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A SIMPLE SIDTR ENDEMIC MODEL TO MAKE TUBERCULOSIS FREE INDIA AND STOP SPREADING

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Abstract. In this paper, we construct a SIDTR model. We develop a system of differential equations for SIDTR (Suspected, Infected, Diagnosed, Treatment and Recovered) model and analyze the outbreak of Tuberculosis (TB) infection and its effect on Indian population. We established theorems on stability analysis conditions for disease free equilibrium and endemic equilibrium. The basic reproduction number R_0 was determined by using the next generation matrix. We attempt to fit our proposed mathematical model by using real world data which was taken from WHO. We expect that this study will be effective on controlling Tuberculosis (TB) spread and also we predicted the future TB infection in India.

Keywords: Tuberculosis (TB); mathematical model; next generation matrix; eigenvalues; stability analysis.

2020 AMS Subject Classification: 37N25, 92B05, 93A30.

1. INTRODUCTION

Tuberculosis (TB) is a serious disease that mainly affect the lungs and it is a type of bacteria. It is an infectious diseases. It is originated by a bacterium called Mycobacterium tuberculosis, which is a member of the Mycobacteriacea family. Tuberculosis (TB) can spread through coughs or sneezes. You cannot get TB from someones clothes, eating utensils, handshake, toilet, drinking glass or other regions where a TB patient's have been contacted. Tuberculosis

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spread quickly in places where people interact or live together closely. People with HIV/AIDS and others with weak immune systems are more likely to get TB than people with good immune systems. Antibiotics drug can treat tuberculosis, but some forms of the bacteria no longer responds to treatments. There are two types of TB infection, latent TB and active TB. Latent TB infection refers to TB bacteria that can exist in your body without getting you ill; as a result, you just have dormant TB germs in your body, which are unable to spread to other people. However, if these germs awaken or become active in your body and multiply, you will become sick with tuberculosis (TB). When TB germs are multiplying in your body (active), this is called active TB disease. These germs usually attack lungs and they can also attack several bodily areas such as the brain, spine or kidneys. There are usually two tests which is used to detect TB infection: blood test or skin test. The most used test is the skin test. Blood tests may occasionally be done to check for TB infection. The top eight countries which has more TB patients count were India (28%), Indonesia (9.2%), Philippines (7%), Nigeria (4.4%), Pakistan (5.8%), Bangladesh (3.6%), China (7.4%) and the Democratic Republic of Congo (2.9%). India was one of the eight nations that accounted for more than two-thirds (68.3%) of all TB cases. The incidence of tuberculosis in India is 210 per 100,000 people for the year 2021. [9].

Abdul et al. [2] have developed a two-strain drug susceptible and resistant TB transmission model where both numerical and analytical model. Their sensitivity analysis of the parameters shows that the most significant factor was the transmission rate of both strains on drug susceptible and resistant TB prevalence. They also examined how treatment rates and amplification affected each other on both drug susceptible and resistant TB spread. They proposed the feasible and optimal strategy to eliminate drug-susceptible TB and resistant TB to lower the cost of treatment in Bangladesh in order to improve treatment rates.

Choi et al. [4] have developed a SEIL model for the TB transmission in South Korea and they focuses on recommending the best TB preventive, control and budget plan for the government to eradicate the disease. Additionally, they have examined the financial plans of the Korean government and the outcomes of their model. The reduction in the number of infected and contagious people will be far from realised if the current Korean government's TB budget is

maintained; in fact, it have increased. However, their model's best control method demonstrates TB eradication.

Fatmawati et al. [6] have investigated the dynamics of TB model with children and adult population using Caputo and Atangana-Baleanu derivative. They found most TB in children is usually not contagious compared to adults. Their graphical results for comparison shows that the Atangana-Baleanu results are more appropriate for the better decrease in infection while the Caputo is less. They concluded from graphical results that rising rates of chemoprophylaxis and treatment rate then the TB infective for both children and adult cases are reduced.

Goudiaby et al. [7] have formulated and analyzed a mathematical equation for the transmission of COVID-19 and TB co-infection. The fundamental characteristics of the two submodels TB and COVID-19 are examined, as well as the potential of coexisting endemic and disease-free equilibrium (bifurcation analysis). They found optimal control methods, and the Pontryagin maximal Principle is used to construct the requirements for the presence of optimal control and the optimality system for the co-infection model.

Kalyan et al. [10] have analyzed the SEIR mathematical model for TB transmission in pandemic situation with time subordinate boundaries. They concluded that the TB model exhibits both local and global asymptotic stability at disease-free equilibrium when the basic reproduction number is less than unity and endemic stability when it is greater than coherence and a bifurcation investigation is carried out using the bifurcation technique devices of the center manifold theory.

Konstantin et al. [13] compared parallel and serial models that describe the progression of TB and used an simplified sub model of TB case detection and simple markovian sub models for two-groups of the progression of TB. More complex models, such as those that use more stages and more detailed information on the patient's health status at detection, as well as those that account for patient heterogeneity, are likely to better approximate the real data. Their research demonstrated the various processes used by the parallel and serial models of active TB progression to explain the increase in the fraction of bacillary TB over time.

Mayowa et al. [14] have examined at the deterministic mathematical model of the coinfection of COVID-19 and TB. In order to analyse the effects of each disease, they employed the

COVID-19 and TB co-infection model that they have developed. Their findings demonstrate that COVID-19 can be completely eradicated in areas where tuberculosis is widespread, and their numerical simulation findings demonstrate that as the rate of co-infection transmission increases, so the risk of TB infection in the community. Additionally, they have used the invasion reproduction number of each diseases to determine the necessary conditions for its invasion.

