BAREKENG: Journal of Mathematics and Its Applications
September 2023 Volume 17 Issue 3 Page 1325–1340
P-ISSN: 1978-7227 E-ISSN: 2615-3017
https://doi.org/10.30598/barekengvol17iss3pp1325-1340

THE DEVELOPMENT OF COVID-19 USING OUTBREAK THE SUSCEPTIBLE, INFECTED AND RECOVERED (*SIR*) MODEL WITH VACCINATION

Dorrah Azis [1*], La Zakaria[2], Tiryono Ruby[3], Muhammad Is'ad Arifaldi[4]

[1,2,3,4]*Mathematics Department, Faculty of Mathematic and Natural Sciences, University of Lampung*
Sumantri Brojonegoro Street, Bandar Lampung, 35141, Indonesia

*Corresponding author's e-mail: * **dorrah.azis@fmipa.unila.ac.id***

Article History:

Received: 06th January 2023
Revised: 9th July 2023
Accepted: 19th July 2023

Keywords:

SIR model;
COVID-19;
Basic reproduction number;
Routh-Hurwitz Criterion

ABSTRACT

The COVID-19 pandemic in 2020 has caused severe problems in Indonesia. The COVID-19 virus epidemic can be modeled using the Susceptible, Infected, and Recovered (SIR) model. This modeling aims to look at the dynamics of COVID-19 to predict when disease-free and endemic disease occurs and to find the basic reproduction number (R_0) for policy making in suppressing the spread of COVID-19. In this article, we describe and solve a research result on the SIR model with an assumption. The assumption in the model is that there is vaccination for the population. There are live stages of research conducted. The first is creating the SIR model and determining the equilibrium points on disease-free and disease-endemic. The Second is getting the basic reproduction number. The third is determining the stability around the equilibrium points using the Routh-Hurwitz criteria. Fourth, create a diagram for the subpopulations state at a specific time using Wolfram Mathematica software. As an implementation of the model created, COVID-19 data at the Batanghari Community Health Center Inpatient UPTD was used. Finally, determine the model error percentage with MAPE. The SIR COVID-19 model was made using eight parameters, namely $N, \alpha, \beta, \tau, \mu, \sigma, \delta, \gamma$, which are all positive. The results showed that the disease-free and disease-endemic equilibrium points were locally asymptotically stable after being analyzed using the Routh-Hurwitz stability criteria. The model trial using data from UPTD Puskesmas Batanghari obtained a stable condition for up to 100 months with a MAPE of 2.8%. From this study, obtained an $R_0 = \frac{\beta\sigma}{\alpha+\mu}$. This means that if you want to reduce the rate of spread, then reduce the number of people who are easily infected (σ) and reduce contacts (β), and increase the healing rate (α).

How to cite this article:
D. Azis, L. Zakaria, T. Ruby and M. I. Arifaldi, "THE DEVELOPMENT OF COVID-19 USING OUTBREAK THE SUSCEPTIBLE, INFECTED, AND RECOVERED (*SIR*) MODEL WITH VACCINATION," *BAREKENG: J. Math. &App.*, vol. 17, iss. 3, pp. 1325-1340, September, 2023.

Journal homepage: *https://ojs3.unpatti.ac.id/index.php/barekeng/*
Journal e-mail: *barekeng.math@yahoo.com; barekeng.journal@mail.unpatti.ac.id*
Research Article • Open Access

1. INTRODUCTION

Mathematical models have played an essential role in explaining the dynamics of the disease. A mathematical model categorizes individuals into Susceptible, Infectious, and Recovered. In several very recent research applied to the COVID-19 epidemic, researchers have developed and used SIR and SEIR-based models with vaccination to overcome the limitations of the conventional SIR model. Mathematical modeling specifically constructed to determine the development of disease outbreaks caused by COVID-19 has not been widely carried out [1]–[9].

Handling the COVID-19 outbreak in Lampung Province involves various groups/communities of society, including academics. Even for Lampung province, dynamic models have not yet been found to solve the problem of the COVID-19 outbreak in terms of the theory of the SIR model, which involves vaccination parameters. The research that has been carried out is to construct the SIR model to determine the development of the COVID-19 outbreak in Lampung Province, especially East Lampung Regency, by involving the parameters of vaccine administration to the community. Using data at the UPTD Puskesmas Batanghari District, East Lampung Regency, the SIR model obtained was implemented to determine the trend of the growth of the COVID-19 outbreak in that place after the people were given the vaccine.

In March 2020, WHO announced that the world was facing a pandemic called Corona Virus Infectious Disease 2019 or COVID-19 [10]. Until October 2020, the number of positive cases of. COVID-19 worldwide has reached 37 million, with deaths reaching 1 million people [11]. The main medium of transmission of the SARS-Cov-2 virus is droplets that can be easily spread when humans interact directly with a certain distance. At the beginning of its spread, the average transmission power of the virus was still quite low, around 2.2 [12]. However, in its development, the SARS-Cov-2 virus underwent mutations so that several new virus variants emerged with higher transmission capabilities, such as in England, South Africa, Brazil, and India [13]. The COVID-19 pandemic is developing so fast that many countries are not ready to adapt since the beginning. WHO has advised focusing the handling of the pandemic on the health aspect by implementing regional isolation and banning activities that involve crowds. However, for some countries, this is not done because they doubt that the COVID-19 pandemic will last quite a long time [14]. One of the other efforts to deal with the spread of COVID-19 is by implementing mass vaccination. For years, vaccines have been proven to reduce the incidence of infectious diseases through the mechanism of the human body's immunity [15]. The COVID-19 vaccine was developed to help the formation of individual body immunity so that the administration of the COVID-19 vaccine is expected to accelerate the formation of group immunity (herd immunity), which will have an impact on reducing the number of infected cases [16]. The vaccination policy has an impact on reducing the number of COVID-19 cases that are still not under control in Indonesia [17]. This is reinforced by [18] which concluded that the severity of disease in individuals who had received the vaccine decreased, so it can be supposed that the vaccine effectively protects individuals from the SARS-CoV-2 variant.

A disease can be modeled mathematically into an epidemiological model. One of the many types of modeling available is the SIR model. The *SIR* model was first introduced in 1927 by Kermack and McKendrick [19]. The SIR model determines the behavior of a pandemic and prediction [20]. This *SIR* model groups individuals in a population into three subpopulations, namely susceptible (groups of individuals who are susceptible to being infected with a disease), infected (groups of individuals infected with disease), recovered (groups of individuals who have recovered from the disease). SIR modeling is a model that is prepared with assumptions about a disease starting from the stage before being infected with a disease, being infected, and until the individual is cured. Mathematical models of infectious diseases based on the classical SIR model are widely used to study the spread of a disease. These models show exciting results, especially in the early period of the pandemic [1]–[4], [21]–[28].The results of this model can be used as an illustration of how to suppress the spread of disease by looking at the effect of vaccination, ideal number of individuals who must be vaccinated, and this model can predict within a certain time, the disease will become endemic. This requires field data to analyze the dynamics of the development of a disease. This modeling aims to determine the basic reproduction number (R_0), which plays a role in decision or policy-making for the authorities in dealing with problems caused by the COVID-19 virus. In addition, this modeling is also to find out whether this disease can disappear or will remain (endemic) in an area and predict when this disease will disappear or remain (endemic) in an area.

