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Estimating the Effective Reproduction Number of Tuberculosis in a Branching Process

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Abstract

Background:
Tuberculosis (TB) remains a major public health challenge in Iran, particularly in border provinces such as Sistan and Baluchestan, where cross-border migration from high TB-burden countries exacerbates transmission dynamics. Accurate estimation of the effective reproduction number (R_t) is crucial for monitoring the epidemic and guiding control strategies, especially in settings with high population mobility.

Methods:
This study employed a branching process model incorporating migration to estimate the Effective Reproduction Number (R_t) of smear-positive pulmonary tuberculosis (SPPTB) in Sistan and Baluchestan Province from March 2011 to March 2022. A Bayesian framework was used to account for uncertainty and integrate prior epidemiological knowledge. Surveillance data from 7.237 registered SPPTB cases were analyzed. The EpiEstim package in R was utilized for dynamic estimation of R_t while descriptive statistics were computed for baseline characteristics and transmission parameters.

Results:
The mean age of patients was 53.24 $\pm$ 21.10 years, and 51.6% were male. Afghan nationals accounted for 33.7% of primary cases, contributing to 32.5% of secondary infections. The estimated mean R_t was 1.10 (95% CrI: 0.93 -1.27), indicating sustained transmission. The mean values for immigration and offspring components were 1.22 and 1.07, respectively, highlighting the influence of migration on local transmission. Fluctuations in R_t over time reflected both internal and imported sources of infection.

Conclusion:
The elevated R_t and the significant contribution of migration emphasize the need for targeted TB control strategies in Sistan and Baluchestan. Cross-border coordination, routine TB screening among migrants, and tailored interventions are critical for reducing transmission. The Bayesian branching process model with immigration offers a robust and context-sensitive tool for epidemic monitoring in high-mobility, high-burden regions.

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Mathematics Subject Classification (2020): xxAxx, xxBxx, xxCxx.

1 Introduction

Tuberculosis (TB) remains a leading cause of morbidity and mortality globally, particularly in regions burdened by poverty, migration, and limited access to healthcare services. Despite progress in TB control, border provinces like Sistan and Baluchestan (S&B) in southeastern Iran continue to face high transmission rates due to socio-economic vulnerabilities and close proximity to high-burden countries such as Afghanistan and Pakistan Rastegar *et al.* (2024). These neighboring countries contribute significantly to cross-border TB transmission, especially in the context of drug-resistant strains and irregular migration patterns Stop T. Partnership (2022).

In such complex epidemiological contexts, the effective reproduction number (R_t) is a critical indicator for understanding disease transmissibility. It reflects the average number of secondary infections caused by an infected individual over time in a partially susceptible population Huisman *et al.* (2022). Accurate and timely estimation of R_t is vital for assessing the impact of interventions and predicting outbreak trajectories. However, traditional compartmental models (e.g., SIR) often fall short in heterogeneous and high-mobility settings like S&B, as they generally assume homogeneous mixing and closed populations (Kucharski et al., 2020).

To address these limitations, this study utilizes a branching process model with immigration, a stochastic modeling framework particularly well-suited for capturing the randomness and heterogeneity of transmission events, especially in regions with frequent population movement. To enhance inference under uncertainty, a Bayesian approach is employed, allowing for integration of prior knowledge and generating credible intervals for parameters such as R_t. Bayesian models are increasingly favored in real-time epidemic analysis due to their flexibility and ability to incorporate uncertainty in reporting, serial interval (SI) distributions, and parameter variability Rastegar *et al.* (2024). SI is defined as the time duration between the onset of symptoms in a primary case and the onset of symptoms in a secondary case infected by the primary one. It is a critical parameter in infectious disease modeling, as it reflects the timing of transmission events and plays a key role in estimating the effective reproduction number (R_t) Gostic *et al.* (2020). Accurate estimation of SI is particularly important for diseases like tuberculosis, where transmission can occur over variable and sometimes extended periods due to long incubation times and delayed diagnosis. In this study, the SI distribution is modeled using a Gamma distribution to capture the right-skewed nature of TB transmission intervals. Incorporating uncertainty in the SI distribution allows for more robust inference of R_t, particularly when using Bayesian frameworks.