Qiuping et al. [16] created a database of TB cases that have been reported from four regions in China from 2005 to 2019. They have classified the reported cases and population under two groups, student and non-student groups, and developed mathematical models (seasonal and nonseasonal) based upon natural history and transmission features of TB. They also demonstrated that the non-student population, which continues to play a significant role in the spread of TB has a high transmissibility of Mycobacterium tuberculosis. The transmission of TB from the non-student population to the student population have a significant impact.

In section 2 we take a look at a mathematical model of SIDTR in a normalised form with some control parameters. In section 3, we study about the equilibrium points of the TB endemic model. In section 4, we find the basic reproduction number R_0. In section 5, we study about the stability analysis of the disease free equilibrium and endemic equilibrium and in section 6 and 7, we discuss about our model and a brief conclusion. In this study, our goal is to see whether TB can be controlled by using our assumptions. We also predicted the TB infection after 2022 in India. Graphs are shown to demonstrate the efficacy of the proposed strategy.

2. METHOD

We frame a five compartmental model on the spread of TB infection among humans. The population is divided into five different groups susceptible $S(t)$, infected $I(t)$, diagnosed $D(t)$, treatment $T(t)$ and recovered $R(t)$. The total population $N(t) = S(t)+I(t)+D(t)+T(t)+R(t)$. The compartmental model is used to construct an SIDTR model by considering TB infection, transmission of disease from one person to another, people who are following the health protocols, people who are taking the preventive measures, person who takes medication and force of infection. A model analysis for SIDTR uses the next generation matrix to acquire the basic reproduction number R_0 and the stability analysis of the SIDTR model for the spread of TB. A discussion is made for SIDTR model and we take data on the number of suspected, infected,

diagnosed, treatment and recovered TB infection cases in India. The important parameters are transmission rate, rate of medication, re-infection rate, latent TB rate and active TB rate. The flow of the individual from one compartment to another compartment is displayed in the following figure:

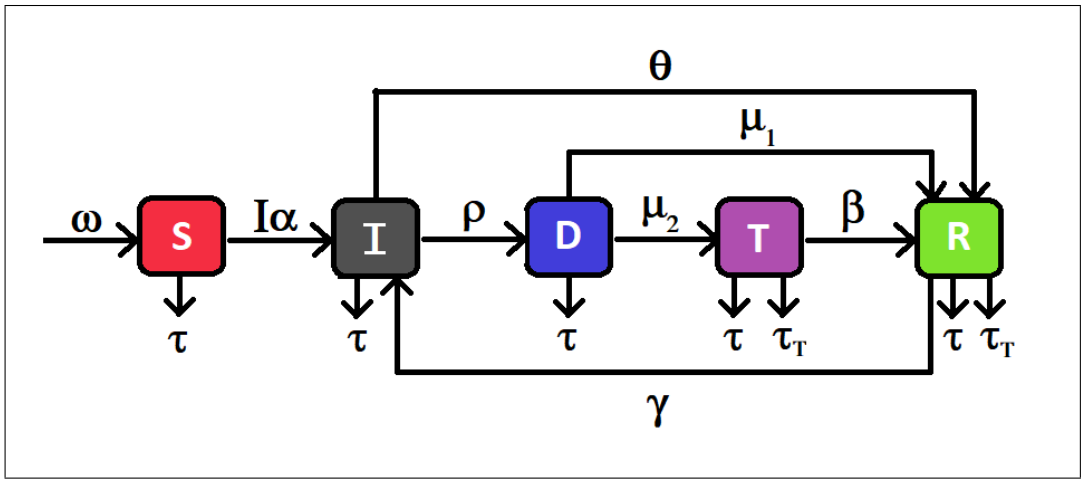

FIGURE 1. SIDTR model for the spread of Tuberculosis infection

This SIDTR model is formulated as a system of linear differential equations:

$$\frac{dS}{dt} = \omega - \tau S - I\alpha S \tag{1}$$

$$\frac{dI}{dt} = I\alpha S + \gamma R - I(\tau + \rho + \theta) \tag{2}$$

$$\frac{dD}{dt} = \rho I - D(\tau + \mu_1 + \mu_2) \tag{3}$$

$$\frac{dT}{dt} = \mu_2 D - T(\tau + \tau_T + \beta) \tag{4}$$

$$\frac{dR}{dt} = \beta T + \theta I + \mu_1 D - R(\tau + \tau_T + \gamma) \tag{5}$$

TABLE 1. Description of parameters

Parameters	Description
ω	Natural birth rate
τ	Natural death rate
τ_T	Death rate due to TB
α	Transmission rate
ρ	Rate of test taken
μ_1	Latent TB rate
μ_2	Active TB rate
β	Recovery rate
θ	Rate of medication
γ	Re-infection rate

3. THE EQUILIBRIUM POINTS

There are two equilibrium points, they are disease free equilibrium and endemic equilibrium. To find these two equilibrium points each of the equation $(1-5)$ must be equal to zero, where,

$$0 = \omega - \tau S - I\alpha S \tag{6}$$

$$0 = I\alpha S + \gamma R - I(\tau + \rho + \theta) \tag{7}$$

$$0 = \rho I - D(\tau + \mu_1 + \mu_2) \tag{8}$$

$$0 = \mu_2 D - T(\tau + \tau_T + \beta) \tag{9}$$

$$0 = \beta T + \theta I + \mu_1 D - R(\tau + \tau_T + \gamma) \tag{10}$$

It has a initial conditions, where $S(0) \geq 0$, $I(0) \geq 0$, $D(0) \geq 0$, $T(0) \geq 0$ and $R(0) \geq 0$.

