

Simulation of the Discrete Time Markov Chain Susceptible Vaccinated Exposed Infected Recovered (DTMC SVEIR) Model with Relapse Cases in the Spread of Tuberculosis*

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Abstract—Tuberculosis (TB) is a contagious disease that primarily affects the lungs and spreads through the air when an infected person coughs, sneezes, or spits. TB remains as a significant global health issue, with millions of cases and deaths annually. There are mathematical epidemiological models that have been developed, including SIR, SEIR, and SVEIR for explaining the spread of disease pattern. The SVEIR model explains the impact of vaccination on disease transmission such as TB. In TB cases, the recovered individuals could be relapsed and be infected again. This study discussed a Discrete Time Markov Chain (DTMC) SVEIR model and applied model simulation to TB disease. The population is divided into five groups such as susceptible, vaccinated, exposed, infected, and recovered. The changes of group's state follow Markov process in discrete time observation. The model is extension from DTMC SEIR with relapse by adding Vaccinated compartment. The model is expressed as transition probability that explain the changes of state in each group. The simulation results indicate that the spread of the disease is significantly influenced by parameters value such as contact rate, vaccination rate, vaccine effectiveness, relapse rate, and recovery rate. If contact rate higher than the recovery rate then the number of infected individuals will increase. The other hand, if vaccination works effectively then the number of susceptible individuals decrease. Lower relapse rates lead to higher recovery numbers, whereas higher relapse rates accelerate reinfection

Keyword: Simulation, DTMC SVEIR Model, relapse cases, Tuberculosis

I. INTRODUCTION

TUBERCULOSIS (TB) is an infectious disease caused by bacteria that most commonly affect the lungs, namely *Mycobacterium tuberculosis*. The disease spreads through the air when a person with TB coughs, sneezes, or spits. Although primarily affecting the lungs, TB can also attack other organs such as the lymphatic system, brain, spine, and kidneys [1]. In 2023, an estimated 10.8 million people worldwide were infected with TB, including 6 million men, 3.6 million women, and 1.3 million children. As many as 1.25 million people

died from TB in 2023, including 161.000 people living with HIV[2]. According to WHO, TB ranked as the 10th leading cause of death worldwide in 2021 [3]. In Indonesia in 2022, TB case detection coverage reached a peak with 724.309 cases discovered (75

An epidemiological model is defined as a mathematical model used to understand how infectious diseases spread in a given population [5], [6]. Epidemic is a situation that infectious disease spreads to a population more than the average number of cases in a short period in a region [7], [8]. Specific characteristics of infectious diseases, such as contact rate, transmission rate, incubation period, recovery rate, vaccination, and others, must be considered as input data when modeling epidemiological systems [9] and [10]. Several models such as SIR, SEIR, and SVEIR have been developed [11]. The SIR model is a basic epidemiological model that divides the population into three groups: susceptible, infected, and recovered [12]. It applies to diseases where infected individuals can spread the disease and eventually recover [13].

However, many infectious diseases have an incubation or latent period, where an infected individual cannot yet transmit the infection [14]. The SEIR model introduces this incubation group [15]. The SVEIR model further extends the SEIR model by incorporating the effect of vaccination on disease transmission. In some diseases like tuberculosis, a recovered individual may experience a relapse. Referring to Allen et al [12] and Allen [16], the DTMC model is appropriate to consider the random effects in disease spread for small populations. This paper develops model that previously has discussed by Nirmala et al [17] by considering relapse cases. Therefore, this study aims to simulate the SVEIR model with relapse cases in tuberculosis spread. The model is analyzed stochastically using a Discrete Time Markov Chain process.

II. METHODOLOGY

This study involves the discussion of the DTMC SVEIR epidemiological model with relapse cases, which is then simulated to depict the spread pattern of tuberculosis [18]. The following are the steps to implement the DTMC SVEIR model for the spread of tuberculosis with relapse cases:

- 1) Construct the DTMC SVEIR epidemiological model with relapse cases, through the following steps:

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- a) Determine the assumptions, random variables, and parameters model.
- b) Define the transition probabilities of the state changes in each group.
- 2) Simulate the DTMC SVEIR model for tuberculosis with relapse cases, through the following steps:
 - a) Determine the values of the contact rate, infection rate, and recovery rate based on the study by Nirmala et al. [17], and the vaccination rate, vaccine efficacy rate, and relapse rate based on Widyaningsih et al. [1],
 - b) Determine the initial values for each group of individuals, namely initial values of $S(0)$, $V(0)$, $E(0)$, $I(0)$, and $R(0)$,
 - c) Generate random data using a uniform distribution to determine the number of susceptible, exposed, infected, and recovered individuals at time t based on the model obtained, using parameter values and initial values specified in steps (a) and (b),
 - d) Plot the simulation of the DTMC SVEIR epidemiological model with relapse cases in tuberculosis,
 - e) Provide an interpretation of the simulation results.

III. RESULT AND DISCUSSION

A. 3.1 DTMC SVEIR Epidemic Model with Relapse Cases

The transmission process of tuberculosis occurs through droplets from patients that are released into the air and inhaled by susceptible individuals. Tuberculosis has an incubation period, which is a phase when individuals have been exposed to the bacteria but do not yet show symptoms and cannot transmit the disease. Although TB is a dangerous infectious disease with high risk, it can be cured with regular and disciplined treatment.