This study proposes a Bayesian branching process model incorporating migration to estimate the effective reproduction number of TB in S&B Province using surveillance data from 2011 to 2022. By accounting for cross-border movement and population heterogeneity, this approach generates more accurate and context-sensitive estimates of R_t, providing valuable insights for targeted TB control interventions. The findings will support evidence-based decision-making in border regions and contribute to the methodological advancement of stochastic epidemic modeling in complex settings.

2 Materials and Methods

2.1 Theoretical Framework

Understanding the spread of infectious diseases like TB requires robust mathematical modeling approaches. These models range from deterministic systems that simulate population-wide trends to stochastic models that account for individual-level transmission variability. In the present study, we employed a stochastic branching process model that incorporated migration to simulate the progression and spread of TB cases. This model is particularly appropriate for diseases with variable transmission patterns and in regions affected by significant population movement.
Branching processes (PB) provide a flexible framework for modeling the generation of secondary infections by each infectious individual, accounting for random variation in transmission. Migration was modeled as a factor influencing the importation and exportation of cases between different regions, reflecting real-world population flows in and out of Sistan and Baluchestan (S&B). Bayesian estimation techniques were applied to infer the R_t, integrating prior epidemiological knowledge with observed data to improve the accuracy of inference under uncertainty. These methods have been shown to be particularly powerful in analyzing real-world epidemic data, especially when integrating social, demographic, and ecological factors Fraser (2007).

We assume that each infectious individual infects a random number of susceptible individuals distributed as a random variable ξ. Let us start with s infected individuals. All infected individuals due to contact with them are called the first generation, and let us denote their number by Z_1. Infected individuals in contact with the first generation form the second generation, with Z_2 individuals, etc. This process can be depicted as a branching process (Figure1).

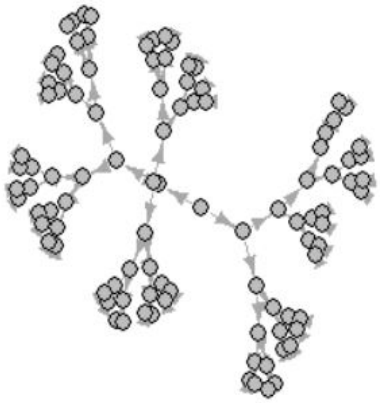


Figure 1: an example of branching process.

Let $\xi_{n,j}$ are independent and identically distributed random variables (i.i.d. r.v.) with the same distribution as ξ. The distribution of ξ is called offspring distribution, and the mean of ξ is denoted by $m = E\xi_{n,j}$. Formally, we define $[Z_n, n = 1, 2, \ldots]$ as follows:

$$
\begin{aligned}
Z_0 &= s \\
Z_1 &= \xi_{1,0} + \cdots + \xi_{s,0} \\
Z_2 &= \xi_{1,1} + \cdots + \xi_{Z_1,1} \\
&\vdots \\
Z_n &= \xi_{1,n} + \cdots + \xi_{Z_{n-1},n} = \sum_{j=1}^{Z_{n-1}} \xi_{n,j}, \quad n = 1, 2, \ldots
\end{aligned}
$$

where $\xi_{n,j}$ is the number of infected by the j-th individual of n-th generation.

The sequence of $(Z_n, n = 1, 2, \ldots)$ is called the Bienaymé–Galton–Watson process (BGWBP).

The event $\{Z_n = 0, \text{ for some } n \geq 1 \mid Z_0 = 1\}$ is called extinction. Denote the probability of extinction $q = P(Z_n = 0, \text{ for some } n \geq 1 \mid Z_0 = 1)$. From the theory of the branching process, it is known that for $m \leq 1$, $q = 1$, and for $m > 1$, $q < 1$.

If the process starts with s individuals, the probability of extinction is $\{Z_n = 0 \text{ for some } n \geq 1 \mid Z_0 = s\} = q^s$.

Depending on whether the offspring mean m is less than, equal to, or greater than 1, the process is called subcritical, critical, and supercritical, respectively.

