

Research Article

On the Optimal Control of HIV-TB Co-Infection and Improvement of Workplace Productivity

Baba Seidu ¹, **Oluwole Daniel Makinde** ² and **Ibrahim Yakubu Seini** ³

¹Department of Mathematics, C. K. Tedam University of Technology and Applied Sciences, Navrongo, Ghana

²Faculty of Military Science, Stellenbosch University, Stellenbosch, South Africa

³Department of Mechanical and Industrial Engineering, School of Engineering, University for Development Studies, Tamale, Ghana

Correspondence should be addressed to Baba Seidu; bseidu@cktutas.edu.gh

Received 15 October 2022; Revised 27 February 2023; Accepted 1 March 2023; Published 18 March 2023

Academic Editor: Andrew Pickering

Copyright © 2023 Baba Seidu et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Human immunodeficiency virus (HIV) and tuberculosis (TB) have long been known to have a synergistic relationship. This is a result of each of the diseases impacting negatively on the immune system of the infected persons. The impact of these diseases on workforce productivity is studied in this paper from the viewpoint of dynamical systems. In this paper, we present a nonlinear ordinary differential equation model to study the dynamics of HIV-TB co-infection and its effect on workforce productivity. The main model is first decoupled into two basic submodels of HIV-only and TB-only models, whose qualitative properties are presented before the qualitative properties of the main model are studied. While the HIV-only model is shown to have a globally asymptotically stable disease-free equilibrium whenever its basic reproduction number is less than unity, the TB-only model is shown to exhibit backward bifurcation under some conditions. To investigate the impact of various intervention strategies on the control of the co-infection and improvement of workforce productivity, five time-dependent controls (involving transmission prevention for the two diseases, therapy for the two diseases, and capacity building for improved workforce productivity) are incorporated into the basic model to form an optimal control problem, which is qualitatively analyzed using Pontryagin's maximum principle and numerically simulated. Incremental cost-effectiveness analysis is conducted with the results of the numerical simulations. It is observed that the most cost-effective strategy for fighting the spread of the co-infection with enhanced productivity is that of combining both preventative and curative measures along with skills training.

1. Introduction

HIV continues to be among the top diseases that place economic burden on governments and individuals, apart from the many lives that are lost through the disease. The disease has claimed over 39 million lives and continues to claim more even with the stepping up of intervention strategies. Tuberculosis (TB) places second only to HIV as a worldwide killer due to a single infectious agent. TB also continues to place huge burden on the world as unacceptable numbers of people continue to get infected and die from the disease. The low-and-middle-income countries continue to bear the brunt of TB, with over 95% of TB deaths occurring in these countries. An estimated 2 billion dollars is required to fill the resource gap required to fully

implement the current intervention strategies [1]. HIV and TB have long since been identified to have a synergistic relationship, with each disease increasing the risk of contracting the other [2, 3]. People living with HIV are said to be about 12–20 times more likely to develop TB than HIV-negative people.

Mathematical models have been used to study the dynamics of infectious diseases. These models are especially useful as they help in improving our understanding about the dynamics and the factors that affect the spread of diseases. Most of the mathematical models that deal with HIV and other related diseases generally appear to follow two trends. The first category involves those that deal with modeling the pathogenesis of the diseases [4–8], while the second category involves those that deal with the effects of demographic and other epidemiological

factors on the spread of the diseases [9–13]. A lot of research on HIV-TB co-infection has been conducted using mathematical modeling in order to study the dynamics and to identify optimal strategies to curb the spread of the two diseases. The work in [14] appears to be among the very first mathematical models that were proposed to study the spread of HIV-TB co-infection. The goal in [14] was to provide a mathematical understanding of the impact HIV had on the spread of TB. Following [14], a mathematical model was developed in [15] to study the spread of HIV and curable TB co-infection within a variable-sized population. The work in [15] was modified by using density-dependent birth and death rates to study the effect of TB on HIV dynamics, and it was observed that effective treatment of TB may have a positive effect in slowing down the surge of HIV [16]. The work in [17] also modified the model in [15] to include the effect of antiretroviral therapy as well as other transmission dynamics of TB. It was observed that TB treatment is equally effective for persons who were infected with both TB and HIV. They also concluded that administering antiretroviral therapy alongside the treatment of latent and active TB infected persons could slow down progression to the AIDS stage. In [18], an earlier model [19] was extended to study the effect of administering antiretroviral therapy at the various phases of TB infection treatment. They observed that early administration of antiretroviral therapy during TB treatment is very effective in reducing disease-induced deaths. Tanvi et al. [20] proposed a model to study the effect of Holling type II TB treatment. To reduce the gap between actual and reported infection infections, the authors of [21] proposed a model to incorporate treatment and detection of TB infection and studied the optimal strategies in controlling the spread of HIV/TB co-infection.

