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SVEAuAdIR model of COVID-19 Transmission

Anindhita Nisitasari*[1], Nur Rokhman[2]
[1]Master Program of Computer Science, FMIPA UGM, Yogyakarta, Indonesia,
[2]Department of Computer Science and Electronics, FMIPA UGM, Yogyakarta, Indonesia
e-mail: ***[1]anindhita.n@mail.ugm.ac.id**, [2]nurrokhman@ugm.ac.id

Abstrak

Pandemi COVID-19 memiliki tingkat penyebaran dan kasus kematian tinggi. Sejumlah penelitian dilakukan untuk membangun model penyebaran COVID-19. Namun demikian, penelitian tersebut belum menggunakan faktor pengaruh vaksinasi. Pada penelitian ini dikembangkan model penyebaran COVID-19 bernama SVEAuAdIR. Model ini pengembangan dari model SEAuAdIR dengan menambahkan faktor pengaruh vaksinasi. Model ini diselesaikan dengan menggunakan metode Runge-Kutta orde empat. Implementasi model dibuat dengan bahasa pemrograman Python. Unjuk kerja model diuji dengan data pasien COVID-19 di Indonesia pada 2 Maret 2020 hingga 30 April 2021 (425) data. Pelaksanaan vaksinasi dimulai tanggal 13 Januari 2021, dilakukan estimasi ulang untuk parameter: laju kontak (β) dan laju vaksinasi (σ). Estimasi ulang menggunakan data sampai dengan 24 April 2021. Data 25 April 2021 hingga 30 April 2021 digunakan sebagai data uji. Hasil uji menunjukkan MAPE sebesar 12%. Sehingga dikatakan model SVEAuAdIR baik digunakan untuk prediksi penyebaran COVID-19. Model SVEAuAdIR memiliki nilai $R_0 = 1{,}36 \times 10^{-7}$. Hal ini menunjukkan tingkat penyebaran COVID-19 yang rendah, sesuai dengan pengaruh vaksinasi. Menggunakan model SVEAuAdIR diprediksi bahwa Indonesia bebas COVID-19 pada tanggal 7 Oktober 2021. Namun, pada tanggal tersebut data aktual menunjukkan kasus baru COVID-19 sebanyak 1393 kasus. Hal ini dimungkinkan karena varian baru COVID-19, vaksinasi yang kurang lancar, atau pelaksanaan pembatasan sosial yang kurang tertib.

Kata kunci*—COVID-19, SVEAuAdIR, Prediksi*

Abstract

The COVID-19 pandemic has a high rate of spread and death cases. A number of studies were conducted to build a model for the spread of COVID-19. However, the study has not used the influence of vaccination. In this study developed a COVID-19 spread model named SVEAuAdIR. This model is developed from the SEAuAdIR model by adding vaccination influence factors. This model was completed using the Runge-Kutta method of the fourth order. The model implementation is created with the Python programming language. The model's performance was tested with COVID-19 patient data in Indonesia from March 2, 2020 to April 30, 2021 (425) data. The implementation of vaccination began on January 13, 2021, re-estimates for parameters: contact rate (β) and vaccination rate (σ). Re-estimate using data until April 24, 2021. Data from April 25, 2021 to April 30, 2021 are used as test data. Test results show mape at 12%. So it is said that the SVEAuAdIR model is good for predicting the spread of COVID-19. The SVEAuAdIR model *has value*$R_0 = 1{,}36 \times 10^{-7}$*. This indicates a low rate of COVID-19 spread, in accordance with the influence of vaccination. Using the SVEAuAdIR model it is predicted that Indonesia is COVID-19 free on October 7, 2021. However, on that date actual data showed 1393 new cases of COVID-19. This is possible due to new variants of COVID-19, less smooth vaccinations, or the implementation of less orderly social restrictions.*

Keywords—*COVID-19, SVEAuAdIR, Forecasting*

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1. INTRODUCTION

The COVID-19 pandemic has captured the world's attention due to its rapid rate of spread and the number of fatalities it has caused. According to the World Health Organization (WHO), the virus is being transmitted by infected individuals. Symptoms of the infection include high fever, shortness of breath, coughing, sneezing, and sometimes a loss of taste or smell. The virus can easily spread through small droplets produced by coughing or sneezing [1].

