BAREKENG: Journal of Mathematics and Its Applications
December 2025 Volume 19 Issue 4 Page 3073–3086
P-ISSN: 1978-7227 E-ISSN: 2615-3017
https://doi.org/10.30598/barekengvol19no4pp3073-3086

SEIR MODELING OF TUBERCULOSIS TRANSMISSION WITH VACCINATION: ESTIMATING THE MINIMUM COVERAGE REQUIRED FOR ELIMINATION IN NORTH SUMATERA

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Article History:
Received: 13th April 2025
Revised: 20th May 2025
Accepted: 8th June 2025
Available online: 1st September 2025

Keywords:
Basic reproduction number;
Equilibrium point;
Mathematical model;
Tuberculosis;
Vaccination.

ABSTRACT

Tuberculosis (TB) remains one of the most significant public health challenges in Indonesia, particularly in North Sumatra Province, which records a relatively high prevalence rate. e–Exposed–Infectious–Recovered) A framework to analyze TB's transmission dynamics and evaluate vaccination's effectiveness as an intervention strategy. The primary objective of this research is to estimate the minimum vaccination coverage required to eliminate TB from the population. The model was built by incorporating vaccination rate parameters into the SEIR mathematical model and applied using regional epidemiological data obtained from the North Sumatra Central Bureau of Statistics. A deterministic approach is employed to simulate the system and derive the basic reproduction number (R_0), which serves as an indicator of disease persistence across various levels of vaccination coverage. The results of numerical simulations performed using 4th-Order Runge Kutta indicate the existence of a critical vaccination threshold required to reduce R_0 below the one-condition that theoretically represents the possibility of disease elimination from the population. These findings provide a quantitative basis for formulating more targeted, data-driven vaccination policies. Calculations based on real-world data reveal that the current R_0 value in North Sumatra remains above one ($R_0 > 1$), suggesting that TB continues to pose a risk of remaining endemic. Simulations were also conducted by varying the vaccination coverage while assuming a constant transmission rate, indicating that a minimum of 87.5% vaccination coverage is required to suppress R_0 below the critical threshold. This study underscores the importance of employing mathematical modeling as a decision-support tool in public health policy. The findings deepen the understanding of TB transmission dynamics and offer a robust quantitative foundation for setting vaccination targets for disease elimination in endemic areas such as North Sumatra.

How to cite this article:

H. Nasution, Mulyono, M. Cyntia S, F. Ahyaningsih and F. N. Zai., "SEIR MODELING OF TUBERCULOSIS TRANSMISSION WITH VACCINATION: ESTIMATING THE MINIMUM COVERAGE REQUIRED FOR ELIMINATION IN NORTH SUMATERA", *BAREKENG: J. Math. & App.*, vol. 19, iss. 4, pp. 3073-3086, December, 2025.

Journal homepage: *https://ojs3.unpatti.ac.id/index.php/barekeng/*
Journal e-mail: *barekeng.math@yahoo.com; barekeng.journal@mail.unpatti.ac.id*
Research Article · Open Access

1. INTRODUCTION

Tuberculosis (TB) is a serious threat to global public health. Tuberculosis (TB) is a prolonged bacterial infectious disease caused by *Mycobacterium tuberculosis* that is a significant health, social, and economic burden worldwide, especially in low- and middle-income countries [1], [2], [3]. Recognized as the world's deadliest infectious disease, it claims more than 4,000 lives every day. The long-term effects of TB on the lungs can increase an individual's risk of developing active TB. Conversely, individuals who have had TB are more vulnerable to reinfection. Despite advancements in prevention and treatment, TB remains widespread in many countries, including Indonesia, where it continues to threaten public health and place a substantial burden on the healthcare system. Furthermore, the bacterium that causes TB, *Mycobacterium tuberculosis*, can also affect other organs such as the liver, lungs, and heart [4].

According to the Global Tuberculosis Report released by the World Health Organization (WHO) in 2023, Indonesia ranks as the country with the second-highest number of tuberculosis (TB) cases globally, following India. The report recorded an estimated 1,060,000 TB cases in Indonesia, with a mortality rate reaching 134,000 deaths. These findings indicate a significantly high disease burden, with an average of approximately 15 people dying from TB every hour in the country. This alarming fact underscores that tuberculosis remains an urgent public health concern in Indonesia, requiring sustained and comprehensive interventions in prevention, early detection, and treatment [5]. Similar patterns of endemic transmission have also been observed in other countries, such as Iran, where the effective reproduction rate of TB remained close to or above 1 in some provinces during 2011-2021, indicating a continued risk of transmission [6]. According to experts, around half of these cases represent newly infected individuals yearly, meaning about 450,000 new TB cases emerge annually. Data from the Ministry of Health of the Republic of Indonesia indicate that around 75% of TB patients are within the most economically productive age group, ranging from 15 to 50. This highlights the significant socio-economic impact of the disease on the nation's workforce.

Regarding regional distribution, North Sumatra ranks second in the highest TB cases, following West Java. In 2022, North Sumatra recorded approximately 83,969 TB cases; however, only 30% of these cases, equivalent to 31,068, were successfully treated. These cases are spread across all regencies and cities within the province.

