COVID-19 TRANSMISSION MODEL WITH DISCRETE TIME APPROACH

D.S. PANGESTU[1], S.T. TRESNA[1], F. INAYATUROHMAT[1], N. ANGGRIANI[2,*]

[1]Master's Program of Mathematics, Department of Mathematics, Padjadjaran University, Jl. Raya Bandung

Sumedang Km. 21, Kab. Sumedang 45363 Jawa Barat, Indonesia

[2]Department of Mathematics, Padjadjaran University, Jl. Raya Bandung Sumedang Km. 21, Kab. Sumedang 45363

Jawa Barat, Indonesia

Abstract: In this research, we developed model of SIR for COVID-19 spread. The model is represented by a deterministic discrete-time model. The model is constructed with divided the population into three compartments, namely Susceptible, Infected, and Recovered denoted by S, I, and R, respectively. This research aims to formulate a model for describing the spread of COVID-19 with a data-driven approach. In this research, the model parameters were estimated using the nonlinear least squares method. The data used are daily cases of COVID-19 data in West Java, Indonesia. In addition, other parameters such as birthrate and mortality rate were calibrated using population data and mortality data in the pre-pandemic period. Finally, through numerical simulation, the population dynamics is observed in the model that has been formed based on the estimated parameters.

Keywords: COVID-19; nonlinear least squares; dynamical theory.

2010 AMS Subject Classification: 92D25,92D30.

1

1. INTRODUCTION

The infectious illness COVID 19 is caused by the SARS-CoV-2 coronavirus, which is a virus that attacks the respiratory system. The World Health Organization (WHO) reported the first occurrence on December 31, 2019, in Wuhan, China [1]. WHO declared COVID-19 a global pandemic on March 11, 2020 [2]. COVID-19 symptoms might occur between 2 and 14 days after infection. COVID-19 infection produces a range of symptoms ranging from mild to severe symptoms. Fever and cough are the most typical symptoms of this illness, however other symptoms may appear. [3].

This pandemic has a fairly large and universal impact, so not only a health crisis is caused by this pandemic, but one of the major aspects of economic growth is the COVID-19 pandemic. Hence, this makes this pandemic an interesting object and strategy to research. COVID-19 researchers are challenged to solve the COVID-19 problem through both vaccines and drugs. Mathematician contribution to addressing the COVID-19 issue is modeling the dynamics of COVID-19 spread throughout the population. The output of the model can be used as a reference for the policy or as input for further research. Mathematical models that have been studied previously include the COVID-19 transmission model considering vaccination and treatment [4]–[6], the model of COVID-19 transmission with waning immunity [7], the mathematical model of the spread of COVID-19 with treatment costs [8],[9] and the mathematics Spread of COVID-19 with the effectiveness of vaccination in reducing health expenditure [10],[11]. This research examined at the spread of COVID-19 in the population. Given that the current data is generally recorded on a daily time frame, the model utilized is a discrete approach. In this research, all parameters used in the model were calibrated and estimated using the collected data. The model created is then analyzed and simulated to accurately describe the population dynamics that occur.

2. MATERIALS AND METHODS

This section describes the materials and methods used in this research.