3.1. The Disease-free Equilibrium Points for SIDTR Model. The points of disease free equilibrium has certain conditions when there is absence of TB infection, where $I = I^0 = 0$, $D = D^0 = 0$, $T = T^0 = 0$ and $R = R^0 = 0$. From (1) - (5), we get disease free equilibrium equations for SIDTR model as follows:

From (6), $0 = \omega - \tau S - I\alpha S \Rightarrow \tau S = \omega \Rightarrow S^0 = \dfrac{\omega}{\tau}$. From (7), (8), (9) and (10), we have $I = I^0 = 0, D = D^0 = 0, T = T^0 = 0$ and $R = R^0 = 0$.

3.2. The Endemic Equilibrium Points for SIDTR Model. The points of equilibrium for endemic are conditions where there is possibilities of the spread of disease, where S=$S^* \neq 0$, I=$I^* \neq 0$, D=$D^* \neq 0$, T=$T^* \neq 0$ and R=$R^* \neq 0$. From (1) to (5), we get the equations for endemic equilibrium for the SIDTR model as follows:

From (6), we have $0 = \omega - \tau S - I\alpha S \Rightarrow \tau S + I\alpha S = \omega$ which implies

$$S = S^* = \frac{\omega}{\tau + I\alpha}. \tag{11}$$

From (7), we have $0 = I\alpha S + \gamma R - I(\tau + \rho + \theta) \Rightarrow -I\alpha S + I(\tau + \rho + \theta) = \gamma R$ which implies

$$I = I^* = \frac{\gamma R}{-\alpha S + \tau + \rho + \theta}. \tag{12}$$

From (8), we have $0 = \rho I - D(\tau + \mu_1 + \mu_2) \Rightarrow D(\tau + \mu_1 + \mu_2) = \rho I$ which implies

$$D = D^* = \frac{\rho I}{\tau + \mu_1 + \mu_2}. \tag{13}$$

From (9), we have $0 = \mu_2 D - T(\tau + \tau_T + \beta) \Rightarrow T(\tau + \tau_T + \beta) = \mu_2 D$ which implies

$$T = T^* = \frac{\mu_2 D}{\tau + \tau_T + \beta} \tag{14}$$

From (10), we have $0 = \beta T + \theta I + \mu_1 D - R(\tau + \tau_T + \gamma) \Rightarrow R(\tau + \tau_T + \gamma) = \beta T + \theta I + \mu_1 D$ which implies

$$R = R^* = \frac{\beta T + \theta I + \mu_1 D}{\tau + \tau_T + \gamma} \tag{15}$$

4. Basic Reproduction Number for SIDTR Model

In our proposed model, disease free equilibrium are I, D, T and R compartments whereas endemic equilibrium are S, I, D, T and R. The basic reproduction number is represented by R_0, an infection where the anticipated number of cases directly caused by one case to many cases in a human population. This is one of the important parameter to consider the long term behavior of an endemic state. It can be described as the total number of secondary cases that each one of the infected person causes during the course of their infectious agent's whole life. The basic reproduction number for a compartment model of the spread of pathogens is derived from

the next generation matrix. The basic reproduction number R_0 for the SIDTR model (1)-(5) is determined using the next generation matrix. We consider $\mathscr{F}(t)$ is the rate of appearance of new infections in compartment, $\mathscr{V}^{-1}(t)$ is the rate at which individuals are transferred out of the compartment and $\mathscr{V}^{+1}(t)$ is the rate at which individuals are transferred into the compartment, where $\mathscr{V}(t) = \mathscr{V}^{-1}(t) - \mathscr{V}^{+1}(t)$ [1].

We consider (2)-(4).

$$\begin{aligned}\frac{dI}{dt} &= I\alpha S + \gamma R - I(\tau+\rho+\theta)\\ \frac{dD}{dt} &= \rho I - D(\tau+\mu_1+\mu_2)\\ \frac{dT}{dt} &= \mu_2 D - T(\tau+\tau_T+\beta)\end{aligned}$$

$$\mathscr{F}(t) = \begin{pmatrix} I\alpha S \\ 0 \\ 0 \end{pmatrix} \text{ and } \mathscr{V}(t) = \begin{pmatrix} -\tau I + \rho I + \theta I + \gamma R \\ \rho I - \tau D + \mu_1 D + \mu_2 D \\ \mu_2 D - \tau T + \tau_T T + \beta T \end{pmatrix}.$$

The Jacobian of $\mathscr{F}(t)$ and $\mathscr{V}(t)$ is obtained by F= Jacobian of $\mathscr{F}(t)$ and V= Jacobian of $\mathscr{V}(t)$.