There is ample evidence that machine learning algorithms can provide efficient predictions in healthcare [2][3]. Nsoesie [4] conducted a systematic review of the approaches used to forecast the dynamics of influenza pandemics and reviewed research papers based on deterministic mass action models, regression models, predictive rules, Bayesian Networks SEIR models, ARIMA forecasting models, among others. Recent studies on COVID-19 have only explored the limited available data through descriptive analysis. The SEIR model is a widely used mathematical approach for studying the spread of infectious diseases, including COVID-19 [5-8]. It has also been used to study the impact of vaccination on the spread of the disease [9][10]. The effects of COVID-19 vaccination, especially in Indonesia, warrant further investigation into the influence of vaccinated individuals on the spread of the disease.

To account for vaccinated individuals, the SEIR model must be modified and named the SVEAuAdIR model. This model can be established by estimating its parameters based on the characteristics of the spread of COVID-19. The SVEAuAdIR model is a problem of initial values, in the form of a system of first-order differential equations, which requires a numerical solution. Ordinary differential equations can be solved using various methods, including the fourth-order Runge-Kutta method [11]. This method has been used in several studies on the spread of COVID-19 but has not considered the impact of vaccinated groups. The fourth-order Runge-Kutta method is an alternative to the Taylor series method, which eliminates the need for derivative calculations. It is more accurate than the Euler method, Heun method, and Taylor series method but requires more iterations. The highest order of the Runge-Kutta method is fifth order [12]. The fourth-order Runge-Kutta method was selected for this study due to its close approximation to the exact value and lower expected number of iterations [13].

2. METHODS

The aim of this study is to predict the number of individuals in the Indonesian population on the SVEAuAdIR model using the fourth-order Runge-Kutta method. The study begins with collecting data on the number of individuals infected with COVID-19 for a period of one year. This data is then used to train the model. During the training process, the data produces estimates of the number of individuals in each group on the SVEAuAdIR model, as well as estimated parameter values. After the model is built, the data is tested to analyze the predicted values. The next step is to determine the phase of disease spread by calculating the values. Error values are also calculated to assess the model's performance, using the accuracy metric of R_0 and MAPE. If the model's MAPE value is less than 90%, it can be considered a successful model. On the other hand, if the MAPE value is greater than 90%, the model is considered to have failed. Finally, the results of the SVEAuAdIR model predictions are implemented.

2.1 Data Source

The data used in this study was collected from various sources. The Indonesian Health Profile was the primary source for obtaining annual data on the number of Indonesians, while data on the number of individuals infected with COVID-19 was obtained from the World Health Organization (WHO). Data on crude birth rate (CBR), crude death rate (CDR), incidence rate, and COVID-19 death rate was obtained from the COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University. Daily data on the number of recovered individuals, individuals who died, and individuals who were vaccinated was obtained from kawalCovid19.id. The data was used to train and test the SVEAuAdIR model, developed to predict the spread of COVID-19 in Indonesia, using the Runge-Kutta method of the fourth order. The accuracy of the model was determined using the R_0 and MAPE values. If the model produced a MAPE value of less than 90%, it was considered successful, and its predictive results were implemented.

2.2 SVEAuAdIR Model

The SVEAuAdIR model used in this study is a compartmental model that describes the spread of COVID-19 in the population by considering the different health states of individuals and the transitions between them. The model considers the dynamics of the disease spread by using the differential equations that describe the flow of individuals from one compartment to another. The model takes into account factors such as birth rate, death rate, infection rate, and recovery rate. The model also considers the effects of vaccination on the spread of the disease by including the number of vaccinated individuals as a parameter. The objective of the study is to use the SVEAuAdIR model to predict the spread of COVID-19 in Indonesia and analyze the effects of vaccine administration on the disease spread. The number of individuals S, E, Au, Ad, I, and R at time t is S(t), V(t), E(t), Au(t), Ad(t), I(t), and R(t), so the number of individuals in the population at time t is

$$N_t = S_t + V_t + E_t + Au_t + Ad_t + I_t + R_t$$

The assumption given to the model is that the population is homogeneous and that rapid tests are used to identify individuals who show no symptoms. The tests are performed on all groups except group I, and individuals in groups Au and Ad are allowed to socialize more because they show no symptoms. The hospital environment facilitates faster recovery for infected individuals due to the limited number of beds and other medical resources. It is also assumed that the recovery rate for infected individuals in the hospital is higher. Therefore, the change in the number of individuals in each group can be fully described by the SVEAuAdIR model (1).