One of the key efforts in preventing the transmission of tuberculosis (TB) is vaccination, particularly through the administration of the *Bacillus Calmette-Guérin* (BCG) vaccine, which is recommended for children over two months of age [7]. Although the BCG vaccine offers protection against TB, its effectiveness is limited and tends to decline with age. It is generally more effective during childhood and does not confer lifelong immunity. Consequently, the incidence of TB remains high every year, especially in countries with a high TB burden.

Various strategies have been implemented to control the spread of TB, including early diagnosis, long-term treatment, public health education, and vaccination programs. Among these strategies, vaccination remains one of the most crucial preventive approaches to reducing transmission rates. However, a critical scientific question arises: what minimum vaccination coverage is required to eliminate TB from a population? Answering this question requires a systematic and quantitative approach. Mathematical modeling is a powerful tool for understanding infectious disease transmission dynamics in this context. Based on previous studies, increased treatment and vaccination coverage reduced the number of TB patients [8]. These models illustrate how humans interact with infectious agents such as bacteria or viruses that can infect healthy individuals and cause disease [9].

Mathematical modeling simplifies complex phenomena into more comprehensible frameworks, offering a solid foundation for analysis and prediction. By applying mathematical concepts, principles, and equations, such models can assess the effectiveness of various disease control strategies, including vaccination. In the context of infectious diseases, mathematical models are especially valuable for estimating optimal vaccination coverage, identifying high-risk groups, and evaluating the long-term impacts of public health interventions [10], [11]. Numerous studies have focused on developing mathematical models to understand better the general spread of infectious diseases [12], [13], [14], [15].

Several researchers have conducted specific research on mathematical modeling of disease transmission. The SEIRS model was used to capture the possibility of re-infection after recovery, applying to Makassar City data [16]. Then the SIR model was used to analyze TB disease by adding therapy parameters, showing that effective treatment can increase the cure rate [17]. In 2019, the TB model was

developed by considering re-infection and analyzing the stability and bifurcation of the system to understand the transition between disease-free and endemic conditions [18].

The TB model was further developed by adding the prevention variable through vaccination, which emphasized the importance of fair and rapid vaccine distribution and attention to vulnerable groups [19]. On the other hand, a non-biological approach has been taken to assess the spread of TB. These approaches show that socioeconomic conditions and population density significantly affect TB transmission [20]. For comparison, this TB model is also identical to the mathematical model of the spread of COVID-19. One of the models used is the SEAQIR model with quarantine intervention, which is relevant for demonstrating the role of intervention strategies in infectious disease control [21].

In this article, the model is developed by modifying the SIR model proposed by [17]. By incorporating an exposed subpopulation (E), the SIR model is extended into a SEIR model. The addition of subpopulation E is because in reality, there are populations that are infected but do not show symptoms of the disease. The constructed model considers a vaccination scenario for susceptible individuals and includes treatment for infected individuals as part of efforts to reduce the transmission rate of TB. The model is formulated as a system of differential equations and analyzed using algebraic methods. To obtain optimal results, the effect of vaccination is evaluated through the basic reproduction number (R_0). The basic reproduction number (R_0) is analyzed in the model because this study is about the spread of disease. In contrast to population dynamics models of animals, plants, etc. that do not require the calculation of R_0 [22], [23]. Additionally, a geometric interpretation of the model is presented through graphical simulations using the 4th Order Runge Kutta numerical method.

2. RESEARCH METHODS

This research employs a combination of a literature review and a case study. The literature review involves collecting various references relevant to the research topic, such as scientific journals, articles, books, and other credible sources. Meanwhile, the case study focuses on the spread of Tuberculosis (TB) in the province of North Sumatra.

The data used in this study consists of actual data related to the transmission of TB. This includes information such as the number of TB cases in each district or city within North Sumatra Province, the total population, birth rates, natural death rates, and deaths caused by TB. These data are utilized to determine key parameters required for the simulation process. Data used, sourced from the Central Bureau of Statistics Health Office of North Sumatra Province in 2024.

The literature review in this study was conducted through an in-depth examination of scholarly sources to develop a comprehensive understanding of Tuberculosis (TB), its demographic characteristics, and the mathematical frameworks employed to model its transmission. The reviewed literature covers compartmental models of infectious disease spread, the SEIR epidemic model, systems of differential equations, equilibrium analysis, eigenvalues and eigenvectors, the basic reproduction number (R_0), and Matlab software simulation techniques.

The methodology employed in addressing the research problem involved the following stages:

1. Conducting a theoretical review of Tuberculosis and relevant studies on the SIR model and its applications;
2. Constructing a compartmental diagram to represent the transmission dynamics of TB incorporating vaccination interventions;
3. Developing a mathematical model to simulate the spread of TB under vaccination strategies;
4. Identifying the equilibrium points of the system obtained when the "zero growth rate" occurs;
5. Calculating and interpreting the basic reproduction number (R_0) using the linearity rule method to assess the potential for disease transmission; and
6. Performing simulations to evaluate the dynamics of TB spread and determine the minimum vaccination threshold required to effectively suppress the disease.

