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Lyapunov Stability Analysis and Simulation of SIR Modelling for COVID-19 Dynamics in Indonesia

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Abstract. The COVID-19 outbreak began to spread in the world in early 2020 and in Indonesia it began to occur in March 2020. The ability to predict potential transmission of COVID-19 will help the government and health workers to prevent and reduce transmission of COVID -19 and as a simulation of the global trend of this pandemic. One of the models that can be used to model epidemiology is SIR modeling. SIR modeling divides the population into three classes, namely Suspect, Infected, and Recovered. By doing a simulation using virus spread parameters such as contact rate, recovery rate can be known how the spread of the virus will occur. In the estimation, you will also get a reproduction number. Reproduction Number (R_0) is the number of people who can be infected or contracted a disease caused by 1 person who has had the disease. If the value of $R_0 > 1$ then each infected individual can infect more than one other individual. If the value of $R_0 < 1$ then an infected individual infects less than one other individual. By constructing the lyapunov function for the SIR model, the disease-free equilibrium state of the model will be found.

Keywords: *COVID-19; SIR model; reproduction number; lyapunov.*

1 Introduction

In December 2019, a mysterious case of pneumonia first appeared in Wuhan, Hubei Province, China. From 18 December to 29 December 2019, it was reported that five patients were treated with Acute Respiratory Distress Syndrome (ARDS). In less than a month, this disease has spread in various other provinces in China, even to other countries such as Thailand, Japan, and South Korea. According to Hui, *et.al* in [1]. The samples studied showed the etiology of the novel coronavirus. Initially, this disease was temporarily named as 2019 novel coronavirus (2019-nCoV), then WHO announced a new name on February 11, 2020, namely Coronavirus Disease (COVID-19) caused by the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-CoV-2). The virus can be

passed from person to person and has spread widely in China and more than 190 other countries and territories.

COVID-19 was first reported in Indonesia on March 2, 2020 with 2 initial cases detected. This virus mainly infects animals, including bats and camels. But currently COVID-19 is spreading through human to human being the main transmission so that the spread of this virus is becoming aggressive. Transmission of the virus occurs from symptomatic patients through droplets that come out when the patient coughs and sneezes. The virus can also be transmitted by touching the hands or face of an infected person, as well as touching the eyes, nose, or mouth after handling items that have been splashed by the saliva of an infected person. Symptoms experienced by patients infected with COVID-19 are divided into 2, namely mild and severe symptoms. For mild symptoms such as headache, cough, sore throat, runny nose, fever, feeling unwell. Then the symptoms can turn into severe symptoms, such as fever which may be quite high if the patient has pneumonia, cough with mucus, shortness of breath, chest pain or shortness of breath and cough, Susilo, *et al*. in [2]

The case of the COVID-19 pandemic that has spread throughout the world has become a topic that is widely discussed by researchers. Researchers do a lot of modeling to be able to find out how COVID-19 will spread in the future. As in the case of the spread of the virus that has happened before, the spread of the COVID-19 virus can be modeled using mathematical models. The model that is commonly used to model cases like this is the SIR model. As done by Kermack and McKendrik in [3]. This model divides the population into several compartment classes.

2 Literature Review

2.1 SIR Model

The SIR model is a mathematical modeling method to model a pandemic case, one of which is COVID-19. In the SIR modeling the population is grouped into 3 classes, namely, Susceptible (S), Infectious (I) and Recovered (R). The susceptible class (S) is an individual who is healthy but has the opportunity and is susceptible to contracting the disease. Infectious (I) class or infected are individuals who are tested positive for infection and have the potential to infect susceptible classes, and Recovered (R) are individuals who are declared cured or died and are assumed to have immunity to the virus so they cannot be infected again. In the Infected class, individuals can cause other individuals to become infected by Cooper, *et.al* in [4].

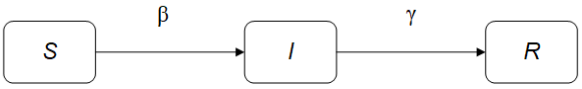

Figure 1 *SIR Model*

Figure 1 shows a flowchart of the dynamics of the SIR model. Furthermore, the SIR model can be expressed in equation (1).