2.1 Data

The data used in this research is data on positive, recovered, died, and active COVID-19 cases in West Java. The data was obtained from the West Java COVID-19 Information and Coordination Center [12]. The data is from June 1, 2021, to June 1, 2022. Other data, such as the demographics of the population of West Java, were obtained from the results of the 2020 Indonesian population census [13]. Figure 1 shows a graph of positive cases, recovered, and died in West Java.
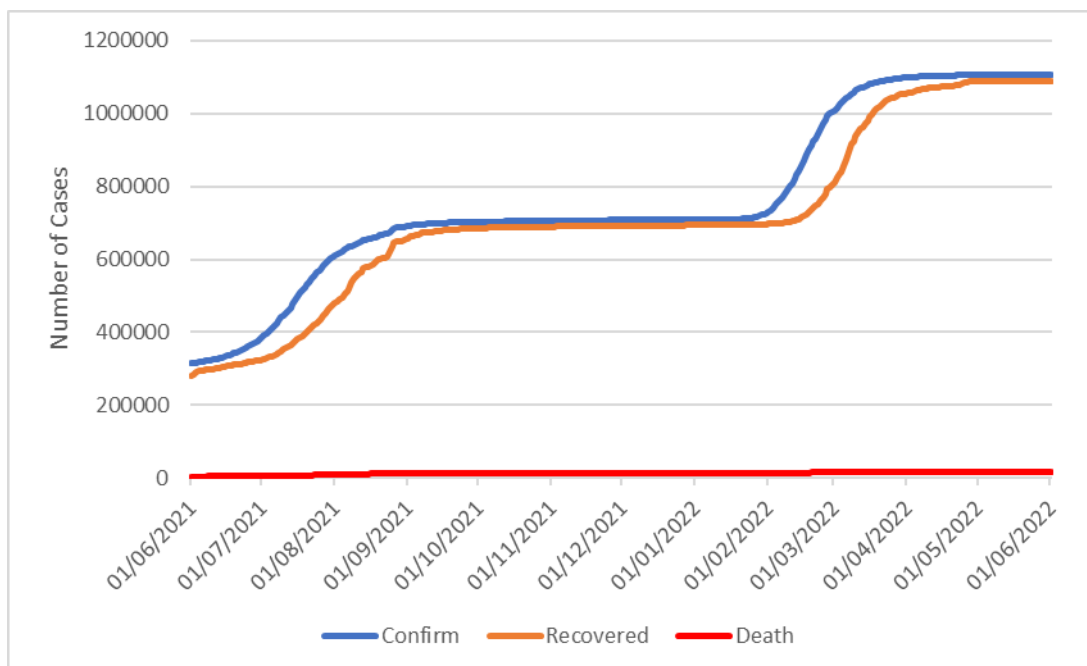

Figure 1. Graph of positive cases, recovered, died in West Java

2.2 Model Formulation

The mathematical model for studying the spread of COVID-19 is represented by a deterministic discrete-time model. The model is constructed by dividing the human population into three compartments such as Susceptible, Infected, and Recovered, denoted by S, I, and R, respectively. The schematic diagram for the COVID-19 model is visualized in Figure 1, with the definition of parameters used in Table 1.

D.S. PANGESTU, S.T. TRESNA, F. INAYATUROHMAT, N. ANGGRIANI

Table 1. Parameters Definition

Parameter	Definition
Λ	Birthrate rate
μ	Mortality rate
d	Mortality rate due to COVID-19
β	Infection rate
α	Recovery rate
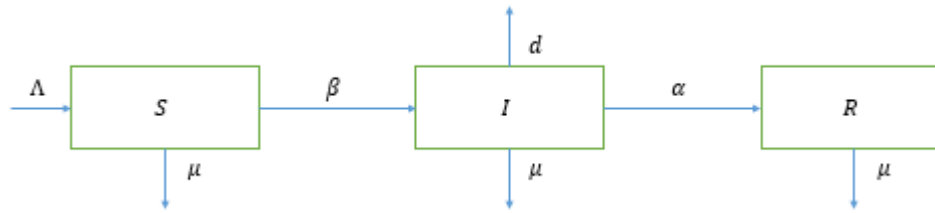
Figure 2. Schematic diagram of the COVID-19 model

According to Figure 2, all compartment decreases because of mortality at the rate of μ. The susceptible (S) increases because of the recruitment at the rate of Λ and decreases because of the infection at the rate of β. The Infected (I) increases because of the infection at the rate β and decreases not only because of the mortality but also mortality due to COVID-19 at the rate of d. The Recovered (R) increases because of the recovery rate at the rate of α. Therefore, the difference equation system for representing the COVID-19 transmission can be written as follows:

$$S_{t+1} = \Lambda + (1 - \mu)S_t - \beta S_t I_t$$
$$I_t = \beta S_t I_t + (1 - \alpha - d - \mu)I_t \qquad (1)$$
$$R_t = \alpha I_t + (1 - \mu)R_t$$

2.3 Parameter Estimation

In this section, there were 5 parameters used in the COVID-19 spread model. Parameters Λ obtained from the results of the 2020 West Java population census, these parameters are calibrated first into daily form before being used in the simulation model. For parameters μ estimated from data on health deaths and deaths due to accidents before the COVID-19 pandemic. So that the parameters are estimated using death data with health causes and accidents in 2019. For parameters, α, β, dan d are estimated using the non-linear least squares method.

