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TREATMENT OF INFECTIOUS DISEASE FOR TUBERCULOSIS (TB) USING FUZZY MATHEMATICAL MODEL

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Abstract. In this paper, we study the fuzzy SIR epidemic model for Tuberculosis (TB) transmission. Here we discussed disease-free equilibrium point, endemic equilibrium point along with basic reproduction numbers at the consequences of different compartment phases. At the disease-free equilibrium point, the tuberculosis (TB) model is said to be both locally and globally asymptotically stable, endemic equilibrium point locally asymptotically stable. Bifurcation and fuzzy basic reproduction value of disease control is suggested. Simulation results show the effect in slowing and stopping the transmission of infectious bacteria virus load.

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Key words and phrases. TB infection model; stability analysis; bifurcation; fuzzy basic reproduction number; fuzzy control system; homotopy perturbation method.

1. Introduction

Mycobacterium tuberculosis, a member of the Mycobacteriaceae family with approximately 200 species, is the bacterium that causes tuberculosis (TB). Although extra-pulmonary TB can affect other organs, pulmonary TB most frequently affects the lungs in people. Through the air, it can spread from person to person. The majority of those who contract the illness are adults; in 2021, men made up 56.5% of people living with the condition, adult women made up 32.5%, and children made up 11%. TB is preventable and curable – Approximately 85% of the people who acquire TB can be successfully treated with a 4–6 month treatment regimen. 10.6 million Persons worldwide had TB diagnoses in 2021, increasing 4.5% from 2020, while 1.6 million patients died from the disease. India was one of the eight nations that accounted for more than two-thirds (68.3%) of all TB cases, with 28% of cases. China (7.4%), the Philippines (7%), Pakistan (5.8%), Nigeria (4.4%), Bangladesh (3.6%), Indonesia (9.2% instances), and the Democratic Republic of the Congo (2.9%) were the other nations [1].

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Swapan Kumar Nandi et al. [2] updated the system by using fuzzy numbers to represent the treatment control and disease transmission rate, then calculating the fuzzy expected value of the affected individuals, and the fuzzy basic reproduction number is evaluated to identify the pathogen threshold condition at which the system undergoes a backward bifurcation. The authors [3], constructed the SIR model with vaccination, and the solution is the number of TB patients tends to decline year by year. Juan Pablo Aparicio et al. [4], have compared the models that are parameterized using demographic, and epidemiological data, and the patterns generated, and also they have discussed the possible causes for the observed historical decline of tuberculosis notifications. Kalyan Das et al. [5], investigated the unique lead of the pandemic TB model for consistent controls of locally as well as globally asymptotically stable at infection-free stability points when the basic reproduction number is not as much as unity and novel endemic harmony when the basic reproduction number is more prominent than unanimity. The authors [6], discussed extensive investigations of casual contacts of highly infectious pulmonary tuberculosis may not be cost-effective, even when contact has been made with those presumed to be vulnerable. Tuberculosis has rightly been given a high profile in the 1990s, but its basic epidemiology must not be forgotten when planning contact investigations.

Samuel Bowong et al. [7], described this model, which deals with the general characteristics of tuberculosis with mass action incidence and two differential infectivity, and the direct Lyapunov approach allows us to demonstrate that the model under consideration is globally stable. Syafruddin Side et al. [8], have highlighted the causes of predicted that the number of infection cases will continue to increase therefore government needs to take preventive measures to control and reduce the number of TB infections in South Sulawesi. Yasin Ucakana et al. [9] study to develop the dynamics of infectious diseases, many mathematical models for tuberculosis diseases and they discussed the accuracy of results for all three models to compare the effect of the vaccination rate. Zohu et al. [11], have discussed improving the efficiency and enlarging the capacity of the treatment to control the spread of disease. Authors [12], carried out the disease-extended model of the number of subsequent infections that are always reduced in infected persons.

Kermack and McKendrick [17] investigate the research of the mathematical SIR model of infectious diseases and epidemics. Zadeh [16] introduced the fuzzy set, fuzzy theory, and the uncertainty fuzzy mathematical model in biology. Some models taking into account the uncertainty of fuzzy model and fuzzy parameter space [13, 15, 18, 19] spared the fuzzy epidemic mathematical models for the human infectious disease. Bhuju et al. [20] highlighted the system of control variable fumigation, proportion of bed net users, and proportion of effectiveness of bed nets are very important parameters for transmission of dengue and they discussed bifurcation values of the system for P_0 are also different for different values of the control variable. Authors [13,21] discussed an epidemic model, a dynamic system with a fuzzy transmission rate and several non-linear models of ordinary differential equations

have been utilized. In this paper, Section 2: Preliminaries, Section 3: Fuzzy SIR Model of TB- Infection, Section 4: deals with fuzzy system analysis, Section 5: deals with a fuzzy model of stability analysis, Section 6: sensitivity analysis, Section 7:fuzzy basic reproduction number, Section 8: deals with the outcomes of numerical simulation, and Section 9: works with the conclusion.

2. Preliminaries

2.1. **Definition (Fuzzy Set).** Let X is a nonempty crisp sets. A fuzzy subset S of X is denoted by $\widetilde{S}$ and is defined as

$$\widetilde{S} = \{(x, \mu_{S(x)}) : x \epsilon X\}$$

Where μ_S: $X \to [0, 1]$ is a membership function associated with a fuzzy set $\widetilde{S}$ which describes the degree of belongingness of x with X. Here we use the membership function $\mu(x)$ to indicate the fuzzy subsets $\tilde{S}$. Also $\mu(x)$ is called fuzzy number if X is the set of real numbers.

