Multi-state Discrete-time Markov Chain SVIRS Model on the Spread of COVID-19

Faihatuz Zuhairoh, Dedi Rosadi*, and Adhitya Ronnie Effendie

***Abstract*—This article discusses the spread of infectious diseases using the multi-state SVIRS model with the assumption that a discrete-time Markov chain (DTMC) occurs in a closed population that is regularly examined. This article aims to generate transition probabilities, which are then used to predict the number of confirmed cases in the next period. The multi-state SVIRS model uses four states, namely susceptible, vaccinated, infected, and recovered, followed by calculating the probabilities of each transition between states that are different from the compartment model. The model was applied to the COVID-19 data in Indonesia, which was analyzed using the statistical software R. The result showed that the transition probability of a person being infected according to the multi-state model with the assumption of DTMC SVIRS on the COVID-19 data was around 25.38% including those with and without vaccination. In comparison, the probability of being recovered was about 92.34%. Then this transition probability was used to predict the confirmed cases of COVID-19 in the next few days. The prediction results were highly accurate with a MAPE value less than 10%. The main contribution of this research is the use of the DTMC assumption, which is a stochastic model in determining the parameters of the differential equation formed by the compartment model and adding the vaccinated state in the model. The vaccinated cases in this article used the proportion of the efficacy of each vaccine used by several susceptible individuals, which, according to WHO recommendations, should be given in two doses. The multi-state model with the assumption of DTMC can model chronic diseases and infectious diseases. This can be seen from the results of the analysis of the COVID-19 data in Indonesia, in which the short-term prediction results had a high level of accuracy.**

***Index Terms*—multi-state model, SVIRS, Markov chain, discrete-time, COVID-19.**

I. Introduction

EPIDEMIOLOGICAL models are divided into deterministic and stochastic models [1]. The deterministic model is formulated in an ordinary differential equation, consequently predicting the same dynamics for an infection process with the same initial conditions. Meanwhile, the stochastic model is a more realistic model because the outbreak does not involve or infect the same person simultaneously, and the uncertainty must be included in the model [2].

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In a deterministic model, the basic reproduction number (R_0) can be used to determine the extinction of an epidemic [3], [4]. Usually, from the deterministic model, the stochastic model inherits the basic reproductive number. However, [5], [6] explains that the Markov chain model in stochastic epidemics has spread of disease with two different possible random variables (i.e., the population transmissions number and the exact reproduction number) provide accurate measurements of disease reach at the beginning of an epidemic or any point during the epidemic process.

A stochastic process can be used to interpret the SVIRS epidemic model. Set of random variables $\{Y_w : w \in T\}$ where each state Y is a function of time w, i.e., number Y_w is observed at any time w is called the stochastic process [7]. The set T denotes the range of observable times for the system. Stochastic processes model how random variables change over time. When sets T can be computed and are equidistant, the stochastic process is a discrete-time process whereas if set T has different distances, it is called a continuous-time process.

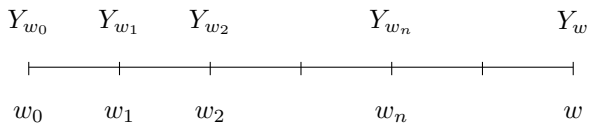


Fig. 1. Discrete-time stochastic process

A basic example of a stochastic process is given in Fig. 1 for discrete times where the state space is determined by the value obtained from a process. The state space depicts the locations where stochastic processes can be detected. The state space in infectious illness modelling is typically limited. The state space of the SVIRS model consists of susceptible, vaccinated, infected, and recovered states.

More discrete-time Markov models have been developed in recent years, including the [8], [9] research which considered a discrete-time model to investigate disease transmission in organized populations. In addition, the next generation matrix method was implemented by [10], [11] to measure the basic reproduction numbers of several models related to the spread of a disease. The authors introduced probabilities in [12] in the models of SI and SIS epidemics of the discrete-time to formulate mortality and cure rates. Disadvantages of the models of SI and SIS epidemics with vertical transmission in discrete time were defined by [13]. In addition, the vaccination discrete-time SIS model was also discussed by [14]. The effect of vaccination on the risk of infection can also be analyzed in the discrete time SIR model [15]. The SEIR and SEIHR epidemic model was developed by [16], [17], a more complex model. Previous research on the SVIR model was carried out by [18], [19] but it was still limited

in deterministic models.

This article discusses the SVIRS stochastic epidemic model with the assumption of discrete-time Markov chains, which describe the spread of COVID-19 where infected people can still be reinfected, regardless of whether they have been vaccinated. It was then followed by predicting confirmed COVID-19 in a short time. In a previous study, we have carried out a long-term prediction of COVID-19 with the Richards curve model [20]. It has been estimated that the transmission of the disease depends on the number of infected individuals, who have been vaccinated with the second dose according to the WHO recommendation and the recovery of the person depends on the cure rate of γ. The rate or severity of each event gives the average number of events per unit of time. Therefore, in the case of recovery, $\frac{1}{\gamma}$ represents the mean time of infection. Populations can be observed at fixed intervals, to control the spread of disease.

This paper aims to model the spread of COVID-19 with a discrete-time SVIRS model and then predict the next few periods using a transition matrix. We used discrete-times, which are analogous to extinction times that describe the length of an epidemic process. Many papers have concentrated on the moment of extinction. Many of them focus on deciding moments, and some even on the distribution of the whole. In this sense, we assume that the mean time of extinction is not affected by the time of birth and death and establishes that the time of extinction follows a simple exponential distribution [21] when the initial distribution is equal to the quasi-stationary distribution. The predicted length of [22], [23] was tested numerically for the models of SI and SIS epidemics of the discrete-time. It is possible to predict the peak and end of an epidemic by predicting COVID-19 using a transition matrix [24] and using a phenomenological model [25].

COVID-19 has caused anxiety among many people. According to experts, a small percentage of people may experience long-term mental health issues that outlast the pandemic. The prolonged duration of quarantine causes anxiety, boredom, and frustration. This is followed by a lack of supply, confusing and uncertain data and information, financial losses, and mental stigma that have an impact on the symptoms of stress and psychological disorders [26]. In Indonesia itself, a large-scale social restriction scheme was implemented but still hopes that economic activities will continue with a number of restrictions to prevent the spread of COVID-19.

This study used transition probabilities with the assumption of DTMC which is a stochastic model in determining the parameters of a differential equation formed by the compartment model. It also added a vaccinated state in the multi-state model. The vaccinated cases in this article used the proportion of the efficacy of each vaccine used by a number of susceptible individuals which, according to the recommendations of the World Health Organization (WHO), should be given in two doses. The vaccines used consisted of five vaccines, namely Sinovac, Sinopharm, Pfizer/BionTech, Moderna, and AstraZeneca/Oxford Vaccine; the Johnson and Johnson vaccine was not included in this study because it requires one dose only.