Nonlinear least-squares is one of the least squares analysis that is used for m observations on a model with n unknown parameters [14]. The objective function of the Nonlinear least squares problem is,

$$f(x) = \frac{1}{2}\sum_{i=1}^{M} \|r_i(x)\|_2^2 = \frac{1}{2}r^T r$$

with the vector $r = (r_1, \ldots, r_m)$ is the residual vector. Because nonlinear least squares problems constitute a transition from nonlinear equations to optimization problems, their solutions reflect this.

3. MAIN RESULTS

3.1. Equilibria Point

In terms of epidemic model analysis, there are two types of equilibria points which are non-endemic and endemic. The non-endemic equilibria point represents the absence of an infected population in the system. To obtain the non-endemic equilibria point, the infected population is set to be at zero $(I^* = 0)$. Based on (1), a non-endemic equilibria point is obtained as follows:

$$Eq_0 = \{S^*, I^*, R^*\} = \left\{\frac{\Lambda}{\mu}, 0, 0\right\} \tag{2}$$

Endemic equilibria represents that the epidemic occurs. Based on (1), an endemic equilibria point is obtained as follows:

$$S^* = \frac{\alpha + d + \mu}{\beta} \tag{3}$$

$$I^* = \frac{\Lambda\beta - \mu\alpha - \mu d - \mu^2}{\beta(\alpha + d + \mu)} \tag{4}$$

$$R^* = -\frac{\alpha(\mu^2 + (\alpha + d)\mu - \Lambda\beta)}{\beta(\alpha + d + \mu)\mu} \tag{5}$$

3.2. Basic Reproduction Ratio

In mathematical epidemiology, the basic reproduction ratio $(\mathcal{R}_0)$ is one of the important things to know [15], [16]. It represents the potential whether the disease is epidemic or not. Hence some interventions can be considered to control the disease spread. We use the next generation matrix [15] to get the basic reproduction ratio, with f as the new infection matrix and v as the

change in the infection matrix (including a decrease by recovery or death due to the disease). The f and v matrix follows:

$$f = [\beta S I] \text{ and } v = [\alpha I + dI + \mu I]$$

The Jacobian matrix for f and v is represented by F and V^{-1}, respectively. We determine the spectral radius (dominant eigenvalue) of the FV^{-1} matrix at the non-endemic equilibria point. Hence, we get:

$$\mathcal{R}_0 = \frac{\beta \Lambda}{\mu(\alpha + d + \mu)}$$

3.3. Stability Analysis

Based on (1), the Jacobian matrix is obtained as follows:

$$J = \begin{bmatrix} -\beta I - \mu + 1 & -\beta S & 0 \\ \beta I & \beta S - \alpha - d - \mu + 1 & 0 \\ 0 & \alpha & 1 - \mu \end{bmatrix}$$

The following theorem gives the local stability of the non-endemic equilibria point:

Theorem 1

The non-endemic equilibria point of the model is locally asymptotically stable if $\mathcal{R}_0 < 1 - \frac{1}{\alpha + d + \mu}$.

Proof

By following [1], substituting the non-endemic equilibria point (2) into the Jacobian matrix, then the characteristic polynomial of $J(Eq_0)$ is obtained as follows:

$$\frac{(\lambda + \mu - 1)^2\big((\lambda + \alpha + d - 1)\mu + \mu^2 - \Lambda\beta\big)}{\mu} = 0$$

From that polynomial, the eigenvalues are known as follows:

$$\lambda_{1,2} = 1 - \mu$$

Based on the eigenvalue, λ_1 and λ_2 will be negative if $\mu > 1$; hence the system is locally stable, then λ_3 must be negative. By considering the polynomial, we obtain

$$\frac{\big((\lambda + \alpha + d - 1)\mu + \mu^2 - \Lambda\beta\big)}{\mu} = 0$$

$$\lambda = \frac{\Lambda\beta - (\alpha + d + \mu)\mu + \mu}{\mu} = \frac{\mathcal{R}_0\big((\alpha + d + \mu)\mu\big) - (\alpha + d + \mu)\mu + \mu}{\mu} < 0$$

$$\mathcal{R}_0\big((\alpha + d + \mu)\mu\big) - (\alpha + d + \mu)\mu + \mu < 0 \rightarrow (\mathcal{R}_0 - 1)(\alpha + d + \mu)\mu < -\mu$$

$$(\mathcal{R}_0 - 1)(\alpha + d + \mu) < -1 \rightarrow \mathcal{R}_0 - 1 < -\frac{1}{(\alpha + d + \mu)}$$

$$\mathcal{R}_0 < 1 - \frac{1}{(\alpha + d + \mu)}$$

This completes the proof.