3. RESULTS AND DISCUSSION

The SEIR (Susceptible–Exposed–Infected–Recovered) epidemic model is a compartmental model used to describe the transmission dynamics of infectious diseases. It divides the population into four subpopulations: susceptible individuals (S), exposed individuals who have been infected but are not yet symptomatic (E), infected individuals who are capable of transmitting the disease (I), and recovered individuals who have gained immunity (R).

3.1 Compartment Diagram SEIR Model

In the Susceptible (S) compartment, the number of individuals increases through births at a rate denoted by π and also includes individuals who fail to acquire immunity after vaccination. On the other hand, the number of susceptible individuals may decrease due to natural deaths, occurring at a rate μ, and due to transitions to the Exposed (E) group resulting from contact with infected individuals, which occurs at a transmission rate β.

The Exposed (E) compartment increases as a result of interactions between susceptible and infected individuals, leading previously susceptible individuals into a latent (incubation) period. The rate of exposure is modeled as $\beta IS/N$, where I is the number of infected individuals, S is the number of susceptibles, and N is the total population. Individuals in the Exposed group may transition to the Infected (I) group at a rate θ, recover directly and move to the Recovered (R) group at a rate γ, or die of natural causes at a rate μ.

This model assumes a constant total population (i.e., no net growth or decline) and that individuals infected and recovered do not return to the susceptible class (i.e., reinfection does not occur). Based on these assumptions, the following is a compartmental diagram illustrating the transmission dynamics of Tuberculosis (TB) using the SEIR model:

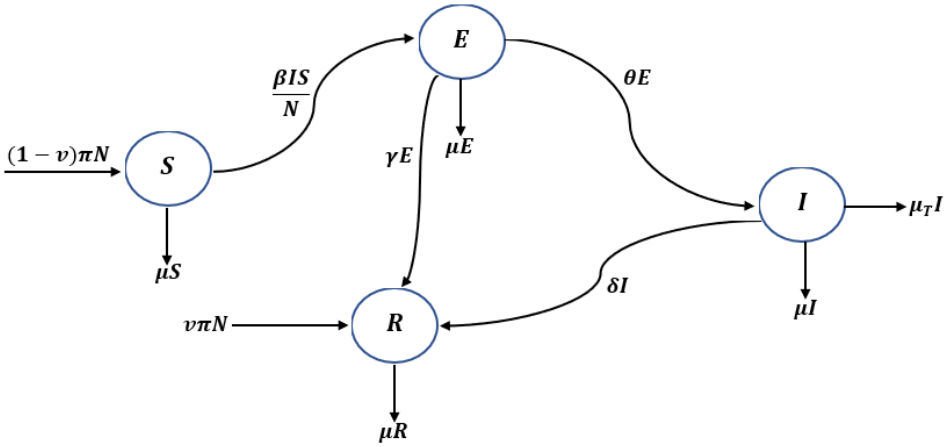

Figure 1. Compartment Diagram of the Distribution of Tuberculosis (TB) Disease with the SEIR Model

3.2 Mathematical Model and Analysis

Figure 1 illustrates the Tuberculosis (TB) transmission mechanism through a flow diagram that depicts the movement of individuals between subpopulations. This diagram systematically represents the dynamics of disease spread and serves as the foundation for formulating a system of differential equations. The mathematical framework employed is a system of dynamic differential equations comprising four main variables, based on the SEIR (Susceptible, Exposed, Infected, Recovered) model. This system captures the rate of change in the number of individuals within each compartment over time.

The following presents the system of differential equations that models the spread of Tuberculosis (TB) using the SEIR approach:

$$\begin{aligned} \frac{dS}{dt} &= (1-v)\pi N - \left(\frac{\beta I}{N} + \mu\right) S \\ \frac{dE}{dt} &= \frac{\beta IS}{N} - (\theta + \gamma + \mu) E \end{aligned} \tag{1}$$

$$\frac{dI}{dt} = \theta E - (\delta + \mu_T + \mu)I$$
$$\frac{dR}{dt} = v\pi N + \gamma E + \delta I - \mu R$$
$$N(t) = S(t) + E(t) + I(t) + R(t)$$

The variables and parameters used are presented in **Table 1**. Parameter values are obtained from the original data by assuming that the data is uniformly distributed. For example, the data shows that the age of death ranges from 63 to 64 years, so the natural mortality rate is 1/63.5.

Table 1. Variable and Parameter Value and Source

Symbol	Definition	Type	Condition	Initial Value	Unit	Source
N	Total number of individuals in the population	Variable	$N \geq 0$	1 (1)	Individuals	BPS
S	Susceptible individuals	Variable	$S \geq 0$	0.91805	Individuals	Data*
E	Exposed individuals	Variable	$E \geq 0$	0.05546	Individuals	Data*
I	Infected individuals	Variable	$I \geq 0$	0.02585	Individuals	Data*
R	Recovered individuals	Variable	$R \geq 0$	0.00064	Individuals	Data*
π	Birth rate	Parameter	$\pi > 0$	0.01569	Per time	Data**
β	Transmission rate of TB leading to infection	Parameter	$\beta > 0$	0.27000	Per time	Data**
θ	Rate of latent TB progressing to active TB	Parameter	$\theta > 0$	0.25000	Per time	Data**
v	Vaccine rate	Parameter	$v > 0$	0.70000	Per time	Data**
δ	Natural recovery rate	Parameter	$\delta > 0$	0.00001	Per time	Assumed
μ_T	Infection death rate	Parameter	$\mu_T > 0$	0.02490	Per time	Data**
μ	Natural death rate	Parameter	$\mu > 0$	0.01569	Per time	Data**
γ	Rate of latent TB to recovery	Parameter	$\gamma > 0$	0.12500	Per time	[24]