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Figure 1 shows a flowchart of the dynamics of the SIR model. Furthermore, the SIR model can be expressed in equation (1). Where N is the total population and according to the existing assumption, namely the population is fixed, then S + I + R = 1. There are parameters β and also γ. Parameter β is the infection rate or it can also be called the contact rate. This parameter controls the speed of spread of the virus which is represented by the probability or probability of transmission from someone who has been infected to someone who is still susceptible or suspected of being in contact with each other. The parameter γ is the healing rate or it can also be called the recovery rate. The parameter γ can also be reversed to 1/γ which is the period of virus infection. The presence of a negative sign on *dS* indicates the change in people who have not been infected with the virus to become infected is always negative. This means the number of healthy people will continue to decrease. From this reduction in the value of healthy people to the addition of the number of people in the equation *dI* who will become sick people and the changes are proportional. The negative sign contained in the *dI* equation indicates the rate of change of a person who was initially infected to recover or die will also always be negative which means that it continues to decrease. This reduction in the number of people will be accommodated in the *dR*, which means the number of people who have recovered from the disease or who died.

2.2 Reproduction Number (R_0)

Reproduction Number (R_0) is the number of people who can be infected or contracted a disease caused by 1 person who has had the disease. This parameter indicates how contagious a disease is. Diseases that have been transmitted to people can be transmitted to other people and then the disease will reproduce

itself. For example, if a disease with a value (R_0) of 3 means that naturally people who have been infected with the disease can transmit the disease to 3 other people.

Reproduction Number (R_0) is mathematically also included in the concept of compartmental modeling as in the SIR model. The calculation of (R_0) is obtained from the infection period and also the contact rate. Assuming the total population (N) is 1 and each person is divided into three classes of SIR compartments, the R_0 equation can be written as in equation (2).

$$R_0 = \beta\gamma^{-1} \quad (2)$$

The value of R_0 is obtained by dividing the level of contact by the period of infection. There are three possibilities for the reproduction number R_0 value.

- If the value of R_0 > 1 then each infected individual can infect more than one other individual. Thus, the epidemic can spread throughout the population.
- If the value of R_0 < 1 then an infected individual infects less than one other individual. Therefore, there is no risk of an epidemic.
- If the value of R_0 = 1 then an infected individual can infect, on average only one other individual. The disease will persist with a steady spread but will not result in an epidemic/pandemic.

2.3 Related Search

The following are some of the studies that also serve as references in this section.

a). The outbreak of COVID-19: An overview by Yi-Chi, *et.al* in [5]

In this research describes the current COVID-19 virus. Also described this type of virus. How the spread of this virus and how much mortality rate can be generated by this virus.

b). Mathematical analysis of COVID-19 by using SIR model with convex incidence rate by [6]

In this study, modeling COVID-19 with the SIR model, then carried out a stability analysis, "the disease-free and endemic equilibrium" Also, the basic reproduction number R0 is derived for the model. Furthermore, the Global Stability is calculated using the Lyapunov Function construction, while the Local Stability is determined using the Jacobian matrix.

3 Exploratory Data Analysis

The data set used was taken from the COVID-19 Data Hub [7]. This data includes all data on COVID-19 in the world. From the data hub, the data used in this study is the COVID-19 Data Repository by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU) [8]. In this JHU dataset, it includes all COVID-19 data in the world. Table 1 shows the detailed features of the JHU dataset.

Table 1 Detailed features of JHU dataset

No	Feature	Feature type
1	*ObservationDate*	Numerical
2	*Confirmed*	Numerical
3	*Infected*	Numerical
4	*Fatal*	Numerical
5	*Recovered*	Numerical
6	*Susceptible*	Numerical
7	*ISO3*	Categorical
8	*Country/Region*	Categorical
9	*Province/State*	Categorical

In Exploratory Data Analysis, the data from JHU will produce data on the dynamics of COVID-19 in Indonesia and dynamics in neighboring countries such as in Southeast Asia and the Australia Region as shown in figures 2 and 3.