$F = \begin{pmatrix} \alpha S & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$. In disease free equilibrium, since (S,I,D,T,R)=(1,0,0,0,0),

$$F = \begin{pmatrix} \alpha & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} (-\tau-\rho-\theta) & 0 & 0 \\ \rho & (-\tau-\mu_1-\mu_2) & 0 \\ 0 & \mu_2 & (-\tau-\tau_T-\beta) \end{pmatrix}.$$

Now finding the inverse of V, we take $A = -\tau-\rho-\theta$, $B = -\tau-\mu_1-\mu_2$ and $C = -\tau-\tau_T-\beta$.

$$adj\, V = \begin{pmatrix} BC & -\rho-C & -\rho\mu_2 \\ 0 & AC & 0 \\ 0 & 0 & AB \end{pmatrix} \text{ and } |V| = ABC.$$

$$\text{Hence} \quad V^{-1} = \begin{pmatrix} \frac{1}{A} & \frac{-\rho}{AB} & \frac{\rho\mu_2}{ABC} \\ 0 & \frac{1}{B} & 0 \\ 0 & 0 & \frac{1}{C} \end{pmatrix} \quad \text{and} \quad FV^{-1} = \begin{pmatrix} \frac{\alpha}{A} & \frac{-\rho\alpha}{AB} & \frac{\rho\mu_2\alpha}{ABC} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

The eigen value of FV^{-1} is obtained from $\begin{vmatrix} \frac{\alpha}{A}-\lambda & \frac{-\rho\alpha}{AB} & \frac{\rho\mu_2\alpha}{ABC} \\ 0 & 0-\lambda & 0 \\ 0 & 0 & 0-\lambda \end{vmatrix} = 0$

$$\Rightarrow \lambda = \frac{\alpha}{\tau+\rho+\theta}, \quad \lambda^2 = 0.$$

The dominant eigen value and the basic reproduction number is,

$$R_0 = \frac{\alpha}{\tau+\rho+\theta} \tag{16}$$

5. Stability Analysis

Theorem 1. *If $R_0 < 1$, then the disease free equilibrium for system (1) - (5) is asymptotically stable.*

Proof. From the equation (1)-(5), we frame the Jacobian matrix J as follows,

$$J = \begin{bmatrix} -\tau - I\alpha & \alpha S & 0 & 0 & 0 \\ I\alpha & \alpha S(-(\tau+\rho+\theta)) & 0 & 0 & \gamma \\ 0 & \rho & -\tau-\mu_1-\mu_2 & 0 & 0 \\ 0 & 0 & \mu_2 & -\tau-\tau_T-\beta & 0 \\ 0 & \theta & \mu_1 & \beta & -\gamma-\tau-\tau_T \end{bmatrix} \tag{17}$$

Jacobian matrix for the disease free equilibrium is given by $S = 1,\ I = 0,\ D = 0,\ T = 0$ and $R = 1$, we obtain matrix J as,

$$J = \begin{bmatrix} -\tau & \alpha & 0 & 0 & 0 \\ 0 & \alpha(-(\tau+\rho+\theta)) & 0 & 0 & \gamma \\ 0 & \rho & -\tau-\mu_1-\mu_2 & 0 & 0 \\ 0 & 0 & \mu_2 & -\tau-\tau_T-\beta & 0 \\ 0 & \theta & \mu_1 & \beta & -\gamma-\tau-\tau_T \end{bmatrix}.$$

Now we have to find the eigen value of J from

$$\begin{vmatrix} -\tau-\lambda & \alpha & 0 & 0 & 0 \\ 0 & \alpha(-(\tau+\rho+\theta))-\lambda & 0 & 0 & \gamma \\ 0 & \rho & -\tau-\mu_1-\mu_2-\lambda & 0 & 0 \\ 0 & 0 & \mu_2 & -\tau-\tau_T-\beta-\lambda & 0 \\ 0 & \theta & \mu_1 & \beta & -\gamma-\tau-\tau_T-\lambda \end{vmatrix} = 0$$

$$\Rightarrow (-\tau-\lambda)(\alpha(-(\tau+\rho+\theta))-\lambda)(-\tau-\mu_1-\mu_2-\lambda)[(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)]$$

$$-\gamma\rho[(\mu_2\beta-\mu_1(-\tau-\tau_T-\beta-\lambda))-(-\tau-\mu_1-\mu_2-\lambda)(\theta(-\tau-\tau_T-\beta-\lambda))]+0=0$$

$$\Rightarrow \lambda=-\tau,\ \lambda=\alpha(-(\tau+\rho+\theta)),\ \lambda=-\tau-\mu_1-\mu_2$$

$$\Rightarrow \lambda_1=-\tau, \quad \lambda_2=-(\tau+\rho+\theta)\alpha, \quad \lambda_3=-\tau-\mu_1-\mu_2 \text{ and } (-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)$$

$$-\gamma\rho[(\mu_2\beta-\mu_1(-\tau-\tau_T-\beta-\lambda))-(-\tau-\mu_1-\mu_2-\lambda)(\theta(-\tau-\tau_T-\beta-\lambda))]=0.$$

As γ stands for re-infection rate, in disease free state there is no possibilities of re-infection, so $\gamma=0$ and hence $(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)-0=0$.

$$\Rightarrow \quad \lambda=-\tau-\tau_T-\beta \text{ and } \lambda=-\gamma-\tau-\tau_T$$

$$\Rightarrow \quad \lambda_4=-\tau-\tau_T-\beta \text{ and } \lambda_5=-\gamma-\tau-\tau_T.$$

It is clear that $\lambda_1,\lambda_2,\lambda_3,\lambda_4,\lambda_5<0$. In λ_2 the parameter α plays a vital role compared to other parameters. α is present only in λ_2 and hence we obtain the following equation

$$\lambda_2=-(\tau+\rho+\theta)\alpha$$

Substitute equation (16) in the above equation, we get

$$\lambda_2=-(\tau+\rho+\theta)R_0(\tau+\rho+\theta)$$

$$=-R_0(\tau+\rho+\theta)$$

$\therefore$ We can conclude that when $R_0<1$ the disease free equilibrium is asymptotically stable. $\square$

Theorem 2. *The endemic equilibrium is stable, if* $R_0>1$.