*Source: *Health Office of North Sumatra Province*
*** Central Bureau of Statistics of North Sumatra Province*

3.3. Mathematic Analysis

The next step is to perform non-dimensionalization of **Equation (1)** in order to reduce the components within the system. Suppose that s, e, i, and r is a proportion with the values $s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, and $r = \frac{R}{N}$ with $s + e + i + r = 1$. Then it can be seen that the domain of the function $D = \{(s, i, t^*, r): e \geq 0, i \geq 0, r \geq 0, e + i + r < 1\}$ is invariant for **Equation (1)**. Then, **Equation (1)** can be written as:

$$\begin{aligned}\frac{ds}{dt} &= (1 - v)\pi - (\beta i + \mu)s \\ \frac{de}{dt} &= \beta i s - (\theta + \gamma + \mu)e \\ \frac{di}{dt} &= \theta e - (\delta + \mu_T + \mu)i \\ \frac{dr}{dt} &= v\pi + \gamma e + \delta i - \mu r\end{aligned} \tag{2}$$

In analyzing the spread of Tuberculosis (TB) using the SEIR model with vaccination, the first step is to determine the equilibrium points. A system is said to be in equilibrium when it no longer changes over time under certain conditions. To identify the equilibrium points of **Equation (2)**, the rate of change of the system is set to zero: $\frac{ds}{dt} = \mathbf{0}$; $\frac{de}{dt} = \mathbf{0}$; $\frac{di}{dt} = \mathbf{0}$ **and** $\frac{dr}{dt} = \mathbf{0}$, so **Equation (2)**:

$$\begin{aligned}(1 - v)\pi - (\beta i + \mu)s &= 0 \\ \beta i s - (\theta + \gamma + \mu)e &= 0 \\ \theta e - (\delta + \mu_T + \mu)i &= 0 \\ \boldsymbol{v\pi + \gamma e + \delta i - \mu r} &= \mathbf{0}\end{aligned} \tag{3}$$

3.3.1. Disease-Free Equilibrium Point (E_0)

The first equilibrium point is the disease-free equilibrium, where the infected subpopulation is absent ($\boldsymbol{i = 0}$). From the differential equation system above, under the disease-free condition ($\boldsymbol{i = 0}$), the equilibrium point is obtained as follows [25]:

1. For $\frac{ds}{dt} = 0$, we obtained:

$$\begin{aligned} (1-v)\pi - (\beta i + \mu)s &= 0 \\ (1-v)\pi - (\mu)s &= 0 \\ \mu s &= (1-v)\pi \\ s &= \frac{(1-v)\pi}{\mu} \end{aligned} \quad (4)$$

2. For $\frac{de}{dt}$ we obtained:

$$\begin{aligned} \beta i s - (\theta + \gamma + \mu)e &= 0 \\ (\theta + \gamma + \mu)e &= \beta i s \\ e &= 0 \end{aligned} \quad (5)$$

3. For $\frac{di}{dt} = 0$:

$$\begin{aligned} \theta e - (\delta + \mu_T + \mu)i &= 0 \\ (\delta + \mu_T + \mu)i &= \theta e \\ i &= 0 \end{aligned} \quad (6)$$

4. For $\frac{dr}{dt} = 0$:

$$\begin{aligned} v\pi + \gamma e + \delta i - \mu r &= 0 \\ v\pi + \gamma e + \delta i &= \mu r \; \mu r \\ r &= \frac{v\pi}{\mu} \end{aligned}$$

So, we obtained:

$$\boldsymbol{E_0 = \left(\frac{(1-v)\pi}{\mu}; 0; 0; \frac{v\pi}{\mu}\right)} \quad (7)$$

3.3.2. Endemic Equilibrium Point (E_1)

The endemic equilibrium point refers to a situation in which there are individuals infected with TB within a given population, or in other words, the value of $i \neq 0$. This equilibrium point can be determined by solving the system of differential equations under the condition $i \neq 0$ specifically by finding the solutions to $\boldsymbol{\frac{ds}{dt} = 0}$; $\boldsymbol{\frac{de}{dt} = 0}$; $\boldsymbol{\frac{di}{dt} = 0}$ **and** $\boldsymbol{\frac{dr}{dt} = 0}$. By assuming $\boldsymbol{x = (1-v)\pi}$; $\boldsymbol{y = \theta + \delta + \mu}$ **and** $\boldsymbol{z = \delta + \mu_T + \mu}$, **Equation (3)** becomes:

$$\boldsymbol{x - (\beta i + \mu)s = 0} \quad (8)$$

$$\boldsymbol{\beta i s - y e = 0} \quad (9)$$

$$\boldsymbol{\theta e - z i = 0} \quad (10)$$

$$\boldsymbol{v\pi + \gamma e + \delta i - \mu r = 0} \quad (11)$$

For **Equation (10)** with: $i \neq 0$:

$$\theta e - zi = 0$$

$$\theta e = zi \iff i = \frac{\theta e}{z} \tag{12}$$

Substitution **Equation (12)** to **Equation (9)**:

$$\beta \frac{\theta e}{z} s - ye = 0$$

$$\beta \frac{\theta e}{z} s = ye \iff s = \frac{yez}{\beta \theta e} = \frac{yz}{\beta \theta} \tag{13}$$