2.2. **Definition (Triangular Fuzzy Number).** A Fuzzy set is called Triangular fuzzy number if the membership value can be represented by a Triangular Function. This function by a three parameters $F(x : a, b, c)$ such as:

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

2.3. **Definition (Fuzzy Measure and Fuzzy Expected Value).** Let Ω be a nonempty set and $P(\Omega)$ denote the set of all subsets of Ω. Then μ: $\Omega \to [0, 1]$ is a fuzzy measure [5], if

(1) $\mu(\phi) = 0$ and $\mu(\Omega) = 1$,
(2) For $A, B \epsilon P(\Omega), \mu(A) \leq \mu(B)$ if $A \subset B$

Let μ: $\Omega \to [0, 1]$ be an uncertain variable, i.e., μ is a fuzzy subset and μ a fuzzy measure on Ω. Then fuzzy expected value (FEV) of μ is the real number, defined by the Sugeno measure [10].

$$FEV(\mu) = \int \mu d\mu = \sup\{\min(\alpha, k(\alpha))\},\ 0 \leq \alpha \leq 1$$

Where $k(\alpha) = \mu\{\omega \in \Omega : \mu(\omega) = \alpha\}$.

3. Fuzzy SIR Model of TB-Infection

In the condition of vital dynamics, the spread of illnesses across susceptible and infected populations has been simulated using the fuzzy SIR model of Tb infection. A SIR epidemic model with fuzzy parameters was suggested in this section. The suggested model is explained using non-linear differential equations. The epidemic model's diagram, as seen in Fig. 1, is made to make the modeling process straightforward. This model for TB infection has three compartments. Susceptible-Infected-Recovered describes them. The schematic model that explains compartments and their rate is shown in Fig. 1. Table 1&2 also included an explanation of variables and parameters.

$$\begin{aligned}
\frac{dS}{dt} &= (1-\vartheta)\sigma N - \left(\frac{\mu(\varepsilon)I}{N} + \rho\right) S + \theta R \\
\frac{dI}{dt} &= \frac{\mu(\varepsilon)I}{N} S - (\tau(\varepsilon) + \rho + \omega) I \\
\frac{dR}{dt} &= \vartheta\sigma N + \tau(\varepsilon) I - (\rho + \theta)
\end{aligned} \tag{1}$$

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

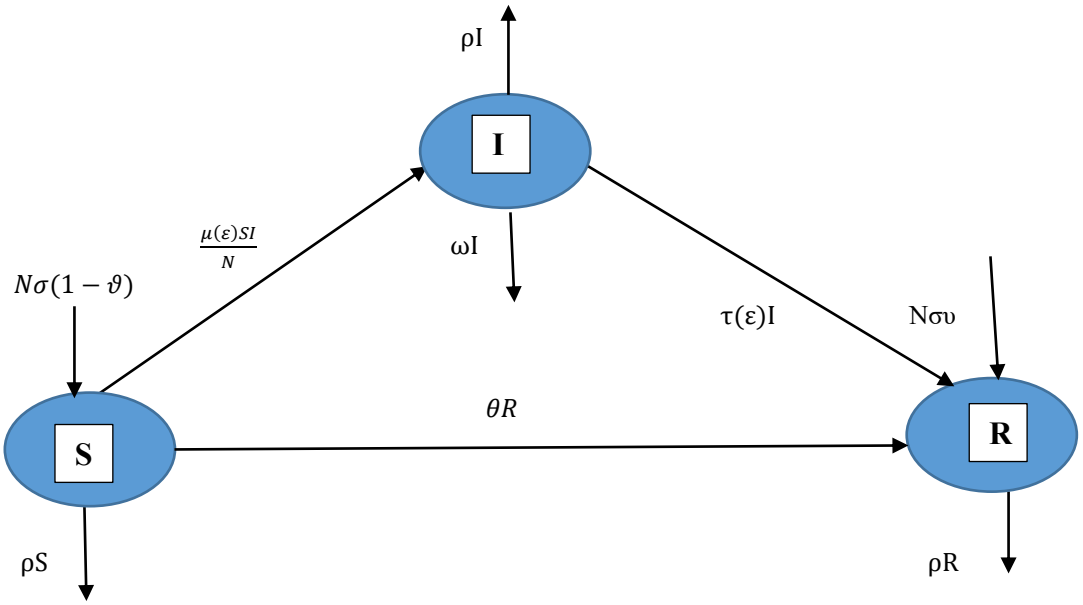

Figure 1. Diagram representation of fuzzy SIR model of TB-infection

3.1. **Properties of the TB Model.** In this section, the fundamental elements of the TB infection model (1) will be looked at. The epidemiological importance of the TB-infection model (1) depends on the presence and uniqueness of the answers to the non-negative for all $t \geq 0$.

TABLE 1. Descriptions of model variables

	Variables
S	Number of Susceptible Population
I	Number of Infected Population
R	Number of Recovery Population

TABLE 2. Descriptions of model parameters

	Parameters
σ	Rate of birth
μ	Rate of Contact
τ	Rate of recovery
ρ	Rate of fatality
θ	Rate of immunity loss
ω	Rate of disease fatality
ϑ	Rate of individuals vaccinated

3.1.1. *Existence and uniqueness.* The follow are the system's initial conditions:

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

Theorem: 1. Identify the existence and uniqueness of the non-negative starting condition model solutions for all $t \geq 0(1)$.

