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Research Article

Analyzing Dynamical Behavior of Tuberculosis Transmission

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Abstract: In this article, we investigated the dynamical behavior of a fuzzy mathematical model with tuberculosis (TB) treatment function. The considered model analyzes fuzzy basic reproduction numbers and stability analysis for both local and global stability conditions around disease-free equilibrium points, as well as its local stability conditions around endemic equilibrium points. We examine the TB model's sensitivity analysis with a focus on the variation of each of its parameters. We propose predicting the extension of the virus load in TB using fuzzy bifurcation. At the end, we have given a numerical simulation to illustrate the outcomes by considering some special types of treatment functions.

***Keywords*:** tuberculosis (TB) infection model, stability analysis, bifurcation, fuzzy basic reproduction number, fuzzy control system, homotopy perturbation method

MSC: 92C50

1. Introduction

The infectious disease tuberculosis is caused by the airborne virus Mycobacterium tuberculosis (TB). TB is one of the most dreadful bacterial causes of human mortality, especially in developing nations. In 2021, 1.6 million individuals worldwide (including 187,000 persons living with HIV) passed away from TB. TB is the second most lethal infectious disease in the world, after COVID-19, and is the 13th greatest cause of death globally (behind HIV and AIDS). Globally, 10.6 million cases of TB were reported in 2021. 6.4 million males, 3.4 million women, and 1.2 million children. TB exists in all nations and among all age groups. However, TB can be treated and avoided. Between 2000 and 2021, it is expected that TB detection and treatment have saved 74 million lives [1].

Latently infected and actively infected are the two different forms of TB infection. Latent infection is a condition in which the patient's body contains dormant (sleeping) TB germs that, although they did not initially produce TB disease, were capable of waking up and becoming active after some time. Patients with latent TB are those who carry the disease. A person with latent TB does not transmit the TB bacterium to those who are prone to contracting the disease. When a person is actively infected, active TB bacteria proliferate in their body and bring on the symptoms of TB disease. Actively infected is a condition in which active TB bacteria breed in the patient's body and cause TB disease symptoms. When a person is actively infected, active TB bacteria proliferate in their body and bring on the symptoms of TB disease. Patients who have active TB are those who are currently infected with the disease. Active TB

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patients can transmit the illness to susceptible individuals. Patients who have latent or active TB are curable, but they lack immunity or resistance. After a given amount of time, those who have recovered from TB may contract the illness again. A population with subpopulations within it can be used to describe the events of a TB bacterial infection. Population groups are susceptible to TB disease; infectious latent patients are a population with latent TB; active infectious patients have active TB disease; and recovered patients have latent TB disease cured.

Takahashi et al. [2] discussed infectious disease behavior in order to make wise decisions could be made regarding the management of its treatment, particularly in the case of a new outbreak of multi-drug-resistant TB. Additionally, the research could examine the application of this model to the spread of other infectious diseases. Through the use of mathematical models such as the Susceptible, Infected, and Recovered (SIR) models and the Susceptible, Exposed, Infected, and Recovered (SEIR) models [3, 4], a number of researchers have advocated compartmental dynamics. Fredlina et al. [5] discussed the modeling of disease spread by vaccination influences using the SIR model. In this research, Castillo-Chavez et al. [6] explained how the dynamic functions, with a main focus on TB prediction and control strategies using simulation techniques.

In 2009, Aparicio et al. [7] focused on three model types: a homogeneous in normal incident model, a non-homogeneous mixing model that includes household contact, and an age structure model. A model is parameterized using demography and epidemic data, as well as a general pattern that is then compared. Taufik and others [8] analyzed the model of vaccinated Tuberculosis with exogenous reinfection has two equilibrium points, there is disease-free and endemic. Ashenaf.et.al [9], studied the model system of ordinary differential equations considering two classes of latently infected individuals, with different risks of becoming TB infectious. The accuracy and sensitivity of identifying the anomalies contained in the data while keeping a low false-positive rate using an adaptive target-level identification approach by Side et al. [10]. The SEIR model was used by Mulbar et al. [11] to analyze tuberculosis transmission.

Nur et al. [12] explained the stability of the dengue-fever infection model. In this paper, Samat et al. [13] discussed the tools for preventing and controlling infectious diseases. Putri et al. [14] utilized the use of vaccines, anti-malarial drugs, and spraying as treatment efforts for the SIR epidemic model. Zaman et al. [15] analyzed how vaccination and treatment of SIR models can be used to solve infectious diseases. In this paper, Edwardo et al. [16] investigated the changes in the dynamics when it ranges between zero and one. Kaddr [17] discussed the phenomenological behavior of a model, which also includes steady state, fundamental reproduction numbers, local and global stability, and bifurcation analysis. In this paper, Satsuma and others [18] focused on the SIR model for transmission, and calculations were done using data on the number of infectious disease cases.