Vaccination is considered one of the most efficient strategies for controlling infectious diseases, especially in terms of cost-benefit ratio. Currently, Bacille Calmette-Guérin (BCG) is the only approved and widely used vaccine for pre-venting tuberculosis, with coverage reaching nearly 90% in countries with high prevalence [19]. Studies show that the BCG vaccine provides protection against pulmonary and extrapulmonary TB for up to 10 years. Although most studies did not follow participants beyond 15 years, five studies still showed measurable protection after that period. Effectiveness declines over time, more rapidly in regions farther from the equator and in individuals sensitive to tuberculin after strict testing [20].

In this study, to describe the dynamics of tuberculosis transmission in accordance with its characteristics, the Susceptible Vaccinated Exposed Infected Recovered (SVEIR) epidemiological model is used [21]. The SVEIR model is an extension of the SIR model that accounts for an incubation period and the vaccination factor in disease transmission [22], [23]. In the case of tuberculosis, individuals who have recovered still have the potential to relapse, which occurs when previously dormant bacteria in the body become active again. Therefore, the relapse rate must be incorporated into this epidemiological model, resulting in the SVEIR model with relapse cases. The

SVEIR model with relapse is derived based on the following assumptions:

- 1) The population size is constant and closed.
- 2) The population is homogeneous, so each individual has the same chances to get infection and to recover.
- 3) Only one disease spreads in the population.
- 4) Birth and death rates are ignored.
- 5) The incubation period and vaccination factors are considered.
- 6) Individuals who have recovered could be relapsed.

In the SVEIR epidemiological model with relapse cases, the population is divided into five groups of individuals, namely susceptible (S), vaccinated (V), exposed (E), infected (I), and recovered (R). The susceptible (S) group consists of individuals who are vulnerable to the disease, the vaccinated (V) group consists of individuals who received vaccination, the exposed (E) group consists of individuals who have been exposed to the disease but have not yet shown symptoms and they cannot yet transmit the disease, the infected (I) group consists of individuals who are infected and capable to transmit the disease, and the recovered (R) group consists of individuals who have been cured of the disease [24].

The SVEIR model describes the dynamics of disease transmission by considering the effects of vaccination, the incubation period, and the possibility of relapse [25]. Individuals move from the susceptible (S) group to the exposed (E) group after contact with an infected individual, at a contact rate of β . Individuals then move from the exposed (E) group to the infected (I) group at an infection rate of σ , and subsequently may recover and move to the recovered (R) group at a recovery rate of γ . Individuals in the recovered (R) group have the possibility of experiencing a relapse and returning to the infected (I) group at a relapse rate of α . In addition, individuals from the susceptible (S) group may receive vaccination and move into the vaccinated (V) group at a vaccination rate of δ , and may return to the susceptible (S) group over time as the vaccine's effectiveness declines, which is represented by a vaccine efficacy rate of θ , indicating the duration of vaccine protection for individuals have been vaccinated. The SVEIR model with relapse is adapted from Widyaningsih et al [1]. In Widyaningsih et al, it was a deterministic model that was stated as differential equations system otherwise in our paper the model is probabilistic and was stated as transition probability. The schematic diagram of the SVEIR model with relapse is shown in Fig. 1.

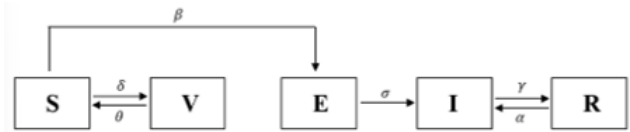


Fig. 1. SVEIR Model Scheme

The number of individuals at time t are denoted by $S(t)$, $V(t)$, $E(t)$, $I(t)$, and $R(t)$. These random variables are assumed to follow discrete time Markov properties [12], [26]. The DTMC SVEIR epidemiological model with a constant

population size of N , can be expressed using four independent random variables, namely $S(t)$, $V(t)$, $E(t)$, and $I(t)$, while $R(t) = N - S(t) - V(t) - E(t) - I(t)$, [27]. If the number of individuals is given by $S(t) = s$, $V(t) = v$, $E(t) = e$, and $I(t) = i$, where s , v , e , and i are the states, then the joint probability function of the DTMC SVEIR epidemiological model is given in Equation (1).

$$P_{(s,v,e,i)}(t) = P\{S(t) = s, V(t) = v, E(t) = e, I(t) = i\} \quad (1)$$

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

The changes in the number of susceptible, vaccinated, exposed, and infected individuals during the time interval Δt can be expressed in terms of transition probabilities. If the change in the number of susceptible individuals during the time interval Δt is j , the change in the number of vaccinated individuals during the time interval Δt is k , the change in the number of exposed individuals during the time interval Δt is l , and the change in the number of infected individuals during the time interval Δt is m , where j, k, l , and m , are states, then referring to Equation (1), the transition probability from s to $s + j$, v to $v + k$, e to $e + l$, and i to $i + m$ over the time interval Δt is given in Equation (2) [28].

$$\begin{aligned} P_{(s+j,v+k,e+l,i+m),(s,v,e,i)}(\Delta t) = \\ P\{S(t+\Delta t) = s+j, V(t+\Delta t) = v+k, \\ E(t+\Delta t) = e+l, I(t+\Delta t) = i+m \mid \\ S(t) = s, V(t) = v, E(t) = e, I(t) = i\} \end{aligned} \quad (2)$$

The transition process in the DTMC SVEIR model with relapse occurs over a very little time interval, such that it is assumed only one individual transitions from state (s, v, e, i) to state $(s + j, v + k, e + l, i + m)$. Therefore, there are seven possible transitions that can occur, from state (s, v, e, i) to $(s - 1, v, e + 1, i)$, from state (s, v, e, i) to $(s - 1, v + 1, e, i)$, from state (s, v, e, i) to $(s + 1, v - 1, e, i)$, from state (s, v, e, i) to $(s, v, e - 1, i + 1)$, from state (s, v, e, i) to $(s, v, e, i - 1)$, from state (s, v, e, i) to $(s, v, e, i + 1)$, and from state (s, v, e, i) to (s, v, e, i) .

