CAUCHY – Jurnal Matematika Murni dan Aplikasi
Volume 11 (1) (2026), Pages 279-289
p-ISSN: 2086-0382; e-ISSN: 2477-3344

Sensitivity Analysis of a Tuberculosis Transmission Model with Incomplete Treatment

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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 Analisys, Tubercolusis.

1. Introduction

Tuberculosis (TB) continues to pose a serious global public health threat, characterized by the complexity of its transmission dynamics and persistent challenges in disease control, particularly related to incomplete treatment and treatment default. Inadequate adherence to TB treatment regimens can result in treatment failure, increased risk of transmission, and the emergence of drug-resistant Mycobacterium tuberculosis strains, which significantly complicate TB eradication efforts. To quantitatively investigate these complex processes, mathematical models such as the SEITR (Susceptible–Exposed–Infected–Treated–Recovered) compartmental model have been widely used as effective tools to describe population interactions and simulate disease dynamics over time.

One of the most critical obstacles in TB control is the high prevalence of treatment non-compliance, where patients discontinue therapy before completing the prescribed regimen. This behavior not only increases the probability of relapse and drug resistance but also sustains ongoing transmission within the community. Consequently, understanding how treatment-related factors influence TB transmission is essential for designing effective intervention strategies. In this

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Submitted: August 29, 2025 Reviewed: September 28, 2025 Accepted: February 6, 2026
DOI: https://doi.org/10.18860/cauchy.v11i1.36325

context, sensitivity analysis plays a fundamental role, as it allows researchers to systematically identify which parameters exert the greatest influence on disease outcomes. Such information is particularly valuable for public health decision-making, as it enables policymakers to prioritize control efforts and allocate resources toward the most impactful intervention targets.

Numerous studies have examined TB transmission dynamics using compartmental models that incorporate treatment mechanisms [1], [2], [3], [4], [5], [6], [7], [8], [9], [10], [11], [12], [13], [14], [15], [16]. These works primarily focus on equilibrium analysis and the local or global stability of disease-free and endemic states. While such analyses are essential for understanding long-term system behavior, they provide limited information regarding how uncertainties in model parameters affect epidemiological predictions. In particular, the study by Ullah et al. [16] proposed a TB model that accounts for treatment and default behavior but did not investigate the sensitivity of model outputs to variations in parameter values.

In practical epidemiological settings, model parameters such as transmission rates, treatment success rates, and default rates are often estimated from incomplete or uncertain data sources. As a result, the reliability of model-based predictions strongly depends on how sensitive the outcomes are to these parameters. Without sensitivity analysis, it is difficult to assess the robustness of model conclusions or to identify which parameters should be targeted most urgently through public health interventions.

The main novelty and scientific contribution of this study lie in conducting a comprehensive parameter sensitivity analysis of the TB model proposed by Ullah et al. [16], with a specific emphasis on treatment adherence and treatment default mechanisms. Unlike previous studies that primarily addressed equilibrium properties and stability conditions, this work explicitly quantifies the relative influence of key epidemiological and treatment-related parameters on critical outcomes such as the basic reproduction number and endemic equilibrium levels. By identifying the most influential parameters driving TB transmission dynamics, this study provides a direct link between mathematical modeling and evidence-based policy design, offering actionable insights for improving TB control strategies, particularly in populations with high rates of treatment non-compliance.

2. Some Concepts

This section presents the fundamental concepts underlying the development of the SIETR model of tuberculosis transmission with incomplete treatment. It introduces the key epidemiological assumptions, compartmental structure, and mathematical framework used to describe the dynamics of disease spread and treatment outcomes. These concepts provide the theoretical basis for formulating the model and facilitate a clear understanding of the relationships among the model components discussed in the subsequent subsections.