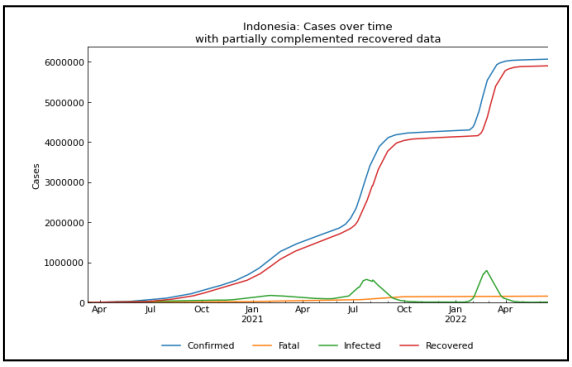

Figure 2 Spread of COVID-19 in Indonesia

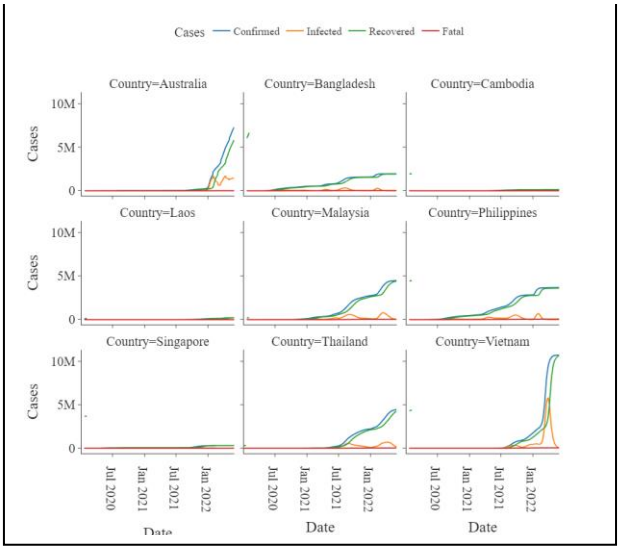

Figure 3 Spread of COVID-19 in nearby country in Southeast Asia and Australia

4 Modelling and Analysis

The modeling carried out will use the SIR model for cases of the spread of COVID-19 in Indonesia until May 31, 2022. The first step is to detect the phase that has been passed so far in Indonesia. Then proceed with the estimation of virus spread parameters for each phase obtained. The distribution parameters include (contact rate, recovery rate and reproduction number). Furthermore, an evaluation of the estimated data with real data is carried out. Then a simulation for the spread of COVID-19 was also carried out with the developed model. Finally, Lyapunov's analysis was carried out on the data results.

In this SIR modeling using python programming with the Covsirphy library in [9]. This library makes it easier for researchers to find out the analysis for COVID-19 in Indonesia and the scenarios created.

4.1 Analisis Trend

S-R trend analysis is used to determine the phases formed during the COVID-19 pandemic. This is used to identify the phases formed during the spread of COVID-19 in Indonesia. Susceptible S and Recovered R show the relationship between the derivatives of the SIR model as follows.

$$\log S_{(R)} = -aR + \log N$$

Where N is the total population, $a = \frac{\beta}{N\gamma}$ is a constant, Balkew in [10]

From equation (3) log S will decrease constantly when there is an increase in R, when the records follow an SIR-derived model, and the parameter values of the model are constant. With logarithmic y-axis scale, plot of (x,y) = (R,S) shows a line. This property is used to determine the phase. A new phase is determined from the change in the slope of the line. S-R slope analysis is performed using Rupture: change point detection in Python [11].

Figure 4 depicts the trend for Susceptible and Recovered until May 30, 2022.

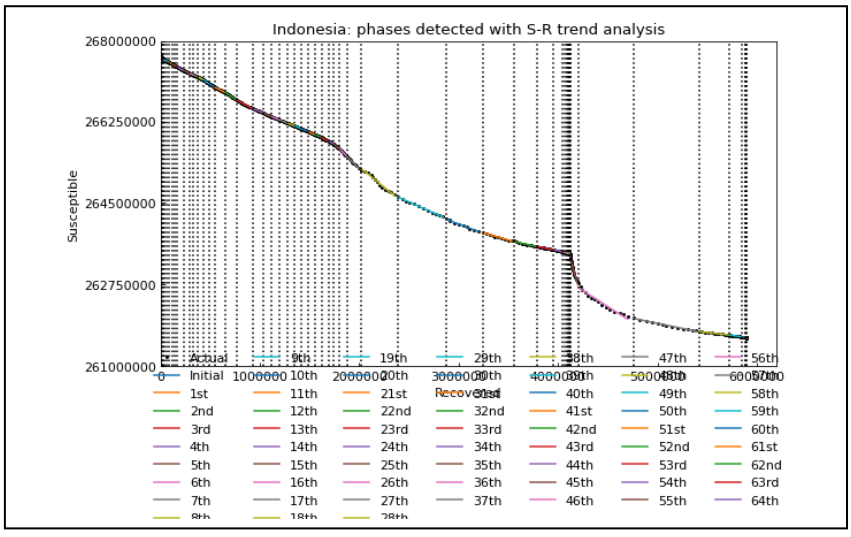

Figure 4 Disease Trend Analysis as of May 31, 2022

From Figure 4 it can be observed that the Susceptible – Recovered trend for COVID-19 in Indonesia consists of 64 phases until May 30, 2022. The phases will change quickly when there is a significant change in Covid cases.