$$\begin{gathered}
S' = \theta N - \beta S(A_u + \xi_i I + \xi_a A_d) - \mu S + \delta R - \sigma S \\
V' = \sigma S - \omega V - \mu V \\
E' = \beta S(A_u + \xi_i I + \xi_a A_d) - p\alpha E - (1-p)\alpha E - \mu E \\
A_u' = p\alpha E - \gamma_0 A_u - \upsilon A_u - \mu A_u \\
A_d' = \upsilon A_u - \eta A_d - \gamma_0 A_d - \mu A_d \\
I' = (1-p)\alpha E + \eta A_d - \left(\gamma_0 + \frac{\gamma_1}{1+bI}\right) I - (\mu + \phi) I \\
R' = \left(\gamma_0 + \frac{\gamma_1}{1+bI}\right) I + \gamma_0 A_d + \gamma_0 A_u - \delta R + \omega V - \mu R
\end{gathered} \tag{1}$$

The system of first-order nonlinear differential equations is given, subject to the initial non-negative condition that $S(0), V(0), E(0), Au(0), Ad(0), I(0)$, and $R(0)$ are all greater than or equal to zero. The parameters Λ, β, μ, and ϕ represent the rates of natural birth, infection, natural death, and death due to COVID-19, respectively. ξ_i and ξ_a denote reductions in I and Ad, respectively, due to isolation at home or in the hospital. The parameters α, γ_0, and δ represent the rate of COVID-19 progression based on the incubation period, natural recovery rate, and temporary loss of immunity. The proportion of exposed individuals who have progressed to asymptomatic individuals is represented by p, while b represents the rate of hospital capacity or number of medics. γ_1 is the rate of improvement in natural recovery due to hospital treatment, η is the level of hospitalization from Ad to I, and ν represents the effort required for early detection of COVID-19 infection. The rate of vaccination is given by σ and the rate of immunity is ω. A transmission diagram that illustrates the spread of disease is shown in Figure 1.

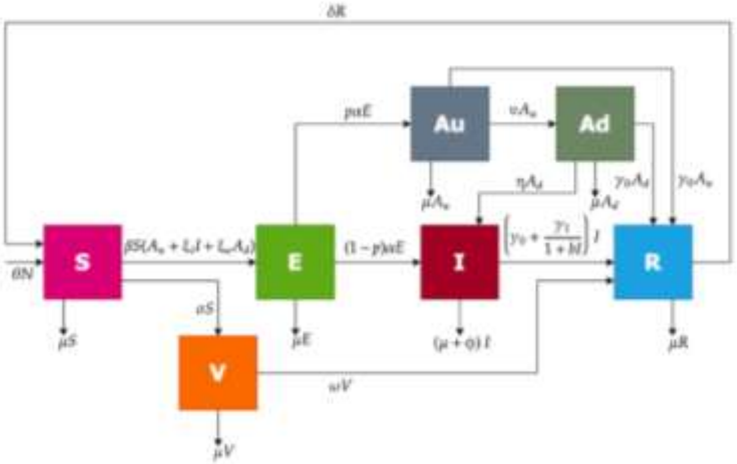

Figure 1 Transmission of COVID-19 SVEAuAdIR Model diagram

The solution to the SVEAuAdIR model in equation (1) is represented by the functions $S(t), V(t), E(t), Au(t), Ad(t), I(t),$ and $R(t)$. These functions represent the number of individuals in each category (S, V, E, Au, Ad, I, and R) at time t. The number of individuals is visualized in graphical form, creating a distinct pattern that illustrates the spread of the disease. The pattern is the result of the completion of the SVEAuAdIR model.

2.3 Fourth Order Runge-Kutta Method

In the SVEAuAdIR model that takes into account vaccinated groups of individuals, the problem is formulated as a first-order differential equation system with initial conditions. The solution can be obtained numerically using the Fourth Order Runge-Kutta method. As stated by Atkinson [18], the Fourth Order Runge-Kutta formula can be used to find the solution of the initial value problem system, as written

$$x_{n+1} = x_n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

with

$$k_1 = h\, f(t_n, x_n)$$
$$k_2 = h\, f\left(t_n + \frac{h}{2}, x_n + \frac{k_1}{2}\right)$$
$$k_3 = h\, f\left(t_n + \frac{h}{2}, x_n + \frac{k_2}{2}\right)$$
$$k_4 = h\, f(t_n + h, x_n + k_3)$$

2.4 MAPE

The accuracy of the model can be evaluated by comparing its output with actual COVID-19 data sets, using the Mean Absolute Percentage Error (MAPE) metric. The MAPE formula is used to calculate this metric

$$MAPE = \frac{1}{n}\sum_{i=1}^{n}\left|\frac{y_i - \hat{y}_i}{y_i}\right|,$$

Where, y_i is the actual value, $\hat{y}_i$ is the predicted value, and n indicates the number of data points. By definition, the lower the value of this performance metric, the better the performance of the forecasting model [19].