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

$$\begin{aligned} X_1 &= (1-\vartheta)\sigma N - \left(\frac{\mu(\varepsilon)I}{N} + \rho\right) S + \theta R \\ X_2 &= \frac{\mu(\varepsilon)I}{N} S - (\tau(\varepsilon) + \rho + \omega)I \\ X_3 &= \vartheta\sigma N + \tau(\varepsilon)I - (\rho + \theta)R \end{aligned} \tag{2}$$

X_k an autonomous continuous function on $\mathbb{R}^3$, since X is an algebraic polynomial, and its partial derivatives are continuous and exist. Thus, for any initial condition $f(0)\epsilon\mathbb{R}^3$, the existence and uniqueness theorem [12] states that a single solution to the system $f' = X(f)$ exists.

3.2. **Feasibility Analysis.**

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

Proof: We analyse the state variables function at the boundary of E in order to prove the theorem, were

$$E = \{(S, I, R)\epsilon\mathbb{R}^3 : 0 \leq S, I, R\}$$

Examine the following constraints, S=R=0, and then read the explanations for each situation below.

(1) At $S = 0$,

$$S' = (1 - \vartheta)\sigma N + \theta R > 0$$

Case: 1

If $S = 0$, $R = 0$ then $S' = (1 - \vartheta)\sigma N$

Case: 2

If $S = 0$, $R > 0$ then $S' > 0$

Since $S' \geq 0$, in order to exit Q, the solution cannot cross this boundary.

(2) At $R = 0$,

$$R' = \vartheta\sigma N + \tau I > 0$$

Case: 1

If $R = 0$, $I = 0$ then $R' = \vartheta\sigma N$

Case: 2

If $R = 0$, $I > 0$ then $R' > 0$

Since $R' \geq 0$, in order to exit Q, the solution cannot cross this boundary.

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

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

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

$$N = (1 - \vartheta)\sigma N + \vartheta\sigma N - \rho(S + I + R)$$

$$\frac{dN}{dt} = (\sigma - \rho)N$$

$$N = \frac{\sigma}{\rho} + (N(0) + \frac{\sigma}{\rho})e^{-\rho t}$$

Therefore, $\lim_{t\to\infty} \sup N \leq \frac{\sigma}{\rho}$.

So, $S(t), I(t), R(t)$ are bounded above by $\frac{\sigma}{\rho}$ on $[0, b)$ for some $b > 0$. Since all variables are bounded below 0 as they are all non-negative. As a result, for some $b > 0$, the solution of the system (2) is bounded on $[0, b)$.

4. Fuzzy Systems

Fuzzy systems are developed by modifying the mathematical model of tuberculosis infection. As a result, depending on the sickness, different human populations have different rates of infection and recovery. The term denoted by $\alpha(\varepsilon)$ is a triangular fuzzy number with a membership function.

$$\alpha(\varepsilon) = \begin{cases} 0, & \texttt{if } \varepsilon < \overline{\varepsilon} - z, \\ \dfrac{\varepsilon - \overline{\varepsilon} + z}{z}, & \textit{if } \overline{\varepsilon} - z \leq \varepsilon \leq \overline{\varepsilon}, \\ 1 & \textit{if } \overline{\varepsilon} \\ \dfrac{-(\varepsilon - \overline{\varepsilon} - z)}{z}, & \textit{if } \overline{\varepsilon} < \varepsilon \leq \ \overline{\varepsilon} + z, \\ 0, & \textit{if } \varepsilon > \overline{\varepsilon} + z. \end{cases} \tag{3}$$

If z is the spread of each of the fuzzy sets that are taken into account by, then the center value is $\overline{\varepsilon}$. 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. Fig. 2 provides a visual representation of $\alpha(\varepsilon)$.

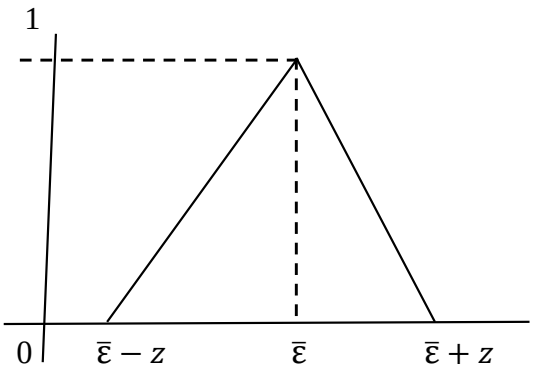

Figure 2. Triangular fuzzy number

Taking into consideration the heterogeneity of the human population. The transmission rate and recovery rate are used as different fuzzy parameters. The rate at which the disease process from susceptible to infectious $(0 \leq \mu(\varepsilon) \geq 1)$ is presummit to be transmitted by the TB virus to the human population. We consider the transmission rate in this model to be a fuzzy number with a membership function $\mu(\varepsilon)$ that varies with the amount of virus load and is given by:

$$\mu(\varepsilon) = \begin{cases} 0, & \textit{if } \varepsilon < \varepsilon_{min}, \\ \dfrac{\varepsilon - \varepsilon_{min}}{\varepsilon_M - \varepsilon_{min}}, & \textit{if } \varepsilon_{min} \leq \varepsilon \leq \varepsilon_M, \\ 1, & \textit{if } \varepsilon_M \leq \varepsilon \leq \varepsilon_{max} \end{cases} \tag{4}$$

Where ε the virus load is ε_{min} is the minimum virus amount indicated for disease transmission. The risk of disease transmission is minimal when a person has less virus inside of them than ε_{min}. The disease transmission rate is maximum and equal to 1 when the virus load ε_M is medium, and ε_{max} is the maximum virus load of an individual in the population. The transmission rate membership function is shown in Figure 3.

