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OPTIMIZING TUBERCULOSIS DYNAMICS THROUGH A COMPARATIVE EVALUATION OF MATHEMATICAL MODELS

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Abstract. Tuberculosis (TB) remains a major public health challenge, requiring precise mathematical modeling to enhance understanding and inform control strategies. Analyzing the dynamics of TB involves studying key model parameters to improve accuracy. This study evaluates six TB models using statistical criteria, including the Sum of Squared Errors (SSE), Akaike Information Criterion (AIC), corrected AIC (AICc), Bayesian Information Criterion (BIC), the difference in AIC (ΔAIC), and Akaike weight. The results show that proposed model 2 outperforms the others, achieving the lowest AIC, AICc, and BIC values while having the highest Akaike weight. These findings underscore the importance of selecting an optimal model for TB dynamics to ensure reliable predictions and effective policymaking.

Keywords: Akaike information criterion; Bayesian information criterion; Δ Akaike information criterion; Akaike weight.

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1. INTRODUCTION

Every year millions of people are infected with tuberculosis (TB), and TB remains one of the leading infectious diseases in the world [1]. Mathematical models are widely used to understand the transmission process of TB and suggest control steps for TB in reality. These models play a crucial role in assessing important quantities, such as the basic reproduction number ($\mathscr{R}_0$), rates of transmission, and the effectiveness of control measures like immunization and therapy [2]. By incorporating real-world data, these models can predict future outbreaks, evaluate public health policies, and guide government in formulating effective TB control strategies. Deterministic and stochastic models help provide a detailed representation of TB dynamics, accounting for both latent infection and active disease phases.

In real-world applications, TB models are tailored to specific populations by incorporating demographic patterns, healthcare accessibility, and socioeconomic factors [2]. To address the challenges of high TB-burden areas like South Asia and Sub-Saharan Africa, models integrate HIV co-infection, drug resistance, and diagnostic delays [3]. The evaluation of intervention strategies, including DOTS, preventive treatments, and vaccination efforts, heavily relies on mathematical models. Bayesian inference and maximum likelihood estimation refine parameter estimation by calibrating models to observed epidemiological data, leading to more precise and trustworthy predictions. A major challenge in real-world TB modeling is ensuring sufficient and reliable data availability [4]. Models may not predict correctly due to lack of comprehensive and reliable health records in high TB-prevalence areas. Researchers can resolve this issue with the help of sensitivity analysis. Sensitivity analysis tells us the impact of each parameter on the model outcomes. In addition, TB models integrate seasonality, migration patterns, and socioeconomic dynamics to better capture real-world transmission trends. Machine learning and increased computational capacity improve TB modeling by integrating extensive data and boosting prediction reliability. Ultimately, TB models serve as valuable decision-making tools for governments and health organizations. By simulating different intervention scenarios, these models help allocate resources effectively, prioritize high-risk groups, and develop targeted policies. For example, models have shown that combining active case detection with preventive

therapy can significantly reduce TB incidence over time. The emergence of new treatments and vaccines will ensure that these models play a key role in advancing TB eradication efforts and improving public health worldwide [5].

Model selection is not uphill task now one can use statistical techniques such as AIC, AICc, BIC, ΔAIC, and Akaike weight. These techniques help us to identify the best model for future predictions. Not only complexity of the model is considered for model selection but also goodness of fit [6]. Using these measures, we can determine which model provides the best explanation for the observed data without overfitting. We have examined six mathematical models for TB. Each model is formulated using system of nonlinear ordinary differential equations. Every model reflects the real picture of TB transmission process. No only these models give importance to role of proper treatment, rate of recovery, contact rate but also short and long latent period. The variations among these models help us to understand the complexities of TB transmission and progression. Therefore, it is necessary to compare the models to understand which model is most suitable for understanding the TB dynamics. One of the most commonly used criteria for the best model selection is AIC. By considering the complexity of the model, AIC tells us how well a model fits the data. AIC value indicates a better fit among the different models. The model having lowest AIC is considered as the best among the other models. However, if the sample size is small, then AIC may be biased and AICc should be used. The term AICc indicates the correction for small sample sizes [7]. Information entropy is the main principle for AIC whereas Bayesian probability is the main principle for BIC. The term BIC is used when the number of parameters is fewer. The comparison between AIC and BIC can provide insights into whether model complexity is justified by improvements in fit [8]. The term ΔAIC, calculated as the difference between a given model's AIC and the lowest AIC value among all models, helps in ranking models. Models with ΔAIC values close to zero are considered the best-fitting models, while those with higher ΔAIC values are less supported by the data [9]. This measure aids in understanding the relative performance of each TB model. Akaike weight, derived from AIC values, quantifies the relative likelihood of each model being the best among the set of models considered. It provides a probabilistic interpretation, indicating how much confidence can be placed in a particular model relative to others [10]. By

computing Akaike weights, researchers can objectively compare and interpret the effectiveness of different TB models.

