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Multi-state SVIRD Model with Continuous-time Markov Chain Assumption on the Spread of Infectious Diseases

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Abstract

The spread of infectious diseases is generally described using mathematical models. This paper discusses the spread of infectious diseases using a multi-state SVIRD model, assuming that a continuous-time Markov chain (CTMC) occurs in a closed population and is examined regularly. This article aims to generate transition probabilities and parameter estimates using the maximum likelihood method. The multi-state SVIRD model assuming CTMC uses a transition intensity and transition probability approach consisting of five primary states: susceptible, vaccinated, infected, recovered, and deceased. The infected state is divided into two: infected before and after being vaccinated. The result is an estimator of transition intensity with sojourn time which is exponentially distributed to produce a transition probability matrix. Then the algorithm for the CTMC SVIRD model is given. The multi-state SVIRD model algorithm can be used directly if the epidemic case is still in single-wave to determine the transition probability. In contrast, for multi-wave cases, it is necessary to detect changepoints to determine wave boundaries to make predictions more accurate. The main contributions of this study are using the CTMC assumption, a stochastic model for determining the parameters of the differential equation formed by the compartment model and adding vaccinated status to the model. In addition, it also provides ways to overcome multi-wave epidemic cases so the prediction results are more accurate.

Keywords: multi-state model, SVIRD, continuous-time, Markov process, epidemic models, multi-wave.

Before we look at style in more detail, the most common mistakes and errors are described:

1. Introduction

The spread of infectious diseases attracts most people's attention because health is essential to life. Without health, people cannot carry out activities to fulfill their needs. Viruses, bacteria, or fungi usually cause infectious diseases through direct or indirect contacts between individuals. The spread of contagious diseases that cannot be controlled for a long time can cause epidemics, and if they spread quickly to various regions of the world, they can become a pandemic.

In epidemiology, mathematical modeling is essential for detecting the spread of infectious diseases and making predictions. Models depict miniature objects, concepts, and scenarios to determine real-world behavior and predict future events (Huppert and Katriel 2013). Mathematical modeling is a model representation that uses mathematical equations.

A multi-state model has been developed by Andersson and Britton (2000) and Hougaard (1999), which discusses modeling that consists of several states. Transitions between states connect them, then Keiding (1991) uses a multi-state model in chronic disease modeling by utilizing the role of different periods. In contrast, Klein and Moeschberger (2003) and Commenges (1999) describe how to overcome incomplete observations in a study. Jones (1994); Zuhairoh, Rosadi, and Effendie (2021) discuss the multi-state modeling process using discrete-time Markov assumptions, and Haberman and Pitacco (1999) describes how multi-state models are used in long-term care insurance. Haberman and Pitacco (1999), explains how to use the maximum likelihood method to estimate transition intensity in a multi-state model, which is then assessed to produce a transition intensity function. One of the assumptions usually used to calculate the transition probability of a multi-state model is the Markov assumption. Markov chains often represent stochastic processes in disease transmission (Hsieh, Chen, and Chang 2002; Hubbard and Zhou 2011; Zhang, Lim, Maiti, Li, Choi, Bozoki, and Zhu 2019). This underlies the researcher to apply the multi-state model with the Markov assumption on the spread of infectious diseases. The multi-state model was previously more often used for chronic disease modeling.

The multi-state model is not equivalent to the Markov model, but both have the concept of state. Markov's assumption states that future events only depend on current events. However, the multi-state model relaxes this assumption by suggesting that other things influence future events, but current events are still the main focus. The previous outcome of an event can affect the future development of a naturally occurring event. The Markov chain describes this stochastic process. Usually, the state space of the Markov chain is kept distinct. The ability to transition to any state depends on the current state and time. This can be seen in infectious disease modeling, where the number of people currently infected determines the probability of a person being infected in the future. To anticipate future conditions, researchers know the current situation where additional information about previous conditions is no longer needed.

The types of infectious disease modeling consist of deterministic, stochastic, and phenomenological models. Classical deterministic modeling has been widely used, including by Triampo, Baowan, Tang, Nuttavut, and Doungchawee (2007); Köhler-Rieper, Röhl, and De Micheli (2020), then a comparison between deterministic and stochastic was developed by Olabode, Culp, Fisher, Tower, Hull-Nye, and Wang (2021); Allen and Burgin (2000) to interpret various epidemic models. Meanwhile, the phenomenological model has been developed in previous studies using the logistic growth model and the expansion of the Richards curve model Zuhairoh and Rosadi (2020, 2022a,b). Because there is a relationship between the multi-state model and the Markov model, we try to use the continuous-time Markov assumption in the multi-state model of the spread of infectious diseases, which consists of five states, namely susceptible, vaccinated, infected, recovered, and deceased, known as SVIRD epidemic model. This model is a type of stochastic model.

A stochastic process is a collection of random variables $\{Y_w : w \in W\}$ where each state Y is a function of time w, i.e., number Y_w is seen at any time w (Britton 2010). Set W represents the number of times the system can be observed. Stochastic processes are mathematical models

that depict how random variables change over time. When the set W is countable, the stochastic process is a discrete-time process and when the set W equals $[0, \infty)$, the stochastic process is a continuous-time process.

Figure 1: Continuous-time stochastic process

Figure 1 illustrates a basic example of a continuous-time stochastic process. In this paper, we use five states representing the spread of infectious diseases assuming a continuous-time Markov chain, which describes the spread of a disease in which there is a vaccinated state so the infected state will be divided into two, namely people infected without vaccination and people infected after being vaccinated. Two things cause the probability of someone dropping out of the model: recovery and death. In our model, there is no transition back to susceptible after recovered.

Another important thing in the multi-state model is transition probability. The transition probabilities can be calculated using the *Kolmogorov forward* and *backward* differential equations (Haberman and Pitacco 1999). A simultaneous differential equation solution is one solution to get the transition probability, but it can also be obtained by a general formula using the Jones (1994) matrix approximation. Transition probabilities are used to predict infected cases in the next few days. Meanwhile, in the multi-state SVIRD model we developed, the transition probability obtained from the compartment model corresponds to the transition between states. Also, it considers the sojourn time in each state.

Prediction results in epidemic models usually apply to single waves. As we know, epidemic cases occur not only in single-wave but also multi-waves, so in this paper, we add a changepoint detection method to overcome this. Therefore, before making predictions, it is necessary to detect the epidemic wave that occurs as a basis for determining the initial limit for data collection. The changepoint detection method is the binary segmentation (BS) method. BS is a method that can be used to find numerous changepoints. At the beginning of the process, the complete dataset is combed through to locate a single changepoint, typically using a similar strategy to CUSUM (Eckley, Fearnhead, and Killick 2011).

The main contribution of this study is the use of multi-state models in modeling the spread of infectious diseases with five states and a continuous-time Markov chain (CTMC) assumption. The difference between this paper and previous research Zuhairoh *et al.* (2021) is that this paper adds the vaccinated state in the model and adds predictions for the following few periods. In addition, it also adds changepoint detection to detect multi-wave epidemic to obtain more accurate prediction results.

This article is structured as follows. We present SVIRD and CTMC models in Sect. 2 that explains the epidemic's evolution. The recursive findings are then presented, and an algorithmic strategy for the random variable distribution is developed to reflect the number of inspections that uncover an active epidemic phase. In Sect. 3, we present the outcomes of our study in the form of transition probabilities derived from the CTMC SVIRD model and estimates of the model's parameters. Section 3 also gives the procedure of the CTMC SVIRD model. Then, in Sect. 4, we applied the CTMC SVIRD model using simulation data and the actual data of COVID-19 in Indonesia. The distinction between the CTMC SVIRD compartment model and the multi-state CTMC SVIRD is the modeling between state changes where the compartment model uses differential equations. In contrast, the probability of transition is used for the multi-state.

2. SVIRD epidemic models using continuous-time Markov chain

2.1. Multi-state model

If $\mathscr{S}$ is a finite state-space and represents states as natural numbers, then $\mathscr{S} = 1, 2, 3, \ldots, N$. Then, if the direct transition set is denoted by $\mathscr{T}$ and $\mathscr{T}$ is a subset of pair set (k, l)

$$\mathscr{T} \subseteq \{(k, l)|k \neq l; k, l \in \mathscr{S}\}, \tag{1}$$

then pair $(\mathscr{S}, \mathscr{T})$ is called a multi-state model.

Characteristic of a multi-state process is affected by the transition probabilities between state k and l following this,

$$p_{kl}(w, u) = \Pr\{Y_u = l|Y_w = k\}. \tag{2}$$

As a result, $p_{kl}(w, u)$ represents the probability that someone is in state k at time w, which moves to state l at time u.

Furthermore, the strength of the transition can effect a multi-state process,

$$\mu_{kl} = \lim_{h \to 0} \frac{p_{kl}}{h}, \qquad k \neq l. \tag{3}$$

Shows the transition intensity to the direct transfer of risk state, if known in advance in state k. Both p_{kl} and μ_{kl} depend on the history and processes owned.

If the present is known, the Markov process is a stochastic process of the past that does no influence on the future. A Markov process is a stochastic model describing a sequence of possible events in which the probability of each event depends only on the state attained in the previous event.

