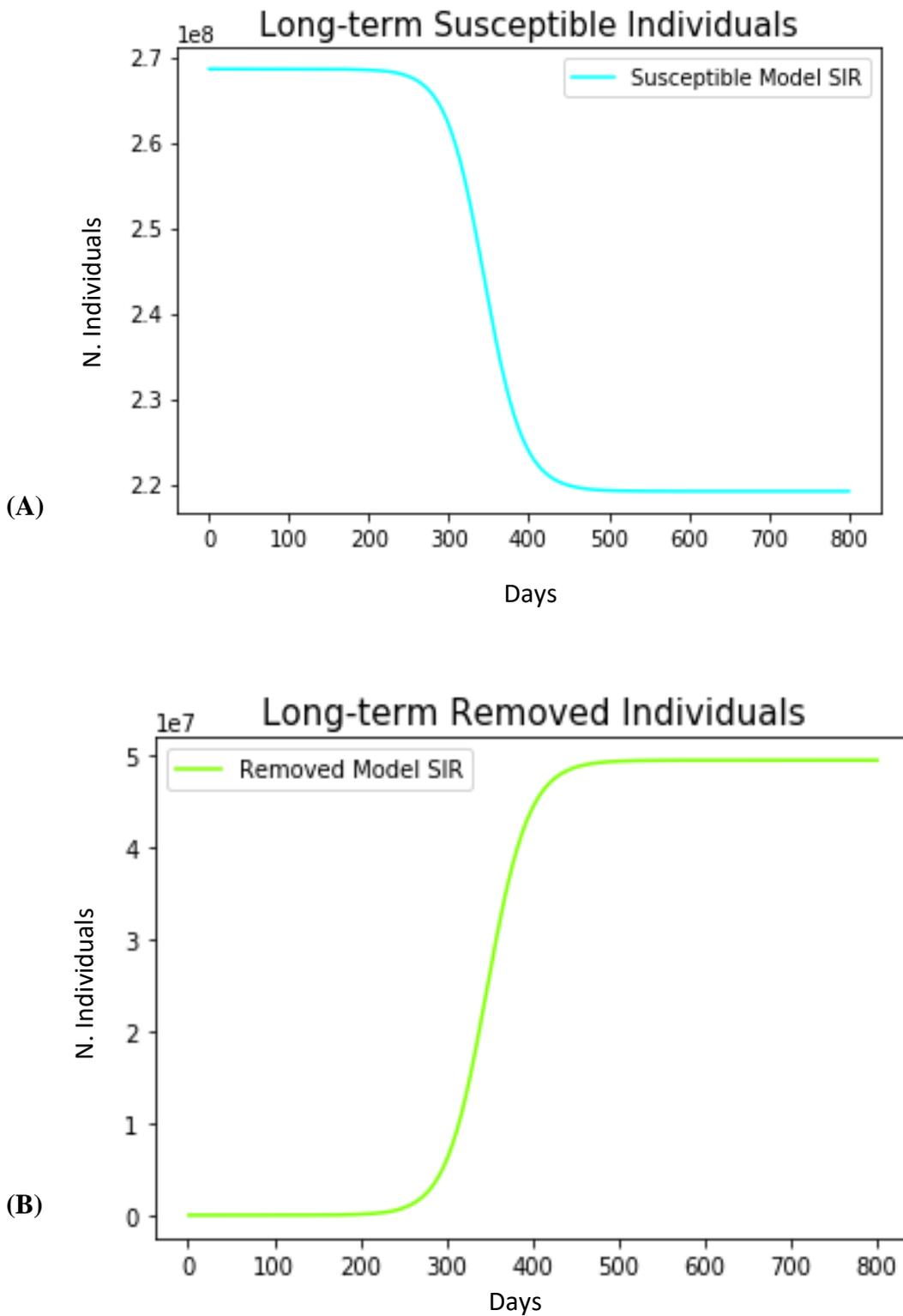


Figure 6. Long-term simulation of susceptible (A) and removed (B) individuals

#### 4. CONCLUSION

In this paper, a study of COVID-19 spread in Indonesia are done using SIR epidemiological model. Several assumptions are made in constructing the model. Least square method is used to estimate the parameters involved in SIR ODEs system. Other parameters are set based on the given data. Result shows that if there is no vaccination applied, COVID-19 is predicted to be exists in Indonesia for 1.9 years from the first emerged case. In other words, it is predicted that COVID-19 will exists until mid January 2022 if there is no vaccination applied.

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