Our aim is to determine which model is best for forecasting TB dynamics. Therefore, six models are selected in this paper. Each model is fitted using real clinical data of Pakistan from WHO [3]. Furthermore AIC, AICc, BIC, ΔAIC, and Akaike weights will be computed for all models. By employing a comparative approach, this study ensures that the selected model is statistically reliable and epidemiologically significant. The results will contribute to refining TB modeling strategies and informing better disease control measures.

2. Material and Methods

TB modeling generally employs a compartmental structure, dividing the population according to disease stages. A widely used approach is the SEIR model, which is modified to reflect the unique aspects of TB transmission and progression [11]. TB differs from many infectious diseases due to its latent stage, during which infected individuals are not yet capable of spreading the disease. Consequently, TB models typically feature compartments like susceptible (S), latent (E), infectious (I), and recovered (R). Certain models also refine this structure by distinguishing between early and late latent stages or between drug-sensitive and drug-resistant TB cases. The spread of TB is mathematically modeled using differential equations, which describe transitions between different disease states. These equations generally incorporate terms representing infection, disease progression, recovery, and the impact of interventions. In TB models, new infections are typically represented by the term βSI, with β as the transmission rate. The latent-to-active progression is controlled by σ, and recovery via treatment occurs at a rate γ. Moreover, TB models often account for reinfection, as individuals who have recovered can become susceptible again. To enhance realism, birth and death rates are also included to capture long-term population dynamics [12].

To incorporate control measures, TB models can be extended with the addition of vaccination, treatment and isolation. A classical example would be the case study for the introduction of Bacillus Calmette-Guérin vaccine (BCG) that alters the susceptible compartment by introducing a population group at a lower susceptibility level. In TB models, treatment interventions are included with compartments for treated individuals and consideration of the emergence of

drug resistance [13]. TB models are often updated to more accurately reflect real world dynamics by including heterogeneity of transmission into the model to capture heterogeneity in aspects such as age, demographics, comorbidities (for example HIV-TB co-infection), and spatial effects. The emergence of new therapies and vaccines will drive the evolution of TB models, incorporating genomic, behavioral, and environmental data to refine their predictions. With this strategy, mathematical modeling continues to play a crucial role in the international effort to combat and eradicate the TB [14]. In this study, a selection of six different models, proposed for comprehension of TB dynamics, is made. The discussion of these models is presented below:

Model 1 (M1): A TB model based upon six epidemiological compartments including susceptible $S(t)$, vaccinated $V(t)$, latent class $L(t)$, active TB $I(t)$, treated class $T(t)$ and recovered class $R(t)$ is introduced in [15]. The model is represented by the following nonlinear system of ordinary differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= \phi + \rho V - \xi SJ - (\tau + \mu)S, \\
\frac{dV}{dt} &= \tau S - \xi(1-\beta)VJ - (\rho + \mu)V, \\
\frac{dL}{dt} &= \xi SJ + \xi(1-\beta)VJ + (1-\theta)\sigma T - (\varepsilon + \mu)L, \\
\frac{dI}{dt} &= \varepsilon L + \theta\sigma T - (\mu + \delta + \omega)I, \\
\frac{dT}{dt} &= \omega I - (\mu + \gamma + \sigma)T, \\
\frac{dR}{dt} &= \gamma T - \mu R.
\end{aligned} \tag{1}$$

The biological parameters and their description are given in Table 1. Furthermore, parameters fitted in the model are (1) are $\tau, \rho, \xi, \beta, \delta, \varepsilon, \theta, \sigma, \gamma$ and ω.

TABLE 1. Biological parameters and their descriptions for the model given in (1).

