



SENSITIVITY ANALYSIS OF A TUBERCULOSIS TRANSMISSION MODEL WITH INCOMPLETE TREATMENT

Joko Harianto^{1*} and Diki Fernandi²

¹*Department of Mathematics, Universitas Cenderawasih, Jayapura, Indonesia*

²*Department of Mathematics, Institut Teknologi Bandung, Bandung, Indonesia*

Abstract

Tuberculosis (TB) remains a major global health concern due to its complex transmission dynamics and frequent treatment interruptions. This study utilizes a SEITR compartmental model to quantitatively analyze the spread and control of TB. The model calculates the basic reproduction number, disease-free equilibrium, and endemic equilibrium to evaluate system stability. Sensitivity analysis identifies key parameters influencing the infected population: effective contact rate, natural mortality rate, population recruitment rate, and treatment rate. Among these, the effective contact rate and natural mortality rate significantly impact disease persistence. The findings suggest that effective TB control can be achieved through early detection and isolation of infectious individuals, timely and proper treatment, improved indoor ventilation, and the consistent use of masks by active TB patients. This model-based approach offers empirical evidence to inform public health policies, highlighting critical intervention points to interrupt TB transmission and improve treatment outcomes.

Keywords: Basic Reproduction Number, Sensitivity Analysis, Tuberculosis.

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1 Introduction

Tuberculosis (TB) continues to pose a serious global public health threat, characterized by the complexity of its transmission dynamics and challenges in its control, particularly concerning the phenomenon of incomplete treatment or treatment default. This condition can lead to treatment failure, an increased risk of further transmission, and the emergence of drug-resistant *Mycobacterium tuberculosis* strains. To quantitatively understand the impact of these factors on the TB epidemic, mathematical models, such as the SEITR (Susceptible–Exposed–Infected–Treated–Recovered) compartment model, have become invaluable tools. These models allow for the representation of interactions among different population groups and the simulation of disease spread over time.

A major barrier to effective tuberculosis (TB) control is the widespread problem of patients not completing their full course of treatment. This non-compliance with medical regimens elevates the likelihood of disease recurrence and facilitates the development of drug-resistant TB strains, while also sustaining the risk of ongoing transmission in the population. Therefore, it is vital to examine the impact of treatment-related factors on the transmission patterns of tuberculosis.

*Corresponding author. E-mail: joharijpr88@gmail.com

Sensitivity analysis, in this regard, offers a vital method for pinpointing the most impactful parameters within epidemiological models, thereby allowing health interventions to be more precisely directed at the primary drivers of disease spread.

Numerous studies have discussed the transmission of TB disease using compartmental models that include treatment factors [1], [2], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14], [15], [16]. These studies generally cover the analysis of both local and global stability of the model's equilibrium points, as well as sensitivity analysis of model parameters. However, article [16] did not include an analysis of model parameter sensitivity. The model can provide insights into disease dynamics, but the accuracy and reliability of its predictions heavily depend on the parameter values used. In the case of TB, these parameters often come from statistical estimations, epidemiological studies, or assumptions based on available data, all of which may have degrees of uncertainty. Therefore, it is important not only to develop models that reflect biological and epidemiological reality but also to understand how sensitive the model's results are to variations in input parameter values.

While prior research has modeled TB transmission and analyzed various treatment factors, a significant gap remains in understanding the sensitivity of these models to changes in key parameters, particularly those tied to treatment behavior and disease progression. Sensitivity analysis plays a crucial role in identifying which variables most influence the outputs of a model, thereby guiding targeted interventions that can yield the greatest epidemiological impact.

This article focuses on the parameter sensitivity analysis of the model discussed in article [16]. Sensitivity analysis is a structured approach to see how responsive a model's outcomes are to different input values. In this context, we will investigate how changes in key parameters, such as the infection rate, incubation period duration, treatment success rate, treatment default rate, and other parameters, affect important epidemiological measures like the basic reproduction number and the endemic equilibrium population size. By identifying which parameters are most influential on TB transmission dynamics, considering incomplete treatment, this analysis is expected to provide more precise guidance for policymakers in designing the most effective and efficient intervention strategies to control the TB epidemic. This insight will also highlight areas where more accurate parameter estimation is critically needed to enhance the reliability of model predictions.