2. RESEARCH METHODS

This research is applied research conducted using secondary data obtained from the UPTD of the Batanghari District Inpatient Health Center related to cases of the spread of the COVID-19 disease that occurred throughout 2020-2021. The steps in this research are given in Figure 1:

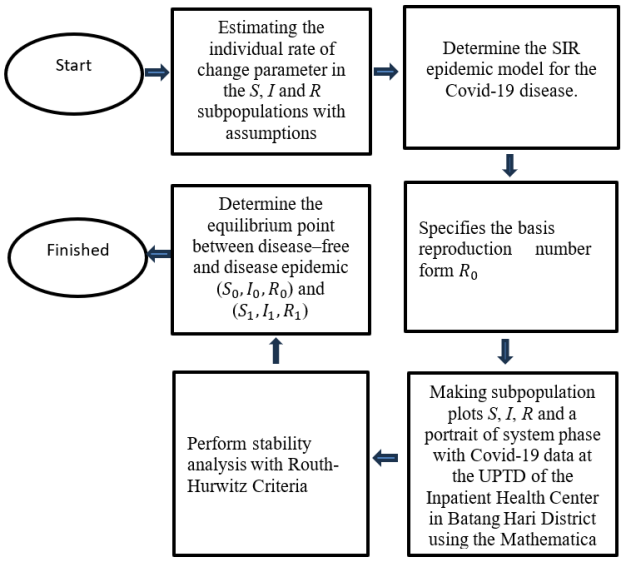

Figure 1. Steps of research diagram

2.1 *SIR* Model

The *SIR* model divides the population into susceptible (*S*), infected (*I*), and recovered (*R*) subpopulations. The number of susceptible, infected, and cured individuals at time t in a row can be written in the form of functions *S*(*t*), *I*(*t*), and *R*(*t*).

The *SIR* model can be used to predict how a disease spreads, the total number of infected, the duration of the epidemic, and estimate various epidemiological parameters such as the number of reproductions. This model can determine how different public health interventions can affect epidemic outcomes [29].

Figure 2. *SIR* model diagram

Information:

S = number of susceptible individuals in the population at the time
I = number of infected individuals in the population at the time
R = number of recovered individuals in the population at the time
α = healing rate from infected to recovered
r = rate of disease transmission from susceptible to infected

The SIR epidemic model is assumed as follows:

$$\frac{dS}{dt} = -rSI \quad (1)$$

$$\frac{dI}{dt} = rSI - \alpha I \quad (2)$$

$$\frac{dR}{dt} = \alpha I \quad (3)$$

2.2 Equilibrium Point

The equilibrium point is used to analyze the model. According to [19], the equilibrium point is the solution of the system of differential equations which is independent of time. In [30], Meyer said the same thing too, the equilibrium condition is a condition where the system does not change over time.

The equilibrium point is divided into 2, as follows:

1. The disease-free equilibrium point is the condition in which no individual is infected with the disease discussed in the population, so $I = 0$.

2. The endemic equilibrium point is a condition where there are infected individuals in the population, so the compartment at the endemic equilibrium point is $I \neq 0$.

Theorem Equilibrium Point [31]:

1. If all the real parts of the eigenvalues of the Jacobian matrix of a system of differential equations are negative, then the equilibrium point of the system is stable.
2. If one eigenvalue of the Jacobian matrix of a system of differential equations is positive, then the equilibrium point of the system is unstable.

2.3 Next Generation Matrix

Suppose there are n infected classes and m uninfected classes. Furthermore, suppose that x is an infected sub-population and y represents an uninfected (susceptible or cured) subpopulation, so that $\dot{x} = \varphi_i(x,y) - \omega_i(x,y)$, and $\dot{y} = g_j(x,y)$, where $i = 1,2,\dots,n$ and $j = 1,2,\dots,m$. $\varphi_i$is the rate of secondary infection in the infected class, and ω_i is the rate of disease progression, death, and recovery resulting in a reduced population of the infected class [32].

Next, Diekmann explain the next generation matrix $\boldsymbol{K}$ is defined, which has the form

$$\boldsymbol{K} = \boldsymbol{F}\boldsymbol{V}^{-1} \tag{4}$$

where $\boldsymbol{F}$ and $\boldsymbol{V}$ are matrix of size $n \times n$, which can also be written as follows:

$$\boldsymbol{F} = \left[\frac{\partial \varphi_i}{\partial y_j}\right] \text{ and } \boldsymbol{V} = \left[\frac{\partial \omega_i}{\partial y_j}\right] \tag{5}$$

2.4 Basic Reproduction Number $(\boldsymbol{R_0})$

The basic reproduction number R_0 can be defined as the average number of infected individuals infected by other infected individuals in a population. A basic reproductive number is a number that shows the number of susceptible individuals who can suffer from diseases caused by one infected individual [33]. According [32], the basic reproduction number, which can be formulated as follows

$$R_0 = \rho(\boldsymbol{K}) = \rho\left(\boldsymbol{F}\boldsymbol{V}^{-1}\right) \tag{6}$$

The same thing regarding the basic reproduction number is denoted by R_0 and is expressed by the following equation [34]:

$$R_0 = \frac{factors\ that\ cause\ disease}{factors\ that\ reduce\ disease} \tag{7}$$

Some of the conditions that will arise, namely:

If $R_0 < 1$, then on average an infected individual produces less than one new infected individual over the course of its infectious period, and the infection cannot grow. The disease will disappear [35].

If $R_0 = 1$, then the disease will persist [34].

If $R_0 > 1$, the each infected individual produces, on average, more than one new infection, and the disease can invade the population. The disease will become an epidemic [35].

2.5 Routh-Hurwitz Stability Criterion

The Routh-Hurwitz stability criterion is used to show a system's stability by taking into account the coefficients of the characteristic equation without calculating the roots directly. If a polynomial equation is a characteristic equation, then this method can determine a system's stability. Thus, the procedures in the Routh-Hurwitz criterion are [31]:

1. The n^{th} order polynomial equation is written in the form:

$$\det(\lambda I - A) = a_n\lambda^n + a_{n-1}\lambda^{n-1} + \cdots + a_1\lambda + a_0 \tag{8}$$

where the coefficients are real numbers and $a_n \neq 0$.