At each level or checkpoint, we modelled the outbreak with the DTMC SVIRS based on the number of infected individuals, individuals who had been vaccinated with the second dose, and individuals who recovered. This article is structured as follows. We presented the DTMC models and SVIRS epidemic models in Section II that explains the evolution of the epidemic. The recursive results were then presented and an algorithmic scheme for the distribution of the random variable was created to reflect the number of inspections to find an active epidemic phase. In Section III, we determine the transition probabilities then estimate the parameters using the maximum likelihood method and provide the procedures for DTMC SVIRS model. Then, we apply the DTMC SVIRS model to the simulation data and COVID-19 data in Indonesia in Section IV and predicted the accuracy of the next few days by calculating the MAPE value. Finally, in Section V, we give a conclusion. The difference between the DTMC SVIRS compartment model and the multi-state DTMC SVIRS was that the modelling between states changed, i.e., the compartment model used differential equations while the multi-state used transition probability.

II. SVIRS Epidemic Models using Discrete-time Markov Chain

A. Discrete-time Markov Chain Model

Let $\{Y_w : w \in T\}$ be a random variable showing the state of the system at time $w \in T = \{0, \Delta w, 2\Delta w, \dots\}$ with discrete state space

$$\{k_0, k_{\Delta w}, k_{2\Delta w}, \dots, k_{w-\Delta w}, k, l\} = S \subset \{0, 1, 2, \dots, N\}$$

If the stochastic process satisfies the required (1), it is a discrete-time Markov chain.

$$\begin{aligned} \Pr[Y_{w+\Delta w} = l | Y_w = k, \dots, Y_{\Delta w} = k_{\Delta w}, Y_0 = k_0] \\ = \Pr[Y_{w+\Delta w} = l | Y_w = k] \\ = p_{kl}(\Delta w) \end{aligned} \tag{1}$$

If at time w, the state of $w + \Delta w$ only depends on the previous state, then this discrete-time process satisfies the Markov property so that a process that occurs no longer requires past events to determine the probability of the next transition. $p_{kl}(\Delta w)$ is the transition probability from state k at time w to state l at time $w+\Delta w$. In this case the transition probability is homogeneous with respect to time.

$$\begin{aligned} \Pr[Y_{w+\Delta w} = l | Y_w = k] = \Pr[Y_{\Delta w} = l | Y_0 = k] \\ = p_{kl}(\Delta w) \end{aligned} \tag{2}$$

The transition from state k to state l in the period Δw is called a one-step transition probability which can be written as $p_{kl}(\Delta w)$. Meanwhile, if it occurs in n-steps, then the transition from state k to state l in the period $n\Delta w$ is given as follows.

$$\Pr[Y_{w+n\Delta w} = l | Y_w = k] = p_{kl}^{(n)}(n\Delta w) \tag{3}$$

Probability $p_{kl}(\Delta w)$ may sometimes be zero.

In a discrete-time Markov chain, transition probability matrix $\mathbf{P}(\Delta w)$ is used to characterize all the possible one-step transitions. Because the state might vary between 0 and N, $\mathbf{P}(\Delta w)$ is the $(N + 1) \times (N + 1)$ matrix. The $\mathbf{P}(\Delta w)$ matrix is shown below.

$$\mathbf{P}(\Delta w) = (p_{kl})k, l \in S$$

or

$$\mathbf{P}(\Delta w) = \begin{bmatrix} p_{00} & p_{01} & \cdots & p_{0l} & \cdots & p_{0N} \\ p_{10} & p_{11} & \cdots & p_{1l} & \cdots & p_{1N} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\ p_{k0} & p_{k1} & \cdots & p_{kl} & \cdots & p_{kN} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\ p_{N0} & p_{N1} & \cdots & p_{Nl} & \cdots & p_{NN} \end{bmatrix}$$

The number of rows in the matrix $P(\Delta w)$ is always equal to 1, so it can be written as (4). Whereas each element of the $P(\Delta w)$ matrix represents a transition between states. For example, the p_{kl} element represents the probability that an individual in state k will transition to state l.

$$\sum_{k=0}^{N} p_{kl}(\Delta w) = 1 \tag{4}$$

The states in the Markov chain are categorized according to their types, namely transient, recurrent, and absorbing state. A state is called transient state if after entering the state k, the process never returns to the state k again. While a state is called recurrent state if after entering the state k, the process will definitely return to the state k again. Therefore, the state k is called a recurrent if and only if it is not a transient. For processes that start from state k and will return to state k defined with $f_{kk} = \sum_{n=1}^{\infty} f_{kk}^{n} = f_{kk}^{1} + f_{kk}^{2} + \dots$. f_{kk} indicates the probability that, processes starting from state k will re-enter to state k. The state k is called recurrent state if $f_{kk} = 1$ and transient state if $f_{kk} < 1$. A state is called absorbing state if after entering the state k, the process will never leave the state k again. This means that no state can be reached from that state.

B. SVIRS Epidemic Models

The SVIRS epidemic model has four compartments, and random variables $S(w), V(w), I(w)$ and $R(w)$ are required. Additional random variable $V(w)$ calculates the number of individuals in the population that have been vaccinated at $w \in T$. $S(w)$ and $I(w)$ computes the number of infectious and susceptible individuals in the population at time $w \in T = \{0, \Delta w, 2\Delta w, \dots\}$ with $S(w), I(w) \in \{0, 1, 2, \dots\}$. $R(w)$ calculates the number of individuals in the population that have recovered at $w \in T$. Recovered individuals will be susceptible again and not immune to COVID-19 infection. The SVIRS epidemic model can be seen in Fig. 2.

The parameters used are defined in Table I.

TABLE I
PARAMETER DEFINITION

Parameter	Definition	Value
β	Infected rate	$\beta \geq 0$
η	Vaccination rate	$\eta \geq 0$
δ	Vaccine effectiveness in reducing infection	$0 < \delta < 1$
γ	Recovery rate	$\gamma > 0$
α	Body immunity waning rate	$\alpha > 0$

Assuming a constant population persists for each value w in the epidemic model,

$$N = S(w) + V(w) + I(w) + R(w)$$

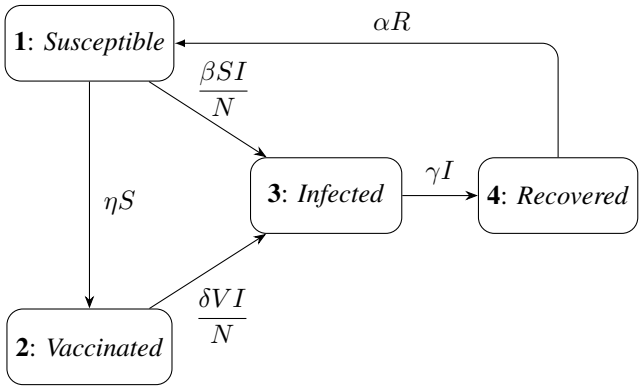


Fig. 2. SVIRS epidemic models

then

$$\frac{dN}{dw} = \frac{dS(w)}{dw} + \frac{dV(w)}{dw} + \frac{dI(w)}{dw} + \frac{dR(w)}{dw} = 0$$

By selecting a sufficiently small time step, we can assume that one transition occurs per step. For time step w, only one of the following can take place:

1) $(s, v, i) \xrightarrow{\Delta w} (s-1, v+1, i) = p_{12}$,
2) $(s, v, i) \xrightarrow{\Delta w} (s-1, v, i+1) = p_{13}$,
3) $(s, v, i) \xrightarrow{\Delta w} (s, v-1, i+1) = p_{23}$,
4) $(s, v, i) \xrightarrow{\Delta w} (s, v, i-1) = p_{34}$,
5) $(s, v, i) \xrightarrow{\Delta w} (s+1, v, i) = p_{41}$,
6) $(s, v, i) \xrightarrow{\Delta w} (s, v, i) = p_{11} = p_{22} = p_{33} = p_{44}$.