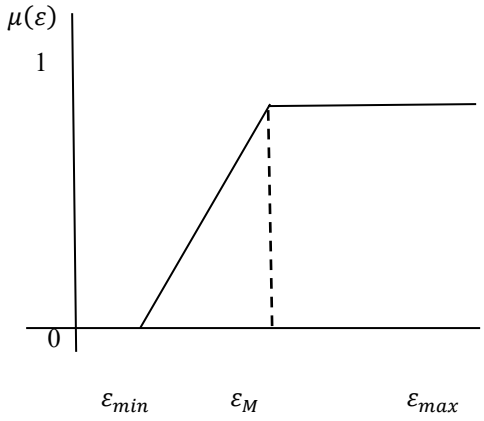

FIGURE 3. Membership function of transmission rate

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

$$\tau(\varepsilon) = \frac{(\pi_0 - 1)}{\varepsilon_{max}}\varepsilon + 1, \quad if\, 0 < \varepsilon < \varepsilon_{max} \tag{5}$$

Where $0 < \pi_0 < 1$, is the population's minimum rate of recovery and ε is the viral load. The recovery rate membership function is shown in Figure 4.

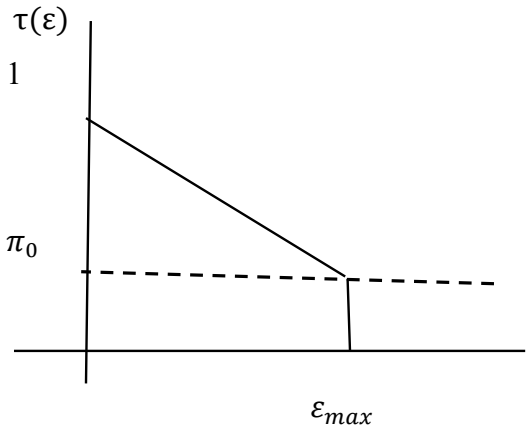

FIGURE 4. Membership function of recovery rate

5. Stability of Fuzzy SIR Model

In order to calculate the stability analysis in this section, we require the equilibrium points and the basic reproduction number. This TB spread model includes two equilibrium points that we have identified.

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

5.1. **Infection-Free Equilibrium.** When there is no TB infection in the human population, that is, when there are no TB-causing infections in the population, M_1 represents the Infection- free equilibrium point, which is a steady state solution.

Let's discuss about, $S_1 = I_1 = R_1 = 0$

The DFE point as $M_1 = (\frac{(1-\vartheta)\sigma N}{\rho}, 0, 0)$

5.2. **Infection Equilibrium.** The Infection equilibrium is defined as the point at which TB disease is present in the human population.

Let's discuss about, $S_2 > 0$, $I_2 > 0$ and $R_2 > 0$

We get the Infection equilibrium point is $M_2 = (S_2, I_2, R_2)$

$$S_2 = \frac{N((\rho+\theta)(1-\vartheta)N\sigma + \theta(\vartheta\sigma N + \tau I))}{(\mu I + N\rho)(\rho+\theta)}$$

$$I_2 = \frac{N((\rho+\theta)(1-\vartheta)N\sigma + \theta(\vartheta\sigma N + \tau I))}{(\mu I + N\rho)(\rho+\theta)}$$

$$R_2 = \frac{\vartheta\sigma N + \tau I}{(\rho+\theta)}$$

5.3. **Basic Reproduction Number.** The basic reproduction number R_0 for the system is determined using the next-generation matrix method [13] to determine R_0:

The basic reproduction number is $R_0 = \frac{\mu(\varepsilon)\sigma(1-\vartheta)}{\rho(\tau(\varepsilon)+\rho+\omega)}$

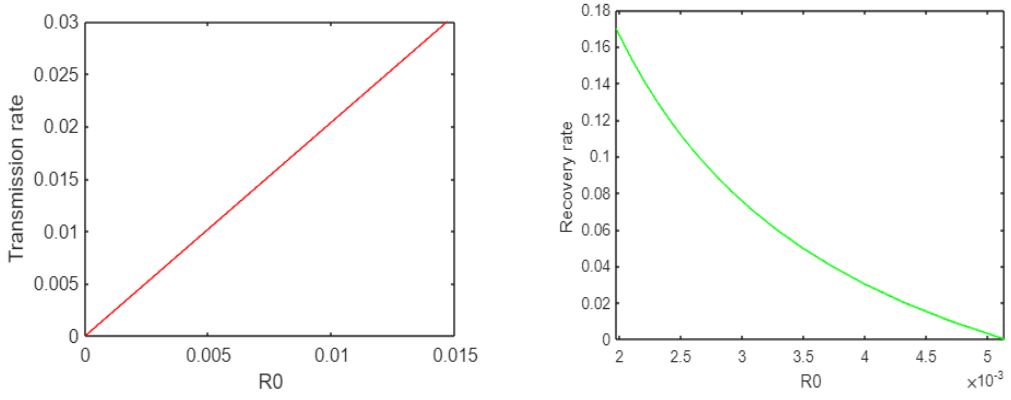

Figure 5. Diagram representation of transmission and recovery rate

5.4. **Local Asymptotically Stable at Equilibrium Points.**

Theorem: 4. The Infection-free equilibrium points $M_1 = (\frac{(1-\vartheta)\sigma N}{\rho}, 0, 0)$ is locally asymptotically stable When $R_0 < 1$, and unstable when $R_0 > 1$.