2. If there is a coefficient of 0 or negative, then there is one root or imaginary roots or has a positive real part which means the system is unstable.
3. If all coefficients are positive, then a matrix which is often called a Routh array, can be formed as follows

$$\begin{vmatrix} \lambda^n & a_n & a_{n-2} & a_{n-4} & \cdots \\ \lambda^{n-1} & a_{n-1} & a_{n-3} & a_{n-5} & \cdots \\ \lambda^{n-2} & b_1 & b_2 & b_3 & \cdots \\ \vdots & c_1 & c_2 & c_3 & \cdots \\ \lambda^0 & \vdots & \vdots & \vdots & \ddots \end{vmatrix} \tag{9}$$

The coefficients $b_1, b_2, \ldots, b_k$ and $c_1, c_2, \ldots, c_k$ can be determined by the following formulas:

$$b_1 = -\frac{1}{a_{n-1}}\begin{vmatrix} a_n & a_{n-2} \\ a_{n-1} & a_{n-3} \end{vmatrix},\ b_2 = -\frac{1}{a_{n-3}}\begin{vmatrix} a_{n-2} & a_{n-4} \\ a_{n-3} & a_{n-5} \end{vmatrix},\ldots$$

$$c_1 = -\frac{1}{b_1}\begin{vmatrix} a_{n-1} & a_{n-3} \\ b_1 & b_2 \end{vmatrix},\ c_2 = -\frac{1}{b_2}\begin{vmatrix} a_{n-3} & a_{n-5} \\ b_2 & b_3 \end{vmatrix},\ldots$$

The scheme is continued until only zeroes appear (both to the right and down wards) [36].

4. The number of unstable roots can be seen in the number of sign changes in the first matrix column (6).
5. The necessary condition for the system to be said to be stable is if the coefficient of the characteristic equation is positive, while the sufficient condition is that each term of the first column of the matrix (6) is positive.

2.6 Mean Absolute Percentage Error (MAPE)

Mean Absolute Percentage Error is a method of finding the average absolute error value in the form of a percentage in a comparison between actual data and existing projection or forecasting data. MAPE is formulated as follows:

$$MAPE = \sum \frac{|A - P|}{n} \times 100\% \tag{10}$$

With
A: Actual data,
P: Forecasting data,
n: Total data.
The percentage of MAPE is divided into four interpretation as follows [37]:

Table 1. MAPE Interpretation

Interpretation of Typical MAPE Value's	
MAPE	**Interpretation**
< 10	Highly Accurate Forecasting
$10 - 20$	Good Forecasting
$20 - 50$	Reasonable Forecasting
> 50	Inaccurate Forecasting

3. RESULTS AND DISCUSSION

3.1 *SIR* Model

The assumptions in the *SIR* model for the COVID-19 disease are as follows:

1. Factors of birth and death are considered. Individuals born into the Susceptible (S) class because the individual is assumed to be healthy but susceptible to COVID-19 disease.
2. The population birth and death rates in each compartment are assumed to be the same so that the total population is constant
3. Migration occurs in the population. No immigrants enter every S, I, and R class.
4. COVID-19 disease can cause death (fatal).
5. Vaccinated individuals fall into class S. Vaccination efficacy is assumed as a percentage. WHO explained that the performance of vaccines could be seen from three measurements, namely through the efficacy, effectiveness, and impact of the vaccine. One type of COVID-19 vaccine is Sinovac. The efficacy of the Sinovac vaccine reaches 65.3% [38].
6. COVID-19 disease can result in re-infection of individuals who have been infected before. However, some individuals have recovered and formed antibodies to the COVID-19 virus.

Based on the assumptions that have been made, the model parameters can be defined as follows:

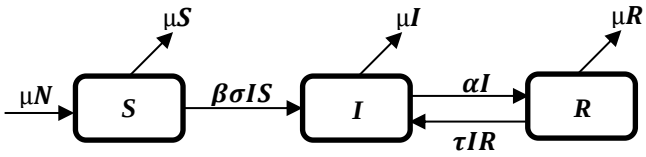

Figure 3. SIR model of COVID-19 disease with vaccination

Information:

N : Total number of individuals in the population (%)

μ : Expresses the birth rate in the S compartment and the death rate in each compartment (%)

β : Expresses the infection rate in compartment S (%)

α : Expresses the healing rate in compartment I (%)

σ: Stating the total number of susceptible individuals (total individuals who are not vaccinated and already vaccinated but infected) (%)

τ: Expresses the rate of reinfection in compartment R (%)

with

$$\sigma = 1 - \delta\gamma \tag{11}$$

δ : Vaccine efficiency (%)

γ : Number of individuals who have been vaccinated (%)

Since the birth rate is considered equal to the number of deaths, the total population will be constant, so $S + I + R = 1$. If the number of births is not equal to the number of deaths, then N is not constant, but the

value is not far from 1 or very close. However, birth and death rates are equated with making this model easy to analyze.

Then the mathematical model of the spread of the COVID-19 disease with vaccination was obtained in the form of a system of differential equations as follows:

$$\frac{dS}{dt} = \mu - \beta\sigma IS - \mu S \tag{12}$$

$$\frac{dI}{dt} = \beta\sigma IS + \tau IR - \alpha I - \mu I \tag{13}$$

$$\frac{dR}{dt} = \alpha I - \mu R - \tau IR \tag{14}$$

where $S(0) > 0, I(0) \geq 0, R(0) > 0;$
$\mu, \beta, \sigma, \delta, \gamma, \tau, \alpha > 0.$

3.2 Equilibrium Point

The equilibrium condition is a condition where the system does not change over time [30].

3.2.1 Disease-Free Equilibrium Point

Disease-free population means that in the population, no one is sick, $I = 0$. This means that no individual has been exposed to COVID-19 or no individual has been infected with COVID-19. Because no individual has been exposed to COVID-19, the transmission rate $(\beta)$and the infected group $(I)$is worth 0.

From the Equation (12), substitute each equation containing the variables $\beta$and I with a value of 0, it is obtained:

$$\begin{aligned} \mu - (0)\sigma(0)S_0 - \mu S_0 &= 0 \\ \mu - \mu S_0 &= 0 \\ -\mu S_0 &= -\mu \\ S_0 &= 1 \end{aligned} \tag{15}$$

Substituting the value $I_0 = 0$ into Equation (14), obtained:

$$\begin{aligned} \alpha(0) - \mu R_0 - \tau(0)R_0 &= 0 \\ -\mu R_0 &= 0 \\ R_0 &= 0 \end{aligned} \tag{16}$$

Then the disease-free equilibrium point is obtained as follows:

$$(S_0, I_0, R_0) = (1,0,0) \tag{17}$$

3.2.2. Disease Endemic Equilibrium Point

Endemic disease means that in the population, there are always individuals who are infected with the disease, meaning that there are individuals who are prone to be exposed to COVID-19, and there are individuals who are infected with COVID-19. Because there are individuals who are exposed to COVID-19, the transmission rate (β) and the infected group (I) are worth $\beta > 0, I \neq 0$. Let (S^*, I^*, R^*) be an endemic equilibrium point. From the Equation (12) for $\sigma > 0$ and $\mu > 0$, we can rewrite the equation as:

$$S^* = \frac{\mu}{I^* \beta\sigma + \mu} \tag{18}$$

Substituting Equation (18) into Equation (13), and then solving it for I^*, we have:

$$I^* = \frac{1}{2}\left(-\frac{\mu(\alpha - \beta\sigma + \mu)}{\beta\sigma(\alpha + \mu)} + \sqrt{\frac{\mu(4\, R^* \beta\sigma\tau(\alpha + \mu) + \mu(\alpha - \beta\sigma + \mu)^2)}{\beta^2\sigma^2(\alpha + \mu)^2}} \right) \tag{19}$$