Kermack and McKendrick [19] originally suggested the infectious disease-to-epidemic mathematical SIR model. We defined fuzzy sets and fuzzy theory, and Zadeh [20] introduced the uncertainty fuzzy mathematical model in biology. Brauer and Castillo-Chavez [21, 22] studied SIR models, in which the transitions are from susceptible to infective to removed, with the removal coming through recovery with full immunity or through death from the disease. The transmission and recovery rates of unknown populations using fuzzy methods were discussed in [24, 25]. The uncertainty of the fuzzy model and fuzzy parameter space of fuzzy epidemic mathematical models for human infectious diseases were discussed in [26, 27].

The potential opportunity for future modeling of infectious disease epidemiology behaviors was thoroughly thorough review in [28, 29]. How a dynamical system can be modeled by fuzzy linguistic rules while taking infectious illness birth and death factors into account [30, 31] Using six separate compartments of SEIOVR, Shah et al. [34] analyzed the spreading and control of COVID-19. Sadek et al. [35] generalized the SEIR model of the spread of COVID-19 with a private focus on the transmissibility of people who were aware of the disease, followed preventative health measures, and made predictions about how COVID-19 will change over the next 1,000 days.

In this research, basic reproduction numbers and fuzzy basic reproduction numbers for investigating the TB infection model, as well as simulations comparing numbers to the homotopy perturbation method (HPM) and Euler's method, are the key topics of discussion. Determining the disease-free equilibrium and endemic equilibrium points allows us to assess the stability of the system. The format of this essay is as follows: Section 2: preliminaries, Section 3: fuzzy TB-infection model, Section 4: basic properties, Section 5 deals with fuzzy system analysis, Section 6 deals with numbers of stability analysis, Section 7: sensitivity analysis, Section 8: fuzzy basic reproduction number, Section 9 deals with the outcomes of numerical simulation, and Section 10 works with the conclusion.

2. Preliminaries

2.1 *Fuzzy sets*

Let X be a nonempty, crisp set. A fuzzy subset T of X is denoted by $\widetilde{T}$ and is defined as

$$\widetilde{T} = \{(x, \beta(x)) : x \in X\}$$

where β: $X \rightarrow [0, 1]$ is a membership function connected to a fuzzy set (T) that expresses the degree to which x belongs to X. In this instance, the membership function (x) is used to denote the fuzzy subset $\widetilde{T}$. If X is a set of real numbers, then (x) is known as a fuzzy number.

2.2 *Triangular fuzzy number*

If the membership value can be represented by a triangular function, the fuzzy set is referred to as a triangular fuzzy number. This function has the following three parameters $F(x: a, b, c)$:

$$F(x:a,b,c) = \begin{cases} 0, & x < a \\ \dfrac{x-a}{b-a}, & a \le x \le b \\ \dfrac{c-x}{c-b}, & b < x \le c \\ 0, & x > c \end{cases}$$

2.3 *Fuzzy expected value*

Let $Z(\beta)$ represent the set of all subsets of β and let it be a nonempty set. Then, the fuzzy measure is X: $\beta \rightarrow [0, 1]$ [30]. If

- $X(\beta) = 0$ and $X(\beta) = 1$,
- for $C, D \in P(\beta)$, $X(C) \le X(D)$ if $C \subset D$.

Let X: $\beta \rightarrow [0, 1]$ be an uncertain variable, meaning that it is a fuzzy subset of and a fuzzy measure on. The real number, as determined by the surgeon measure, is the fuzzy expected value (FEV) of [26].

$$FEV(X) = \int XdX = \sup\{\min(\alpha, k, (\alpha))\}, \quad 0 \le \alpha \le 1$$

where $k(\alpha) = X\{\omega \int \beta : \mu(\omega) \ge \alpha\}$.

3. Model of fuzzy TB infection

We looked at a compartmental TB mathematical model, in which the entire human population is divided into three categories based on natural features. S is the proportion of Susceptible people, I is the proportion of Infected people, and R is the proportion of Recovery people. The fuzzy parameters x, y, δ, and ω are constants. The population in this model is assumed to be constant, so ω is the transmission rate from susceptible people to infected people, and δ is the recovery rate from infected people to become recovered people. x is the rate of birth, and y is the death rate due to the disease of TB. The system of nonlinear differential equations of such models is given by [33]:

$$\begin{aligned}\frac{dS}{dt} &= x - \left(\frac{\omega(\theta)I}{N} + y\right)S \\ \frac{dI}{dt} &= \frac{\omega(\theta)I}{N}S - \left(\delta(\theta)I + \right)I \\ \frac{dR}{dt} &= \delta(\theta)I - yR\end{aligned} \tag{1}$$