2.1. SIETR Model of Tuberculosis Transmission with Incomplete Treatment

According to [16], 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, according [16], 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 [17]. Based on model (eq:seitrsystem) 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

$$S^* = \frac{\pi}{xI^* + \eta}, \quad E^* = \frac{h_2 I^*}{\alpha}, \quad T^* = \frac{\gamma I^*}{h_3}, \quad R^* = \frac{p\theta\gamma}{\eta h_3} I^*, \quad I^* = \frac{\eta}{x}(R_0 - 1),$$

and

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

2.3. Sensitivity Analisys

According to [18], 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:

$$I_x^A = \frac{\partial A}{\partial x} \cdot \frac{x}{A} \tag{2}$$

where A is the variable to be analyzed while x is the parameter [19].

3. Result and Discussion

This section presents the results and discussion of the SIETR model of tuberculosis transmission with incomplete treatment. The analysis begins with a sensitivity study of the basic reproduction number to identify the most influential parameters affecting disease transmission. It is followed by a sensitivity analysis of the infected population to further examine the impact of key parameters on infection dynamics. Finally, numerical simulations are provided to illustrate the behavior of the model and support the analytical findings.

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 [20], [21], [22], [23], [24].

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 Eq. (2), the sensitivity index is illustrated in Fig. 1.

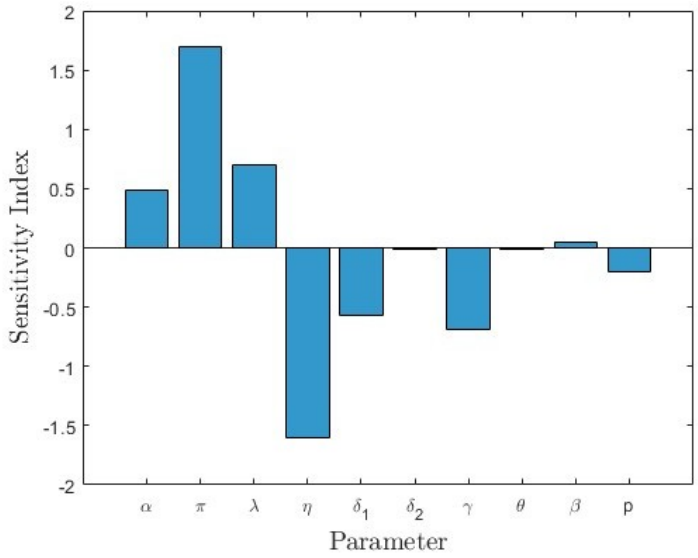

Figure 1: Sensitivity index of the basic reproduction number

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 Fig. 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.

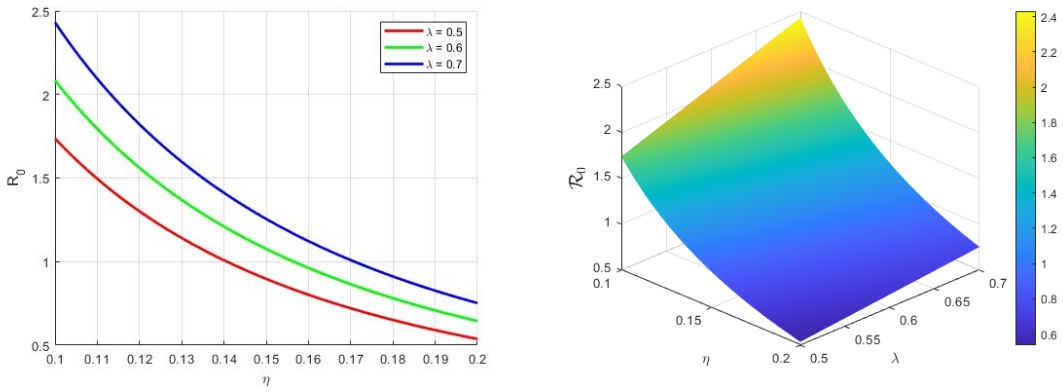

Figure 2: Effect of λ variation on η and the basic reproduction number R_0.

The simulations in Fig. 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 Analisys 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.