The transition from (s, v, e, i) to state $(s - 1, v, e + 1, i)$ indicates the movement of an individual from the susceptible group to the exposed group. This transition occurs due to disease transmission from infected individuals to susceptible individuals. If there are i infected individuals in group I , then there is a probability that $\frac{i}{N}$ individuals make direct contact with those in the susceptible group S . If β represents the contact rate, the probability of transition from state (s, v, e, i) to state $(s - 1, v, e + 1, i)$ within the time interval Δt is given in Equation (3).

$$P_{(s-1,v,e+1,i),(s,v,e,i)}(\Delta t) = \beta \frac{i}{N} s \Delta t \quad (3)$$

The transition from state (s, v, e, i) to state $(s - 1, v + 1, e, i)$ represents the movement of an individual from the susceptible group to the vaccinated group. This transition occurs when one individual receives a vaccination, resulting in an increase in the number of individuals in group V . If δ denotes the vaccination rate, then the probability of transition from state (s, v, e, i) to

state $(s - 1, v + 1, e, i)$ within the time interval Δt is given in Equation (4).

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

The transition from state (s, v, e, i) to state $(s + 1, v - 1, e, i)$ represents the movement of an individual from the vaccinated group back to the susceptible group. This transition occurs because vaccination does not provide perfect or permanent protection; over time, individuals may return to group S . If θ denotes the vaccine efficacy decay rate, then the probability of transition from state (s, v, e, i) to state $(s + 1, v - 1, e, i)$ within the time interval Δt is given in Equation (5).

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

The transition from state (s, v, e, i) to state $(s, v, e - 1, i + 1)$ represents the movement of an individual from the exposed group to the infected group. This transition occurs as the bacteria in the individual's body become active and clinical symptoms begin to appear. If σ denotes the infection rate, then the probability of transition from state (s, v, e, i) to state $(s, v, e - 1, i + 1)$ within the time interval Δt is given in Equation (6).

$$P_{(s,v,e-1,i+1),(s,v,e,i)}(\Delta t) = \sigma e \Delta t \quad (6)$$

The transition from state (s, v, e, i) to state $(s, v, e, i - 1)$ represents the movement of an individual from the infected group to the recovered group. This transition occurs when an individual in the infected group is declared recovered. If γ denotes the recovery rate, then the probability of transition from state (s, v, e, i) to state $(s, v, e, i - 1)$ within the time interval Δt is given in Equation (7).

$$P_{(s,v,e,i-1),(s,v,e,i)}(\Delta t) = \gamma i \Delta t \quad (7)$$

The transition from state (s, v, e, i) to state $(s, v, e, i + 1)$ represents the movement of an individual from the recovered group back to the infected group. This transition occurs when an individual in the recovered group, who was previously declared cured, experiences a relapse. If α denotes the relapse rate, then the probability of transition from state (s, v, e, i) to state $(s, v, e, i + 1)$ within the time interval Δt is given in Equation (8).

$$P_{(s,v,e,i+1),(s,v,e,i)}(\Delta t) = \alpha r \Delta t \quad (8)$$

The transition from state (s, v, e, i) to state (s, v, e, i) indicates that no state change occurs. This condition arises when none of the groups experience an increase or decrease in the number of individuals. The transition probability from state (s, v, e, i) to state (s, v, e, i) within the time interval Δt is given in Equation (9).

$$P_{(s,v,e,i),(s,v,e,i)}(\Delta t) = 1 - b \Delta t \quad (9)$$

where, $b = (\beta \frac{i}{N} s + \delta s + \theta v + \sigma e + \gamma i + \alpha r)$.

In a little time interval, the probability of more than one individual transitioning from one state to another is zero.

Base on summary from Equation (3) to Equation (9), within the time interval Δt the DTMC SVEIR epidemiological model with relapse can be written in Equation (10).

$$P_{(s+j,v+k,e+l,i+m),(s,v,e,i)}(\Delta t) = \begin{cases} \beta \frac{i}{N} s \Delta t, & (j,k,l,m) = (-1,0,1,0) \\ \delta s \Delta t, & (j,k,l,m) = (-1,1,0,0) \\ \theta v \Delta t, & (j,k,l,m) = (1,-1,0,0) \\ \sigma e \Delta t, & (j,k,l,m) = (0,0,-1,1) \\ \gamma i \Delta t, & (j,k,l,m) = (0,0,0,-1) \\ \alpha r \Delta t, & (j,k,l,m) = (0,0,0,1) \\ 1 - b \Delta t, & (j,k,l,m) = (0,0,0,0) \\ 0, & \text{others.} \end{cases} \quad (10)$$