Substituting Equation (19) into Equation (14), and then solving it for R^*, we have:

$$R^* = a - b \tag{20}$$

Where:

$$a = \frac{1}{2\tau^3}(\beta\sigma\tau\mu + \beta\sigma\mu^2 - \tau\mu^2 + \alpha(2\tau^2 + \beta\sigma\mu - \tau\mu)$$

$$b = \tau^3 \sqrt{\frac{\left(\alpha^2(2\beta\sigma\tau(2\tau-\mu)+\beta^2\sigma^2\mu+\tau^2\mu)+\mu(\tau\mu-\beta\sigma(\tau+\mu))^2+2\alpha\mu(\beta\sigma\tau(\tau-2\mu)+\tau^2\mu+\beta^2\sigma^2(\tau+\mu))\right)}{(\tau^6\mu)}}$$

By selecting and setting parameter values that satisfy $\sigma > 0 \wedge \mu > 0 \wedge \left(\left(\alpha \geq \mu \wedge \left(\left(\beta = \frac{\alpha+\mu}{\sigma} \wedge \tau > 0\right) \vee \left(\tau > \frac{\mu(\alpha-\beta\sigma+\mu)}{\alpha} \wedge 0 < \beta < \frac{\alpha+\mu}{\sigma}\right)\right)\right) \vee \left(0 < \alpha < \mu \wedge 0 < \beta \leq \frac{\alpha+\mu}{\sigma} \wedge \tau > \frac{\mu(\alpha-\beta\sigma+\mu)}{\alpha}\right)\right)$ and substituting them into **Equation (20)**, **Equation (19)** and **Equation (3)**, the equilibrium point () will be obtained. Finally, we have the COVID-19 endemic equilibrium point for is as follows:

$$(S, I, R) = (S^*, I^*, R^*) \tag{21}$$

3.3 Basic Reproduction Number

The first step is to form a Jacobian matrix of the compartments containing infected individuals, namely I and R as follows:

$$\boldsymbol{J}(I,R) = \begin{pmatrix} \frac{d(\beta\sigma IS + \tau IR - \mu I - \alpha I)}{dI} & \frac{d(\beta\sigma IS + \tau IR - \mu I - \alpha I)}{dR} \\ \frac{d(\alpha I - \tau IR - \mu R)}{dI} & \frac{d(\alpha I - \tau IR - \mu R)}{dR} \end{pmatrix}$$

$$\boldsymbol{J}(I,R) = \begin{pmatrix} \beta\sigma S + \tau R - \mu - \alpha & \tau I \\ \alpha - \tau R & -\tau I - \mu \end{pmatrix} \tag{22}$$

Next, substituting the disease-free equilibrium point (17) into the Jacobian matrix (22), we get:

$$\boldsymbol{J}(1,0,0) = \begin{pmatrix} \beta\sigma(1) + \tau(0) - \mu - \alpha & \tau(0) \\ \alpha - \tau(0) & -\tau(0) - \mu \end{pmatrix}$$

$$\boldsymbol{J}(1,0,0) = \begin{pmatrix} \beta\sigma - \mu - \alpha & 0 \\ \alpha & -\mu \end{pmatrix} \tag{23}$$

Since $\boldsymbol{J} = \boldsymbol{F} - \boldsymbol{V}$, by using manipulation, the Jacobian matrix (23) can be formed as follows:

$$\boldsymbol{J}(1,0,0) = \begin{pmatrix} \beta\sigma & 0 \\ \alpha & 0 \end{pmatrix} - \begin{pmatrix} \mu + \alpha & 0 \\ 0 & \mu \end{pmatrix}$$

$$\boldsymbol{F} = \begin{pmatrix} \beta\sigma & 0 \\ \alpha & 0 \end{pmatrix} \text{ and } \boldsymbol{V} = \begin{pmatrix} \mu + \alpha & 0 \\ 0 & \mu \end{pmatrix} \tag{24}$$

Next, looking for the inverse of the matrix $\boldsymbol{V}$, we get:

$$\boldsymbol{V}^{-1} = \frac{1}{\mu(\mu + \alpha)} \begin{pmatrix} \mu & 0 \\ 0 & \mu + \alpha \end{pmatrix}$$

$$\boldsymbol{V}^{-1} = \begin{pmatrix} \frac{1}{(\mu + \alpha)} & 0 \\ 0 & \frac{1}{\mu} \end{pmatrix} \tag{25}$$

The next step is to find $R_0 = \rho(\boldsymbol{F} \cdot \boldsymbol{V}^{-1})$. Then obtained:

$$R_0 = \rho(F \cdot V^{-1})$$

$$R_0 = \rho\left(\begin{pmatrix} \beta\sigma & 0 \\ \alpha & 0 \end{pmatrix} \cdot \begin{pmatrix} \frac{1}{(\mu + \alpha)} & 0 \\ 0 & \frac{1}{\mu} \end{pmatrix}\right)$$

$$R_0 = \rho \begin{pmatrix} \frac{\beta\sigma}{(\mu+\alpha)} & 0 \\ \frac{\alpha}{(\mu+\alpha)} & 0 \end{pmatrix} \tag{26}$$

To get R_0, the next step is to find the biggest eigenvalue of **Equation (26)** as follows:

$$|\boldsymbol{F}\cdot\boldsymbol{V}^{-1} - \lambda\boldsymbol{I}| = \left| \begin{pmatrix} \frac{\beta\sigma}{(\mu+\alpha)} & 0 \\ \frac{\alpha}{(\mu+\alpha)} & 0 \end{pmatrix} - \begin{pmatrix} \lambda & 0 \\ 0 & \lambda \end{pmatrix} \right|$$

$$\rightarrow |\boldsymbol{F}\cdot\boldsymbol{V}^{-1} - \lambda\boldsymbol{I}| = \begin{vmatrix} \frac{\beta\sigma}{(\mu+\alpha)} - \lambda & 0 \\ \frac{\alpha}{(\mu+\alpha)} & -\lambda \end{vmatrix}$$

$$\rightarrow \lambda\left(\lambda - \frac{\beta\sigma}{(\mu+\alpha)}\right) = 0$$

$$\lambda_1 = 0 \text{ and } \lambda_2 = \frac{\beta\sigma}{\mu+\alpha} \tag{27}$$