This study addresses that gap by conducting a comprehensive parameter sensitivity analysis of a TB compartmental model, based on the framework discussed in article [16]. Unlike prior works that focused on equilibrium analysis or global stability, this study evaluates how variations in parameters such as infection rate, treatment success rate, treatment default rate, and incubation period affect TB outcomes. Our findings indicate that parameters related to treatment adherence and progression duration have the most significant impact on TB transmission dynamics. By pinpointing these high-impact variables, the study not only enhances the reliability and applicability of epidemiological models but also provides actionable insights for public health decision-making. These results can inform more effective treatment protocols and resource allocation strategies, especially in settings with high rates of treatment non-compliance.

2 Some Concepts

2.1 SIETR Model of Tuberculosis Transmission with Incomplete Treatment

According to [17], the spread of infectious diseases in a population can be mathematically modeled using the SEITR model. In this model, the population is divided into five mutually exclusive groups: susceptible (S), exposed (E), actively infected or infectious (I), under treatment (T), and recovered (R). New individuals enter the population through the susceptible class with a recruitment rate π . Transmission of infection occurs when a susceptible individual comes into close contact with an infectious or on-treatment individual, with a transmission rate of

$\lambda S(t)(I(t) + \beta T(t))$, where λ is the effective contact rate, and β ($0 \leq \beta < 1$) describes the decrease in infectiousness due to treatment. The natural mortality rate of the entire population is expressed by η , while disease-induced mortality occurs in the infectious and treatment classes at rates δ_1 and δ_2 , respectively, where δ_1 is greater than δ_2 . The movement of individuals from the exposed class to the infectious class is controlled by the parameter α , while γ indicates the treatment rate of infectious individuals. Individuals who have undergone treatment will leave class T at a rate θ , where some ($p\theta T$) successfully recover and enter class R , while the rest $((1-p)\theta T)$ return to being exposed due to ineffective treatment. The value of p ($0 < p \leq 1$) indicates the treatment success rate. Individuals who are in the exposed stage cannot transmit the disease, while individuals on treatment still have the potential to transmit based on the WHO TB report.

The susceptible population increases through recruitment at a rate of π and decreases due to infection following contact with infectious individuals (I) or those undergoing treatment (T), the latter having reduced infectivity, represented by the modification factor β . Additionally, natural death among susceptible individuals occurs at a rate η . The exposed class (E) increases as susceptible individuals become infected, and decreases due to progression to the infectious stage at a rate α and natural death at a rate η . Furthermore, individuals from the treatment class (T) who fail to recover (with probability $1 - p$) may return to the exposed stage at a rate θ . The infectious population (I) grows as exposed individuals transition into the infectious stage and decreases due to natural mortality (η), disease-induced death (δ_1), and movement into treatment (γ). The treatment class (T) increases as infectious individuals begin therapy, and decreases due to natural death, TB-induced death (δ_2), and treatment exit either due to success or failure at a rate θ . Recovered individuals enter the R compartment following successful treatment, with a proportion p exiting the treatment stage at rate θ . This class also decreases through natural death at rate η . Based on these assumptions, a system of differential equations is developed that represents the dynamics of disease spread in the population.

$$\begin{aligned}\frac{dS}{dt} &= \pi - \lambda S(I + \beta T) - \eta S, \\ \frac{dE}{dt} &= \lambda S(I + \beta T) - (\eta + \alpha)E + (1 - p)\theta T, \\ \frac{dI}{dt} &= \alpha E - (\eta + \delta_1 + \gamma)I, \\ \frac{dT}{dt} &= \gamma I - (\eta + \delta_2 + \theta)T, \\ \frac{dR}{dt} &= p\theta T - \eta R.\end{aligned}\tag{1}$$

2.2 Fixed Point and Basic Reproduction Number

The disease-free fixed point of the proposed TB transmission model can be obtained by equating the right-hand side of the model equation system to zero and $E = I = T = 0$. From this process, the following results are obtained:

$$P_0 = (S, E, I, T, R) = \left(\frac{\pi}{\eta}, 0, 0, 0, 0 \right).$$

Furthermore, the value of the basic reproduction number will be found using the Next Generation Matrix (NGM) method **Driessche2002**. Based on model (eq:seitrssystem) and P_0 , the following correspondence matrices are obtained:

$$F = \begin{bmatrix} 0 & \frac{\lambda\pi}{\eta} & \frac{\lambda\beta\pi}{\eta} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} \eta + \alpha & 0 & -(1-p)\theta \\ -\alpha & \eta + \delta_1 + \gamma & 0 \\ 0 & -\gamma & \eta + \delta_2 + \theta \end{bmatrix}$$