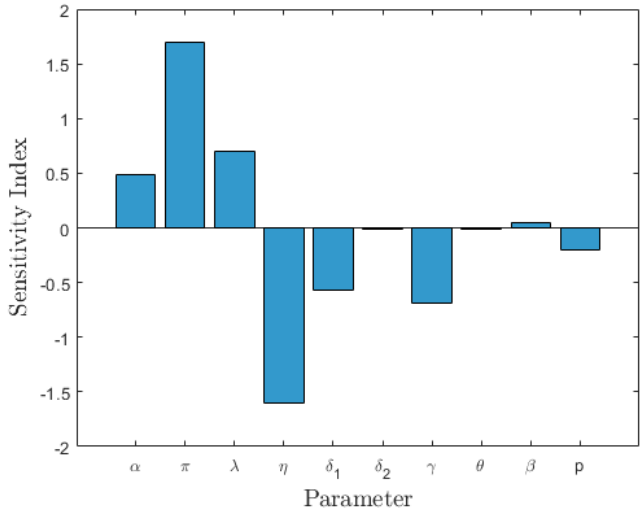

Figure 3: Sensitivity index of the infected population

Based on Fig. 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

Fig. 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.

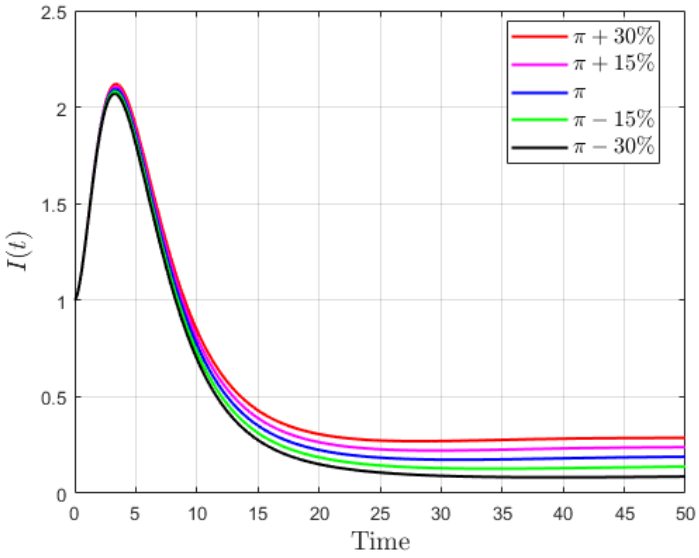

Figure 4: Effect of (π) variation on infected population

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

Fig. 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.

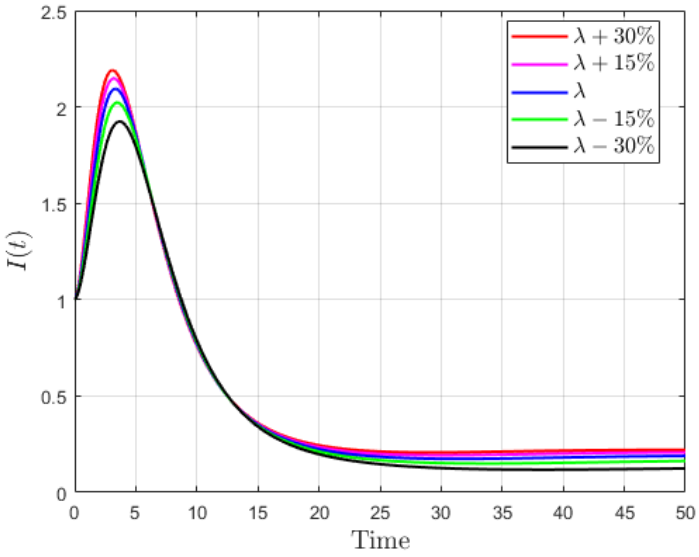

Figure 5: Effect of (λ) variation on infected population

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

Fig. 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.

