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Dynamics of Tuberculosis Transmission Model with Reinfection Issues

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Abstract Tuberculosis (TB) is a global epidemic caused by *Mycobacterium tuberculosis*. In this article, we study the dynamics of the TB transmission model with reinfection issues. It is demonstrated that the basic reproduction number R_0 defines the TB transmission dynamics. If $R_0 < 1$, only TB free equilibrium exists which is globally asymptotically stable, and when $R_0 > 1$, thus, there occurs endemic equilibrium, and the TB takes over. A bifurcation analysis was conducted by employing the bifurcation techniques of center manifold theory, both analytical and numerical solutions guarantee the occurrence of transcritical bifurcation at $R_0 = 1$. We also discussed the global stability of endemic equilibrium employing the approach of Lyapunov function. Numerical investigations illustrated that increase in reinfection value results in a huge force of infection. However, reinfection among treated individuals play an important role in the control of TB infection.

Keywords Tuberculosis; reinfection; stability analysis; bifurcation analysis.

Mathematics Subject Classification 46N60, 92B99.

1 Introduction

Tuberculosis (TB) is a starring health menace across the globe. The TB outbreak is generally caused by *Mycobacterium tuberculosis* (Mtb) [1], and it is highly infectious with significant mortality. However, TB is both preventable and curable. Isoniazid is utilized to keep people who are latently infected with Mtb from acquiring the disease, and multiple-drug regimens are very effective at treating active TB cases [2]. Mtb typically affects the lungs, but it can also affect other organs in the human body. In 2021, an estimated 10 million people became ill with TB, and 1.5 million died from the disease worldwide. TB is transmitted from person to person through the air. When people with lung tuberculosis cough, sneeze, or spit, they release TB germs into the air. In order to become infected, a person only needs to inhale a few of these germs. Approximately one-quarter of the world's population is infected with tuberculosis

(TB), which means they have been infected by TB bacteria but are not (yet) ill with disease and cannot transmit it [1]. The longer duration of latency in MTB infection adds uncertainty to the onset of active disease and complicates understanding disease development [3–5].

Reinfection is a situation where by individuals who haveing previously treated can be reinfected as a result of low immunity [2–4,6]. A reinfection event can be attributed to a TB episode in a significant number of cases. More cases of TB due to reinfection could be anticipated in high incidence regions compared to low incidence regions because reinfection is more likely in high incidence regions than low incidence regions, demonstrating that higher prevalence of Mtb is the main risk for TB reinfection [6]. Olaniyi [7] presented optimal control analysis of a TB model with exogenous re-infection and incomplete treatment Athithan and Ghosh [8] designed a mathematical modeling of TB infection with exogenous re-infection by assessing the impacts of case detection and treatment. Yang et al studied global stability analysis of two models with incomplete treatment for TB in the absence of exogenous re-infection employing Lyapunov functions. Okuonghae and Aihie [9] investigated the synergetic effects of case detection and direct observation therapy strategy (DOTS) on TB transmission in Nigeria by incorporating exogenous re-infection and endogenous reactivation of latent TB cases. Individuals who have had TB before and have it again have a substantially higher risk of having TB disease than those who have never had the infection. More research is needed, but scientists believe that certain people may be more susceptible to TB than others for unknown reasons [10].

Mathematical biology is an exciting and fast growing field. Most of the current topics of mathematical biology consist of the formulation and analysis of various mathematical models,often in the forms of difference equations or differential equations. One of the most important ways for capturing mathematics in structure, which is an essential subject to apply in real life, is modeling [21]. In recent years, mathematical models are developed and applied in the area of mathematical biology are found in many references, for example, epidemic models [11–14], eco-epidemiological models [15, 16, 18], preypredator models [16, 19], and also used to understand epidemiological phenomena.

The basic reproduction number is a crucial quantity in epidemic models because it determines whether a disease may be controlled in the community. When the basic reproduction number is greater than one, each infectious individual will produce more than one new case; when it is less than one, the illness will become extinct in the community [22]. In reality, in most epidemic models, the bifurcation at $R_0 = 1$ is transcritical (forward), implying that $R_0 < 1$ has no endemic equilibrium. Furthermore, in recent years, several scholars (see [3, 4, 23]) have discovered another form of bifurcation at $R_0 = 1$, known as backward bifurcation, in several epidemic models, and this form of bifurcation verifies the existence of multiple endemic equilibria of the given system when $R_0 < 1$. Khajanchi et al. [4] studied the dynamical model of TB infection with exogenous reinfections and endogenous reactivation. They demonstrated that their model displays two various types of bifurcation: one is backward bifurcation and another is transcritical. Kar and Mondal [3] discovered that their model undergoes the phenomenon of backward bifurcation and can have a multiple endemic equilibria if $R_0 < 1$ given that the probability of reinfection exceeds a critical value.

Uys et al. [6] have investigated a mathematical model on TB reinfection. They accepted that the rate of reinfection is a multiple of the rate of first-time infection. Yang and Raimundo [24] used a deterministic model to assess the effect of multiple infections and prolonged latency on the transmission of recurrent TB. Their findings indicate that reinfection of treated people is

trifling, disputing that such a pathway increases non-linearity and makes the model mathematically difficult. The models of Kar and Mondal [3] and Feng et al. [25] were all based on the assumption that individuals went through a long latency period before TB reactivated to clinically active TB.

The dynamical behaviour of a deterministic model of TB with vaccination and contact rate has been formulated and analysed by [26]. Their result suggested that vaccination coverage is insufficient to control TB and that the effective contact rate significantly impacts TB spread. The authors in [27] studied the dynamical behavior of compartmental models of TB with vaccination and saturated incidence rate. Their findings revealed that the first effective strategy to combat TB spread is to limit contact between TB-infected and vulnerable people. The second significant finding is improving access to treatment for latently infected individuals. Finally, they demonstrated that the BCG vaccination has a significant role in TB prevention and that children's immunization should be continued. A dynamical model of TB with health education and early therapy influence has been examined in [28]. The theoretical analysis of their models revealed that the disease free equilibrium is globally asymptotically stable if $R_0 < 1$, while the endemic equilibrium is globally asymptotically stable when $R_0 > 1$. Mathematical results revealed that both health education and early therapy have a strong influence on TB burden reduction.

The main objective of this article is to study the effect of the reinfection among treated people as well as theoretical and numerical solutions. For this reason, we employed the well-known $S_\iota, E_\iota, I_\iota, R_\iota$ model. The present article is categorized into six sections. The description of the dynamical model of TB with reinfection model is presented in section 2. In section 3, some theoretical aspects and a stability analysis of a nonlinear model for the basis of equilibrium points are given. In the section 4, we study the existence and uniqueness of the solutions for the dynamics $S_\iota, E_\iota, I_\iota, R_\iota$ model. In section 5, numerical solutions are held some simulations are given to validate the results. In the end, our conclusions and findings was given in section 6.

2 Model Description

In this article, the TB model with reinfection among the people who have been treated is considered. The model is modification from TB transmission models developed by [3, 29–31]. The modification model extends the [31] by including a latently infected class and the re-infection so that the model will be in the form of the $S_\iota E_\iota I_\iota R_\iota E_\iota$ model. The latently infected class has been considered because there is a long incubation period in TB disease and also re-infection because of low immunity. This model is also the same as developed by [3] but with standard incidence function instead of bilinear incidence and incorporation of death due to TB, has been considered. We ignored exogenous re-infection which is left open to be the future study. Immigration of infectives was removed from the model o [29, 30] because E_ι and I_ι compartments became most individual that is sick and can not travel while the recovered class has been included because individuals who are infected with Mtb can be recovered due to treatment and move to recovered compartment R_ι at the rate γ (although some of the live bacilli are still with them).