Consider a continuous-time stochastic process $\{Y_w; w \geq 0\}$, with a finite (or denumerably infinite) state-space $\mathscr{S}$. We say that $\{Y_w : w \geq 0\}$ is a CTMC if, for any n and each finite set of time $(0 \leq) w_0 < \cdots < w_{n-1} < w_n < u$ and Markov property is satisfied Haberman and Pitacco (1999): responding set of states $k_0, \ldots, k_{n-1}, k_n, l$ in $\mathscr{S}$ with

$$\Pr\{Y_{w_0} = k_0 \wedge \cdots \wedge Y_{w_{n-1}} = k_{n-1} \wedge Y_{w_n} = k_n \wedge Y_u = l\} > 0,$$

the following property (the so-called Markov)

$$\Pr\{Y_u = l|S_{w_0} = k_0 \wedge \cdots \wedge Y_{w_n} = k_n\} = \Pr\{Y_u = l|Y_{w_n} = k_n\}. \tag{4}$$

2.2. Model of a continuous-time Markov chain

The fundamental difference with the discrete-time Markov chain model is that for continuous-time there is an event where a person will settle in a particular state for an unknown time before transitioning to the next state. Suppose $\{Y_w : w \in W\}$ is a random variable showing the condition of the system at moment $w \in W = [0, \infty)$. Random variable $\{Y_w : w \in W\}$ of CTMC if each time series $w_0, w_1, \ldots, w_{n-1}, w_n, u, w$ with $w_0 < w_1 < \cdots < w_{n-1} < w_n < u < w$, random variable $\{Y_w : w \in W\}$ satisfies the following equation:

$$\begin{aligned} P[Y_w = l|Y_u = k, Y_{w_n} = k_n, \ldots, Y_{w_0} = k_0] &= P[Y_w = l|Y_u = k] \\ &= p_{kl}(w - u). \end{aligned} \tag{5}$$

As seen in the Equation 5, the continuous-time process satisfies the Markov property, which asserts that the process at time w is exclusively dependent on the prior state at time u. But unlike the discrete-time case, there is no smallest "next time" until the next transition, there is a continuum of such possible times t. Similarly, we represent the likelihood that the process will shift from state k at time u to state l at time w, to $p_{kl}(w - u)$. We also suppose that

$p_{kl}(w-u)$ does not depend on w at any given time, implying that the process is time and space homogenous

$$P[Y_w = l|Y_u = k] = P[Y_{w-u} = l|Y_0 = k] = p_{kl}(w-u). \tag{6}$$

Y_u will remain in its present state for $\Delta w = w-u$ unit time before transitioning to Y_w with a transition probability of $p_{kl}(wu) = p_{kl}(\Delta w)$. Sojourn time is the time required for a process to transition from state k to state l. In general, for two consecutive states k_n and k_{n+1}, a continuous-time process in state k_n, at time w_n will remain in state k_n until $w_{n+1} - w_n$, at which point it will transition to k_{n+1}. The intervention between k_n and k_{n+1} is denoted by W_n. Together with the homogeneous time, the stochastic process's memoryless property provides the sojourn time memoryless for CTMC. Consider the conditional probability that $W_n > u + w$ with $W_n > u$ demonstrate this,

$$\Pr(W_n > u + w|W_n > u),$$

for $W_n > u$, the process will stay in state k_n every time $w_n + s$ when $0 \leq s \leq u$, so $Y_{w_n+s} = k_n$ for $0 \leq s \leq u$. Also, for $W_n > u + w$, the process will stay in state k_n every time $w_n + s$ when $0 \leq s \leq u + w$, so $Y_{w_n+s} = k_n$ for $0 \leq s \leq u + w$.

Using Markov's property, the conditional probability can be written as follows

$$\Pr(W_n > u + w|W_n > u) = \Pr(Y_{w_n+s} = k_n : u \leq s \leq u + w|Y_{w_n+u} = k_n).$$

Because the random process is time homogeneous.

$$\Pr(W_n > u + w|W_n > u) = \Pr(Y_{w_n+s} = k_n : 0 \leq s \leq w|Y_{w_n} = k_n),$$

and also

$$\Pr(W_n > u + w|W_n > u) = \Pr(Y_{w_n+s} = k_n : 0 \leq s \leq w) = \Pr(W_n > w).$$

This shows that W_n has a memoryless distribution, which means that W_n is Exponentially distributed. Suppose $\Pr(W_n > w) = H_n(w)$, we get

$$H_n(w) = e^{-\lambda_n w}, \tag{7}$$

where $\lambda_n > 0$ denotes the parameter's value. Below is an illustration of cumulative distribution function $F_n(w)$

$$F_n(w) = 1 - e^{-\lambda_n w}. \tag{8}$$

2.3. SVIRD epidemic models

The SVIRD epidemic model has five states: susceptible, vaccinated, infected, recovered, and deceased. This model has random variables $S(w), V(w), I(w), R(w)$ and $D(w)$ whose meanings are explained in Table 1. An illustrative representation of the mathematical model can be seen in Figure 2. Susceptible individuals are represented by **S**, and vaccinated individuals are represented by **V**. Infected individuals are represented by **I**, divided into two states: infected unvaccinated and infected vaccinated. Recovered individuals are represented by **R**. Deceased individuals are represented by **D**. Here, we assume that the vaccine is effective in severe cases, which means that deaths come from unvaccinated individuals. In addition, in this model, it is assumed that there is immunity in individuals who have been infected with the disease so there is no more transition out of the recovered state.

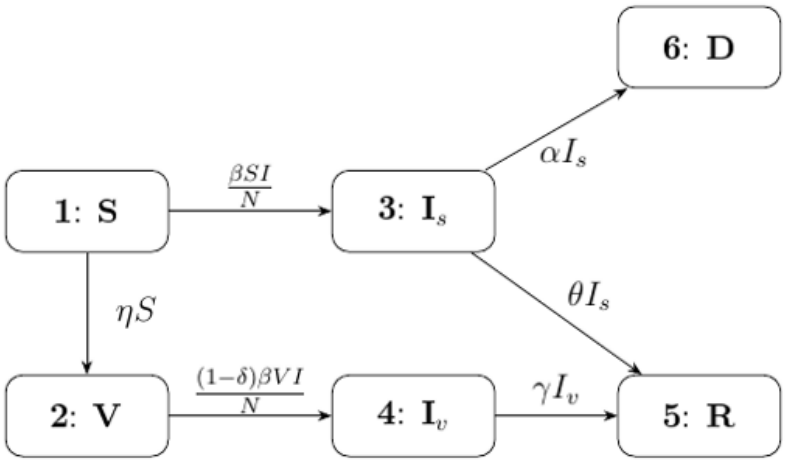

Figure 2: SVIRD epidemic models

We can assume that one transition occurs per step by selecting a sufficiently small time step. Only one of the following events can occur within time step w.

1. $(s, v, i_s, i_v, r) \xrightarrow{\Delta w} (s-1, v+1, i_s, i_v, r) = p_{12}$,
2. $(s, v, i_s, i_v, r) \xrightarrow{\Delta w} (s-1, v, i_s+1, i_v, r) = p_{13}$,
3. $(s, v, i_s, i_v, r) \xrightarrow{\Delta w} (s, v-1, i_s, i_v+1, r) = p_{24}$,
4. $(s, v, i_s, i_v, r) \xrightarrow{\Delta w} (s, v, i_s-1, i_v, r+1) = p_{35}$,
5. $(s, v, i_s, i_v, r) \xrightarrow{\Delta w} (s-1, v, i_s-1, i_v, r) = p_{36}$,
6. $(s, v, i_s, i_v, r) \xrightarrow{\Delta w} (s-1, v, i_s, i_v-1, r+1) = p_{45}$,
7. $(s, v, i_s, i_v, r) \xrightarrow{\Delta w} (s, v, i_s, i_v, r, d) = p_{11} = p_{22} = p_{33} = p_{44} = p_{55} = p_{66}$.

Table 1: Basic notation

Notation	Description
$S(w)$	Number of susceptible at time w
$V(w)$	Number of vaccinated at time w
$I_s(w)$	Number of infected from the susceptible state at time w
$I_v(w)$	Number of infected from the vaccinated state at time w
$R(w)$	Number of recovered at time w
$D(w)$	Number of deceased at time w
β	Infection rate
η	Vaccination rates
δ	Efficacy rates
γ	Recovery rate after vaccination
θ	Recovery rate before vaccination
α	Mortality rate

The path in the SVIRD models is defined as a G series of states with sojourn times.

$$G = ((s_0, v_0, i_{s0}, i_{v0}, r_0), W_0, (s_1, v_1, i_{s1}, i_{v1}, r_1), W_1, \ldots, (s_k, v_k, i_{sk}, i_{vk}, r_k), W_k, (k, l, m, n, o)).$$

This shows that the initial state of the system was $(s_0, v_0, i_{s0}, i_{v0}, r_0)$. The system then changed to $(s_1,\ v_1,\ i_{s1},\ i_{v1},\ r_1)$ after W_0 time units. The system remained in state $(s_1,\ v_1,\ i_{s1},\ i_{v1},\ r_1)$ for W_1 units of time before transitioning to state $(s_2, v_2, i_{s2}, i_{v2}, r_2)$, and so on.

The statistics result (vaccine efficacy) are often presented as a proportional decrease in disease attack rate (A_r) between the unvaccinated (A_u) and vaccinated (A_v), or can be derived from the vaccinated group's relative risk (R_r). The basic formula is written as (Orenstein, Bernier, Dondero, Hinman, Marks, Bart, and Sirotkin 1985):

$$V_e = \frac{A_u - A_v}{A_u} \times 100\%. \tag{9}$$

2.4. Generator matrices

CTMC can be explained accurately by the probability of transition between states and the average duration spent in each stage. The likelihood of a state changing creates an embedded discrete-time Markov chain. The average time spent in each state is exponentially distributed for time between events. We next show how to use a very small transition probability $p_{kl}(\Delta w)$ to form an embedded CTMC and find the average time between events.

To begin, we derive generator matrix $\mathbf{Q}$ from transition rate q_{kl}, which is a one-sided derivative of the extremely small transition probability at $w = 0$. To calculate the transition rate, we assume that probability $p_{kl}(\Delta w)$ is continuous and differentiated at $\Delta w \geq 0$. There are no transitions in time period $\Delta w = 0$ and subsequent periods

$$p_{kl}(0) = 0, \qquad k \neq l,$$

and

$$p_{kl}(0) = 1, \qquad k = l,$$

to obtain the rate q_{kl} where $k \neq l$, can be calculated with

$$\begin{aligned} q_{kl} &= \lim_{\Delta w \to 0^+} \frac{p_{kl}(\Delta w) - p_{kl}(0)}{\Delta w} \\ &= \lim_{\Delta w \to 0^+} \frac{p_{kl}(\Delta w)}{\Delta w}. \end{aligned}$$

In this case, we have $\sum_{l=0}^{N} p_{kl}(\Delta w) = 1$, so that the following equation is obtained

$$1 - p_{kk}(\Delta w) = \sum_{l=0, l\neq k}^{N} p_{kl}(\Delta w).$$

Next we have,

$$\begin{aligned} q_{kk} &= \lim_{\Delta w \to 0^+} \frac{p_{kk}(\Delta w) - 1}{\Delta w} \\ &= \lim_{\Delta w \to 0^+} \frac{-\sum_{l\neq k} p_{kl}(\Delta w)}{\Delta w} \\ &= -\sum_{l=0, l\neq k}^{N} q_{kl}. \end{aligned}$$

The relationship between very small transition probability p_{kl} and transition rate q_{kl} can be written as $p_{kl}(\Delta w) = q_{kl}\dot{\Delta} w + o(\Delta w)$ and $p_{kk}(\Delta w) - 1 = q_{kk}\dot{\Delta} w + o(\Delta w)$. Rate of q_{kl} is used to form the following generator matrix.

$$\mathbf{Q} = \begin{bmatrix} q_{00} & q_{10} & \cdots & q_{k0} & \cdots & q_{N0} \\ q_{01} & q_{11} & \cdots & q_{k1} & \cdots & q_{N1} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\ q_{0l} & q_{1l} & \cdots & q_{kl} & \cdots & q_{Nl} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots \\ q_{0N} & q_{1N} & \cdots & q_{kN} & \cdots & q_{NN} \end{bmatrix}$$

The transition probability from state k to state l for the embedded DTMC is determined using a matrix generator

$$\frac{q_{kl}}{\sum_{k \neq l} q_{kl}}. \tag{10}$$

The likelihood of transitioning from k to l is 0 in an integrated DTMC. In state k, the average exponential interevent time is $\frac{-1}{q_{kk}}$, where $q_{kk} = \lambda_i$ denotes the exponential time distribution rate for state k.

