BAREKENG: Journal of Mathematics and Its Applications
March 2024 Volume 18 Issue 1 Page 0303–0312
P-ISSN: 1978-7227 E-ISSN: 2615-3017
https://doi.org/10.30598/barekengvol18iss1pp0303-0312

ANALYSIS AND SIMULATION OF THE SIR MODEL ON THE SPREAD OF COVID-19 BY CONSIDERING THE VACCINATION FACTOR

Atika Ratna Dewi [1]*, Ridho Ananda [2], Utti Marina Rifanti[3], Nadia Putri Anggraeni[4], Miko Ardian[5]

[1,4,5] *Data Science Study Program, Faculty of Informatics, Institut Teknologi Telkom Purwokerto*
[2] *Industrial Engineering Study Program, Faculty of Industrial Engineering and Design, Institut Teknologi Telkom Purwokerto*
[3] *Telecommunications Engineering Study Program, Faculty of Telecommunications and Electrical Engineering, Institut Teknologi Telkom Purwokerto*
D. I. Panjaitan Street No. 128, Purwokerto, 53147, Indonesia

*Corresponding author's e-mail: * **atika@ittelkom-pwt.ac.id***

ABSTRACT

Article History:

Received: 25th August 2023
Revised: 2nd December
Accepted: 1st January 2023

Keywords:

Basic Reproduction Ratio Number;
Covid-19;
Model Simulation;
SIR Model;
Vaccination.
.

COVID-19 is a serious respiratory disease that can be fatal for those affected. Governments have tried various strategies to conquer the Covid-19 pandemic. One of them is to vaccinate people six years old and over. The vaccination program aims to form herd immunity so that the number of confirmed positive cases can be reduced. The purpose of this research is to form a mathematical model of the SIR (Susceptible-Infected-Recovery) spread of COVID-19 by considering vaccination factors. The SIR model is combined with a vaccination factor to forestall the unfolding of COVID-19. The research method includes deriving models of nonlinear differential equation systems, solving qualitative models, deriving the basic reproduction ratio (R_0), analysis of equilibrium points, and building simulation models. This model has an asymptotically stable disease-free equilibrium point. At the same time, the endemic equilibrium point is unstable. Model simulation is obtained by using different parameter values. This is proven through the outcomes of the model analysis. Vaccination coverage is a key parameter that can be controlled to reduce R_0 so that the pandemic ends soon.

How to cite this article:

A. R. Dewi, R. Ananda, U. M. Rifanti, N. P. and M. Ardian., "ANALYSIS AND SIMULATION OF THE SIR MODEL ON THE SPREAD OF COVID-19 BY CONSIDERING THE VACCINATION FACTOR," *BAREKENG: J. Math. & App.*, vol. 18, iss. 1, pp. 0303-0312, March, 2024.

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

COVID-19 is a virus that belongs to the same group as SARS and MERS [1]. As stated in NBC News (2020), the spread of this coronavirus has been determined by WHO to be a pandemic condition starting in March 2020 [2]. A pandemic is an epidemic condition that has spread over a huge area, across a country or continent, usually affecting many people [3]. This virus is transmitted through droplets from someone infected with COVID-19 when sneezing or coughing [4]. This viral infection causes symptoms such as sore throat, tremors, high fever, shortness of breath, dry cough, headache, nausea, vomiting, and diarrhea in patients.[5]. There are quite a number of impacts caused by this pandemic. In the Education sector, for example, teaching and learning are currently being held online, which, of course, encounters many obstacles [6]. The economic sector has also experienced a downturn due to this pandemic. As a result, many business actors have had to close their operations because turnover has dropped dramatically [7].

The government is currently pursuing various strategies to break the cycle of transmission of COVID-19. One of the preventive measures is to give vaccines to people who are at least six years old. This is to protect the public from the risk factors for contracting this virus [8]. Based on data from the Indonesian Ministry of Health in February 2022, the coverage of vaccine dose 1 reached 90%, dose 2 reached 64%, and dose 3 reached 3%. Knowing the results of the strategy for tackling the COVID-19 outbreak is certainly not easy, therefore, an appropriate simulation model can be useful in determining policy steps.

The mathematical model of the epidemic was created as a tool to devise strategies to stem the spread of the disease. Apart from that, mathematical models are also used to predict future outbreaks to avoid pandemics [9]. The epidemic model was first introduced in 1927 by W.O. Kermack and Mc. Kendrick, namely in the form of a SIR model. In the SIR model, there are three subpopulations, namely people who are susceptible to infection, infected, and recovered.

