



SIMULATION OF DISCRETE-TIME MARKOV CHAIN SUSCEPTIBLE VACCINATED INFECTED RECOVERED SUSCEPTIBLE (DTMC SVIRS) STOCHASTIC EPIDEMIC MODEL ON THE SPREAD OF TUBERCULOSIS DISEASE IN CENTRAL JAVA

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Abstract

One of the infectious diseases that is still a public health challenge in Indonesia is tuberculosis (TB). This study is intended to model the spread of TB disease in Central Java using the Discrete-Time Markov Chain Susceptible Vaccinated Infected Recovered Susceptible (DTMC SVIRS) stochastic epidemic model. This model categorizes the population into four groups: susceptible, vaccinated, infected, and recovered. The transition probabilities between these groups are obtained based on transmission, vaccination, vaccine failure, vaccine effectiveness, recovery, and waning immunity rates. Parameter values were estimated using TB data from the Central Java Health Profile. Simulations were performed with different transmission rate treatments to analyze their effect on epidemic dynamics. The results show that the higher transmission rate, the longer it takes to reach the peak of epidemic and the more individuals are infected, which indicates a more serious epidemic. The model predicts that the epidemic will continue timelessly due to waning immunity and remaining susceptibility. The SVIRS model provides an overview of the spread of TB in Central Java.

Keywords: *Stochastic, DTMC, SVIRS, Epidemic, Tuberculosis*

A. Introduction

There are many infectious diseases or contagious diseases that can endanger human health. One of the infectious diseases is tuberculosis. Tuberculosis (TB) is an infectious disease that can be transmitted when people with TB are talking, coughing, sneezing, or singing so that their sputum will be spread through the air and then the air that is contaminated will be inhaled by other individuals [1]. Tuberculosis is caused by *Mycobacterium tuberculosis* entering the respiratory system and infecting the lungs [2]. However, the disease can also infect other organs such as bones, brain tissue, and other organs.

Tuberculosis is one of the top ten diseases with the highest mortality rate in the world with the number of new cases increasing every year. Indonesia has the second highest number of TB cases after India, which is 1.02 million cases.

Provinces that contribute the most TB cases are provinces with high population density, namely East Java, Central Java, and West Java with a total of 44% of cases in Indonesia [3].

Vaccination is one of the most effective ways to protect yourself from TB. [4]. A vaccine has been developed by health practitioners to prevent tuberculosis, namely the Bacillus Calmette Guerin (BCG) vaccine. The BCG vaccine is a vaccine made from live bacteria causing tuberculosis that has been weakened so that healthy individuals who are injected with the BCG vaccine will form immunity to tuberculosis disease and the bacteria will not infect the individual concerned [5]. BCG vaccine is generally given in one dose to newborns before the age of 1 month as basic immunization.

According to Lekone and Finkenstadt in a research journal written by Nurlazuardini et al (2016) [6], there is mathematical modeling to model the spread of infectious diseases to find out the pattern. The mathematical model consists of two models, namely deterministic models and stochastic models. According to Mode and Sleeman in a journal written by Maisura et al (2018) [7], the deterministic model tends to be incomplete. This is because the deterministic model is unable to explain the variations and uncertainties that exist in epidemic models, so stochastic models are needed to consider the random influences of individuals.

Kristiandari et al (2023) [8] modeled diphtheria disease in Indonesia using DTMC SVIR. In this study, two simulations were performed with different population sizes, the initial number of infected individuals, and the initial number of individuals who received the vaccine. The result of this study is that the epidemic will end when there is an increase in the number of individuals who get the vaccine and the number of individuals who recover. Therefore, it can be said that the number of individuals who get the vaccine affects the epidemic.

Zuhairah et al (2022) [9] researched the modeling of the spread of COVID-19 disease using DTMC SVIRS. This study concluded that by using the DTMC SVIRS model, short-term predictions for COVID-19 in Indonesia are very accurate. This is known from the low average MAPE value which is 5.7% for the prediction of COVID-19 cases in Indonesia.

Tilahun et al (2020) [10] in their research on the spread of tuberculosis (TB) using SVIRS stochastic modeling. This research begins by forming a deterministic model first as a comparison. Then stochastic modeling is carried out because, in the deterministic model, there are several limitations due to the neglect of random influences. This study concludes that the number of individuals infected with TB will continue to decrease if individuals are given vaccines and followed by proper

treatment. This research also says that stochastic models can provide a more accurate representation of real events than deterministic models.

