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Sensitivity Analysis of the SIRD Model for TB-Related Life Insurance Claims in Southeast Sulawesi

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Abstract

Tuberculosis (TB) remains a major public health challenge in Indonesia and generates significant mortality-related risk for the life insurance sector. This study develops an integrated Susceptible–Infected–Recovered–Deceased (SIRD) model to analyze TB transmission dynamics in Southeast Sulawesi and to estimate related life insurance claims. The model is calibrated using regional TB data from 2021–2023 and validated against 2024 observations. Analytical results include equilibrium analysis and the basic reproduction number, while long-term dynamics are examined through scenario-based simulations. Epidemiological outcomes are translated into actuarial projections by converting cumulative TB-related deaths into annual incremental deaths and expected insurance claims under optimistic, baseline, and pessimistic scenarios. Parameter sensitivity is assessed using Latin Hypercube Sampling and Partial Rank Correlation Coefficients. The results show that the transmission rate is the most influential determinant of the present value of TB-related insurance claims, followed by the recovery rate, whereas TB-induced mortality has a smaller but significant effect. These findings highlight that reducing transmission and improving treatment effectiveness can simultaneously mitigate public health impacts and lower long-term insurance liabilities, demonstrating the relevance of integrating epidemiological modeling with actuarial risk assessment.

Keywords: Life Insurance Claims, Numerical Simulation, Sensitivity Analysis, SIRD Model, Tuberculosis.

1 Introduction

Tuberculosis (TB) is an infectious disease caused by Mycobacterium tuberculosis and transmitted through the air. A single cough or sneeze from a TB patient can release approximately 3,000 germs into the air [1]. Tuberculosis remains one of the deadliest infectious diseases in the world. According to the Global Tuberculosis Report 2023 [2] released by the World Health Organization (WHO), Indonesia ranks second in the number of TB cases after India, with over 1 million new cases and approximately 136,000 deaths each year [3].

In Southeast Sulawesi, surveys from the past three years show that the number of TB cases continues to increase [4]. Additionally, TB patients with non-communicable comorbidities, such as diabetes and heart disease, have a prevalence of up to 11.81% [5] and are more likely to utilize inpatient services. This condition makes TB not only a public health problem but also an economic burden, including for the health and life insurance industry.

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In this context, the SIRD (Susceptible–Infected–Recovered–Deceased) mathematical model is relevant for describing the dynamics of TB spread and estimating the number of deaths [6], making it useful for projecting potential life insurance claims.

Although tuberculosis exhibits a latent phase, the use of a SIRD model without an explicit latent compartment remains appropriate at the population level. The limited empirical data on the number of individuals in the latent or exposed phase is also an important consideration, as this variable is rarely fully available in local health reports, making a model without a latent compartment more realistic to implement with the existing actual data. Previous studies on COVID-19 [7] [8] and TB-HIV [9] dynamics have shown that simplified SIRD-type models can produce reliable epidemic projections when parameters are properly calibrated. In line with this, Sirait et al. (2023) emphasize that SIR-type compartmental models remain widely used due to their simplicity, stability, and ease of integration with economic and actuarial frameworks. Since this study focuses on the cumulative death compartment as a proxy for tuberculosis-related mortality risk in life insurance applications, the SIRD framework provides a parsimonious and practically relevant modeling approach.

Research on mathematical modeling of infectious diseases has been developing for a long time since it was introduced by Kermack and McKendrick in 1927 [10]. Basic models like SIR and SEIR are used to predict disease dynamics by dividing the population into compartments based on infection status. As it developed, this model was modified by adding compartments and parameters, such as Vaccinated [11], [12], [13], [14], Deceased [15], [16], [17], and time delay [18], [19]. On the other hand, several studies have conducted sensitivity analyses of parameters [20], [21], [22], [23], research on life insurance projections [24], [25], [26], and the integration of epidemiological models into actuarial science [27], [28], [29]. However, research specifically linking infectious disease spread models with projections of life insurance claims in Indonesia is still very limited, particularly for tuberculosis cases.

This research combines the analysis of TB epidemic dynamics with life insurance claim projections within an integrated SIRD model framework. Unlike previous studies that generally only highlighted either the spread of disease or financial calculations separately, this research combines both to provide a more comprehensive picture of the epidemic's impact. Additionally, a sensitivity analysis was conducted on epidemiological parameters to identify the factors most influential on the size of insurance claims so that the results could serve as a basis for decision-making in the healthcare and insurance industries. Through this approach, this research presents novelty by developing an SIRD model that not only describes the dynamics of tuberculosis but also directly links it to the estimation of financial risk due to the death of the insured.

The content of this paper is organized as follows: Section 2 describes the methodology, including model construction, simulation scenarios, and sensitivity analysis. Section 3 presents the results and discussion, emphasizing model validation, projections for life insurance claims based on data, and parameter sensitivity analysis. Finally, Section 4 provides conclusions and outlines key policy implications.

2 Methods

This study employs a theoretical-computational approach by constructing an SIRD (Susceptible–Infected–Recovered–Deceased) mathematical model to simulate the dynamics of tuberculosis spread in Southeast Sulawesi and its implications for life insurance claims.

The SIRD model is formulated as a system of differential equations with four main compartments (S, I, R, D). The analysis was conducted by calculating the basic reproduction number (R0) using the next generation matrix method [30] and by analysing the stability of the equilibrium points using the Routh-Hurwitz criterion [31]. Model validation was performed by comparing simulation results using initial value data from 2023 with actual case data from 2024.