Research on disease epidemic models with disease control strategies has been widely studied. Study [10] predicting COVID-19 in Indonesia with the SIR model. Research on the effect of lockdown control strategies and limited treatment was carried out by [11] [12]. One of the epidemic model studies with prevention efforts is the research of Nisa Aulia, Muhammad Kharis, and Supriyono [13]. This study develops a mathematical model of the SIR influenza epidemic by considering the success of vaccination. Research on the SIR mathematical model of the spread of COVID-19 can be seen in [14]. Some of the parameters considered in this model include vaccine effectiveness, medical protocol effectiveness, and treatment effectiveness. In addition, research on mathematical models of the spread of COVID-19 can also be found at [15][16][17][18][19]. Therefore, this study analyzes the mathematical model for the COVID-19 epidemic, which is in the form of the SIR model, taking into account the vaccination factor. The model obtained is then searched for the equilibrium point and analyzed for its stability. The next step is to look for the basic reproduction ratio (Ro) to show the incidence of epidemics in the population. Then, a model simulation of the spread of COVID-19 is be carried out with the vaccination factor.

2. RESEARCH METHODS

2.1 Types of Research

This type of research is a literature review based on real everyday phenomena. This real phenomenon is then described in the form of a mathematical equation and presented in the form of a compartment diagram. In this study, the authors collected data on COVID-19 cases on the Indonesian Ministry of Health's website from March to December 2021. This is because the vaccination program was only implemented in January 2021.

2.2 Research Steps

The following is a flowchart of the research used:

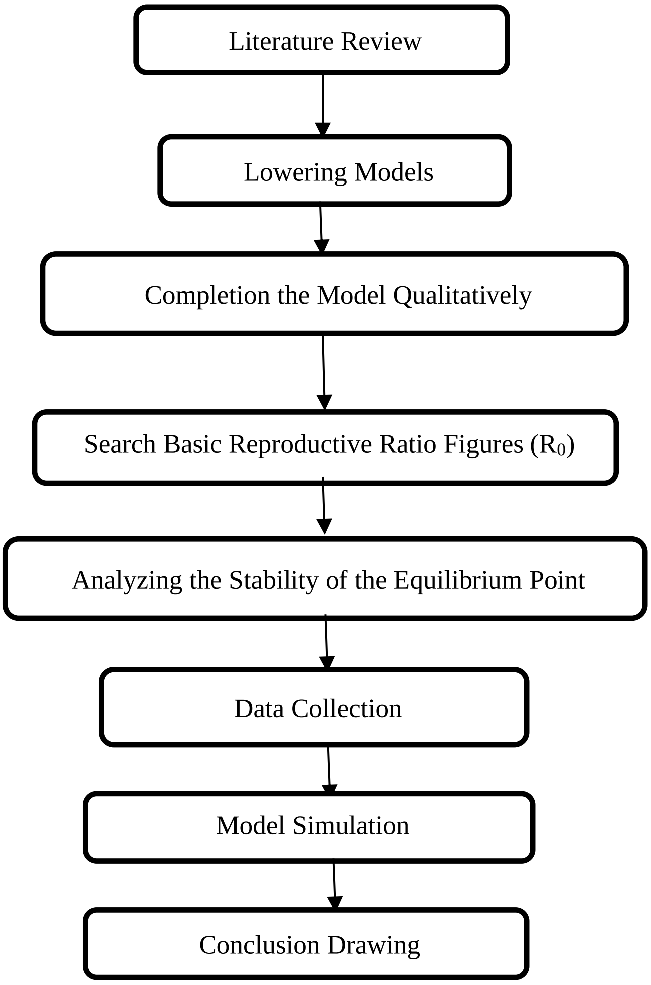

Figure 1. Research Flowchart

a. Lowering Models

The model was grouped into three *SIR* subpopulations, namely susceptible, infected, and recovery humans. Then, formulate the *SIR* model based on predetermined assumptions and use the parameters used with the three *SIR* subpopulation groups. The model formed is a system model of nonlinear differential equations.

b. Completing the Model Qualitatively

Finding the equilibrium point from the resulting *SIR* model equation. When $I = 0$, a disease-free equilibrium point is reached, while when $I \neq 0$, an endemic equilibrium point is reached.