$$P_{(s+j,v+k,e+l,i+m),(s,v,e,i)}(\Delta t) = \begin{cases} 7.2197 \times 10^{-6} \frac{i}{N} s \Delta t, & (j,k,l,m) = (-1,0,1,0) \\ 5.8082 \times 10^{-5} s \Delta t, & (j,k,l,m) = (-1,1,0,0) \\ 1.8265 \times 10^{-4} v \Delta t, & (j,k,l,m) = (1,-1,0,0) \\ 2.04 \times 10^{-2} e \Delta t, & (j,k,l,m) = (0,0,-1,1) \\ 6.4297 \times 10^{-4} i \Delta t, & (j,k,l,m) = (0,0,0,-1) \\ 1.4301 \times 10^{-5} r \Delta t, & (j,k,l,m) = (0,0,0,1) \\ 1 - b \Delta t, & (j,k,l,m) = (0,0,0,0) \\ 0, & \text{others.} \end{cases} \quad (11)$$

where $S(0) > 0, V(0) > 0, E(0) > 0, I(0) > 0, R(0) \geq 0$, and all parameters $\beta, \delta, \theta, \sigma, \gamma, \alpha$ are positive.

The absorbing state occurs if $i = 0$ and $r = 0$ the epidemic can't reignite, every individual is susceptible or vaccinated. Unlike standard SVEIR, relapse ($R \rightarrow I$) prevents R -only states from being absorbing. The next state depends only on current (s,v,e,i,r) . It is finite states model with the size in each compartment grows combinatorially with N .

B. Model Simulation

The simulation based on the DTMC SVEIR model is conducted to illustrate the pattern of tuberculosis transmission using parameter values for contact rate, infection rate, and recovery rate as referred to in the study by Nirmala et al. [17], as well as vaccination rate, vaccine efficacy rate, and relapse rate as referred to in the study by Widyaningsih et al. [1].

According to Nirmala et al. [17], the parameters for contact rate and recovery rate were calculated based on annual tuberculosis data from 2022, sourced from the 2022 Tuberculosis Control Program Report, while the infection rate parameter was calculated based on the Guidelines of the Indonesian Ministry of Health, Directorate General of P2PTB, 2016. The contact rate parameter was obtained by dividing the number of confirmed tuberculosis cases by the population of Indonesia in 2022, resulting in a daily contact rate of 7.2197×10^{-6} . The infection rate was calculated using the transition rate or mean time method, resulting in a daily infection rate of 2.04×10^{-2} . The recovery rate was calculated by dividing the number of recovered cases by the total number of TB cases in 2022, yielding a daily recovery rate of 6.4297×10^{-4} .

The study by Widyaningsih et al. [1] calculated parameter values using data from the Data and Information Centre, the World Bank, and the WHO during the period 2004–2014. Based on this data, the daily vaccination rate was 5.8082×10^{-5} , the daily vaccine efficacy rate was 1.8265×10^{-4} , and the daily relapse rate was 1.4301×10^{-5} . Based on Equation (10), the DTMC SVEIR epidemiological model with relapse for tuberculosis transmission patterns can be expressed in Equation (11).

The model simulation uses a constant population size of $N = 1000$ assuming no birth or death rates, with initial values $S(0) = 925, V(0) = 20, E(0) = 20, I(0) = 35$, and $R(0) = 0$ over a time period of $t = 1000$ days.

The steps of simulation procedure refer from [29] and [30] explains below:

- 1) Set the initial number of S, V, E, I and R
- 2) Set the value of parameters
- 3) Compute the transition probabilities for each state changes, equation (11)
- 4) Generate random number according to three previous conditions
- 5) Update states
- 6) Continue until $I = 0, E = 0$ or maximum time step reached

The results of the DTMC SVEIR model simulation with relapse for tuberculosis transmission in Indonesia are shown in Fig. 2.

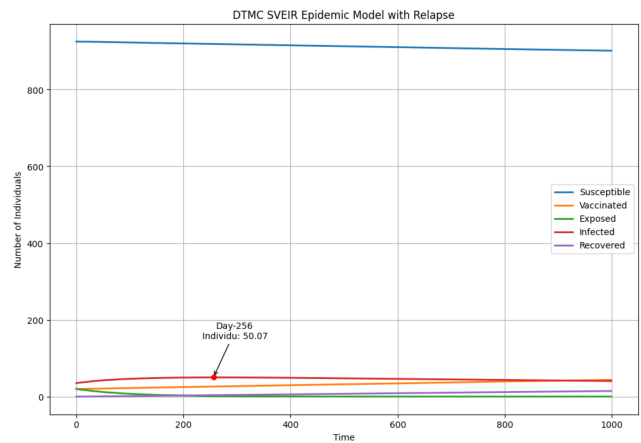


Fig. 2. Initial Simulation Result

Figure 2 shows a few fluctuations that reflect the dynamics of tuberculosis transmission. The number of susceptible individuals decreases gradually until the end of the simulation, while the number of individuals in the vaccinated group continues to increase. The number of individuals in the exposed group also declines steadily, approaching zero by the end of the simulation. The number of infected individuals rises in the early stages of the simulation and then gradually

decreases, while the number of individuals in the recovered group increases slowly over time. The simulation begins with 35 infected individuals, and the epidemic reaches its peak at day 248 with 50 infected individuals. At $t = 1000$ the epidemic has not yet completely ended, with $S(1000) \approx 902$, $V(1000) \approx 43$, $E(1000) \approx 0$, $I(1000) \approx 40$, and $R(1000) \approx 15$.