For the SVIRS models, we define the path as a U sequence of states with sojourn times.

$$U = ((s_0, v_0, i_0), \Delta w, (s_{\Delta w}, v_{\Delta w}, i_{\Delta w}), \Delta w, \dots, (s, v, i), \Delta w, (k, l, m))$$

This indicates that the system begins in state (s_0, v_0, i_0). The system then changes to state $(s_{\Delta w}, v_{\Delta w}, i_{\Delta w})$ after the period Δw unit of time. The system stays in state $(s_{\Delta w}, v_{\Delta w}, i_{\Delta w})$ for Δw other units of time before moving on to the next state, and so on.

The statistical results (vaccine efficacy) are often presented as derived from the vaccinated group's relative risk (R_r), or a proportional decrease in disease attack rate (A_r) between the unvaccinated (A_u) and vaccinated (A_v). The basic formula is written as [27]:

$$V_e = \frac{A_u - A_v}{A_u} \times 100\% \tag{5}$$

III. RESULTS

A. Transition Probabilities of a DTMC SVIRS Model

Models that are formed based on the assumptions such as variables, parameters, and model in Fig. 2 can be mathematically expressed using the following equation system.

$$\begin{aligned} \frac{dS(w)}{dw} &= -\frac{\beta S(w) I(w)}{N} - \eta S(w) + \alpha R(w) \\ \frac{dV(w)}{d(w)} &= -\frac{\delta V(w) I(w)}{N} + \eta S(w) \\ \frac{dI(w)}{d(w)} &= \frac{\beta S(w) I(w)}{N} + \frac{\delta V(w) I(w)}{N} - \gamma I(w) \\ \frac{dR(w)}{dw} &= \gamma I(w) - \gamma R(w) \end{aligned}$$

The probability of the transition that occurs between states in Fig. 2 is written in (6-11)

$$p_{(s,v,i)\to(s-1,v+1,i)}(\Delta w) = \eta s\Delta w \quad (6)$$

$$p_{(s,v,i)\to(s-1,v,i+1)}(\Delta w) = \frac{\beta si}{N}\Delta w \quad (7)$$

$$p_{(s,v,i)\to(s,v-1,i+1)}(\Delta w) = \frac{\delta vi}{N}\Delta w \quad (8)$$

$$p_{(s,v,i)\to(s,v,i-1)}(\Delta w) = \gamma i\Delta w \quad (9)$$

$$p_{(s,v,i)\to(s+1,v,i)}(\Delta w) = \alpha r\Delta w \quad (10)$$

$$p_{(s,v,i)\to(s,v,i)}(\Delta w) = 1-\left(\frac{\beta si}{N}+\frac{\delta vi}{N}+\eta s+\gamma i+\alpha r\right)\Delta w \quad (11)$$

Equation (6) shows the transition probability from susceptible to vaccinated, (7) shows the transition probability from susceptible to infected, (8) shows the transition probability from vaccinated to infected, (9) shows the transition probability from infected to recovered, (10) shows the transition probability from recovered back to susceptible, and (11) shows the transition probability settling in a given state.

The transition probability from the DTMC SVIRS epidemic model written with $\left(p_{(s,v,i)\to(s+k,v+l,i+m)}(\Delta w)\right)$ is given as follows.

$$p(\Delta w)=\begin{cases}\eta s\Delta w, & (k,l,m)=(-1,1,0)\\ \frac{\beta}{N}si\Delta w, & (k,l,m)=(-1,0,1)\\ \frac{\delta vi}{N}\Delta w, & (k,l,m)=(0,-1,1)\\ \gamma i\Delta w, & (k,l,m)=(0,0,-1)\\ \alpha r\Delta w, & (k,l,m)=(1,0,0)\\ 1-\Big(\eta s+\frac{\beta si}{N}si & \\ +\frac{\delta vi}{N}+\gamma i+ & \\ \alpha r\Big)\Delta w, & (k,l,m)=(0,0,0)\\ 0, & \text{otherwise}\end{cases} \quad (12)$$

The DTMC SVIRS epidemic model is the transition probability from state (s,v,i) to state $(s+k,v+l,i+m)$, which is expressed in (12). The number of individual groups S,V,I, and R can be determined at any given time using (12), and the initial values are given first.

The transition matrix formed in the SVIRS model will be more complex than the SIR model because it is an ordered pair of three states, namely (s,v,i). The time step Δw must be chosen so that all transition probabilities fall within the interval [0,1]. However, applying the Markov property, the difference equation satisfied by probability $p_{(s,v,i)}(w+\Delta w)$ can be expressed in terms of the transition probabilities:

$$\begin{aligned}p_{(s,v,i)}(w+\Delta w) = {}& p_{(s-1,v+1,i)}(w)\eta(s-1)\Delta w + p_{(s-1,v,i+1)}(w)\\ & \frac{\beta}{N}(s-1)(i+1)\Delta w + p_{(s,v-1,i+1)}(w)\\ & \frac{\delta}{N}(v-1)(i+1)\Delta w + p_{(s,v,i-1)}(w)\\ & \gamma(i-1)(\Delta w) + p_{(s+1,v,i)}(w)\\ & \alpha(N-s-v-i)\Delta w + p_{(s,v,i)}(w)\\ & \left(1-\left[\eta s+\frac{\beta si}{N}+\frac{\delta vi}{N}+\gamma i+\alpha r\right]\right)\Delta w\end{aligned} \quad (13)$$