Substitution **Equation (13)** to **Equation (8)**:

$$e = \frac{\beta \theta x - xyz}{\beta \theta yz} \tag{14}$$

Substitution **Equation (14)** to **Equation (12)**:

$$i = \frac{1}{z}\left[\frac{\beta \theta x - xyz}{\beta yz}\right] \tag{15}$$

Substitution **Equation (14)** and **Equation (15)** to **Equation (11)**,

$$v\pi + \gamma e + \delta i - \mu r = 0$$

$$v\pi + \gamma e + \delta i = \mu r \iff r = \frac{v\pi}{\mu} + \frac{\gamma}{\mu}\left(\frac{\beta \theta x - xyz}{\beta \theta yz}\right) + \delta \frac{1}{\mu z}\left[\frac{\beta \theta x - xyz}{\beta yz}\right] \tag{16}$$

In this way, an endemic equilibrium point is produced, namely:

$$E_1 = \left(\frac{yz}{\beta \theta}, \frac{\beta \theta x - xyz}{\beta \theta yz}, \frac{1}{z}\left[\frac{\beta \theta x - xyz}{\beta yz}\right], \frac{v\pi}{\mu} + \frac{\gamma}{\mu}\left(\frac{\beta \theta x - xyz}{\beta \theta yz}\right) + \delta \frac{1}{\mu z}\left[\frac{\beta \theta x - xyz}{\beta yz}\right]\right) \tag{17}$$

3.3.3. Basic Reproduction Number (R_0)

The basic reproduction number is a measure that indicates the expected number of new infections per unit of time in a fully susceptible population, caused by a single infected individual. This value R_0 is calculated using the method introduced by [26], by constructing a matrix that includes only the subpopulations involved in the transmission of the infection. This matrix is known as the next generation matrix. The basic reproduction number, denoted as, is defined as the largest non-negative eigenvalue of the matrix. The next generation matrix consists of two main components, namely F and V^{-1} , which are defined as follows:

$F_1 := \beta si$

$F_2 := 0$

$V_1 := (\theta + \gamma + \mu)e$

$V_2 = -\theta e + (\delta + \mu + \mu_T)$

The matrix F and V are obtained by finding the Jacobian matrix of the functions $F_1 := (F_1, F_2)$ and $V := (V_1, V_2)$. Then the disease-free equilibrium solution (E_0) is substituted into the matrices F dan V.

$$F := \begin{bmatrix} 0 & \beta s \\ 0 & 0 \end{bmatrix} = \begin{bmatrix} 0 & \frac{\beta(1-v)\pi}{\mu} \\ 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \theta + \gamma + \mu & 0 \\ -\theta & \delta + \mu + \mu_T \end{bmatrix}$$

The NGM matrix is the product of matrices $F \cdot V^{-1}$.

$$NGM = F.V^{-1} = \begin{bmatrix} 0 & \frac{\beta(1-v)\pi}{\mu} \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\theta+\gamma+\mu} & 0 \\ \frac{}{(\delta+\mu+\mu_T)(\theta+\gamma+\mu)} & \frac{1}{\delta+\mu} \end{bmatrix}$$

$$= \begin{bmatrix} \frac{\beta\theta(1-v)\pi}{\mu(\delta+\mu+\mu_T)(\theta+\gamma+\mu)} & \frac{\beta(1-v)\pi}{\mu(\delta+\mu+\mu_T)} \\ 0 & 0 \end{bmatrix}$$

Since the number is the spectral radius (dominant eigenvalue) of the NGM matrix, we obtain

$$R_0 = \frac{\beta\theta(1-v)\pi}{\mu(\delta+\mu+\mu_T)(\theta+\gamma+\mu)} \tag{18}$$

Based on **Equation (18)**, we can find that the smaller the value of v, the larger R_0 will be. So, it can be obtained that the vaccination rate can reduce the number of patients because R_0 goes to 0 if the vaccination rate goes to 1. Then, by substituting the initial parameter values from **Table 1** into **Equation (18)**, the basic reproduction number was found to be R_0=2.22229, indicating that R_0 >1. This result suggests that, at the time the study was conducted, the transmission dynamics of Tuberculosis in North Sumatra still had the potential to become endemic **[27]**, **[28]**. A reproduction number greater than one implies that, on average, each infected individual can transmit the disease to more than one susceptible person, allowing the infection to persist and spread within the population unless effective control measures are implemented.