Tuberculosis infectious disease can be modeled using the Susceptible Vaccinated Infected Recovered Susceptible (SVIRS) stochastic epidemic model because tuberculosis is a type of disease that can be controlled by vaccination and can be reinfected even though the patient has recovered. This research will use the Discrete-Time Markov Chain Susceptible Vaccinated Infected Recovered Susceptible (DTMC SVIRS) model. This study is expected to provide knowledge on the pattern of tuberculosis spread in Central Java, the effectiveness of vaccination, and assist in the formulation of health policy strategies related to tuberculosis.

B. Methods

This research will be conducted by re-deriving the SVIRS model based on literature studies and then applying it to tuberculosis disease by simulation. The steps needed to solve the problems in this research are as follows:

1. Modeling the DTMC SVIRS, which includes:
 - a. Explaining the phenomenon of disease spread in the DTMC SVIRS model.
 - b. Determining the assumptions of the DTMC SVIRS.
 - c. Determining parameters and random variables for the DTMC SVIRS.
 - d. Determining the transition probability of the DTMC SVIRS on the spread of tuberculosis disease.
2. Simulate and interpret the DTMC SVIRS epidemic model, which includes:
 - a. Determining the number of initial individuals belonging to the Susceptible (S), Vaccinated (V), Infected (I), and Recovered (R) groups in a population.
 - b. Determining the value of each parameter used which is estimated using annual data on tuberculosis disease in 2018-2021 referred from the Central Java Health Profile Book [11-14].
 - c. Generating random numbers with uniform distribution to determine the number of individuals in each group at each time t .
 - d. Obtaining the model and giving an interpretation of the simulation results.

C. Results and Discussion

1. *Modeling the DTMC SVIRS*

Disease spread occurs when susceptible individuals make contact with infected individuals. Vaccination is one of the many ways to control the spread of infectious diseases. Vaccinations are given to newborn babies as an attempt to create immunity to various diseases from an early age. In some diseases, infected individuals who have recovered can still be re-infected even after receiving the vaccine. The mathematical model that matches these properties is the Susceptible Vaccinated Infected Recovered Susceptible (SVIRS) model.

The rederivation of the DTMC SVIRS epidemic model refers to the DTMC SVIRS epidemic model researched by Zuhairah et al [9]. The assumptions in the DTMC SVIRS epidemic model are as follows:

- a. The spread of disease occurs in a constant and closed population so that no individual enters or leaves the population.
- b. The population is homogeneous so that each individual has the same characteristics and the same chance of being infected and recovering.
- c. The pure birth rate is equal to the pure death rate.
- d. Consider vaccinations.
- e. Infected individuals who have recovered can still be reinfected even after receiving the vaccine.

The SVIRS stochastic epidemic model categorizes the population into four groups, namely Susceptible (S), Vaccinated (V), Infected (I), and Recovered (R). Susceptible (S) groups are healthy individuals who are prone and at risk of being infected with the disease, Vaccinated (V) are individuals who have received the vaccine, Infected (I) are individuals who are infected with the disease and can transmit the disease to other individuals, and Recovered (R) are individuals who have recovered and can still be re-infected. Disease spread in the SVIRS model occurs when individuals from group S move to group V with a vaccination rate α , group V moves to group I with a vaccine failure rate δ , group V moves to group S with a vaccine effectiveness rate λ , group S moves to group I with a transmission rate β , group I moves to group R with a recovery rate γ , and group R moves to group S with an immune waning rate η . The flow of disease spread with the SVIRS model is shown in Figure 1.

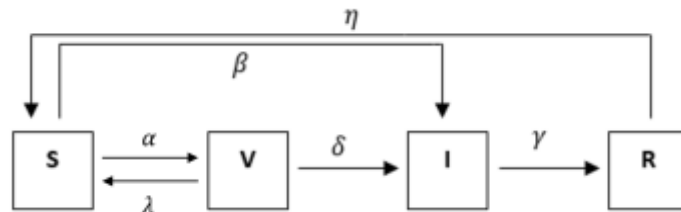


Figure 1. Pattern of Disease Spread with SVIRS Model

The number of individuals in groups S, V, I , and R at time t are expressed as $S(t), V(t), I(t)$, and $R(t)$. In the DTMC SVIRS stochastic epidemic model, there are three independent random variables, namely $S(t), V(t)$, and $I(t)$. If the total number of individuals in a population is expressed as N , then $R(t) = N - S(t) - V(t) + I(t)$. At time t , the number of susceptible individuals is denoted as $S(t) = s$, the number of vaccinated individuals is represented by $V(t) = v$, and the number of infected individuals is expressed as $I(t) = i$. Thus, the joint probability function of the DTMC SVIRS stochastic epidemic model is obtained as follows:

$$p_{(s,v,i)}(t) = P[P(S(t) = s, V(t) = v, I(t) = i)]$$

where $s, v, i = 0, 1, 2, \dots, N$ and $t = 0, \Delta t, 2\Delta t, \dots$

The number of individuals in each group can change over time. The value of the change of susceptible to infected individuals at time interval Δt is j , the value of the change from vaccinated to susceptible at time interval Δt is k , and the value of the change from infected to recovered at time interval Δt is l . Thus, the movement from state s to state $s + j$, from state v to state $v + k$, and from state i to state $i + l$ are called transitions. The transition probability of the DTMC SVIRS epidemic model is as follows:

$$\begin{aligned} P_{(s+j,v+k,i+l),(s,v,i)}(\Delta t) &= P[(S(t + \Delta t), V(t + \Delta t), I(t + \Delta t)) \\ &= (s + j, v + k, i + l) | (S(t), V(t), I(t)) = (s, v, i)] \end{aligned}$$

where Δt is a one-time infected period that is assumed to be chosen small enough. So that at most one change in state occurs during the time interval Δt .

When a susceptible group individual has transmitted the disease from an infected group individual, the susceptible group will move to the infected group. This means there is a transition from state (s, v, i) to state $(s - 1, v, i + 1)$. If there are as many as i individuals in the population N , then the probability of an infected individual interacting with a susceptible individual is denoted as $\frac{i}{N}$. If the transmission rate is β , then the transition probability from state (s, v, i) to state $(s - 1, v, i + 1)$ is

$$P_{(s-1,v,i+1),(s,v,i)}(\Delta t) = \beta \frac{i}{N} s \Delta t \quad (1)$$

When susceptible group individuals get vaccinated, the susceptible group will move to the vaccinated group and there is a transition from state (s, v, i) to state $(s - 1, v + 1, i)$. If the vaccination rate is α , then the transition probability from state (s, v, i) to state $(s - 1, v + 1, i)$ is

$$P_{(s-1,v+1,i),(s,v,i)}(\Delta t) = \alpha s \Delta t \quad (2)$$

If the vaccination received by the vaccinated group is successful, the vaccinated group will move to the susceptible group, which means there is a transition from state (s, v, i) to state $(s + 1, v - 1, i)$. If the vaccine effectiveness rate is λ , then the transition probability from state (s, v, i) to state $(s + 1, v - 1, i)$ is

$$P_{(s+1,v-1,i),(s,v,i)}(\Delta t) = \lambda v \Delta t \quad (3)$$

If the vaccination received by the vaccinated group of individuals fails, it makes the vaccinated group of individuals get infected when they interact with infected individuals and move to the infected group. This means that there is a transition from state (s, v, i) to state $(s, v - 1, i + 1)$. If there are as many as i individuals in the population N , the probability of an infected individual making contact with a vaccinated individual is $\frac{i}{N}$. If the vaccine failure rate is δ , then the transition probability from state (s, v, i) to state $(s, v - 1, i + 1)$ is

$$P_{(s,v-1,i+1),(s,v,i)}(\Delta t) = \delta \frac{i}{N} v \Delta t \quad (4)$$

As the infected individuals have recovered from their infection, the infected group will move to the recovered group. This means there is a transition from state (s, v, i) to state $(s, v, i - 1)$. If the recovery rate is γ , then the transition probability from state (s, v, i) to state $(s, v, i - 1)$ is

$$P_{(s,v,i-1),(s,v,i)}(\Delta t) = \gamma i \Delta t \quad (5)$$

When a recovered individual moves to susceptible, there is a transition from state (s, v, i) to state $(s + 1, v, i)$. The transition occurs because individuals who have recovered do not have permanent immunity so they can still be reinfected. If the rate of immune waning is η , then the transition probability from state (s, v, i) to state $(s + 1, v, i)$ is

$$P_{(s+1,v,i),(s,v,i)}(\Delta t) = \eta r \Delta t \quad (6)$$

If there is no addition or subtraction of individuals from each group, it means that there is no state transition or it can be said that there is a transition from state (s, v, i) to state (s, v, i) . The transition probability from state (s, v, i) to state (s, v, i) is

$$P_{(s,v,i),(s,v,i)}(\Delta t) = 1 - \left[\beta \frac{i}{N} s + \alpha s + \lambda v + \delta \frac{i}{N} v + \gamma i + \eta r \right] \Delta t \quad (7)$$