The value of R_0 is the spectral radius of FV^{-1} , so the value of R_0 is:

$$R_0 = \frac{\alpha\lambda\pi}{\eta} \cdot \frac{(\eta + \delta_2 + \theta + \beta\gamma)}{(\eta + \alpha)(\eta + \delta_1 + \gamma)(\eta + \delta_2 + \theta) - (1 - p)\theta\alpha\gamma}$$

The endemic fixed point of model 1 is obtained by equalizing the right-hand side of the system, so that the fixed point value is obtained as follows

$$P_1 = (S^*, E^*, I^*, T^*, R^*)$$

where

$$S^* = \frac{\pi}{xI^* + \eta}, \quad E^* = \frac{h_2I^*}{\alpha}, \quad T^* = \frac{\gamma I^*}{h_3}, \quad R^* = \frac{p\theta\gamma}{\eta h_3}I^*, \quad I^* = \frac{\eta}{x}(R_0 - 1),$$

and

$$x = \frac{\lambda(h_3 + \beta\gamma)}{h_3}.$$

2.3 Sensitivity Analysis

According to [17], sensitivity analysis is conducted to assess the role of each parameter in influencing the dynamics of the spread of a disease. To assess the influence of each parameter on the spread of the disease, a sensitivity index is used. This index, known as the normalized sensitivity index, is obtained by performing the derivative of variable A against parameter x , then normalizing it. The index is defined as follows:

$$I_x^A = \frac{\partial A}{\partial x} \cdot \frac{x}{A} \quad (2)$$

where A is the variable to be analyzed while x is the parameter [18].

3 Result and Discussion

3.1 Sensitivity Analysis for Basic Reproduction Number

The basic reproduction number, denoted as R_0 , describes the average number of new individuals infected by a single infected person over the course of its transmission, in a population where all members are still susceptible to infection [19], [20], [21], [22], [23].

Sensitivity analysis of R_0 aims to identify the parameters that most influence the magnitude of the R_0 value, so that disease control efforts can be carried out more effectively and purposefully. The sensitivity analysis is conducted using parameter values based on [16], as presented in Table 1.

Table 1: Parameter values used in the sensitivity analysis of R_0 based on [16].

Parameter	Value
π	0.2
λ	0.7
α	0.25
η	0.1
δ_1	0.15
δ_2	0.05
γ	0.2
θ	0.1
β	0.1
p	0.9

Furthermore, based on Table 1 and Equation (2), the sensitivity index is illustrated in Figure 1.

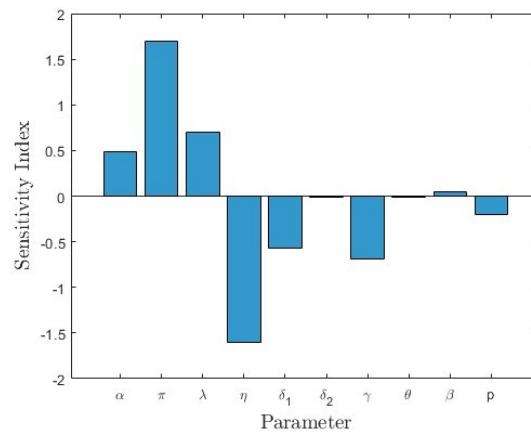


Figure 1: Sensitivity index of the basic reproduction number

Next, we will look at the relationship between changes in parameter values and changes in R_0 values, as presented in Table 2.

Table 2: Comparison of parameter value changes to the basic reproduction number $R_0 = 2.4309$.