Proof: The Jacobian matrix of the system of equation (2), which is given by, is used to determine the stability of the disease's free equilibrium.

$$J(M_1) = \begin{bmatrix} -\rho & -\mu(1-\vartheta)\sigma & \theta \\ 0 & \mu(1-\vartheta)\sigma - (\tau+\rho+\omega) & 0 \\ 0 & \tau & -(\rho+\theta) \end{bmatrix} \tag{6}$$

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

$$|J - XI| = 0$$

$$(-\rho - X)(\mu(1-\vartheta)\sigma - (\tau+\rho+\omega) - X)(-(\rho+\theta) - X) = 0$$

Therefore, $X = \vartheta, \sigma, \mu, \tau, \rho, \theta$ and ω

$$C_1X^3 + C_2X^2 + C_3X + C_4 = 0 \tag{7}$$

The Routh-Hurwitz criterion [19] states that the system of equations is locally asymptotically stable if the roots of the equations $C_1 - C_4 > 0$ and $C_2C_3 - C_1C_4 > 0$ are both negative. The system's Infection-free equilibrium point is locally asymptotically stable because of $R_0(\varepsilon) < 1$.

Theorem: 5. The Infection 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 establish the stability of the Infection equilibrium, we may determine that $|J - \mu I| = 0$ using the Jacobian matrix of the system of equations (6&7). The roots of the equations $C_1 - C_4 > 0$ and $C_2C_3 - C_1C_4 > 0$ are both negative by the Routh-Hurwitz criterion [19]. As a result, the system's Infection equilibrium point will be locally asymptotically stable if $R_0(\varepsilon) > 1$.

5.5. **Globally Asymptotically Stable for Infection-free Equilibrium Point.** In this subsection, we will simply analyze the TB model's Infection-free equilibrium point.

Theorem: 6. The Infection-free equilibrium points $M_1 = (\frac{(1-\vartheta)\sigma N}{\rho}, 0, 0)$ are globally asymptotically stable When $R_0 < 1$ and unstable when $R_0 > 1$.

Proof: The Lyapunov function W_1 for our model is $W_1(t, S, I, R) = A_1 I$

We find that

$$\frac{dW_1}{dt} = A_1 \left[\frac{\mu}{N} S - (\tau + \rho + \omega)\right] I$$

By choosing A_1 as $\frac{1}{\mu(1-\vartheta)\sigma-(\tau+\rho+\omega)}$, it is clear that

$$\frac{dw_1}{dt} = 0 \text{ iff } I = 0$$

When time approaches infinity, we found that S approaches 0 and R approaches 0 when we substituted $I = 0$ in our model system of equations. Lasalle's invariance principle states that the system of equations is stable at 0 as a result. The system is hence globally asymptotically stable at 0. As a result, the system is universally stable at M_1.

5.6. **Bifurcation.** The Infection-free equilibrium point is stable, if $R_0(\varepsilon) < 1$, then the equations (1) is at a bifurcation point when $R_0(\varepsilon) = 1$

$$R_0(\varepsilon) = \frac{\mu(\varepsilon)\sigma(1-\vartheta)}{\rho(\tau(\varepsilon) + \rho + \omega)}$$

$$1 = \frac{\mu(\varepsilon)\sigma(1-\vartheta)}{\rho(\tau(\varepsilon) + \rho + \omega)}$$

Let ε^* be the bifurcation value of the system, then ε^* is the solution of the equation

$$\rho(\tau(\varepsilon) + \rho + \omega = \mu(\varepsilon)\sigma(1-\vartheta)$$

The value of bifurcation,

$$\varepsilon^* = \frac{\varepsilon_{max}((\varepsilon_M - \varepsilon_{min})\rho(1 + \rho + \omega) + \varepsilon_{min}\sigma(1-\vartheta))}{\sigma(1-\vartheta)\varepsilon_{max} - (\varepsilon_M - \varepsilon_{min})\rho(\pi_0 - 1)}$$

Where $\varepsilon^* \leq \varepsilon_M$.

In this way, if a virus ε is transmitted in some people, it should be noted that is not higher than ε^*. This provides ε^* a fuzzy parameter connected to the control of the TB infection virus.

6. Sensitivity Analysis

The impact of each parameter on the transmission of disease is revealed via sensitivity analysis. Together including experimental design, this understanding is important for the reduction of nonlinear models and information assimilation [20]. Sensitivity analysis is widely utilized to assess how parameter values influence model predictions since mistakes in data collection and expected parameter values are common. Because they significantly affect R_0, it is utilized to highlight the characteristics that educational interventions should concentrate on. According to sensitivity indices, we may assess the corresponding change in a variable when a parameter changes.