$$S + I + R = N,\ S(0) > 0,\ I(0) > 0,\ R(0) \geq 0$$

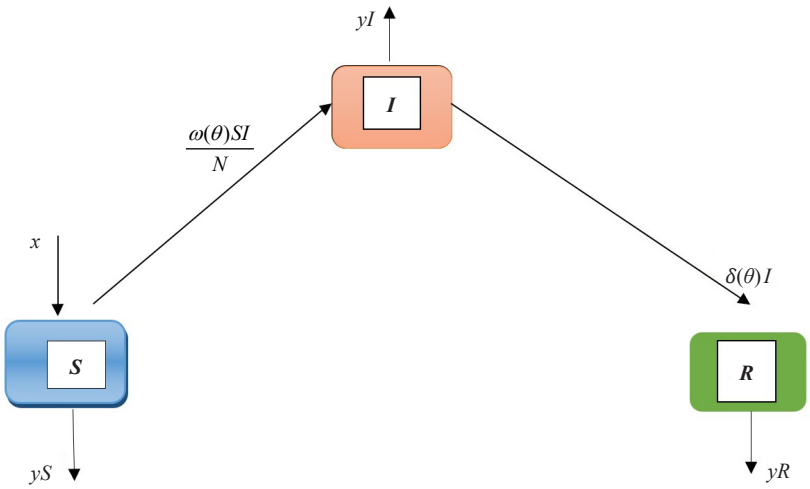

Figure 1. Diagrammatic representation of fuzzy SIR Model

4. Fundamental properties of the TB infection model

Here, the basic components of the TB infection model (1) will be examined. The existence and uniqueness of the solutions to the nonnegative for all $t \geq 0$ must be proven for the TB infection model (1) in order for it to have epidemiological significance.

4.1 *Existence and uniqueness*

The system's initial conditions are as follows:

$$S > 0,\ I\,(0) > 0,\ R(0) \geq 0$$

Theorem 1. For all $t \geq 0$, indicate the existence and uniqueness of the solutions to the nonnegative initial condition model (1).

Proof. Let $y(t) \in \mathbb{R}^3$ where $y(t) = (S(\theta), I(\theta), R(\theta))$. The form of the system of equation (1) is represented as $y' = f.(y)$. Let f_j be the vector field's components, where $j = 1, 2, 3$, and 4. Then,

$$\begin{aligned}f_1 &= x - \frac{\omega(\theta)I}{N}S - yS \\ f_2 &= \frac{\omega(\theta)I}{N}S - \delta(\theta)I - yI \\ f_3 &= \delta(\theta)I - yR\end{aligned} \tag{2}$$

As f_j is an autonomous continuous function on $\mathbb{R}^3$, its partial derivatives are continuous and exist because f is an algebraic polynomial. As a result, given any initial condition $y(0) \in \mathbb{R}^3$, the existence and uniqueness theorem [25] states that there is only one solution to the system $y' = f(y)$.

4.2 *Feasibility*

Theorem 2. Explain that for all t greater than 0, the solutions of system (2) are positive.

Proof. Understanding how the state variables work at the limits of Q allows us to prove the theorem.

$$Q = \{(S, I, R) \in \mathsf{R}^3 : 0 \leq S, I, R\}$$

Consider the following limits, $S = R = 0$, and read the discussion for each situation below.

1. At

$$S = 0,$$
$$S' = x > 0.$$

Since $S' > 0$ in order to exit Q, this line cannot be crossed by the solution.

2. At

$$R = 0,$$
$$R' = \delta I > 0.$$

Case 1. If $R = 0$, $I = 0$ then $R' = 0$.

Case 2. If $R = 0$, $I > 0$ then $R' > 0$.

Since $R' \geq 0$, in order to exit Q, this line cannot be crossed by the solution.

Theorem 3. Show that for some $b > 0$, the solutions to system (1) are constrained to the range $[0, b)$.

Proof. Thus, $S(t)$, $I(t)$, and $R(t)$ are all bounded on $[0, b)$.

From (1), we have $N = S + I + R$;

$$\frac{dN}{dt} = x - \omega$$
$$N = \frac{x}{\omega} + (N(0) + \frac{x}{\omega})e^{-\omega t}.$$

Therefore, $\limsup_{t \to \infty} N \leq \frac{x}{\omega}$.

Therefore, for some $b > 0$, $S(t)$, $I(t)$, and $R(t)$ are bound above by x on $[0, b)$. Since they are all nonnegative, all variables are constrained below 0. As a result, the solution of the system (2) is constrained to the range $[0, b)$ for some $b > 0$.

5. Fuzzy system analysis

By updating the mathematical model of TB infection, fuzzy systems are created. As a result, the rate of infection and recovery among the human population varies depending on the illness. A triangular fuzzy number with a membership function is the term represented by $\alpha(\theta)$.

$$\alpha(\theta)=\begin{cases}0, & \text{if } \theta<\bar{\theta}-b,\\ \dfrac{\theta-\bar{\theta}+b}{b}, & \text{if } \bar{\theta}-b\le\theta\le\bar{\theta},\\ 1, & \text{if } \bar{\theta}.\\ \dfrac{-(\theta-\bar{\theta}-b)}{b}, & \text{if } \bar{\theta}<\theta\le\bar{\theta}+b,\\ 0, & \text{if } \theta>\bar{\theta}+b.\end{cases} \tag{3}$$

If b is the spread of each of the fuzzy sets assumed by and the center value is $\bar{\theta}$, then the linguistic variable's classification for a fixed is given as weak, medium, and high in this fuzzy model, representing the triangular fuzzy number. Each classification can be shown as a fuzzy, triangular number. Figure 2 clearly demonstrates $\alpha(\theta)$.