Let us denote by Y the total progeny of BGWBP or the total number of infected individuals by the end of the outbreak. It is defined as follows:

- The generation sizes can then be written as the collection $\{Z_n; n = 1, 2, \ldots, n\}$.
- The process $\{Z_n; n \geq 0\}$ can be recursively defined using the representation

$$Y = Z_n = \sum_{j=1}^{Z_{n-1}} \xi_{n,j}, \quad n = 1, 2, \ldots \tag{1}$$

The probability distribution of $\xi_{n,j}$ for all n and j is

$$P(\xi_{n,j} = k) = p_k \qquad k \geq 0 \tag{2}$$

The sequence $\{p_k : k \geq 0\}$ is referred to as the offspring distribution.

Branching process with immigration

A useful and realistic modification of the BP is the incorporation of an immigration component into the population from an outside source. More precisely, the branching process with immigration (BPI) is defined as

$$X_t = \sum_{j=1}^{X_{t-1}} \xi_{t,j} + I_t, \qquad t = 1, 2, \ldots \tag{3}$$

where $\xi_{n,j}$ are the same as in (1), and I_n is the number of immigrants entering the n-th generation from an outside source. The random variables $I_1, I_2, \ldots$ are assumed to be independent and identically distributed (i.i.d.) and are independent of the process $\{\xi_{n,j}; j \geq 1, n \geq 1\}$.

We denote their distribution by

$$P(I_j = j) = q_j, \quad j \geq 0.$$

Let $E(I_1) = b$, $Var(I_1) = v^2$.

Bayesian estimation of the offspring means in branching processes

The Bayesian estimation method is one of the most commonly used methods developed to estimate R_t in real-time through equation (3), which relies on a branching process model. In a branching process, each infected individual can produce a random number of secondary infections, and the total number of infections at any given time is the sum of all the infections produced by each infected individual.

The branching process $\{X_t; t \geq 0\}$ was defined in (3)

Where $\xi_{t,j}$ can be interpreted as the number of new cases produced by the j^{th} infected case in the t^{th} generation. The probability distribution of $\xi_{t,j}$ for all t and j is

$$P(\xi_{t,j} = k) = p_k \qquad k \geq 0$$

The sequence $\{p_k : k \geq 0\}$ is referred to as the offspring distribution. Most often we do not have data on the number of infected ones by each infectious, but on the total number of infected individuals for a given time (X_t). The Poisson process in the branching process by assuming that the number of new cases at any given time is a random variable that follows a Poisson distribution is referred to as the offspring distribution, with the mean of this distribution being the product of R_t and the sum of the past incidence X_{t-s} of cases, weighted by w_s, the probability mass function of the generation time (the time between infection in a case and their infector). In practice, as infection is difficult to observe, the incidence of symptomatic cases can be used instead and w_s can be approximated by SI.

$$p_k = \frac{\exp(-R_t)R_t^k}{k!} \qquad k \geq 0$$

The model assumes that the incidence of new cases on day t, X_t, can be represented by a Poisson process:

$$X_t \sim \text{Pois}\left(R_t \sum_{s=1}^{t} X_{t-s} w_s\right) \tag{4}$$

In practice, as the infection is difficult to observe, the incidence of symptomatic cases can be used instead and SI can approximate w_s. Parametric models for the SI such as the Gamma, Weibull, and log-normal distributions are widely used to model infectious diseases Cowling *et al.* (2009). Compared to the other distributions, the Gamma distribution has a more flexible shape, which allows it to fit a wider range of SI distributions, including those with shorter or longer tails. The Gamma distribution is also a more natural choice when the SI is measured in discrete time units, such as days or hours, as it models the probability of observing a certain number of days between the onset of symptoms in the primary and secondary cases. The Weibull and log-normal distributions are also similar to the Gamma distribution in terms of empirical form Firth (1988). Here, we assume a Gamma distribution for the SI distribution. The estimation of the shape and scale parameters of the Gamma distribution for the SI can be achieved using the method of uncertainty on the SI distribution as described in Cori *et al.* (2020).