TABLE 3. Parameters of sensitivity analysis

Parameters	**Sensitivity value**
σ	1
μ	1
τ	-0.622260
ρ	1
ω	-0.35648
ϑ	-1

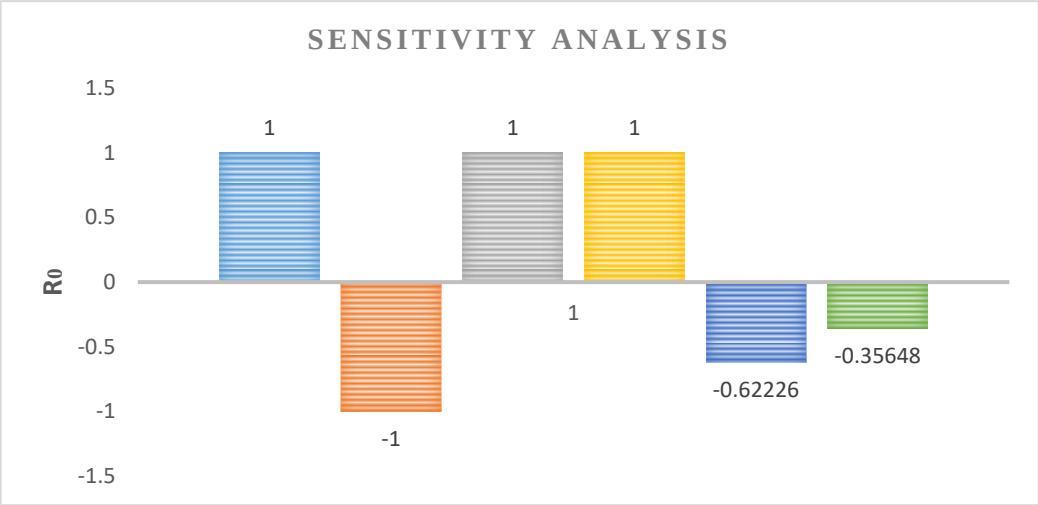

FIGURE 6. Diagram representation of sensitivity analysis

7. Fuzzy Basic Reproduction Number

The fuzzy basic reproduction number is [21] given by

$$R_F = \frac{1}{\pi_0} FEV[\pi_0 R_0(\varepsilon)]$$

To obtain FEV we need to define the fuzzy measure of ε

where $FEV(\pi_0 R_0(\varepsilon)) = sup\{inf(\beta, k(\beta))\}, 0 \leq \beta \leq 1,$

$k(\beta) = \varepsilon\{v : \pi_0 R_0(\varepsilon) \geq \beta\} = \varepsilon(Y)$, which is a fuzzy measure. By implementing the fuzzy measure, we determine FEV. The possibility measure is provided for this purpose by,

$$\varepsilon(Y) = supX(\varepsilon),\ \forall\, v \in Y,\ Y \subset R$$

From $FEV(\pi_0 < R_0(\varepsilon))$, it is clear that $R_0(\varepsilon)$ is not decreasing with ε, where the set, $Y = [\overline{\varepsilon}, \varepsilon_{max}]$, and $\overline{\varepsilon}$ is the solution of the following equation

$$\frac{\pi_0 \mu(\varepsilon)\sigma(1-\vartheta)}{\rho(\tau(\varepsilon) + \rho + \omega)} = \beta$$

Thus, $k(\beta) = v[\varepsilon', \varepsilon_{max}] = sup\rho(\varepsilon)$ with $\varepsilon' \leq \varepsilon \leq \varepsilon_{max}$, where $k(0) = 1$ and $k(1) = \rho(\varepsilon_{max})$.

Weak, medium, and strong virus loads are the three main types used to categorize the amount of virus in the cell population of the human body, which was thought to have linguistic significance.

Case 1: The viral load in this situation is low. (i.e.) when $\overline{\varepsilon} + z \leq \varepsilon_{min}$.

Here $\mu(\varepsilon) = 0$ and $\tau(\varepsilon) = \frac{(\pi_0 - 1)}{\varepsilon_{max}}\varepsilon + 1$. We have calculated $FEV[\pi_0 R_0(\varepsilon)]$.

$$FEV[\pi_0 R_0(\varepsilon)] = sup\{\min(\beta, v(\varepsilon))\}, = 0$$

$$R_{f0} = \frac{1}{\pi_0} FEV[\pi_0 R_0(\varepsilon)] = 0$$

In case we obtain $R_{f0} = 0$. It means. Hence, we can come to the conclusion that the illness will disappear.

Case 2: The infection load in this situation is Medium. (i.e.) when $\overline{\varepsilon} - z \geq \varepsilon_{min}$ and $\overline{\varepsilon} + z \leq \varepsilon_M$.

Here $\mu(\varepsilon) = \frac{\varepsilon - \varepsilon_{min}}{\varepsilon_M - \varepsilon_{min}}$ and $\tau(\varepsilon) = \frac{\pi_0 - 1}{\varepsilon_{max}}\varepsilon + 1$

We have calculated $FEV[\pi_0 R_0(\varepsilon)]$.

$$FEV[\pi_0 R_0(\varepsilon)] = sup\{\min(\beta, k(\beta))\}, \ 0 \leq \beta \leq 1$$

When $0 < \beta < 1$ with β is the solution of the following equation.

$$\frac{\pi_0 \mu(\varepsilon)\sigma(1 - \vartheta)}{\rho(\tau(\varepsilon) + \rho + \omega)} = \beta$$