4.2 Parameter Estimation

In making estimates for the SIR model, the parameters that have been obtained in the previous phase determination are used. Parameters estimated in this study include contact rate β, recovery rate γ. In Optuna using metod which is a Hyperparameter Optimization Framework written in Python language. Optuna uses TPA + CMA – ES mixed method (tree-structured Parzen estimators + Covariance matrix adaptation evolution strategy) to find the best estimation of the parameters [12].

In the SIR model, there are 3 estimation parameters, namely contact rate β, recovery rate γ and reproduction number R_0. In Figure 5, it can be observed that the estimated values for the contact rate β, recovery rate γ and reproduction number R_0 parameters up to May 31, 2022.

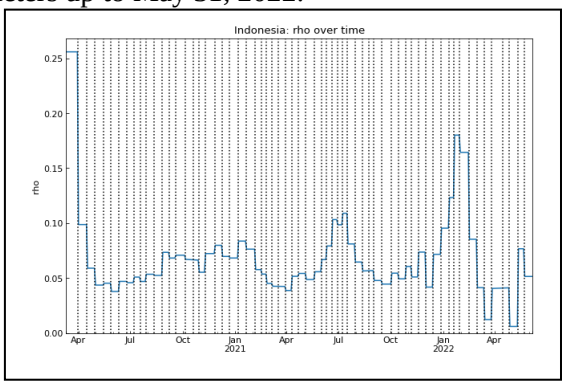

Figure 5 Contact rate COVID-19 in Indonesia

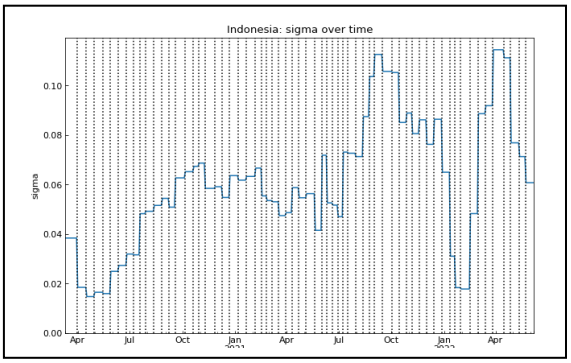

Figure 6 Recovery rate COVID-19 in Indonesia

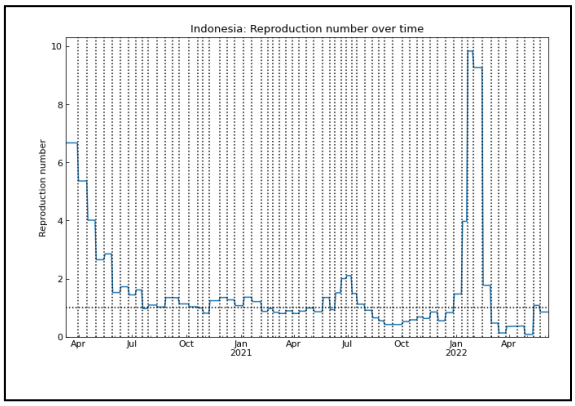

Figure 7 Reproduction number COVID-19 in Indonesia

4.3 Model Evaluation

From the estimation results obtained, it is necessary to evaluate the data results by comparing them with the actual data available. This evaluation is carried out on the following matrices including MAE, MSE, MSLE, RMSE, RMSLE, and MAPE. In Figure 8, it can be seen that the comparison of the estimation results to the actual data from the infected cases.