Next, the model will be simulated under three conditions. The Simulation 1 varies the contact rate(β) relative to the recovery rate(γ). Simulation 2 varies the vaccination rate (δ) relative to the vaccine efficacy rate (θ), while the other parameter values are assumed to remain constant, as presented in Table I.

TABLE I
PARAMETER VALUES FOR SIMULATION 1 AND SIMULATION 2

Simulation	Parameter Values	Conditions
Simulation 1 $\gamma = 6.4297 \times 10^{-4}$	$\beta = 7.2197 \times 10^{-7}$	$\beta < \gamma$
	$\beta = 6.4297 \times 10^{-4}$	$\beta = \gamma$
	$\beta = 7.2197 \times 10^{-2}$	$\beta > \gamma$
Simulation 2 $\theta = 1.8265 \times 10^{-4}$	$\delta = 5.8082 \times 10^{-6}$	$\delta < \theta$
	$\delta = 1.8265 \times 10^{-4}$	$\delta = \theta$
	$\delta = 5.8082 \times 10^{-2}$	$\delta > \theta$

The Simulation 1 is conducted to examine the effect of the contact rate on how rapidly the disease spreads within a population. In this simulation, the contact rate β is evaluated under conditions $\beta < \gamma$, $\beta = \gamma$, and $\beta > \gamma$, while the recovery rate (γ) and other parameters remain constant.

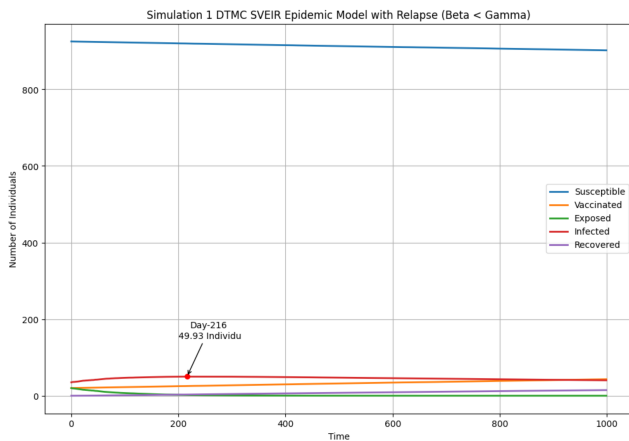


Fig. 3. Simulation Result for Parameter $\beta < \gamma$

Figure 3 shows the simulation results with the contact rate parameter (β) being lower than the recovery rate (γ). The results indicate that the number of individuals in the susceptible group decreases gradually until the end of the simulation, while the number of individuals in the vaccinated group continues to increase. The exposed group shows a decline in the number of individuals until it approaches zero by the end of the simulation. The number of infected individuals rises at the beginning of the simulation and then slowly declines, whereas the recovered group experiences a slow increase over time. The epidemic peaks at day 216 with

50 infected individuals. At $t = 1000$, the epidemic has not yet ended, with $S(1000) \approx 901$, $V(1000) \approx 44$, $E(1000) \approx 0$, $I(1000) \approx 40$, and $R(1000) \approx 15$.

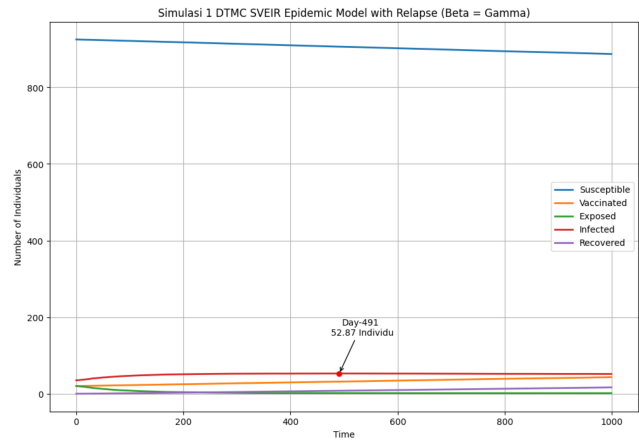


Fig. 4. Simulation Result for Parameter $\beta = \gamma$

Figure 4 presents the simulation results when the contact rate parameter (β) is equal to the recovery rate (γ). The results show that the number of individuals in the susceptible group continues to decline, while the number of individuals in the vaccinated group keeps increasing. The exposed group shows a significant decline throughout the simulation. The number of infected individuals increases up to the middle of the simulation period and then slowly decreases, whereas the recovered group experiences a gradual increase over time. The epidemic peaks at day 491 with 53 infected individuals. At $t = 1000$, the epidemic has not fully ended, with $S(1000) \approx 887$, $V(1000) \approx 43$, $E(1000) \approx 2$, $I(1000) \approx 52$, and $R(1000) \approx 16$.