All simulations and sensitivity analyses were performed in Python 3.12 using standard

scientific libraries, under three epidemiological scenarios (optimistic, baseline, and pessimistic). Sensitivity analysis was conducted employing the Latin Hypercube Sampling (LHS) method and the Partial Rank Correlation Coefficient (PRCC) [32] using the SciPy.stats package. The analytical findings are used to determine the most significant factors for claim forecasts, thereby establishing a foundation for policy suggestions in the health and life insurance sectors.

3 Results and Discussion

This section presents the key results and their interpretation in relation to the study objectives. The discussion begins with the construction and analysis of the SIRD model, including equilibrium and stability properties. It then proceeds to simulation results, scenario-based projections, and sensitivity analysis. Comparisons with observed data are provided to validate the model, while scenario analysis illustrates the range of potential epidemiological and financial outcomes. Overall, the results demonstrate how variations in TB transmission dynamics directly affect projected life insurance claims and highlight the critical role of parameter sensitivity in risk evaluation.

3.1 Model Construction

This study extends the classical SIR model for infectious disease transmission into an SIRD model specifically formulated for tuberculosis (TB) [1]. The population is divided into four mutually exclusive compartments: Susceptible (S), Infected (I), Recovered (R), and Deceased (D). The total population is denoted by $N = S + I + R + D$, with each compartment expressed as a proportion of the total population.

It is assumed that susceptible individuals become infected through contact with infectious individuals, infected individuals can either recover or die from TB, and natural deaths occur uniformly across all living compartments. Births are included at a constant rate μ, maintaining population balance. The deceased compartment $D(t)$ represents the cumulative number of TB-related deaths and does not feed back into the other compartments.

The compartmental flow is illustrated in Fig. 1, and the description of all variables and parameters is summarized in Table 1.

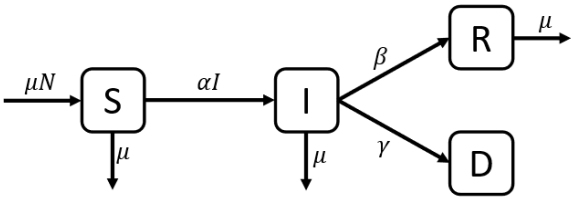

Figure 1: Compartmental diagram for the transmission dynamics of TB.

This model partitions the compartment into four sections. Susceptible individuals (S) may be infected with tuberculosis. Infected individuals (I) are those afflicted with tuberculosis. Recovered individuals (R) are those who have successfully overcome TB. Individuals who have succumbed to tuberculosis are classified under category D. Fig. 1 and Table 1 illustrate the compartment diagram and associated variables.

For numerical stability and generalization, the system was transformed into proportional form by dividing each compartment by N, yielding $s = S/N, i = I/N, r = R/N$, and D/N. During simulation, population conservation was maintained, and for interpretative clarity, the results were normalized relative to the living population ($s + i + r = 1$), while $d(t)$ was tracked separately as cumulative mortality. This normalization allows the model to describe changes in the internal composition of the surviving population without distortion from cumulative deaths. Considering these assumptions, the dynamics of tuberculosis transmission are governed by the

Table 1: Variables and parameters

Symbol	Description	Unit/Interpretation
(N)	Total population	-
(S(t))	Number (or proportion) of susceptible individuals	persons or proportion
(I(t))	Number (or proportion) of infected individuals with active TB	persons or proportion
(R(t))	Number (or proportion) of recovered individuals	persons or proportion
(D(t))	Cumulative deaths due to TB	persons
(α)	Transmission (infection) rate	per person per year
(β)	Recovery rate	per year
(γ)	TB-induced mortality rate	per year
(μ)	Natural birth and death rate	per year

following system of nonlinear ordinary differential equations:

$$\frac{ds}{dt} = \mu - \alpha si - \mu s \tag{1}$$

$$\frac{di}{dt} = \alpha si - \beta i - \gamma i - \mu i \tag{2}$$

$$\frac{dr}{dt} = \beta i - \mu r \tag{3}$$

$$\frac{dd}{dt} = \gamma i. \tag{4}$$

subject to the initial condition: $s(0) + i(0) + r(0) = 1$.

3.2 Equilibrium Points and Basic Reproduction Number (R_0)

The equilibrium points of the proportional SIRD model are obtained by setting all time derivatives to zero in the system of Eqs. (1)–(4).

$$\mu - \alpha si - \mu s = 0 \tag{5}$$

$$\alpha si - (\beta + \gamma + \mu)i = 0 \tag{6}$$

$$\beta i - \mu r = 0 \tag{7}$$

Because $D(t)$ represents the cumulative number of deaths and does not feed back into the system, it is excluded from the equilibrium analysis. Setting the derivatives equal to zero yields two equilibrium points.

3.2.1 Disease-Free Equilibrium

When there are no TB-infected people in the community, this is known as the disease-free equilibrium point (E_0) [33]. This state implies that there are no infections in the population.

$$E_0 = (s, i, r) = (1, 0, 0). \tag{8}$$

3.2.2 Endemic Equilibrium (EE)

The endemic equilibrium point (E_1) refers to the condition in which individuals within the population are afflicted with tuberculosis [33]. When $i \neq 0$, solving the steady-state equations gives

$$\begin{aligned} E_1 &= (s^*, i^*, r^*) \\ &= \left(\frac{\beta + \gamma + \mu}{\alpha}, \frac{\mu(\alpha - (\beta + \gamma + \mu))}{\alpha(\beta + \gamma + \mu)}, \frac{\beta(\alpha - (\beta + \gamma + \mu))}{\alpha(\beta + \gamma + \mu)} \right). \end{aligned} \tag{9}$$

The endemic equilibrium exists only when $\alpha > \beta + \gamma + \mu$.