Following Reich *et al.* (2009), we perform Bayesian parametric estimation of the SI distribution from such data using data augmentation Markov Chain Monte Carlo (MCMC). If we use a Gamma-distributed SI distribution offset by one day, the MCMC estimation procedure leads to a joint posterior sample for the parameters of the chosen distribution, i.e., a list of possible sets of parameter values, with each parameter set corresponding to a single step in the MCMC chain. Each parameter set, i, in the posterior sample is then converted into a discrete probability mass function, $w_s(i)$. $(s = 0, 1, 2, \ldots)$ as follows: The probability of the SI lasting 0-time steps, $w_s(0)$, is set to 0 as in Cori et al. (2013), and the probability $w_s(i)$ for any other timestep $s = 1, 2, 3, \ldots$ is obtained by integrating the probability density function defined by this parameter set between $s-0.5$ and $s+0.5$. For each i, the function $w_s(i)$ is then renormalized to sum to 1. The posterior sample of SI distributions, $w_s(i)$. $(i = 1, 2, \ldots, n)$, is then used along with disease incidence time series to estimate the R_t as described in the following Cori *et al.* (2013).

As defined by Cori et al. (2013), R_t is a measure of the transmission potential of an infectious disease at a specific point in time. X_t is calculated as the ratio of the number of new infected cases at time t, denoted by I_t, and the total infection potential across all infected individuals at time t, denoted by Λ_t. If there is a single SI distribution $w_s(i)$. $(s = 1, 2, \ldots)$,

representing the probability of a secondary case arising a period s after the primary case, each incident case that appeared at a previous time step $t-s$ contributes to the current infectiousness at a relative level given by w_s Cori *et al.* (2013).

Therefore, conditional on w_s, t can be computed as

$$\Lambda_t = \sum_{s=1}^{t} X_{t-s} w_s$$

Given a SI distribution w_s, data on the total number of incident cases up to the previous time step $(X_1, X_2, \ldots, X_{t-1})$, and R_t, the expected number of incident infected cases at time t is

$$E(X_t | X_1, X_2, \ldots, X_{t-1}, w_s) = R_t \Lambda_t$$

Assuming that the number of cases at time step t is drawn from a Poisson distribution. Cori *et al.* (2020), we assume that R_t is constant over a time period $[t-\tau, t]$, with τ representing the length of the time window over which R_t is estimated. Given R_t and conditional on the previous incidence data $X_0, X_1, \ldots, X_{t-1}$, is then

$$P(X_t | X_0, X_1, \ldots, X_{t-1}, w_s, R_t) = \frac{(R_t\Lambda_t)^{X_t} \exp(-R_t\Lambda_t)}{X_t!} = \prod_{k=t-\tau}^{t} \frac{(R_t\Lambda_k)^{X_k} \exp(-R_t\Lambda_k)}{X_k!}$$

To estimate the R_t of pulmonary tuberculosis, we used the number of total infected individuals Λ_k at a given time k, with a time window of $\tau = 7$ days, and the SI distribution w_s. We employed a Gamma distribution prior and conjugated it with the Poisson likelihood to derive an analytical formulation of the posterior distribution of R_t Thompson *et al.* (2019).

Using a Bayesian framework with a Gamma-distributed prior for R_t as in Cori *et al.* (2013), the posterior distribution of R_t given past incidence data and conditional on the SI distribution, w_s, is

$$\begin{aligned}
&P(R_t \mid X_0, X_1, \ldots, X_{t-\tau}, X_{t-\tau+1}, \ldots, X_t, w_s) \\
&\propto P(X_{t-\tau}, X_{t-\tau+1}, \ldots, X_t \mid X_0, X_1, \ldots, X_{t-\tau-1}, w_s, R_t) P(R_t) \\
&= \left(\prod_{k=t-\tau}^{t} \frac{(R_t\Lambda_k)^{X_k} \exp(-R_t\Lambda_k)}{X_k!} \right) \left(\frac{R_t^{a-1} \exp\left(-\frac{R_t}{b}\right)}{\Gamma(a) b^a} \right) \\
&= R_t^{a+\sum_{k=1}^{t} X-1} \exp\left(-R_t \left(\sum_{k=t-\tau}^{t} \Lambda_k + \frac{1}{b} \right) \right) \times \prod_{k=t-\tau}^{t} \frac{(\Lambda_k)^{X_k}}{X_k!}
\end{aligned} \tag{5}$$