Proof. From equation (17) jacobian matrix for the endemic equilibrium is given by $S \neq 0, I \neq 0, D \neq 0, T \neq 0$ and $R \neq 0$, we assume as $S = 1, I = 1, D = 1, T = 1$ and $R = 1$.

$$J = \begin{bmatrix} -\tau-\alpha & \alpha & 0 & 0 & 0 \\ \alpha & -(\tau+\rho+\theta)\alpha & 0 & 0 & \gamma \\ 0 & \rho & -\tau-\mu_1-\mu_2 & 0 & 0 \\ 0 & 0 & \mu_2 & -\tau-\tau_T-\beta & 0 \\ 0 & \theta & \mu_1 & \beta & -\gamma-\tau-\tau_T \end{bmatrix} \tag{18}$$

Now we have to find the eigen value J from

$$\begin{vmatrix} -\tau-\alpha-\lambda & \alpha & 0 & 0 & 0 \\ \alpha & -(\tau+\rho+\theta)\alpha-\lambda & 0 & 0 & \gamma \\ 0 & \rho & -\tau-\mu_1-\mu_2-\lambda & 0 & 0 \\ 0 & 0 & \mu_2 & -\tau-\tau_T-\beta-\lambda & 0 \\ 0 & \theta & \mu_1 & \beta & -\gamma-\tau-\tau_T-\lambda \end{vmatrix} = 0$$

$\Rightarrow (-\tau-\alpha-\lambda)(\alpha(-(\tau+\rho+\theta))-\lambda)(-\tau-\mu_1-\mu_2-\lambda)[(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)]-\gamma[\rho(\mu_2\beta-\mu_1(-\tau-\tau_T-\beta-\lambda))-(-\tau-\mu_1-\mu_2-\lambda)(\theta(-\tau-\tau_T-\beta-\lambda))]+\alpha^2[-\tau-\mu_1-\mu_2-\lambda(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)]-\gamma[-\tau-\mu_1-\mu_2-\lambda(0)]=0$

$\Rightarrow \quad \lambda_1 = -\tau-\alpha, \lambda_2 = -(\tau+\rho+\theta)\alpha$ and $(-\tau-\mu_1-\mu_2-\lambda)[(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)]-\gamma[\rho(\mu_2\beta-\mu_1(-\tau-\tau_T-\beta-\lambda))-(-\tau-\mu_1-\mu_2-\lambda)(\theta(-\tau-\tau_T-\beta-\lambda))]+\alpha^2[-\tau-\mu_1-\mu_2-\lambda(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)]=0$

$\Rightarrow \quad (-\tau-\mu_1-\mu_2-\lambda)(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)(1+\alpha^2)-\gamma[\rho(\mu_2\beta-\mu_1(-\tau-\tau_T-\beta-\lambda))-(-\tau-\mu_1-\mu_2-\lambda)(\theta(-\tau-\tau_T-\beta-\lambda))]=0$

According to Kermack-Mc Kendrick model [12], once they are recovered they are immune for life time. Therefore we assume $\gamma = 0$ and hence

$$(-\tau-\mu_1-\mu_2-\lambda)(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)(1+\alpha^2)-0=0$$

Since we have to prove $R_0 > 1$, we consider equation (16), we take

$$\frac{\alpha}{\tau+\rho+\theta} > 1 \Rightarrow \alpha > \tau+\rho+\theta$$

$$\Rightarrow \quad (-\tau-\mu_1-\mu_2-\lambda)(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)(1+\alpha^2)=0$$

$$\Rightarrow \quad (-\tau-\mu_1-\mu_2-\lambda)(-\tau-\tau_T-\beta-\lambda)(-\gamma-\tau-\tau_T-\lambda)=0$$

$$\Rightarrow \quad \lambda=-\tau-\mu_1-\mu_2, \quad \lambda=-\tau-\tau_T-\beta, \quad \lambda=-\gamma-\tau-\tau_T$$

$$\Rightarrow \quad \lambda_3=-\tau-\mu_1-\mu_2, \quad \lambda_4=-\tau-\tau_T-\beta, \quad \lambda_5=-\gamma-\tau-\tau_T$$

$\therefore$ We can conclude that endemic equilibrium is stable if $R_0>1$. □

6. Result and Discussion

A discussion is done by using initial values for S,I,D,T and R which is evaluated from the data of India from 2021 to 2022 and is given in the table 2.

TABLE 2. Initial values of the SIDTR model for TB in India

Variable	Value	Reference
$S(0)$	279,835,917	[5]
$I(0)$	111,934,366	[5]
$D(0)$	100,460,273	[5]
$T(0)$	9,041,424	Assumption
$R(0)$	7,233,139	[5]

The following table 3 shows the values of the parameters of the SIDTR model for TB in India.