In this section, a four compartmental TB model with reinfection is introduced. This model can describe the relationship between the population of susceptible individual, exposed individual, infected individual and recovered individual. The dynamics of the population of the

susceptible individual S_ι, exposed individual E_ι, infected individual I_ι, and recovered individual R_ι are as follows;

$$\begin{aligned}
\frac{dS_\iota}{dt} &= \Lambda - \frac{\beta S_\iota I_\iota}{N_\iota} - \mu S_\iota, \\
\frac{dE_\iota}{dt} &= \frac{\beta S_\iota I_\iota}{N_\iota} + \frac{\sigma \beta I_\iota R_\iota}{N_\iota} - (\kappa + \mu) E_\iota, \\
\frac{dI_\iota}{dt} &= \kappa E_\iota - (\mu + \delta + \gamma) I_\iota, \\
\frac{dR_\iota}{dt} &= \gamma I_\iota - \frac{\sigma \beta I_\iota R_\iota}{N_\iota} - \mu R_\iota.
\end{aligned} \tag{1}$$

with

$$N_\iota = S_\iota + E_\iota + I_\iota + R_\iota,$$

where

$$\lambda = \frac{\beta I_\iota}{N_\iota}, \tag{2}$$

of which equation (2) is represented by force of infection so that the model system (1) can be rewritten as

$$\begin{aligned}
\frac{dS_\iota}{dt} &= \Lambda - \lambda S_\iota - \mu S_\iota, \\
\frac{dE_\iota}{dt} &= \lambda S_\iota + \sigma \lambda R_\iota - (\kappa + \mu) E_\iota, \\
\frac{dI_\iota}{dt} &= \kappa E_\iota - (\mu + \delta + \gamma) I_\iota, \\
\frac{dR_\iota}{dt} &= \gamma I_\iota - \sigma \lambda R_\iota - \mu R_\iota.
\end{aligned} \tag{3}$$

with the initial condition

$$S_{\iota 0} \geq 0, E_{\iota 0} \geq 0, I_{\iota 0} \geq 0, R_{\iota 0} \geq 0. \tag{4}$$

In the system (3) above, the susceptible compartment is increased by recruiting individuals, either by immigration or birth, into the population at the constant rate Λ. The term μ is taken to be natural death rate. The susceptible individuals become infected at a rate $\frac{\beta I_\iota}{N_\iota}$, represented by λ, known as standard incidence. The exposed compartment becomes infectious and progresses to active infected at a constant rate κ. Infected individuals are recovered at the rate γ and diminished due to TB induced death rate at the rate δ. The treated compartment revert to the exposed compartment as a result of low immunity at the constant rate σ.

2.1 Clinical Assumptions of the TB Model with Reinfection

The biological assumptions of the model are as follows:

- There is a constant recruitment rate to the susceptible population and natural cause death affects individuals in all compartments, with an extra TB-induced death rate in the infected class;
- The population which goes from susceptible to infected class is taken to be standard incidence and it is of the form $\frac{\beta I_\iota}{N_\iota}$
- The recovered individual may be again infected by infectious individual [3].

Therefore, based on the above description and assumptions, the basic TB Model lead to following system of non-linear differential equations, the schematic diagram Figure 1 below, and the parameters indicated in the diagram are explained in Table 1.

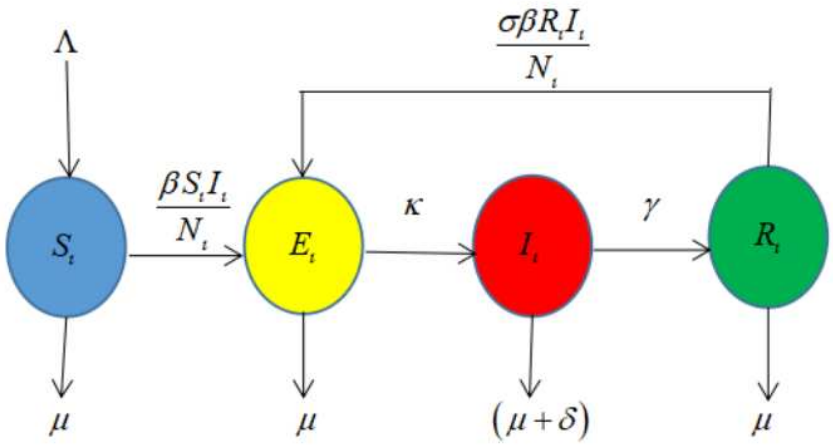

Figure 1: Schematic Diagram of the TB Model with Reinfection.

Table 1: Description of the State Variables and Parameters of the System (3)

State Variables	**Explanation**
S_ι	Individuals susceptible to TB
E_ι	Not yet infected, still in latent period
I_ι	Actively infected individuals
R_ι	Recovered from TB infection
N_ι	Human population size
Parameters	
Λ	Inflow of recruitment rate into susceptible class
β	Effective transmission rate
μ	Natural death rate
κ	Progression rate from E_ι to I_ι
γ	recovery rate
σ	Re-infection among the treated individuals
δ	TB induced death rate

3 Basic Properties of the TB Model with Reinfection

The basic properties of the TB Model with reinfection (3) are explored in this section. This analysis is crucial when examining the dynamical behavior of a disease model since it demonstrates if the model is epidemiologically relevant and mathematically well-posed, that is, if the model and its predictions are confirmed [32–34].

Theorem 1 *Let initial data be* $\{(S_{\iota 0}, E_{\iota 0}, I_{\iota 0}, R_{\iota 0}) \geq 0\} \in \Phi$. *Therefore, the set solution of* $\{S_\iota(t), E_\iota(t), I_\iota(t), R_\iota(t)\}$ *of the TB Model with reinfection* (3) *is non-negative for all* $t > 0$.

Proof The method described in [16, 17], is applied. We use the first equation to consider the non-linear system of (3), which clearly shows that

$$\frac{dS_\iota}{dt} + (\lambda(t) + \mu)S_\iota > 0,$$

utilizing an integrating factor gives

$$\frac{d}{dt}\left[S_\iota \, exp\left(\int_0^t (\lambda(\epsilon) + \mu\right) d\epsilon\right] > 0. \tag{5}$$

Using the initial conditions (4) and integrating (5) results in

$$S_\iota(t) > S_{\iota 0} exp\left[-\left(\int_0^t (\lambda(\epsilon) + \mu\right) d\epsilon\right] > 0, \; \forall t > 0. \; \square$$

Likewise, it is provable that $E_\iota(t) > 0, I_\iota(t) > 0, R_\iota(t) > 0 \; \forall \; t > 0$.

3.1 Invariant Region

Theorem 2 *The region* Φ *is positively-invariant and all the solution are enclosed in* $\Phi \in R_+^4$.

Proof Summation of model system (3) is given by

$$\frac{dN_\iota}{dt} = \frac{dS_\iota}{dt} + \frac{dE_\iota}{dt} + \frac{dI_\iota}{dt} + \frac{dR_\iota}{dt}. \tag{6}$$

We can observe that by applying the standard comparison theorem [35], which yields

$$\frac{dN_\iota}{dt} = \Lambda - \mu N_\iota - \delta I_\iota(t). \tag{7}$$

In the absence of TB infection, there is no death from TB transmission, (that is, $\delta = 0$), hence the rate of change of the total population size in equation (7) is given as

$$\frac{dN_\iota}{dt} \leq \Lambda - \mu N_\iota. \tag{8}$$

From (8) above, we obtain

$$N_\iota(t) = \frac{\Lambda}{\mu} + \left(N_{\iota 0} - \frac{\Lambda}{\mu}\right) e^{-\mu t}. \tag{9}$$

As $t \longrightarrow \infty$, the value of $N_\iota \longrightarrow \frac{\Lambda}{\mu}$. This shows that N_ι is bounded above by $\frac{\Lambda}{\mu}$ as the value of t goes to infinity. But initially, we said that $S_{\iota 0} \geq 0, E_{\iota 0} \geq 0, I_{\iota 0} \geq 0, R_{\iota 0} \geq 0$. Therefore, $N_\iota = S_\iota + E_\iota + I_\iota + R_\iota \geq 0$. That is $N_\iota \geq 0$, which means $0 \leq N_\iota$. Therefore

$$0 \leq N_\iota \leq \frac{\Lambda}{\mu}. \tag{10}$$

Hence, in Φ, the TB model with reinfection is well-posed epidemiologically. Thus, it is sufficient to study the dynamics of the basic TB model in Φ. So, we can conclude that all the solution set of the system model (3) is bounded in Φ, where

$$\Phi = \left\{ (S_\iota, E_\iota, I_\iota, R_\iota) \in \mathbb{R}^4_+ : 0 \leq N_\iota \leq \frac{\Lambda}{\mu} \right\}. \square \tag{11}$$

4 Model Analysis

In this section, we shall examine the equilibrium solutions, obtain the basic reproduction number, conduct the stability analysis of the TB-free equilibrium (TFE), endemic equilibrium (EE), the local and global stability of both TB-free and endemic equilibrium.