Based on Lewis [20], *MAPE* values are interpreted into 4 categories

1. $MAPE < 10\%$, The results of predictions are very accurate,
2. $MAPE\ 10 - 20\%$, The results of predictions are good,
3. $MAPE\ 20 - 50\%$, The results of predictions are still reasonable,
4. $MAPE > 10\%$, The results of predictions are weak or inaccurate.

2.5 Basic Reproduction Number

The value of R_0 provides insight into the transmission of the disease and is a key focus for epidemiologists studying new cases [21]. Simply put, R_0 represents the average number of people who can be infected by one person over a given period of time. If R_0 is less than 1, the spread of the disease is expected to come to a halt. If R_0 is equal to 1, the spread of the disease is stable or endemic. If R_0 is greater than 1, the spread of the disease is increasing and intervention is needed. The R_0 value for the SVEAuAdIR model can be calculated using the formula provided in equation (2).

$$R_0 = \frac{\beta\theta N(\alpha\mu^2+\alpha\mu\nu+\alpha\mu\gamma_0+\alpha\mu\eta+\alpha\nu\eta+\alpha\gamma_0\eta-\alpha\nu p\eta)}{\mu(\eta+\mu)(\mu+\nu+\gamma_0)(\alpha+\mu+\alpha p)(\mu+\phi+\gamma)} \tag{2}$$

3. RESULTS AND DISCUSSION

The SVEAuAdIR model in equation (1) is used to predict the number of infected individuals based on available data. The study takes into account natural births and deaths, as well as temporary immunity loss, since the population is assumed not to be constant over short periods. It also considers the movement of individuals from one compartment to another, such as from S to E, E to I, and I to R, which adjusts the standard SIR models proposed by Hethcote [22], SEIR models for COVID-19 predictions in India [21], and SEAuAdIR by Aldila [23]. As a result, the equation for the SVEAuAdIR model used to make predictions with Indonesian data is presented as follows.

$$\begin{aligned}
S' &= \theta N - \frac{\beta SI}{N} - \frac{\sigma SI}{N} - \mu S + \delta R \\
V' &= \frac{\sigma SI}{N} - \omega V - \mu V \\
E' &= \frac{\beta SI}{N} - (p+1)\alpha E - \mu E \\
Au' &= p\alpha E - (\nu + \gamma_0) Au - \mu Au \\
Ad' &= \nu Au - (\eta + \gamma_0) Ad - \mu Ad \\
I' &= \alpha E + \eta Ad - \gamma I - \mu I - \phi I \\
R' &= \omega V + (Ad + Au)\gamma_0 + \gamma I - \mu R - \delta R
\end{aligned} \tag{3}$$

The parameters used in the SVEAuAdIR model (3) add up to thirteen in total. These parameters are $\theta, \mu, \phi, \beta, \sigma, \omega, \alpha, p, \nu, \eta, \gamma, \gamma_0$ and δ. The estimation of these parameters is based on data from March 2, 2020 to January 31, 2021 for some parameters, while others are obtained from the decline source of the SVEAuAdIR model (3). The estimated values of the parameters are $0.018, 0.007, 0.007, 0.94 \times 10^{-7}, 0.001, 0.167, 0.250, 0.420, 0.367, 0.060, 0.946, 0.270$ and 0.011. After substituting these parameter values into equation system (3), and given the initial value of the SVEAuAdIR model of COVID-19 spread, the equation is written as follows.