Parameter	+5%	-5%
α	2.4648	2.3944
π	2.5524	2.3093
λ	2.5524	2.3093
η	2.2529	2.6306
δ_1	2.3905	2.4726
δ_2	2.4288	2.4330
γ	2.3877	2.4760
θ	2.4283	2.4336
β	2.4399	2.4219
p	2.4169	2.4450

Based on Table 2, it can be seen that a sensitivity index with a positive value indicates that an increase in the parameter value will result in an increase in the basic reproduction number R_0 . Conversely, a negative sensitivity index indicates that an increase in the parameter value will lead to a decrease in R_0 . For example, the sensitivity index obtained for the parameter α is 0.2894, which means that if α increases (decreases) by 10%, it causes R_0 to increase (decrease) by 2.894%. Similarly, the parameter η has a sensitivity index of -1.5492 , indicating that if η increases (decreases) by 10%, R_0 will decrease (increase) by 15.492%. This type of analysis also applies to other parameters. Based on the sensitivity index values, the parameters that have the most influence on R_0 are π , λ , and η .

Furthermore, simulations are carried out to better visualize the effect of these parameters on the value of R_0 under varying conditions. In this simulation, the values $\lambda = 0.5$, $\lambda = 0.6$, and $\lambda = 0.7$ are selected, while η is varied over the interval $0 \leq \eta \leq 0.2$. The simulation results are shown in Figure 2. Based on the figure, it is observed that as the value of λ increases, the value of R_0 also increases, while as the value of η increases, R_0 decreases. This behavior aligns with the sensitivity indices, where λ has a positive sensitivity index and η has a negative one.

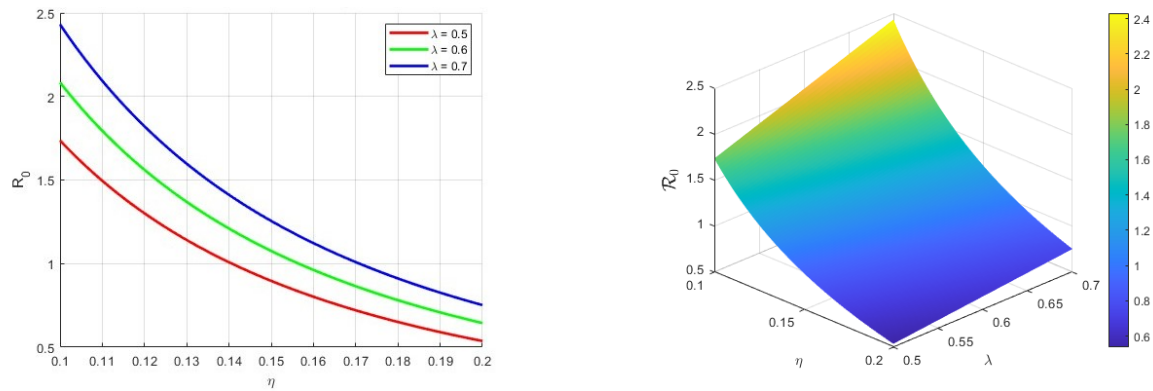


Figure 2: Effect of λ variation on η and the basic reproduction number R_0 .

The simulations in Figure 2 provide critical insight into how changes in the effective contact rate (λ) and the natural mortality rate (η) affect the basic reproduction number (R_0). As observed, increases in λ lead to a higher R_0 , while increases in η correspond to a reduction in R_0 . These findings highlight the pivotal role of contact reduction strategies, such as early case detection, contact tracing, and isolation of infectious individuals, in lowering the transmission potential. Furthermore, improving general health conditions and reducing comorbidities that elevate mortality may indirectly contribute to a more favorable disease dynamic by altering η .

From a policy perspective, these results underscore the importance of targeted interventions that modulate transmission and treatment pathways. For instance, public health programs aimed at increasing awareness, reducing diagnostic delays, and ensuring treatment adherence can significantly influence λ and, consequently, suppress R_0 below the threshold level required for sustained transmission. Incorporating these model insights into tuberculosis (TB) control strategies can enable better resource optimization and support more effective intervention planning.

3.2 Sensitivity Analysis for Infected Population

Sensitivity analysis of the infected population (I) was conducted to determine the parameters that have the most influence on the size of the infected population, so that efforts to control the spread of infection can be carried out more optimally. This analysis uses parameter values taken from [16], as listed in Table 1.

