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Mathematical analysis of the SEIRD model for the spread of tuberculosis in Bangladesh

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ABSTRACT

The Susceptible-Infected-Recovered (SIR) model is a mathematical framework commonly used to understand how infectious diseases spread within a population. Building on this foundation, we examine an extended model known as the Susceptible-Exposed-Infected-Recovered-Deceased (SEIRD) model. This model is applied to study the spread of multidrug-resistant tuberculosis (MDR-TB), a critical and growing public health concern in Bangladesh. To evaluate the model, we use the basic reproduction number, which is calculated through the next-generation matrix method. The results indicate that when the reproduction number is below a certain threshold, the disease-free equilibrium is locally stable and the infection gradually disappears. However, if the reproduction number exceeds that threshold, the system's equilibrium points become locally asymptotically stable. In this study, we also carry out numerical simulations to assess the impact of MDR-TB in Bangladesh over the period from 2008 to 2020.

1. Introduction

Tuberculosis is a global pandemic and a contagious disease caused by *Mycobacterium tuberculosis*. The bacteria are transmitted through the air in a manner similar to the common cold, although tuberculosis does not usually resolve on its own. Most tuberculosis (TB) infections will occur when the immune system successfully combats the bacterial infection, preventing further spreading and stopping its growth. Only people who have active tuberculosis can transmit the illness. According to the World Health Organization (WHO), a small percentage of 11 individuals, ranging from 5% to 10%, will pose a risk of transmission to others. Without treatment, everyone is projected to spread the infection to approximately 10 to 15 people annually (WHO, 2023).

It is thought that people have had tuberculosis for thousands of years. Skeletal remnants demonstrate that TB was present in early people (4000 BCE) and that tuberculosis was discovered. In the spines of 3000-2400 BCE Egyptian mummies. It wasn't attributed to a single illness until the 1820s because of its diverse range of symptoms. Johann Lukas Schonlein coined the term "tuberculosis" in 1834 (Barberis et al., 2017). *Mycobacterium tuberculosis*, the bacterium that causes tuberculosis, was discovered by Robert Koch, a Nobel Prize laureate, in 1882. In the early 1900s, Albert Calmette and his colleagues achieved the first successful immunization against tuberculosis with the development of the Bacillus Calmette–Guérin (BCG) vaccine (WHO, 2023; Shaman et al., 2011).

WHO estimates that the microorganism TB bacillus presently afflicts one-third of people worldwide. TB is a disease of the poor, and most cases result in deaths in the developing world, of which Asia accounts for more than half (Loddenkemper and Murray, 2021). From the peak of 141 cases, the predicted global incidence rate is decreasing very slowly. From 288 cases per 100,000 people in 2002 to 128 cases per 100,000 people in 2010. Since 1990, the death rate has likewise decreased by 40%, and the total number of deaths is also declining. Globally, the percentage of people successfully treated reached its highest level at 87% in 2009.

One of the most concerning aspects of the antibiotic resistance pandemic is multidrug-resistant tuberculosis (MDR-TB), which is caused by *Mycobacterium tuberculosis* that is resistant to both

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isoniazid and rifampicin (RMP), with or without resistance to other medications (Falzon et al., 2011). About 3% of all newly diagnosed individuals worldwide have MDR-TB. RMP resistance found by a molecular diagnostic assay (like Xpert) is frequently the first indication of the presence of MDR-TB. Except in exceptional circumstances where additional test results verifying RMP resistance are not available, no patient ought to be prescribed a "standardized" MDR-TB regimen solely based on the findings of an Xpert test (Lange et al., 2019).

The failure of programs intended to guarantee individuals with tuberculosis receive a full recovery is reflected in the larger number of patients who have previously received anti-tuberculosis medication. The most significant factor contributing to the development of MDR-TB is incomplete and poor therapy; however, host genetic factors may also play a role. We have proposed a model and run through a numerical as well as statistical analysis to have an outline of the MDR-TB situation in Bangladesh.

2. Model formation

A very well-known model is Susceptible-Infected-Recovered (SIR), which can be used to learn more about how various treatments, including social distancing or immunizations, can affect the transmission of disease by adjusting these parameters. However, SIR is suitable for diseases where the latent period is negligible or absent.

To analyze the transmission dynamics of MDR-TB and evaluate the impact of a short-term treatment strategy, we perform a Susceptible-Exposed-Infected -Recovered-Deceased (SEIRD) compartmental model. The SEIRD model provides a mathematical framework to assess the spread and control of the epidemiological parameters and evaluate the potency of short-term treatment. Considering the probable increases in the population of vulnerable individuals noted in the synopsis.