3.4 Simulation

The SEIR model simulation for Tuberculosis (TB) cases in North Sumatra was conducted using MATLAB 2022b. MATLAB was utilized to calculate the proportions of each initial variable value, generate random values for selected parameters, and visualize the disease transmission dynamics numerically. This numerical simulation supports the analytical findings that will be discussed further in the subsequent section.

In this case, the basic reproduction number R_0 obtained indicates that each infected individual can transmit the disease to an average of 2.22229 other individuals in a fully susceptible population. A value of $R_0 > 1$ suggests the potential for the disease to become endemic, as the infection can spread exponentially and persist over time.

The simulation results demonstrate that a high R_0 leads to a rapid increase in the proportion of the population in the Infected (I) and Exposed (E) compartments during the early stages of transmission. However, with the implementation of vaccination, the spread of TB is eventually brought under control, as indicated by the stabilization of each compartment's proportion by the end of the simulation period.

The simulation results illustrating the dynamics of TB transmission in North Sumatra are presented in **Figure 2**.

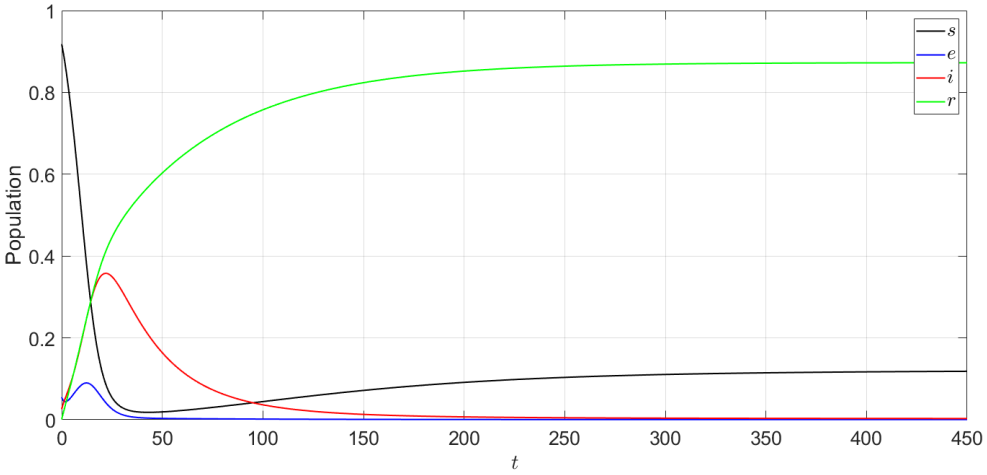

Figure 2. Graph of TB Spread in North Sumatra

The parameter values used in this simulation were obtained from the 2023 data provided by the Health Office of Medan. The parameters applied are as follows: π = 0.01569, β = 0.47, γ = 0.125, δ = 0.00001, μ =

0.01569, and μ_T = 0.0249. By applying these parameters, the endemic equilibrium point (non-disease-free equilibrium) was determined as E_1= (s, e, i, r), with a basic reproduction number of R_0=2.33815. This R_0value indicates that each infected individual is expected to transmit the disease to approximately 2.33815 other individuals in a fully susceptible population. Since R_0>1, the disease has the potential to persist within the population for an extended period, suggesting the likelihood of an endemic state. A higher reproduction number also leads to a rapid initial increase in the proportion of individuals in the Infected (I) and Exposed (E) compartments.

To assess the impact of vaccination on the transmission of Tuberculosis among active individuals, a variation in the vaccination rate parameter v was conducted. The results showed that the basic reproduction number (R_0) could be reduced to below 1, with the minimum threshold achieved at v = 0.87 (referring to **Table 2**, it can be obtained that the value of $R_0 < 1$ when $v = 0.87$). When R_0<1, the disease will naturally die out from the population, as each infected individual transmits the disease to fewer than one susceptible individual on average **[27]**, **[28]**. In this scenario, the parameter ω remains essential in accelerating the recovery process and minimizing the number of infections before the disease is completely eradicated. Variations in vaccine values with other parameters constant are presented in **Table 2**.

Tabel 2. Variation in Vaccine Values v and Value Of R_0

v	R_0
0	7.407634
0.05	7.037253
0.1	6.666871
0.5	3.703817
0.7	2.222290
0.87	0.962992

To determine the minimum effective vaccination rate, simulations were conducted using various values of the vaccination parameter v, as presented in **Table 2**. The simulation was applied to each subpopulation, namely the susceptible, exposed, infected, and recovered groups. The results illustrate the dynamic behavior of Tuberculosis (TB) transmission under different vaccination scenarios. These simulations provide valuable insights into how varying vaccination coverage levels influence the spread of TB within the population.