B. Parameter Estimation for DTMC SVIRS Model

According to the discrete-time SVIRS model with transition probability in (13), it is possible to estimate parameters η,β,δ,γ and α by the maximum likelihood method. The likelihood function of the DTMC SVIRS model is

$$\begin{aligned}L(\eta,\beta,\delta,\gamma,\alpha) &= \Pr(X(w=0)=(s_0,v_0,i_0))\\ &= \prod_{\substack{i,m,v,\\ l,s,k=0}}^{N}\left(p_{(s,v,i)\to(k,l,m)}\right)^{n_{(s,v,i)(k,l,m)}}\end{aligned} \quad (14)$$

where $n_{(s,v,i)(k,l,m)}$ is the number of transitions calculated from state (s,v,i) to state (k,l,m). So (14) can be written as

$$\begin{aligned}&L(\eta,\beta,\delta,\gamma,\alpha)=\\ &\prod_{i=1}^{N}\prod_{v=0}^{N}\prod_{s=0}^{N}\left(p_{(s,v,i)\to(s-1,v+1,i)}\right)^{n_{(s,v,i),(s-1,v+1,i)}}\\ &\left(p_{(s,v,i)\to(s-1,v,i+1)}\right)^{n_{(s,v,i),(s-1,v,i+1)}}\\ &\left(p_{(s,v,i)\to(s,v-1,i+1)}\right)^{n_{(s,v,i),(s,v-1,i+1)}}\\ &\left(p_{(s,v,i)\to(s,v,i-1)}\right)^{n_{(s,v,i),(s,v,i-1)}}\\ &\left(p_{(s,v,i)\to(s+1,v,i)}\right)^{n_{(s,v,i),(s+1,v,i)}}\\ &\left(p_{(s,v,i)\to(s,v,i)}\right)^{n_{(s,v,i),(s,v,i)}}\end{aligned} \quad (15)$$

We have the likelihood function's logarithm.

$$\begin{aligned}&\log L(\eta,\beta,\delta,\gamma,\alpha)=\\ &\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\Big[n_{(s,v,i),(s-1,v+1,i)}\log(\eta s)+\\ &n_{(s,v,i),(s-1,v,i+1)}\log(\frac{\beta si}{N})+n_{(s,v,i),(s,v-1,i+1)}\\ &\log(\frac{\delta vi}{N})+n_{(s,v,i),(s,v,i-1)}\log(\gamma i)+\\ &n_{(s,v,i),(s+1,v,i)}\log(\alpha r)+n_{(s,v,i),(s,v,i)}\\ &\log\left(1-\left[\eta s+\frac{\beta si}{N}+\frac{\delta vi}{N}+\gamma i+\alpha r\right]\right)\Big]\end{aligned} \quad (16)$$

Taking the partial derivative of the likelihood function's logarithm with respect to η, we have

$$\frac{\partial\log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial\eta}=\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s-1,v+1,i)}\left(\frac{1}{\eta}\right)-\frac{n_{(s,v,i),(s,v,i)}s}{\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] \quad (17)$$

if derived against β, we have

$$\frac{\partial\log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial\beta}=\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s-1,v,i+1)}\left(\frac{1}{\beta}\right)-\frac{n_{(s,v,i),(s,v,i)}si}{N\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] \quad (18)$$

if derived against δ, we have

$$\frac{\partial \log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial \delta} = \sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s,v-1,i+1)}\left(\frac{1}{\delta}\right) - \frac{n_{(s,v,i),(s,v,i)}vi}{N\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] \tag{19}$$

if derived against γ, we have

$$\frac{\partial \log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial \gamma} = \sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s,v,i-1)}\left(\frac{1}{\gamma}\right) - \frac{n_{(s,v,i),(s,v,i)}i}{\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] \tag{20}$$

if derived against α, we have

$$\frac{\partial \log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial \alpha} = \sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s+1,v,i)}\left(\frac{1}{\alpha}\right) - \frac{n_{(s,v,i),(s,v,i)}r}{\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] \tag{21}$$

The first step to estimate the η parameter is that the likelihood equation is equal to zero. So the value of $\hat{\eta}$ is as follows.

$$\frac{\partial \log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial \eta} = 0$$

Therefore, we have that

$$\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s-1,v+1,i)}\left(\frac{1}{\eta}\right) - \frac{n_{(s,v,i),(s,v,i)}s}{\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] = 0$$

$$\left(\frac{1}{\eta}\right)\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s-1,v+1,i)}\right] - \sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[\frac{n_{(s,v,i),(s,v,i)}s}{\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] = 0$$

Suppose $\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s-1,v+1,i)}\right] = N_{\eta_{kl}}$ is the total number of individuals who transitioned from susceptible state to vaccinated state in the period $t = 1$ to N. Whereas

$$\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[\frac{n_{(s,v,i),(s,v,i)}s}{\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] = N_{\eta_{kk}}$$

is the number of people who have remained in the susceptible state divided by the entire population minus the number of people who have moved between states. More simply, parameter estimate value can be written as follows.

$$\hat{\eta} = \frac{N_{\eta_{kl}}}{N_{\eta_{kk}}} \tag{22}$$

The estimation results of the β parameter with the maximum likelihood function written as $\hat{\beta}$ are obtained as follows.

$$\frac{\partial \log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial \beta} = 0$$

Suppose $\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s-1,v,i+1)}\right] = N_{\beta_{kl}}$ is the total number of individuals who transitioned from susceptible state to infected state in the period $t = 1$ to N. Whereas

$$\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[\frac{n_{(s,v,i),(s,v,i)}si}{N\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] = N_{\beta_{kk}}$$

is the number of people who have remained in the susceptible and infected state divided by the entire population minus the number of people who have moved between states. Therefore, we have that

$$\hat{\beta} = \frac{N_{\beta_{kl}}}{N_{\beta_{kk}}} \tag{23}$$

The estimation results of the δ parameter with the maximum likelihood function written as $\hat{\delta}$ are obtained as follows.

$$\frac{\partial \log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial \delta} = 0$$

Suppose $\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s,v-1,i+1)}\right] = N_{\delta_{kl}}$ is the total number of individuals who transitioned from vaccinated state to infected state in the period $t = 1$ to N. Whereas

$$\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[\frac{n_{(s,v,i),(s,v,i)}vi}{N\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] = N_{\delta_{kk}}$$

is the number of people who have remained in the vaccinated and infected state divided by the entire population minus the number of people who have moved between states. Therefore, we have that

$$\hat{\delta} = \frac{N_{\delta_{kl}}}{N_{\delta_{kk}}} \tag{24}$$

The estimation results of the γ parameter with the maximum likelihood function written as $\hat{\gamma}$ are obtained as follows.

$$\frac{\partial \log L(\eta,\beta,\delta,\gamma,\alpha)}{\partial \gamma} = 0$$

Suppose $\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[n_{(s,v,i),(s,v,i-1)}\right] = N_{\gamma_{kl}}$ is the total number of individuals who transitioned from infected state to recovered state in the period $t = 1$ to N. Whereas

$$\sum_{i=1}^{N}\sum_{v=0}^{N}\sum_{s=0}^{N}\left[\frac{n_{(s,v,i),(s,v,i)}i}{\left(1-\eta s-\frac{\beta si}{N}-\frac{\delta vi}{N}-\gamma i-\alpha r\right)}\right] = N_{\gamma_{kk}}$$

is the number of people who have remained in the infected state divided by the entire population minus the number of people who have moved between states. Therefore, we have that

$$\hat{\gamma} = \frac{N_{\gamma_{kl}}}{N_{\gamma_{kk}}} \tag{25}$$

The estimation results of the α parameter with the maximum likelihood function written as $\hat{\alpha}$ are obtained as follows.

$$\frac{\partial \log L(\eta, \beta, \delta, \gamma, \alpha)}{\partial \alpha} = 0$$

Suppose $\sum_{i=1}^{N} \sum_{v=0}^{N} \sum_{s=0}^{N} \left[n_{(s,v,i),(s+1,v,i)} \right] = N_{\alpha_{kl}}$ is the total number of individuals who transitioned from recovered state to susceptible state in the period $t = 1$ to N. Whereas

$$\sum_{i=1}^{N} \sum_{v=0}^{N} \sum_{s=0}^{N} \left[\frac{n_{(s,v,i),(s,v,i)} r}{\left(1 - \eta s - \frac{\beta s i}{N} - \frac{\delta v i}{N} - \gamma i - \alpha r\right)} \right] = N_{\alpha_{kk}}$$

is the number of people who have remained in the recovered state divided by the entire population minus the number of people who have moved between states. Therefore, we have that

$$\hat{\alpha} = \frac{N_{\alpha_{kl}}}{N_{\alpha_{kk}}} \tag{26}$$

C. Procedure for DTMC SVIRS Model

The procedure needed to apply the DTMC SVIRS model is depicted below.