where a and b are the shape and scale parameters of the Gamma distributed prior to R_t. We used a Gamma-distributed prior, conjugated to the Poisson likelihood, to obtain an analytical formulation of the posterior distribution of R_t. According to the expression above, the posterior distribution for R_t given the incidence data, conditional on the SI distribution w_s, is a Gamma distribution with the shape parameter $a + \sum_{k=t-\tau}^{t} X_k$, and the scale parameter $\frac{1}{\sum_{k=t-\tau}^{t} \Lambda_k(w_s) + \frac{1}{b}}$.

To select the parameters a and b for the Gamma prior distribution of R_t, we should consider the type of branching process the data represents. If the data is from a subcritical branching process, we set the mean of the Gamma distribution to be less than one. For a critical branching process, we set the mean to equal one. We set the mean to be greater than one for a supercritical branching process. This approach ensures that the prior distribution reflects the expected behavior of the branching process based on the underlying data. To obtain a sample from the full posterior distribution for R_t given both the incidence and the SI data, we consider each possible SI distribution $w_s(i)$ $(i = 1, \ldots, n)$. For each i, we draw a sample of size m from the Gamma posterior distribution of R_t, given the incidence data and conditional on the SI distribution $w_s(i)$. We thereby obtain a sample of size $n \times m$ drawn from the posterior distribution of R_t given both the incidence and SI data, from which the posterior mean and 95% credible intervals of R_t can be computed Cori *et al.* (2013), Nishiura and Chowell (2014), McBryde *et al.* (2009), Wallinga and Lipsitch (2007).

2.2 Statistical Analysis

Descriptive statistics were computed to summarize the data, with continuous variables expressed as mean ± standard deviation (SD) and categorical variables reported as frequencies and percentages. The chi-square goodness-of-fit test was applied to evaluate distribution uniformity across qualitative variables. All statistical analyses were performed using SPSS (v22.0), R (v4.2.1), and Microsoft Excel (2014), with a significance threshold of $p < 0.05$ for hypothesis testing. For dynamic estimation of the effective reproduction number (R_t), we implemented a Bayesian inference framework, which accounts for uncertainty by integrating prior epidemiological knowledge with observed transmission data. The EpiEstim package in R was employed to model R_t over time, providing time-varying estimates of disease spread.

2.3 Study Population and Data Source

This study utilized a national historical cohort design, analyzing data from March 2011 to March 2022 obtained from the Health Deputy of Zahedan University of Medical Sciences. The dataset included 7.237 reported cases of SSPTB, diagnosed and registered across S&B province. Given their higher infectivity and public health significance, SSPTB cases were specifically selected to better assess transmission dynamics and estimate reproduction numbers (R_t).

3 Result

A total of 7.237 new smear-positive pulmonary tuberculosis patients were included in this study. The mean age of the patients was 53.24 ± 21.10 years, with a notable age distribution: 2.9% were under 15 years, 22.9% were aged 15–35, 35.3% were 36–63, and 38.9% were over 64 years. Age distribution differences were statistically significant ($P < 0.001$). The cohort comprised 51.6% males and 48.4% females, with a significant gender difference ($P < 0.001$). The majority of patients were Iranian (83.2%), while 16.8% were of other nationalities, a difference that was also statistically significant ($P < 0.001$).

Table 2 presents descriptive statistics of R_t and related parameters for pulmonary tuberculosis (PTB) in Iran from 2018 to 2022, highlighting the dynamic nature of TB transmission in Sistan and Baluchestan. The mean R_t during this period was 1.10, with a 95% credible interval of $(0.93, 1.27)$, indicating that, on average, each infectious individual caused more than one secondary case—suggesting ongoing transmission. This value, which remained above the epidemic threshold, reflects a persistent risk of disease spread. Notably, the immigration mean (b) ranged from 0.72 to 2.27, with an average of 1.22, emphasizing the significant contribution of migration to local TB dynamics. The results indicate that R_t was not solely driven by internal transmission (offspring mean of 1.07) but was also meaningfully influenced by cross-border and internal migration, which introduced new infections into the population.