The SEIRD model is divided into five components. The class of susceptible individuals is denoted by $S(t)$. The people who were exposed to TB are denoted by $E(t), I(t)$ is the class of individuals who are infected, and $R(t)$ stands for the people who are recovering after their illness has been cured. In conclusion, $D(t)$ is the representation of the illness that leads to death.

It now divides the entire population $N(t)$ into five distinct classes. That is $N(t) = S(t) + E(t) + I(t) + R(t) + D(t)$. New people will join the population with a fraction of $(1-\rho-\tau)\,\Delta N, \rho\Delta N, \tau\Delta N$ going into susceptible, exposed, and infected groups, accordingly. The compartmental description of the model is represented visually in Fig. 1.

A detailed exploration of the parameter (Table 1) and the following system of differential equations describes the SEIRD model for the spread of tuberculosis among immigrants.

$$\begin{aligned}
\frac{dS}{dt} &= (1-\rho-\tau)\Delta N - (\gamma I + \varepsilon)S + \mu R \\
\frac{dE}{dt} &= \rho\Delta N + \gamma SI - (\beta + \varepsilon)E \\
\frac{dI}{dt} &= \tau\Delta N + \beta E - (\varepsilon + \omega + \delta)I \\
\frac{dR}{dt} &= \delta I - \varepsilon R - \mu R \\
\frac{dD}{dt} &= (S+E)\varepsilon + (\varepsilon + \omega)I
\end{aligned} \tag{1}$$

Table 1: A detailed explanation of the parameters

Parameters	Description
γ	Rate of contact susceptible to the exposed class
β	Rate of transmission of those exposed to infections
δ	Recovery progression rate
ε	Natural death rate at each class
ω	The rate of infection deaths
μ	The rate of recovery for susceptible
ΔN	The recruitment rate

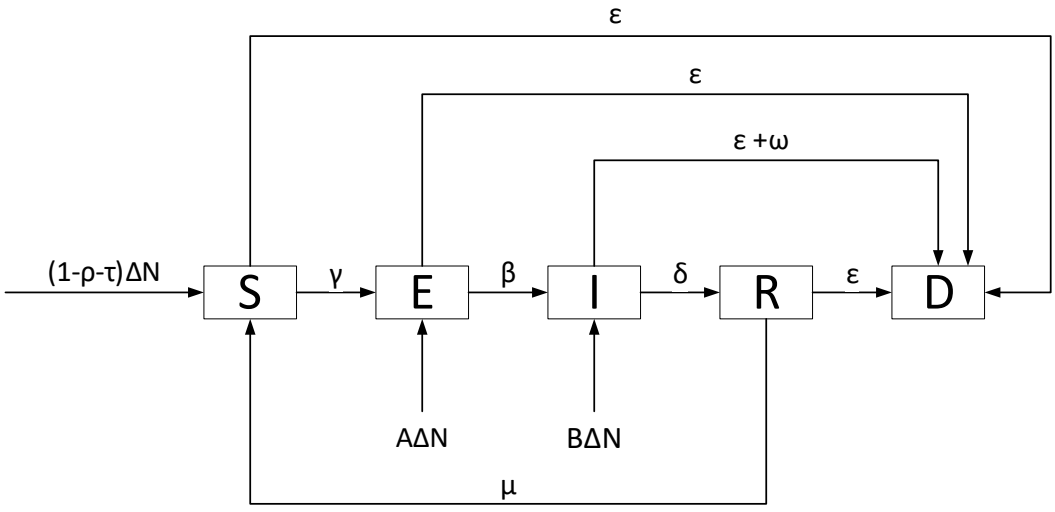

Fig. 1: Schematic diagram of the model

2.1. The model's mathematical analysis

Some fundamental principles need to be shown to validate the model. We will go over the terminology in brief.