1) Derive the DTMC SVIRS model
   a) COVID-19 spreads if there is a contact between an infected individual and an individual susceptible to the disease then recovers and is not immune to the disease before being vaccinated; this is in accordance with the characteristics of the SVIRS mathematical model. Although vaccination has been carried out, a person is still likely to be infected but with mild symptoms that rarely cause death. The SVIRS epidemic model, divides individuals into four states, namely susceptible (S), i.e., the state of an individual who is healthy but can be infected with the disease, vaccinated (V), i.e., the state of an individual who has been vaccinated with the second shot but is still possible to be infected with COVID-19 with mild symptoms, infected (I), i.e., the condition of infected individuals, including those who have been and have not been vaccinated, and recovered (R), i.e., the state of individuals recovering from the disease. The number of individuals in each state S, V, I, and R at time w is expressed as $S(w), V(w), I(w)$, and $R(w)$.
   b) Specify the DTMC SVIRS epidemic model assumptions.
   The population is considered to be constant, thus the population size is fixed, or $S(w) + V(w) + I(w) + R(w) = N$, where N is the total number of individuals in a population.
   c) Specify the transition probability of the DTMC SVIRS epidemic model
   The possibility that an individual can move from one state to another only concerns one individual who transitions at a very small time interval. Therefore, at time interval δw, the probability of the transition with the number of individuals moving by more than one is zero. Equations (6-11) show the transition probability of the DTMC SVIRS epidemic model which is written as (12).
2) Simulate a COVID-19 disease spread pattern using the DTMC SVIR model. The DTMC SVIRS model algorithm is as follows.
   a) Calculate the value of each parameter utilized $(\eta, \beta, \delta, \gamma, \alpha)$ based on the number of transitions that occur between states and those that remain in each state, and the number of the population used N.
   b) Create a transition probability matrix based on the existing data, with the following details.
      i) Calculate (p_{13}) using $\left(\frac{\beta S(w) I(w)}{N}\right) \Delta w$ from susceptible state and (p_{23}) using $\left(\frac{\delta V(w) I(w)}{N}\right) \Delta w$ from vaccinated state.
      ii) Calculate (p_{12}) using $\eta S(w) \Delta w$ to transition from susceptible to vaccinated state.
      iii) Calculate (p_{34}) using $\gamma I(w) \Delta w$ to transition from infected to recovered state.
      iv) Calculate (p_{41}) using $\alpha R(w) \Delta w$ to transition back to susceptible after recovered.
      v) Calculate the probability of no increase in the number of infected using $1 - (p_{12} + p_{13})$.
   c) Draw a graph of $S(w), V(w), I(w)$ and $R(w)$ for the next several periods.
   d) Provide interpretation of the simulation results.

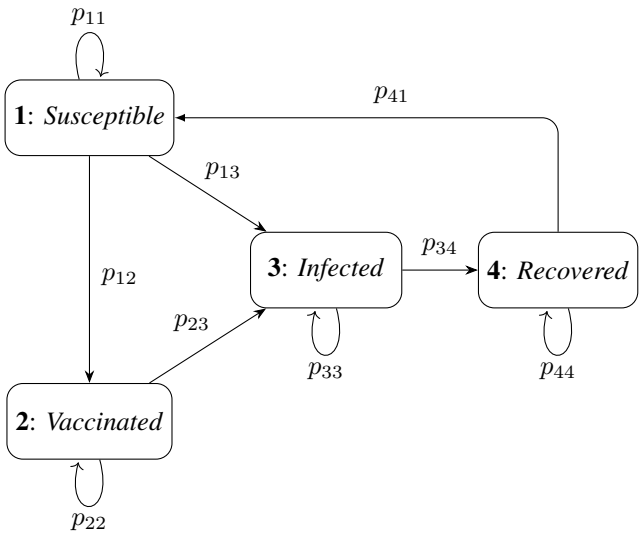


Fig. 3. Transition probability of multi-state DTMC SVIRS model

In this paper, the R software was used to assist the analysis and prediction of the COVID-19 data. We used an algorithm based on the COVID-19 data in Indonesia to illustrate an example of a DTMC SVIRS epidemic model. The multi-state DTMC SVIRS model can be seen in Fig. 3. Fig. 3 shows the transition probability among states, where p_{11} represents the probability that someone remains in a susceptible state during the observation period. p_{12} expresses the transition probability of a person from a susceptible to vaccinated state during the observed period and so on.

Although there is no optimum prediction model for COVID-19, but we can choose a suitable model for the desired prediction results. Deterministic epidemiological mod-

els, such as the SVIR-type model, rely significantly on estimated parameters such as R_0 and can provide a broad variety of predictions in a short amount of time. This is valuable for reference, but its capacity to support real-time decision-making may be restricted. The DTMC model with empirical probability has the advantage of not requiring any complicated estimation procedures. In this present study, the DTMC model has been proven to be more flexible and accurate for short-term prediction. Meanwhile, to make a long-term prediction, this model is less accurate, making it difficult to predict when the epidemic will end.

IV. Application

A. Application of DTMC SVIR Model using Data Simulation

We used the previously mentioned algorithm to simulate a DTMC SVIRS model. In this case, it is assumed that the population of the outbreak is 100 people with the initial condition being that there are two infected people. In this example, the infected rate (β) is 0.08, the vaccination rate (η) is 0.6, the efficiency of the vaccine in preventing infection (δ) is 0.00392, the recovery rate (γ) is 0.234, and the time between consecutive occurrences is 0.01.

Fig. 4 shows a simulation using different values of parameter β while the other parameters remain the same. The values of parameter β consist of 0.02, 0.04, 0.06, and 0.08. Fig. 4 shows that the higher the rate of disease infection, the faster the transition of people who are in a susceptible state to both the vaccinated state and the infected state. In addition, when the value of β changes, the vaccinated and infected curves also change. At the value of β = 0.02, the vaccinated curve is higher than the infected curve, and it will move continuously as the value of β increases, so the position of the infected curve is higher than the vaccinated curve.