3.2.3 Basic Reproduction Number (R_0)

To ascertain whether the transmission of TB within a community will cease or endure throughout time, it is essential to calculate the fundamental reproduction number R_0. This statistic denotes the mean number of new infections caused by a single infected individual in a completely susceptible group. The R_0 equation in the SIRD model was formulated utilizing the Next Generation Matrix (NGM) method [34], taking into account the infection rate, recovery rate, and mortality rate associated with tuberculosis. Let,

$$F = \alpha si, \quad V = (\beta + \gamma + \mu)i \tag{10}$$

The Jacobi matrix was derived from the two matrices, F and V, so

$$\begin{aligned} K &= FV^{-1} \\ &= \alpha s \left(\frac{1}{\beta + \gamma + \mu} \right) \\ &= \frac{\alpha s}{\beta + \gamma + \mu}. \end{aligned}$$

By substituting $s = 1$ by E_0, the fundamental reproduction number is determined.

$$R_0 = \frac{\alpha}{(\beta + \gamma + \mu)}. \tag{11}$$

The value of R_0 reflects the transmission potential of tuberculosis (TB). A reduction in the transmission rate α, or an increase in the recovery (β) or TB mortality (γ) rates, decreases R_0, which indicates effective disease control. Therefore, interventions focusing on treatment adherence and early detection can significantly reduce R_0 below unity. If $R_0 < 1$, each infectious individual generates less than one new infection and the disease will eventually die out. If $R_0 > 1$, the infection can invade the population and persist at the endemic equilibrium [33].

3.3 Stability Analysis

The stability of the disease-free equilibrium (E_0) and the endemic equilibrium (E_1) was analyzed using the Jacobian matrix [31] and the Routh–Hurwitz criteria. From Eqs. (1)–(3) the resultant Jacobian matrix is derived as follows:

$$Jf(x) = \begin{bmatrix} -(\alpha i + \mu) & -\alpha s & 0 \\ \alpha i & \alpha s - (\beta + \gamma + \mu) & 0 \\ 0 & \beta & -\mu. \end{bmatrix} \tag{12}$$

At the DFE by Eq. (8), the Jacobian matrix of the SIRD system is derived as:

$$J(E_0) = \begin{bmatrix} -\mu & -\alpha & 0 \\ 0 & \alpha - (\beta + \gamma + \mu) & 0 \\ 0 & \beta & -\mu \end{bmatrix} \tag{13}$$

The characteristic equation is obtained as:

$$(\lambda + \mu)^2(\lambda - \alpha + \beta + \gamma + \mu) = 0. \tag{14}$$

We acquire $\lambda = -\mu, \quad \lambda = -\mu$ and $\lambda = \alpha - (\beta + \gamma + \mu)$, then we get

$$\begin{aligned} \lambda &= \alpha - (\beta + \gamma + \mu) \\ &= R_0(\beta + \gamma + \mu) - (\beta + \gamma + \mu) \\ &= (\beta + \gamma + \mu)(R_0 - 1). \end{aligned} \tag{15}$$

If $\lambda < 0$, then $R_0 < 1$. E_0 will exhibit local asymptotic stability if R_0 is less than 1. Therefore, E_0 is locally asymptotically stable if $R_0 < 1$; otherwise, it is unstable [35].

For the endemic equilibrium $E_1 = (s^*, i^*, r^*)$, the Jacobian matrix of the SIRD system is derived as:

$$J(E_1) = \begin{bmatrix} \lambda + (\alpha i + \mu) & \alpha s & 0 \\ -\alpha i & \lambda - (\alpha s - (\beta + \gamma + \mu)) & 0 \\ 0 & \beta & -\mu \end{bmatrix}. \tag{16}$$

The characteristic equation is obtained as:

$$(\lambda + \mu)(\lambda^2 + a\lambda + b) = 0, \tag{17}$$

where

$$a = -\alpha s + \alpha i + \beta + \gamma + 2\mu \tag{18}$$

$$b = \alpha i(\beta + \gamma + \mu) - \alpha s\mu - \mu(\beta + \gamma + \mu). \tag{19}$$

Let

$$\begin{aligned} H_1 = |a| &= -\alpha s + \alpha i + \lambda + \mu \\ &= x + \alpha i + x + \mu \\ &= \alpha i + \mu > 0, \end{aligned} \tag{20}$$

Now please be advise that

$$s^* = \frac{\beta + \gamma + \mu}{\alpha} \tag{21}$$

$$\alpha s^* = \beta + \gamma + \mu \tag{22}$$

So we get

$$\begin{aligned} H_2 &= \left| \begin{bmatrix} a & 0 \\ 1 & b \end{bmatrix} \right| = ab \\ &= (\alpha i + \mu)(\alpha i(\beta + \gamma + \mu)) > 0. \end{aligned} \tag{23}$$

According to the Routh–Hurwitz [31] stability criterion, the EE is locally asymptotically stable if and only if $H_1 > 0$ and $H_2 > 0$, which occurs when the basic reproduction number $R_0 = \frac{\alpha}{\beta+\gamma+\mu} > 1$.

Hence, the stability analysis indicates a transcritical bifurcation at $R_0 = 1$, marking the transition from a disease-free state to a persistent endemic state as the transmission potential exceeds the critical threshold.

3.4 Simulation

A simulation of the SIRD model was performed to gain a quantitative understanding of the dynamics of tuberculosis transmission and its effects on life insurance claims, utilizing published epidemiological data. This simulation seeks to illustrate the interactions across compartments (Susceptible, Infected, Recovered, and Deceased) during a designated timeframe, while also providing a foundation for estimating mortality rates and assessing the potential financial impact of insurance.