3. Results

3.1. Probabilities of transition in a CTMC SVIRD model

The following equation system can be used to express compartement models that are derived from the assumptions such as variables, parameters, and model shown in Figure 2.

$$\begin{aligned}
\frac{dS(w)}{dw} &= -\frac{\beta S(w) I_s(w)}{N} - \eta S(w) + o(\Delta w), \\
\frac{dV(w)}{dw} &= -\frac{(1-\delta)\beta V(w) I_v(w)}{N} + \eta S(w) + o(\Delta w), \\
\frac{dI_s(w)}{dw} &= \frac{\beta S(w) I_s(w)}{N} - \theta I_s(w) - \alpha I_s(w) + o(\Delta w), \\
\frac{dI_v(w)}{dw} &= \frac{(1-\delta)\beta V(w) I_v(w)}{N} - \gamma I_v(w) + o(\Delta w), \\
\frac{dR(w)}{dw} &= \theta I_s(w) + \gamma I_v(w) + o(\Delta w), \\
\frac{dD(w)}{dw} &= \alpha I_s(w) + o(\Delta w).
\end{aligned}$$

The transition probability between states in Figure 2 is written as follows.

$$p_{12}(\Delta w) = \eta s \Delta w + o(\Delta w), \tag{11}$$

$$p_{13}(\Delta w) = \frac{\beta s i_s}{N} \Delta w + o(\Delta w), \tag{12}$$

$$p_{24}(\Delta w) = \frac{(1-\delta)\beta v i_v}{N} \Delta w + o(\Delta w), \tag{13}$$

$$p_{35}(\Delta w) = \theta i_s \Delta w + o(\Delta w), \tag{14}$$

$$p_{36}(\Delta w) = \alpha i_s \Delta w + o(\Delta w), \tag{15}$$

$$p_{45}(\Delta w) = \gamma i_v \Delta w + o(\Delta w), \tag{16}$$

$$p_{kk}(\Delta w) = 1 - \left(\frac{\beta s i_s}{N} + \frac{(1-\delta)\beta v i_v}{N} + \eta s + \theta i_s + \alpha i_s + \gamma i_v \right) \Delta w + o(\Delta w). \tag{17}$$

Equation (11) shows the probability of transition from susceptible to vaccinated, Equation (12) shows the probability of transition from susceptible to infected unvaccinated, Equation (13) shows the probability of transition from vaccinated to infected vaccinated, Equation (14) shows the probability of transition from infected unvaccinated to recovered, Equation (15) shows the probability of transition from infected unvaccinated to deceased, Equation (16) shows the probability of transition from infected vaccinated to recovered, and the last Equation (17) shows the probability of transition settling in a given state where $k = 1, 2, 3, 4, 5, 6$.

The parameters used in Equation (11-17) will be estimated using the maximum likelihood method which will be described in the next subsection. In the compartment model, parameter values are usually derived based on differential equations that have been created based on the epidemic model, whereas in this study, based on the transition intensity with exponentially distributed sojourn time.

The transition probability from the CTMC SVIRD epidemic model written as $\left(p_{(s,v,i_s,i_v,r)\to(s+k,v+l,i_s+m,i_v+n,r+o)}(\Delta w)\right)$ is given as follows

$$p(\Delta w)=\begin{cases}\eta s\Delta w+o(\Delta w), & (k,l,m,n,o)=(-1,1,0,0,0)\\ \frac{\beta}{N}si_s\Delta w+o(\Delta w), & (k,l,m,n,o)=(-1,0,1,0,0)\\ \frac{(1-\delta)}{N}\beta vi_v\Delta w+o(\Delta w), & (k,l,m,n,o)=(0,-1,0,1,0)\\ \theta i_s\Delta w+o(\Delta w), & (k,l,m,n,o)=(0,0,-1,0,1)\\ \alpha i_s\Delta w+o(\Delta w), & (k,l,m,n,o)=(0,0,-1,0,0)\\ \gamma i_v\Delta w+o(\Delta w), & (k,l,m,n,o)=(0,0,0,-1,1)\\ 1-\left(\eta s+\frac{\beta si_s}{N}+\frac{(1-\delta)\beta vi_v}{N}+\theta i_s+\right. & \\ \left.\alpha i_s+\gamma i_v\right)\Delta w+o(\Delta w), & (k,l,m,n,o)=(0,0,0,0,0)\\ o(\Delta w) & \text{otherwise.}\end{cases}\tag{18}$$

The CTMC SVIRD epidemic model is the probability of transition from state (s,v,i_s,i_v,r) to state $(s+k,v+l,i_s+m,i_v+n,r+o)$, which is denoted by Equation (18). Using Equation (18) the number of groups S,V,I,R, and D may be computed at any given moment, with the initial values provided first.

3.2. Parameter estimation for CTMC SVIRD model

According to the time-continuous SVIRD model with transition probability in Equation (18), it is possible to estimate parameters $\eta,\beta,\delta,\theta,\alpha$ and γ by the maximum likelihood method. This process contains a total of n transitions. At any point in time, all observations occur inside time interval (w_0,w), where $w\geq w_n$, and there is no transition between time intervals (w_n,w). The likelihood function is

$$L(\eta,\beta,\delta,\theta,\alpha,\gamma)=\prod_{i=0}^{n-1}\left(\lambda_{s_i}e^{-\lambda_{s_i}W_i}\right)\left(p_{s_i,s_{i+1}}\right)\left(e^{-\lambda_{s_n}\left(t-\sum_{i=0}^{n-1}W_i\right)}\right),\tag{19}$$

where $\lambda_{s_i}e^{-\lambda_{s_i}W_i}$ is the probability of sojourn time W_i in state s_i, $p_{s_i\to s_{i+1}}$ is the probability of transition from state s_i to s_{i+1} and $e^{-\lambda_{s_n}\left(w-\sum_{i=0}^{n-1}W_i\right)}$ is the probability that no additional transitions occur after time s_n up to time w. We observe that $\sum_{i=0}^{n-1}W_i=w_k$. Let $w-w_n=W_n$, so

$$e^{-\lambda_{s_n}\left(w-\sum_{i=0}^{n-1}W_i\right)}=e^{-\lambda_{s_n}(W_n)}.$$

As a result, Equation (19) may be written as follows.

$$L(\eta,\beta,\delta,\theta,\alpha,\gamma)=e^{-\lambda_{s_n}(W_n)}\prod_{i=0}^{n-1}\left(\lambda_{s_i}e^{-\lambda_{s_i}W_i}\right)\left(p_{s_i,s_{i+1}}\right),\tag{20}$$

for the time-continuous SVIRD model, there are five types of transitions that can occur, namely the transition between (s,v,i_s,i_v,r) and $(s-1,v+1,i_s,i_v,r)$ (susceptible to vaccinated), (s,v,i_s,i_v,r) to $(s-1,v,i_s+1,i_v,r)$ (susceptible to infected unvaccinated), (s,v,i_s,i_v,r) to $(s,v-1,i_s,i_v+1,r)$ (vaccinated to infected vaccinated), (s,v,i_s,i_v,r) to $(s,v,i_s-1,i_v,r+1)$ (infected unvaccinated to recovered), (s,v,i_s,i_v,r) to (s,v,i_s-1,i_v,r) (infected unvaccinated to deceased), and (s,v,i_s,i_v,r) to $(s,v,i_s,i_v-1,r+1)$(infected vaccinated to recovered).

Suppose $(w_{\eta_1},w_{\eta_2},\ldots,w_{\eta_a})$ is the set of times when there is a transition from (s,v,i_s,i_v,r) to $(s-1,v+1,i_s,i_v,r)$, $(w_{\beta_1},w_{\beta_2},\ldots,w_{\beta_b})$ is the set of times when there is a transition from (s,v,i_s,i_v,r) to $(s-1,v,i_s+1,i_v,r)$, $(w_{\delta_1},w_{\delta_2},\ldots,w_{\delta_c})$ is the set of times when there is a transition from (s,v,i_s,i_v,r) to $(s,v-1,i_s,i_v+1,r)$, $(w_{\theta_1},w_{\theta_2},\ldots,w_{\theta_d})$ is the set of times when there is a transition from (s,v,i_s,i_v,r) to $(s,v,i_s-1,i_v,r+1)$, $(w_{\alpha_1},w_{\alpha_2},\ldots,w_{\alpha_e})$ is the set of times when there is a transition from (s,v,i_s,i_v,r) to (s,v,i_s-1,i_v,r), and $(w_{\gamma_1},w_{\gamma_2},\ldots,w_{\gamma_f})$ is the set of times when there is a transition from (s,v,i_s,i_v,r) to $(s,v,i_s,i_v-1,r+1)$.

This means that the first transition from (s, v, i_s, i_v, r) to $(s-1, v+1, i_s, i_v, r)$, occurs at w_{η_a}, the first transition from (s, v, i_s, i_v, r) to $(s-1, v, i_s+1, i_v, r)$ occurs at w_{β_b}, the first transition from (s, v, i_s, i_v, r) to $(s, v-1, i_s, i_v+1, r)$ occurs at w_{δ_c}, the first transition from (s, v, i_s, i_v, r) to $(s, v, i_s-1, i_v, r+1)$ occurs at w_{θ_d}, the first transition from (s, v, i_s, i_v, r) to (s, v, i_s-1, i_v, r) occurs at w_{α_e}, and the first transition from (s, v, i_s, i_v, r) to $(s, v, i_s, i_v - 1, r + 1)$ occurs at w_{γ_f}. There are a transitions from susceptible to vaccinated, b transitions from susceptible to infected unvaccinated, c transitions from vaccinated to infected vaccinated, d transitions from infected unvaccinated to recovered, e transitions from infected unvaccinated to deceased, and f transitions from infected vaccinated to recovered. There is a total of n transitions in the system from state s_0 to state s_n.