$$\begin{gathered}
S' = 0.017\,N - \frac{0.94\times10^{-7}\,SI}{N} - \frac{0.037\,SI}{N} - 0.006\,S + 0.011\,R \\
V' = \frac{0.037\,SI}{N} - 0.167\,V - 0.006\,V \\
E' = \frac{0.94\times10^{-7}\,SI}{N} - (0.420+1)\,0.250\,E - 0.006\,E \\
Au' = 0.420\ \times\ 0.250\,E - (0.367+\ 0.230)Au - 0.006\,Au \\
Ad' = 0.367\,Au\ -\ (\,0.190\ +\ 0.230)\,Ad - 0.006\,Ad \\
I' = 0.250\,E\ +\ 0.190\,Ad\ -\ 0.946\,I - 0.006\,I - 0.031\,I \\
R' = 167\,V\ +\ (\,Ad\ +\ Au\,)0.230\ +\ 0.946\,I - 0.007\,R - 0.011\,R, \\
\big(S(0), V(0), E(0), Au(0), Ad(0), I(0), R(0)\big) = \begin{pmatrix} 257180929 \\ 11741559 \\ 1647138 \\ 3898 \\ 1647138 \\ 4402 \\ 3804 \end{pmatrix}
\end{gathered} \tag{4}$$

The solution of the initial value problem system described by equation (4) can be determined using the Fourth Order Runge-Kutta algorithm for a 5-day period. The algorithm was implemented in a python program and the results were displayed in a table showing the estimated number of individuals in each of the compartments S, V, E, Au, Ad, I, and R for each day from day 0 to day 5. These results can then be compared to actual COVID-19 data to assess the accuracy of the model.

The MAPE results of 12% indicate that the SVEAuAdIR model is fairly accurate in predicting the spread of COVID-19 in terms of the number of infected individuals in different groups (S, V, E, Au, Ad, I, and R). The model can be used to make predictions for the next 2 weeks based on the data available. However, it's important to note that the accuracy of the model's predictions may be impacted by various factors such as changes in intervention measures, the evolution of the virus, and the availability and quality of data. Thus, it's important to continually assess and update the model to ensure its accuracy.

SVEAuAdIR model (4) is used to predict over the next 2 weeks. Selected a new initial value is on the date of the last data in this study April 30, 2021 which is 30 April 2021

$$\big(S(0), V(0), E(0), Au(0), Ad(0), I(0), R(0)\big) = \begin{pmatrix} 256445157 \\ 12422253 \\ 1672880 \\ 5389 \\ 1672880 \\ 5500 \\ 5313 \end{pmatrix} \tag{5}$$

The prediction of the number of individuals in the SVEAuAdIR model (4) is conducted through a python program set to forecast data for up to 365 days ahead. The solution of the SVEAuAdIR model (4) is obtained by utilizing the Fourth Order Runge-Kutta algorithm and the initial value in equation (5). The pattern of the number of consecutive SVEAuAdIR individuals is depicted in Figures 2 and 6.

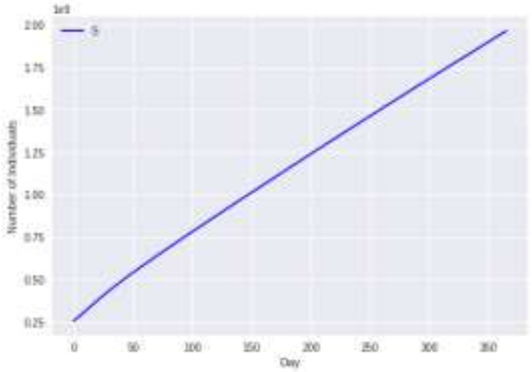

Figure 2 Pattern of the number of individuals S for 365 days

In addition, Figure 6 shows the number of R individuals increasing every day, which indicates that the number of individuals recovering from COVID-19 is increasing. This is in line with the efforts to increase public awareness of the importance of following health protocols and providing adequate treatment to those who are infected. The increasing number of recovered individuals also indicates that the spread of COVID-19 is slowing down.

However, it is important to note that the prediction model is based on assumptions and can be affected by many factors such as changes in behavior, changes in health protocols, and the emergence of new variants of the virus. Therefore, it is necessary to continually monitor and update the model to ensure its accuracy and relevance in predicting the spread of COVID-19.

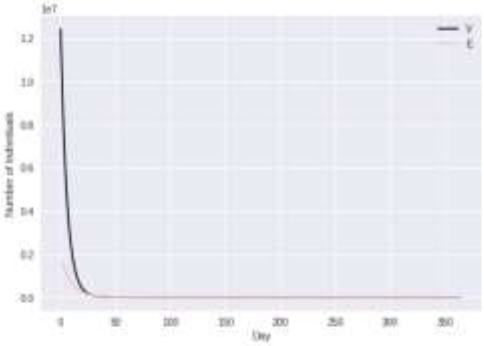

Figure 3 Pattern of the number of individuals V and E for 365 days

In Figure 5, the pattern of the number of infected individuals (I) shows an increase in the number of individuals from day 0 to the 20th day. After the 20th day, the number of infected individuals starts to decrease and continues to decrease until it reaches a stable value. This decrease in the number of infected individuals indicates that health care has been carried out effectively and that the number of individuals who are detected and treated increases.