c. Looking for Basic Reproductive Ratio (R_0)

Basic reproduction ratio numbers are used to determine conditions in populations with or without epidemic disease.

d. Analyzing the stability of the equilibrium point

After obtaining the equilibrium point, then, an analysis of the equilibrium point is carried out so that the behavior of the model can be identified.

e. Data Collection

The collection process was carried out secondary, namely by collecting data on the Indonesian Ministry of Health's website from March to December 2021. The data collected was in the form of data on the number of active cases of COVID-19, recovered, died, and those who had been vaccinated.

f. Model Simulation

The model simulation was carried out by taking values for each parameter so that the number of susceptible humans (S) can be obtained, the number of people who are confirmed positive for COVID-19 (I), the number who have recovered (R), and the basic reproduction ratio number. The model simulation is displayed in graphical form for each population.

g. Conclusion Drawing

In the final stage, a comprehensive study was carried out to draw conclusions about the resulting mathematical model.

3. RESULTS AND DISCUSSION

The COVID-19 epidemic model with the vaccination factor is derived from a system of nonlinear differential equations. Next, analyze the disease-free and endemic equilibrium points and look for the formula for the basic reproduction ratio (R_0) to find out the factors that influence the model.

3.1 Covid-19 Epidemic Model with Vaccination Factors

Mathematical models can be formed by considering several assumptions related to the problem to be modeled. The following assumptions are used in the mathematical modeling of COVID-19 with the vaccination factor, namely:

a. Increase or decrease in the number of people caused by birth or death.

b. The human birth rate is fixed.

c. Everyone is born healthy.

d. People who have recovered will not be exposed to the COVID-19 virus again.

Variables and parameters are defined in **Table 1**:

Table 1. Variables and Parameters of the COVID-19 Model with Vaccination

Notation	Meaning	Type	Condition	Unit
S	Number of humans susceptible to infection	Variable	$S \geq 0$	person
I	Number of humans infected	Variable	$I \geq 0$	person
R	Number of people have recovered	Variable	$R \geq 0$	person
δ	The rate of increase in human susceptibility to infection	Parameter	$\delta \geq 0$	person/day
α	COVID-19 spread rate	Parameter	$0 < \alpha \leq 1$	
μ	Natural death rate	Parameter	$0 < \mu < 1$	per day
β	The cure rate of infected humans	Parameter	$0 < \beta < 1$	per day
σ	The death rate due to COVID-19	Parameter	$0 < \sigma < 1$	per day
θ	Vaccination rates	Parameter	$0 < \phi < 1$	per day
N	Total human population	Parameter	$N > 0$	person

The SIR model of the spread of COVID-19 with the vaccination factor is obtained by developing the set assumptions and parameters. Schematically, the *SIR* model of the spread of COVID-19 with the vaccination factor can be presented in a compartment diagram (**Figure 2**).

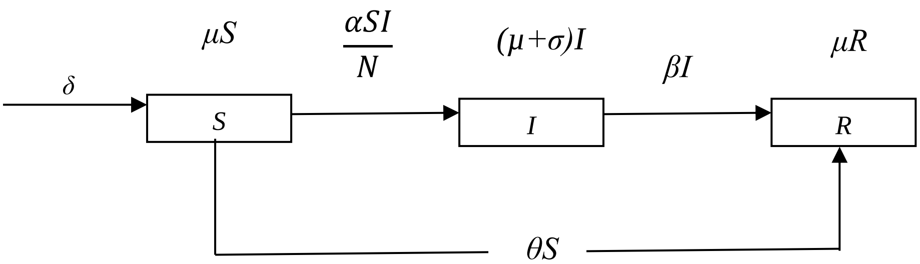

Figure 2. COVID-19 Model Compartment Diagram with Vaccination Factors

The *SIR* model with the vaccination factor obtained from the spread of COVID-19 is in the form of a system of differential equations as follows:

$$\begin{aligned} \frac{dS}{dt} &= \delta - \frac{\alpha SI}{N} - \mu S - \theta S \\ \frac{dI}{dt} &= \frac{\alpha SI}{N} - (\beta + \mu + \sigma)I \\ \frac{dR}{dt} &= \beta I + \theta S - \mu R \end{aligned} \tag{1}$$