3.4.1 Parameter Estimation

The aim of this section is to estimate the unknown parameters of the SIRD model Eqs. (1)-(3) using annual tuberculosis case data for Southeast Sulawesi. The demographic parameters such as the natural mortality rate (μ) is derived from regional population statistics. The natural mortality rate is approximated as the inverse of the average life expectancy of the Indonesian population in 2021 (71.36 years)[1], resulting in $\mu \approx 0.014013453$ per year.

The SIRD model parameters were calibrated using the Nonlinear Least Squares (NLS) [36] approach to ensure that the model accurately represents the transmission dynamics of tuberculosis (TB) in Southeast Sulawesi. The estimation was conducted by minimizing the sum of squared residuals between the observed and simulated trajectories of the infected (I) and recovered (R) compartments. The estimation is based on cumulative TB cases from 2021 to 2023, compiled from the Indonesian Ministry of Health's Data and Information Center[2] [3] [4]. The parameters estimated in this process include the transmission rate (α), recovery rate (β), and TB-induced mortality rate (γ), while the natural mortality rate ($\mu = 0.0140$) and birth rate ($\Lambda = \mu N_0$) were fixed according to demographic assumptions.

Parameter uncertainty was quantified using bootstrap resampling (1000 iterations), from which 95% confidence intervals were derived. All simulations were conducted using proportional data to maintain population consistency and numerical stability, following methodologies described by [37] and [38] , which demonstrated the effectiveness of bootstrap techniques in quantifying parameter uncertainty in non-linear models.

The final estimated parameters are presented in Table 2. The basic reproduction number was calculated as $R_0 = 2.763$, indicating that, on average, a single infectious individual could generate approximately 2.76 secondary infections under baseline conditions.

Table 2: Calibrated Parameters and 95% Confidence Intervals

Parameter	Value	95% Confidence Interval	Remark
α	0.34734	0.3130 – 0.3762	Fitted
β	0.09860	0.0924 – 0.0986	Fitted
γ	0.01312	0.0105 – 0.0131	Fitted
μ	$\frac{1}{71.36}$	-	Demographic assumption

The model demonstrated excellent agreement with the observed data, with the Root Mean Square Error (RMSE) and Mean Absolute Percentage Error (MAPE) [39] for the infected compartment being 0.000112 and 4.18%, respectively. The overall model performance metrics are summarized in Table 3.

Table 3: Goodness-of-fit metrics

Variable	RMSE	MAE	MAPE (%)	R^2	Interpretation
Infected	0.000112	0.000081	4.18	0.98	Excellent fit
Recovered	0.000086	0.000070	16.73	0.95	Acceptable fit
Deceased	0.000011	0.000008	9.82	0.96	Excellent fit

External validation using 2024 data further confirmed the model's reliability. The predicted number of infected individuals for 2024 ($I_{pred} = 7132$) was close to the actual reported value ($I_{obs} = 6524$), corresponding to an absolute difference of 608 cases and a prediction error (MAPE) of 9.32%. Fig. 2 illustrates this validation, where the model projection (dashed line) closely

[1] https://www.bps.go.id/id/statistics-table/2/NTAxIzI=/angka-harapan-hidup-ahh-menurut-provinsi-dan-jenis-kelamin.html

[2] https://repository.kemkes.go.id/book/1288

[3] https://kemkes.go.id/id/profil-kesehatan-indonesia-2022

[4] https://kemkes.go.id/id/profil-kesehatan-indonesia-2023

follows the observed epidemic trajectory (blue line), confirming the robustness of the calibrated model for subsequent scenario simulations and actuarial applications.

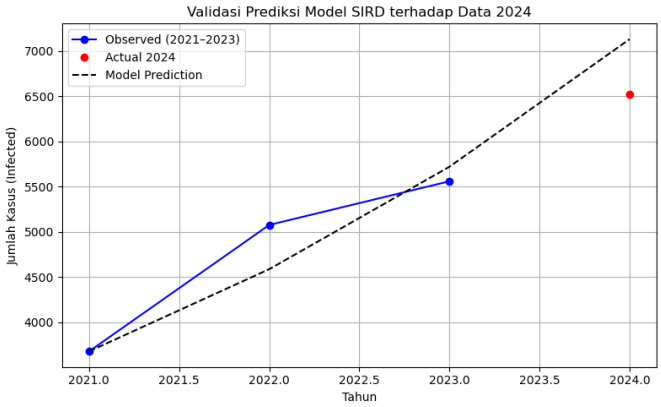

Figure 2: Validation of the SIRD Model Prediction against 2024 Data.

3.4.2 Baseline and Scenario Simulation

The simulation commences with data sourced from the official repository of Statistics of Southeast Sulawesi Province (BPS-Statistics Indonesia)[5], indicating a population of 2,749,010 (N) individuals distributed across four compartments. Using the year 2021 [c] as a baseline for the model, we write the initial conditions as $S(0) = N - 3678 - 759 - 191, I(0) = 3678, R(0) = 759$, and $D(0) = 191$. The baseline simulation was conducted using the calibrated parameters listed in Table 2 to describe the long-term TB dynamics in the population. Fig. 3 shows the baseline SIRD trajectories expressed in normalized proportions relative to the living population.