4.1 Existence of TB-Free Equilibrium State,(T^0)

This is achieved if there is no TB infection in the community, means that the number of exposed, infected and recovered people are zero, that is ($E_\iota, I_\iota \,\text{and}\, R_\iota = 0$). The TB free equilibrium of TB model with reinfection (3) is obtained and is given by (12),

$$T^0 = (S_\iota, E_\iota, I_\iota, R_\iota) = \left(\frac{\Lambda}{\mu}, 0, 0, 0 \right). \tag{12}$$

4.2 Existence of Endemic Equilibrium State,(T^*)

The endemic equilibrium (EE) is the state at which the disease break-out and is persistent in a population. The EE for the TB model with reinfection (3) is given by $T^* = (S^*_\iota, E^*_\iota, I^*_\iota, R^*_\iota)$:

$$T^* = (S^*_\iota, E^*_\iota, I^*_\iota, R^*_\iota) = \left[\frac{\Lambda}{\lambda+\mu}, \frac{\lambda\Lambda(\sigma\lambda+\mu)(\mu+\gamma+\delta)}{(\lambda+\mu)(G_0-G_1)}, \frac{\kappa\Lambda(\sigma\lambda+\mu)\lambda}{(\lambda+\mu)(G_0-G_1)}, \frac{\kappa\gamma\Lambda\lambda}{(\lambda+\mu)(G_0-G_1)} \right]. \tag{13}$$

where

$$G_0 = (\kappa+\mu)(\mu+\delta+\gamma)(\sigma\lambda+\mu), \,\text{and}\, G_1 = \kappa\sigma\lambda\gamma.$$

4.3 Basic Reproduction Number

The basic reproduction number of the TB model with reinfection (3) represented by R_0, is the average number of secondary infections caused by a single index case in a completely susceptible community [22,36]. It is significant as a threshold parameter in the analysis of epidemic models, such as TB [38]. The R_0 shall be calculated following the next generation approach employed by [36]. The R_0 is $\rho(FV^{-1})$, where ρ is the spectral radius,

$$F = \begin{pmatrix} 0 & \beta \\ 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} (\kappa+\mu) & 0 \\ -\kappa & (\mu+\delta+\gamma) \end{pmatrix}.$$

The inverse of V denoted by V^{-1} is

$$V^{-1} = \begin{pmatrix} \frac{1}{(\kappa+\mu)} & 0 \\ \frac{\kappa}{(\kappa+\mu)(\mu+\delta+\gamma)} & \frac{1}{(\mu+\delta+\gamma)} \end{pmatrix}.$$

Thus, the basic reproduction number for this TB model with reinfection is given by:

$$R_0 = \frac{\beta\kappa}{(\kappa+\mu)(\mu+\delta+\gamma)}. \tag{14}$$

If $R_0 < 1$, it signifies that the probability of new cases of disease persisting in the community is insufficient for the TB to occur, whereas, when $R_0 > 1$, the disease will then become widespread, causing a major decrease in the population of susceptible individuals [37].

4.4 Local Stability of the TB Disease-Free Equilibrium

Theorem 3 *The TFE, of the TB model with reinfection* (1) *given by* (3)*, is locally asymptotically stable (LAS) when $R_0 < 1$ and unstable if $R_0 > 1$.*

Proof The Jacobian matrix of the TB model with reinfection (3) at TFE state (T^0) is then given by

$$J(T^0) = \begin{bmatrix} -\mu & 0 & -\beta & 0 \\ 0 & -(\kappa+\mu) & \beta & 0 \\ 0 & \kappa & -(\mu+\delta+\gamma) & 0 \\ 0 & 0 & \gamma & -\mu \end{bmatrix}. \tag{15}$$

The eigenvalue of (15) are given by

$$\left|J(T^0) - \alpha I\right| = 0,$$

where $J(T^0)$ denotes Jacobian matrix at TFE, The Jacobian derived from (15) has the following characteristics equation:

$$J(T^0) = \begin{vmatrix} -\mu-\alpha & 0 & -\beta & 0 \\ 0 & -(\kappa+\mu)-\alpha & \beta & 0 \\ 0 & \kappa & -(\mu+\delta+\gamma)-\alpha & 0 \\ 0 & 0 & \gamma & -\mu-\alpha \end{vmatrix} = 0. \tag{16}$$

Evaluating along the first column

$$\begin{aligned} (-\mu-\alpha)(-\mu-\alpha)\left[-(\kappa+\mu)-\alpha)(-(\mu+\delta+\gamma)-\alpha)-\kappa\beta\right] &= 0, \\ (\mu+\alpha)^2\left[(\kappa+\mu)(\mu+\delta+\gamma)+(\kappa+\mu+\mu+\delta+\gamma)\alpha+\alpha^2-\kappa\beta\right] &= 0, \\ (\mu+\alpha)^2\left[\alpha^2+(\kappa+2\mu+\delta+\gamma)\alpha+(\kappa+\mu)(\mu+\delta+\gamma)(1-R_0)\right] &= 0, \\ (\mu+\alpha)^2 f(\alpha) &= 0, \end{aligned} \tag{17}$$

where $f(\alpha) = \alpha^2 + (\kappa+2\mu+\delta+\gamma)\alpha + (\kappa+\mu)(\mu+\delta+\gamma)(1-R_0)$.

Clearly, $\alpha_1 = -\mu$, $\alpha_2 = -\mu$ while $f(\alpha)$ has no sign change only if $R_0 < 1$. Hence, the solution of $f(\lambda)$ are all real and negative which implies that α_3 and α_4 are negative if $R_0 < 1$. Following the Routh Hurwitz stability criterion, we conclude that the TFE point is locally asymptotically stable. □

4.5 Global Stability of the TB Free Equilibrium

Global Stability of TFE, T^0, for $R_0 \leq 1$: Inspired by [39–41], where we already know that TFE state T^0 is locally asymptomatically stable if $R_0 < 1$. and unstable if $R_0 > 1$ [36,38]. We shall construct a Lyapunov function to prove the global stability of TFE. Define a Lyapunov function as follows:

$$L = A_1 E_\iota + A_2 I_\iota, \tag{18}$$

Differentiating equation (18) with respect to time, we have

$$\frac{dL}{dt} = A_1 \frac{dE_\iota}{dt} + A_2 \frac{dI_\iota}{dt}, \tag{19}$$

Substitute the values of $\frac{dE_\iota}{dt}$ and $\frac{dI_\iota}{dt}$ into equation (19), we get

$$\frac{dL}{dt} = A_1 \left[\frac{\beta S_\iota I_\iota}{N_\iota} + \frac{\sigma \beta I_\iota R_\iota}{N_\iota} - (\kappa + \mu) E_\iota \right] + A_2 \left[\kappa E_\iota - (\mu + \delta + \gamma) I_\iota \right]. \tag{20}$$

After some algebraic calculations,

$$A_1 = 1 \text{ and } A_2 = \frac{A_1}{\kappa}(\kappa + \mu), \tag{21}$$

such that

$$\frac{dL}{dt} \leq \frac{(\kappa + \mu)(\mu + \gamma + \delta)}{\kappa}(R_0 - 1) I_\iota. \tag{22}$$

Thus, if $R_0 < 1$, then $\frac{dL}{dt}$ is negative. Hence the largest compact invariant set in Φ is the singleton set T^0. Therefore, LaSalles invariant principle [40,41] then implies that T^0 is globally asymptotically stable in Φ.