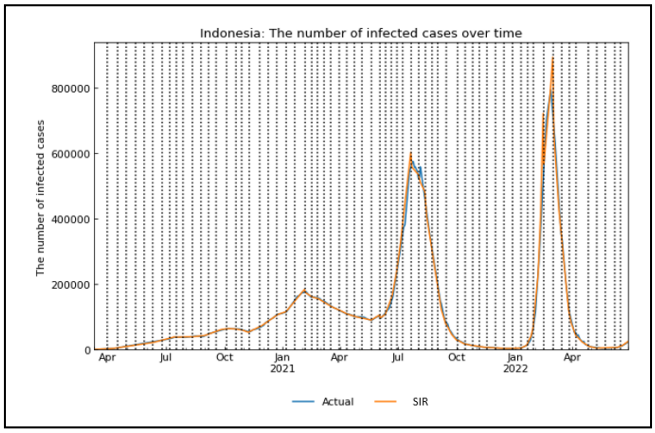

Figure 8 Number of Infected cases in Indonesia

From table 2, an error matrix is obtained for cases of the spread of COVID-19 in Indonesia. The value of each matrix obtained can be said to be quite small, this indicates that the estimation results compared to the actual data are quite close.

Table 2 SIR model evaluation for COVID-19 in Indonesia

Metrics	SIR
MAE	51851.520
MSE	6646987632.895
MSLE	36.175
RMSE	71302.102
RMSLE	6.014
MAPE	0.394

4.4 Simulation pandemic with SIR model

The simulation for the pandemic in Indonesia has several limitations, including:

- Scenario simulation using the SIR model to predict cases of the spread of COVID-19 in Indonesia
- The parameters used for the last simulation use the parameters from the last phase.
- The simulation is carried out with a time span of 30 days after May 30, 2022. It is necessary to limit the time range due to changes in parameters within a certain time so that it cannot be carried out with a long time span.

The simulation results as shown in Figure 8 are known after 30 days of infected cases, there will be 19540 cases.

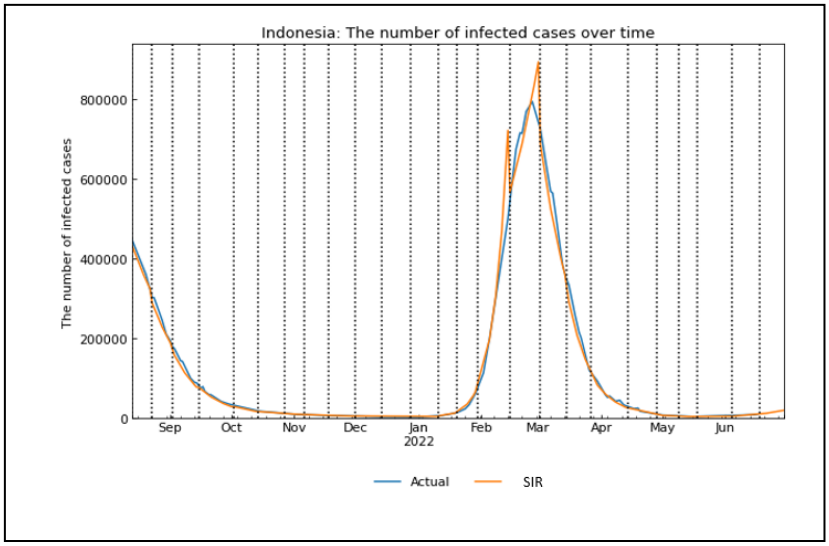

Figure 9 Simulation result with SIR model

4.5 Lyapunov Analysis

The classic SIR model assumes the individuals recover with immunity. We can define $x_1 = S/N$, $x_2 = I/N$, and $x_3 = R/N$, we can rewrite the SIR model into the form such as equations (5)

$$\begin{bmatrix} \dot{x}_1 \\ \dot{x}_2 \\ \dot{x}_3 \end{bmatrix} = \begin{bmatrix} -\beta x_1 x_2 \\ \beta x_1 x_2 - \gamma x_2 \\ \gamma x_2 \end{bmatrix} \quad (5)$$

with $0 \leq x_1 \leq 1$, $0 \leq x_2 \leq 1$, $0 \leq x_3 \leq 1$, and $x_1 + x_2 + x_3 = 1$.