For $0 < \beta < 1$ we divide into three Parts. $k(\beta)$ for $0 \leq \beta \leq 1$

$$k(\beta) = \begin{cases} 1, & \text{if } 0 < \beta \leq \pi_0 R_0(\overline{\varepsilon}), \\ \rho(\overline{\varepsilon}), & \text{if } \pi_0 R_0(\overline{\varepsilon}) < \beta \leq \pi_0 R_0(\overline{\varepsilon} + z) \\ 0, & \text{if } \pi_0 R_0(\overline{\varepsilon} + z) < \beta \leq 1 \end{cases}$$

So, if $\pi_0 > 0$, $k(\beta)$ is continuous and decreasing function with $k(0) = 1$ and $k(1) = 0$. Hence, $FEV(\pi_0 R_0(\varepsilon))$ is the fixed point of k and R_{f0}

$$\pi_0 R_0(\overline{\varepsilon}) \leq FEV(\pi_0 R_0(\varepsilon)) \leq \pi_0 R_0(\overline{\varepsilon} + z),$$

$$R_0(\theta) = R_{f0} = R_0(\varepsilon + z)$$

Due to the fact that the function $R_0(\varepsilon)$ is increasing and continuous, the intermediate value theorem states that ε with $\overline{\varepsilon} < \varepsilon < \overline{\varepsilon} + z$ exists such that,

$$R_{f0} = R_0(\varepsilon) > R_0(\overline{\varepsilon})$$

There is a sufficient virus load that R_0 and $R_0(\overline{\varepsilon})$ are equal. Also, due to the medium amount of virus, the average amount of secondary illnesses R_{f0} is greater than the typical number of secondary illnesses $R_0(\overline{\varepsilon})$.

Case 3: The infection load in this situation is high. (i.e.) when $\overline{\varepsilon} + z \leq \varepsilon_M$ and $\overline{\varepsilon} + z \leq \varepsilon_{max}$.

Here $\mu(\varepsilon) = 1$ and $\tau(\varepsilon) = \frac{(\pi_0 - 1)}{\varepsilon_{max}}\varepsilon + 1$, we have calculated $FEV[\pi_0 R_0(\varepsilon)]$.

$$FEV[\pi_0 R_0(\varepsilon)] = sup\{\min(\beta, k(\beta))\},\ 0 \leq \beta \leq 1$$

When $0 < \beta < 1$ with β is the solution of the following equation.

$$\frac{\pi_0 \mu(\varepsilon)\sigma(1-\vartheta)}{\rho(\tau(\varepsilon) + \rho + \omega)} = \beta$$

For $0 < \beta < 1$ we divide into three Parts. $k(\beta)$ for $0 \leq \beta \leq 1$

$$k(\beta) = \begin{cases} 1, & \text{if } 0 < \beta \leq \pi_0 R_0(\overline{\varepsilon}), \\ \rho(\overline{\varepsilon}), & \text{if } \pi_0 R_0(\overline{\varepsilon}) < \beta \leq \pi_0 R_0(\overline{\varepsilon} + z) \\ 0, & \text{if } \pi_0 R_0(\overline{\varepsilon} + z) < \beta \leq 1 \end{cases}$$

Since the function of k is continuous and decreasing, we can directly calculate $FEV[\pi_0 R_0(\varepsilon)]$ and R_{f0}.

$$\pi_0 R_0(\varepsilon) \leq FEV(\varepsilon_0 R_0(\varepsilon)) \leq \pi_0 R_0(\overline{\varepsilon} + z),$$

$$R_0(\varepsilon) = R_{f0} = R_0(\varepsilon + z)$$

Thus, $R_{f0} > 1$; We can deduce that the illness will be widespread.

If the population's transmission and infection rates are not zero, we are able to calculate the fuzzy basic reproduction number of the fuzzy TB infection model.

$$R_0(\varepsilon) = R_{f0} = R_0(\varepsilon + z)$$

7.1. **Fuzzy Control System.** In this part, we've examined that fuzzy basic reproduction numbers and the Bifurcation Parameter ε^* can be used to influence the estimation of the TB disease.

Case (a). Amount of virus is low. Here, the minimum virus amount $\varepsilon < \varepsilon^*$ denotes that when the basic reproduction number falls to zero, the system will be free of sickness because the basic reproduction number is less than unity.

Case (b). Amount of virus is medium.

(1) If $\varepsilon < \varepsilon^*$ the system will be infection-free since the basic reproduction number is less than unity.
(2) A bifurcation around the infection-free equilibrium occurs if $\varepsilon = \varepsilon^*$, which means that $R_0(\varepsilon) = 1$ and that this phenomenon has previously been demonstrated.
(3) If $\varepsilon > \varepsilon^*$, the system will be endemic since the basic reproduction number is greater than unity.

Case (c). Amount of virus is strong. Here, $\varepsilon \in [\varepsilon_{min}, \varepsilon_M]$, and by applying this, we obtain $R_0(\varepsilon) = \frac{1}{\pi_0}$. As a result, the parameter determines how quickly the disease spreads. Three scenarios regarding the disease's spread are possible in this situation.

(1) If $0 \leq \varepsilon < 1$, then $R_0(\varepsilon) < 1$. As a result, the illness will disappear from the person.

(2) If $0 = \varepsilon = \varepsilon^*$ during a bifurcation, the system exhibits increased trend approaching the infection-free equilibrium.

(3) If $\varepsilon > \varepsilon^*$, then $R_0(\varepsilon) > 1$. So, in this scenario, the disease would propagate using a compartmentalised SIR epidemic model.