As the world strives to increase productivity to match its increasing population, it is important for the working class to remain healthy. We note however that majority of the people infected with HIV and TB are those in their active working years. This leads to declining workforce productivity, reduced household incomes, and increased poverty. The question of how HIV-TB co-infection impacts workplace productivity is thus pertinent. The research studies discussed so far have provided the basic framework for modeling HIV-TB co-infection. However, not so much research has been done on the impact of infectious diseases on workforce evolution/dynamics. The pioneering work of Okosun et al. [22] is probably one of the first to present a mathematical modeling approach to describe the impact of HIV on workforce productivity. They sought to study the optimal strategies in controlling the spread of HIV and improving productivity using the least cost and observed that the most cost-effective strategy is to use infection preventative measures together with skills improvement measure. Following [22], Seidu and Oluwale [9] proposed an industrial HIV model to determine the optimal control of workforce productivity and HIV spread in the presence of carefree individuals. In a related work [12], a model was proposed to study the impact of HIV-malaria co-infection on workforce productivity. Through cost-effectiveness analysis, they observed that preventative measures are the most cost-effective strategy in the fight against the spread of the co-infection and improved productivity. Also, the work in [23] presented an optimal control problem to study the impact of carefree attitude towards safe sex on the transmission

dynamics of HIV and workforce productivity. In this current paper, the goal is to incorporate the concept of workforce productivity developed in [9, 22, 23] to propose an industrial HIV-TB co-infection model which describes the dynamics of the co-infection and its effects on a typical workforce. Thus, this paper presents a deterministic mathematical model that describes the dynamics of HIV and TB infections in a homogeneously mixed workforce.

The remainder of the paper is organized as follows. Section 2 discusses the formulation of the model in focus. In Section 3, the full model is decomposed into two basic submodels (namely, the HIV-only model and the TB-only submodel) and their qualitative analysis is presented. The qualitative properties of the full model are discussed in Section 4. In Section 5, the main model is extended into an optimal control problem which is qualitatively analyzed using Pontryagin's maximum principle. In Section 6, numerical experimentation of the resulting optimal control is performed and the results are discussed. The main conclusions of the work are finally presented in Section 7.

2. Formulation of the Mathematical Model

Consider a homogeneously mixed workforce of size $N(t)$ consisting of Susceptibles, $S(t)$, and Infectives, $I(t)$. The infectives consist of those employees who are either HIV or TB infected or both. Thus, the infectives consist of the following:

- (1) HIV-only infected persons, some of whom are productive, I_{ph} , and others are nonproductive, I_{nh} .
- (2) Employees without HIV who are exposed to TB, E_p , who are assumed to be productive.
- (3) Employees with only active TB infection, I_{nt} . These people are assumed to be nonproductive.
- (4) Employees in the latent state of TB who have contracted HIV; those who are productive, I_{pht} and those who are nonproductive, I_{nht} .
- (5) Employees, with active TB and HIV infection, I_{nd} , who are assumed to be nonproductive.
- (6) Employees who had only TB and recovered, R_p , who are assumed to be productive.
- (7) AIDS patients, $A(t)$, who are assumed to be nonproductive.

Thus, the total workforce population is given by

$$N = S + I_{ph} + I_{nh} + E + I_{nt} + R_p + I_{pht} + I_{nht} + I_{nd} + A. \quad (1)$$

In the subscripts, we use p, n, a, t , and d to represent productive, nonproductive, HIV, TB, and dually infected, respectively.

HIV/AIDS is spread through contact with an infected person while TB is contracted through inhaling of air containing droplets which are left in the air when an infected person sneezes without covering. Individuals susceptible to HIV (S, E, I_{nt} , and R_p) are assumed to get infected through contact with HIV-infected persons ($I_{nh}, I_{nh}, I_{nht}, I_{pht}, I_{nd}$) with a force of infection $\lambda_h = (\beta_h c_h (I_{ph} + I_{nh} + I_{pht} + I_{nht} + I_{nd})/N)$. The

parameters β_h and c_h , respectively, represent the probability of infection per contact and the average number of contacts per infected person. Due to differences in the immune systems of people, a fraction f_1 of Susceptibles who are infected with HIV only move to the productive HIV-infective class, I_{ph} , and the remaining fraction, $1 - f_1$, moves to the nonproductive HIV-only infective class, I_{nh} . Thus, the rate of progression of fully susceptible individuals into the I_{ph} and I_{nh} classes is $f_1\lambda_h$ and $(1 - f_1)\lambda_h$, respectively. Individuals in the E_p and I_{nt} classes progress to classes I_{nht} and I_{nd} at rates $\xi_1\lambda_h$ and $\xi_2\lambda_h$, respectively, where $\xi_1 > 1$ and $\xi_2 > \xi_1$ are modification parameters that account for increased susceptibility due to the TB infection. Individuals in the R_p class get HIV-only infection to join the I_{ph} and I_{nh} at rates $f_1\lambda_h$ and $(1 - f_1)\lambda_h$, respectively. Individuals susceptible to TB (S , I_{ph} , I_{nh} , and R_p) get infected with TB through contact with TB-infected persons (I_{nt} and I_{nd}) with a force of infection $\lambda_T = (\beta_T c_T (I_{nt} + I_{nd})/N)$.