Parameter	Description
ϕ	Recruitment rate of individuals into the susceptible population
τ	Vaccination rate
ρ	Vaccine waning rate
ξ	Transmission rate
β	Vaccine effectiveness
μ	Natural mortality rate
δ	Mortality rate due to disease
ε	Progression rate from latent TB to active TB
θ	Probability of treatment failure
σ	Transfer rate of individuals into the treated class
γ	Recovery rate of treated individuals
ω	Treatment rate for individuals with active TB

Model 2 (M2): A nonlinear 5 by 5 system of ordinary differential equations is generated with the help of transmission dynamics of TB in [16]. The number of compartments in which the total population is classified are: susceptible $S(t)$, vaccinated $V(t)$, exposed $E(t)$, infected $I(t)$, and recovered $R(t)$. The model is shown below:

$$
\begin{aligned}
\frac{dS}{dt} &= \Lambda + \theta V - \zeta S - \beta SI - \mu S,\\
\frac{dV}{dt} &= \zeta S - \omega\beta VI - \theta V - \mu V,\\
\frac{dE}{dt} &= \beta SI + \omega\beta VI - p\beta EI - (k+\mu)E + \sigma\beta IR,\\
\frac{dI}{dt} &= p\beta EI + kE - (\mu+\tau+\delta)I,\\
\frac{dR}{dt} &= \tau I - \sigma\beta IR - \mu R.
\end{aligned}
\tag{2}
$$

The biological parameters and their description are given in Table 2. Furthermore, parameters fitted in the model are (2) are $\omega, \theta, \zeta, \delta, \beta, \sigma, \kappa, \tau$ and p.

TABLE 2. Description of parameters used in the TB model (2).

Parameter	**Description**
Λ	Recruitment of individuals through birth or immigration
ω	Reduction in infection risk due to vaccination
θ	Rate at which vaccine immunity wanes
ζ	Vaccination rate of susceptible individuals
μ	Natural mortality rate
δ	TB-induced mortality rate
β	Transmission rate of infection
σ	Rate of reinfection among treated individuals
κ	Rate of progression from latent to active TB
τ	Recovery rate from TB
p	Rate of exogenous reinfection

Model 3 (M3): Another TB model has been proposed in [17] that captures the essential dynamics of TB transmission, considering vaccination, progression, recovery, and reinfection. The nonlinear system of ordinary differential equations is given by:

$$
\begin{aligned}
\frac{dS}{dt} &= \Pi - \kappa_1 \frac{SI}{N} - \kappa_2 \frac{SW}{N} - (\mu + \alpha)S + \theta V, \\
\frac{dV}{dt} &= \alpha S - \mu V - \theta V, \\
\frac{dE}{dt} &= \kappa_1 \frac{SI}{N} + \kappa_2 \frac{SW}{N} - (\mu + \beta + r_1)E, \\
\frac{dI}{dt} &= \beta E + \phi R - (\mu + d + \tau + r_2)I, \\
\frac{dT}{dt} &= \tau I - (r_3 + d + \mu)T, \\
\frac{dR}{dt} &= r_1 E + r_2 I + r_3 T - (\phi + \mu)R, \\
\frac{dW}{dt} &= \psi I - bW.
\end{aligned} \tag{3}
$$

The biological parameters and their description are given in Table 3. Furthermore, parameters fitted in the model are (3) are κ_1, κ_2, α, θ, β, r_1, ϕ, d, τ, r_2, r_3, ψ and b.

TABLE 3. Description of parameters used in the TB model (3).

Parameter	Description
Π	Recruitment rate of individuals through birth or immigration
κ_1	Infection rate due to direct contact with infected individuals
κ_2	Infection rate due to indirect exposure from the environment
α	Vaccination rate of susceptible individuals
θ	Vaccine waning rate
μ	Natural death rate
β	Transmission rate of infection
r_1	Recovery rate of exposed individuals
r_2	Recovery rate of infected individuals
r_3	Recovery rate of treated individuals
τ	Treatment rate of infected individuals
d	Disease-induced death rate
ϕ	Reinfection rate of recovered individuals
ψ	Shedding rate of the virus from infected individuals
b	Clearance rate of pathogens in the environment