4.6 Endemic Equilibrium

To obtain the existence of endemic equilibrium point for the system model (2), represented by $T^* = (S_\iota, E_\iota, I_\iota, R_\iota)$ given in (13). The system model (1) are solved in terms of force of infection in equation (2) at a steady state which satisfy the following

$$\frac{I_\iota}{N_\iota} = \frac{\kappa\sigma\lambda^2 + \kappa\mu\lambda}{(\sigma(\mu + \delta + \gamma) + \kappa\sigma)\lambda^2 + (G_0 + \mu(\mu + \delta + \gamma) + \kappa(\mu + \gamma)\lambda + G_1}, \tag{23}$$

using (23) in (2) yields

$$\lambda = \frac{\beta\kappa\sigma\lambda^2 + \beta\kappa\mu\lambda}{G_2\lambda^2 + G_3\lambda + G_1}. \tag{24}$$

where

$$G_2 = \sigma(\mu + \delta + \gamma) + \kappa\sigma,$$
$$G_3 = G_0 + \mu(\mu + \delta + \gamma) + \kappa(\mu + \gamma).$$

Cross multiply (24), we have

$$\Rightarrow \lambda(G_2\lambda^2 + G_3\lambda + G_1) = \beta\kappa(\sigma\lambda + \mu)\lambda,$$

$$G_2\lambda^2 + (G_3 - \beta\kappa\sigma)\lambda + \mu(\kappa+\mu)(\mu+\delta+\gamma) - \beta\kappa\mu = 0,$$
$$G_2\lambda^2 + (G_3 - \beta\kappa\sigma)\lambda + \mu(\kappa+\mu)(\mu+\delta+\gamma)(1-R_0) = 0. \quad (25)$$

The equation (25) can be written as

$$G_2\lambda^2 + G_4\lambda + G_5 = 0. \quad (26)$$

where

$$G_4 = G_3 - \beta\kappa\sigma,$$
$$G_5 = \mu(\kappa+\mu)(\mu+\delta+\gamma)(1-R_0)$$

The endemic equilibrium of the TB model with reinfection (1) can be achieved by solving λ from (25), and replacing the values λ into the expressions in (13). The quadratic equation (26) can be examined for the possibility of multiple endemic equilibria when $R_0 < 1$. Notice that the coefficient G_2 is always positive of the quadratic equation (25) and G_5 is positive or negative if R_0 is less or greater than one. The following outcome, therefore, is established.

Theorem 4 *The TB model with reinfection* (1)

1. *has a unique endemic equilibrium if* $G_5 < 0 \Leftrightarrow R_0 > 1$;
2. *a unique endemic equilibrium when if* $(G_4 < 0 \, and \, G_5 = 0)$ *or* $G_2^2 - 4G_2G_5 = 0$ *;*
3. *one or more than one endemic equilibrium when* $G_5 > 0, G_4 < 0$ *and* $G_2^2 - 4G_2G_5 > 0$*;*
4. *no endemic equilibrium otherwise.*

4.7 Bifurcation Analysis of The Model

Primarily, bifurcation theory deals with the change in stability criteria of a system of differential equations. The point where changes in stability occurs is known as bifurcation value. The bifurcation property for the developed model shall be examined employing the idea of center manifold studied in Theorem 4.1 of [42]. To examine the local stability of the TB model with reinfection T^* [43]. Let the bifurcation parameter be $\beta = \beta^0$. Firstly, we obtained the bifurcation parameter at $R_0 = 1$. Thus

$$\frac{\beta\kappa}{(\kappa+\mu)(\mu+\delta+\gamma)} = 1,$$

therefore

$$\beta = \beta^0 = \frac{(\kappa+\mu)(\mu+\delta+\gamma)}{\kappa}. \quad (27)$$

To investigate the use of centre manifold theory in [42], it is convenient to make simplification and transform the variables on the TB model with reinfection (3). This is done by rewriting our system model (3). Let

$$x_1 = S_\iota, x_2 = E_\iota, x_3 = I_\iota \, \text{and} \, x_4 = R_\iota,$$

so that

$$N_\iota = x_1 + x_2 + x_3 + x_4.$$

More so, by using the vector notation $V = (x_1, x_2, x_3, x_4)^T$, the TB model with reinfection (3) can be restated in the form of $dV/dt = (f_1, f_2, f_3, x_4)^T$ as follows

$$\begin{aligned}
\frac{dx_1}{dt} &= \Lambda - \lambda x_1 - \mu x_1 = f_1,\\
\frac{dx_2}{dt} &= \lambda x_1 + \sigma\lambda x_4 - (\kappa + \mu)\, x_2 = f_2,\\
\frac{dx_3}{dt} &= \kappa x_2 - (\mu + \delta + \gamma)\, x_3 = f_3,\\
\frac{dx_4}{dt} &= \gamma x_3 - \sigma\lambda x_4 - \mu x_4 = f_4.
\end{aligned} \tag{28}$$

where

$$\lambda = \frac{\beta(x_3)}{N_\iota}, \tag{29}$$

The Jacobian of the basic model system (28), evaluated at the TFE, T^0 (denoted by $J(T^0)$), is given by

$$J(T^0) = \begin{pmatrix} -\mu & 0 & -\beta & 0\\ 0 & -(\kappa+\mu) & \beta & 0\\ 0 & \kappa & -(\mu+\delta+\gamma) & 0\\ 0 & 0 & \gamma & -\mu \end{pmatrix}. \tag{30}$$

The linearized system of the transformed model system (28) with $\beta = \beta^0$ chosen as a bifurcation parameter has a simple zero eigenvalue. We then calculate the right eigenvector W and the left eigenvector V which are associated with the zero eigenvalue of the Jacobian of (31) at (denoted by J_{β^0}) chosen such that $J(T_0)W = 0$ and $VJ(T_0) = 0$ with $VW = 1$, where

$$\begin{aligned} W &= [w_1, w_2, w_3, w_4]\\ V &= [v_1, v_2, v_3, v_4]. \end{aligned}$$

Then

$$J(T^0) = \begin{pmatrix} -\mu & 0 & -\beta & 0\\ 0 & -(\kappa+\mu) & \beta & 0\\ 0 & \kappa & -(\mu+\delta+\gamma) & 0\\ 0 & 0 & \gamma & -\mu \end{pmatrix} \begin{pmatrix} w_1\\ w_2\\ w_3\\ w_4 \end{pmatrix} = \begin{pmatrix} 0\\ 0\\ 0\\ 0 \end{pmatrix}. \tag{31}$$

$$\begin{aligned}
&-\mu w_1 - \beta w_3 = 0,\\
&-(\kappa+\mu)w_2 + \beta w_3 = 0,\\
&\kappa w_2 - (\mu+\delta+\gamma)w_3 = 0,\\
&\gamma w_3 - \mu w_4 = 0.
\end{aligned} \tag{32}$$

Solving (32), gives

$$\begin{aligned}
w_1 &= -\frac{\beta w_3}{\mu},\\
w_2 &= -\frac{\beta w_3}{\kappa+\mu},\\
w_3 &> 0\,(\text{can take any value}),\\
w_4 &= \frac{\gamma w_3}{\mu}.
\end{aligned} \tag{33}$$

Similarly, it is easy to obtain the left eigenvectors denoted as $V = (v_1, v_2, v_3, v_4)^T$ with $VJ(T^0) = 0$, gives

$$J(T^0)V_i = (v_1, v_2, v_3, v_4)\begin{pmatrix} -\mu & 0 & -\beta & 0 \\ 0 & -(\kappa+\mu) & \beta & 0 \\ 0 & \kappa & -(\mu+\delta+\gamma) & 0 \\ 0 & 0 & \gamma & -\mu \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \\ 0 \\ 0 \end{pmatrix}. \tag{34}$$

i.e.,

$$\begin{aligned} &-\mu v_1 = 0 \Rightarrow v_1 = 0, \\ &-(\kappa+\mu)v_2 + \kappa v_3 = 0, \\ &-\beta v_1 + \beta v_2 - (\mu+\delta+\gamma)v_3 + v_4 = 0, \\ &-\mu v_4 = 0 \Rightarrow v_4 = 0. \end{aligned} \tag{35}$$

Solving(35), gives

$$\begin{aligned} &v_1 = v_4 = 0, \\ &v_2 = \frac{\kappa}{(\kappa+\mu)}v_3, \\ &v_3 > 0 \,(\text{can take any value}). \end{aligned} \tag{36}$$

For the computation of a and b. The computation of coefficient bifurcations, a and b has been mentioned in [42]. Its known that when both coefficients are non-negative, then the system undergoes a backward bifurcation and otherwise forward bifurcation will occur.
It is convenient to find both a and b defined by [42] as follows:

For a, gives

$$a = \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k(0,0)}{\partial x_i \partial x_j}, \tag{37}$$

$$a = -\frac{2\beta(\frac{\sigma\gamma\Lambda}{\mu} + \Lambda)(\delta\Lambda + \kappa\Lambda + \frac{\kappa\gamma\Lambda}{\mu} + \Lambda\mu + \gamma\Lambda)\mu}{(\kappa+\mu)\Lambda^3} < 0, \tag{38}$$

Similarly, for b, gives

$$b = \sum_{k,i=1}^{4} v_k w_i \frac{\partial^2 f_k(0,0)}{\partial x_i \partial \varphi}(0,0). \tag{39}$$

$$b = \frac{\kappa}{\kappa+\mu} + \frac{\kappa\gamma\sigma}{(\kappa+\mu)\mu} > 0. \tag{40}$$

Observing from the signs of coefficient of a and b the direction of bifurcation is transcritical (forward) since coefficient of a is negative and b is positive. By item iv of Theorem presented in [42] , we conclude that the basic TB model exhibits forward bifurcation at $R_0 = 1$. Thus, establishing that unique endemic equilibrium is locally asymptotically stable if $R_0 > 1$. The figure below shows force of infection $'\lambda'$ versus basic reproductive number $'R_0'$ which exhibits a forward transcritical bifurcation for the chosen numerical data: $\gamma = 2$, $\beta = 0.02$, $\mu = 0.015$, $\Lambda = 9$, $\kappa = 0.0005$, $\delta = 0.2$, $\sigma = 0.5$. Figure 2 depicts the bifurcation diagram of the TB model with reinfection (1) as the basic reproduction number (R_0) is varied. A critical value occurs, that is, BP, which corresponds to transcritical bifurcation. Generally, we have two branches

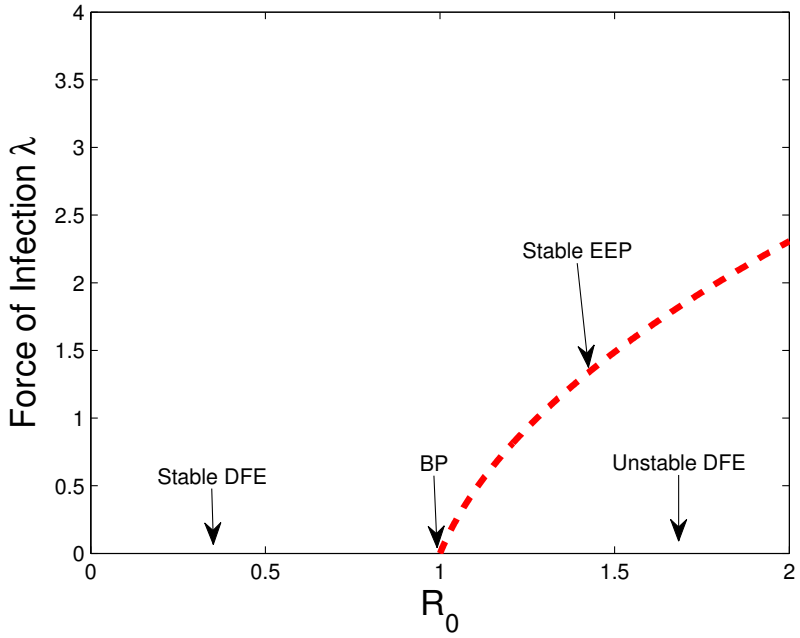

Figure 2: Bifurcation diagram of the basic TB model of system (1) demonstrating force of infection λ as R_0 varies with threshold BP represents forward or transcritical bifurcation.

of steady states: (i) the upper branch corresponding to stable endemic equilibria, EEP; and (ii) the lower branch corresponds disease free equilibria, DFE, which can be stable or unstable depending on the magnitudes of R_0. Similar to our theoretical analysis section, the value of R_0 quantity can be estimated using Equation (14). The emergence of alternate stable states is observed, with both endemic and disease-free equilibria being stable. The convergence to any of these stable states relies upon the initial abundance of individuals in the population, when $R_0 > 1$, only EEP is stable, leading to TB disease outbreak. Also observed is that as R_0 reduced and lies below BP point, i.e., $R_0 < BP$, DFE is stable in this case. Eventually, this condition eliminates the disease.

4.8 Global Stability of Endemic Equilibrium

Theorem 5 *The endemic equilibrium of the TB model with reinfection* $T^* = (S_\iota^*, E_\iota^*, I_\iota^*, R_\iota^*)$ *is asymptotically globally stable if* $R_0 > 1$.

Proof Following the method considered by [44], the following positive definite Lyapunov function can be considered:

$$L(S_\iota, E_\iota, I_\iota, R_\iota) = \left(S_\iota - S_\iota^* - S_\iota^* \ln\frac{S_\iota^*}{S_\iota}\right) + \left(E_\iota - E_\iota^* - E_\iota^* \ln\frac{E_\iota^*}{E_\iota}\right) + \left(I_\iota - I_\iota^* - I_\iota^* \ln\frac{I_\iota^*}{I_\iota}\right) + \left(R_\iota - R_\iota^* - R_\iota^* \ln\frac{R_\iota^*}{R_\iota}\right). \tag{41}$$

The derivatives of $L(S_\iota, E_\iota, I_\iota, R_\iota)$ with respect to t produced

$$\frac{dL}{dt} = \frac{(S_\iota - S_\iota^*)}{S_\iota}\frac{dS_\iota}{dt} + \frac{(E_\iota - E_\iota^*)}{E_\iota}\frac{dE_\iota}{dt} + \frac{(I_\iota - I_\iota^*)}{I_\iota}\frac{dI_\iota}{dt} + \frac{(R_\iota - R_\iota^*)}{R_\iota}\frac{dR_\iota}{dt}, \tag{42}$$

Substituting the expressions given in (1) into (42) gives:

$$\begin{aligned}\frac{dL}{dt} &= \frac{(S_\iota - S^*)}{S_\iota}(\Lambda - (\lambda+\mu)S_\iota) + \frac{(E_\iota - E_\iota^*)}{E_\iota}(\lambda S_\iota + \sigma\lambda R_\iota - (\kappa+\mu)E_\iota)\\ &\quad + \frac{(I_\iota - I_\iota^*)}{I_\iota}(\kappa E_\iota - (\gamma+\mu+\delta)I_\iota) + \frac{(R_\iota - R_\iota^*)}{R_\iota}(\gamma I_\iota - (\sigma\lambda+\mu)R_\iota),\end{aligned} \tag{43}$$

Simplifying (43), we obtain

$$\begin{aligned}\frac{dL}{dt} &= \frac{(S_\iota - S_\iota^*)}{S_\iota}(\Lambda - (\lambda+\mu)(S_\iota - S_\iota^*)) + \frac{(E_\iota - E_\iota^*)}{E_\iota}(\lambda(S_\iota - S_\iota^*) + \sigma\lambda(R_\iota - R_\iota^*)\\ &\quad - (\kappa+\mu)(E_\iota - E_\iota)) + \frac{(I_\iota - I_\iota^*)}{I_\iota}(\kappa(E_\iota - E_\iota^*) - (\gamma+\mu+\delta)(I_\iota - I_\iota^*)\\ &\quad + \frac{(R_\iota - R_\iota^*)}{R_\iota}(\gamma(I_\iota - I_\iota^*) - (\sigma\lambda+\mu)(R_\iota - R_\iota^*)).\end{aligned} \tag{44}$$