The transition of an individual from one state to another occurs at such a small time interval that only one individual can transition. Therefore, the transition probability with the number of individuals who move more than one in the time interval Δt is zero. The DTMC SVIRS stochastic epidemic model formed from the transition probabilities can be expressed as follows:

$$p_{(s+j,v+k,i+l),(s,v,i)} \Delta t = \begin{cases} \beta \frac{i}{N} s \Delta t, & (j, k, l) = (-1, 0, 1) \\ \alpha s \Delta t, & (j, k, l) = (-1, 1, 0) \\ \lambda v \Delta t, & (j, k, l) = (1, -1, 0) \\ \frac{\delta v i}{N} \Delta t, & (j, k, l) = (0, -1, 1) \\ \gamma i \Delta t, & (j, k, l) = (0, 0, -1) \\ \eta r \Delta t, & (j, k, l) = (1, 0, 0) \\ 1 - z, & (j, k, l) = (0, 0, 0) \\ 0, & \text{otherwise} \end{cases} \quad (8)$$

where $z = \left[\beta \frac{i}{N} + \alpha s + \lambda v + \frac{\delta v i}{N} + \gamma i + \eta r \right] \Delta t$, $S(0) > 0$, $V(0) \geq 0$, $I(0) > 0$, $R(0) \geq 0$ also $\beta, \alpha, \lambda, \delta, \gamma$, and η are positive.

2. Simulation of DTMC SVIRS Model

Based on the obtained DTMC SVIRS model, a simulation of the model was performed on the spread of tuberculosis disease in Central Java. The parameters used in the simulation of the DTMC SVIRS model of tuberculosis disease were estimated using annual data on tuberculosis disease from 2018 to 2021 referred from the Central Java Health Profile Book.

The data gives an estimated transmission rate parameter (β) of 3.960×10^{-6} . This means that there are an average of 3960 infected individuals for every 10^9 susceptible individuals who interact with an infected individual. The estimation is obtained from the average number of infected individuals (I) divided by the population size N in the same year. The estimation of the vaccination rate (α) is obtained as 3.941×10^{-5} which means that there are an average of 3941 individuals getting vaccinated from 10^8 susceptible individuals every day. This is obtained from the average number of vaccinated individuals (V) divided by the number of susceptible individuals (S) in the same year. The vaccine failure rate (δ) is estimated to be 5.47945×10^{-4} . This means that there are an average of 547945 individuals who remain infected with TB disease from 10^9 vaccinated individuals every day even though they have been vaccinated. This rate is obtained from the average BCG vaccine failure rate, which is 20% [15]. The vaccine effectiveness rate (λ) was found to be 2.191781×10^{-3} which means that there are an average of 2191781 individuals who become susceptible to TB disease again from

10^9 vaccinated individuals every day. This estimation is obtained from the average BCG vaccine success rate, which is 80% [15]. The estimation of the recovery rate (γ) is obtained as 1.5221×10^{-5} , which means that infected individuals have a probability of recovering from TB disease of 1.5221×10^{-5} . The probability is obtained from 1 per TB infection period, which is for an average of 6 months [16]. The immune waning rate parameter (η) is 1.368927×10^{-3} which means that there are an average of 1368927 recovered individuals who become susceptible to TB disease again from 10^9 recovered individuals. This result is obtained from 1 per period of loss of immunity to TB disease, which is an average of 2 years [17].

In this simulation, a constant population of $N = 10,000$ with no consideration of death and birth rates as well as initial values of $S(0) = 9700, V(0) = 50, I(0) = 250$, and $R(0) = 0$. The simulation was carried out three times with the treatment of changing the transmission rate parameter (β), namely $\beta < \gamma$, which corresponds to the initial parameters estimated, $\beta = \gamma$, and $\beta > \gamma$. The following is a simulation of the DTMC SVIRS stochastic epidemic model on the spread of TB disease.