Model 4 (M4): Based on the compartmental model description and the assumptions, a TB model has been proposed in [18] which is a system of six coupled nonlinear first-order ordinary differential equations as shown below:

$$
\begin{aligned}
\frac{dS}{dt} &= \Lambda - \beta SI + \theta V + \gamma R - (\tau + \mu)S, \\
\frac{dV}{dt} &= \tau S - (1-\omega)\beta VI - (\theta + \mu)V, \\
\frac{dE}{dt} &= \beta SI + \varepsilon\beta RI + (1-\omega)\beta VI - (\rho + \kappa + \mu)E, \\
\frac{dI}{dt} &= \kappa E - (\alpha + \mu + \delta)I \\
\frac{dT}{dt} &= \rho E + \alpha I - (r + \mu)T, \\
\frac{dR}{dt} &= rT - \varepsilon\beta RI - (\gamma + \mu)R.
\end{aligned}
\tag{4}
$$

The above system is a baseline model of TB transmission dynamics in the absence of targeted intervention strategies. The biological parameters and their description are given in Table 4. Furthermore, parameters fitted in the model (4) are $\beta, \kappa, r, \gamma, \varepsilon, \delta, \theta, \tau, \alpha, \omega$ and ρ.

TABLE 4. Description of parameters in the TB model (4).

Parameter	Description
μ^{-1}	Average human lifespan
Λ	Rate of new individuals entering the population
β	Rate of TB transmission
κ	Rate at which latent TB progresses to active TB
r	Recovery rate from TB
γ	Loss of immunity due to waning effects
ε	Correction factor for reinfection probability
μ	Natural death rate of individuals
δ	Death rate due to TB infection
θ	Rate of immunity loss due to vaccine waning
τ	Vaccination rate of the population
α	Rate at which active TB patients seek treatment
ω	Effectiveness of the vaccine
ρ	Rate at which latent TB patients seek treatment

Proposed Model 1 (PM1): To study TB transmission, we have proposed a mathematical model for TB. The developed model has six compartments: Susceptible $S(t)$, Slow Exposed $E_1(t)$, Fast Exposed $E_2(t)$, Infected $I(t)$, Treated $T(t)$ and Recovered $R(t)$. The resulting 6 by 6 system of nonlinear ordinary differential equations is formulated as follows:

$$
\begin{aligned}
\frac{dS}{dt} &= \lambda - \frac{c\beta_1 SI}{N} - \frac{c\beta_2 SI}{N} - \mu S,\\
\frac{dE_1}{dt} &= \frac{c\beta_1 SI}{N} + \frac{1}{2}(1-\eta_3)\delta T - (k_1+\mu)E_1,\\
\frac{dE_2}{dt} &= \frac{c\beta_2 SI}{N} + \frac{1}{2}(1-\eta_3)\delta T - (k_2+\mu)E_2,\\
\frac{dI}{dt} &= \eta_1 k_1 E_1 + \eta_2 k_2 E_2 + \eta_3 \delta T - (\gamma+\mu+\sigma_1)I,\\
\frac{dT}{dt} &= \gamma I - (\mu+\delta+\sigma_2+\alpha)T,\\
\frac{dR}{dt} &= \alpha T + (1-\eta_1)k_1 E_1 + (1-\eta_2)k_2 E_2 - \mu R,
\end{aligned}
\tag{5}
$$

with initial conditions $S(0) > 0$, $E_1(0) \geq 0$, $E_2(0) \geq 0$, $I(0) \geq 0$, $T(0) \geq 0$ and $R(0) \geq 0$. The biological parameters and their description are given in Table 5. Furthermore, parameters fitted in the model (5) are $c, \beta_1, \beta_2, \eta_1, \eta_2, k_1, k_2, \gamma, \delta$ and α.

TABLE 5. Biological interpretation of parameters in the proposed TB model (5).

Parameter	**Description**
λ	Recruitment rate
c	Contact rate between susceptible and infected individuals
β_1	The probability of leaving the compartment S and joining the slow exposed compartment
β_2	The probability of leaving the compartment S and joining the fast exposed compartment
η_1	The probability of leaving the compartment E_1 and joining the I compartment
η_2	The probability of leaving the compartment E_2 and joining the I compartment
k_1	The rate of transfer from E_1 to I
k_2	The rate of transfer from E_2 to I
γ	The rate of treatment
η_3	The failure of treatment
δ	The rate of transfer from T to I
α	The rate of recovery
μ	Natural death rate
σ_1	TB induced death
σ_2	Death during TB treatment