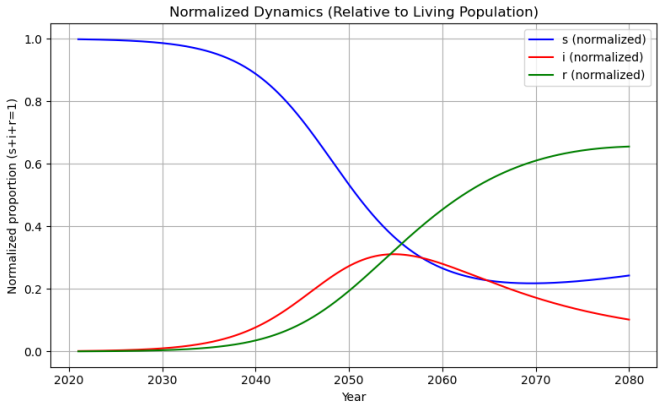

Figure 3: Validation of the SIRD Model Prediction against 2024 Data Normalized baseline dynamics of the SIRD model (2021–2080) relative to the living population.

Fig. 3 presents the normalized baseline dynamics of the calibrated SIRD model for the period 2021–2080. The trajectories exhibit a typical epidemic pattern, where the susceptible proportion $s(t)$ declines steadily as infection spreads, the infected proportion $i(t)$ increases to a single peak before subsiding, and the recovered proportion $r(t)$ rises monotonically. The model preserves population balance throughout the simulation, with the total proportion of all compartments $(s + i + r + d)$ remaining close to 1 (minimum = 1.000, maximum = 1.028).

By 2080, the compartmental proportions reach $s = 0.223, i = 0.094, r = 0.603$, and $d = 0.109$, indicating that roughly 60% of the population has recovered and about 11% has died from TB by

[5] https://sultra.bps.go.id/id/statistics-table/1/NDU5NSMx/penduduk--laju-pertumbuhan-penduduk--distribusi-persentase-penduduk--kepadatan-penduduk--dan-rasio-jenis-kelamin-menurut-kabupaten-kota-di-provinsi-sulawesi-tenggara--2020--2023--dan-2024.html

the end of the horizon. When normalized relative to the living population ($s+i+r=1$), the final distribution becomes $s_{rel}=0.243, i_{rel}=0.102$, and $r_{rel}=0.655$. This implies that among the surviving population, approximately two-thirds are recovered and immune, one-quarter remain susceptible, and about 10% are still infected.

Overall, the baseline simulation suggests that TB transmission stabilizes after mid-century as the susceptible pool becomes depleted, leading the system toward an endemic equilibrium characterized by $R_0>1$ and a persistent but declining infection prevalence.

To evaluate the effect of parameter uncertainty on TB transmission dynamics, three scenarios were simulated by varying the key epidemiological parameters by ±20% [33] from their calibrated baseline values, while keeping the natural death rate (μ) constant. The parameter settings and the resulting basic reproduction numbers (R_0) are summarized in Table 4.

Table 4: Scenario settings and resulting basic reproduction numbers (R_0)

Scenario	α	β	γ	μ	Parameter change	R_0
Optimistic	0.277872	0.118320	0.010496	0.014013	$\alpha-20\%, \beta+20\%, \gamma-20\%$	1.945
Baseline	0.347340	0.098600	0.013120	0.014013	-	2.763
Pessimistic	0.416808	0.078880	0.015744	0.014013	$\alpha+20\%, \beta-20\%, \gamma-20\%$	3.873

The results show that the basic reproduction number decreases from $R_0=3.837$ in the pessimistic scenario to $R_0=1.945$ in the optimistic case, with a baseline value of $R_0=2.763$ (Figure 4). Although all values remain greater than one, indicating that TB transmission persists endemically, the magnitude of R_0 directly reflects the potential for epidemic intensity and duration under varying epidemiological conditions

Fig. 4 compares the infected trajectories across the three scenarios. In the pessimistic scenario, characterized by higher transmission (+20%) and lower recovery (−20%), the infected proportion rises rapidly, peaking near 0.42 of the population around 2045 before declining. The baseline scenario exhibits a moderate peak (~ 0.30) around 2053, while the optimistic scenario, with reduced transmission and improved recovery, shows a delayed and flattened peak (~ 0.16) near 2068. These patterns demonstrate that strengthening recovery and reducing transmission can significantly postpone and reduce the infection burden over time.

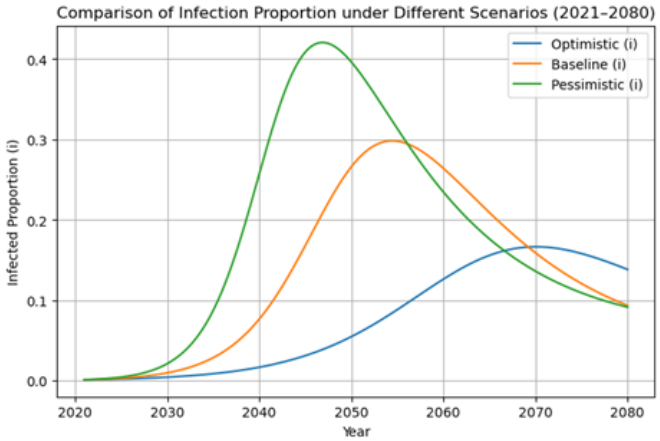

Figure 4: Comparison of infection trajectories ($i(t)$) across scenarios during 2021–2080.) relative to the living population.

Figs. 5–7 collectively show that improved recovery and reduced transmission substantially delay the epidemic peak and lower cumulative TB mortality, while adverse parameter shifts accelerate infection spread and increase long-term deaths.