Now let us open the bracket in (44) and simplify to have

$$\begin{aligned}\frac{dL}{dt} &= \frac{(S_\iota - S_\iota^*)}{S_\iota}\Lambda - \frac{(S_\iota - S_\iota^*)^2}{S_\iota}(\lambda+\mu) + \frac{(E_\iota - E_\iota^*)}{E_\iota}\lambda(S_\iota - S_\iota^*) + \sigma\lambda\\ &\quad (R - R_\iota^*) - \frac{(E_\iota - E_\iota^*)^2}{E_\iota}(\kappa+\mu) + \frac{(I_\iota - I_\iota^*)}{I_\iota}\kappa(E_\iota - E_\iota^*) - \frac{(I_\iota - I_\iota^*)^2}{I_\iota}\\ &\quad (\gamma+\mu+\delta) + \frac{(R_\iota - R_\iota^*)}{R_\iota}\gamma(I_\iota - I_\iota^*) - \frac{(R_\iota - R_\iota^*)^2}{R_\iota}(\sigma\lambda+\mu).\end{aligned} \tag{45}$$

$$\begin{aligned}\frac{dL}{dt} &= \left(1 - \frac{S_\iota^*}{S_\iota}\right)\Lambda - \frac{(S_\iota - S_\iota^*)^2}{S_\iota}(\lambda+\mu) + \left(1 - \frac{E_\iota^*}{E_\iota}\right)(\lambda S_\iota - \lambda S_\iota^*) + (\sigma\lambda R_\iota - \sigma\lambda R_\iota^*)\\ &\quad - \frac{(E_\iota - E_\iota^*)^2}{E_\iota}(\kappa+\mu) + \left(1 - \frac{I_\iota^*}{I_\iota}\right)(\kappa E_\iota - \kappa E_\iota^*) - \frac{(I_\iota - I_\iota^*)^2}{I_\iota}(\gamma+\mu+\delta)\\ &\quad + \left(1 - \frac{R_\iota^*}{R_\iota}\right)(\gamma I_\iota - \gamma I_\iota^*) - \frac{(R_\iota - R_\iota^*)^2}{R_\iota}(\sigma\lambda+\mu)).\end{aligned} \tag{46}$$

$$\begin{aligned}\frac{dL}{dt} &= \Lambda - \frac{S_\iota^*}{S_\iota}\Lambda - \frac{(S_\iota - S_\iota^*)^2}{S_\iota}(\lambda+\mu) + \lambda S_\iota - \lambda S_\iota^* + \sigma\lambda R_\iota - \sigma\lambda R_\iota^*\\ &\quad - \lambda S_\iota\frac{E_\iota^*}{E_\iota} + \lambda S_\iota^*\frac{E_\iota^*}{E_\iota} - \sigma\lambda R_\iota\frac{E_\iota^*}{E_\iota} + \sigma\lambda R_\iota^*\frac{E_\iota^*}{E_\iota} - \frac{(E_\iota - E_\iota^*)^2}{E_\iota}(\kappa+\mu)\\ &\quad + \kappa E_\iota - \kappa E_\iota^* - \kappa E_\iota\frac{I_\iota^*}{I_\iota} + \kappa E_\iota^*\frac{I_\iota^*}{I_\iota} - \frac{(I_\iota - I_\iota^*)^2}{I_\iota}(\gamma+\mu+\delta)\\ &\quad + \gamma I_\iota - \gamma I_\iota^* - \gamma I_\iota\frac{R_\iota^*}{R_\iota} + \gamma I_\iota^*\frac{R_\iota^*}{R_\iota} - \frac{(R_\iota - R_\iota^*)^2}{R_\iota}(\sigma\lambda+\mu).\end{aligned} \tag{47}$$

Group positive terms together and negative terms together, we get

$$\frac{dL}{dt} = \Lambda + \lambda S_\iota + \gamma I_\iota^* + \frac{R_\iota^*}{R_\iota} + \kappa E_\iota^* + \frac{I_\iota^*}{I_\iota} + \gamma I_\iota + \sigma\lambda R_\iota^* + \frac{E_\iota^*}{E_\iota} + \kappa E_\iota + \lambda S_\iota^* \frac{E_\iota^*}{E_\iota} + \sigma\lambda R_\iota - \frac{S_\iota^*}{S_\iota}\Lambda$$
$$- \lambda S_\iota^* - \sigma\lambda R_\iota^* - \lambda S_\iota \frac{E_\iota^*}{E_\iota} - \sigma\lambda R_\iota \frac{E_\iota^*}{E_\iota} - \kappa E_\iota^* - \kappa E_\iota \frac{I_\iota^*}{I_\iota} - \gamma I_\iota^* - \gamma I_\iota \frac{R_\iota^*}{R_\iota} - \frac{(S_\iota - S_\iota^*)^2}{S_\iota}(\lambda + \mu)$$
$$- \frac{(E_\iota - E_\iota^*)^2}{E_\iota}(\kappa + \mu) - \frac{(I_\iota - I_\iota^*)^2}{I_\iota}(\gamma + \mu + \delta) - \frac{(R_\iota - R_\iota^*)^2}{R_\iota}(\sigma\lambda + \mu) \tag{48}$$

$$\frac{dL}{dt} = (\Lambda + \lambda S_\iota + \gamma I_\iota^* + \frac{R_\iota^*}{R_\iota} + \kappa E_\iota^* + \frac{I_\iota^*}{I_\iota} + \gamma I_\iota + \sigma\lambda R_\iota^* + \frac{E_\iota^*}{E_\iota} + \kappa E_\iota + \lambda S_\iota^* \frac{E_\iota^*}{E_\iota} + \sigma\lambda R_\iota,) - (\frac{S_\iota^*}{S_\iota}\Lambda$$
$$- \lambda S_\iota^* - \sigma\lambda R_\iota^* - \lambda S_\iota \frac{E_\iota^*}{E_\iota} - \sigma\lambda R_\iota \frac{E^*}{E_\iota} - \kappa E_\iota^* - \kappa E \frac{I^*}{I} - \gamma I^* - \gamma I \frac{R^*}{R} - \frac{(S - S^*)^2}{S}(\lambda + \mu)$$
$$\frac{(E_\iota - E_\iota^*)^2}{E_\iota}(\kappa + \mu) - \frac{(I_\iota - I_\iota^*)^2}{I}(\gamma + \mu + \delta) - \frac{(R_\iota - R_\iota^*)^2}{R_\iota}(\sigma\lambda + \mu). \tag{49}$$

$$\frac{dL}{dt} = M_1 - M_2,$$

where

$$M_1 = \Lambda + \lambda S_\iota + \gamma I_\iota^* + \frac{R_\iota^*}{R_\iota} + \kappa E_\iota^* + \frac{I_\iota^*}{I} + \gamma I_\iota + \sigma\lambda R_\iota^* + \frac{E_\iota^*}{E_\iota} + \kappa E_\iota + \lambda S_\iota^* \frac{E_\iota^*}{E_\iota} + \sigma\lambda R_\iota, \tag{50}$$

$$M_2 = \frac{S_\iota^*}{S_\iota}\Lambda - \lambda S_\iota^* - \sigma\lambda R_\iota^* - \lambda S_\iota \frac{E_\iota^*}{E_\iota} - \sigma\lambda R_\iota \frac{E_\iota^*}{E_\iota} - \kappa E_\iota^* - \kappa E_\iota \frac{I_\iota^*}{I_\iota} - \gamma I_\iota^* - \gamma I_\iota \frac{R_\iota^*}{R_\iota} - \frac{(S_\iota - S_\iota^*)^2}{S_\iota}$$
$$(\lambda + \mu) - \frac{(E_\iota - E_\iota^*)^2}{E_\iota}(\kappa + \mu) - \frac{(I_\iota - I_\iota^*)^2}{I_\iota}(\gamma + \mu + \delta) - \frac{(R_\iota - R_\iota^*)^2}{R_\iota}(\sigma\lambda + \mu). \tag{51}$$

$\frac{dL}{dt} \leq 0$ if M_1 is less than M_2.

$\frac{dL}{dt} = 0$ if and only if $S_\iota = S_\iota^*, E_\iota = E_\iota^*, I_\iota = I_\iota^*, R_\iota = R_\iota^*$.

Therefore, the largest invariant impact invariant set in ,$\{(S_\iota^*, E_\iota^*, I_\iota^*, R_\iota^*) \in \Phi : \frac{dL}{dt} = 0\}$, is the singleton set T^*, where T^* is the endemic equilibrium of the system (1). Therefore, by Lasalles Invariant principle, it implies that T^* is globally asymptotically stable in Φ if M_1 is less than M_2 [44]. Therefore, the largest invariant impact invariant set in ,$\{(S_\iota^*, E_\iota^*, I_\iota^*, R_\iota^*) \in \Phi : \frac{dL}{dt} = 0\}$, is the singleton set T^*, where T^* is the endemic equilibrium of the system (1). Therefore, by LaSalles Invariance principle, it implies that T^* is globally asymptotically stable in Φ if M_1 is less than M_2 [44].