Since the first two equations do not depend on the third equation (constant population size), it is possible to focus on the first two equations as mentioned by Gui and Yong in [13] so the equation is simplified to

$$\begin{bmatrix} \dot{x}_1 \\ \dot{x}_2 \end{bmatrix} = \begin{bmatrix} -\beta x_1 x_2 \\ \beta x_1 x_2 - \gamma x_2 \end{bmatrix} \quad (6)$$

and the closed set $\Gamma = \{(x_1,\ x_2) \in \Re_+^2 : x_1 + x_2 \leq 1\}$

Equilibria are points where the states do not change with time, i.e.,

$$\begin{bmatrix} -\beta x_1 x_2 \\ \beta x_1 x_2 - \gamma x_2 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix} \quad (7)$$

The epidemiological interpretation requires the solution of equations. (5) with an initial value of $x_1 = 1$, that is, all individuals are free of disease (healthy). This state is an equilibrium point, $E_0 \Leftrightarrow [x_1 = 1,\ x_2 = 0]$, usually named as disease free equilibrium point. Furthermore we show that the system have a continuum of equilibria which are solutions $(x_{1\infty},\ x_{2\infty})$ of $x_{1\infty} x_{2\infty} = 0$, $x_{2\infty}(\beta x_{1\infty} - \gamma) = 0$, where $x_{1\infty} = \lim_{t\to\infty} x_1(t)$ and $x_{2\infty} = \lim_{t\to\infty} x_2(t)$. There is a continuum of equilibria $(x_{1\infty},\ 0)$ with arbitrary $x_{1\infty}$, $0 \leq x_{1\infty} \leq 1$, or in other word, the equilibria are non-isolated, Fraser, *et.al* in [14]

Theorem : The disease free equilibrium point, E_0, is stable if $\Re_0 < 1$.

Proof : If $\Re_0 < 1$ the dominant eigenvalue is 0, so we conclude that the linearization method is inconclusive. To prove the stability of E_0, when $\Re_0 < 1$, we can define $\xi_1 = x_1 + 1$, such that the function (6) can be translated as shown in (8)

$$\begin{bmatrix} \dot{\xi}_1 \\ \dot{\xi}_2 \end{bmatrix} = \begin{bmatrix} -\beta(\xi_1 + 1)\xi_2 \\ \beta(\xi_1 + 1)\xi_2 - \gamma\xi_2 \end{bmatrix} \tag{8}$$

We consider candidate for the Lyapunov function such as:

$$V(\xi_1,\ \xi_2) = \frac{1}{2}(\xi_1 + 1 + \xi_2)^2 + \frac{1}{2}\xi_2^2 - \frac{1}{2} \tag{9}$$

The function in (9) is a globally positive definite. Evaluating the time derivative of $V(\xi_1,\ \xi_2)$ along Eqs. (8), which is applied to the disease-free equilibrium point

$$\frac{dV}{dt} = (\xi_1 + 1 + \xi_2)\left(\frac{d\xi_1}{dt} + \frac{d\xi_2}{dt}\right) + \xi_2\frac{d\xi_2}{dt} \tag{10}$$

$$\frac{dV}{dt} = (\xi_1 + 1)\left(\xi_2 - \frac{\gamma}{\beta}\right)\beta\xi_2 - \gamma\xi_2 - \gamma\xi_2^2 \tag{11}$$

Since $0 \le \xi_1 \le 1$ and $0 \le \xi_2 \le 1$, the value of $\xi_2 - \frac{\gamma}{\beta} < 0$ when $\frac{1}{\Re_0} = \frac{\gamma}{\beta} > 1$, such that $\frac{dV}{dt} < 0$. It is shown that $\frac{dV}{dt}(\xi = 0) = 0$, this implies that $\frac{dV}{dt}(\xi)$ in (11) is a negative definite. Therefore, by Mahayana, et.al in [15], we may conclude that the disease-free equilibrium point E_0 is stable when $\Re_0 < 1$.

5 Conclusion

The conclusions obtained from this research are.

a) The SIR epidemiological model is a machine learning concept that can be used for simulation and analysis of cases of the spread of COVID-19 in Indonesia. Modeling is done by dividing the time of the pandemic in Indonesia into several phases with each spreading parameter. These parameters are contact rate, recovery rate and reproduction number.

b) From the estimation results with MAPE value 0.394, it is found that the evaluation value is good compared to the actual data, this shows that the estimation are close to the actual data.

c) Lyapunov's analysis also shows that when the reproduction number value is less than 1 ($R_0 < 1$) it is said that the disease-free equilibrium point is stable.

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