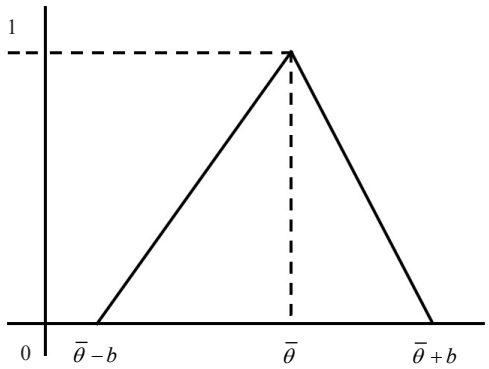

Figure 2. Triangular fuzzy number

Taking into consideration the heterogeneity of the human population, the transmission rate and recovery rate are used as two fuzzy parameters. The rate at which the disease progresses from susceptible to infectious $(0\le\omega(\theta)\ge 1)$ is presumed to be provided by the TB virus. We take the spread rate in this model to be a fuzzy number with a membership function $\omega(\theta)$ that depends on the quantity of virus load and is given by:

$$\omega(\theta)=\begin{cases}0, & \text{if } \theta<\theta_{\min},\\ \dfrac{\theta-\theta_{\min}}{\theta_M-\theta_{\min}}, & \text{if } \theta_{\min}\le\theta\le\theta_M,\\ 1, & \text{if } \theta_M\le\theta\le\theta_{\max}.\end{cases} \tag{4}$$

Where is the virus load, $\theta_{\min}$ is the minimum virus quantity necessary for disease transmission. The risk of disease transmission is minimal when a person has less virus inside of them than $\theta_{\min}$. The disease transmission rate is maximum and equal to 1 when the virus load θ_M is medium, and $\theta_{\max}$ is the maximum virus load of an individual in the population. The transmission rate membership function is shown in Figure 3.

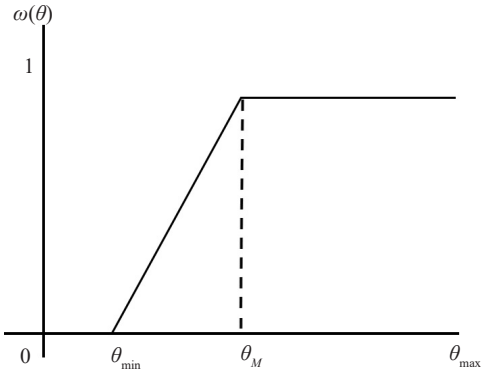

Figure 3. Membership function of transmission rate

Let $\delta(\theta)$ be the virus load-dependent recovery rate from infectious TB illnesses. The length of time it takes to recover from the illness increases with the virus load. As a result, in this model, we use the membership function $\delta(\theta)$ to treat the recovery rate as a fuzzy value.

$$\delta(\theta) = \frac{(\pi_{\min} - 1)}{\theta_{\max}}\theta + 1, \text{ if } 0 < \theta < \theta_{\max} \tag{5}$$

where $0 < \pi_{\min} < 1$, represents the population's minimal recovery rate and is the viral load. The recovery rate membership function is shown in Figure 4.

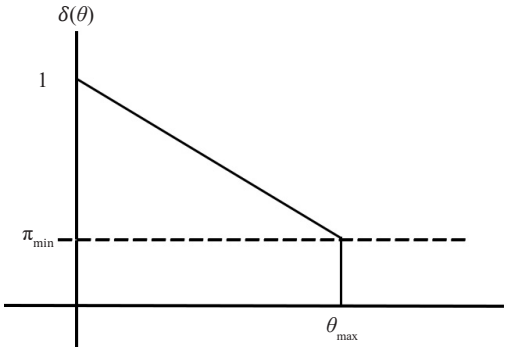

Figure 4. Membership function of recovery rate

6. Fuzzy model of stability analysis

We require both the equilibrium points and the basic reproduction number in order to calculate the stability analysis in this section. We have identified two equilibrium points in this TB spread model.

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$$

6.1 *Disease free equilibrium*

When there is no TB infection in the human population, that is, when there are no TB-causing illnesses in the population, P_1 stands for the disease-free equilibrium point, which is a steady-state solution.

Let us consider $S_1 = 0$, $I_1 = 0$, $R_1 = 0$.

$$\text{The disease-free equilibrium point as } P_1 = (\frac{x}{y}, 0, 0).$$

6.2 *Endemic equilibrium*

The attack disease still exists and is still spreading throughout the endemic equilibrium.

Let us consider $S_2 > 0$, $I_2 > 0$, and $R_2 > 0$.

We get the endemic equilibrium point

$$P_2 = \left(\frac{(\delta + y)N}{\omega}, \frac{\omega x - y(\delta + y)N}{\omega(\delta + y)}, \frac{\delta I}{y} \right).$$

6.3 *Basic reproduction number*

The next-generation matrix approach [32] is used to determine the fundamental reproduction number R_0 for the system.

The basic reproduction number is $R_0 = \dfrac{\omega(\theta)}{y(\delta(\theta) + y)}$.