Figure 2 depicts the monthly trends SSPTB incidence, R_t, and SI distribution in Sistan and Baluchestan Province from March 2011 to March 2022. The epidemic curve shows fluctuating case counts with peaks reaching 75 monthly cases and troughs near zero, indicating intermittent outbreaks superimposed on endemic transmission. R_t estimates varied between 0.0–2.0, with sustained periods above 1.0, suggesting ongoing transmission, while sharp declines likely reflected intervention impacts. The SI distribution peaked at low probabilities (0.00–0.02), consistent with rapid transmission in close-contact settings. Notably, incidence peaks correlated with R_t surges (> 1.5), revealing periodic epidemic growth phases amidst generally stable endemic transmission patterns.

Table 1: **Baseline Characteristics and Risk Factors of New Smear-Positive Pulmonary Tuberculosis Patients in S&B province (n = 7237).**

Characteristics		**New smear-positive PTB patients**	**P Value**
Age (year)	Mean±SD	53.24±21.10	–
Age (year)	<15 (n %)	211 (2.9)	<0.001*
	15–35 (n %)	1655 (22.9)	
	36–63 (n %)	2556 (35.3)	
	>64 (n %)	2815 (38.9)	
Gender	Female (n %)	3501 (48.4)	<0.001*
	Male (n %)	3736 (51.6)	
Nationality	Iranian (n %)	6022 (83.2)	<0.001*
	Others (n %)	1215 (16.8)	

* Significant at a level of 0.05

Table 2: Descriptive statistics of R_t and SI of PTB disease in Iran during 2011–2022

descriptive statistics	Mean (b) (Immigration Mean Estimation)	SD (b) (Immigration Standard deviation Estimators)	Mean (m) (Offspring Mean Estimation)	SD (m) (Offspring Standard deviation Estimation)	Mean (R_t) Total	SD (R_t) Total
Minimum	0.72	0.10	0.63	0.04	0.64	0.039
1st Quartile	0.99	0.13	0.91	0.05	0.92	0.051
Median	1.17	0.14	0.98	0.06	1.02	0.054
Mean	1.22	0.15	1.07	0.06	1.10	0.057
3rd Quartile	1.37	0.16	1.21	0.07	1.25	0.062
Maximum	2.27	0.28	2.01	0.10	2.05	0.098
95%Crl	(0.77, 1.67)		(0.89, 1.25)		(0.93, 1.27)	

* Standard deviation (SD), 95% credible interval (95% Crl).

4 Discussion:

A total of 7.237 new smear-positive pulmonary tuberculosis (SPPTB) cases were analyzed from March 2011 to March 2022 in S&B Province. Most patients were Iranian nationals (83.2%), while 16.8% were of other nationalities, predominantly Afghan. Descriptive statistics of R_t during 2018–2022 showed a mean R_t of 1.10 (SD = 0.057), with a 95% credible interval (Crl) of $(0.93, 1.27)$. The immigration mean (b) was 1.22 and offspring mean (m) was 1.07, indicating a notable contribution of immigration to transmission dynamics. The maximum estimated R_t reached 2.05, emphasizing periods of intense transmission risk. These results highlight the dual role of internal and external (migration-related) factors in maintaining TB transmission in the region.

Tuberculosis remains a significant public health concern in regions with high population mobility, such as S&B. This province, situated on Iran's southeastern border, is uniquely vulnerable due to its proximity to Afghanistan and Pakistan-countries with some of the highest TB and drug-resistant TB incidence rates globallyWorld Health Organization (2021). In the current study, 16% of SPPTB cases were Afghan nationals. This high transmission rate from migrants strongly implicates cross-border movement in sustaining TB transmission.