2.2. Equilibrium

Equilibrium describes the stability of an epidemic or pandemic model by referencing its current state. At equilibria, the values of the system (1)'s left side will be zero as follows:

$$\frac{dS(t)}{dt} = 0, \frac{dE(t)}{dt} = 0, \frac{dI(t)}{dt} = 0, \frac{dR(t)}{dt} = 0, \frac{dD(t)}{dt} = 0$$

Where there is no infection, the equilibrium points are called the disease-free equilibrium points. Thus, the system maintains an equilibrium that is always disease-free, $E_0(S, 0,0,0) = (1,0,0,0)$. The places where an infection is present

are referred to as an endemic equilibrium. The endemic equilibrium point of system (1) is thus,

$$S = \frac{(1-\rho-\tau)\Delta N+\mu R}{\gamma I+\varepsilon} = S^*, E = \frac{\rho\Delta N+\gamma SI}{\beta+\varepsilon} = E^*, \quad I = \frac{\tau\Delta N+\beta E}{\varepsilon+\omega+\delta} = I^*, R = \frac{\delta I}{\varepsilon+\mu} = R^*$$

So, the unique endemic equilibrium of the system (1) is denoted by $E^* = (S^*, E^*, I^*,)$.

2.3. Basic reproduction number

We can obtain the reproduction number by using the next generation matrix, as described in the references (Brauer et al., 2008). If we define $X = (E, I)$, then we can derive the following from system (1)

$$\frac{dX}{dt} = F - V \; ; \qquad F = \begin{pmatrix} \gamma SI \\ 0 \end{pmatrix} \qquad V = \begin{pmatrix} (\beta+\varepsilon)E \\ -\beta E+(\varepsilon+\omega+\delta)I \end{pmatrix}$$

The coordinates of system (1)'s disease-free equilibrium points are $E_0 = (0,0,1,0)$. The derivatives of the system with respect to E and I were calculated at $E_0 = (0,0,1,0)$ are:

$$F = \begin{pmatrix} 0 & \gamma \\ 0 & 0 \end{pmatrix} \qquad V^{-1} = \begin{pmatrix} \frac{1}{\beta+\varepsilon} & 0 \\ \frac{1}{(\beta+\varepsilon)(\varepsilon+\omega+\delta)} & \frac{1}{\varepsilon+\omega+\delta} \end{pmatrix}.$$

The system (1)'s next-generation matrix is

$$\mathrm{F}V^{-1} = \begin{pmatrix} \frac{\gamma\beta}{(\beta+\varepsilon)(\varepsilon+\omega+\delta)} & \frac{\gamma}{\varepsilon+\omega+\delta} \\ 0 & 0 \end{pmatrix}.$$

The eigenvalues of the matrix are

$$\lambda_1 = 0, \lambda_2 = \frac{\gamma\beta}{(\beta+\varepsilon)(\varepsilon+\omega+\delta)}.$$

Hence, the maximum eigenvalue of the matrix is R_0(Reproduction number),

$$R_0 = \frac{\gamma\beta}{(\beta+\varepsilon)(\varepsilon+\omega+\delta)}.$$

Theorem 1: In system (1), the no-disease equilibrium points E_0 are stable, and it locally and gradually approaches zero if the value of R_0 is smaller than one. The infection equilibrium point E_0 becomes unstable when R_0 is larger than one, but it becomes locally stable when R_0 equals one.

Proof: At E_0, the system (1)'s Jacobian matrix is shown below,

$$J(E_0) = \begin{pmatrix} \lambda+\varepsilon & 0 & -\gamma & \alpha \\ 0 & \lambda+\varepsilon+\beta & \gamma & 0 \\ 0 & \beta & \lambda+\varepsilon+\omega+\delta & 0 \\ 0 & 0 & \delta & \lambda+\varepsilon+\mu \end{pmatrix} \qquad (2)$$

Or,

$$(\lambda+\varepsilon)(\lambda+\varepsilon+\mu)\{(\lambda+\varepsilon+\beta)(\lambda+\varepsilon+\omega+\delta)-\gamma\beta\} = 0$$
$$\therefore \lambda+\varepsilon = 0$$

Or,

$$\lambda = -\varepsilon < 1$$
$$\lambda+\varepsilon+\mu = 0$$

Or,

$$\lambda = -(\varepsilon+\mu) < 1$$
$$(\lambda+\varepsilon+\beta)(\lambda+\varepsilon+\omega+\delta)-\gamma\beta = 0$$

Or,

$$\lambda^2 + \lambda C_1 + C_2 = 0$$

$$C_1 > 0$$
$$C_2 = (\varepsilon+\beta)(\varepsilon+\omega+\delta)-\gamma\beta$$
$$= (\varepsilon+\beta)(\varepsilon+\omega+\delta) - R_0(\beta+\varepsilon)(\varepsilon+\omega+\delta) > 0$$

If $R_0 < 1$, the Routh-Hurwitz criteria are satisfied. There is a negative real portion for each of the equations of eigenvalues (van den Driessche and Watmough, 2002). A steady state value of one is reached when one of the eigenvalues is zero, which gives exact details about the system (2). Furthermore, system (1) is locally asymptotically stable because all the eigenvalues have negative portion. So, R_0 must be less than one (Mekonen et al., 2021).