3.4 Parameter Estimation Results

Table 2 shows the results of the parameter estimate utilized in this research.

Table 2. Parameter Estimation Results

Parameter	Definition	Value
Λ	Birthrate rate	3.0411E-05
μ	Mortality rate	3.85316E-07
d	Mortality rate due to COVID-19	0.0006568
β	Infection rate	0.05874
α	Recovery rate	1.47E-09

The parameters presented in Table 2 were then used to simulate the COVID-19 spread model numerically in this research. Before being used in numerical simulations, the parameter estimation results are checked first, evaluating the accuracy of the model against the data used. Figure 3 shows the plot between model predictions and data on COVID-19 cases in West Java.
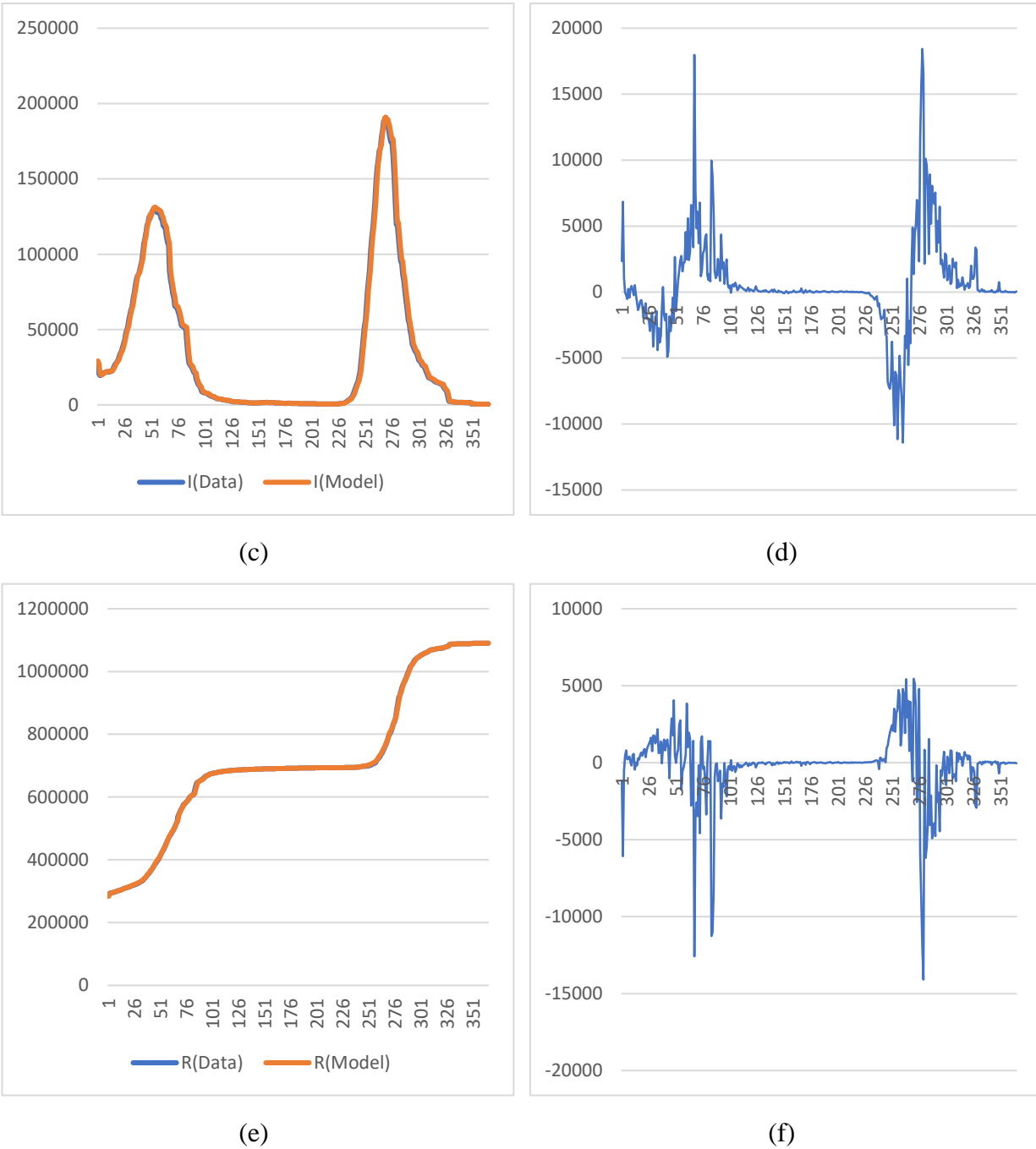