Lastly, the pattern of the number of recovered individuals (R) can be seen in Figure 6. The graph shows a steady increase in the number of recovered individuals from day 0 to day 365. This increase in the number of recovered individuals indicates that the number of individuals who have recovered from COVID-19 is increasing.

In conclusion, the SVEAuAdIR model provides an accurate prediction of the number of susceptible, vaccinated, exposed, asymptomatic, detected, infected, and recovered individuals in the spread of COVID-19. The results from the MAPE calculation show that the prediction has a good accuracy of around 12%. The prediction from the model can be used to provide insight and guidance for the decision-making process in addressing the COVID-19 pandemic.

This rapid increase in the number of individuals infected with COVID-19 can be attributed to several factors, such as increased exposure to the virus, lack of personal protective measures, and lack of compliance with health protocols. After reaching the peak on the 3rd day, the number of individuals infected with COVID-19 began to decrease until it stabilized on the 50th day. This decrease in the number of individuals infected with COVID-19 can be attributed to the efforts of the government and healthcare professionals to reduce the spread of the virus, such as increasing the number of COVID-19 testing, increasing the number of hospitals, and increasing the number of individuals who have received the vaccine.

It is important to note that the predictions in Figure 5 should be interpreted with caution as it is based on the data available at the time the model was developed and may not accurately reflect the current situation. Additionally, various factors, such as changes in population size and behavior, can affect the spread of the virus and therefore, the accuracy of the predictions.

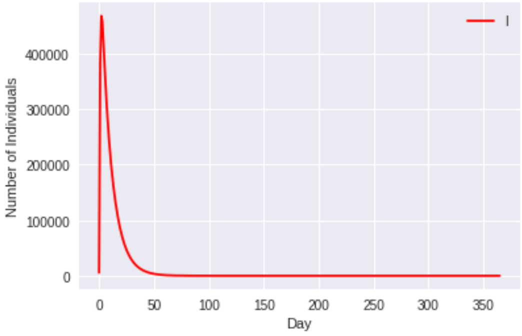

Figure 4 Pattern of the number of individuals I for 365 days

If we observe the pattern of the number of individuals infected with COVID-19, there was a decrease after May 3, 2021, until the 112th day (August 20, 2021), when there were 19,042 individuals. The number of infected individuals continued to decrease until the 160th day

(October 7, 2021), when there were no infected individuals. Figure 5 shows that from day 160 to day 365, there is no change in the pattern due to the predictive value that converges to zero. This is because the data is discrete.

If the number of infected individuals is zero on the 160th day (October 7, 2021), it means that no one is infected with COVID-19 on that day. After that day, there are no more individuals infected with COVID-19 in Indonesia. This situation is called "COVID-19 disease-free," and it was predicted that Indonesia would be COVID-19 free on October 7, 2021. The Indonesian Ministry of Health aimed to stop the spread of COVID-19 by the end of 2021. However, actual data from kawalcovid.id [17] during this study showed that there were still new cases of COVID-19 on October 7, 2021. On that day, there were 1393 new cases, indicating that Indonesia did not achieve its target of being COVID-19 free by the end of 2021.

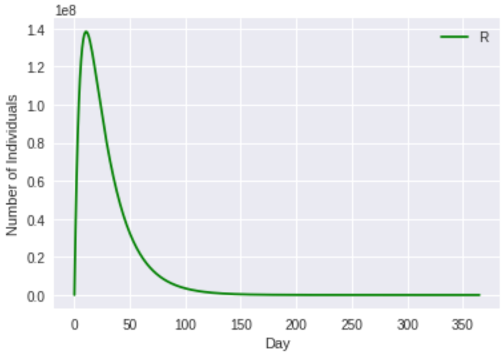

Figure 5 Pattern of the number of individuals R for 365 days

As seen in Figure 6, the behavior pattern of the number of individuals who have recovered from COVID-19 (R) over 365 days showed an increase on day 0, reaching its peak on the 14th day at 138,368 individuals. The peak of individuals who recovered was due to the increased availability of treatments. After the 14th day, there was a decrease in the number of individuals who have recovered, which is believed to be due to more individuals having temporary immunity that eventually wears off, making them vulnerable again.