Because all variables are positive, so $\lambda_2 > \lambda_1$. Then obtained R_0 as follows:

$$R_0 = \frac{\beta\sigma}{\mu+\alpha} \quad , \mu+\alpha \neq 0 \tag{28}$$

3.4 Stability Analysis

After obtaining the model equilibrium point, the next step is to perform stability analysis for each equilibrium point (S_0, I_0, R_0) and (S_1, I_1, R_1). As the first step in analyzing the equilibrium point, it is necessary to linearize the system of differential **Equation (12)**, **Equation (13)**, and **Equation (14)**. For example:

$$f(S,I,R) = \mu - \beta\sigma IS - \mu S \tag{29}$$

$$g(S,I,R) = \beta\sigma IS + \tau IR - \alpha I - \mu I \tag{30}$$

$$h(S,I,R) = \alpha I - \mu R - \tau IR \tag{31}$$

By linearizing **Equation (29)**, we get:

$$\frac{df}{dS} = \frac{d(\mu - \beta\sigma IS - \mu S)}{dS} = -\beta\sigma I - \mu$$

$$\frac{df}{dI} = \frac{d(\mu - \beta\sigma IS - \mu S)}{dI} = -B\sigma S$$

$$\frac{df}{dR} = \frac{d(\mu - \beta\sigma IS - \mu S)}{dR} = 0$$

Then linearize **Equation (30)**. Then obtained:

$$\frac{dg}{dS} = \frac{d(\beta\sigma IS + \tau IR - \alpha I - \mu I)}{dS} = \beta\sigma I$$

$$\frac{dg}{dI} = \frac{d(\beta\sigma IS + \tau IR - \alpha I - \mu I)}{dI} = \beta\sigma S + \tau R - \alpha - \mu$$

$$\frac{dg}{dR} = \frac{d(\beta\sigma IS + \tau IR - \alpha I - \mu I)}{dR} = \tau I$$

Then linearize **Equation (31)**. Then obtained:

$$\frac{dh}{dS} = \frac{d(\alpha I - \mu R - \tau IR)}{dS} = 0$$

$$\frac{dh}{dI} = \frac{d(\alpha I - \mu R - \tau IR)}{dI} = \alpha - \tau R$$
$$\frac{dh}{dR} = \frac{d(\alpha I - \mu R - \tau IR)}{dR} = -\mu - \tau I$$

The result of linearization will be the elements of the Jacobian matrix, which has the following general Jacobian:

$$J = \begin{bmatrix} -\beta\sigma I - \mu & -\beta\sigma S & 0 \\ \beta\sigma I & \beta\sigma S + \tau R - \alpha - \mu & \tau I \\ 0 & \alpha - \tau R & -\mu - \tau I \end{bmatrix} \quad (32)$$

3.4.1 Disease-Free Equilibrium Point Stability Analysis

By substituting the disease-free equilibrium point value in **Equation (17)** into the Jacobian matrix (32), we get:

$$J_0 = \begin{bmatrix} -\mu & -\beta\sigma & 0 \\ 0 & \beta\sigma - \alpha - \mu & 0 \\ 0 & \alpha & -\mu \end{bmatrix} \quad (33)$$

Next, look for the eigenvalues of the matrix (33). So, the characteristic equation for the Jacobian matrix (33), which is analyzed by substituting the disease-free equilibrium point, can be written as follows:

$$det\begin{bmatrix} \lambda + \mu & -\beta\sigma & 0 \\ 0 & \lambda - \beta\sigma + \alpha + \mu & 0 \\ 0 & \alpha & \lambda + \mu \end{bmatrix} = 0$$

$$(\lambda + \mu)^2(\alpha - \beta\sigma + \lambda + \mu) = 0 \quad (34)$$

Then the eigenvalues obtained are $\lambda_1 = -\mu$ and $\lambda_2 = \beta\sigma - \alpha - \mu$. It can be seen that the value of λ_1 is clearly negative, and λ_2 is not necessarily negative. For that, it will be proved that λ_2 is negative. It is known that the condition for the disease-free equilibrium point is said to be stable if $R_0 < 1$. From **Equation (28)** known value $R_0 = \frac{\beta\sigma}{\alpha+\mu}$. Then obtained:

$$\frac{\beta\sigma}{\alpha + \mu} < 1$$
$$\beta\sigma < \alpha + \mu$$
$$\beta\sigma - \alpha - \mu < 0$$

Because $\lambda_2 = \beta\sigma - \alpha - \mu$. Then obtained:

$$\lambda_2 < 0$$

Based on the Routh-Hurwitz criteria, every eigenvalue that exists is the same, namely negative. As a result, there is no change in sign. It can be concluded that the disease-free equilibrium point is locally asymptotically stable.

3.4.2 Disease Endemic Equilibrium Point Stability Analysis

Consider an endemic equilibrium **Equation (21)**. Let the point $(S_1, I_1, R_1) = (S^*, I^*, R^*) = (S, I, R)$. By substituting the disease-free equilibrium point value in **Equation (21)** into the Jacobian matrix (32), we get:

$$J = \begin{bmatrix} -\beta\sigma I_1 - \mu & -\beta\sigma S_1 & 0 \\ \beta\sigma I_1 & \beta\sigma S_1 + \tau R_1 - \alpha - \mu & \tau I_1 \\ 0 & \alpha - \tau R_1 & -\mu - \tau I_1 \end{bmatrix} \quad (35)$$

Next, look for the eigenvalues of the matrix (35). So the characteristic equation for the Jacobian matrix (35), which is analyzed by substituting the disease-free equilibrium point, can be written as follows:

$$det\begin{bmatrix} -\beta\sigma I_1 - \mu & -\beta\sigma S_1 & 0 \\ \beta\sigma I_1 & \beta\sigma S_1 + \tau R_1 - \alpha - \mu & \tau I_1 \\ 0 & \alpha - \tau R_1 & -\mu - \tau I_1 \end{bmatrix} = 0$$

$I_1\tau(-\alpha + \tau R_1)(\lambda + I_1\beta\sigma + \mu) + (\lambda + \tau I_1 + \mu)\big(S_1 I_1\beta^2\sigma^2 + (\lambda + I_1\beta\sigma + \mu)(\alpha + \lambda - S_1\beta\sigma + R_1\tau + \mu)\big) = 0$

$\lambda^3 + \lambda^2(\alpha - S_1\beta\sigma + I_1\beta\sigma + I_1\tau + R_1\tau + 3\mu) + \lambda(2I_1\beta\sigma\mu$
$-2S_1\beta\sigma\mu + 2I_1\tau\mu + 2R_1\tau\mu + 3\mu^2 + I_1\alpha\beta\sigma - S_1I_1\beta\sigma\tau$
$+{I_1}^2\beta\sigma\tau + I_1R_1\beta\sigma\tau + 2I_1R_1\tau^2 + 2\alpha\mu) + 2{I_1}^2R_1\beta\sigma\tau^2$
$+I_1\alpha\beta\sigma\mu - S_1I_1\beta\sigma\tau\mu + {I_1}^2\beta\sigma\tau\mu + I_1R_1\beta\sigma\tau\mu$
$+2I_1R_1\tau^2\mu + \alpha\mu^2 - S_1\beta\sigma\mu^2 + I_1\beta\sigma\mu^2 + I_1\tau\mu^2$
$+R_1\tau\mu^2 + \mu^3 = 0$