Theorem 2: If the value of R_0 is larger than 1, then the equilibrium points E^* in the system are locally asymptotically stable (Shahrear et al., 2021).

Proof: At $E^* = (S^*, E^*, I^*, R^*)$, the Jacobian matrix of the system (1) is

$$J(E^*) = \begin{pmatrix} -(\gamma I^*+\varepsilon) & 0 & -\sigma S^* & \alpha \\ \gamma I^* & -(\beta+\varepsilon) & \sigma S^* & 0 \\ 0 & \beta & -(\varepsilon+\omega+\delta) & 0 \\ 0 & 0 & \delta & -(\varepsilon+\mu) \end{pmatrix} \qquad (3)$$

Trace $J(E^*) = -(\gamma I^*+\varepsilon)-(\rho+\mu)-(\varepsilon+\omega+\delta)-(\varepsilon+\mu) < 0$
$detJ(E^*) = (\gamma I^*+\varepsilon)(\beta+\varepsilon)(\varepsilon+\omega+\delta)(\varepsilon+\mu) - \gamma\beta S^*(\varepsilon+\beta)(\gamma I^*+\varepsilon) + \gamma^2\beta S^* I^*$
$(\varepsilon+\mu) - \mu\gamma\beta\delta I^*$

$= (R_0 - 1)\frac{\gamma\beta - AB - AB^2C^3(\gamma I^* - \varepsilon)}{AB} - \gamma\beta S^* A(\gamma I^* + \varepsilon) + \gamma^2\beta S^* I^* D(\gamma I^* + \varepsilon) - \gamma^2\beta\delta I^*$
$= (R_0 - 1) - (X + Y + Z) + F > 0.$

New det $(J(E^*)) > 0$ provided conditions. If $R_0 > 1$ and provided the condition $F > (X + Y + Z)$. In system (3), the endemic equilibrium points E^* have a negative real section (Shahrear et al., 2021). Consequently, system (3)'s endemic equilibrium point E^* is asymptotically locally stable.

3. Data estimation

Several sources, such as World Meter and National Tuberculosis Control Program (NTP), were used to gather data for this model. After compiling data from multiple sources, we utilized Microsoft Excel to calculate the parameters. Table 2 displays the data that we gathered from 2008 to 2020. The data we presently have will be used to obtain the data for the various classes, as indicated in Table 2, which shows the initial values of various variables.

Table 2: Initial values of variables

Parameters	Values
N	144500000
S	12491858
E	132000000
I	4721
R	3063
D	358

Now, here we can consider (Das et al., 2023),

$$\zeta_i = Average\left(\sum_{j=1}^{n} \frac{(n_i)_{j+1} - (n_i)_{j-1}}{(n_i)_{j+1}}\right); \qquad i = 1,2,3,4$$

Here, the first parameter $(n_1)_{j+1}$ represents the present-day infection rate, and the second parameter $(n_1)_{j-1}$ represents the infection rate of the previous day. Similarly, $(n_2)_{j+1}$ and $(n_2)_{j-1}$ represent the personnel who have been cured of tuberculosis on the present day and the day before (Shahrear et al., 2021). Finally, the death rate is denoted by $(n_3)_{j+1}$ and $(n_3)_{j-1,}$ respectively. The symbols $and\ \zeta_3$ respectively represent the values of γ, δ, ω.

Using the equations, we have managed to calculate the infection rate from the credible data successfully set that we successfully procured from NTP and other organizations (Das et al., 2023; Kuddus et al., 2022). By using these values from Table 3, we can now start the system to generate a prediction of the Tuberculosis situation in Bangladesh (Okuonghae and Omosigho, 2011).