TABLE 3. Parameter value of the SIDTR model for TB in India

Parameter	Description	Value	Reference
ω	Natural birth rate	17.163	[3]
τ	Natural death rate	0.047	[11]
τ_T	Death rate due to TB	0.01	[11]
α	Transmission rate	0.6	[11]
ρ	Rate of test taken	0.95	Assumption
μ_1	Latent TB rate	0.09	[11]
μ_2	Active TB rate	0.91	Assumption
β	Recovery rate	0.840	[15]
θ	Rate of medication	0.8	Assumption
γ	Re-infection rate	0.63	[15]

The system $(1)-(5)$ is evaluated for the different set of parameters satisfying the conditions of the stability analysis of disease free equilibrium and endemic equilibrium. In the numerical simulation, we have represented x axis as months and y axis as the total number of cases who are affected by TB in India.

Figure 2 represent the SIDTR graph of TB in India from 2021 to 2022 and figure 3 represent the SIDTR graph of TB in India from 2021 to 2031. The disease free equilibrium stability is shown in figure 4. Figure 5 represent the analysis of endemic equilibrium. If this trend continues, the analysis of disease free equilibrium from 2021 to 2031 is shown in figure 6 and it shows that we will get TB free India in 2027 to 2028. The analysis of the endemic equilibrium from 2021 to 2031 is shown in figure 7 and it shows that we will get TB free India in 2029 to 2030. Figure 8 represent the infected populations for various values of α, figure 9 represent the diagnosed populations for various values of α, figure 10 represent the treated populations for various values of α, figure 11 represent the recovered populations for various values of α, figure 12 represent the treated populations for various values of θ and figure 13 represent the recovered populations for various values of θ.

We predicted that India will become TB free in 2031 if the same situation continues, but by using our SIDTR mathematical model we can predict that in disease free state if people follows social distancing from TB affected people and aware of TB infection we can make TB free India in 2027 to 2028 and in endemic state if people takes proper medication, social distancing and aware of TB infection we can make TB free India in 2029 to 2030. Whereas WHO [5] suggested that India will become free from TB during 2030 and 2035.