6.4 *Stability analysis*

6.4.1 *Local asymptotically stable at equilibrium points*

Theorem 4. The disease-free equilibrium points $P_1 = \left(\dfrac{(1-\vartheta)\sigma N}{\rho}, 0, 0 \right)$ is locally asymptotically stable, when $R_0 < 1$ unstable and when $R_0 > 1$.

Proof. The stability of the disease' free equilibrium is obtained by using the Jacobian matrix of the system of equation (2), which is given by

$$J(P_1) = \begin{bmatrix} -y & -\omega \dfrac{x}{Ny} & 0 \\ 0 & \omega \dfrac{x}{Ny} - \delta - y & 0 \\ 0 & \delta & -y \end{bmatrix}. \tag{6}$$

At the disease-free equilibrium point, the characteristic equation is

$$\begin{aligned} |J - \lambda I| &= 0. \\ (-y - \lambda)(\omega \frac{x}{Ny} - \delta - y - \lambda)(-y - \lambda) &= 0. \\ (-y - \lambda)^2 (\omega \frac{x}{Ny} - \delta - y - \lambda) &= 0. \end{aligned}$$

Therefore, $\lambda = y, \delta, \omega, x, N$

$$B_1 \lambda^3 + B_2 \lambda^2 + B_3 \lambda + B_4 = 0. \tag{7}$$

Where,

$$B_1 = Ny.$$
$$B_2 = 3Ny^2 + Ny\delta - \omega x.$$
$$B_3 = 3Ny^3 + 2Ny^2\delta - 2y\omega x.$$
$$B_3 = Ny^4 + Ny^3\delta - y^2\omega x.$$

According to the Routh-Hurwitz criterion [15], the roots of the equations B_1- $B_4 > 0$ and B_2B_3 - $B_1B_4 > 0$ both are negative, indicating that the system of equations is locally asymptotically stable. As a result of $R_0(\theta) < 1$, the disease-free equilibrium point for the system is locally asymptotically stable.

Theorem 5. The endemic equilibrium points $M_2 = (S_2, I_2, R_2)$, when $R_0 < 1$ and unstable when $R_0 > 1$ is locally asymptotically stable.

Proof. To acquire the endemic equilibrium's stability Using the Jacobian matrix of the system of equations (6) and (7), we can conclude that $|J - \mu I| = 0$. According to the Routh-Hurwitz criterion [15], the roots of the equations B_1 - $B_4 > 0$ and B_2B_3 - $B_1B_4 > 0$ both are negative. As a result, if $R_0(\theta) > 1$, the endemic equilibrium point of the system will be locally asymptotically stable.

6.4.2 *Globally asymptotically stable for disease-free equilibrium point*

In this sub section, to analysis only disease-free equilibrium point of the TB model.

Theorem 6. The disease-free equilibrium points $P_1 = (\frac{x}{y}, 0, 0)$ is globally asymptotically stable, when $R_0 < 1$ and unstable when $R_0 > 1$.

Proof. The Lyapunov function V_1 for our model is $V_1(t, S, I, R) = C_1 I$.

We find that

$$\frac{dv_1}{dt} = C_1\left[\omega\frac{x}{Ny} - \delta - y\right]I \ .$$

By choosing C_1 as $\frac{1}{\omega\frac{x}{Ny} - \delta - y}$,

$$\frac{dv_1}{dt} = 0 \text{ if } I = 0 \ .$$

When we substituted $I = 0$ in our model system of equations, we discovered that S approaches 0 and R approaches 0 as time approaches infinity. As a result, according to Lasalle's invariance principle, the system of equations is stable at 0. As a result, at 0, the system is globally asymptotically stable. Hence, the system is globally asymptotically stable at P_1.

6.5. *Bifurcation*

If R_0 (θ) <1, the disease-free equilibrium point is stable; otherwise, R_0(θ) = 1 causes a bifurcation in equation (1).

$$1 = \frac{\omega(\theta)}{y(\delta(\theta) + y)}$$

If θ^* is the system's bifurcation value, then θ^* is the equation's solution.

$$y(\delta(\theta) + y) = \omega(\theta)$$

The value of bifurcation,

$$\theta^* = \frac{\theta_{\max}(\theta_M - \theta_{\min})y^2}{A\theta_{\max}(\theta - \theta_{\min}) - ((\pi_{\min} - 1)\theta + \theta_{\max})y(\theta_M - \theta_{\min})}$$

where $\theta^* \leq \theta_M$. In this way, if a virus is transmitted to some people, it should be noted that it is not higher than θ^*. This makes θ^* a fuzzy parameter connected to the control of the TB infection virus.

7. Sensitivity analysis

In this part, we conduct a sensitivity analysis to assess the resilience of the model when parameter values change as a result of parameter estimation uncertainty. We concentrate on how the fundamental reproduction number (R_0) responds to changes in the related factors.