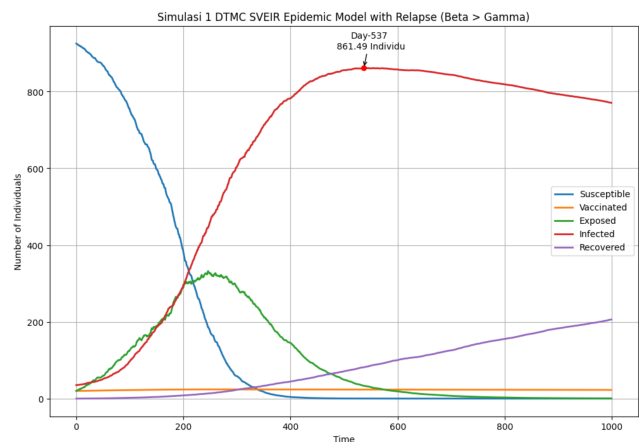


Fig. 5. Simulation Result for Parameter $\beta > \gamma$

Figure 5 shows the simulation results with the contact rate parameter (β) greater than the recovery rate (γ). The simulation results show that the number of individuals in the susceptible group declines significantly until it nearly reaches zero by the end of the simulation, while the number of individuals in the vaccinated group initially increases slightly

and then gradually decreases. The exposed group also shows a significant change, starting with 20 individuals and rising sharply to a peak of 331 individuals at day 260, before dropping drastically to near zero. The number of infected individuals increases and reaches its peak at day 537 with 861 infected individuals, then slowly decreases, while the number of individuals in the recovered group continues to increase. At $t = 1000$, the epidemic has not fully ended, with $S(1000) \approx 0$, $V(1000) \approx 22$, $E(1000) \approx 0$, $I(1000) \approx 769$, and $R(1000) \approx 209$.

The results of Simulation 1 indicate that the contact rate (β) and recovery rate (γ) have a significant influence on the dynamics of disease transmission. When the contact rate is less than or equal to the recovery rate, the number of infected individuals remains relatively low, and the epidemic progresses more slowly. In contrast, when the contact rate is greater than the recovery rate, the number of infected individuals increases sharply, and the epidemic becomes more widespread.

The Simulation 2 aims to understand how variations in vaccination rate and vaccine efficacy affect the dynamics of disease transmission. In this simulation, the vaccination rate δ is evaluated under conditions $\delta < \theta$, $\delta = \theta$, and $\delta > \theta$, while the vaccine efficacy rate (θ) and other parameters remain constant.

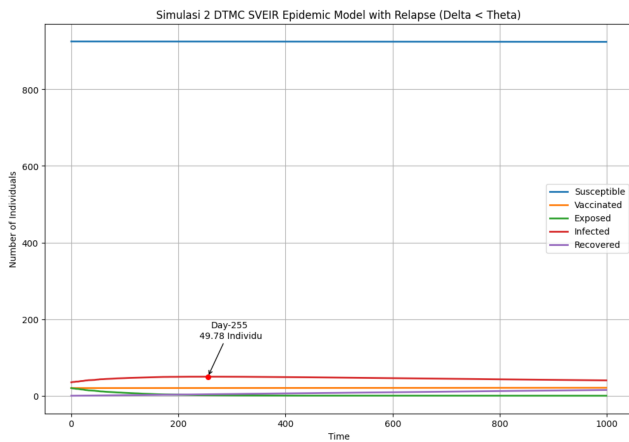


Fig. 6. Simulation Result for Parameter $\delta < \theta$

Figure 6 shows the simulation results with the vaccination rate parameter (δ) being lower than the vaccine efficacy rate (θ). The results indicate that most of the population remains in the susceptible group with no significant changes, and similarly, the number of vaccinated individuals increases by only one. The number of individuals in the exposed group decreases to near zero by the end of the simulation. The number of infected individuals increases early in the simulation and then slowly declines, while the recovered group gradually increases. The epidemic peaks at day 255 with 50 infected individuals. The epidemic has not fully ended, with $S(1000) \approx 924$, $V(1000) \approx 21$, $E(1000) \approx 0$, $I(1000) \approx 41$, and $R(1000) \approx 14$ until the last time simulation.

Figure 7 shows the simulation results with the vaccination rate (δ) equal to the vaccine efficacy rate (θ). The results

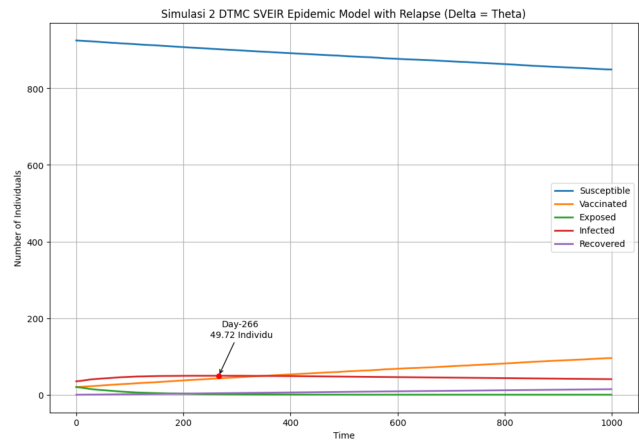


Fig. 7. Simulation Result for Parameter $\delta = \theta$

indicate a continuous decline in the number of susceptible individuals, while the number of vaccinated individuals increases significantly. The exposed group declines steadily until it nearly reaches zero by the end of the simulation. Infected individuals experience a slight increase early in the simulation, while the recovered group gradually increases until the end. The epidemic peaks at day 266 with 50 infected individuals. The epidemic has not fully ended, with $S(1000) \approx 848$, $V(1000) \approx 96$, $E(1000) \approx 0$, $I(1000) \approx 41$, and $R(1000) \approx 15$ until the end time of simulation.