Individuals who are exposed to TB and are in the latent stage of the infection are assumed incapable of transmitting the disease. Due to differences in the immune systems of people, a fraction, f_2 , of the susceptible individuals infected with TB only move to the exposed class, E_p , and are assumed to be productive since exposed persons in the latent stage mostly do not show clinical symptoms of TB infection and usually appear and feel healthy, while the remaining fraction moves to the infective class. People in the TB-exposed classes E_p , I_{ph} , and I_{nht} are assumed to progress to the active TB-infected classes, I_{nt} , I_{nd} , and I_{nd} , respectively, at rates θ , $\eta_1\theta$ and $\eta_2\theta$, respectively. The parameters $\eta_1 > 1$ and $\eta_2 > 1$ are modification parameters due to increased possibility of progressing to infectiousness because of the impact of HIV infection. The progression of people in the I_{nht} and I_{ph} classes to the active stage of TB leads to dual infection. People who recover from TB-

only infection, R_p , are assumed to be re-infected with TB at the rate $\rho\lambda_T$ where $\rho < 1$ is a modification parameter accounting for the increased immunity that leads to reduced susceptibility due to their previous TB infection (individuals who recover from TB are known to often have some increased partial immunity from the disease). HIV-infected people, I_{ph} , I_{nh} , I_{ph} , I_{nht} , and I_{nd} , are assumed to progress to the AIDS class, A , at rates δ , $\kappa_1\delta$, $\kappa_2\delta$, $\kappa_3\delta$, and $\kappa_4\delta$ where $1 < \kappa_1 < \kappa_2 < \kappa_3 < \kappa_4$ are modification parameters that account for increased chances of failure of HIV treatment due to either lower immunity or TB infection. It is assumed that TB-infected people in classes, I_{ph} and I_{nd} , are treated of TB to join the R_p and I_{nht} classes at rates r and $\tau_2 r$, respectively, where $\tau_2 < 1$ is a modification parameter accounting for reduced rate of recovery due to HIV infection of people in the I_{nd} class. Administration of HAAR drugs is assumed to lead to reduced viral load which in turn leads to people in the I_{nh} and I_{nht} moving to the I_{ph} class at rates σ and $\tau_3\sigma$ where $\tau_3 < 1$ is a modification parameter that accounts for reduced reduction of viral load in people within the I_{nht} class due to the TB infection. Dual infection results when individuals infected with either disease also get infected with the other. Thus, dual infection results from HIV-only infected persons getting infected with TB, TB-only infected persons getting infected with HIV, and HIV-infected persons in the latent stage of TB infection progressing to the active stage of TB infection.

Individuals in all classes are assumed to have a natural death rate of μ , whereas individuals in TB-infected classes I_{nt} , I_{nd} suffer TB-induced death rate of μ_T and individuals in the AIDS class, A , suffer an AIDS-induced death rate of μ_h . The dynamics described above are represented in Figure 1.

The mathematical model that describes the dynamics of HIV-TB infection in a workforce describe thus far is given by the following set of differential equations:

$$\left. \begin{aligned}
 \frac{dS_p}{dt} &= Q - (\lambda_h + \lambda_T + \mu)S_p \\
 \frac{dI_{ph}}{dt} &= f_1\lambda_h(S_p + R_p) + \sigma I_{nh} - (\tau_1\lambda_T + k_1)I_{ph} \\
 \frac{dI_{nh}}{dt} &= (1 - f_1)\lambda_h(S_p + R_p) - (\tau_1\lambda_T + k_2)I_{nh} \\
 \frac{dE_p}{dt} &= f_2\lambda_T(S_p + \rho R_p) - (\xi_1\lambda_h + k_3)E_p \\
 \frac{dI_{ph}}{dt} &= \tau_1 f_2 \lambda_T I_{ph} + \sigma I_{nht} - k_4 I_{ph} \\
 \frac{dI_{nht}}{dt} &= \tau_1 (1 - f_2)\lambda_T I_{nh} + \xi_1\lambda_h E_p + \tau_2 r I_{nd} - k_5 I_{nht} \\
 \frac{dI_{nt}}{dt} &= (1 - f_2)\lambda_T(S_p + \rho R_p) + \theta E_p - (\xi_2\lambda_h + k_6)I_{nt} \\
 \frac{dR_p}{dt} &= r I_{nt} - (\rho\lambda_T + \lambda_h + \mu)R_p \\
 \frac{dI_{nd}}{dt} &= \xi_2\lambda_h I_{nt} + \tau_1\lambda_T [f_2 I_{nh} + (1 - f_2)I_{ph}] + \theta(\eta_1 I_{nht} + \eta_2 I_{ph}) - k_7 I_{nd} \\
 \frac{dA}{dt} &= \delta(I_{ph} + \kappa_1 I_{nh} + \kappa_2 I_{ph} + \kappa_3 I_{nht} + \kappa_4 I_{nd}) - k_8 A
 \end{aligned} \right\} \quad (2)$$