Table 1. Parameters of sensitivity analysis

Parameters	Sensitivity value
y	-0.890566
ω	1
δ	-0.9896

8. Fuzzy basic reproduction number

By examining the stability of the equilibrium point, the fundamental reproduction number R_0 can be determined. For the TB infection model $R_0 = \frac{\omega(\theta)}{y(\delta(\theta) + y)}$, which rises with the virus load, this cannot be a fuzzy set because it can be more than 1, and it increases with the virus load. Therefore, $R_0(\theta)$ must be less than 1. The basic reproduction number R_0 is obtained through the analysis of the stability of the equilibrium point. For the TB infection model, $R_0 = \frac{\omega(\theta)}{y(\delta(\theta) + y)}$, which increases with an increase in the virus load, this cannot be a fuzzy set as it can be greater than 1. So, have $R_0(\theta)$ to be less than 1.

Thus, $\pi_{\min} R_0(\theta) \leq 1$, whereby $\pi_{\min} R_0(\theta)$ is a fuzzy set, $FEV[\pi_{\min} R_0(\theta)]$ is well defined. We previously found the FEV values of $R_0(\theta)$, $\omega(\theta)$, < 1 and $\delta(\theta) < 1$.

As we know that $\omega(\theta) < 1$, we obtain $\frac{\omega(\theta)}{y(\delta(\theta) + y(\theta))} < 1$. In this view, we introduce the fuzzy basic reproduction number [26-30].

The fuzzy basic reproduction number is given by

$$R_F = \frac{1}{\pi_{\min}} FEV\ [\pi_{min} R_0].$$

To obtain FEV, we need to define fuzzy measure of θ.

Where $FEV\ (\pi_{\min} R_0(\theta)) = \sup, 0 \leq \beta \leq 1.$

$k(\beta) = \theta\{v : \pi_{\min} R_0(\theta) \geq \beta\} = \theta(Y)$, which is a fuzzy measure. We find FEV by using the fuzzy measure. For this purpose, the possibility measure is given by

$$\theta(Y) = \sup \rho(\theta), \forall, \mu \in Y,\ Y \subset R$$

From $FEV(\pi_{\min} < R_0(\theta)$, it is clear that $R_0(\theta)$ is not decreasing with θ, where the set $X = [\overline{\theta}, \theta_{\max}]$ and θ is the solution of the following equation:

$$\frac{\pi_{\min}\omega(\theta)}{y(\delta(\theta)+y)} = \beta$$

Thus, $[k(\beta) = w[\theta', \theta_{\max}] = \sup \rho(\theta)$ with $\theta' \le \theta \le \theta_{\max}$, where $k(0) = 1$ and $k(1) = \rho(\theta_{\max})$.

Weak, medium, and strong virus loads are the three categories used to categorize the amount of virus in the human population, which was taken as a linguistic connotation. The heterogeneity of the human population of weak, medium, and strong virus loads shown in Figure 5.

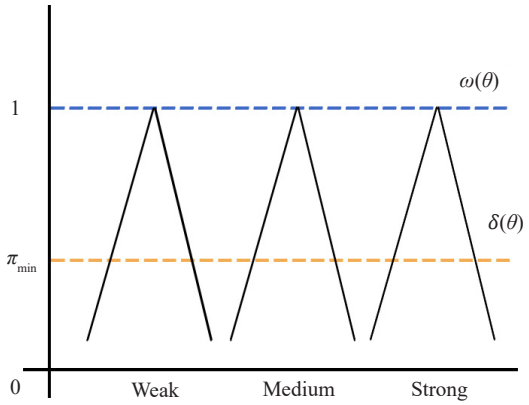

Figure 5. Heterogeneity of the human population

i) Weak ($\theta_{\min}$)

The viral load in this instance is low (i.e.) when $\overline{\theta} + b \le \theta_{\min}$.

Here, $\omega(\theta) = 0$ and $\delta(\theta) = \frac{(\pi_{\min} - 1)}{\theta_{\max}}\theta + 1$, we have calculated $FEV[\pi_{\min} R_0(\theta)]$.

$$FEV[\pi_{\min} R_0(\theta)] = \sup\{\min(\beta, w(\theta))\}, = 0$$

$$R_F \quad \frac{1}{\pi_{\min}} FEV[\pi_{\min} R_0(\theta)] \quad 0$$

In case we obtain $R_F = 0$, we might draw the conclusion that the illness will vanish.

ii) Medium (θ_M)

The viral burden in this instance is medium (i.e.) when and $\overline{\theta} - b \ge \theta_{\min}$ and $\overline{\theta} + b \le \theta_M$.