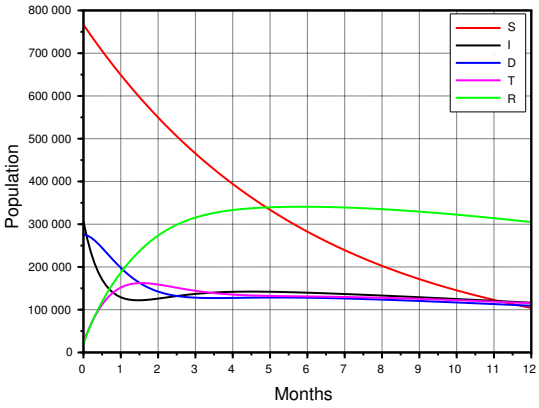

FIGURE 2. SIDTR graph of TB in India from 2021-22

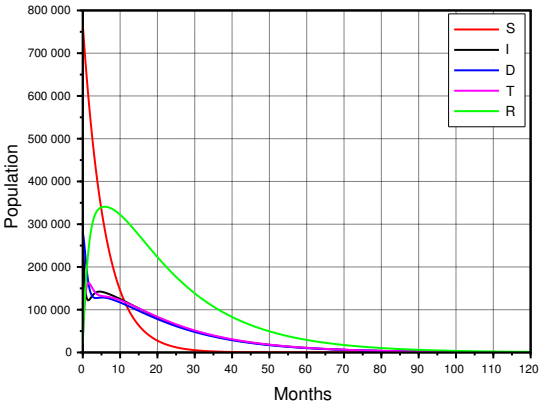

FIGURE 3. SIDTR graph of TB in India from 2021-31

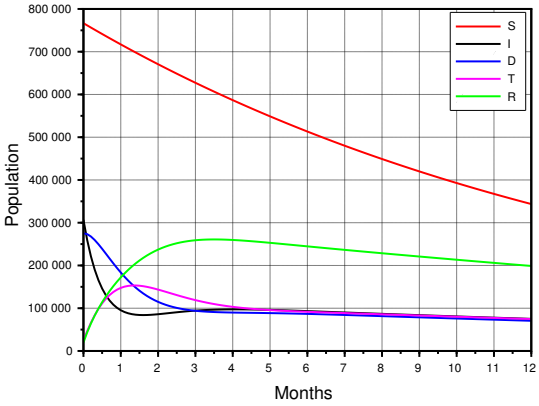

FIGURE 4. Analysis of disease free equilibrium from 2021-22

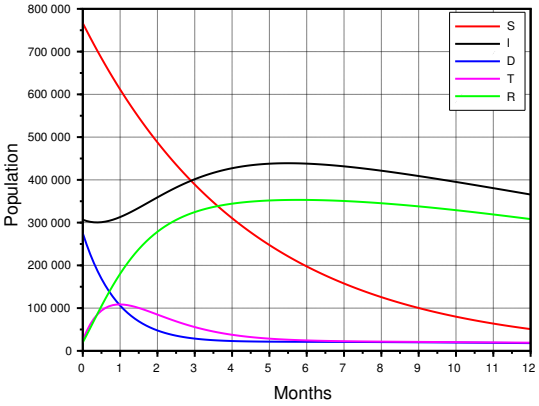

FIGURE 5. Analysis of endemic equilibrium from 2021-22

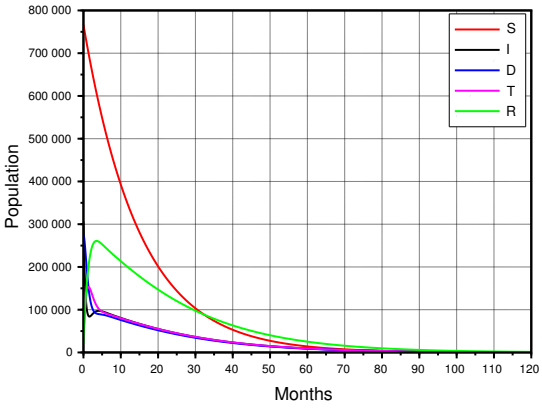

FIGURE 6. Analysis of disease free equilibrium from 2021-31

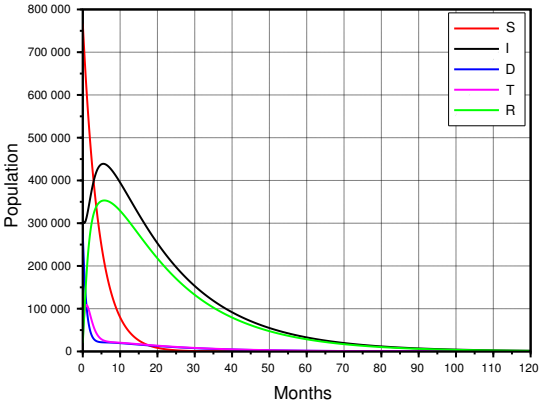

FIGURE 7. Analysis of endemic equilibrium from 2021-31

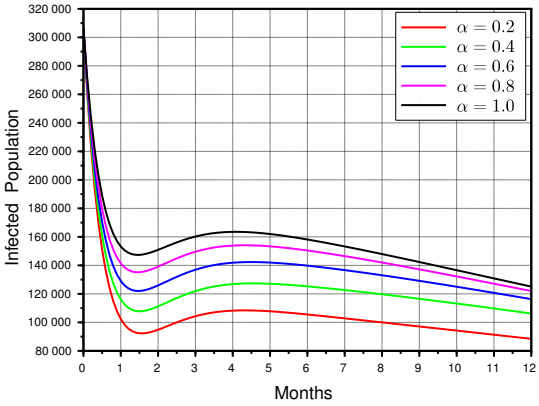

FIGURE 8. The curves of the infected populations for different values of α

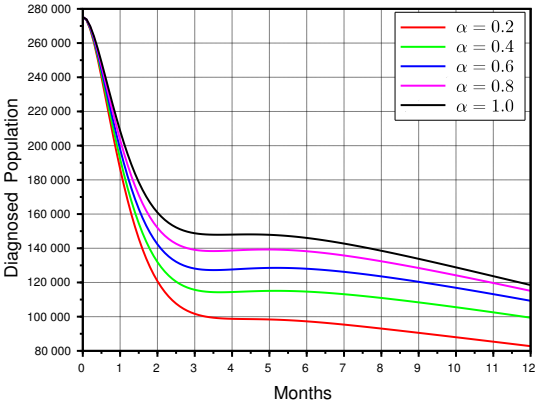

FIGURE 9. The curves of the diagnosed populations for different values of α

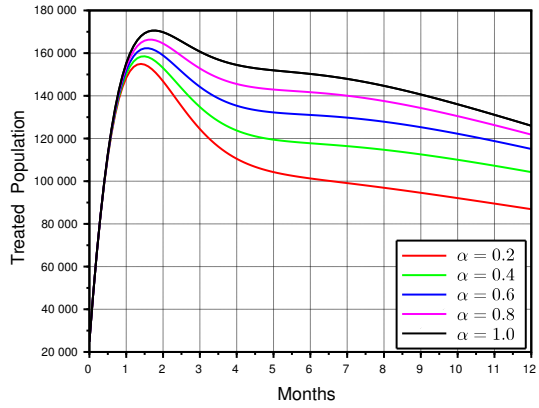

FIGURE 10. The curves of the treated populations for different values of α

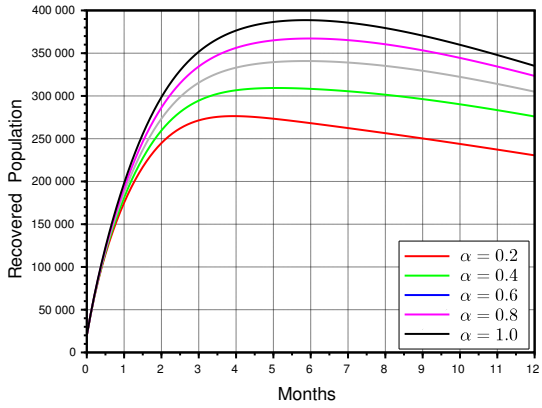

FIGURE 11. The curves of the recovered populations for different values of α

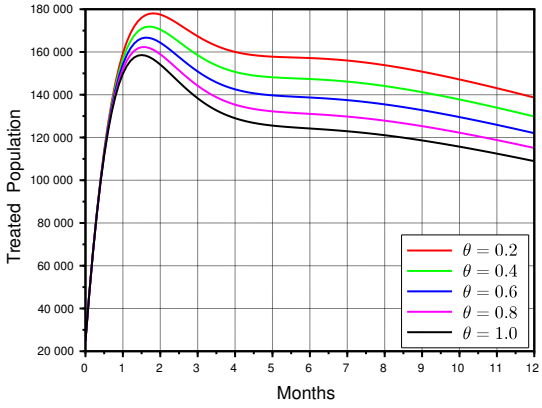

FIGURE 12. The curves of the treated populations for different values of θ

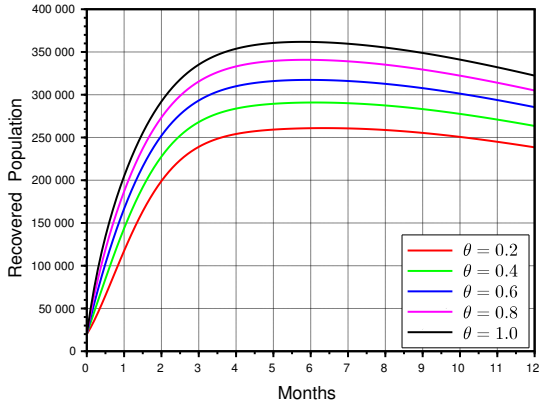

FIGURE 13. The curves of the recovered populations for different values of θ

7. CONCLUSION

In this article we have discussed Tuberculosis spread in India during 2021 to 2022. We have modeled SIDTR mathematical model for TB as a system of linear differential equations and examined disease transmission. We found that TB is easily controllable in disease free state by using medication, social distancing and aware of TB infection. However, in the endemic state, TB is not easily controllable by using medication, social distancing and aware of TB infection alone. The stability of the disease free equilibrium is asymptotically stable when $R_0 < 1$ and the endemic equilibrium is stable when $R_0 > 1$. The results illustrate that the transmission rate and rate of medication have biggest influence on basic reproduction number. This implies that the control, prevention and proper medication of TB concentrate more on spread prevention campaign. Campaign focused on people at increased risk of TB infection that motivate them to take precaution such as the use of ventilation systems, protective masks, keeping infectious people separate from other people and the regular screening of health care for TB people will be more effective. It is better to give treatment to the latent TB infected people in order to avoid them from spreading, however people affected with active TB needs medication and proper care, where occurrence rate is high. The best course of action will be to treat affected persons and isolate them so that their contact rate with other people is reduced and minimising the risk of disease spread. If people takes proper medication and aware of TB infection we can make TB free India in 2029 to 2030.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