Fig. 5 shows a simulation using different values of parameter η while the other parameters remain the same. The values of parameter η consist of 0.2, 0.4, 0.6, and 0.8. Fig. 5 shows that the higher the vaccination rate, the more likely the infection rate to lower among people who are in the vaccinated state, the lower the peak of the infected curve as shown in Fig. 5.

Fig. 6 shows a simulation using different values of parameter δ while the other parameters remain the same. The values of parameter δ consist of 0.002, 0.004, 0.006, and 0.008. Fig. 6 shows a change in neither the susceptible nor recovered curves because parameter δ represents the transition probability of a person from a vaccinated state to an infected state. The higher the number of people vaccinated, the lower the probability of contracting the disease.

Fig. 7 shows a simulation using different values of parameter γ while the other parameters remain the same. The values of parameter γ consist of 0.2, 0.4, 0.6, and 0.8. Fig. 7 shows that if there is an increase in the cure rate, the epidemic will end more quickly. As for the infected curve, the higher the value of parameter γ, the lower the infected curve.

B. Application of DTMC SVIRS Model using COVID-19 Data

The infectious disease used in this model was COVID-19 which is still spreading today. The data used were Indonesia's

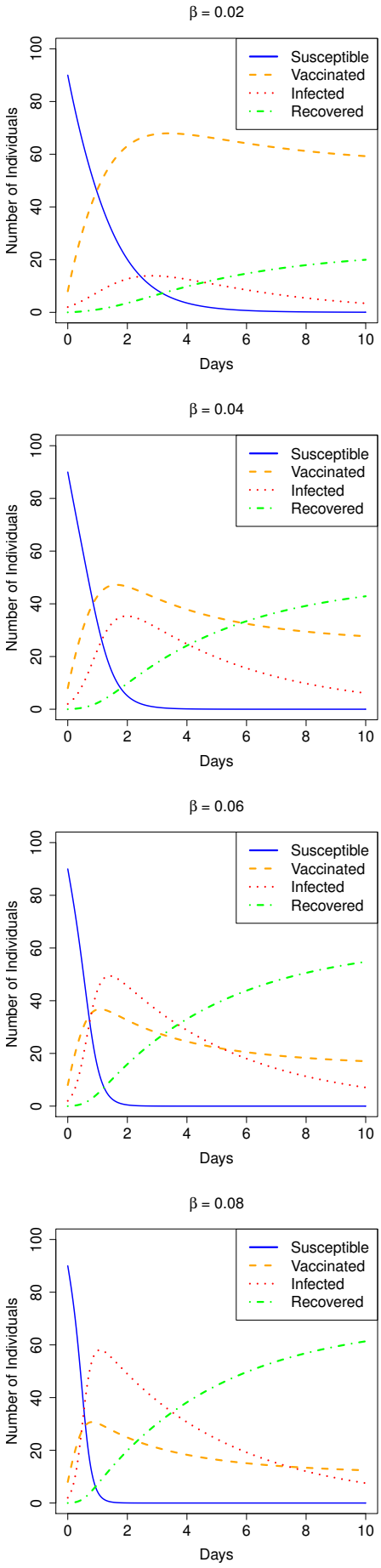
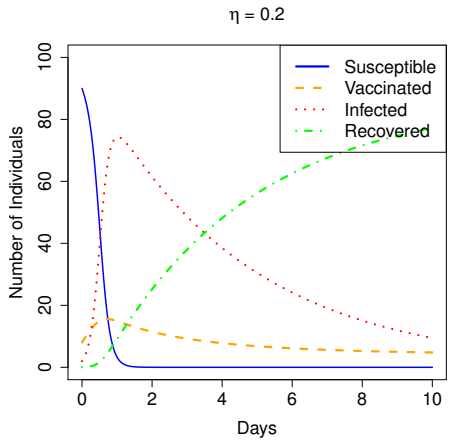
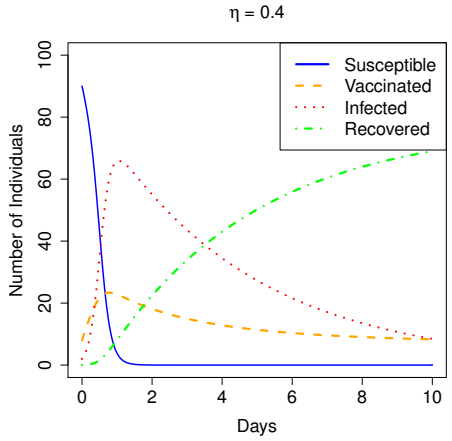
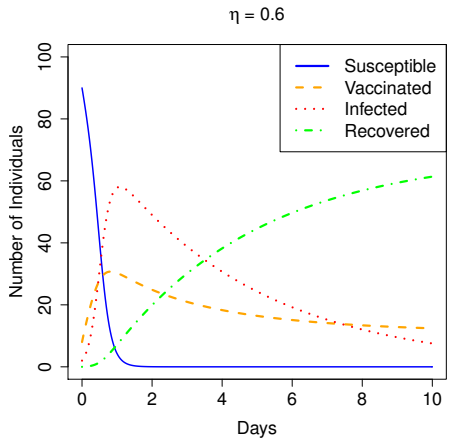


Fig. 4. Simulation of a DTMC SVIR model with different values of infected rate (β) parameters







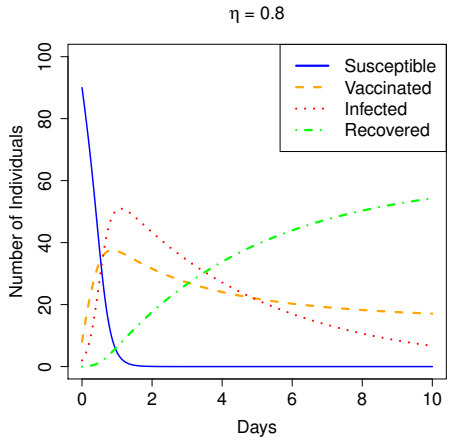
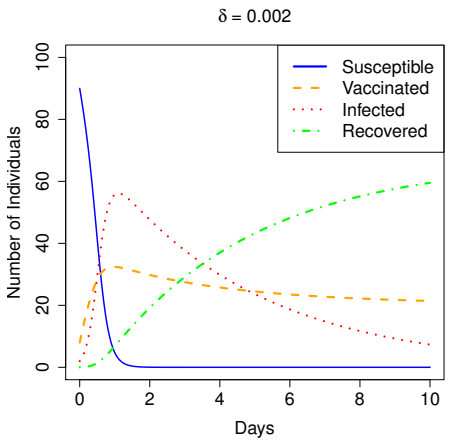
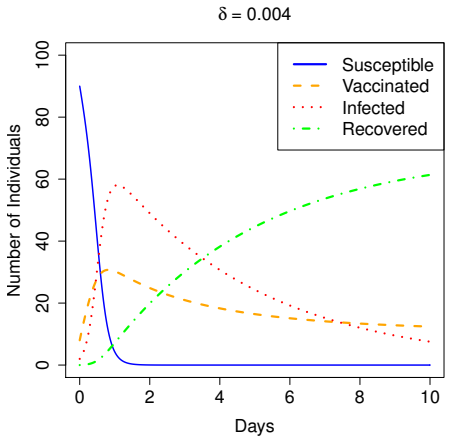
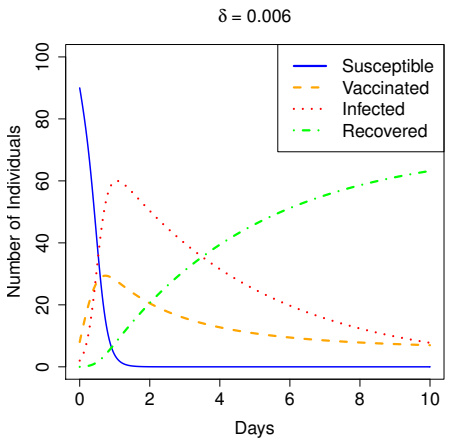