(a)

(b)

(c)

(d)

(e)

(f)
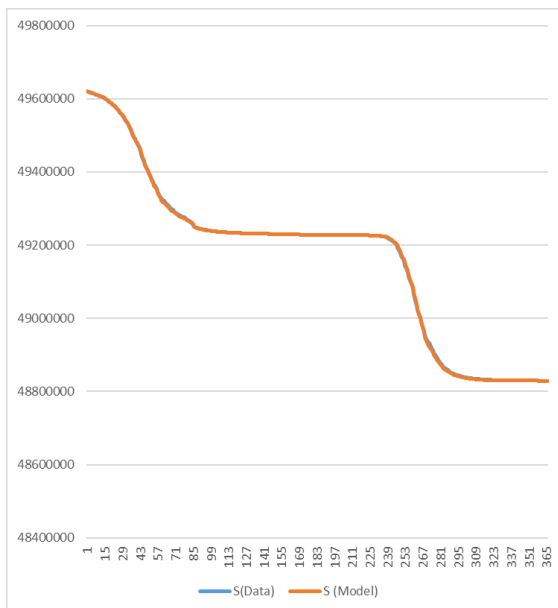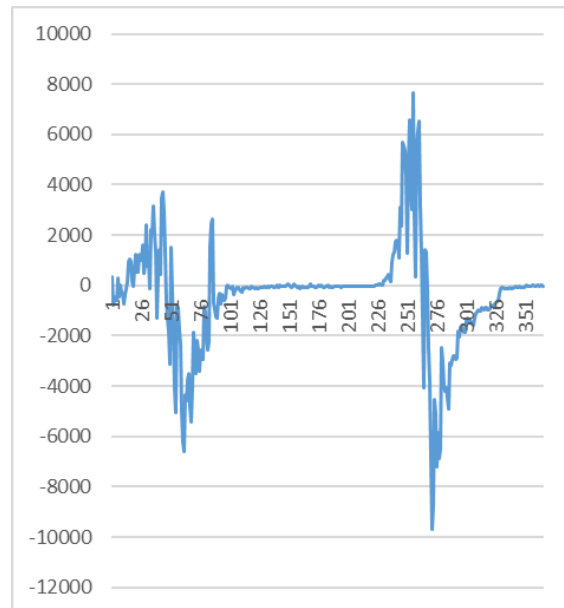
Figure 3. Comparison between model predictions and data (a) S compartment (b) S residual (c) I compartment (d) I residual (e) R compartment (b) R residual

Figure 3 compares the data plot and the predicted model results plot. At first glance, it can be seen that the prediction results of the model are close to the data, even though there are still errors in the prediction results. For example, in Figure 3 (b), (d), (f) the residuals from each compartment in the population are shown. Based on this residual plot, it can be seen that there are errors that are not visible at a glance, and several periods of time are also found where the errors that occur have increased. However, in general, it can be concluded that the parameters used are fit for use in numerical simulations.