5 Numerical Investigations and Discussions

This section, presents the numerical simulation solutions of the TB model with reinfection. To demonstrate the solutions, we utilized MATLAB software. The diagram displayed below

confirm the solutions employing the initial conditions and parameter values of the proposed model. In this situation, we have taken the parameter values from the published literature papers, by estimation and assumption and they are presented in Table 2. In addition, $S_\iota = 0.99, E_\iota = 0.01, I_\iota = 0$ and $R_\iota = 0$.

Table 2: The Parameters and Baseline Values of the System (1)

Parameters	**Baseline values**	**Ranges**	**References**
Λ	3,768,410	[3,000,000, 4,000,000]	[45]
μ	0.02041	[0.0143,0.03]	[46]
β	Variable	$[0.1 - 1]$	Assumed
σ	0.25	[0-1]	[3, 47]
κ	0.05	[0.005,0.05]	[48]
γ	1.5	[0.5, 2.5]	[45]
δ	0.413	[0.2, 0.6]	[49]

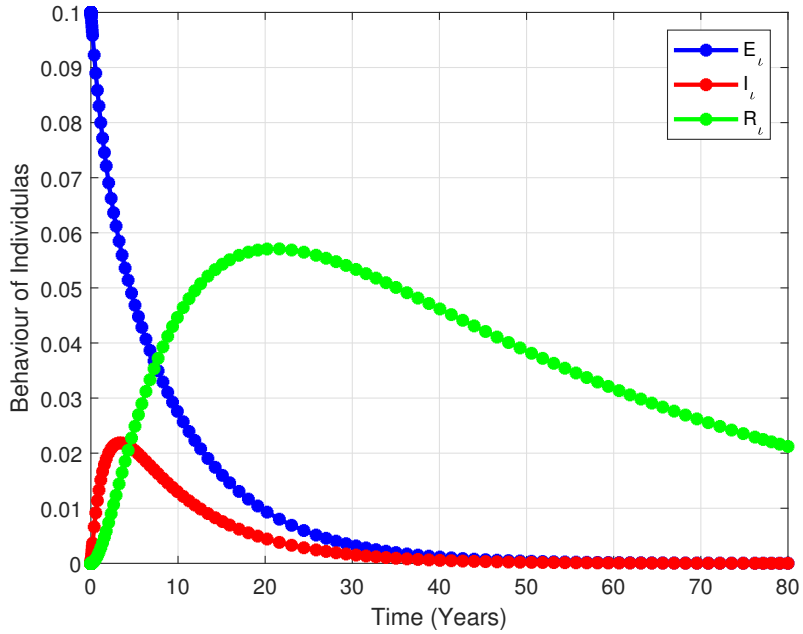

Figure 3: Simulations of system (1) showing the behaviour of individuals when $\beta = 0.2433$, which gives $R_0 < 1$.

Figure 3 illustrates the variation of the system model (1) as a function of time (years) which gives $R_0 = 0.4183 < 1$. This figure depicts the global stability of the TB-free equilibrium with $\beta = 0.2344$ and all parameter values as specified in Table 2. The diagram shows that the trajectories of the solution of the system model (1) converge to the disease-free equilibrium T_0. This figure implies that the TB will not invade the population if $R_0 < 1$, verifying that the TB-free equilibrium is GAS if $R_0 < 1$.

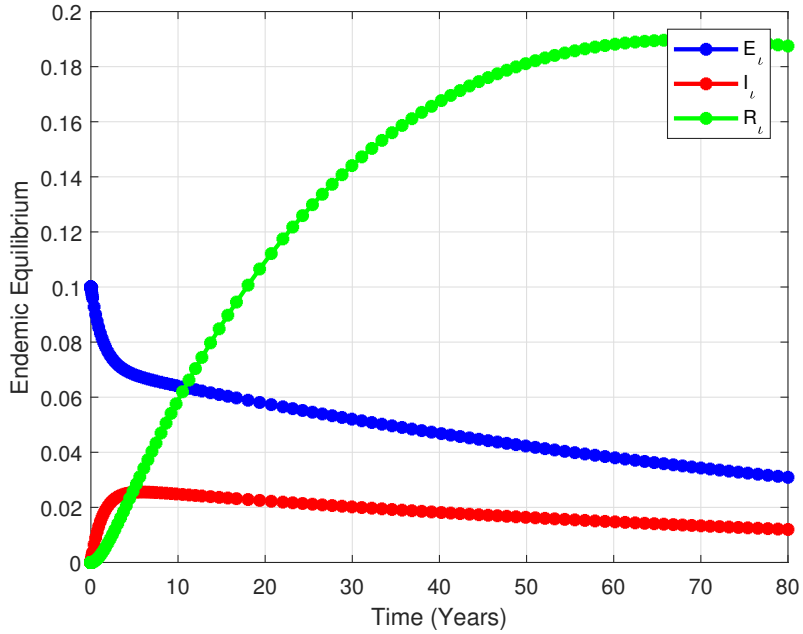

Figure 4: Simulations of system (1) showing the behaviour of individuals when $\beta = 0.5433$, which gives $R_0 > 1$.

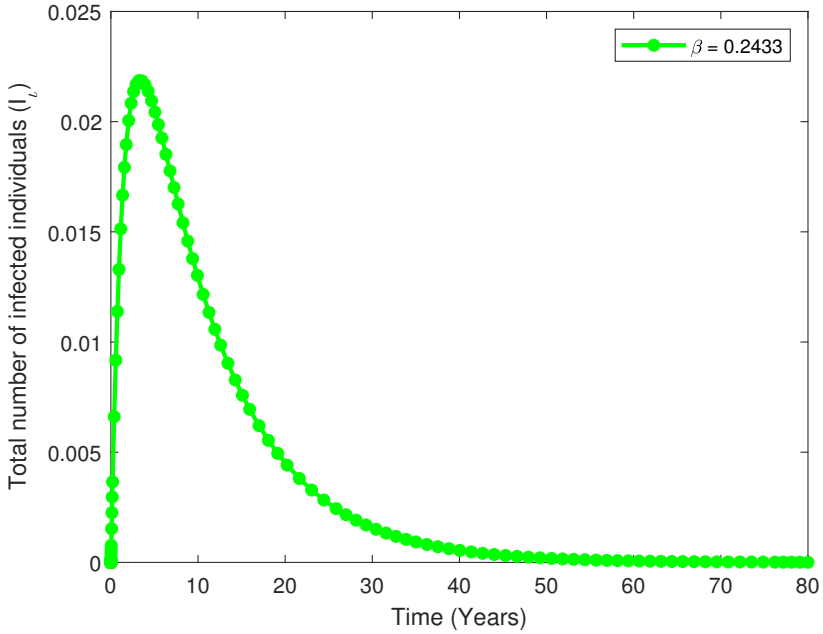

Figure 5: Simulations of system (1) showing the total number of infected individuals using different initial conditions $(S_\iota = 0.9, E_\iota = 0.1, I_\iota = 0, R_\iota = 0)$ with $\beta = 0.2433$ and $R_0 = 0.4183 < 1$.

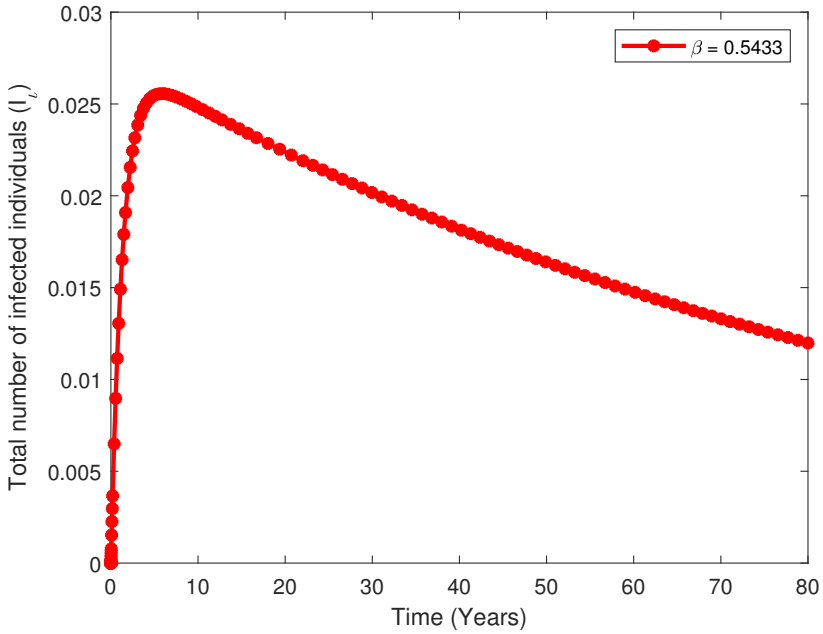

Figure 6: Simulations of system (1) showing the total number of infected individuals using different initial conditions ($S_\iota = 0.9, E_\iota = 0.1, I_\iota = 0, R_\iota = 0$) with $\beta = 0.5433$ and $R_0 = 1.1192 > 1$.