3.1. Sensitivity analysis

In the proposed SEIRD model, we gain our basic reproduction number by using the formula below,

$$R_0 = \frac{\gamma\beta}{(\beta+\varepsilon)(\varepsilon+\omega+\delta)} = 0.4425$$

By using the following formula, we have the sensitivity parameters,

$$I_\gamma^{R_0} = \frac{\beta}{(\beta+\varepsilon)(\varepsilon+\omega+\delta)}\frac{\gamma}{R_0} = 0.999$$
$$I_\delta^{R_0} = -\frac{\gamma\beta}{\beta+\varepsilon}\frac{1}{(\varepsilon+\omega+\delta)^2}\frac{\delta}{R_0} = -0.4980$$
$$I_\omega^{R_0} = -\frac{\gamma\beta}{(\beta+\varepsilon)(\varepsilon+\omega+\delta)^2}\frac{\omega}{R_0} = -0.4224$$

Table 3: Parameter estimation

Parameters	Values
γ	0.1617
δ	0.1277
μ	0.001
β	0.048
ε	0.02041
ω	0.1083
ρ	0.2
τ	0.1
ΔN	0.984

The following outcomes are obtained from the indices' analysis:

1. Based on the value, it follows that an increase of 10% in γ causes the same 10% rise in |9.9999| = 0.9999 of Ro, which has the potential to cause an epidemic. On the other hand, a 10% drop in σ causes a 10% drop in |9.999| = 0.9999 of R_0, greatly lowering the value of R_0. This emphasizes how crucial it is to lower the rate of σ to stop the illness from spreading. To achieve this, governments and the WHO are supporting actions like social distancing and following protocols to stop the Tuberculosis disease.
2. The value of $I_\delta^{R_0}$ is negative, meaning that a 10% increase (or decrease) in δ causes a 10% increase (or decrease) in |− 0.4980| of R_0, which is equal to 0.04980. This emphasizes how crucial it is to keep Tuberculosis patients isolated to stop the illness from spreading.
3. In a similar vein, the value of $I_\omega^{R_0}$ is negative, meaning that a 10% increase or decrease in ω will result in a 10% increase or decrease in |− 0.4224| of R_0, which is equal to 0.04224. This emphasizes how crucial it is to keep Tuberculosis patients apart to stop the illness from spreading.

4. Numerical simulations

The model was simulated using MATLAB/Python by the fourth-order Runge-Kutta (RK4) method, and fourth-order polynomial regression was used to verify the result that was derived from the data we obtained from the National Tuberculosis Control Program for the period 2008 to 2020, based on the data in Tables 2 and 3. The MATLAB/Python figures for the Sensitivity Analysis of the proposed SEIRD model are shown in Fig. 2-5.

Now, let's analyze the MATLAB/Python systems output. We used the information from Tables 2 and 3 to solve the proposed SEIRD model and characterize the MDR-TB scenario in Bangladesh for the years 2008 to 2020. The infection rate first rose based on the data shown in Fig. 2. Then it dropped slightly. The infection rate was higher after 2016. The recovery rate gradually increased in the given period, along with the death rate, in Figs. 3 and 4.

The recovery rate and death rate were highest in 2018 and 2020, as per the solution graph of the model in Fig. 5. The different trends in the number of infections, recoveries, and deaths are shown in Figs. 6-9.