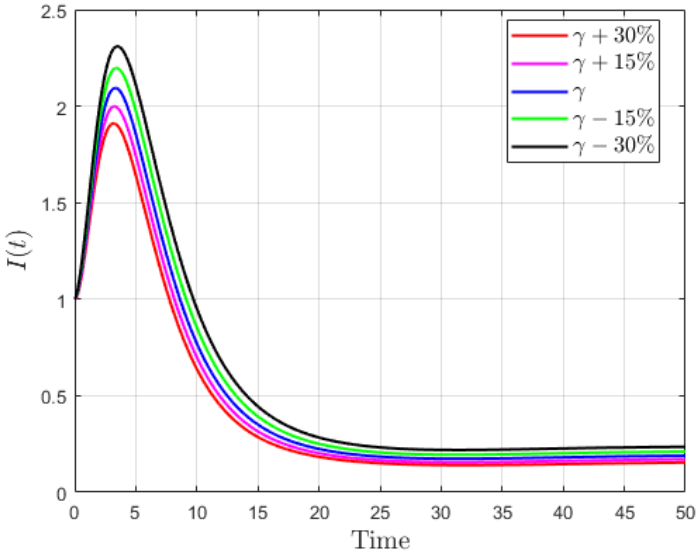

Figure 6: Effect of (γ) variation on infected population

4. Conclusion

This study presents a comprehensive parameter sensitivity analysis of a tuberculosis (TB) transmission model with incomplete treatment, based on the SEITR framework. The main scientific contribution of this work lies in the systematic application of sensitivity analysis to a TB model that explicitly incorporates treatment default, which, to the best of our knowledge, has not been sufficiently explored in previous studies. Unlike earlier research that primarily focused

on equilibrium behavior and stability properties, this study quantifies the relative influence of epidemiological and treatment-related parameters on key model outputs, thereby enhancing the practical relevance of mathematical modeling for TB control.

The sensitivity analysis reveals that the parameters η, π, and λ exert the strongest influence on the basic reproduction number (R_0), while η, π, γ, and λ are the dominant drivers of the infected population size. These results highlight the critical role of treatment adherence and effective contact reduction in shaping TB transmission dynamics. From a public health perspective, the findings suggest that interventions should prioritize reducing the effective contact rate (λ) through early diagnosis, isolation of infectious individuals, improved ventilation in high-risk environments, and consistent mask usage. In addition, strengthening treatment programs to minimize treatment default (π) through patient education, digital adherence monitoring, and community-based supervision can substantially reduce disease persistence. Improving treatment rates (γ) by ensuring timely access to healthcare services and sufficient medical resources is also essential for accelerating recovery and interrupting transmission.

Despite these contributions, this study has several limitations. The model relies on parameter values obtained from secondary sources and assumptions, which may not fully capture the heterogeneity of real-world TB transmission. Moreover, the model does not account for important factors such as HIV co-infection, drug resistance, socioeconomic conditions, or spatial heterogeneity, all of which are known to significantly affect TB epidemiology.

Future research can extend this work in several directions. More accurate parameter estimation can be achieved through primary data collection and advanced statistical inference techniques. The model may also be expanded to incorporate additional epidemiological features such as HIV-TB co-infection, multidrug-resistant TB, and healthcare system capacity. Furthermore, spatial modeling and cost-effectiveness analysis of intervention strategies could provide deeper insights into regional TB patterns and support evidence-based resource allocation. These extensions would enhance the realism of the model and further strengthen its applicability as a decision-support tool for TB control policies.

CRediT Authorship Contribution Statement

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

During the preparation of this work the authors used Generative AI in order to enhance language clarity and readability, ensuring cautious and careful application. After using this tool/service, the authors reviewed and edited the content as needed and takes full responsibility for the content of the publication.

Declaration of Competing Interest

The authors declare no competing interests.

Funding and Acknowledgments

This research received no external funding.

Data and Code Availability

Data and code sharing are not applicable.

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