Transition probability from (s, v, i_s, i_v, r) to $(s - 1, v + 1, i_s, i_v, r)$ (susceptible to vaccinated vaccinated) is calculated using matrix $\mathbf{Q}$

$$p_{12} = \frac{\eta s}{\eta s + \dfrac{(1-\delta)\beta v i_v}{N} + \gamma i_v}. \tag{21}$$

Transition probability from (s, v, i_s, i_v, r) to $(s - 1, v, i_s + 1, i_v, r)$ (susceptible to infected non-vaccinated) is

$$p_{13} = \frac{\dfrac{\beta s i_s}{N}}{\dfrac{\beta s i_s}{N} + \theta i_s + \alpha i_s}. \tag{22}$$

Transition probability from (s, v, i_s, i_v, r) to $(s, v - 1, i_s, i_v + 1, r)$ (vaccinated to infected vaccinated) is

$$p_{24} = \frac{\dfrac{(1-\delta)\beta v i_v}{N}}{\eta s + \dfrac{(1-\delta)\beta v i_v}{N} + \gamma i_v}. \tag{23}$$

Transition probability from (s, v, i_s, i_v, r) to $(s, v, i_s - 1, i_v, r + 1)$ (infected non-vaccinated to recovered) is

$$p_{35} = \frac{\theta i_s}{\dfrac{\beta s i_s}{N} + \theta i_s}. \tag{24}$$

Transition probability from (s, v, i_s, i_v, r) to $(s, v, i_s - 1, i_v, r)$ (infected non-vaccinated to deceased) is

$$p_{36} = \frac{\alpha i_s}{\dfrac{\beta s i_s}{N} + \alpha i_s}. \tag{25}$$

Transition probability from (s, v, i_s, i_v, r) ke $(s, v, i_s, i_v - 1, r + 1)$ (infected vaccinated to recovered) is

$$p_{45} = \frac{\gamma i_v}{\eta s + \dfrac{(1-\delta)\beta v i_v}{N} + \gamma i_v}. \tag{26}$$

After obtaining the equation of each transition probability between states, the next step is to form the likelihood function then to look for the logarithm of the likelihood function and the partial derivative of the logarithm of the likelihood function for each parameter used. The detailed description can be found in "Appendix 1".

Maximum likelihood estimate $\hat{\eta}$ is the value of η such that

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

Therefore, we have

$$\hat{\eta} = \frac{a}{\sum_{i=0}^{n} [S(w_i) W_i]}, \tag{27}$$

in the same way the value of parameter β is obtained as follows.

$$\hat{\beta} = \frac{b}{\sum_{i=0}^{n}\left[\frac{S(w_i)I_s(w_i)W_i}{N}\right]}, \tag{28}$$

in the same way the value of the parameter δ is obtained as follows.

$$\hat{\delta} = \frac{c}{\sum_{i=0}^{n}\left[\frac{V(w_i)I_v(w_i)W_i}{N}\right]}, \tag{29}$$

in the same way the value of the parameter θ is obtained as follows.

$$\hat{\theta} = \frac{d}{\sum_{i=0}^{n}[I_s(w_i)W_i]}, \tag{30}$$

in the same way the value of the parameter α is obtained as follows.

$$\hat{\alpha} = \frac{e}{\sum_{i=0}^{n}[I_v(w_i)W_i]}, \tag{31}$$

in the same way the value of the parameter γ is obtained as follows.

$$\hat{\gamma} = \frac{f}{\sum_{i=0}^{n}[I_s(w_i)W_i]}. \tag{32}$$

3.3. The algorithm for CTMC SVIRD models

Using real data, parameter values can be determined based on Equation (27-32), while using simulation data, the likelihood function can be determined using the program. The algorithm of the CTMC SVIRD epidemic model is as follows.

1. Initialize the values of $\eta, \beta, \delta, \theta, \alpha, \gamma$, the total population of N, and the duration of the w_{end} outbreak .
2. Determine the number of individuals in each state $S(k), V(k), I_s(k), I_v(k), R(k),\ D(k)$ and $w(k)$.
3. Determine the value of each transition probability between states.
4. Plot times $w(k)$ against the number of infections at each time, $I(k)$.

The detailed algorithm can be found in algorithm 1.

In this paper, we use R software and Matlab to assist in simulating and predicting the COVID-19 data in Indonesia. We use an algorithm based on the COVID-19 data in Indonesia to illustrate an example of the CTMC SVIRD epidemic model where the source code can be seen at https://github.com/fzuhairoh/Multi-state-SVIRD-model.git

Algorithm 1 CTMC SVIRD Epidemic Model

INITIALISE:

The values of $\eta, \beta, \delta, \theta, \alpha, \gamma$, the total population of N, and the duration of the w_{end} outbreak.

Set $k = 1, I_s(1) =$ number of infected on the first day,

$S(1) = N - I_s(1)$,

$V(1) = I_v(1) = R(1) = D(1) = w(1) = 0$,

$I(k) = I_s(k) + I_v(k)$.

ITERATE:

while $I(k) > 0$ and $w(k) < w_{end}$ **do**

Let $a = \eta S(k)$, $b = \dfrac{\beta S(k) I_s(k)}{N}$, $c = \dfrac{(1-\delta)\beta V(k) I_v(k)}{N}$,

$d = \theta I_s(k)$, $e = \alpha I_s(k)$, and $f = \gamma I_v(k)$.

Calculate $p_{12} = \dfrac{a}{a+c+f}$; $p_{13} = \dfrac{b}{b+d+e}$; $p_{24} = \dfrac{c}{a+c+f}$;

$p_{35} = \dfrac{d}{b+d}$; $p_{36} = \dfrac{e}{b+e}$; $p_{45} = \dfrac{f}{a+c+f}$.

Selects two random numbers u_1 and u_2 from a uniform distribution of (0, 1).

if $0 < u_1 \leq p_{12}$ **then**,

$S(k+1) = S(k) - 1; V(k+1) = V(k) + 1; I_v(k+1) = I_v(k); R(k+1) = R(k);$

else if $p_{12} < u_1 \leq p_{24}$ **then**

$S(k+1) = S(k); V(k+1) = V(k) - 1; I_v(k+1) = I_v(k) + 1; R(k+1) = R(k);$

else $p_{24} < u_1 \leq 1$

$S(k+1) = S(k); V(k+1) = V(k); I_v(k+1) = I_v(k) - 1; R(k+1) = R(k) + 1.$

end if

if $0 < u_1 < p_{13}$ **then**,

$S(k+1) = S(k) - 1; I_s(k+1) = I_s(k) + 1; R(k+1) = R(k);$

else $p_{13} < u_1 \leq 1$

$S(k+1) = S(k); I_s(k+1) = I_s(k) - 1; R(k+1) = R(k) + 1.$

end if

if $0 < u_1 \leq p_{13}$ **then**,

$S(k+1) = S(k) - 1; I_s(k+1) = I(k) + 1; D(k+1) = D(k);$

else $p_{13} < u_1 \leq 1$,

$S(k+1) = S(k); I_s(k+1) = I_s(k) - 1; D(k+1) = D(k) + 1.$

end if

Utilize the following method to determine the timing of the next event u_2 as

$w(k+1) = w(k) - \dfrac{\ln(u_2)}{a+c+f} - \dfrac{\ln(u_2)}{b+d} - \dfrac{\ln(u_2)}{b+e}.$

end while

OUTPUT:

Plot times $w(k)$ against the number of infections at each time, $I(k)$.

4. Application

4.1. Application of CTMC SVIRD model using data simulation

We use the previously mentioned algorithm to simulate a CTMC SVIRD model. In this case, we use data on the COVID-19 cases in Indonesia with a population of 2,000,000 people with initial conditions, there were 38,694 people who had been vaccinated, 17,261 people who were infected without vaccination, 8,860 people who were infected after being vaccinated, 8,577 people who recovered, and 82 people who died. According to COVID-19 data in Indonesia on 7 February 2022. In this example, the vaccination rate (η) is 0.676, the infected rate (β) is 0.443, the efficacy rates (δ) is 0.120, the recovery rate after vaccination (γ) is 0.780, the recovery rate before vaccination (θ) is 0.250, and mortality rate (α) is 0.021.

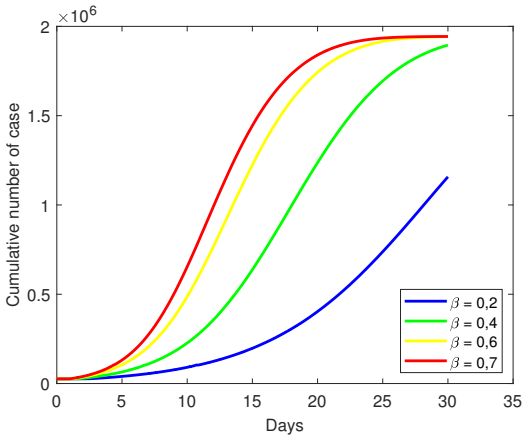

Figure 3: Simulation of a CTMC SVIRD model with different values of infected rate (β) parameters

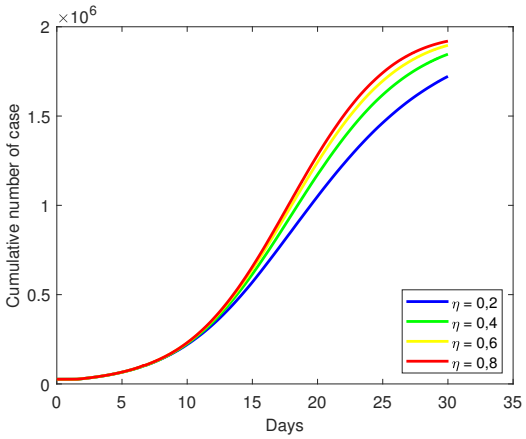

Figure 4: Simulation of the CTMC SVIRD model with varying vaccination rate (η) parameter values

Figure 3 depicts a simulation in which β is varied while the other parameters remain constant. The parameter β has values of 0.1, 0.3, 0.5, and 0.9. Figure 3 demonstrates that the growth in the number of infected individuals is proportional to the infection rate. Several studies have revealed that someone who has been infected with COVID-19 but has not yet shown any clinical signs and symptoms is known to infect others. The more often this occurs, the more difficult the control the spread of the disease, the higher the transmission rate of COVID-19. Figure 3 also shows the greater the value of β, the faster the infected cases will reach the

peak.