Here, $\omega(\theta) = \frac{\theta - \theta_{\min}}{\theta_M - \theta_{\min}}$ and $\delta(\theta) = \frac{\pi_{\min} - 1}{\theta_{\max}}\theta + 1.$

We have calculated $FEV[\pi_{\min} R_0(\theta)]$.

$$FEV\ [\pi_{\min} R_0(\theta)] = \sup\{\min(\beta, k(\beta))\}, 0 \le \beta \le 1$$

When $0 < \beta < 1$ with the answer to the following equation is β.

$$\frac{\pi_{\min}\omega(\theta)}{y(\delta(\theta)+y)} = \beta$$

For $0 < \beta < 1$, $k(\beta)$ for $0 \le \beta \le 1$,

$$k(\beta) = \begin{cases} 1, & \text{if } 0 < \beta \le \gamma_0 R_0(\overline{\theta}), \\ \rho(\overline{\theta}), & \text{if } \tau_{\min} R_0(\overline{\theta}) < \beta \le \tau_{\min} R_0(\overline{\theta}+b) \\ 0, & \text{if } \tau_{\min} R_0(\overline{\theta}+b) < \beta \le 1. \end{cases}$$

So, if $\pi_{\min} > 0, k(\beta)$ is continuous and decreasing function with $k(0) = 1$ and $k(1) = 0$. Hence, $FEV(\pi_{\min}\gamma_0 R_0(\theta))$ is the fixed point of k and R_F.

$$\pi_{\min} R_0(\overline{\theta}) \le FEV(\pi_{\min} R_0(\theta)) \le \pi_{\min} R_0(\overline{\theta}+b)$$
$$R_0(\theta) \le R_F \le R_0(\theta+b).$$

Due to the fact that the function $R_0(\theta)$ is growing and continuous, the intermediate value theorem states that with θ with $\overline{\theta} < \theta < \overline{\theta}+b$ exists, such that

$$R_F = R_0(\theta) > R_0(\overline{\theta}).$$

There is enough virus load in this area for R_0 and $R_0(\theta)$ to be equal. Additionally, due to the medium amount of virus, the average number of secondary cases R_F is higher than the average number of secondary cases $R_0(\overline{\theta})$.

iii) Strong ($\theta_{\max}$)

The viral burden in this instance is high (i.e.) when $\overline{\theta}+b \le \theta_M$ and $\overline{\theta}+b \le \theta_{\max}$.

Here, $\omega(\theta) = 1$ and $\delta(\theta) = \frac{(\tau_{\min}-1)}{\theta_{\max}}\theta$, we have calculated $FEV\left[\tau_{\min} R_0(\theta)\right]$.

$$FEV[\tau_{\min} R_0(\theta)] = \sup\left\{\min\left(\beta, k\left(\beta\right)\right)\right\}, \quad 0 \le \beta \le 1$$

When $0 < \beta < 1$, the answer to the following equation is β.

$$\frac{\pi_{\min}\omega(\theta)}{y(\delta(\theta)+y)} = \beta$$

For $0 < \beta < 1$, $k(\beta)$ for $0 \le \beta \le 1$,

$$k(\beta) = \begin{cases} 1, & \text{if } 0 < \beta \le \pi_{\min} R_0(\overline{\theta}), \\ \rho(\overline{\theta}), & \text{if } \pi_{\min} R_0(\overline{\theta}) < \beta \le \pi_{\min} R_0(\overline{\theta}+b), \\ 0, & \text{if } \pi_{\min} R_0\left(\overline{\mu}+b\right) < \beta \le 1. \end{cases}$$

Since k has a continuous and decreasing function $FEV[\pi_{\min} R_0(\theta)]$ and R_F, we can calculate its value directly.

$$\pi_{\min} R_0(\bar{\theta}) \le FEV(\pi_{\min} R_0(\theta)) \le \pi_{\min} R_0(\bar{\theta}+b)$$
$$R_0(\theta) \le R_F \le R_0(\theta).$$

As a result, $R_F > 1$ leads us to believe that the disease will be endemic. If the population's transmission and recovery rates are not zero, we can calculate the fuzzy basic reproduction number for the fuzzy TB infection model.

$$R_0(\theta) \le R_F \le R_0(\theta+b)$$

8.1 *Fuzzy control system*

In this subsection, we examined the control of TB disease estimation using fuzzy basic reproduction number and bifurcation value θ^*.

i) The virus load is low in this case (i.e.) when $\bar{\theta}+b \le \theta_{\min}$. R_F is the fuzzy basic reproduction number. It means that the disease will be eradicated.

ii) In this instance, the viral burden is medium (i.e.) if $\bar{\theta}-b \ge \theta_{\min}$ and $\bar{\theta}+b \le \theta_M$. There is a virus load in which R_0 and $R_0(\theta)$ coincide. Furthermore, due to the medium amount of virus, the average number of secondary cases R_F is higher than the number of secondary cases R_0 ($\bar{\theta}$).

iii) The virus load in this case is high (i.e.) when $\bar{\theta}+b \le \theta_M$ and $\bar{\theta}+b \le \theta_{\max}$. As a result of $R_F > 1$, the disease will be endemic.

9. Numerical simulation result

We examine the simulation analysis of the provided system of nonlinear differential equations in this part (1). Since the dynamics of the human population are described by these equations, which include intervention options, the model of TB infection in the simulation is compared to Euler's approach and the HPM. The parameter values x = 1449401, y = 0.001167, 0.5, and 0.111111 [33] are used for numerical simulation.

The results of comparing the proposed model's solutions using HPM and Euler's technique are shown in Figures 6, 7, 8, 9, 10, and 11, where days are plotted along the x axis and susceptible, infected, or recovered are plotted along the y axis. Since in each case, the two curves have the same pattern and behavior, the HPM generated the model's reliable and accurate findings, which are demonstrated by the excellent convergence of the HPM and Euler's method solutions. For 100 consecutive days, we calculate analytical and numerical values.