REFERENCES

[1] M. Aakash, C. Gunasundari, Effect of partially and fully vaccinated individuals in some regions of India: A mathematical study on COVID-19 outbreak, Commun. Math. Biol. Neurosci. 2023 (2023), 25. https://doi.org/10.28919/cmbn/7825.

[2] M.A. Kuddus, E.S. McBryde, A.I. Adekunle, et al. Mathematical analysis of a two-strain tuberculosis model in Bangladesh, Sci. Rep. 12 (2022), 3634. https://doi.org/10.1038/s41598-022-07536-2.

[3] India birth rate. https://www.macrotrends.net/countries/IND/india/birth-rate.

[4] S. Choi, E. Jung, Optimal tuberculosis prevention and control strategy from a mathematical model based on real data, Bull Math Biol. 76 (2014), 1566–1589. https://doi.org/10.1007/s11538-014-9962-6.

[5] WHO, Global tuberculosis report 2022. World Health Organization, Geneva, 2022.

[6] Fatmawati, M. Altaf Khan, E. Bonyah, et al. A mathematical model of tuberculosis (TB) transmission with children and adults groups: A fractional model, AIMS Math. 5 (2020), 2813–2842. https://doi.org/10.3934/math.2020181.

[7] M.S. Goudiaby, L.D. Gning, M.L. Diagne, et al. Optimal control analysis of a COVID-19 and tuberculosis co-dynamics model, Inform. Med. Unlocked. 28 (2022), 100849. https://doi.org/10.1016/j.imu.2022.100849.

[8] India census (Total population). https://www.census.gov/popclock/world/in.

[9] https://www.drishtiias.com/daily-updates/daily-news-analysis/world-tuberculosis-report-2022-who.

[10] K. Das, B.S.N. Murthy, Sk.A. Samad, et al. Mathematical transmission analysis of SEIR tuberculosis disease model, Sensors Int. 2 (2021), 100120. https://doi.org/10.1016/j.sintl.2021.100120.

[11] K.G. Mekonen, S.F. Balcha, L.L. Obsu, A. Hassen, Mathematical modeling and analysis of TB and COVID-19 coinfection, J. Appl. Math. 2022 (2022), 2449710. https://doi.org/10.1155/2022/2449710.

[12] W.O. Kermack, A.G. McKendrick, A contribution to the mathematical theory of epidemics, Proc. R. Soc. Lond. A. 115 (1927), 700-721. https://doi.org/10.1098/rspa.1927.0118.

[13] K.K. Avilov, A.A. Romanyukha, E.M. Belilovsky, et al. Mathematical modelling of the progression of active tuberculosis: Insights from fluorography data, Infect. Dis. Model. 7 (2022), 374-386. https://doi.org/10.1016/j.idm.2022.06.007.

[14] M.M. Ojo, O.J. Peter, E.F.D. Goufo, et al. A mathematical model for the co-dynamics of COVID-19 and tuberculosis, Math. Computers Simul. 207 (2023), 499-520. https://doi.org/10.1016/j.matcom.2023.01.014.

[15] S. Kasereka Kabunga, E.F. Doungmo Goufo, V. Ho Tuong, Analysis and simulation of a mathematical model of tuberculosis transmission in Democratic Republic of the Congo, Adv. Differ. Equ. 2020 (2020), 642. https://doi.org/10.1186/s13662-020-03091-0.

[16] Q. Chen, S. Yu, J. Rui, et al. Transmissibility of tuberculosis among students and non-students: an occupational-specific mathematical modelling, Infect. Dis. Poverty. 11 (2022), 117. https://doi.org/10.1186/s40249-022-01046-z.