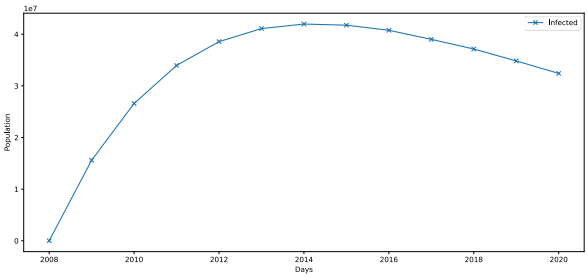

Fig. 2: Rate of infection

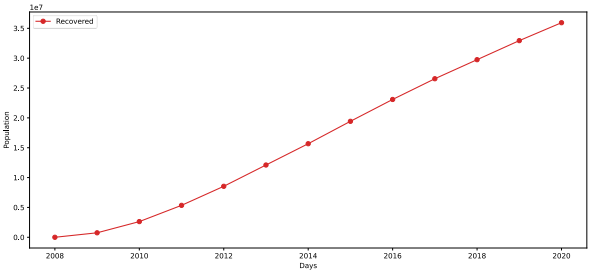

Fig. 3: Rate of recovery

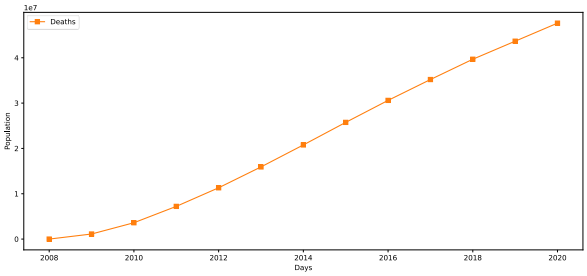

Fig. 4: Rate of death

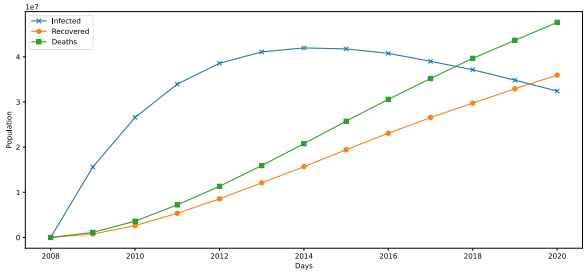

Fig. 5: The solution of the SEIRD model by MATLAB

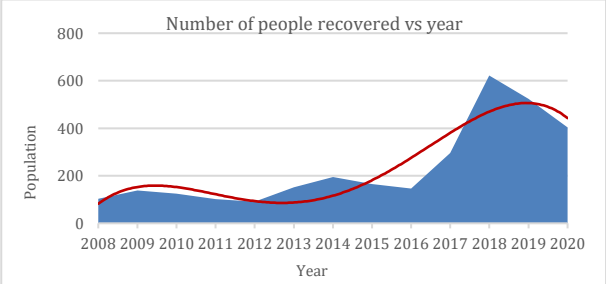

Fig. 6: Polynomial regression of infected people

The trendline derived from fourth-order polynomial regression is represented by the red line. The trendline depicts that over time, the death rate has stayed essentially unchanged. Fig. 9 indicates the number of people who were infected, recovered, and died from 2008 to 2020. The pie chart is based on the number of cases registered during a specific period. It is evident from the pie chart that the number of recoveries is less than the number of infected people, which indicates that the recovery rate in this period was notable. We can also observe this in Figs. 6-9. Fig. 6 shows the polynomial regression for infected people per year. It shows that the number of infections gradually increased by the year 2020. All over, there was a clear growth in the infection number. On the other hand, the number of recoveries is shown in Fig. 7. The number of recoveries eventually increased in the given period.

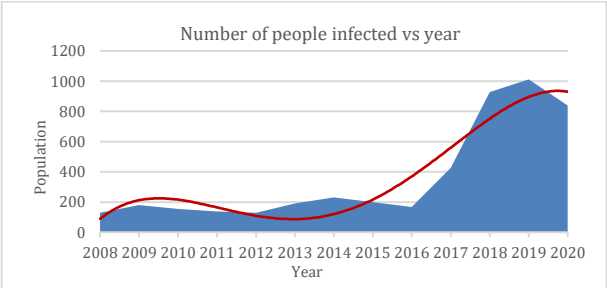

Fig. 7: Polynomial regression of recovered people

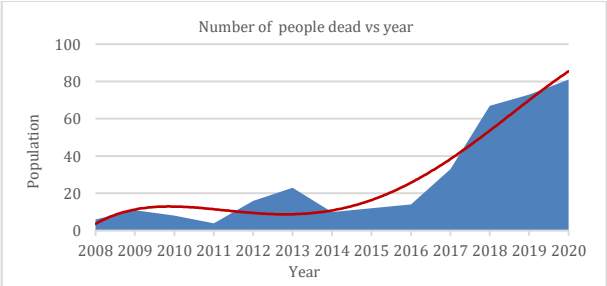

Fig. 8: Polynomial regression of dead people

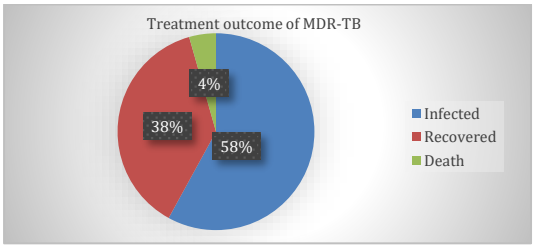

Fig. 9: Treatment outcome of MDR-TB case registered from 2008 to 2020

During the whole period, sometimes it increased and at some points, it decreased comparatively from the previous year. However, a good recovery rate is visible compared to the infection number. Lastly, the number of people who died during that period is less than the infection and recovery numbers.

5. Statistical analysis

Statistical analysis was carried out to summarize and better understand the Tuberculosis data reported in Bangladesh from 2008 to 2020. The data used in this analysis were taken from Table 2 and processed using Microsoft Excel. The results are

presented through descriptive statistics (Table 4) and graphical representation (Fig. 10).