Proposed Model 2 (PM2): Last but not the least, another TB model has been proposed by authors of this paper. It may be noted that the manuscript consisting of this model is under consideration. In this model, there are four compartments in which total population is divided. Each compartment is non-intersecting. The associated system of nonlinear ODEs is as follows:

$$
\begin{aligned}
\frac{dS}{dt} &= \lambda - \frac{\beta SI}{N} - \mu S, \\
\frac{dE}{dt} &= \frac{\beta SI}{N} - (\mu + k)E, \\
\frac{dI}{dt} &= \eta kE - (\alpha + z)I - (\mu + \sigma)I, \\
\frac{dR}{dt} &= (1-\eta)kE + (\alpha + z)I - \mu R,
\end{aligned} \tag{6}
$$

The biological parameters and their description are given in Table 6. Furthermore, parameters fitted in the model (6) are $\beta, \alpha, \eta, k, \sigma$ and z.

TABLE 6. Parameters describing the biological mechanism in the model (6).

Parameter	Description
λ	Recruitment rate
β	Contact rate between susceptible and infected
α	Progression from I to R
η	Probability that E will join I
k	Progression from E to I
μ	Natural death rate
σ	Death rate in I due to TB
z	Rate of therapy

3. MODEL SELECTION CRITERIA

In this section, our aim is to discuss the model selection criteria. There are six TB models studied for the model selection using different statistical measures. These statistical techniques are Akaike Information Criterion (AIC), the corrected Akaike Information Criterion (AICc), the Bayesian Information Criterion (BIC), the difference in AIC (ΔAIC), and Akaike weight. These criteria assist in selecting the most suitable model by balancing goodness-of-fit with complexity, preventing overfitting.

3.1. Akaike Information Criterion. The Akaike Information Criterion (AIC) is a key statistical measure used to compare models by considering both fit and complexity. It is mathematically defined as:

$$AIC = -2\ln L + 2k, \tag{7}$$

where

- L is the likelihood function of the model, given the data,
- k is the number of estimated parameters in the model.

A smaller AIC value suggests a more suitable model, balancing fit and complexity. The penalty term $2k$ mitigates over-fitting by imposing a cost on excessive parameters.

3.2. Corrected Akaike Information Criterion. When AIC is biased as sample size is small, then corrected Akaike Information Criterion (AICc) is used. The AICc adjusts AIC by adding a correction term. The associated formula is as follows:

$$AICc = AIC + \frac{2k(k+1)}{n-k-1}, \tag{8}$$

where

- n is the sample size,
- k is the number of parameters.

As the sample size n increases, AICc approaches AIC. However, for smaller datasets, AICc offers a more accurate estimate by applying a stricter penalty on models with numerous parameters.

3.3. Bayesian Information Criterion. Derived from Bayesian probability principles, the Bayesian Information Criterion (BIC) provides a framework for model selection. It is expressed as:

$$BIC = -2\ln(L) + k\ln(n), \tag{9}$$

where

- L is the *likelihood function*,
- k is the *number of parameters*,
- n is the *sample size*.

Unlike AIC, BIC imposes a stronger penalty on models with more parameters as it includes the $\ln(n)$ term, making it more conservative in selecting complex models.

3.4. Difference in AIC. The relative performance of models is assessed using ΔAIC, which is computed as:

$$\Delta_i = AIC_i - AIC_{\min}, \tag{10}$$

where

- AIC_i is the AIC of model i,
- $AIC_{\min}$ is the lowest AIC value among all models.

Models with $\Delta\text{AIC} \leq 2$ are considered highly competitive, while models with $\Delta\text{AIC} \geq 10$ have considerably less support.

3.5. Akaike Weight. To compare model probabilities, the Akaike weight for model i is given by:

$$w_i = \frac{e^{-\Delta_i/2}}{\sum_{j=1}^{J} e^{-\Delta_j/2}}, \tag{11}$$

where

- w_i is the Akaike weight for model i, representing its relative likelihood.
- e is the base of the natural logarithm (≈ 2.718).
- Δ_i is the ΔAIC for model i.
- J is the total number of candidate models.
- $\sum_{j=1}^{J} e^{-\Delta_j/2}$ is the normalization factor ensuring that all Akaike weights sum to 1.

Akaike weight provides the probability that a given model is the best among a set of competing models.