3.2 Disease-Free and Endemic Equilibrium Points

The disease-free equilibrium point is obtained when $I=0$ from the system (1) as follows

$$K_0 = (S^{\cdot}, 0, R^{\cdot}) = \left(\frac{\delta}{\mu+\theta}, 0, \frac{\theta\delta}{(\mu+\theta)\mu}\right) \tag{2}$$

Furthermore, to obtain the endemic equilibrium point, it is assumed to be $I \neq 0$. Based on the system (1), the endemic equilibrium point is obtained

$$K_1 = (S^*, I^*, R^*) \tag{3}$$

where:

$$S^* = \frac{(\beta+\mu+\sigma)N}{\alpha}$$

$$I^* = \frac{-\delta\alpha + N\beta\mu + N\mu^2 + N\mu\sigma + N\theta\beta + N\mu\theta + N\theta\sigma}{\alpha(\beta+\mu+\sigma)}$$

$$R^* = -\frac{(-\beta\delta\alpha + N\mu\beta^2 + \beta N\mu^2 + \beta N\mu\sigma - \beta N\theta\mu - \beta N\theta\sigma - N\theta\mu^2 - 2N\theta\mu\sigma - N\theta\sigma^2)}{\alpha(\beta+\mu+\sigma)\mu}$$

3.3 Basic Reproductive Ratio Figures (R_0)

The basic reproduction ratio for this case is obtained by using the next-generation operator approach, namely

$$R_0 = \left(\frac{\alpha\mu}{(\mu+\theta)(\beta+\mu+\sigma)}\right) \tag{4}$$

Based on the value of R_0, the following analysis is obtained:

a. If the value of α is greater and the value $(\mu + \theta)(\beta + \mu + \sigma)$ is smaller, the result is $R_0 > 1$. This means that there is a greater chance of an outbreak of disease or a pandemic occurring.

b. If the value of α is smaller and the value $(\mu + \theta)(\beta + \mu + \sigma)$ is greater, it will produce $R_0 < 1$. This means that there is a little chance of an outbreak of disease or no outbreak at all.

3.4 Stability Analysis Equilibrium Point

Analysis of the stability of the system's equilibrium point is carried out by first determining the eigenvalues of matrix A. The stability of the equilibrium point of the system can be determined based on the eigenvalues of matrix A in **Theorem 1** below.

Theorem 1 [20]

If matrix A on the system $\dot{x} = Ax$ is a matrix of coefficients with eigenvalues $\lambda_1,\ \lambda_2,\ \cdots, \lambda_n$, and $(\ \lambda_k)$ is the real part of the eigenvalues λ_k, hence the stability of the equilibrium point $x^* = 0$ of system solutions $\dot{x} = Ax$ said

a. Stable, if $(\ \lambda_k) \leq 0,\ \forall k = 1,\ 2,\ \cdots,\ n.$

b. Asymptotically stable, if $(\ \lambda_k) < 0,\ \forall k = 1,\ 2,\ \cdots,\ n$

c. Not stable, if $(\ \lambda_k) > 0,\ for\ a\ k.$

3.4.1 Stability of Model Behavior at Disease-Free Equilibrium Points

Theorem 2. If $R_0 < 1$ then the equilibrium point K_0 is asymptotically stable.

Proof:
The stability of the model's behavior at the disease-free equilibrium point was analyzed from the eigenvalues obtained based on the following Jacobian matrix.

$$\left| J_{\left(\frac{\delta}{\mu+\theta},0,\frac{\theta\delta}{(\mu+\theta)\mu}\right)} - \lambda I \right| = \left| \left(-(\mu+\theta) - \lambda\ \frac{\alpha\mu}{(\mu+\theta)}\ 0\ 0\ \frac{\alpha\mu}{(\mu+\theta)} - (\beta+\mu+\sigma) - \lambda\ 0\ \theta\ \beta\ -\mu-\lambda \right) \right| = 0 \qquad (5)$$

The eigenvalues of **Equation (5)** are

$$\lambda_1 = -\mu,\ \lambda_2 = -(\mu+\theta), \lambda_3 = -\left(-\frac{\alpha\mu}{(\mu+\theta)} + (\beta+\mu+\sigma)\right).$$

Eigenvalues $\lambda_1, \lambda_2, \lambda_3 < 0$ have a negative real part, so according to **Theorem 1**, the equilibrium point $K_0 = (S^{\cdot}, 0, R^{\cdot}) = (\frac{\delta}{\mu+\theta}, 0, \frac{\theta\delta}{(\mu+\theta)\mu})$ is asymptotically stable.