Table 4 provides descriptive statistics for the number of infected, recovered, and deceased individuals over the study period. These statistics include measures of central tendency, variability, and distribution shape, which help describe the overall behavior of the data.

The average number of infected individuals is 362.85, with a relatively large standard deviation of 330.94. This indicates that the number of infections varied widely from year to year. The positive skewness value (1.322) shows that the infection data are right-skewed, meaning that a few years with very high infection numbers influenced the distribution. The wide range of 883 further confirms large fluctuations in infection counts during the study period. The recovery data show a mean value of 235.62 and a standard deviation of 174.22, indicating noticeable variation in the number of recovered individuals. Similar to infection data, recovery counts also exhibit positive skewness (1.395), suggesting that some years experienced much higher recovery numbers than others. The range of recoveries is 531, which reflects substantial differences across years. The kurtosis value indicates a distribution that is slightly flatter than a normal distribution. For deaths, the mean number is 27.54, with a standard deviation of 27.49. Although the overall number of deaths is much lower than infection and recovery counts, the data still show variability across years. The positive skewness value (1.232) indicates a right-skewed distribution, while the negative kurtosis value (−0.112) suggests a flatter distribution compared to a normal curve. The range of deaths is 77, showing that mortality numbers were not constant over time.

Fig. 10 presents histograms for infection, recovery, and death cases from 2008 to 2020. The histograms clearly show that infection and recovery numbers increased steadily from 2008 and reached their highest levels around 2012. After that, both declined and reached their lowest levels around 2017. A moderate increase is observed in 2018 and 2019, followed by a sharp rise in 2020.

In contrast, the number of deaths remained much lower throughout the study period. Death cases peaked around 2010 and then gradually declined until 2017. A slight increase occurred in 2018 and 2019, followed by a noticeable rise in 2020.

Overall, the statistical analysis shows that infection and recovery numbers experienced large variations over time, while death counts remained comparatively low. All three variables exhibit positive skewness, indicating that a small number of years with high values influenced the distributions. These results provide a clear quantitative overview of Tuberculosis trends in Bangladesh during the study period and support the findings obtained from the numerical simulations.

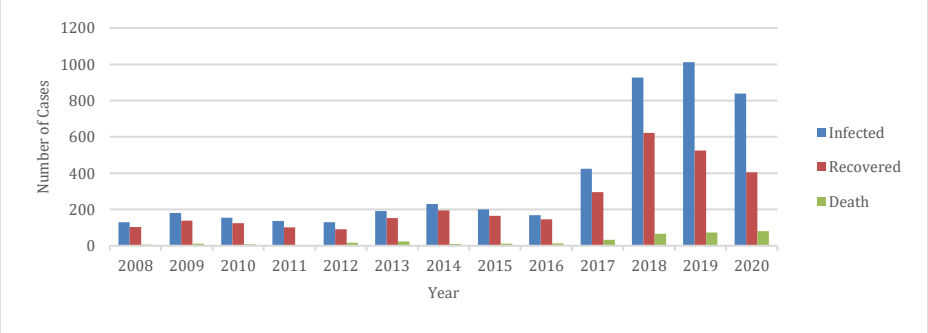

Fig. 10: Histogram based on infection, recovery, and death from 2008-2020

Table 4: Descriptive statistics on data 2008- 2020

Statistic	Infected	Recovery	Death
N	13	13	13
Mean	362.85	235.62	27.54
Standard error of Mean	91.786	48.32	7.626
Median	191	152	14
Mode	129	91[a]	4[a]
Standard deviation	330.938	174.221	27.494
Variance	109520.14	30352.923	755.936
Skewness	1.322	1.395	1.232
Standard error of Skewness	0.616	0.616	0.616
Kurtosis	0.016	0.782	-0.112
Standard error of Kurtosis	1.191	1.191	1.191
Range	883	531	77
Minimum	129	91	4
Maximum	1012	622	81
Sum	4717	3063	358

a: Multiple modes exist. The smallest value is shown

6. Discussion

In Bangladesh, poverty is one of the main causes of TB. Infection and disease susceptibility are increased by malnutrition, substandard housing, and restricted access to medical care. The model is created according to the socio-economic structure of Bangladesh. The treatment of MDR-TB is

comparatively more expensive than non-drug-resistant TB, which makes it more challenging to claim. In addition, the period of the treatment is long enough to cause many to quit. Furthermore, they lack sufficient awareness regarding tuberculosis. Our research unequivocally demonstrates that a noteworthy example of MDR-TB has been discovered. Despite this, the death rate is not particularly high. Better outcomes require adequate medical treatment, healthcare accessibility, free medications, public knowledge, and sufficient staff. Although a lot has changed in the last few years, more work needs to be done to eradicate tuberculosis (Kuddus et al., 2021). For additional research and development, policymakers can count on these points.