Figures 6 and 9 illustrate how long susceptible individuals can go without becoming ill. Only a small number of people acquire the illness. Figures 7, 10, and 11 demonstrate how the population of infectious people might suddenly decline if we increase the amount of virus or the amount of fumigation. As seen in Figures 8 and 11, the number of TB cases has reduced, while the number of those who have recovered has increased. A decline in the number of susceptible populations is seen along with this increase. Thus, it may be said that the TB epidemic is under control.

i) Euler's method

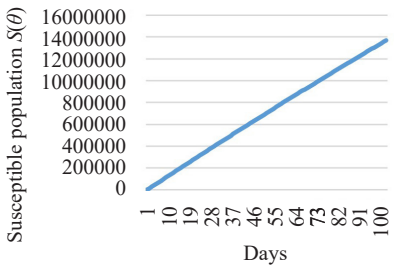

Figure 6. Susceptible population

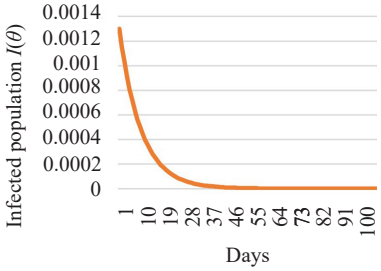

Figure 7. Infected population

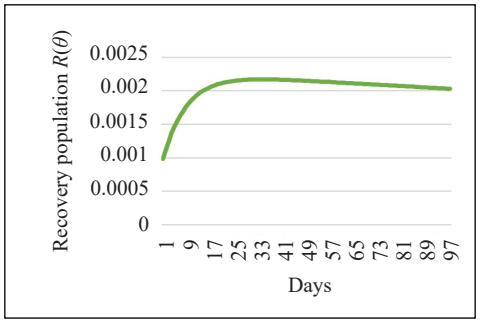

Figure 8. Recovery population

ii) HPM

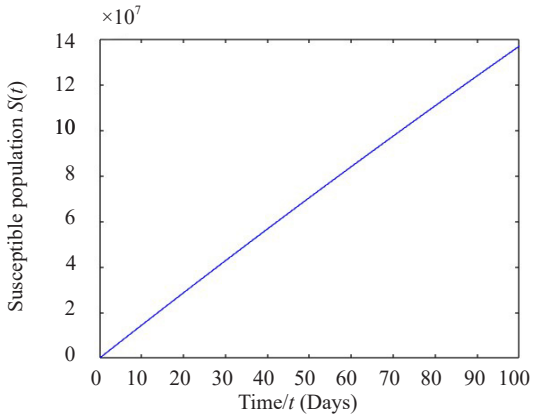

Figure 9. Susceptible population

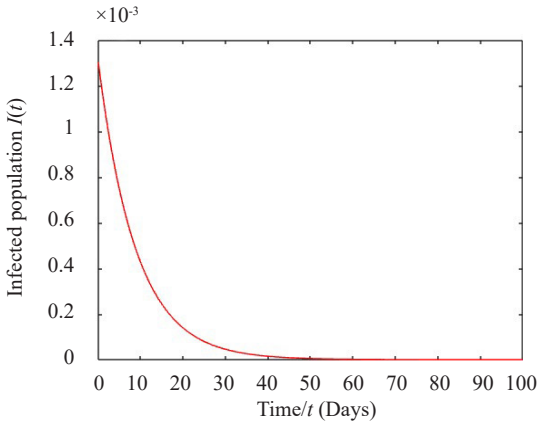

Figure 10. Infected population

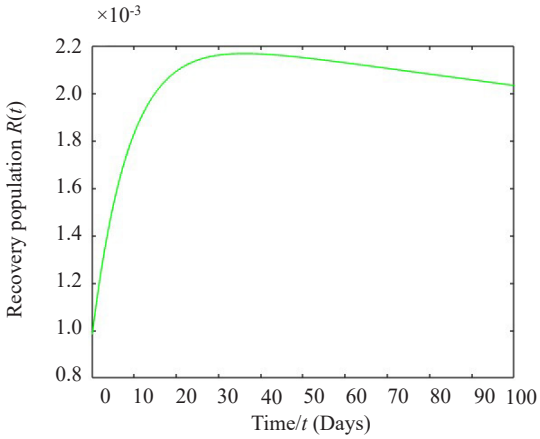

Figure 11. Recovery population

10. Conclusions

In this paper, we have proposed and studied the SIR mathematical model for TB in a fuzzy environment. The stability analysis, equilibrium points, sensitivity analysis, fuzzy basic reproduction numbers, and bifurcation have been

covered. Also, we have given plots of both exact and approximate solutions and shown the effect of delaying and halting the spread of the infectious bacteria viral load. In the future, from the clinical data of TB patients, we can classify multimodal features, reducing the interpretation of TB categorization

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Conflict of interest

The authors declare no conflict of interest.

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