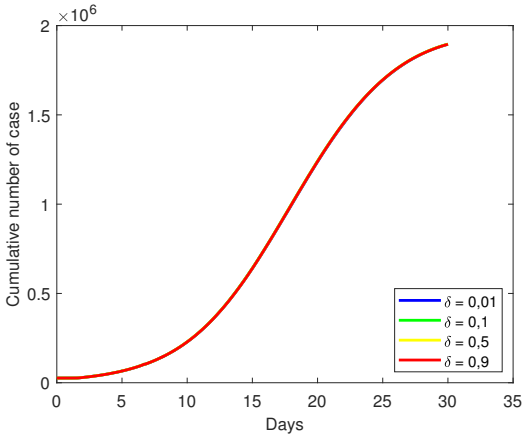

Figure 5: Simulation of a CTMC SVIRD model with varying vaccination efficacy in preventing illness (δ) parameters

Figure 4 depicts a simulation in which η is varied while the remaining parameters remain constant. The parameter η has values of 0.3, 0.5, 0.7, and 0.9. As illustrated in Figure 4, the higher the vaccination rate, the lower the probability of infection among vaccinated individuals, and the faster the cumulative peaks. Vaccination aims to make a person's immune system able to recognize and quickly fight bacteria or viruses that cause infection. The goal to be achieved with the provision of the COVID-19 vaccine is to reduce morbidity and mortality due to this virus. Although not 100% able to protect a person from being infected with COVID-19, this vaccine can reduce the possibility of severe symptoms and complications due to COVID-19. In addition, the COVID-19 vaccination aims to promote the formation of herd immunity. This is important because some people cannot be vaccinated for specific reasons.

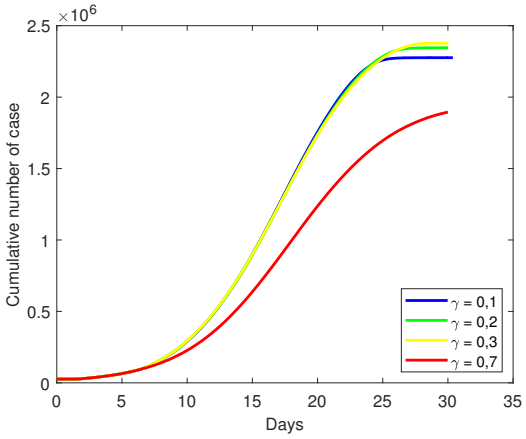

Figure 6: Simulation of a CTMC SVIRD model with varying parameters for the recovery rate after vaccination (γ)

Figure 5 depicts a simulation in which δ is varied while all other parameters remain constant. The parameter δ has values of 0.1, 0.5, 0.7, and 0.9. Figure 5 indicates that the increase in the value of δ has little effect on the infection curve. As we know, there is a low probability of vaccinated people to be infected with COVID-19. According to the Center for Disease Control and Prevention (CDC), even if a person becomes infected with COVID-19 after being vaccinated, it has been known that vaccination can reduce the severy of symptoms and time of infection. In addition, the infected vaccinated person is less likely to be treated or at

a lower risk of death compared to those infected unvaccinated.

Figure 6 depicts a simulation in which γ is varied while the other parameters remain constant. The parameter γ has values of 0.1, 0.3, 0.5, and 0.9. Figure 6 indicates that if the rate of recovery increases, the epidemic will stop more quickly. As for the infected curve, the parameter γ has a negative correlation with the slope of the infected curve.

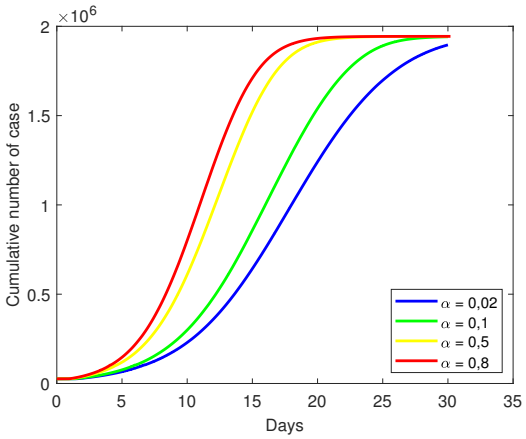

Figure 7: Simulation of a CTMC SVIRD model with varying parameters for mortality rate (α)

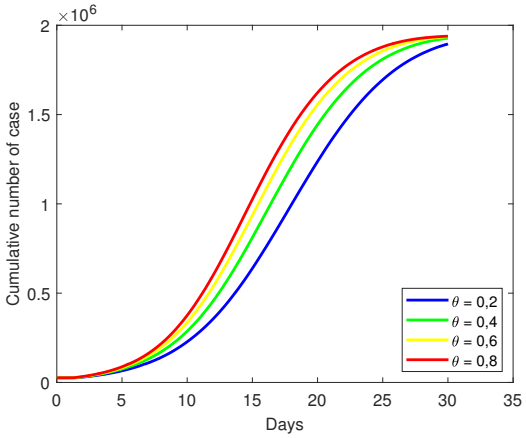

Figure 8: Simulation of a CTMC SVIRD model with varying pre-vaccination recovery rate (θ) parameters

Patients are said to have recovered when they have finished undergoing isolation. The criteria for patients to have completed isolation vary, depending on the cases. For asymptomatic cases, patients are said to have recovered after completing ten days of isolation. Patients with mild symptoms are declared to have recovered if they have no longer shown fever and respiratory problems and if they have completed ten days of isolation three days of isolation without symptoms. COVID-19 patients with severe symptoms may get a positive test result from the real-time-reverse transcription-polymerase chain reaction (RT-PCR) even though they have recovered. This is because the patient with severe symptoms still has the body of the Coronavirus in his/her body, but the virus is no longer dangerous.

Figure 7 depicts a simulation in which α is varied while the other parameters remain constant. The parameter α has values of 0.1, 0.5, 0.7, and 0.9. Figure 7 shows that if there is an increase in the number of mortality due to COVID-19 disease, it causes the infection curve to become more sloping as well as Figure 8 which shows the same thing, namely if there is an increase

in the recovery rate of patients without vaccination, it also causes a decrease in the infection curve. This is because both recovered and deceased states are an absorption state, which means that if someone enters that state, he/she will not transition to another state.

4.2. Application of CTMC SVIRD model using COVID-19 data

Due to data limitations, in the application using actual data, we simplify the model into six states as shown in Figure 2 with the following explanation.

1. The three vaccinated states are combined into one, with the vaccinated state containing individuals who have been vaccinated with at least the first and second doses, in accordance with the type of vaccine used in Indonesia, namely Sinovac, Sinopharm, Pfizer/BioNTech, Moderna, and AstraZeneca/Oxford.

2. The infected state items are divided into two: infected before vaccination and infected after vaccination.

3. The four recovered states are merged into one, which is the transition goal from the infected unvaccinated to infected vaccinated states.

4. The used data begin with the presence of individuals who have received at least the first and second doses of vaccination.

5. If it is still a single-wave epidemic, it is possible to estimate the parameters and determine the transition probability directly. However, if it is a multi-wave epidemic, it is necessary to detect changepoints to assess each wave boundary that appears to obtain better prediction results. The changepoint detection method used in this paper is a binary segmentation method whose algorithm can be seen in algorithm 2.

The binary segmentation method algorithm developed by Eckley *et al.* (2011) is as follows.

Algorithm 2 Binary Segmentation (BS) Method.

INPUT:
A set of data of the form, $(x_1, x_2, \ldots, x_n)$.
A test statistic $\Lambda(\cdot)$ dependent on the data.
An estimator of changepoint position $\hat{\tau}(\cdot)$.
A rejection threshold $\mathcal{C}$.

INITIALISE:
Let $\mathcal{C} = \emptyset$, and $S = \{[1, n]\}$.

ITERATE:
while $S \neq \emptyset$ **do**
  Choose an element of S; denote this element as $[s, t]$.
  if $\Lambda(x_{s:t}) < C$ **then**,
    remove $[s, t]$ from S.
  else if $\Lambda(x_{s:t}) \geq C$ **then**
    remove $[s, t]$ from S;
    calculate $r = \hat{\tau}(x_{s:t}) + s - 1$, and add r to $\mathcal{C}$;
    If $r \neq s$ add $[s, r]$ to S;
    If $r \neq t - 1$ add $[r + 1, t]$ to S.
  end if
end while

OUTPUT:
the set of changepoints recorded $\mathcal{C}$.

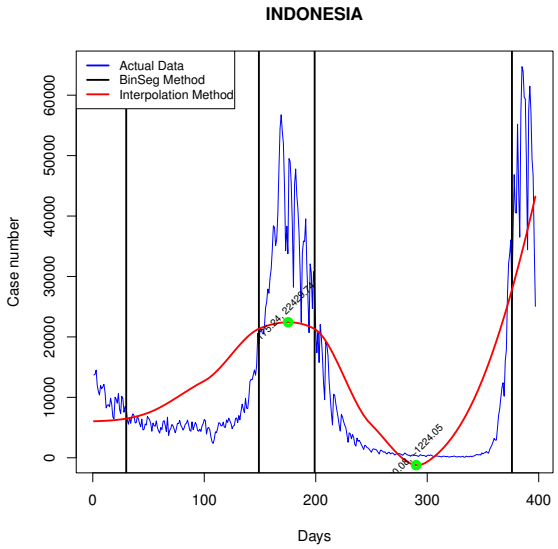

Figure 9: Changepoint detection for COVID-19 data in Indonesia

The data used were data on the COVID-19 cases in Indonesia starting from January 28, 2021, to February 28, 2022. Then changepoint detection was carried out using the binary segmentation method to determine the wave boundary, as shown in Figure 9. The wave used was the last, starting on February 7, 2022.