3.4.2 Stability of Model Behavior at Endemic Equilibrium Points

Theorem 3. If $R_0 > 1$ then the equilibrium point K_1 is asymptotically stable.

Proof:

The stability of the model's behavior at the endemic equilibrium point is analyzed from the eigenvalues obtained based on the following Jacobian matrix

$$J = \frac{\partial F}{\partial x}(S^*, I^*, R^*) = \left| -\frac{\alpha I^*}{N} - \mu - \theta\ \ -\frac{\alpha S^*}{N}\ \ 0\ \ \frac{\alpha I^*}{N}\ \ \frac{\alpha S^*}{N} - (\beta+\mu+\sigma)\ 0\ \theta\ \beta\ -\mu \right| \qquad (6)$$

The eigenvalues obtained from **Equation (6)** are

$$\begin{aligned} \lambda_1 &= -\frac{(\delta\alpha - \sqrt{B})}{2A}, \\ \lambda_2 &= -\frac{(\delta\alpha + \sqrt{B})}{2A} \\ \lambda_3 &= (\beta+\mu+\sigma)^2\left(-\frac{(\delta\alpha+\sqrt{C})}{2A}\right), \\ \lambda_4 &= -\mu \end{aligned} \qquad (7)$$

where:

$A = (\beta + \mu + \sigma)N$

$$B = -8N\beta\delta\alpha\mu + 24N^2\beta\theta\mu\sigma - 8N\beta\delta\alpha\sigma - 8N\mu\delta\alpha\sigma + 4N^2\mu^4 + 24N^2\beta\mu^2\sigma + 12N^2\beta\theta\mu^2 + 12N^2\beta^2\theta\mu - 4N\beta^2\delta\alpha + 12N^2\beta^2\mu\sigma + 12N^2\beta\mu\sigma^2 + 12N^2\beta\theta\sigma^2 + 12N^2\beta^2\theta\sigma - 4N\mu^2\delta\alpha + 12N^2\mu^2\theta\sigma + 12N^2\mu\theta\sigma^2 - 4N\sigma^2\delta\alpha + 12N^2\beta\mu^3 + 12N^2\beta^2\mu^2 + 4N^2\beta^3\mu + 4N^2\beta^3\theta + 12N^2\mu^3\sigma + 4N^2\mu^3\theta + 12N^2\mu^2\sigma^2 + 4N^2\sigma^3\mu + 4N^2\sigma^3\theta + \delta^2\alpha^2$$

$\lambda_1 < 0$ will be fulfilled if $B > 0$ and $\delta\alpha > \sqrt{B}$

$\lambda_2 < 0$ will be fulfilled if $B > 0$

$\lambda_3 < 0$ will be fulfilled if $C > 0$

Eigenvalues $\lambda_1, \lambda_2, \lambda_3, \lambda_4 < 0$ have a negative real part if these conditions are met. According to **Theorem 1**, the equilibrium point $K_1 = (S^*, I^*, R^*)$ is asymptotically stable.

3.5 Simulation of the COVID-19 Epidemic Model with Vaccination Factors

The COVID-19 epidemic simulation model with vaccination is generated from the parameter values given in **Table 2** as follows:

Table 2. Model Simulation Parameter Values

Notation	Meaning	Value	Reference
$S(0)$	Number of humans susceptible to infection	273860000	[21]
$I(0)$	Number of humans infected	4258552	[22]
$R(0)$	A number of people have recovered	4114905	[22]
δ	Rate of increase in human susceptibility to infection	4493	[21]
α	COVID-19 spread rate	0.8	assume
μ	Natural death rate	0.2	assume
β	Cure rate	0.01	assume
σ	The death rate due to COVID-19	0.03	assume
θ	Vaccination rates	0.1	assume
R_0	Basic reproduction ratio figure	2.22	assume