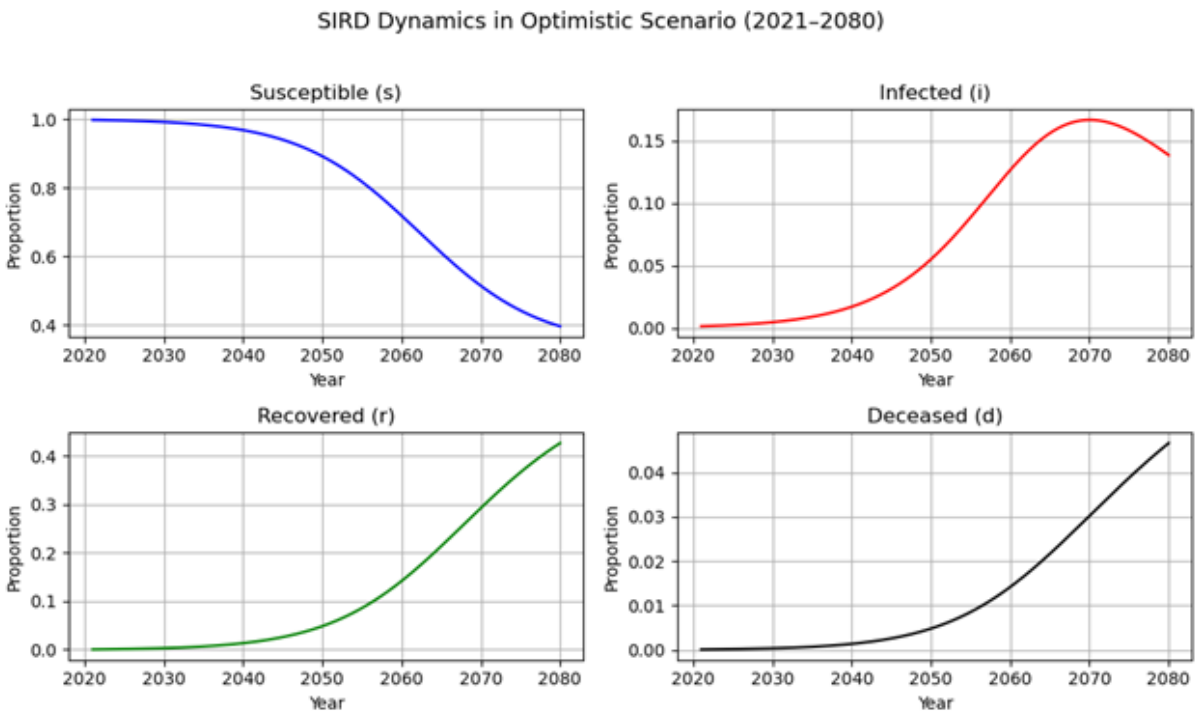

Figure 5: SIRD compartmental dynamics in the optimistic scenario (2021–2080).

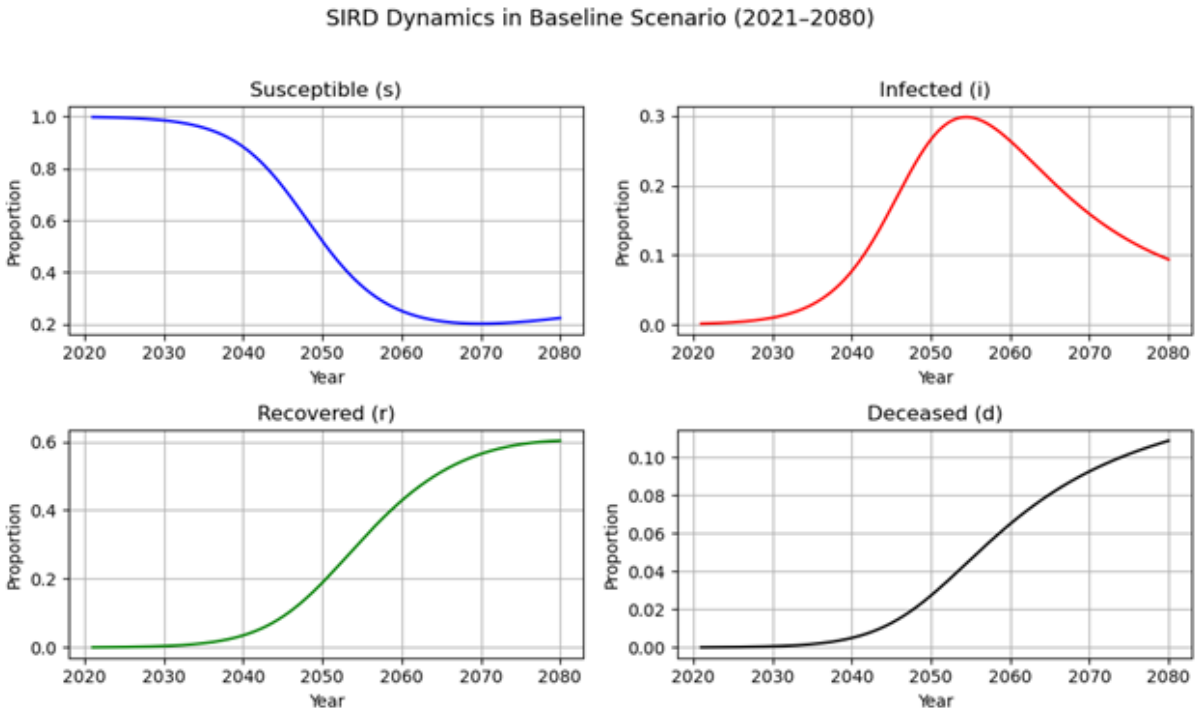

Figure 6: SIRD compartmental dynamics in the baseline scenario (2021–2080).