Fig. 5. Simulation of a DTMC SVIR model with different values of vaccination rate (η) parameters







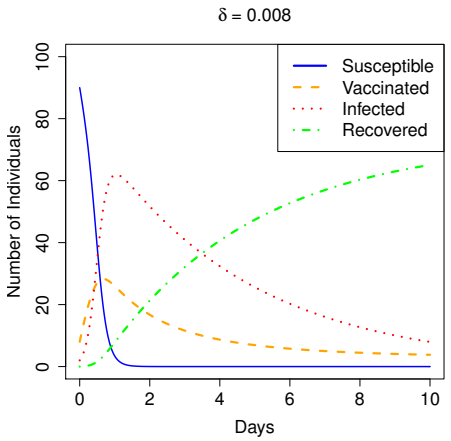


Fig. 6. Simulation of a DTMC SVIR model with different values of vaccine effectiveness in reducing infection (δ) parameters

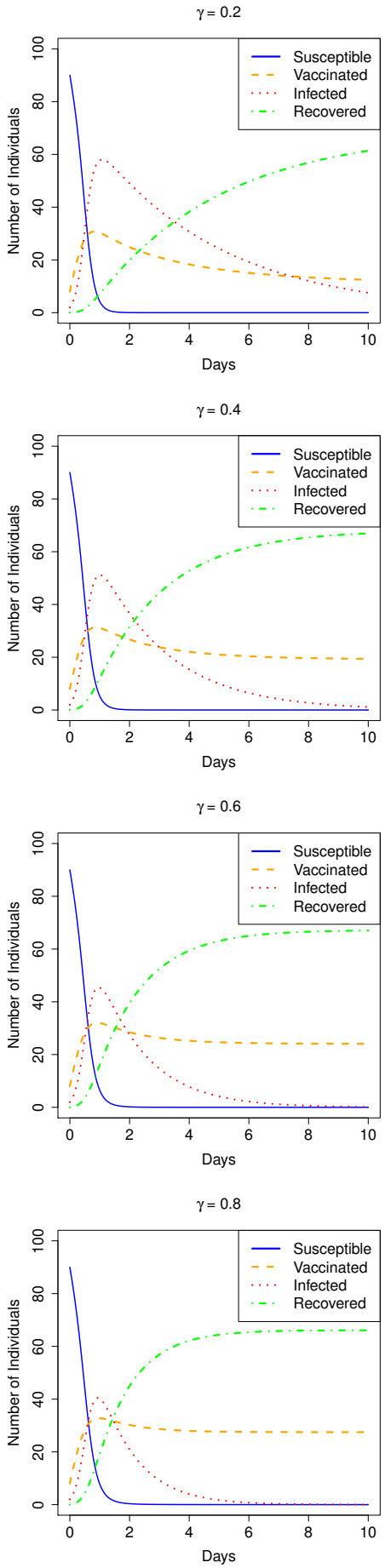


Fig. 7. Simulation of a DTMC SVIR model with different values of recovery rate (γ) parameters

COVID-19 cases taken between March 2, 2020, and August 31, 2021. From the data obtained on August 31, 2021, the number of suspected individuals was 164,364,896, the number of individuals vaccinated with the second shot was 36,034,132, the number of infected cases was 4,089,801 and the number of recovered individuals was 3,776,891. Thus, the number of people involved in this study was 208,265,720 [28].

Based on the total number of susceptible individuals, vaccinated, infected with COVID-19, then declared recovered, the obtained data are presented as follows.

1) The COVID-19 infection rate in Indonesia was 1.96%. It was obtained from the total number of the infected individuals divided by N, so the value of $p_{13} = 0.0196$. The transition probability of those vaccinated with the second shot was obtained from the quotient of the number of people vaccinated divided by N, resulting in $p_{12} = 0.1730$. Since it was a transition probability matrix where the number of rows had to be equal to 1, the value of $p_{11} = 1 - 0.0196 - 0.1730 = 0.8074$. This indicated the probability that a person would remain susceptible during the observation period.
2) The probability of a vaccinated person being infected with COVID-19 was $p_{23} = 1 - 0.6608 = 0.3392$. This value was obtained from 1 minus the proportion of efficacy of the five types of vaccines used in Indonesia including Sinovac, Sinopharm, Pfizer/BionTech, Moderna, and AstraZeneca/Oxford Vaccine. According to WHO, the efficacy of the five types of vaccines is as follows.

TABLE II
VACCINE TYPE EFFICACY

Types of Vaccines	Efficacy (E)	Proportion (P)	$E \times P$
Sinovac	63.00 %	77,26	48.68 %
Sinopharm	78.10 %	0.38	0.30 %
Pfizer/BionTech	95.00 %	3.81	3.62 %
Moderna	93.00 %	5.82	5.42 %
AstraZeneca/Oxford	63.47 %	12.72	8.07 %

The Johnson and Johnson vaccine was not included in the study because this vaccine was approved in Indonesia starting in September 2021 and it requires one dose only, while this article used vaccination data collected until August 2021. The amount from the efficacy column multiplied by the proportion of each vaccine is 66.08%. So the value of $p_{22} = 0.6608$. This showed the possibility that a person was able to survive from the COVID-19 virus because of getting vaccinated.

3) The recovered rate for COVID-19 in Indonesia was 92.34%. This percentage was obtained from the dividend between the number of people who recovered from COVID-19 infection and the number of people infected during the selected time period. The value of $p_{34} = 0.9234$. Meanwhile, the value of $p_{33} = 1 - 0.9234 = 0.0766$. This showed the probability that someone would remain in the infected state within the period of observation.

Thus, the following transition probability matrix can be

formed for the DTMC SVIR and DTMC SVIRS models.

$$\mathbf{P}_{SVIR} = \begin{bmatrix} 0.8074 & 0.1730 & 0.0196 & 0.0000 \\ 0.0000 & 0.6608 & 0.3392 & 0.0000 \\ 0.0000 & 0.0000 & 0.0766 & 0.9234 \\ 0.0000 & 0.0000 & 0.0000 & 1.0000 \end{bmatrix}$$

and

$$\mathbf{P}_{SVIRS} = \begin{bmatrix} 0.8074 & 0.1730 & 0.0196 & 0.0000 \\ 0.0000 & 0.6608 & 0.3392 & 0.0000 \\ 0.0000 & 0.0000 & 0.0766 & 0.9234 \\ 1.0000 & 0.0000 & 0.0000 & 0.0000 \end{bmatrix}$$

The transition probabilities of each state are illustrated in Fig. 8, where the direction of the arrow denotes the direction of transition between states and the circle denotes the state used in the case of COVID-19. **S** represents susceptible, **V** represents vaccinated, **I** represents infected, and **R** represents recovered.