The study calculated the basic reproductive number (R_0) for the SVEAuAdIR model (4) to determine how the disease spreads when vaccinated. The R_0 value was calculated using the formula in equation (2) with the parameter values used in the model. The resulting R_0 value for the SVEAuAdIR model (4) is $R_0 = 1.36 \times 10^{-7} N$, where N represents the population of Indonesia. The R_0 value falls in the range of $0 < R_0 < 1$, indicating that the disease spread is close to disease-free. When compared to the R_0 value based on Aldila's study [23], which did not consider the vaccination process, the R_0 value obtained in the SVEAuAdIR model (4) tends to be smaller. This may be due to the estimated parameters of the contact rate parameter being lowered and the rate of vaccination being increased. The decrease in the contact rate parameter or the rate of infection is due to the implementation of social distancing policies by the government, while the increase in the rate of vaccination is due to more and more people receiving vaccines to prevent COVID-19 infection. Therefore, based on the results of the R_0 value for the SVEAuAdIR model (4) in this study, it can be concluded that the implementation of COVID-19 vaccination can reduce the rate of spread of COVID-19 compared to those who do not receive the vaccine.

4. CONCLUSIONS

This study developed a new deterministic compartment model to evaluate the spread of COVID-19 among human populations. The model takes into account several important factors, including hidden cases, rapid testing to identify such cases, limitations on medical resources, social distancing, quarantine and isolation measures, and vaccination programs in Indonesia. The model consists of seven variables and has been subjected to rigorous analysis. The analysis of the SVEAuAdIR model yielded the following results.

The model is a modification of the basic SEIR model, which was later refined into the SVEAuAdIR model. The model is represented by equation (1), with $S(0) \geq 0, V(0) \geq 0, E(0) \geq 0, Au(0) \geq 0, Ad(0) \geq 0, I(0) \geq 0$, and $R(0) \geq 0$, along with the parameters Λ, β, μ, and ϕ, which respectively represent the natural birth rate, infection rate, natural death rate, and death rate due to COVID-19. Additionally, parameters ξ_i and ξ_a denote a reduction from β to I and Ad, respectively, due to isolation at home or in the hospital. Further, α, γ_0, and δ represent the rate of development of COVID-19 based on the incubation period, natural recovery rate, and temporary loss of immunity. Parameter p describes the proportion of exposed individuals who have progressed to asymptomatic individuals, while b represents the rate of hospital capacity or the number of medics. γ_1 is the rate of improvement in natural recovery due to hospital treatment, η represents the level of hospitalization from Ad to I, and ν represents the necessary effort for early detection of COVID-19 infection. Finally, parameter σ denotes vaccination rates and parameters ω represent immune rates. The SVEAuAdIR model is represented by a first-order nonlinear differential equations system.

The accuracy of the SVEAuAdIR model is measured using Mean Absolute Percentage Error (MAPE) values. The average of all MAPE values from each individual group was found to be 12%. Based on the MAPE results, it can be concluded that the SVEAuAdIR model is a good prediction model, and can therefore be used to predict the spread of COVID-19 disease in Indonesia.

The pattern of COVID-19 spread in Indonesia can be discerned from the number of individuals infected (I). Beginning on day 0, the pattern of infections increased and then decreased until reaching zero individuals on the 160th day (October 7, 2021), indicating no new cases of COVID-19. This situation, in which there are no longer individuals infected with COVID-19, is called a COVID-19 disease-free state, and it was predicted that Indonesia would achieve this state by October 7, 2021. The Indonesian Ministry of Health set a target to stop the spread of COVID-19 by the end of 2021. However, as of the study's date, new cases of COVID-19 were still being reported. On October 7, 2021, for example, there were 1,393 new cases of COVID-19, demonstrating that Indonesia's target of becoming COVID-19 disease-free by the end of 2021 was not achieved.

The R_0 value for the SVEAuAdIR model is $R_0 = 1.36 \times 10^{-7} N$, which falls within the range of $0 < R_0 < 1$. This indicates that the spread of the disease is close to being disease-free. Based on the results of the R_0 value in this study, it can be concluded that the rate of COVID-19 spread can be reduced through COVID-19 vaccination, compared to those who are not vaccinated.

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