4. Interpretation of Model Selection Criteria

AIC and AICc favor models that balance goodness of fit and complexity, with AICc being preferred for small sample sizes due to its additional correction. BIC, on the other hand, imposes a stronger penalty on model complexity, making it more conservative in selecting simpler models as the sample size increases. The ΔAIC value helps assess how much worse a model

is compared to the best model, providing a relative measure of model performance. Akaike weights assign probabilities to each model and the model with the highest weight is considered to be the best model and can be used for future prediction. It should be noted that the model should have at least 90% weight to be considered for future prediction. Furthermore, if no model has weight 90% then sum of models will be considered for model's selection.

In this study, we compare the models based on these criteria to determine the most suitable TB model for the data set. Table 7 presents the statistical comparison of six different models based on various criteria, including the SSE, k, AIC, AICc, BIC, ΔAIC, and w_i. These criteria help to determine the model that best fits the data while balancing complexity and goodness of fit. Lower values of AIC, AICc, and BIC indicate a better model, whereas Akaike weight represents the probability of a model being the most appropriate among the compared models. Analyzing the results, we notice that **PM1**, **M1**, **M2** and **PM2** have significantly lower SSE, suggesting they provide a closer fit to the data. Furthermore, the proposed model **(PM1)** has the lowest SSE compared to other models. SSE measures the difference between the observed and predicted values, with a lower value indicating a better accuracy. While **M3** has the highest number of parameters ($k = 14$), its AIC (131.75) and BIC (341.75) values indicate that it is not optimal in terms of model selection criteria.

In Table 7 and Figure 1, (plot A & B), it is emphasized that **PM2** outperforms all other models with the lowest AIC (107.78) and AICc (120.23), indicating that it provides the best trade-off between model complexity and fit. AICc, which adjusts AIC for small sample sizes, shows a significant difference between **PM2** and the other models. The BIC values in Table 7 and Figure 2, (plot A), also follow the same trend, further confirming that **PM2** is the best among the six models. Lower BIC values reinforce the idea that this model is the most efficient when penalizing for complexity. Based on the difference in AIC (ΔAIC) in Table 7 and Figure 2, (plot B), models **PM2** and **PM1** have the strongest support among the candidate models. A smaller ΔAIC indicates that these models provide the best balance between fit and complexity. Models with higher ΔAIC values are less likely to be the best choice. Therefore, **PM2** and **PM1** emerge as the most plausible models based on AIC comparison. The Akaike weight (w_i) in Table 7 and Figure 3, further supports this conclusion, with **PM2** achieving a value of 0.94504, which

means it has a 94.504% probability of being the best model among the six. In contrast, the second-best model is **PM1** having a weight of only 0.018935. This emphasizes that **PM2** is the most suitable model in terms of model selection in this research study. Model **PM2** stands out as the most suitable option, as it optimally balances accuracy and complexity. With the lowest selection criteria values and the highest Akaike weight, it proves to be the most reliable model for practical applications.

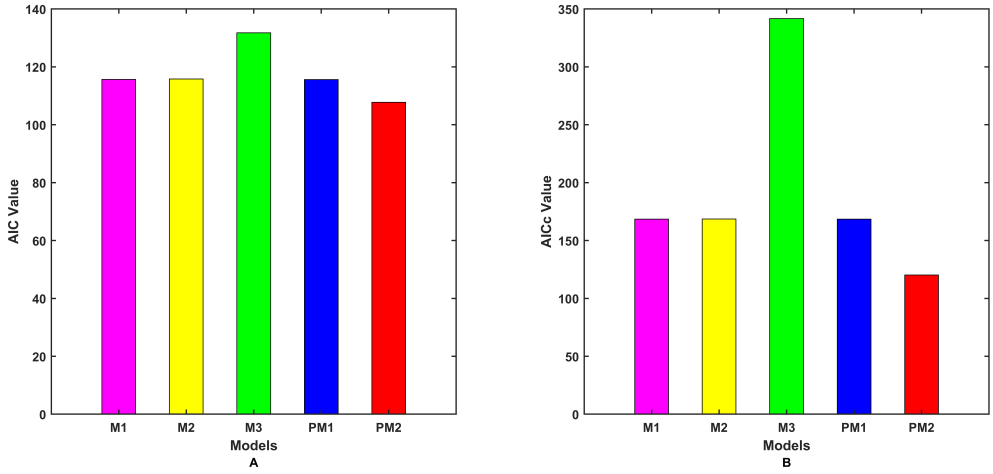

FIGURE 1. AIC and AICc values of every model under consideration.