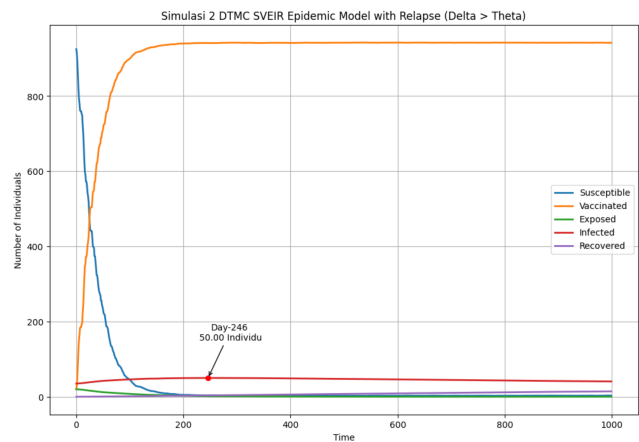


Fig. 8. Simulation Result for Parameter $\delta > \theta$

Figure 8 shows the simulation results with the vaccination rate (δ) greater than the vaccine efficacy rate (θ). The results show a drastic shift in the susceptible and vaccinated groups early in the simulation. The susceptible group initially declines rapidly, then the rate of decrease slows down. Meanwhile, the vaccinated group increases quickly and stabilizes at 942 individuals. The number of individuals in the exposed group continues to decline until nearly zero by the end. Infected individuals increase slightly early in the simulation, while the recovered individuals gradually increase. The epidemic peaks at day 246 with 50 infected individuals. By the end

of the simulation, the epidemic has not fully ended, with $S(1000) \approx 3$, $V(1000) \approx 942$, $E(1000) \approx 0$, $I(1000) \approx 40$, and $R(1000) \approx 15$.

The results of Simulation 2 show that the vaccination rate (δ) and vaccine efficacy rate (θ) significantly affect disease transmission dynamics, particularly in the susceptible and exposed groups. When the vaccination rate is higher than the vaccine efficacy rate, the number of individuals in the susceptible group decreases more significantly, in line with the increase in the vaccinated group.

The Simulation 3 is conducted by gradually increasing the relapse rate (α), while the values of the other parameters are held constant, as shown in Table II. This simulation is intended to examine the effect of relapse rate on disease transmission.

TABLE II
PARAMETER VALUES FOR SIMULATION 3

Simulation	Parameter Values
Simulation 3	$\alpha = 1.4301 \times 10^{-6}$
	$\alpha = 1.4301 \times 10^{-4}$
	$\alpha = 1.4301 \times 10^{-2}$
	$\alpha = 1.4301$

From the variations in parameter values presented in Table II, the following simulation results were obtained.

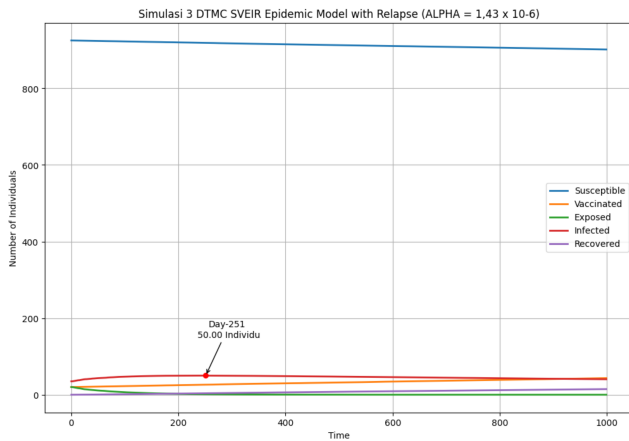


Fig. 9. Simulation Result for Parameter $\alpha = 1.4301 \times 10^{-6}$

Figure 9 shows the results of Simulation 3 with $\alpha = 1.43 \times 10^{-6}$. The results indicate that the number of individuals in the susceptible group decreases slowly, while the vaccinated group increases. The exposed group declines steadily until near zero. The number of infected individuals rises and reaches a peak at day 251 with 50 infected individuals, then decreases. Meanwhile, the recovered group shows a gradual increase in the number of recovered individuals. At day 1000, the epidemic has not fully ended, with $S(1000) \approx 901$, $V(1000) \approx 44$, $E(1000) \approx 0$, $I(1000) \approx 41$, and $R(1000) \approx 14$.

Figure 10 shows the results of Simulation 3 with $\alpha = 1.43 \times 10^{-4}$. The simulation shows that the number of susceptible individuals decreases slowly over time, while the vaccinated group shows a consistent increase. The number of exposed

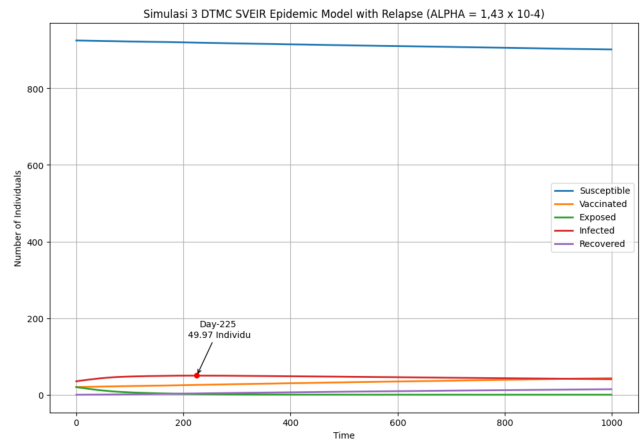


Fig. 10. Simulation Result for Parameter $\alpha = 1.4301 \times 10^{-4}$

individuals drops sharply to near zero. The infected group rises and peaks at day 225 with 50 infected individuals, then decreases. The recovered group shows a gradual increase in the number of recovered individuals until the end of the simulation. By the end of the simulation period, the epidemic has not yet ended, with $S(1000) \approx 901$, $V(1000) \approx 43$, $E(1000) \approx 0$, $I(1000) \approx 41$, and $R(1000) \approx 14$.