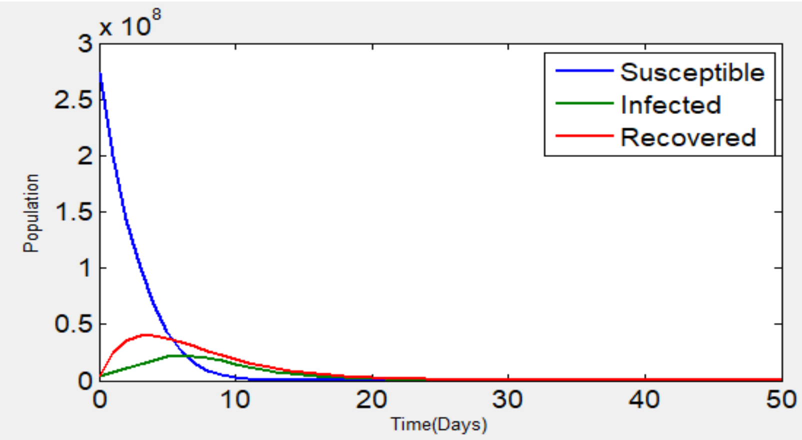

Figure 3. Graph of the COVID-19 Model with Vaccination at the Endemic Equilibrium Point with a Vaccination Rate of 0.1

The following will present a graph with different parameter values θ (vaccination rate), namely:

a. If the value of the vaccination parameter is changed to 0.3, then the value is obtained

b. $R_0 = 1.333$ and the graph in **Figure 4**:

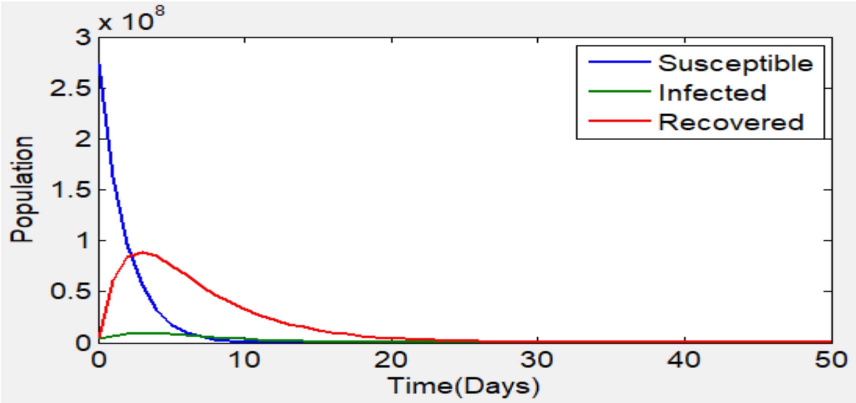

Figure 4. Graph of the COVID-19 Model with Vaccination at the Endemic Equilibrium Point with a Vaccination level of 0.3

c. If the value of the vaccination parameter is changed to 0.6 then the value is obtained $R_0 = 0.833$ and the graph in **Figure 5**:

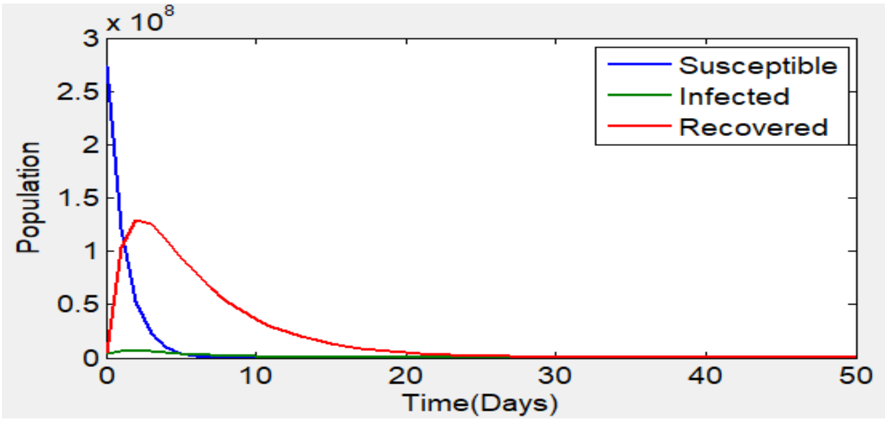

Figure 5. Graph of the COVID-19 Model with Vaccination at the Endemic Equilibrium Point with a Vaccination rate of 0.6

d. If the value of the vaccination parameter is changed to 0.9 then the value is obtained
e. $R_0 = 0.606$ and the graph in **Figure 6**:

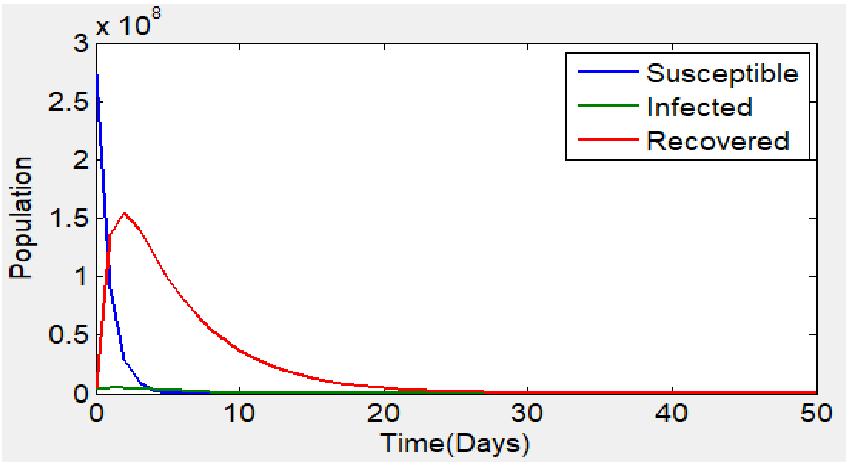

Figure 6. Graph of the COVID-19 Model with Vaccination at the Endemic Equilibrium Point with a Vaccination rate of 0.9

Figure 3 - **Figure 6** shows that the greater the vaccination rate (the other parameter values are constant), the lower the R_0 value. **Figure 3** - **Figure 6** also shows that the number of people infected has decreased over time as vaccination coverage has increased. At the same time, the number of people who have recovered continues to grow as the vaccination parameters increase. This means that the level of vaccination

is very influential on the population. For this reason, a comprehensive vaccination program is needed for members of the public so that the COVID-19 pandemic ends soon.

4. CONCLUSIONS

a. The spread of COVID-19 with the vaccination factor can be modeled into a system of nonlinear differential equations.

b. In the COVID-19 distribution model, the vaccination factor has an asymptotically stable disease-free equilibrium point. Meanwhile, the endemic equilibrium point is unstable.

c. The basic reproduction ratio figure formula for the model is

$$R_0 = \left(\frac{\alpha\mu}{(\mu+\theta)(\beta+\mu+\sigma)}\right)$$

If the value of α is greater and the value$(\mu+\theta)(\beta+\mu+\sigma)$ is smaller, then the value of R_0 is greater than one $(R_0 > 1)$, meaning there is a greater chance of an outbreak of disease or a pandemic occurring. If the value of α is smaller and the value $(\mu+\theta)(\beta+\mu+\sigma)$ is greater, then the value of R_0 is smaller than one $(R_0 < 1)$. This means that there is little chance of an outbreak of disease or no outbreak at all.

d. Model simulations carried out using different vaccination levels show that the presence of the vaccination factor reduces the value R_0.

e. The limitation and future direction of this research is that vaccination is made a separate variable.

ACKNOWLEDGMENT

The author expresses his appreciation and gratitude to the Ministry of Education and Culture for funding this research through the 2022 Beginner Lecturer Research (PDP) scheme.

REFERENCES

[1] T. Hu, Y. Liu, M. Zhao, Q. Zhuang, L. Xu, and Q. He, "A Comparison of COVID-19, SARS and MERS," *PeerJ*, vol. 8, pp. 1–30, 2020.

[2] C. Siemaszko, "Coronavirus Outbreak Labeled a Pandemic by World Health Organization," 2020. [Online]. Available: https://www.nbcnews.com/health/health-news/coronavirus-outbreak-labeledpandemic-world-health-organization-n1155741. [Accessed: 27-Mar-2020].

[3] N. Mascie Taylor and K. Moji, "Pandemics," *J. Peace Nucl. Disarm.*, vol. 4, no. S1, pp. 47–59, 2021.

[4] W. H. Organization, "QA for Public," 2020. [Online]. Available: https://www.who.int/indonesia/news/novel-coronavirus/qa-for-public. [Accessed: 05-Sep-2020].

[5] M. Sukmana and F. A. Yuniarti, "The Pathogenesis Characteristics and Symptom of COVID-19 in the Context of Establishing a Nursing Diagnosis," *J. Kesehat. Pasak Bumi Kalimantan*, vol. 3, no. 1, p. 21, 2020.