3.5 Numerical Simulation

The aim of this numerical simulation is to figure out the population dynamics in the COVID-19 spread model. The numerical simulation in this research uses the parameters presented in Table 2. Figure 2 shows the population dynamics of COVID-19 in West Java.
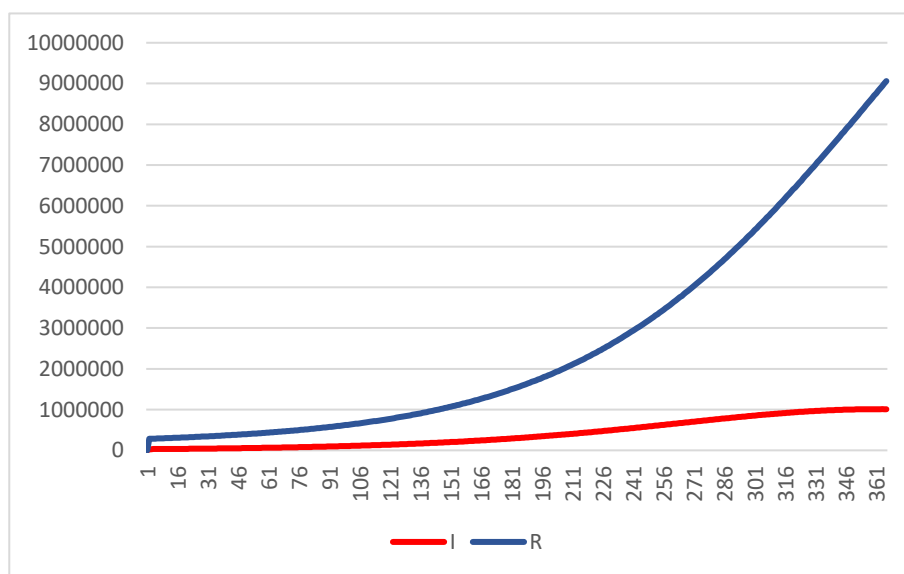

Figure 4. S, I, R Population Dynamics in West Java

Figure 4 shows population dynamics on the spread of COVID-19 in West Java. Based on Figure 4, it is found that the susceptible population will continue to decrease over time, while the infected and recovered populations will continue to increase. For more detailed observations, Figure 5 shows population I and R dynamics on the spread of COVID-19 in West Java.
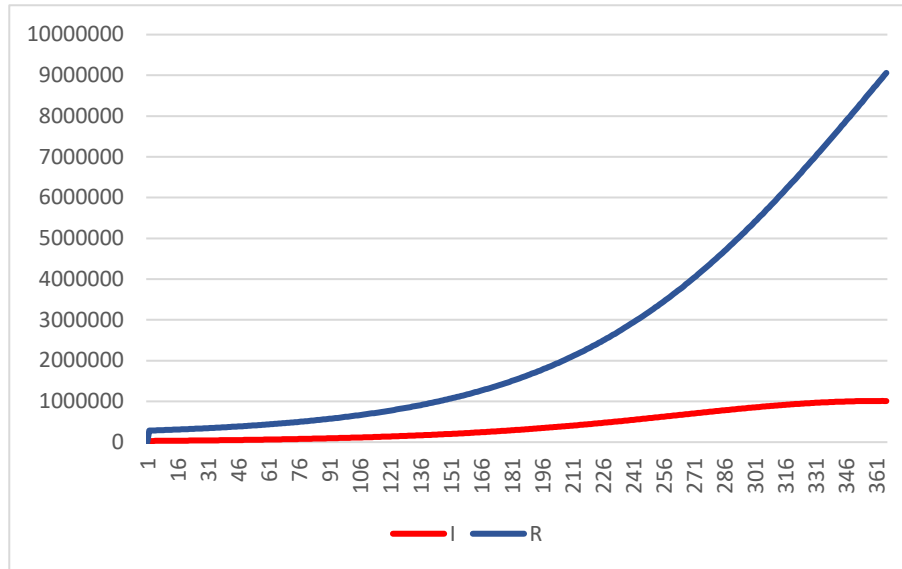
Figure 5. I, R Population Dynamics in West Java

Based on Figure 5. It was found that the increase in the recovered population was much more significant than the increase in the infected population, or as the pandemic progressed, the number of people who recovered would be much higher than the number of people infected with COVID-19.