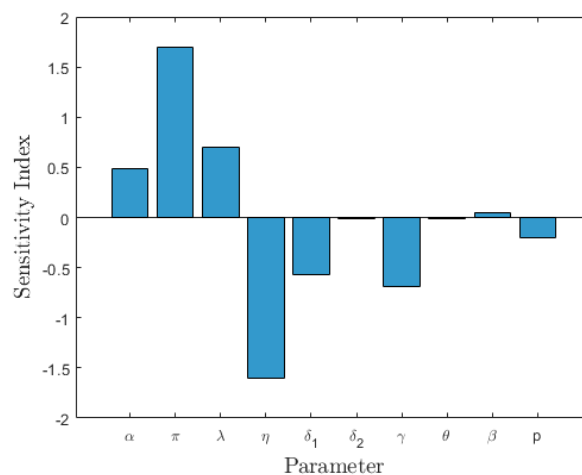


Figure 3: Sensitivity index of the infected population

Based on Figure 3, it can be seen that the parameters π , η , and λ are the most influential factors on changes in the number of infected individuals, both positively and negatively. The parameter π has the greatest positive influence, indicating that an increase in π leads to a significant rise in the number of infected individuals. In contrast, the parameter η shows the strongest negative effect, suggesting that an increase in η has the potential to substantially reduce the size of the infected population.

3.3 Simulation

In this section, we will simulate several parameters to see how the effect of parameter variation affects the infected population.

3.3.1 Effect recruitment rate (π) to infected population

Figure 4 shows that as the parameter value π increases, the number of infected individuals also increases. Sensitivity analysis indicates that a 30% increase in π results in approximately a 49.8% increase in the infected population. The value of π itself is influenced by various factors, including socio-cultural aspects, economic conditions, government policies, and health-related factors. Therefore, government initiatives such as promoting family planning programs can be considered as strategic efforts to reduce the number of infected individuals by controlling the growth rate represented by π .

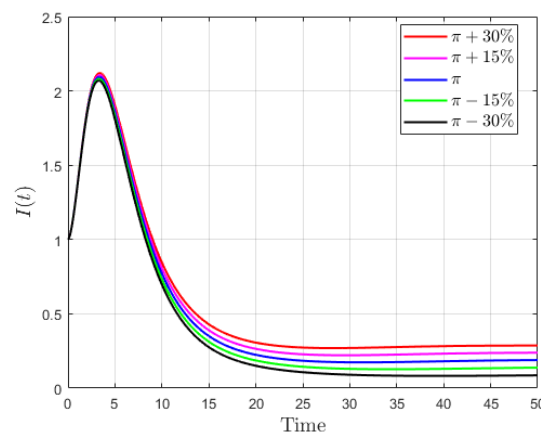


Figure 4: Effect of (π) variation on infected population

3.3.2 Effect effective contact rate (λ) to infected population.

Figure 5 shows that an increase in the value of λ is directly proportional to the increase in the number of infected individuals. Based on sensitivity analysis, a 30% increase in λ is estimated to result in approximately a 19.8% increase in the number of infected cases. Therefore, it is crucial to implement measures aimed at reducing λ , such as early detection and isolation of active TB patients, effective and timely treatment, improving the quality of room ventilation, and encouraging the use of masks by active TB patients. These efforts can significantly reduce λ and help break the chain of transmission.

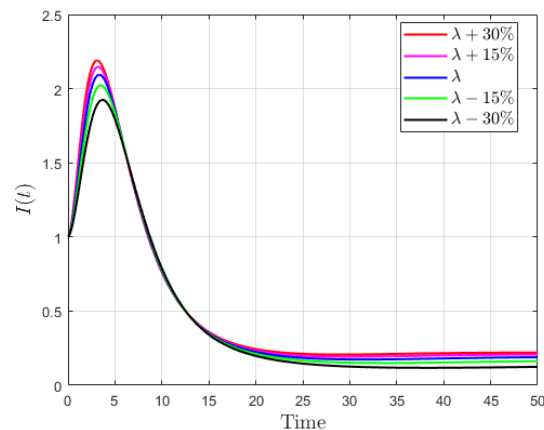


Figure 5: Effect of (λ) variation on infected population

3.3.3 Effect treatment rate of infectious individuals (γ) to infected population

Figure 6 shows that as the value of γ increases, the number of infected individuals decreases. According to the sensitivity analysis results, a 30% increase in γ can reduce the infected population by approximately 19.8%. This indicates that a faster or broader treatment rate plays an important role in reducing the spread of infection. Therefore, accelerating case management efforts can be achieved by improving access to healthcare services and promoting the more widespread use of medical technology.