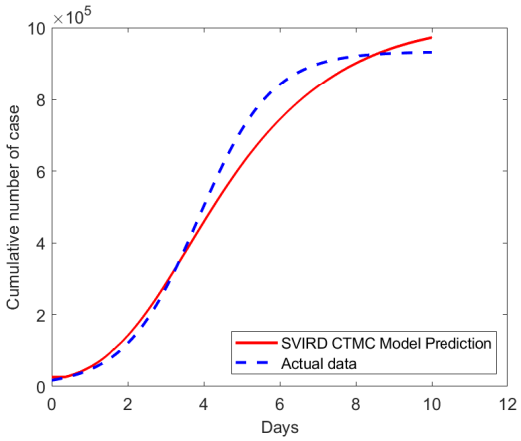

Figure 10: Comparison of the curves of COVID-19 infection cases with actual data

Table 2: Prediction results for COVID-19 cases in Indonesia using CTMC SVIRD

Date	Actual Data	Short-term Prediction
2022/03/1	24,728	46,781
2022/03/2	40,920	41,623
2022/03/3	37,259	36,616
2022/03/4	26,347	31,906
2022/03/5	30,156	27,582
2022/03/6	24,867	23,687
2022/03/7	21,380	20,231

Table 2 shows that the prediction results using CTMC SVIRD had a mean absolute percentage error value (MAPE) of 18.91%. This means that the prediction results were categorized as a good prediction because it fell in the range of 10 % - 20%.

5. Conclusion

A multi-state model that assumes CTMC can model both chronic and infectious disease. This multi-state CTMC model differs from the classical compartment model in that, according to the CTMC assumption, the transition probabilities must be used to define the relationship between states when a multi-state model is employed. This article employs five conditions: susceptible, vaccinated, infected, recovered, and deceased. The infected state is divided into infected vaccinated and unvaccinated. Then the equation to calculate the transition probability and estimate the parameters of the CTMC SVIRD model is given. Finally, the working procedure of the CTMC SVIRD model is given, which is equipped with a changepoint detection method to get accurate prediction results for multi-wave epidemic cases. The short-term prediction results were categorized as a good prediction with MAPE of 18.91%.

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Appendix 1

The likelihood function is transformed into

$$
\begin{aligned}
&\prod_{i=0}^{n-1}\left(\lambda_{s_i}e^{-\lambda_{s_i}W_i}\right)\left(p_{s_i\to s_{i+1}}\right)= \\
&\left[\prod_{p=w_{\eta_1}}^{w_{\eta_a}}\left(\eta S(p)+\frac{\beta S(p)I_s(p)}{N}+\frac{(1-\delta)\beta V(p)I_v(p)}{N}+\theta I_s(p)+\alpha I_s(p)+\gamma I_v(p)\right)\right. \\
&\exp\left(-\left(\eta S(p)+\frac{\beta S(p)I_s(p)}{N}+\frac{(1-\delta)\beta V(p)I_v(p)}{N}+\theta I_s(p)+\alpha I_s(p)+\gamma I_v(p)\right)W_p\right) \\
&\left.\left(\frac{\eta S(p)}{\eta S(p)+\frac{\beta S(p)I_s(p)}{N}+\frac{(1-\delta)\beta V(p)I_v(p)}{N}+\theta I_s(p)+\alpha I_s(p)+\gamma I_v(p)}\right)\right]\times \\
&\left[\prod_{q=w_{\beta_1}}^{w_{\beta_b}}\left(\eta S(q)+\frac{\beta S(q)I_s(q)}{N}+\frac{(1-\delta)\beta V(q)I_v(q)}{N}+\theta I_s(q)+\alpha I_s(q)+\gamma I_v(q)\right)\right. \\
&\exp\left(-\left(\eta S(q)+\frac{\beta S(q)I_s(q)}{N}+\frac{(1-\delta)\beta V(q)I_v(q)}{N}+\theta I_s(q)+\alpha I_s(q)+\gamma I_v(q)\right)W_q\right) \\
&\left.\left(\frac{\frac{\beta S(q)I_s(q)}{N}}{\eta S(q)+\frac{\beta S(q)I_s(q)}{N}+\frac{(1-\delta)\beta V(q)I_v(q)}{N}+\theta I_s(q)+\alpha I_s(q)+\gamma I_v(q)}\right)\right]\times \\
&\left[\prod_{r=w_{\delta_1}}^{w_{\delta_c}}\left(\eta S(r)+\frac{\beta S(r)I_s(r)}{N}+\frac{(1-\delta)\beta V(r)I_v(r)}{N}+\theta I_s(r)+\alpha I_s(r)+\gamma I_v(r)\right)\right.
\end{aligned}
$$

$$\exp\left(-\left(\eta S(r)+\frac{\beta S(r)I_s(r)}{N}+\frac{(1-\delta)\beta V(r)I_v(r)}{N}+\theta I_s(r)+\alpha I_s(r)+\gamma I_v(r)\right)W_r\right)$$
$$\left(\frac{\frac{(1-\delta)\beta V(r)I_v(r)}{N}}{\eta S(r)+\frac{\beta S(r)I_s(r)}{N}+\frac{(1-\delta)\beta V(r)I_v(r)}{N}+\theta I_s(r)+\alpha I_s(r)+\gamma I_v(r)}\right)\Bigg]\times$$
$$\left[\prod_{x=w_{\theta_1}}^{w_{\theta_d}}\left(\eta S(x)+\frac{\beta S(x)I_s(x)}{N}+\frac{(1-\delta)\beta V(x)I_v(x)}{N}+\theta I_s(x)+\alpha I_s(x)+\gamma I_v(x)\right)\right.$$
$$\exp\left(-\left(\eta S(x)+\frac{\beta S(x)I_s(t)}{N}+\frac{(1-\delta)\beta V(x)I_v(x)}{N}+\theta I_s(x)+\alpha I_s(x)+\gamma I_v(x)\right)W_x\right)$$
$$\left(\frac{\theta I_s(x)}{\eta S(x)+\frac{\beta S(x)I_s(x)}{N}+\frac{(1-\delta)\beta V(x)I_v(x)}{N}+\theta I_s(x)+\alpha I_s(x)+\gamma I_v(x)}\right)\Bigg]\times$$
$$\left[\prod_{y=w_{\alpha_1}}^{w_{\alpha_e}}\left(\eta S(y)+\frac{\beta S(y)I_s(y)}{N}+\frac{(1-\delta)\beta V(y)I_v(y)}{N}+\theta I_s(y)+\alpha I_s(y)+\gamma I_v(y)\right)\right.$$
$$\exp\left(-\left(\eta S(y)+\frac{\beta S(y)I_s(y)}{N}+\frac{(1-\delta)\beta V(y)I_v(y)}{N}+\theta I_s(y)+\alpha I_s(y)+\gamma I_v(y)\right)W_y\right)$$
$$\left(\frac{\alpha I_s(y)}{\eta S(y)+\frac{\beta S(y)I_s(y)}{N}+\frac{(1-\delta)\beta V(y)I_v(y)}{N}+\theta I_s(y)+\alpha I_s(y)+\gamma I_v(y)}\right)\Bigg]\times$$
$$\left[\prod_{z=w_{\gamma_1}}^{z_{\gamma_f}}\left(\eta S(z)+\frac{\beta S(z)I_s(z)}{N}+\frac{(1-\delta)\beta V(z)I_v(z)}{N}+\theta I_s(z)+\alpha I_s(z)+\gamma I_v(z)\right)\right.$$
$$\exp\left(-\left(\eta S(z)+\frac{\beta S(z)I_s(z)}{N}+\frac{(1-\delta)\beta V(z)I_v(z)}{N}+\theta I_s(z)+\alpha I_s(z)+\gamma I_v(z)\right)W_z\right)$$
$$\left.\left(\frac{\gamma I_v(z)}{\eta S(z)+\frac{\beta S(z)I_s(z)}{N}+\frac{(1-\delta)\beta V(z)I_v(z)}{N}+\theta I_s(z)+\alpha I_s(z)+\gamma I_v(z)}\right)\right]$$

It can then be simplified into the following equation.

$$\prod_{i=0}^{n-1}\left(\lambda_{s_i}e^{-\lambda_{s_i}W_i}\right)\left(p_{s_i\to s_{i+1}}\right)=$$
$$\left[\prod_{p=w_{\eta_1}}^{w_{\eta_a}}\eta S(p)\exp\left(-\left(\eta S(p)+\frac{\beta S(p)I_s(p)}{N}\right)W_p\right)\right.$$
$$\left.\exp\left(-\left(\frac{(1-\delta)\beta V(p)I_v(p)}{N}+\theta I_s(p)+\alpha I_s(p)+\gamma I_v(p)\right)W_p\right)\right]\times$$
$$\left[\prod_{q=w_{\beta_1}}^{w_{\beta_b}}\frac{\beta S(q)I_s(q)}{N}\exp\left(-\left(\eta S(q)+\frac{\beta S(q)I_s(q)}{N}\right)W_q\right)\right.$$
$$\left.\exp\left(-\left(\frac{(1-\delta)\beta V(q)I_v(q)}{N}+\theta I_s(q)+\alpha I_s(q)+\gamma I_v(q)\right)W_q\right)\right]\times$$
$$\left[\prod_{r=w_{1-\delta_1}}^{w_{\delta_c}}\frac{(1-\delta)\beta S(r)I_v(r)}{N}\exp\left(-\left(\eta S(r)+\frac{\beta S(r)I_s(r)}{N}\right)W_r\right)\right.$$
$$\left.\exp\left(-\left(\frac{(1-\delta)\beta V(r)I_v(r)}{N}+\theta I_s(r)+\alpha I_s(r)+\gamma I_v(r)\right)W_r\right)\right]\times$$
$$\left[\prod_{x=w_{\theta_1}}^{w_{\theta_d}}\theta I_s(x)\exp\left(-\left(\eta S(x)+\frac{\beta S(x)I_s(x)}{N}\right)W_x\right)\right.$$

$$\exp\left(-\left(\frac{(1-\delta)\beta V(x)I_v(x)}{N}+\theta I_s(x)+\alpha I_s(x)+\gamma I_v(x)\right)W_x\right)\Bigg]\times$$
$$\Bigg[\prod_{y=w_{\alpha_1}}^{w_{\alpha_e}}\alpha I_s(y)\exp\left(-\left(\eta S(y)+\frac{\beta S(y)I_s(y)}{N}\right)W_y\right)$$
$$\exp\left(-\left(\frac{(1-\delta)\beta V(y)I_v(y)}{N}+\theta I_s(y)+\alpha I_s(y)+\gamma I_v(y)\right)W_y\right)\Bigg]\times$$
$$\Bigg[\prod_{z=w_{\gamma_1}}^{w_{\gamma_f}}\gamma I_v(z)\exp\left(-\left(\eta S(z)+\frac{\beta S(z)I_s(z)}{N}\right)W_z\right)$$
$$\exp\left(-\left(\frac{(1-\delta)\beta V(z)I_v(z)}{N}+\theta I_s(z)+\alpha I_s(z)+\gamma I_v(z)\right)W_z\right)\Bigg]$$