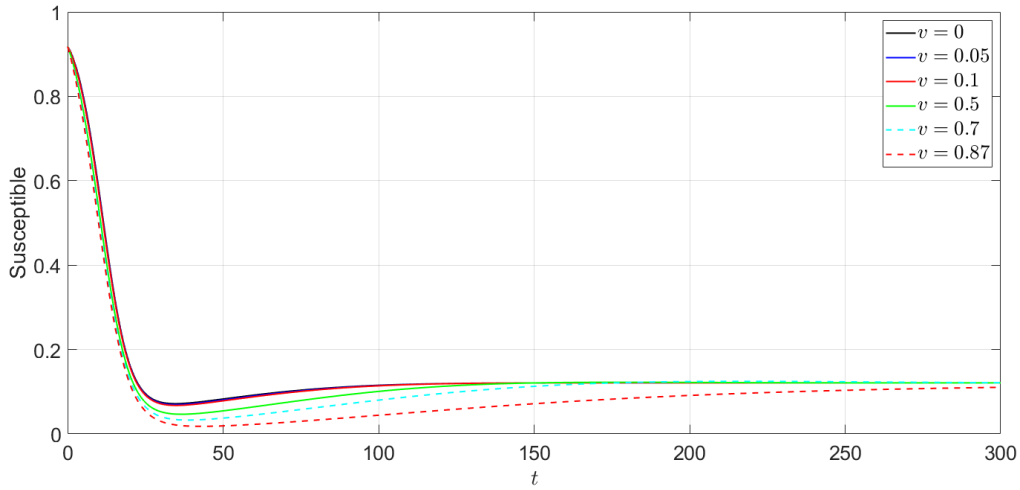

Figure 3. Susceptible Dynamics Graph with Vaccine Value Variations

Figure 3 illustrates the dynamics of the susceptible population proportion over time about Tuberculosis (TB), based on variations in the vaccination parameter value v. The graph demonstrates how increased vaccination coverage influences the reduction of individuals susceptible to TB infection. A sharp decline is observed in the proportion of the susceptible population across all curves, indicating a rise in initial infections or transitions to other compartments (exposed or infected). As the value of v increases, population resistance to infection improves significantly, as evidenced by the stable proportion of uninfected individuals toward the end of the simulation. This suggests that higher vaccination rates are crucial in limiting TB transmission and maintaining long-term disease control.

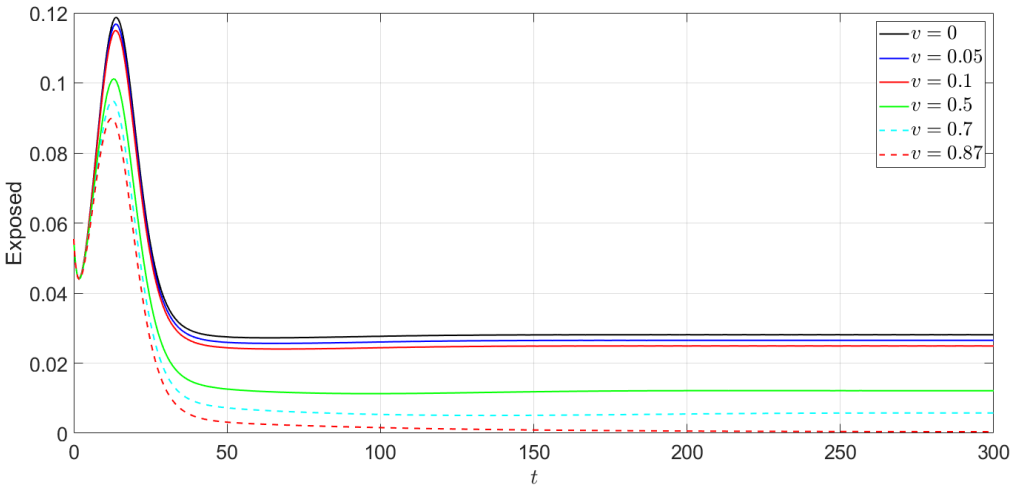

Figure 4. Exposed Dynamics Graph with Vaccine Value Variations

Figure 4 illustrates the dynamics of the Exposed subpopulation over time under various levels of vaccination coverage (v). All curves exhibit an initial peak, reflecting a rise in individuals who have been recently exposed to TB. Following this peak, the proportion of Exposed individuals decreases and eventually stabilizes. As the vaccination rate v increases, the peak and the steady-state values of the Exposed population decrease significantly. This indicates that higher vaccination coverage effectively reduces the number of individuals transitioning to the Exposed class, limiting the potential progression to active infection (Infected). The higher the proportion of vaccination administered, the lower the number of individuals susceptible to TB infection**.** Notably, when $v = 0.87$, the Exposed subpopulation decreases drastically, approaching zero at a certain time point. This finding highlights the significant impact of vaccination in reducing the transmission rate of Tuberculosis within the population.