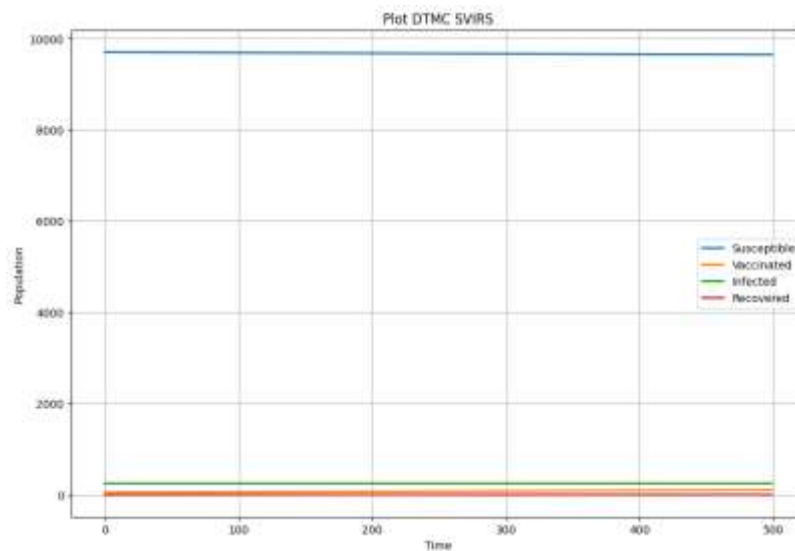


Figure 2. Simulation Results of DTMC SVIRS Epidemic Model with Parameters $\beta = 3.960 \times 10^{-6}, \alpha = 3.941 \times 10^{-5}, \delta = 5.47945 \times 10^{-4}, \lambda = 2.191781 \times 10^{-3}, \gamma = 1.5221 \times 10^{-5}$, and $\eta = 1.368927 \times 10^{-3}$

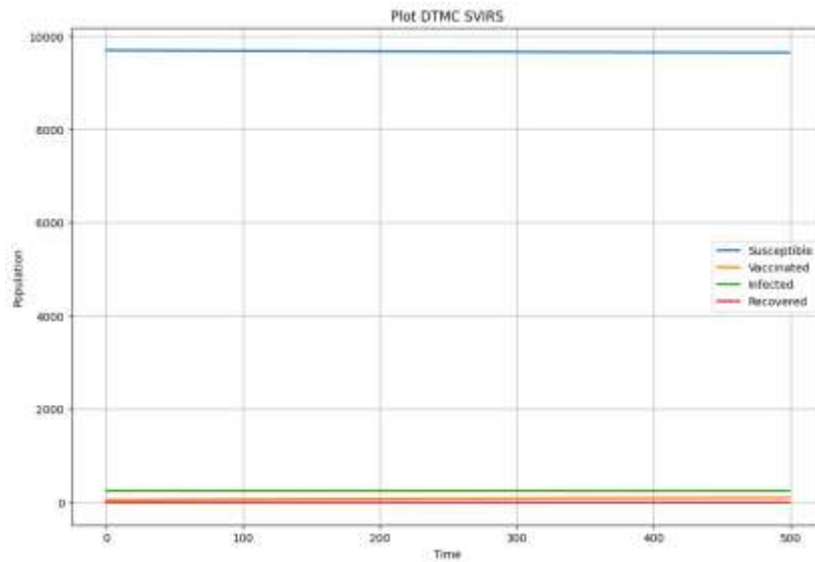


Figure 3. Simulation Results of DTMC SVIRS Epidemic Model with Parameters $\beta = 1.5221 \times 10^{-5}$, $\alpha = 3.941 \times 10^{-5}$, $\delta = 5.47945 \times 10^{-4}$, $\lambda = 2.191781 \times 10^{-3}$, $\gamma = 1.5221 \times 10^{-5}$, and $\eta = 1.368927 \times 10^{-3}$