4. CONCLUSION

We developed a deterministic discrete-time model of SIR for COVID-19 spread. This research is focusing on a data-driven approach and numerical simulation to formulate a COVID-19 population dynamics in West Java, Indonesia. The model has two equilibrias: the non-endemic equilibria which is stable when $\mathcal{R}_0 < 1$ and the endemic equilibria. The infection rate, the recovery rate, and the mortality rate due to COVID-19 were estimated using the non-linear least-squares method. While the birthrate and the mortality rate were calibrated using population data and mortality data in the pre-pandemic period. The result of the parameter estimation using a non-linear least squares is fitting the data very well. Finally, the population dynamics are observed through numerical simulation of the model. The susceptible continuously decreases while the recovered always increases in a year.

CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

REFERENCES

[1]   WHO, Coronavirus disease 2019 (COVID-19). situation report–57, (2020).

https://www.who.int/publications/m/item/situation-report---57.

[2]   WHO, Coronavirus disease 2019 (COVID-19) situation report–51, (2020).

https://www.who.int/publications/m/item/situation-report---51

[3]   CDC, CDC FAQ on COVID-19, (2020). https://www.cdc.gov/coronavirus/2019-ncov/vaccines/faq.html.

[4]   M.L. Diagne, H. Rwezaura, S.Y. Tchoumi, et al. A mathematical model of COVID-19 with vaccination and treatment, Comput. Math. Methods Med. 2021 (2021), 1250129. https://doi.org/10.1155/2021/1250129.

[5]   M. Yavuz, F.Ö. Coşar, F. Günay, et al. A new mathematical modeling of the COVID-19 pandemic including the vaccination campaign, Open J. Model. Simul. 09 (2021), 299–321. https://doi.org/10.4236/ojmsi.2021.93020.

[6]   G. Webb, A COVID-19 epidemic model predicting the effectiveness of vaccination in the US, Infect. Dis. Rep. 13 (2021), 654–667. https://doi.org/10.3390/idr13030062.

[7]   F. Inayaturohmat, N. Anggriani, A.K. Supriatna, Optimal control and sensitivity analysis of COVID-19 transmission model with the presence of waning immunity in West Java, Indonesia, Commun. Math. Biol. Neurosci., 2022 (2022), 19. https://doi.org/10.28919/cmbn/7124.

[8]   S. Torres-Rueda, S. Sweeney, F. Bozzani, et al. Stark choices: exploring health sector costs of policy responses to COVID-19 in low-income and middle-income countries, BMJ Glob. Health. 6 (2021), e005759. https://doi.org/10.1136/bmjgh-2021-005759.

[9]   P. Dudine, K.-P. Hellwig, S. Jahan, A framework for estimating health spending in response to COVID-19, IMF Working Papers. 2020 (2020), 1-43. https://doi.org/10.5089/9781513550220.001.

[10] J.E. Marco-Franco, P. Pita-Barros, S. González-de-Julián, et al. Simplified mathematical modelling of uncertainty: Cost-effectiveness of COVID-19 vaccines in Spain, Mathematics. 9 (2021), 566. https://doi.org/10.3390/math9050566.

[11] F.G. Sandmann, N.G. Davies, A. Vassall, et al. The potential health and economic value of SARS-CoV-2 vaccination alongside physical distancing in the UK: a transmission model-based future scenario analysis and economic evaluation, Lancet Infect. Dis. 21 (2021), 962–974. https://doi.org/10.1016/s1473-3099(21)00079-7.

[12] Pikobar, Statistik Kasus COVID-19 Provinsi Jawa Barat, (2022). https://dashboard.jabarprov.go.id/id/dashboard-pikobar/trace/statistik (accessed Jun. 16, 2022).

[13] BPS, Result of 2020 population census of Jawa Barat Province, (2021). https://bekasikab.bps.go.id/pressrelease/2021/02/08/617/hasil-sensus-penduduk-2020-di-provinsi-jawa-barat.html

[14] A. Sanfelice Bazanella, L. Campestrini, D. Eckhard, Iterative optimization, in: Data-Driven Controller Design, Springer Netherlands, Dordrecht, 2012: pp. 69–88. https://doi.org/10.1007/978-94-007-2300-9_4.

[15] O. Diekmann, J.A.P. Heesterbeek, M.G. Roberts, The construction of next-generation matrices for compartmental epidemic models, J. R. Soc. Interface. 7 (2009), 873–885. https://doi.org/10.1098/rsif.2009.0386.

[16] P. van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci. 180 (2002), 29–48. https://doi.org/10.1016/s0025-5564(02)00108-6.