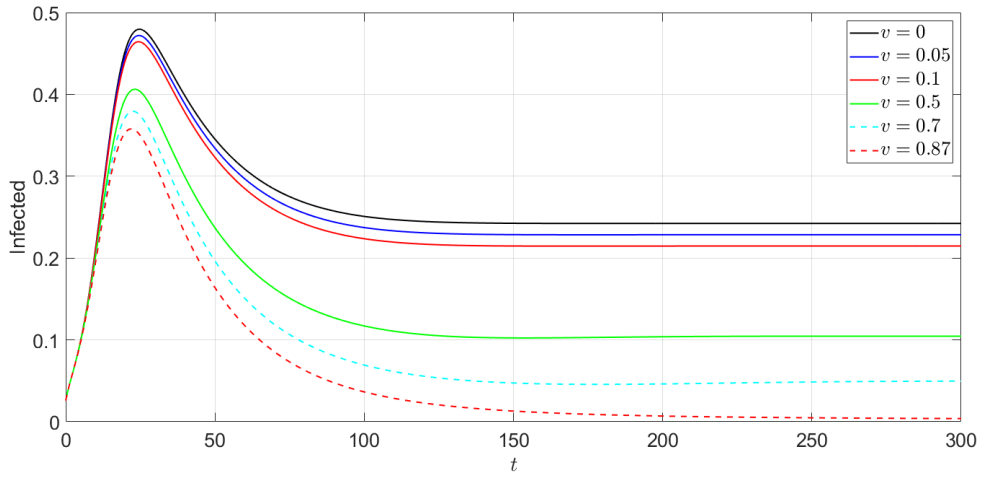

Figure 5. Infected Dynamics Graph with Vaccine Value Variations

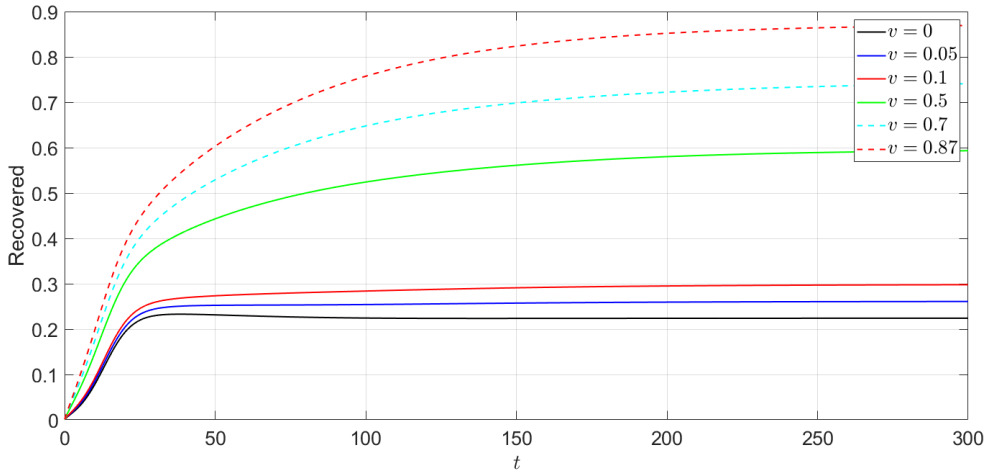

Figure 6. Recovered Dynamics Graph with Vaccine Value Variations

Figure 5 illustrates the dynamics of the Infected subpopulation over time under various levels of vaccination coverage (v). All curves show the relationship between vaccines and individual infection rates. The higher the proportion of vaccines to the population, the lower the infection rate. Finally, as shown in proportion $v = 0.87$, the total infected population was at zero, meaning that TB disease could disappear from the North Sumatra region. This also interprets $R_0 < 1$. It can be concluded that increasing the number of vaccines has a positive impact on suppressing the rate of spread of TB. Through simulation illustrations, it can be shown that at least 87% of 87% of the population will disappear or become extinct from the region. **Figure 6** illustrates the relationship between recovered and vaccination. The graph concludes that the higher the proportion of vaccination in the population, the faster the recovery rate.

4. CONCLUSION

The dynamics of tuberculosis (TB) transmission in North Sumatra indicate that vaccination interventions have significant potential to reduce the number of infected individuals. Results from mathematical modeling simulations show that expanding vaccination coverage can effectively suppress disease transmission, even when vaccine efficacy does not reach 100%. Increasing vaccination coverage plays a critical role in slowing the rate of transmission and reducing the long-term prevalence of infection. Empirical data analysis yields a basic reproduction number (R_0) of 2.22229 (R_0> 1), indicating that TB still has the potential to spread actively within the region. Furthermore, increasing the vaccination coverage parameter (v) has been shown to have a significant impact on reducing the number of TB cases. This study also identifies the vaccination threshold required to bring the R_0 value below 1, which is a necessary condition to transition from an endemic to a non-endemic state. Simulation results suggest that a high level of vaccination coverage is required to halt endemic TB transmission. With a transmission rate of 0.47, the minimum proportion of the population that needs to be vaccinated is estimated at 87.5% to achieve the threshold necessary to eliminate TB transmission in North Sumatra. Further exploration can be done by estimating parameters to predict TB patients.

AUTHOR CONTRIBUTIONS

Hamidah Nasution: Conceptualization and Methodology. Mulyono: F Writing - Review and Editing. Maria Cyntia S: Data Curation and Project Administration. Faiz Ahyaningsih: Software and Formal Analysis. Fidelis Nofertinus Zai: Software, Visualization, and Writing - Original Draft. All authors discussed the results and contributed to the final manuscript.

FUNDING STATEMENT

This research was funded by BOPTN of Universitas Negeri Medan and the Contract Number: 0055/UN33.8/PPKM/PPT/2024.

ACKNOWLEDGEMENT

The authors thank Universitas Negeri Medan for sponsoring this research through the Applied Research program in 2024. The authors are also thankful to the editors and reviewers who have supported us in improving this manuscript.

CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest to report.

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