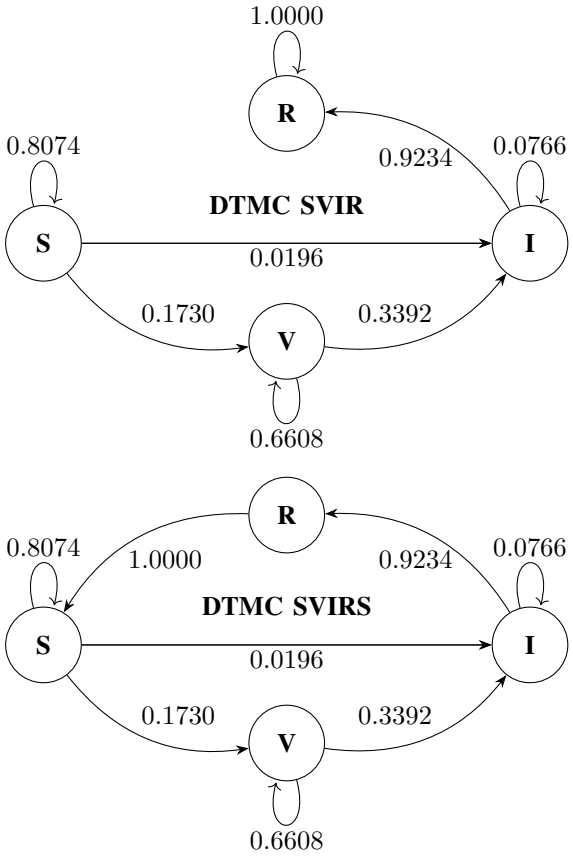


Fig. 8. Comparison of the DTMC SVIR and DTMC SVIRS COVID-19 transition probability plots

The difference between the transition probabilities of the DTMC SVIR and DTMC SVIRS models only lies in the fourth line. The DTMC SVIR model no longer transitions to another state after the individual is in the recovered state p_{44} = 1. Meanwhile in the DTMC SVIRS model, all recovered individuals will return to the susceptible state because there is no immunity to COVID-19, so p_{41} = 1, meaning that every recovered individual will return to susceptible regardless of whether they have been vaccinated.

TABLE III
PREDICTION RESULTS WITH DTMC SVIRS ON COVID-19 CASES IN INDONESIA

Date	Actual	Prediction	MAPE (%)
2021/09/1	10,337	10,537	1.93
2021/09/2	8,955	8,927	0.31
2021/09/3	7,797	8,045	3.18
2021/09/4	6,727	6,651	1.13
2021/09/5	5,403	5,865	8.55
2021/09/6	4,413	5,234	18.60
2021/09/7	7,201	6,674	7.32
2021/09/8	6,731	7,052	4.77

Transition matrices $\mathbf{P}_{SVIR}$ and $\mathbf{P}_{SVIRS}$ can be plotted as shown in Fig. 8 which shows the transition probability between states where the difference is that the DTMC SVIRS model has a transition back to a susceptible state while the DTMC SVIR model does not.

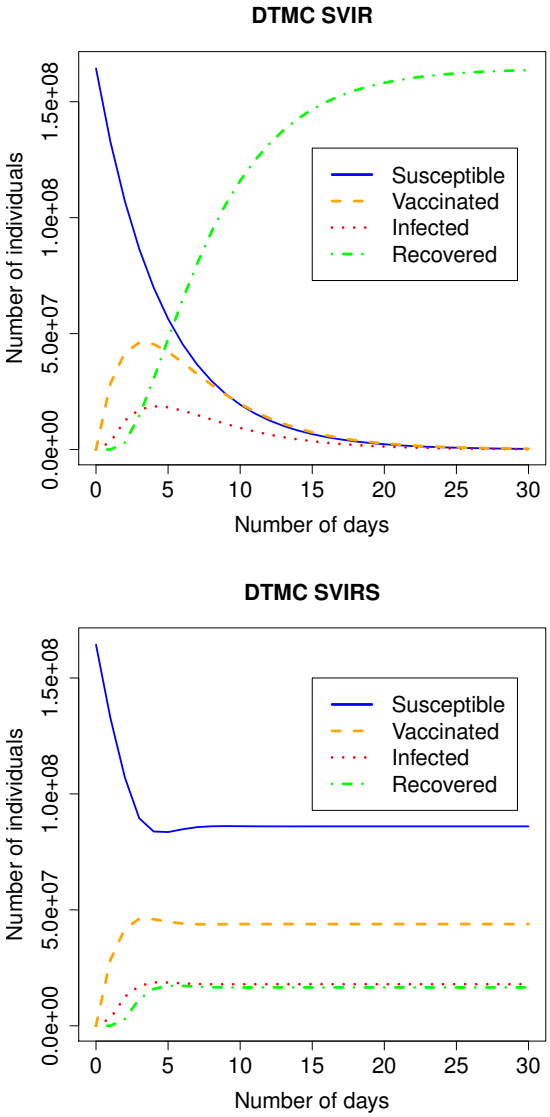


Fig. 9. A comparison of COVID-19 prediction in Indonesia with DTMC SVIR and DTMC SVIRS models

The transition probability matrix that was obtained previously can predict the number of patients over the next several

days. Due to the Markov chain's nature stating that today's events affect the next event, each of the data in this study was used to predict the next period. Then the predicted results and MAPE values were calculated and the results are as shown in Table III. Table III shows that the prediction results using DTMC had an average MAPE value of 5.7%.

The plot of the COVID-19 data in Indonesia by entering the parameter values, namely the rate of transmission, vaccination, and cure, can be seen in Fig. 9. With the spread of COVID-19 in Indonesia, which was modelled with DTMC SVIR, the number of susceptible individuals will reach 0 over time. In the DTMC SVIRS model, the number of individuals in a susceptible state will never reach 0 because every recovered individual will return to a susceptible state. Even though they have been vaccinated, there is no immunity in COVID-19 cases, so it is very suitable to model the spread of COVID-19 with the SVIRS model.

V. Conclusion

The multi-state model with the DTMC assumption can model not only chronic diseases but also infectious diseases. This multi-state DTMC model is different from the compartment model with the DTMC assumption stating that if the multi-state model is used, the transition probability should be used to determine the relationship among states. This paper uses four states of COVID-19 infection, namely susceptible, vaccinated, infected, and recovered. After finding the transition probability between the states, short-term predictions on the COVID-19 data in Indonesia were made. The results obtained have a highly accurate prediction with a MAPE value lower than 10%.

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