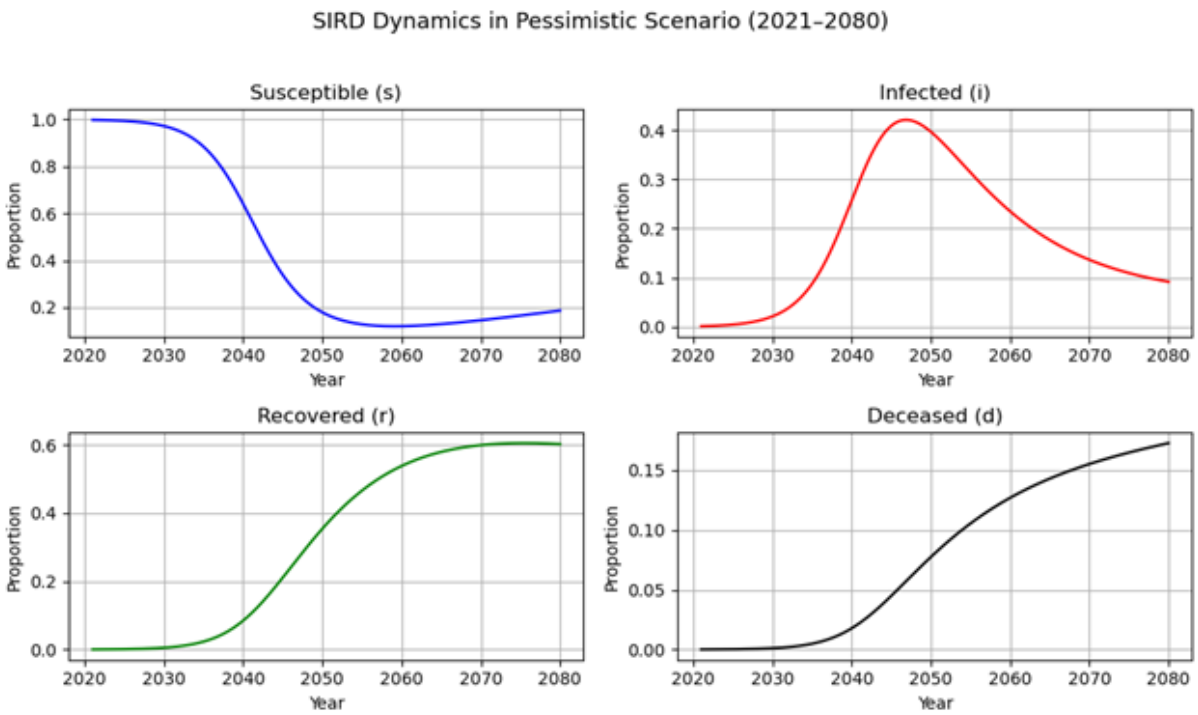

Figure 7: SIRD compartmental dynamics in the baseline scenario (2021–2080).

Overall, this sensitivity analysis confirms that modest changes (±20%) in key parameters can substantially alter TB progression, affecting both peak magnitude and timing. Hence, interventions that effectively reduce transmission and increase recovery rates are crucial to suppressing long-term TB persistence and minimizing its demographic impact.

3.4.3 Actuarial Translation of Model Outcomes

The epidemiological outcomes generated by the SIRD model are translated into life insurance claim projections using fundamental actuarial principles. In particular, the cumulative number of tuberculosis-related deaths $D(t)$ is transformed into annual incremental deaths $\Delta D_t = D(t) - D(t-1)$, which represent the number of new death events occurring in year t. This transformation is essential to avoid double counting and to ensure that insurance claims are associated only with newly mortality events in each period, consistent with standard actuarial practice.

The expected life insurance claims arising from TB-related mortality in year tare calculated using the following formulation:

$$C_t = \rho \times B \times \Delta D_t \times v^t. \tag{24}$$

where ρ denotes the insurance coverage rate (the proportion of TB-related deaths that result in an insurance claim), Brepresents the average benefit paid per death claim (in nominal terms), $v = (1+i)^{(} - 1)$ is the annual discount factor, and is the discount rate. Claims are assumed to be paid at the end of each year in which TB-related deaths occur, which is consistent with annual reporting and settlement conventions in the life insurance industry.

This formulation is grounded in the actuarial principle of expected present value for contingent payments and aligns with existing literature that integrates epidemic models with insurance risk assessment.[40] developed an actuarial framework linking pandemic-driven mortality to insurance liabilities, while [41] and [42] demonstrated how compartmental epidemic models can be combined with actuarial valuation techniques to project claims and reserves under time-varying mortality conditions. In this study, the actuarial framework is adapted by directly incorporating the

annual incremental deaths ΔD_t obtained from the calibrated SIRD model, thereby ensuring that projected claims reflect the dynamic evolution of disease-induced mortality rather than static or cumulative measures.

The base-case actuarial parameters employed in this study are as follows. The coverage rate ρ is set to 0.29 based on data reported by the Indonesian Life Insurance Association (AAJI)[6], which indicates approximately 81.76 million insured individuals out of a national population of around 281 million. Due to the unavailability of insurance penetration data specific to Southeast Sulawesi, this national estimate is adopted as the most reasonable proxy. The average death benefit per claim B is set at IDR $17,628,855$, derived from official AAJI ,statistics that report total claims and benefits paid relative to the number of beneficiaries. This value reflects actual claim payments rather than maximum sums assured and therefore provides a realistic measure of the financial burden borne by the life insurance industry.

To maintain analytical tractability and to emphasize epidemiological dynamics rather than financial market volatility, a fixed annual discount rate of 6.2% is applied. This rate corresponds to the yield on 10-year Indonesian government bonds according to market data[7] and is used as a risk-free reference rate in line with actuarial valuation practices and IFRS 17 guidance. While stochastic interest rate modelling may further refine claim valuation, the fixed-rate assumption is sufficient for isolating the impact of TB transmission dynamics on insurance liabilities.