Then obtained:
$a_0 = 1$
$a_1 = \alpha - S_1\beta\sigma + I_1\beta\sigma + I_1\tau + R_1\tau + 3\mu$
$a_2 = 2I_1\beta\sigma\mu - 2S_1\beta\sigma\mu + 2I_1\tau\mu + 2R_1\tau\mu + 3\mu^2 + I_1\alpha\beta\sigma - S_1I_1\beta\sigma\tau + {I_1}^2\beta\sigma\tau + I_1R_1\beta\sigma\tau + 2I_1R\tau^2 + 2\alpha\mu$
$a_3 = 2{I_1}^2R_1\beta\sigma\tau^2 + I_1\alpha\beta\sigma\mu - S_1I_1\beta\sigma\tau\mu + {I_1}^2\beta\sigma\tau\mu + I_1R_1\beta\sigma\tau\mu + 2I_1R\tau^2\mu + \alpha\mu^2 - S_1\beta\sigma\mu^2 + I_1\beta\sigma\mu^2 + I_1\tau\mu^2 + R_1\tau\mu^2 + \mu^3$

Forming an Array-Routh based on the above equation, we get:

$$\begin{vmatrix} \lambda^3 & \alpha_0 & \alpha_2 \\ \lambda^2 & \alpha_1 & \alpha_3 \\ \lambda & \left(\frac{\alpha_1\alpha_2 - \alpha_0\alpha_3}{\alpha_1}\right) & 0 \end{vmatrix}$$

The next step is to analyze α_0, α_1, and $\left(\frac{\alpha_1\alpha_2-\alpha_0\alpha_3}{\alpha_1}\right)$There is no change in signs of a stable condition. The condition for a disease to be endemic is $S, I, R > 0$. Each case will create a different compartment value, meaning that the difference between the compartments is absolute.

Then obtained:
$\alpha_1\alpha_2 - \alpha_0\alpha_3 = I_1\alpha^2\beta\sigma + |I_1 - S_1|I_1\alpha\beta^2\sigma^2 + |I_1 - S_1|I_1\alpha\beta\sigma\tau + 2R_1\alpha\beta\sigma\tau + {S_1}^2I_1\beta^2\sigma^2\tau + |I_1 - 2S_1|{I_1}^2\beta^2\sigma^2\tau + |I_1 - S_1|I_1R_1\beta^2\sigma^2\tau + 2I_1R_1\alpha\tau^2 + |I_1 - S_1|{I_1}^2\beta\sigma\tau^2 + |I_1 - 3S_1|S_1I_1R_1\beta\sigma\tau^2 + I_1{R_1}^2\beta\sigma\tau^2 + 2I^2R_1\tau^3 + 2I_1{R_1}^2\tau^3 + 2\alpha^2\mu + |6I_1 - 4S_1|\alpha\beta\sigma\mu + 2{S_1}^2\beta^2\sigma^2\mu + |2I_1 - 4S_1|S_1I_1\beta^2\sigma^2\mu + 4I_1\alpha\tau\mu + 4R_1\alpha\tau\mu + |6I_1 - 6S_1|I_1\beta\sigma\tau\mu + |6I_1 - 4S_1|R_1\beta\sigma\tau\mu + 2{I_1}^2\tau^2\mu + 8R_1{I_1}^2R_1\mu + 2{R_1}^2\tau^2\mu + 8\alpha\mu^2 + |8I_1 - 8S_1|\beta\sigma\mu^2 + 8I_1\tau\mu^2 + 8R_1\tau\mu^2 + 8\mu^3$
$\alpha_1\alpha_2 - \alpha_0\alpha_3 > 0$

$\alpha_1 = \alpha + |I_1 - S_1|\beta\sigma + I_1\tau + R_1\tau + 3\mu$
$\alpha_1 > 0$

In this case, $\alpha_1\alpha_2 - \alpha_0\alpha_3$ and α_1 are clearly positive, so it can be concluded that $\frac{\alpha_1\alpha_2-\alpha_0\alpha_3}{\alpha_1}$ is positive. Then all column one in Array Routh is positive. So, this equation is asymptotically stable. This means that the disease will remain in a population.

3.5 Model Application

This simulation aims to test the balance points that have been formed following the Routh-Hurwitz criteria. This simulation uses the following equation:

$$S_{n+1} = S_n + \mu N - \beta\sigma I_n S_n - \mu S_n \quad (36)$$
$$I_{n+1} = I_n + \beta\sigma I_n S_n + \tau I_n R_n - \alpha I_n - \mu I_n \quad (37)$$
$$R_{n+1} = R_n + \alpha I_n - \mu R_n - \tau I_n R_n \quad (38)$$

The application of this model uses data obtained from the UPTD Puskesmas Batanghari, as follows:

Table 2. Parameter values in COVID-19 data at Health Center UPTD Batanghari

Parameter	Value Parameter
N(Total Population)	100% (24.977)
μ(Death and Birth Rate)	2% (Assumption)
β (Transmission or Infection Rate)	100% (Assumption)
α(Recovery Rate)	66% (138 of 206)
γ(Total Vaccinated)	65% (16.361 of 24.977)
δ(Vaccine Efficacy)	65% (Sinovac Standard)
τ(Reinfection Rate)	50% (Assumption)
I (Infected Individual)	0,82% (206 of 24.977)

With initial values $S_1: 0.9868$, $I_1: 0.0082$, and $R_1: 0.005$. Subtitute **Equation (36)**, **Equation (37)**, and **Equation (38)** with existing parameter values. Then obtained:

$$S_2 = S_1 + \mu - \beta(1-\delta\gamma)I_1 S_1 - \mu S_1$$
$$S_2 = 0.9868 + 2\% - 100\% \times (1 - 65\% \times 70\%) \times 0.0082 \times 0.9868 - 2\% \times 0.9868$$
$$\boldsymbol{S_2 = 0,979498204}$$

$$I_2 = I_1 + \beta(1-\delta\gamma)I_1 S_1 + \tau I_1 R_1 - \alpha I_1 - \mu I_1$$
$$I_2 = 0.000132495 + 100\% \times (1 - 65\% \times 70\%) \times 0.000132495 \times 0.999847505 + 10\% \times 0.000132495 \times 0.00002 - 20\% \times 0.000132495 - 2\% \times 0.000132495$$
$$\boldsymbol{I_2 = 0.000175545}$$

$$R_2 = R_1 + \alpha I_1 - \mu R_1 - \tau I_1 R_1$$
$$R_2 = 0.00002 + 20\% \times 0.000132495 - 2\% \times 0.00002 - 10\% \times 0.000132495 \times 0.00002$$
$$\boldsymbol{R_2 = 0.000046}$$

Continued until the 100^{th} iteration, so that the graph is obtained as follows:

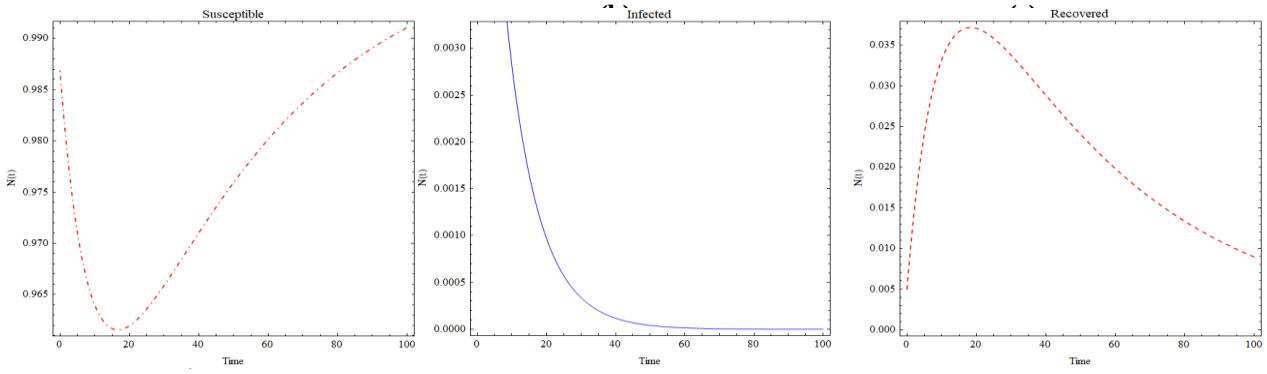

Figure 4. Graph of the SIR Model for Covid 19 Data at Batanghari Health Center. (a) Population conditions for individuals who are healthy but susceptible to COVID-19, (b) Population conditions for individuals infected with COVID-19, and (c) Population conditions for individuals who have been given the COVID-19 vaccine.

Based on the resulting graph, it can be seen that the dynamics of the development of COVID-19 are monitored to be conducive, and the condition is stable for the next 100 months. It can be concluded that the

decisions or policies implemented by the government and Health Center are correct. However, they must continue to apply health protocols properly so that there is no spike in unwanted infections.

3.6 MAPE

To find out the errors that exist in the forecasting process, the data in the Batanghari Health Center UPTD in months 1, 2, 3, 4, and 5 in 2022 with forecasting results with the SIR COVID-19 model in months 1, 2, 3, 4, and 5 in 2022.

Table 3. Comparison of Data for Months 1, 2, 3, 4, and 5 in 2022

Months	Model *SIR* COVID-19 (A)	Health Center (P)	$\Delta\|A-P\|$
1	12.239	10	2.239
2	10.965	11	0.035
3	9.796	7	2.796
4	8.761	8	0.761
5	7.837	9	1.163
Total	49.598	45	6.994

Then it can be obtained that the average absolute error or Mean Absolute Error (MAPE) is

$$MAE = \frac{\Delta|A-P|}{n} = \frac{6{,}994}{5} = 1.3988$$

$$MAPE = \frac{1.3988}{49.598} = 0.028202 = 2.8\%$$

4. CONCLUSIONS

Our research results can be explained as follow:

1. The COVID-19 SIR Model, made locally asymptotically stable at the balance point of disease-free and endemic disease, means that this disease can disappear and remain in an area.
2. The effect of the vaccination given is to inhibit the spike in infection. We can pay attention to the basic reproduction number A in handling this case.
3. Based on the application of the model to the data at the Batanghari Health Center UPTD, we obtained that the dynamics of the COVID-19 development monitored to be conducive, and the condition was stable for the next 100 months, with a Mean Absolute Percentage Error (MAPE) percentage of 2.8% which it's Highly Accurate Forecasting

ACKNOWLEDGEMENT

All authors would like to thank the academic community at the University of Lampung and LPPM at the University of Lampung for supporting and funding the research and publication of this article.

REFERENCES

[1] E. Callaway, "The race for coronavirus vaccines: a graphical guide," *Nature*, vol. 580, no. 7805, pp. 576–577, 2020, doi: doi:10.1038/d41586-020-01221-y.
[2] A. Ajbar, R. T. Alqahtani, and B. Mourad, "Dynamics of an SIR-Based COVID-19 Model With Linear Incidence Rate, Nonlinear Removal Rate, and Public Awareness," *Front. Phys.*, vol. 9, no. 634251, pp. 1–13, 2021, doi: https://doi.org/10.3389/fphy.2021.634251.
[3] B. Wacker and J. Schlüter, "Time-continuous and time-discrete SIR models revisited: theory and applications," *Adv. Differ. Equations*, vol. 2020, no. 556, pp. 1–44, 2020, doi: doi.org/10.1186/s13662-020-02995-1.
[4] Z. Liao, P. Lan, Z. Liao, Y. Zhang, and S. Liu, "TW-SIR: time-window based SIR for COVID-19 forecasts.," *Sci. Rep.*, vol. 10, no. 1, 2020, doi: https://doi.org/10.1038/s41598-020-80007-8.
[5] A. Mortellaro and P. Ricciardi-Castagnoli, "From vaccine practice to vaccine science: The contribution of human immunology to the prevention of infectious disease," *Immunol. Cell Biol.*, vol. 89, no. 3, pp. 332–339, 2011, doi: 10.1038/icb.2010.152.