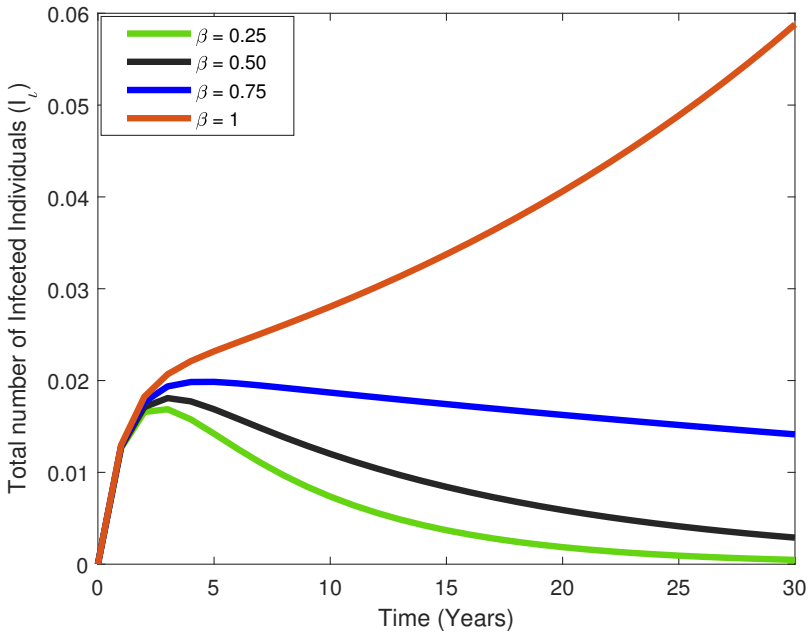

Figure 7: The effect of transmission rate (β) on the total number of infected individuals.

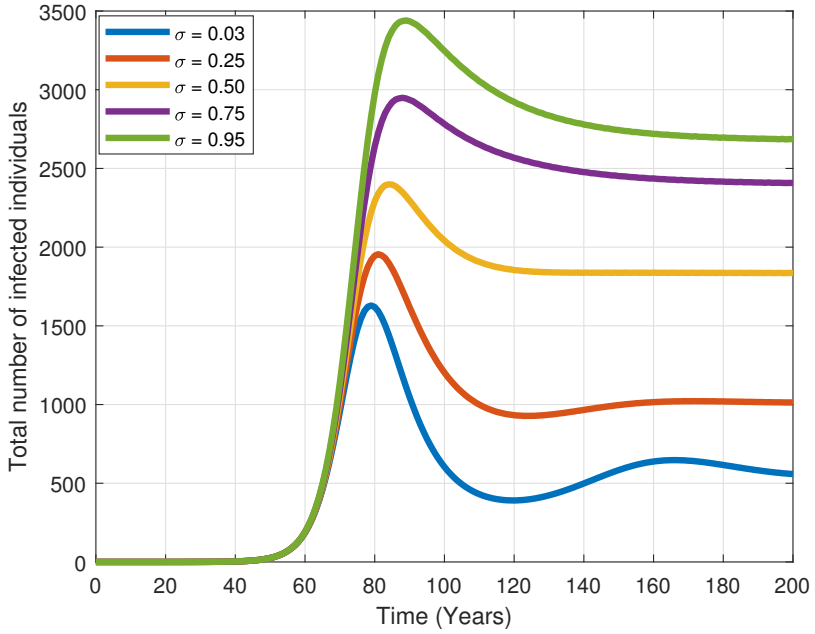

Figure 8: The effect of re-infection among the treated individuals (σ) on the total number of infected individuals.

Figure 4 represents the variation of the system model (1) as a function of time (years), which gives $R_0 = 1.1192 > 1$. The figure shows that the global stability of the endemic equilibrium T^* is locally asymptotically stable with $\beta = 0.5344$ and all parameter values as specified in Table 2. From the diagram, it can be seen that the trajectories of the solution of the system model (1) converge to the endemic equilibrium point T^*; this shows that TB transmission persists in the population if $R_0 > 1$, which verifies the justification for the statement that endemic equilibrium is GAS if $R_0 > 1$.
Figure 5 shows the time-series plot for the infected population (I_ι) for $\beta = 0.2433$ which gives $R_0 = 0.4183$ with all other parameter values as specified in Table 2. The curve converges to the TFE, with different initial population sizes, $(S_\iota = 0.9, E_\iota = 0.1, I_\iota = 0, R_\iota = 0)$.
Figure 6 shows the time-series plot for the infected population (I_ι) for $\beta = 0.5433$ which gives $R_0 = 1.1192$ with all other parameter values as specified in Table 2. The curve converges to the endemic equilibrium T^*, with different initial population sizes, $(S_\iota = 0.9, E_\iota = 0.1, I_\iota = 0, R_\iota = 0)$.
Figure 7 illustrates the impact of transmission rate (β) on the total number of infected individuals as we vary $\beta = 1$, 0.75 0.50, 0.25. As β decreases, the peak becomes less pronounced and drastically reduced. For small value of β there will be no peak, and the total number of infected individuals decreases directly to zero. Epidemiologically, as anticipated, a decrease in contact rate yields a productive positive impacts in the dynamics of TB infection with a reduction in the total number infected individuals.
Figure 8 demonstrates the impact of re-infection among the treated individuals σ between 0.03 and 0.95. [3] stated that people that have been treated can re-infect as a result of low immunity. Increasing σ results in a huge force of infection, which causes the TB infection. Similarly, it

can be clearly observed that, with a lower threshold value of the reinfection among the treated individuals σ, the infection rate is low. For high values of σ, the infection rate is higher; see figure 8, which shows that decreasing the value of σ from 0.95 to 0.03 brings down the number of infected individuals. Epidemiologically, we observed that a reduction in TB cases emerge due to low value of the reinfection parameter. This result is in agreement with previous results on endemic TB transmission [3].

6 Conclusions

In this article, the dynamic behavior of the TB model with reinfection was formulated. The boundedness of the TB model with reinfection was proved. The invariant region in which the solutions of the basic TB model are biologically meaningful was also obtained. Mathematical analysis shows that the TB model with reinfection (1) at the TB-free case is locally and globally asymptotically stable whenever the associated basic reproductive number $R_0 < 1$. In addition, when associated basic reproductive number $R_0 > 1$, the TB model with reinfection (1) are both locally and globally asymptotically stable. This means that TB infection will disappear if $R_0 < 1$, and otherwise will be prevalent when $R_0 > 1$. Theorem 4 and Theorem 5 verify that R_0 is the keys threshold for eradicating the disease. A detailed analysis of the TB model with reinfection (1) based on the use of the center manifold theory, demonstrates the existence of transcritical bifurcation phenomenon, where there is an exchange of stability from the disease-free equilibrium to endemic equilibrium points at $R_0 = 1$. Finally, some numerical investigations are performed for the verification of the theoretical results. Numerical investigation illustrated that when the reinfection value is increase, it results into a huge force of infection. However, the population of infected individuals does not go to extinction even at equilibrium state.

- To consider a stochastic model approach. This will result in more realistic TB model dynamics.
- Since the spread of TB affects all age groups, it is crucial to consider the dynamics of the TB model by incorporating an age-structured model.
- Real data will also be considered because collecting data for TB patients is difficult in epidemiological models; as a result, we use data collected or estimated from literature sources. Once we have real-world data for TB patients, we can compare it to theoretical outcomes.
- Analyzing the dynamics of the TB model using a fractional order differential equation (FODE). It will be extremely interesting to use a FODE to examine the dynamics of TB model.
- To consider a different control strategies which remain the important factors that contribute to a decreased of the infection.

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