The elevated R_t values estimated in this study support these concerns. The mean R_t of 1.10, exceeding the threshold of 1, indicates that the epidemic is self-sustaining. The immigration mean (1.22) being higher than the offspring mean (1.07) suggests that imported cases via migration are a major driver of ongoing transmission. These findings are consistent

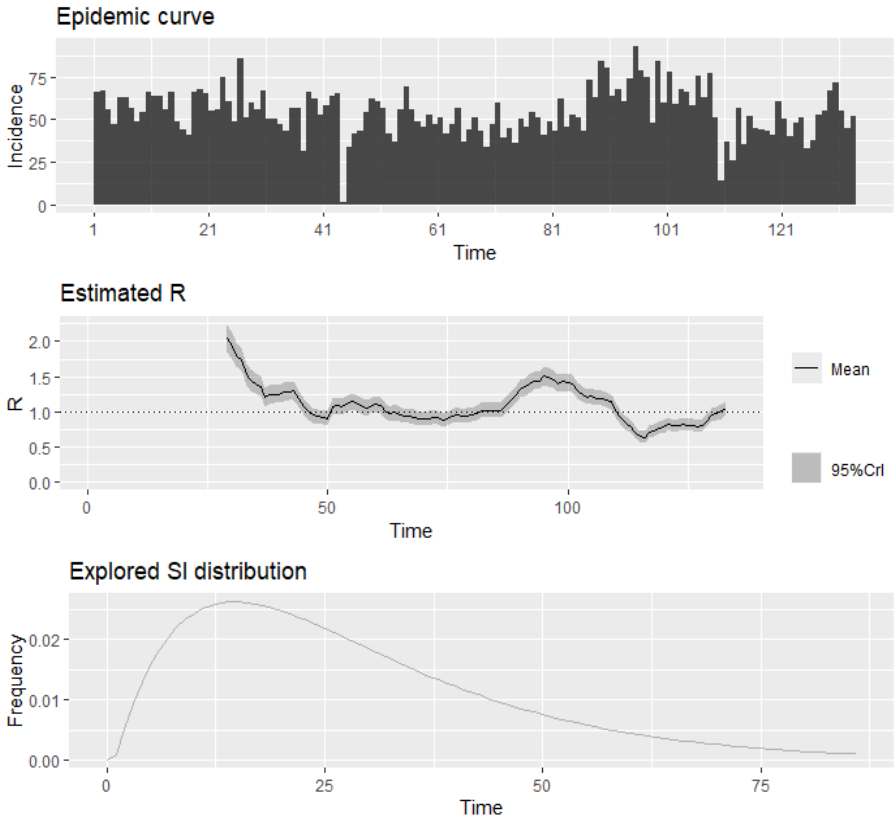


Figure 2: New cases, R_t and SI of SPPTB in SB province from March 2011 to March 2022 monthly.

with previous literature that highlights how population displacement and migration amplify the spread of infectious diseases, especially TB Kimbrough *et al.* (2012).

Bayesian estimation through branching process modeling provided robust insight into the dynamic contribution of both internal transmission and migration. The use of such probabilistic models is particularly valuable in high-mobility regions where surveillance data may be incomplete or uncertain Cori *et al.* (2017). These findings further underline the importance of integrating border health monitoring systems, routine TB screening among migrants, and culturally adapted treatment services in TB control programs.

5 Conclusion

The findings of this study underscore that the R_t of TB in Sistan and Baluchestan is influenced not only by internal community transmission but significantly by immigration from neighboring high-burden countries. The observed R_t levels above 1 highlight the need for urgent and targeted interventions. Given S&B's geographic location and socio-political context-including porous borders and high population mobility-the elevated R_t underscores the need for targeted TB control strategies that address both transmission and migration-related risks. To reduce TB transmission, especially smear-positive cases that are more infectious, Iran's national TB control strategy must include comprehensive policies addressing migrant health. These include routine screening, cross-border coordination, and ensuring access to care for undocumented populations. Addressing these factors is essential for achieving TB elimination goals in this high-risk region.

List of abbreviations

BP	Branching Process
TB	Tuberculosis
PTB	Pulmonary tuberculosis
SPPTB	Smear-positive pulmonary tuberculosis
EXTB	Extra-pulmonary tuberculosis
R_t	Effective reproduction number
SI	Serial Interval
S&B	Sistan and Baluchestan

Ethics approval and consent to participate

Informed consent was waived by the Research Ethics Committee of Mashhad University of Medical Sciences, Code: IR.MUMS.FHMPM.REC.1401.054.

Consent for publication

Not Applicable

Competing interests

The authors declare that they have no conflicts of interest.

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