[6] P. Thapa, "Predicating COVID19 Epidemic in Nepal Using the SIR Model," *Stud. Syst. Decis. Control*, vol. 358, no. September, pp. 229–237, 2021, doi: 10.1007/978-3-030-69744-0_14.
[7] O. Diekmann, J. A. P. Heesterbeek, and J. A. J. Metz, "On the definition and the computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous populations," *J. Math. Biol.*, vol. 28, no. 4, pp. 365–382, 1990, doi: 10.1007/BF00178324.
[8] W. F. Putra, "Analisis Efikasi dan Efektivitas Vaksin COVID-19 terhadap Varian SARS-CoV-2: Sebuah Tinjauan Literatur," *J. Kedokt. Meditek*, vol. 28, no. 1, pp. 107–119, 2022, doi: 10.36452/jkdoktmeditek.v28i1.2243.
[9] C. van Oosterhout, N. Hall, H. Ly, and K. M. Tyler, "COVID-19 evolution during the pandemic–Implications of new SARS-CoV-2 variants on disease control and public health policies," *Virulence*, vol. 12, no. 1, pp. 507–508, 2021, doi: 10.1080/21505594.2021.1877066.
[10] J. Li *et al.*, "Epidemiology of COVID-19 : A Systematic Review and Meta-analysis of Clinical Epidemiology of COVID-19 : A systematic review and meta-analysis of clinical characteristics, risk factors , and outcomes," *Med. Virol.*, pp. 1–10, 2020, doi: 10.1002/jmv.26424.
[11] WHO, "Coronavirus disease (COVID-19)," 2020. [Online]. Available: https://www.who.int/docs/default-source/coronaviruse/situation-reports/20201012-weekly-epi-update-9.pdf
[12] J. Sun *et al.*, "COVID-19 : Epidemiology , Evolution , and Cross-Disciplinary Perspectives," no. January, 2020.
[13] C. Van Oosterhout, N. Hall, H. Ly, and K. M. Tyler, "COVID-19 evolution during the pandemic – Implications of new SARS-CoV-2 variants on disease control and public health policies," *Virulence*, vol. 12, no. 1, pp. 507–508, 2021, doi: 10.1080/21505594.2021.1877066.
[14] S. Setiati and M. K. Azwar, "Dilemma of Prioritising Health and the Economy During COVID-19 Pandemic in Indonesia," *Acta Med Indones*, vol. 52, no. 3, pp. 196–198, 2020.
[15] A. Mortellaro and P. Ricciardi-Castagnoli, "From vaccine practice to vaccine science : the contribution of human immunology to the prevention of infectious disease," *Immunol. Cell Biol.*, vol. 89, pp. 332–339, 2011, doi: 10.1038/icb.2010.152.
[16] WHO, "Tanya Jawab : Lockdown dan herd immunity," 2021. who.int/indonesia/news/novel-coronavirus/qa/qa-lockdown-and-herd-immunity (accessed Jun. 10, 2020).
[17] N. M. Nasir, I. S. Joyosemito, B. Boerman, and I. Ismaniah, "Kebijakan Vaksinasi COVID-19 : Pendekatan Pemodelan Matematika Dinamis Pada Efektivitas Dan Dampak Vaksin Di Indonesia," *J. Abdimas UBJ*, vol. 4, no. 2, pp. 191–204, 2021.
[18] W. F. Putra, "Analisis Efikasi dan Efektivitas Vaksin COVID-19 terhadap Varian SARS-CoV-2 : Sebuah Tinjauan Literatur Analysis the Efficacy and Effectivity of COVID-19 Vaccines to the SARS-CoV-2 Variants : A Literature Review," *Meditek*, vol. 28, no. 1, pp. 107–119, 2022, doi: https://doi.org/10.36452/jkdoktmeditek.v28i1.2243.
[19] W. O. Kermarck and A. G. McKendrick, "A Contribution to the Mathematical Theory o f Epidemics.," in *The Royal Society London A*, Royal Society, 1927, pp. 700–721. doi: 10.1098/rspa.1927.0118.
[20] P. Thapa, "Predicating COVID19 epidemic in Nepal using the SIR model," *Artif. Intell. COVID-19.*, 2021, doi: 10.1007/978-3-030-69744-0_14.
[21] M. A. Shereen, S. Khan, A. Kazmi, N. Bashir, and R. Siddique, "COVID-19 infection: origin, transmission, and characteristics of human coronaviruses.," *J. Adv. Res.*, vol. 24, no. 2020, pp. 91–98, 2020, doi: 10.1016/j.jare.2020.03.005.
[22] Y. F. Lin *et al.*, "Spread and Impact of COVID-19 in China: A Systematic Review and Synthesis of Predictions From Transmission-Dynamic Models. Frontiers in Medicine, 7. doi:10.3389/fmed.2020.00321," *Front. Med.*, vol. 7, no. 321, pp. 1–11, 2020, doi: doi:10.3389/fmed.2020.00321.
[23] Q. Griette and P. Magal, "Clarifying predictions for COVID-19 from testing data: The example of New York State.," *Infect. Dis. Model.*, vol. 6, pp. 273–283, 2021, doi: https://doi.org/10.1016/j.idm.2020.12.011.
[24] Z. Liu, P. Magal, and G. Webb, "Predicting the number of reported and unreported cases for the COVID- 19 epidemics in China, South Korea, Italy, France, Germany and United Kingdom," *J. Theor. Biol. 509, 110501.*, vol. 509, no. 110501, 2021, doi: doi:10.1016/j.jtbi.2020.110501.
[25] A. J. Kucharski, T. W. Russell, J. Diamond, C., Liu, Y., Edmunds, S. Funk, and R. M. Eggo, "Early dynamics of transmission and control of COVID-19: a mathematical modelling study.," *Lancet Infect. Dis.*, vol. 20, pp. 1–7, 2020, doi: https://doi.org/10.1016/S1473-3099(20)30144-4.
[26] E. S. Kurkina and E. M. Koltsova, "Mathematical Modeling of the Propagation of COVID-19 Pandemic Waves in the World.," *Comput. Math. Model.*, vol. 32, no. 2, pp. 147–170, 2021, doi: doi:10.1007/s10598-021-09523-0.
[27] A. Lobo *et al.*, "COVID-19 epidemic in Brazil: where we at?," *Int. J. Infect. Dis.*, vol. 97, pp. 382–385, 2020, doi: doi:10.1016/j.ijid.2020.06.044.
[28] K. Roosa *et al.*, "Real-time forecasts of the COVID-19 epidemic in China from February 5th to February 24th, 2020.," *Infect. Dis. Model.*, vol. 5, no. 2020, pp. 256–263, 2020, doi: 10.1016/j.idm.2020.02.002.
[29] H. W. Hethcote, "The mathematics of infectious diseases," *SIAM Rev.*, vol. 42, no. 4, pp. 599–653, 2000, [Online]. Available: http://www.siam.org/journals/sirev/42-4/37190.html
[30] K. R. Meyer, "Normal forms for the general equilibrium," *Funkc. Ekvacioj*, vol. 27, pp. 261–271, 1984.
[31] G. J. Olsder and J. W. van der Woude, *Mathematical Systems Theory*, Second. Delft, The Netherland: Delft Univrsity Press, 1997.
[32] O. Diekmann, J. A. P. Heesterbeek, and J. A. J. Metz, "On the definition and the computation of the basic reproduction ratio Ro in models for infectious diseases in heterogeneous populations," *J. Math. Biol*, vol. 28, pp. 365–382, 1990.
[33] A. Faruk, "Model Epidemik Tuberkulosis Seir dengan Terapi pada Individu Terinfeksi," *J. Penelit. Sains*, vol. 18, no. 3, pp. 99–104, 2016, doi: 10.56064/jps.v18i3.16.
[34] J. Giesecke, *Modern Infectious Disease Epidemiology*, Third. CRC Press Taylor & Francis Group, 2017.
[35] P. Van Den Driessche and J. Watmough, "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission," *Math. Biosci. 180*, vol. 180, pp. 29–48, 2002, [Online]. Available: http://www.math.unb.ca/?watmough.
[36] F. R. Gantmacher, *The theory of matrices*. Chelsea Publishing Company, 1959.
[37] C. D. Lewis, *Demand Forecasting and Inventory Control: A computer aided learning approach*, vol. 2. Woodhead Publishing Ltd, 1997.
[38] WHO, "Evaluation of COVID-19 vaccine effectiveness," 2021. https://www.who.int/publications/i/item/WHO-2019-nCoV-

vaccine_effectiveness- measurement-2021