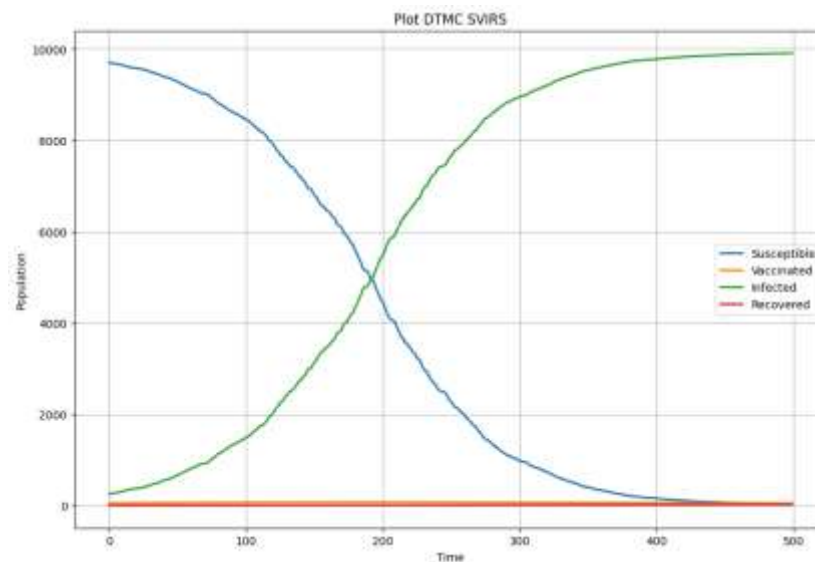


Figure 4. Simulation Results of DTMC SVIRS Epidemic Model with Parameters $\beta = 0.03960$, $\alpha = 3.941 \times 10^{-5}$, $\delta = 5.47945 \times 10^{-4}$, $\lambda = 2.191781 \times 10^{-3}$, $\gamma = 1.5221 \times 10^{-5}$, and $\eta = 1.368927 \times 10^{-3}$

Figure 2 is a simulation of the epidemic model of tuberculosis disease with parameter values according to the estimation obtained previously. The parameter value used in this simulation is $\beta = 3.960 \times 10^{-6} < \gamma = 1.5221 \times 10^{-5}$. As a result, the change in the number of individuals in each group is not significant. Based on the simulation results, it can be seen that the number of susceptible

individuals (S) is decreasing, the number of vaccinated individuals (V) is increasing, the number of infected individuals (I) is decreasing, and the number of recovered individuals (R) is increasing over time. The peak of the epidemic occurred at time 1 with 250 infected individuals and the lowest number of infected individuals occurred at time 493 with 249 infected individuals.

Figure 3 shows the simulation of the epidemic model of tuberculosis disease with the parameter value $\beta = \gamma = 1.5221 \times 10^{-5}$. Just like in the previous simulation, the change in the number of individuals in each group is not significant. However, the change is more noticeable than in the previous simulation. Based on the simulation results, it can be seen that the number of susceptible individuals (S) is decreasing, the number of vaccinated individuals (V) is increasing, the number of infected individuals (I) tends to increase, and the number of recovered individuals (R) is also increasing over time. The peak of the epidemic occurred at time 489 with 250 infected individuals and the lowest number of infected individuals occurred at time 2 with 249 infected individuals.

Figure 4 shows a simulation of the epidemic model of tuberculosis disease with a parameter value of $\beta = 0.03960 > \gamma = 1.5221 \times 10^{-5}$. The change in the number of individuals in this simulation looks quite significant than the previous two simulations. Based on the simulation results, it can be seen that the number of susceptible individuals (S) is decreasing, the number of vaccinated individuals (V) is increasing until around time 200 and tends to decrease until the end of the simulation, the number of infected individuals (I) is increasing, and the number of recovered individuals (R) is also increasing over time. The peak of the epidemic occurred at time 498 with 9914 infected individuals and the lowest number of infected individuals occurred at time 1 with 250 infected individuals.

Based on the three simulations that have been performed, it can be concluded that the greater the transmission rate (β), the longer it will take to reach the peak of the epidemic and the greater the number of infected individuals. The spread pattern also shows that the epidemic will not end. This is because at any period, infected individuals still exist and never reach zero.

D. Conclusion

Based on the results and discussion, it can be concluded that:

1. The DTMC SVIRS epidemic model in the form of transition probabilities is expressed in equation 8.
2. Simulation of the DTMC SVIRS epidemic model on the spread of tuberculosis disease in Central Java using parameters with the treatment of $\beta < \alpha$, $\beta = \alpha$, and $\beta > \alpha$ concludes that the greater the transmission rate (β), the longer it takes to reach the peak of the epidemic and the greater the number of infected individuals. The spread pattern also shows that the epidemic cannot end because at any period, infected individuals still exist and never reach zero. This is because individuals who have recovered do not have permanent immunity and are susceptible again. So, susceptible individuals will never run out and can continue to be infected.

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