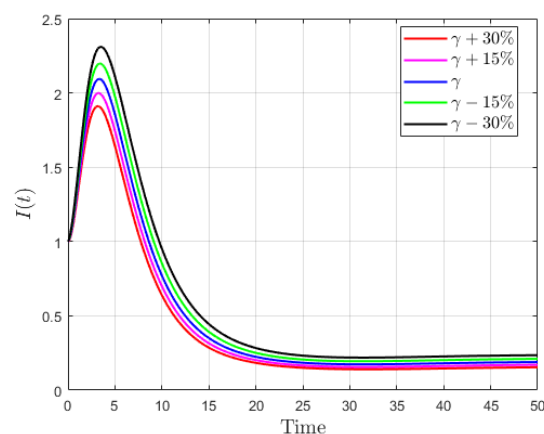


Figure 6: Effect of (γ) variation on infected population

4 Conclusion

The sensitivity analysis of the tuberculosis (TB) transmission model with incomplete treatment has provided crucial insights into the most influential parameters affecting disease dynamics. The results indicate that η , π , and λ significantly impact the basic reproduction number (R_0), while η , π , γ , and λ are key determinants of the number of infected individuals. These findings underscore the importance of targeted interventions to effectively control TB transmission, leading to a strategic emphasis on managing these critical parameters. Specifically, efforts to reduce the effective contact rate (λ) are paramount for breaking the chain of transmission. This can be achieved through early detection and isolation of active TB cases, improving the quality of room ventilation, and encouraging the use of masks by infected individuals. Optimizing the natural mortality rate (η) and the treatment rate (γ) requires ensuring timely and effective access to

healthcare, while addressing the fraction of incomplete treatment (π) highlights the need for strategies that improve treatment adherence and completion.

To further refine our understanding of TB dynamics and develop more robust control strategies, several research directions are proposed. Parameter estimation can be improved through primary data collection, leveraging advanced statistical methods, and applying geographical or demographic stratification. The model could also be expanded to include additional variables such as HIV co-infection, drug resistance, socioeconomic factors, healthcare system capacity, and vaccination coverage. Furthermore, incorporating behavioral aspects such as health-seeking behavior, stigma, and adherence to public health recommendations could enhance the model's realism. Another valuable step would be conducting cost-effectiveness analyses to evaluate different intervention strategies and guide optimal resource allocation. Finally, spatial modeling could be introduced to better understand the geographic distribution and clustering of TB cases.

The conclusion would be more impactful when accompanied by practical examples of implementation. For instance, primary data collection can be carried out through field surveys targeting TB patients in areas with high treatment default rates. Spatial aspects can be integrated by mapping TB case distributions using Geographic Information Systems (GIS). To incorporate socioeconomic variables or HIV co-infection, the model can be extended using secondary data obtained from health department records or household surveys. Cost-effectiveness evaluations may be performed by comparing community-based interventions and clinical-based approaches through cost-per-TB-case-prevented analysis. Including such examples not only makes the future research directions more realistic but also more actionable for both researchers and policymakers in designing data-driven and sustainable public health interventions for TB control.

CRedit Authorship Contribution Statement

Author One: Introduction, SIETR Model of Tuberculosis Transmission with Incomplete Treatment, Sensitivity Analysis for Basic Reproduction Number, Conclusion, Conceptualization, Methodology, Writing–Original Draft, Supervision, Project Administration.

Author Two: Fixed Point and Basic Reproduction Number, Sensitivity Analysis, Sensitivity Analysis for Infected Population, Simulation (Effect of recruitment rate π , effective contact rate λ , and treatment rate γ to infected population), Data Curation, Formal Analysis, Writing–Review Editing, Software, Validation, Visualization.

Declaration of Generative AI and AI-assisted technologies

No generative AI or AI-assisted technologies were used during the preparation of this manuscript.

Declaration of Competing Interest

The authors declare no competing interests.

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