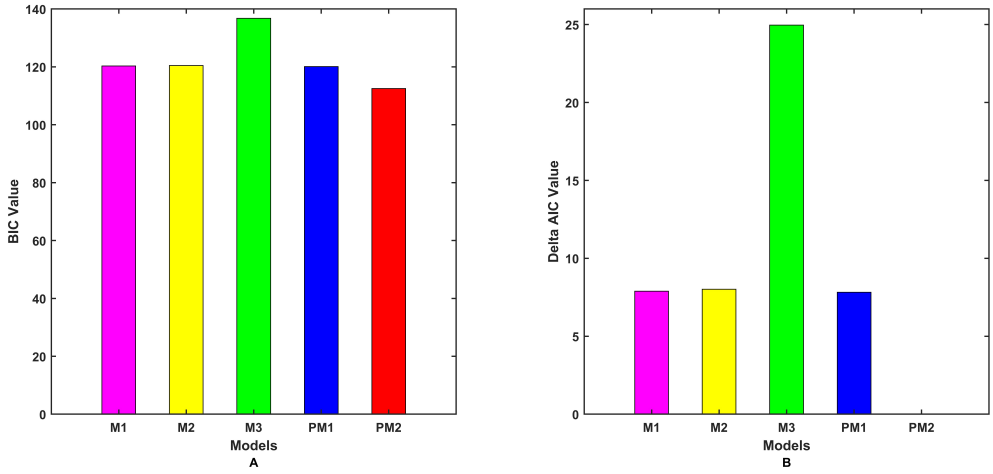

FIGURE 2. BIC and Delta AIC values of every model under consideration.

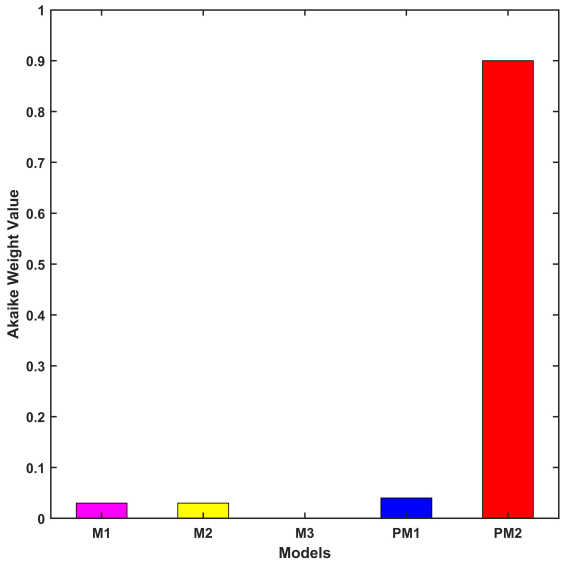

FIGURE 3. Akaike weight values of every model under consideration.

TABLE 7. Statistical evaluation of six models based on different selection metrics.

Model	SSE	k	AIC	AICc	BIC	ΔAIC	Akaike weight
Model 1	4201.1363	11	115.67	168.47	124.83	7.89	0.018326
Model 2	4232.9452	10	115.8	168.6	124.96	8.014	0.017188
Model 3	7604.1123	14	131.75	341.75	143.42	23.97	5.887e-06
Model 4	5703.5561	12	122.87	200.87	132.86	15.08	5.0136e-04
Proposed Model 1	4185.0178	11	115.6	168.4	124.77	7.82	0.018935
Proposed Model 2	4229.4494	7	107.78	120.23	113.61	0.0000	0.94504

5. CONCLUSION AND FUTURE REMARKS

In conclusion, this study compared six mathematical epidemiological TB models, revealing that **PM2** is the most suitable one, as indicated by its lowest AIC (107.78), AICc (120.23), and BIC (113.61) values. The Akaike weight further supports this conclusion, assigning a

94.504% probability to its suitability. While **PM1** and **M1** also demonstrated relatively good performance, their higher selection criteria values suggest they are less optimal. These findings underscore the importance of balancing the complexity and accuracy of the model in epidemiological modeling. Future research could improve this work by incorporating factors such as seasonality, intervention strategies, or stochastic effects to improve the reliability of the model and its application in TB control policies.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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