The likelihood function is denoted by the following.

$$L(\eta,\beta,\delta,\theta,\alpha,\gamma)=$$
$$\exp\left(-\left(\eta S(w_n)+\frac{\beta S(w_n)I_s(w_n)}{N}+\frac{(1-\delta)\beta V(w_n)I_v(w_n)}{N}+\theta I_s(w_n)+\alpha I_s(w_n)+\alpha I_v(w_n)\right)W_n\right)$$
$$\prod_{p=w_{\eta_1}}^{w_{\eta_a}}\left[\eta S(p)\exp\left(-\left(\eta S(p)+\frac{\beta S(p)I_s(p)}{N}+\frac{(1-\delta)\beta V(p)I_v(p)}{N}+\theta I_s(p)+\alpha I_s(p)+\gamma I_v(p)\right)W_p\right)\right]\times$$
$$\prod_{q=w_{\beta_1}}^{w_{\beta_b}}\left[\frac{\beta S(q)I_s(q)}{N}\right.$$
$$\left.\exp\left(-\left(\eta S(q)+\frac{\beta S(q)I_s(q)}{N}+\frac{(1-\delta)\beta V(q)I_v(q)}{N}+\theta I_s(q)+\alpha I_s(q)+\gamma I_v(q)\right)W_q\right)\right]\times$$
$$\prod_{x=w_{\delta_1}}^{w_{\delta_c}}\left[\frac{(1-\delta)\beta V(x)I_v(x)}{N}\right.$$
$$\left.\exp\left(-\left(\eta S(x)+\frac{\beta S(x)I_s(x)}{N}-\frac{(1-\delta)\beta V(x)I_v(x)}{N}+\theta I_s(x)+\alpha I_s(x)+\gamma I_v(x)\right)W_r\right)\right]\times$$
$$\prod_{x=w_{\theta_1}}^{w_{\theta_d}}\left[\theta I_s(x)\exp\left(-\left(\eta S(x)+\frac{\beta S(x)I_s(x)}{N}+\frac{(1-\delta)\beta V(x)I_v(x)}{N}+\theta I_s(x)+\gamma I_s(x)+\gamma I_s(x)\right)W_x\right)\right]\times$$
$$\prod_{y=w_{\alpha_1}}^{w_{\alpha_e}}\left[\alpha I_s(y)\exp\left(-\left(\eta S(y)+\frac{\beta S(y)I_s(y)}{N}+\frac{(1-\delta)\beta V(y)I_v(y)}{N}+\theta I_s(y)+\alpha I_s(y)+\gamma I_v(y)\right)W_y\right)\right]\times$$
$$\prod_{z=w_{\gamma_1}}^{w_{\gamma_f}}\left[\gamma I_v(z)\exp\left(-\left(\eta S(z)+\frac{\beta S(z)I_s(z)}{N}+\frac{(1-\delta)\beta V(z)I_v(z)}{N}+\theta I_s(z)+\alpha I_s(z)+\gamma I_v(z)\right)W_z\right)\right]$$

We have obtained the logarithm of the likelihood function

$$\log L(\eta,\beta,\delta,\theta,\alpha,\gamma)=$$
$$-\left(\eta S(w_n)+\frac{\beta S(w_n)I_s(w_n)}{N}+\frac{(1-\delta)\beta V(w_n)I_s(w_n)}{N}+\theta I_s(w_n)+\alpha I_s(w_n)+\gamma I_v(w_n)\right)W_n+$$
$$\sum_{p=w_{\eta_1}}^{w_{\eta_a}}\left[\log\left(\eta S(p)\right)-\left(\eta S(p)+\frac{\beta S(p)I_s(p)}{N}+\frac{(1-\delta)\beta V(p)I_v(p)}{N}+\theta I_s(p)+\alpha I_s(p)+\gamma I_v(p)\right)W_p\right]+$$
$$\sum_{q=w_{\beta_1}}^{w_{\beta_b}}\left[\log\left(\frac{\beta S(q)I_s(q)}{N}\right)-\right.$$
$$\left.\left(\eta S(q)+\frac{\beta S(q)I_s(q)}{N}+\frac{(1-\delta)\beta V(q)I_v(q)}{N}+\theta I_s(q)+\alpha I_s(q)+\gamma I_v(q)\right)W_q\right]+$$
$$\sum_{r=w_{\delta_1}}^{w_{\delta_c}}\left[\log\left(\frac{(1-\delta)\beta S(r)I_s(r)}{N}\right)-\right.$$
$$\left.\left(\eta S(r)+\frac{\beta S(r)I_s(r)}{N}+\frac{(1-\delta)\beta V(r)I_v(r)}{N}+\theta I_s(r)+\alpha I_s(r)+\gamma I_v(r)\right)W_r\right]+$$

$$\sum_{x=w_{\theta_1}}^{w_{\theta_d}}\left[\log\left(\theta I_s(x)\right)-\left(\eta S(x)+\frac{\beta S(x)I_s(x)}{N}+\frac{(1-\delta)\beta V(x)I_v(x)}{N}+\theta I_s(x)+\alpha I_s(x)+\gamma I_v(x)\right)W_x\right]+$$
$$\sum_{y=w_{\alpha_1}}^{w_{\alpha_e}}\left[\log\left(\alpha I_s(y)\right)-\left(\eta S(y)+\frac{\beta S(y)I_s(y)}{N}+\frac{(1-\delta)\beta V(y)I_v(y)}{N}+\theta I_s(y)+\alpha I_s(y)+\gamma I_v(y)\right)W_y\right]+$$
$$\sum_{z=w_{\gamma_1}}^{w_{\gamma_f}}\left[\log\left(\gamma I_s(z)\right)-\left(\eta S(z)+\frac{\beta S(z)I_s(z)}{N}+\frac{(1-\delta)\beta V(z)I_v(z)}{N}+\theta I_s(z)+\alpha I_s(z)+\gamma I_v(z)\right)W_z\right]$$

Using the partial derivative of the logarithm of the likelihood function with respect to η, we obtain

$$\begin{aligned}\frac{\partial \log L(\eta,\beta,\delta,\theta,\alpha,\gamma)}{\partial\eta} =& -S(w_n)W_n+\sum_{p=w_{\eta_1}}^{w_{\eta_a}}\left[\frac{1}{\eta}-\left(S(p)\right)W_p\right]-\sum_{q=w_{\beta_1}}^{w_{\beta_b}}[S(q)W_q]-\\ &\sum_{r=w_{\delta_1}}^{w_{\delta_c}}[S(r)W_r]-\sum_{x=w_{\theta_1}}^{w_{\theta_d}}[S(x)W_x]-\sum_{y=w_{\alpha_1}}^{w_{\alpha_e}}[S(y)W_y]-\sum_{z=w_{\gamma_1}}^{w_{\gamma_f}}[S(z)W_z]\\ =& -S(w_n)W_n+\sum_{p=w_{\eta_1}}^{w_{\eta_a}}\left(\frac{1}{\eta}\right)-\left(\sum_{p=w_{\eta_1}}^{w_{\eta_a}}[S(p)W_p]+\sum_{q=w_{\beta_1}}^{w_{\beta_b}}[S(q)W_q]+\right.\\ &\left.\sum_{r=w_{\delta_1}}^{w_{\delta_c}}[S(r)W_r]+\sum_{x=w_{\theta_1}}^{w_{\theta_d}}[S(x)W_x]+\sum_{y=w_{\alpha_1}}^{w_{\alpha_e}}[S(y)W_y]+\sum_{z=w_{\gamma_1}}^{w_{\gamma_f}}[S(z)W_z]\right)\\ =& -S(w_n)W_n+\sum_{p=w_{\eta_1}}^{w_{\eta_a}}\left(\frac{1}{\eta}\right)-\sum_{i=0}^{n-1}[S(i)W_i]\\ =&\frac{a}{\eta}-\sum_{i=0}^{n}[S(i)W_i]\end{aligned}$$

Using the partial derivative of the logarithm of the likelihood function with respect to β, we obtain

$$\begin{aligned}\frac{\partial \log L(\eta,\beta,\delta,\theta,\alpha,\gamma)}{\partial\beta} =& -\left[\frac{S(w_n)I_s(w_n)}{N}\right]W_n+\sum_{q=w_{\beta_1}}^{w_{\beta_b}}\left[\frac{1}{\beta}-\left(\frac{S(q)I_s(q)}{N}\right)W_q\right]-\\ &\sum_{p=w_{\eta_1}}^{w_{\eta_a}}\left[\left(\frac{S(p)I_s(p)}{N}\right)W_p\right]-\sum_{r=w_{\delta_1}}^{w_{\delta_c}}\left[\left(\frac{S(r)I_s(r)}{N}\right)W_r\right]-\\ &\sum_{x=w_{\theta_1}}^{w_{\theta_d}}\left[\left(\frac{S(x)I_s(x)}{N}\right)W_x\right]-\sum_{y=w_{\alpha_1}}^{w_{\alpha_e}}\left[\left(\frac{S(y)I_s(y)}{N}\right)W_y\right]-\\ &\sum_{z=w_{\gamma_1}}^{w_{\gamma_f}}\left[\left(\frac{S(z)I_s(z)}{N}\right)W_z\right]\\ =& -\left[\frac{S(w_n)I_s(w_n)}{N}\right]W_n+\sum_{p=w_{\beta_1}}^{w_{\beta_b}}\left(\frac{1}{\beta}\right)-\left(\sum_{p=w_{\eta_1}}^{w_{\eta_a}}\left[\left(\frac{S(p)I_s(p)}{N}\right)W_p\right]+\right.\\ &\sum_{q=w_{\beta_1}}^{w_{\beta_b}}\left[\left(\frac{S(q)I_s(q)}{N}\right)W_q\right]+\sum_{r=w_{\delta_1}}^{w_{\delta_c}}\left[\left(\frac{S(r)I_s(r)}{N}\right)W_r\right]+\\ &\sum_{x=w_{\theta_1}}^{w_{\theta_d}}\left[\left(\frac{S(x)I_s(x)}{N}\right)W_x\right]+\sum_{y=w_{\alpha_1}}^{w_{\alpha_e}}\left[\left(\frac{S(y)I_s(y)}{N}\right)W_y\right]+\\ &\left.\sum_{z=w_{\gamma_1}}^{w_{\gamma_f}}\left[\left(\frac{S(z)I_s(z)}{N}\right)W_z\right]\right)\\ =& -\left[\frac{S(w_n)I_s(w_n)}{N}\right]W_n+\sum_{p=w_{\beta_1}}^{w_{\beta_a}}\left(\frac{1}{\beta}\right)-\sum_{i=0}^{n-1}\left[\left(\frac{S(q)I_s(q)}{N}\right)W_q\right]\end{aligned}$$

$$= \frac{b}{\beta} - \sum_{i=0}^{n} \left[\left(\frac{S(q)I_s(q)}{N} \right) W_q \right]$$