8. Numerical Simulation Result

We examine the simulation analysis of the provided system of non-linear differential equations by using homotopy perturbation method. The simulation for numerical simulation, the parameter values $\sigma = 0.0162512$, $\mu = 0.0039008$, $\tau = 0.173955$, $\rho = 0.005939$, $\theta = 0.192632$, $\omega = 0.0996568$ and $\vartheta - 0.95$ [3] are utilized.

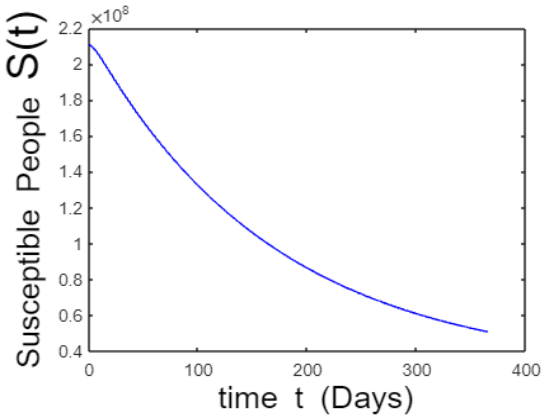

Figure 7. Susceptible population

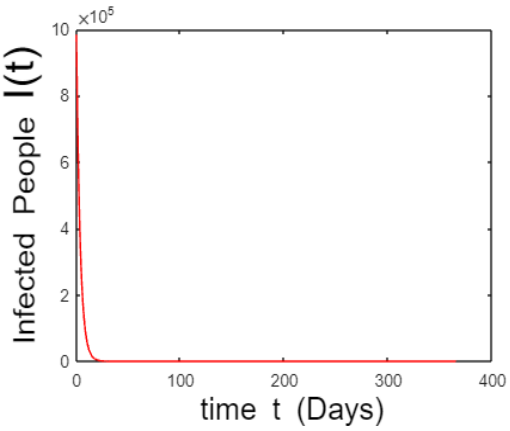

Figure 8. Infected population

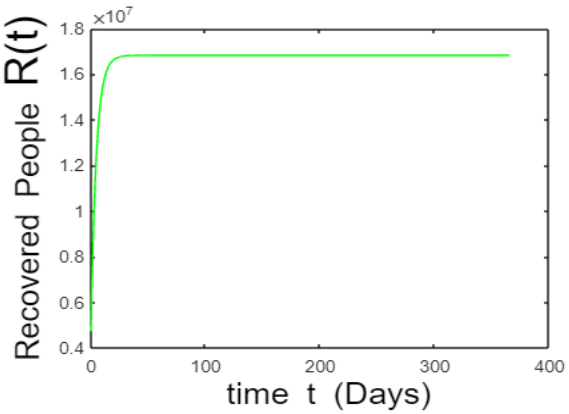

FIGURE 9. Recovery population

Figure 7 indicates that out of 216414500 persons, 210691233 were vulnerable.The line will converge to a point after crossing the peak point and then begin a steady decline. This indicates that the presumed population will likely decrease at some point in the future.Regarding Figure 8, 984000 out of 216414500 people were infected. As time goes on, the number of infected people decreases gradually, dropping sharply near to the x-axis.Considering Figure 9, From 216414500 individuals, 4739267 were recovered; this indicates that the proportion of healthy people has grown over time. The rate of recovery from infection is more than the rate of death of the recovered class, and the rate of disease transmission from suspect to infected is unable to spread, which is the reason of the increase.

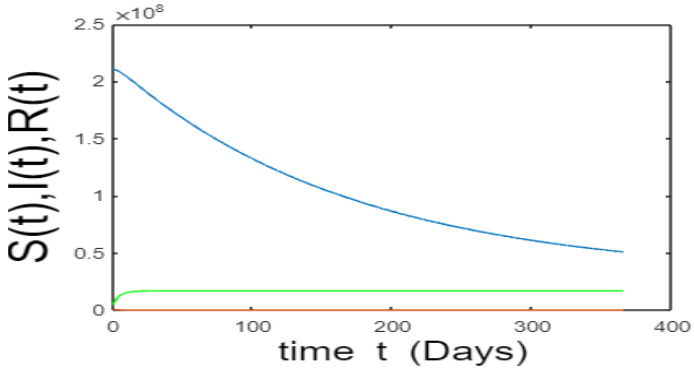

FIGURE 10. SIR model

Figure 10 SIR model Shows susceptible, infected and recovered human population be plotted in the graph of fuzzy environment. From this figure, it is seen that as the value of susceptible and infected is increases, then all the human population gradually decrease. So, it is concluded that the tuberculosis (TB) takes proper treatment, the disease will be control.

9. Conclusions

In this study, we explored for a mathematical model of tuberculosis (TB) in fuzzy environment. For models with fuzzy parameters, the stability analysis, equilibrium points, and basic reproduction number are examined. For $R_0(\varepsilon) < 1$ and $R_0(\varepsilon) > 1$, the points of endemic equilibrium and disease-free equilibrium are locally asymptotically stable and the points of disease-free equilibrium are globally asymptotically stable. We calculated the sensitivity analysis, the fuzzy basic reproduction number, and the bifurcation. The impact on reducing and preventing the spread of the infectious bacterium virus load is demonstrated by simulation findings.

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Authors' Contributions

All the authors contributed significantly in writing this article. The authors read and approved the final manuscript.

Conflicts of Interest

The authors declare that they have no competing interests.

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