The actuarial translation is conducted under three epidemiological scenarios. This scenario-based approach ensures that projected life insurance claims do not rely on a single set of assumptions and allows for a realistic assessment of downside and upside risk. The resulting total nominal claims and their present values are summarized in Table 5.

Table 5: Projected Total Life Insurance Claims

Scenario	Total Nominal Claim (IDR)	Total Present Value (PV) (IDR)
Optimistic	632,813,107,154	60,964,536,091
Baseline	1,475,187,463,787	206,994,910,293
Pessimistic	2,347,952,335,089	430,697,480,924

Table 5 indicates that projected life insurance claims increase markedly from the optimistic to the pessimistic scenario, consistent with higher tuberculosis transmission and mortality in the SIRD model. The baseline scenario results in total nominal claims of IDR 1.48 trillion with a present value of IDR 207.0 billion, representing the expected actuarial impact under current conditions in Southeast Sulawesi. These findings confirm that variations in TB epidemiological parameters translate directly into significant differences in life insurance claim projections, supporting the relevance of sensitivity analysis for actuarial risk assessment.

It should be emphasized that the actuarial translation presented in this study focuses on aggregate claim projections at the population level rather than individual policy pricing or reserve valuation. Nevertheless, the framework provides a robust quantitative bridge between epidemiological modeling and actuarial risk assessment, offering valuable insights for insurers and policymakers in evaluating the financial consequences of infectious disease dynamics.

3.4.4 Sensitivity Analysis

The PRCC results in Table 6 indicate that the transmission rate (α) is the most influential parameter affecting the present value of tuberculosis-related life insurance claims, exhibiting a strong positive correlation ($PRCC = 0.86, p < 0.001$) . This finding implies that increases in TB transmission intensity lead to a substantial rise in projected insurance liabilities. The

[6] https://www.antaranews.com/berita/4126605/aaji-total-tertanggung-industri-asuransi-jiwa-capai-8176-juta-orang?utm

[7] https://tradingeconomics.com/indonesia/government-bond-yield

recovery rate (β) shows a significant negative correlation with projected claims ($PRCC$ =-0.37, $p < 0.001$), confirming that improved treatment outcomes reduce mortality-driven insurance risk. Meanwhile, the TB-induced mortality rate (γ) has a positive but weaker correlation ($PRCC = 0.26, p < 0.001$), indicating that disease severity contributes to claim growth, although its impact is less dominant than transmission dynamics. Overall, the sensitivity analysis demonstrates that parameters governing disease spread are the primary drivers of actuarial risk in tuberculosis-related life insurance claims.

Table 6: PRCC Results

Scenario	Total Nominal Claim (IDR)	Total Present Value (PV) (IDR)
Optimistic	632,813,107,154	60,964,536,091
Baseline	1,475,187,463,787	206,994,910,293
Pessimistic	2,347,952,335,089	430,697,480,924

4 Conclusion

This study develops an integrated SIRD-based framework to analyze the sensitivity of tuberculosis transmission dynamics and its implications for life insurance claim projections in Southeast Sulawesi. By calibrating the model using regional epidemiological data and validating it against observed cases, the proposed approach demonstrates that the SIRD model is capable of reliably capturing long-term TB dynamics and cumulative mortality patterns relevant for actuarial applications. Scenario simulations further show that variations in key epidemiological parameters substantially affect both the timing and magnitude of infections, as well as the projected number of TB-related deaths.

From an actuarial perspective, the translation of epidemiological outcomes into expected life insurance claims provides a quantitative link between public health dynamics and financial risk. The sensitivity analysis using PRCC reveals that the transmission rate is the most influential determinant of the present value of TB-related insurance claims, followed by the recovery rate, while TB-induced mortality plays a comparatively smaller but still significant role. These findings highlight that interventions aimed at reducing transmission and improving treatment effectiveness not only mitigate public health impacts but also substantially lower long-term insurance liabilities. Consequently, the proposed framework offers practical insights for insurers in assessing epidemic-driven mortality risk and for policymakers in prioritizing disease control strategies with broader economic implications.

Several limitations should be acknowledged. The model does not explicitly incorporate a latent or exposed compartment, and insurance coverage rates are approximated using national-level data due to limited regional information. In addition, a fixed discount rate is assumed to isolate epidemiological effects from financial market uncertainty. Future research may extend this framework by incorporating latent-stage dynamics, heterogeneous population structures, stochastic interest rates, or region-specific insurance penetration data. Despite these limitations, the present study provides a parsimonious and robust foundation for integrating infectious disease modeling with actuarial risk assessment, particularly in the context of tuberculosis-related life insurance claims in Indonesia.

CRediT Authorship Contribution Statement

Asriani Arsita Asni: Conceptualization, Methodology, Supervision, Project Administration, Funding Acquisition, Writing – Original Draft Preparation, Software **Fitriyani:** Data Curation, Formal Analysis, Validation, Writing – Original Draft Preparation, Writing – Review & Editing, Software **Ira Puspita:** Investigation.

Declaration of Generative AI and AI-assisted technologies

During the preparation of this work, the authors used ChatGPT-4o to enhance clarity, grammar, and readability. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

Declaration of Competing Interest

The authors declare no competing interests.

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Data Availability

The data used in this study were obtained from publicly accessible PDF reports published on the official website of the Indonesian Ministry of Health, as well as archived records provided by the Southeast Sulawesi Provincial Health Office.

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