Using the partial derivative of the logarithm of the likelihood function with respect to δ, we obtain

$$\begin{aligned}
\frac{\partial \log L(\eta,\beta,\delta,\theta,\alpha,\gamma)}{\partial \delta} =& - \left[\frac{(1-\delta)\beta V(w_n) I_v(w_n)}{N} \right] W_n + \sum_{r=w_{\delta_1}}^{w_{\delta_c}} \left[\frac{1}{\delta} - \left(\frac{(1-\delta)\beta V(r) I_v(r)}{N} \right) W_r \right] - \\
& \sum_{p=w_{\eta_1}}^{w_{\eta_a}} \left[\left(\frac{(1-\delta)\beta V(p) I_v(p)}{N} \right) W_p \right] - \sum_{q=w_{\beta_1}}^{w_{\beta_b}} \left[\left(\frac{(1-\delta)\beta V(q) I_v(q)}{N} \right) W_q \right] - \\
& \sum_{x=w_{\theta_1}}^{w_{\theta_d}} \left[\left(\frac{(1-\delta)\beta V(x) I_v(x)}{N} \right) W_x \right] - \sum_{y=w_{\alpha_1}}^{w_{\alpha_e}} \left[\left(\frac{(1-\delta)\beta V(y) I_v(y)}{N} \right) W_y \right] - \\
& \sum_{z=w_{\gamma_1}}^{w_{\gamma_f}} \left[\left(\frac{(1-\delta)\beta V(z) I_v(z)}{N} \right) W_z \right] \\
=& - \left[\frac{(1-\delta)\beta V(w_n) I_v(w_n)}{N} \right] W_n + \sum_{p=w_{\delta_1}}^{w_{\delta_c}} \left(\frac{1}{\beta} \right) - \\
& \left(\sum_{p=w_{\eta_1}}^{w_{\eta_a}} \left[\left(\frac{(1-\delta)\beta V(p) I_v(p)}{N} \right) W_p \right] + \sum_{p=w_{\beta_1}}^{w_{\beta_b}} \left[\left(\frac{(1-\delta)\beta V(q) I_v(q)}{N} \right) W_q \right] \right. \\
& \sum_{r=w_{\delta_1}}^{w_{\delta_c}} \left[\left(\frac{(1-\delta)\beta V(r) I_v(r)}{N} \right) W_r \right] + \sum_{x=w_{\theta_1}}^{w_{\theta_d}} \left[\left(\frac{(1-\delta)\beta V(x) I_v(x)}{N} \right) W_x \right] \\
& \left. + \sum_{y=w_{\alpha_1}}^{w_{\alpha_e}} \left[\left(\frac{(1-\delta)\beta V(y) I_v(y)}{N} \right) W_y \right] + \sum_{z=w_{\gamma_1}}^{w_{\gamma_f}} \left[\left(\frac{(1-\delta)\beta V(z) I_v(z)}{N} \right) W_z \right] \right) \\
=& - \left[\frac{(1-\delta)\beta V(w_n) I_v(w_n)}{N} \right] W_n + \sum_{r=w_{\delta_1}}^{w_{\delta_c}} \left(\frac{1}{\delta} \right) - \sum_{i=0}^{n-1} \left[\left(\frac{(1-\delta)\beta V(r) I_v(r)}{N} \right) W_r \right] \\
=& \frac{c}{\delta} - \sum_{i=0}^{n} \left[\left(\frac{(1-\delta)\beta V(r) I_v(r)}{N} \right) W_r \right]
\end{aligned}$$

Using the partial derivative of the logarithm of the likelihood function with respect to θ, we obtain

$$\begin{aligned}
\frac{\partial \log L(\eta,\beta,\delta,\theta,\alpha,\gamma)}{\partial \theta} =& - I_s(w_n) W_n + \sum_{x=w_{\theta_1}}^{w_{\theta_d}} \left[\frac{1}{\theta} - (I_s(x)) W_x \right] - \sum_{p=w_{\eta_1}}^{w_{\eta_a}} [I_s(p) W_p] - \\
& \sum_{q=w_{\beta_1}}^{w_{\beta_b}} [I_s(q) W_q] - \sum_{r=w_{\delta_1}}^{w_{\delta_c}} [I_s(r) W_r] - \sum_{y=w_{\alpha_1}}^{w_{\alpha_e}} [I_s(y) W_y] - \sum_{z=w_{\gamma_1}}^{w_{\gamma_f}} [I_s(z) W_z] \\
=& - I_s(w_n) W_n + \sum_{x=w_{\theta_1}}^{w_{\theta_d}} \left(\frac{1}{\theta} \right) - \left(\sum_{p=w_{\eta_1}}^{w_{\eta_a}} [I_s(p) W_p] + \sum_{q=w_{\beta_1}}^{w_{\beta_b}} [I_s(q) W_q] + \right. \\
& \left. \sum_{r=w_{\delta_1}}^{w_{\delta_c}} [I_s(r) W_r] + \sum_{x=w_{\theta_1}}^{w_{\theta_d}} [I_s(x) W_x] + \sum_{y=w_{\alpha_1}}^{w_{\alpha_e}} [I_s(y) W_y] + \sum_{z=w_{\gamma_1}}^{w_{\gamma_f}} [I_s(z) W_z] \right) \\
=& - I_s(w_n) W_n + \sum_{x=w_{\theta_1}}^{w_{\theta_d}} \left(\frac{1}{\theta} \right) - \sum_{i=0}^{n-1} [I_s(i) W_i] \\
=& \frac{d}{\theta} - \sum_{i=0}^{n} [I_s(i) W_i]
\end{aligned}$$

Using the partial derivative of the logarithm of the likelihood function with respect to α, we

obtain

$$\begin{aligned}\frac{\partial \log L(\eta,\beta,\delta,\theta,\alpha,\gamma)}{\partial \alpha} =& - I_s(w_n)W_n + \sum_{y=w_{\alpha_1}}^{w_{\alpha_e}} \left[\frac{1}{\alpha} - (I_s(y))\, W_y\right] - \sum_{p=w_{\eta_1}}^{w_{\eta_a}} [I_s(p)W_p] - \\ & \sum_{q=w_{\beta_1}}^{w_{\beta_b}} [I_s(q)W_q] - \sum_{r=w_{\delta_1}}^{w_{\delta_c}} [I_s(r)W_r] - \sum_{x=w_{\theta_1}}^{w_{\theta_e}} [I_s(x)W_x] - \sum_{z=w_{\gamma_1}}^{w_{\gamma_f}} [I_s(z)W_z] \\ =& - I_s(w_n)W_n + \sum_{x=w_{\alpha_1}}^{w_{\alpha_e}} \left(\frac{1}{\alpha}\right) - \left(\sum_{p=w_{\eta_1}}^{w_{\eta_a}} [I_s(p)W_p] + \sum_{q=w_{\beta_1}}^{w_{\beta_b}} [I_s(q)W_q] + \right. \\ & \left. \sum_{r=w_{\delta_1}}^{w_{\delta_c}} [I_s(r)W_r] + \sum_{x=w_{\theta_1}}^{w_{\theta_d}} [I_s(x)W_x] + \sum_{y=w_{\alpha_1}}^{w_{\alpha_e}} [I_s(y)W_y] + \sum_{z=w_{\gamma_1}}^{w_{\gamma_f}} [I_s(z)W_z] \right) \\ =& - I_s(w_n)W_n + \sum_{x=w_{\alpha_1}}^{w_{\alpha_e}} \left(\frac{1}{\alpha}\right) - \sum_{i=0}^{n-1} [I_s(i)W_i] \\ =& \frac{e}{\alpha} - \sum_{i=0}^{n} [I_s(i)W_i]\end{aligned}$$

Using the partial derivative of the logarithm of the likelihood function with respect to γ, we obtain

$$\begin{aligned}\frac{\partial \log L(\eta,\beta,\delta,\theta,\alpha,\gamma)}{\partial \gamma} =& - I_v(w_n)W_n + \sum_{z=w_{\gamma_1}}^{w_{\gamma_f}} \left[\frac{1}{\gamma} - (I_v(z))\, W_z\right] - \sum_{p=w_{\eta_1}}^{w_{\eta_a}} [I_v(p)W_p] - \\ & \sum_{q=w_{\beta_1}}^{w_{\beta_b}} [I_v(q)W_q] - \sum_{r=w_{\delta_1}}^{w_{\delta_c}} [I_v(r)W_r] - \sum_{x=w_{\theta_1}}^{w_{\theta_e}} [I_v(x)W_x] - \sum_{y=w_{\alpha_1}}^{w_{\alpha_d}} [I_v(y)W_y] \\ =& - I_v(w_n)W_n + \sum_{x=w_{\gamma_1}}^{w_{\gamma_f}} \left(\frac{1}{\gamma}\right) - \left(\sum_{p=w_{\eta_1}}^{w_{\eta_a}} [I_v(p)W_p] + \sum_{q=w_{\beta_1}}^{w_{\beta_b}} [I_v(q)W_q] + \right. \\ & \left. \sum_{r=w_{\delta_1}}^{w_{\delta_c}} [I_v(r)W_r] + \sum_{x=w_{\theta_1}}^{w_{\theta_d}} [I_v(x)W_x] + \sum_{y=w_{\alpha_1}}^{w_{\alpha_e}} [I_v(y)W_y] + \sum_{z=w_{\gamma_1}}^{w_{\gamma_f}} [I_v(z)W_z] \right) \\ =& - I_v(w_n)W_n + \sum_{z=w_{\gamma_1}}^{w_{\gamma_e}} \left(\frac{1}{\gamma}\right) - \sum_{i=0}^{n-1} [I_v(i)W_i] \\ =& \frac{f}{\gamma} - \sum_{i=0}^{n} [I_v(i)W_i]\end{aligned}$$

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