[6] A. Kurniawati, "The Impact of COVID-19 Pandemic on Learning in Indonesia," *J. Media Komun. Pendikan Teknol. dan Kejuru.*, vol. 8, no. 2, pp. 16–21, 2021.

[7] L. Saryani and A. Sayuti Pulungan, "Impact of The COVID-19 Pandemic on The Indonesian Economy," *Int. J. Educ. Res. Soc. Sci.*, vol. 2, no. 5, pp. 996–1007, 2021.

[8] L. Mery, A. Rahmah, and A. S. R. Wulandari, "Regulation of The Provision of COVID-19 Vaccination in Indonesia as The Implementation of State Obligations in line with The Indonesian Constitution," *Sasi*, vol. 27, no. 4, p. 451, 2021.

[9] A. Afzal, C. A. Saleel, S. Bhattacharyya, N. Satish, O. D. Samuel, and I. A. Badruddin, "Merits and Limitations of Mathematical Modeling and Computational Simulations in Mitigation of COVID-19 Pandemic: A Comprehensive Review," *Arch. Comput. Methods Eng.*, vol. 29, no. 2, pp. 1311–1337, 2022.

[10] B. A. Wahyudi and I. Palupi, "Prediction of the Peak COVID-19 Pandemic in Indonesia using SIR Model," *J. Teknol. dan Sist. Komput.*, vol. 9, no. 1, pp. 49–55, 2021.

[11] A. P. Putra and S. A. Z. Abidin, "Aplication of SEIR Model in COVID-19 and the Effect of Lockdown on Reducing the Number of Active Cases," vol. 5, no. 2, pp. 185–192, 2020.

[12] U. M. Rifanti, A. R. Dewi, N. Nurlaili, and S. T. Hapsari, "Model Matematika COVID-19 dengan Sumber Daya Pengobatan yang Terbatas," *Limits J. Math. Its Appl.*, vol. 18, no. 1, p. 23, 2021.

[13] N. Aulia and M. Kharis, "Pemodelan Matematika Epidemi Influenza dengan Memperhatikan Peluang Keberhasilan Vaksinasi dan Kekebalan Tetap," *J. Math. UNNES*, vol. 5, no. 2, 2016.

[14] M. Abdy, S. Side, S. Annas, W. Nur, and W. Sanusi, "An SIR Epidemic Model for COVID-19 Spread with Fuzzy Parameter:

The Case of Indonesia," *Adv. Differ. Equations*, vol. 2021, no. 1, 2021.

[15] S. I. Vinitsky, A. A. Gusev, V. L. Derbov, P. M. Krassovitskiy, F. M. Pen'kov, and G. Chuluunbaatar, "Reduced SIR Model of COVID-19 Pandemic," *Comput. Math. Math. Phys.*, vol. 61, no. 3, pp. 376–387, 2021.

[16] M. Imran, M. Wu, Y. Zhao, E. Beșe, W. Alonazi, and M. J. Khan, "Mathematical Modelling of SIR for COVID-19 Forecasting," *Rev. Argentina Clínica Psicológica*, vol. XXX, pp. 218–226, 2021.

[17] S. Annas, M. Isbar Pratama, M. Rifandi, W. Sanusi, and S. Side, "Stability Analysis and Numerical Simulation of SEIR Model for Pandemic COVID-19 Spread in Indonesia," *Chaos, Solitons and Fractals*, vol. 139, 2020.

[18] M. N. Alenezi, F. S. Al-Anzi, and H. Alabdulrazzaq, "Building a Sensible SIR Estimation Model for COVID-19 Outspread in Kuwait," *Alexandria Eng. J.*, vol. 60, no. 3, pp. 3161–3175, 2021.

[19] X. Liu, "A simple, SIR-like but Individual-Based Epidemic Model: Application in Comparison of COVID-19 in New York City and Wuhan," *Results Phys.*, vol. 20, no. August 2020, 2021.

[20] W. Boyce and R. DiPrima, *Elementary Differential Equations with Boundary Value Problems*, 10th ed. New Jersey: Prentice-Hall, 2012.

[21] [BPS] Badan Pusat Statistik, "Berita Resmi Statistik," *Bps.Go.Id*, no. 27, pp. 1–52, 2019.

[22] Kemenkes, "Dashboard COVID-19," *COVID-19*, 2021. [Online]. Available: https://dashboardcovid19.kemkes.go.id/. [Accessed: 20-May-2021].