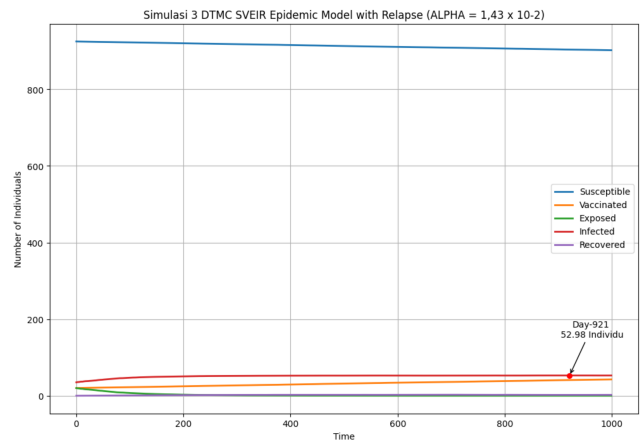


Fig. 11. Simulation Result for Parameter $\alpha = 1.4301 \times 10^{-2}$

Figure 11 shows the results of Simulation 3 with $\alpha = 1.43 \times 10^{-2}$. The results indicate that the number of individuals in the susceptible group decreases slowly, while the vaccinated group shows an upward trend over time. The number of exposed individuals drops sharply to near zero. The infected group increases and reaches a peak at day 921 with 53 infected individuals. Meanwhile, the recovered group increases very slowly throughout the simulation, with only 2 recovered individuals by the end. At day 1000, the population distribution is recorded as $S(1000) \approx 901$, $V(1000) \approx 43$, $E(1000) \approx 0$, $I(1000) \approx 53$, and $R(1000) \approx 2$. Based on this condition, it can be concluded that the epidemic has not yet ended because the number of infected individuals remains relatively high.

Figure 12 shows the results of Simulation 3 with $\alpha = 1.43$.

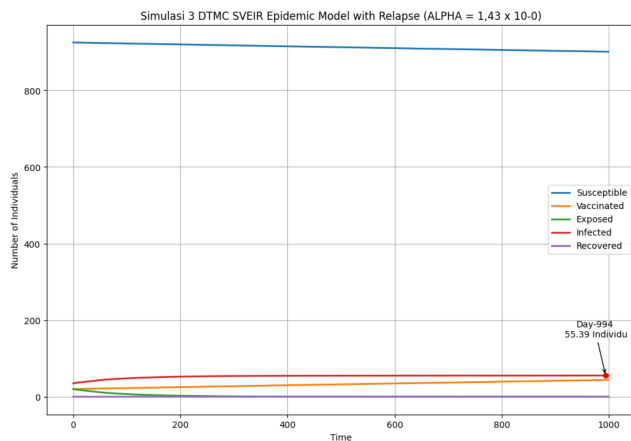


Fig. 12. Simulation Result for Parameter $\alpha = 1.4301$

The results show that the number of individuals in the susceptible group tends to decrease slowly, while the vaccinated group increases continuously. The number of individuals in the exposed group drops sharply to near zero. The number of infected individuals continues to increase and reaches its peak at day 994 with 56 infected individuals. Meanwhile, the recovered group shows no significant changes, with zero recovered individuals recorded by the end of the simulation. At day 1000, the population is recorded as $S(1000) \approx 901$, $V(1000) \approx 43$, $E(1000) \approx 0$, $I(1000) \approx 55$, and $R(1000) \approx 0$. Based on these results, it can be concluded that the epidemic has not ended, as the number of infected individuals remains high and no individuals have recovered by the end of the simulation.

The results of Simulation 3 indicate that the relapse rate (α) has a substantial impact on disease transmission, especially in the infected and recovered groups. When the relapse rate is low, the number of individuals in the recovered group tends to increase, and the number of infected individuals gradually decreases after peaking. Conversely, when the relapse rate is high, individuals who have recovered are reinfected more quickly, making it difficult for the recovered group to grow and keeping the infected group large until the end of the simulation period. This demonstrates that the higher the relapse rate, the more difficult it is for the epidemic to end.

From a public health point of view, these findings highlight the need for stronger measures. Vaccination coverage and effectiveness must be improved, and infectious individuals should be identified and isolated more quickly. Recovery and immunity also need to be supported, otherwise the epidemic may settle at a high level of infection for a long time. Without these improvements, the disease will continue to circulate, creating lasting health and social impacts.

IV. CONCLUSIONS

Based on the results of the four simulations conducted, it can be concluded that the dynamics of disease transmission are strongly influenced by parameters such as contact rate,

vaccination rate, vaccine efficacy rate, relapse rate, and recovery rate. A contact rate that is higher than the recovery rate leads to an increase in the number of infected individuals and accelerates the spread of the epidemic. Meanwhile, a vaccination rate that is higher than the vaccine efficacy rate can reduce the number of susceptible individuals and enhance population protection through vaccination. The relapse rate also plays a critical role: a low relapse rate allows for an increase in the number of recovered individuals, whereas a high relapse rate results in individuals becoming reinfected more quickly. Overall, controlling these parameters is essential in efforts to break the chain of disease transmission and support the end of an epidemic. This study does not consider for migration; therefore, it cannot be applied to dynamic populations. Future research needs to develop a model for dynamic populations.

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