To define global targets and track progress toward TB elimination, our TB model helps estimate the global burden of TB. Funding for TB control initiatives can be increased with the assistance of this model's forecast. It will provide a shared foundation for understanding the disease and evaluating various approaches.

7. Conclusion

We found that the disease spreads rapidly throughout Bangladesh as more people contract it. Almost nine people die from tuberculosis every hour, and effective treatment is not available. It has long-term treatment of several months, and the diagnosis is not easy in every case. Most cases are drug-sensitive and respond favorably to combined traditional treatment. In the case of delaying finishing a prescribed course of treatment and poor management, it promotes the development of multidrug-resistant tuberculosis (MDR-TB). From the period 2008 to 2020, in Fig. 9, there was an increasing infection rate, and the recovery rate was close enough to the infection rate based on the data, and the death rate was lower. We can conclude that our prediction was almost accurate after comparing our results with the actual scenario that was provided to us. Currently, many of the model's essential parameters are assumed to be derived from trustworthy sources, such as World Meter (UN, 2022). A monthly registration system for tuberculosis patients is maintained by the National Tuberculosis Control Program (NTP). We gathered the data from their workplace, then we used Python 3.x in Jupyter Notebook to clean and process it all. If the required information can be supplied precisely or if it is present in government-provided sources, the proposed SEIRD model will produce a more accurate prediction. There were some restrictions while performing the studies, such as misclassification of the patient's treatment history, which is possible because of working with large data, which can cause restrictions to the study. The lack of networking data and molecular epidemiology may also present a limitation for the study's conclusion (Ershova et al., 2015). The process period of treatment is not fixed; sometimes, it can take a long time to cure.

As far as we are aware, the World Health Organization has reported that Bangladesh has one of the highest incidences of TB cases worldwide and a significant burden of TB and MDR-TB (WHO, 2023). 30 countries exhibit a high frequency of MDR-TB. In 2018, the National Notifiable Diseases Surveillance of Australia received 1,438 TB notifications, representing a rate of 5.8 per 100,000 population, consistent with the preceding three years. According to the Australian Department of Health, 93 cases of TB were detected where the carriers of TB were from Bangladesh. The WHO Global TB Report in 2017 estimated that the national prevalence of MDR-TB is 1.6% among newly diagnosed patients and 29% among cases that have already received treatment. The risk of progression is higher (40-50%) in children <5 years, especially in the first 12 months after infection (Cheng et al., 2020; Knight et al., 2019; Farina et al., 2022). The situation regarding treatment is concerning, particularly in consideration of achieving the objectives outlined by the World Health Organization's End TB Strategy (Anozie et al., 2024). However, treating DR-TB infections is more difficult and less optimistic, which contributes to the TB pandemic's ongoing tenacity. Additionally, COVID-19, HIV co-infection, low patient compliance, and inappropriate treatment methods in many regions of the world typically restrict TB control attempts (Alsayed and Gunosewoyo, 2023). Moreover, the reported incidence of very or very serious financial impact resulting from their tuberculosis condition was comparatively high among all patients (Evans et al., 2024). The WHO recommends clofazimine (WHO, 2023), which may help shorten treatment periods for drug-susceptible TB patients. However, no research has been done to assess the dose-exposure relationship in patients with drug-resistant TB, and it is uncertain what the ideal dosage is for this condition (Abdelwahab et al., 2020). The occurrence of adverse events highlights the need for regular monthly care monitoring through clinical examination and laboratory investigations (Khan et al., 2024). Since we developed this model and obtained findings from 2008 to 2020, we expect that MDR-TB will peak between the beginning of 2012 and 2016. We monitored the situation in line with the model for the set time. Using our method, we performed a statistical study and discovered a similar outcome. We saw an upward trend that then turned downward at the beginning of 2016. However, the generated model has helped us to have an overview of the MDR-TB situation in Bangladesh, briefly and significantly.

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Compliance with ethical standards

Conflict of interest

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

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