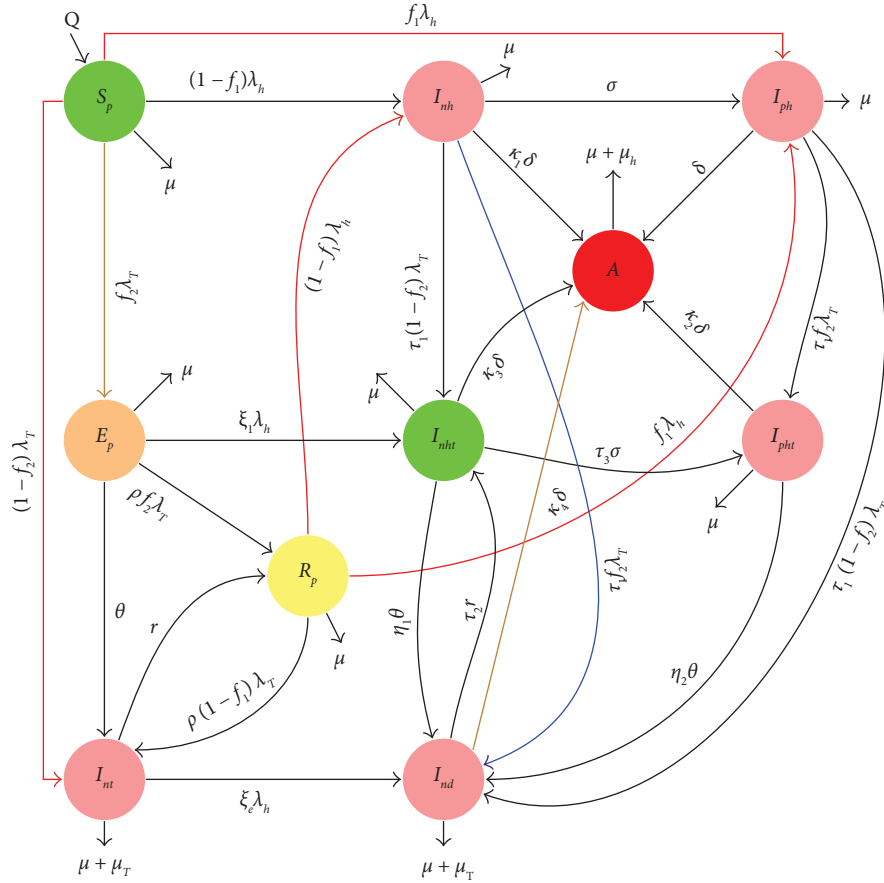


FIGURE 1: Schematic diagram of the industrial HIV-TB model.

where

$$\begin{aligned}
 k_1 &= \delta + \mu, & k_2 &= \sigma + \kappa_1\delta + \mu, & k_3 &= \theta + \mu, & k_4 &= \eta_2\theta + \kappa_2\delta + \mu, \\
 k_5 &= \eta_1\theta + \kappa_3\delta + \sigma + \mu, & k_6 &= r + \mu + \mu_T, & k_7 &= \tau_2r + \kappa_4\delta + \mu + \mu_T, & k_8 &= \mu + \mu_h.
 \end{aligned} \tag{3}$$

It should be noted that model (2) can be decomposed into two single-disease infection models, namely, the HIV-only model and the TB-only model. In the next few sections, each of the two basic models is discussed before the full model is discussed. The parameters of the model and their values used for numerical simulation purposes only are presented in Table 1.

3. Qualitative Analysis of the Submodels

In this section, we break the main model into two submodels, namely, the HIV-only model and the TB-only model. This is done by setting all parameters and variables related to TB infection to zero in the full model (2) to get the HIV-only model and vice versa.

TABLE 1: Description of model parameters and baseline values.

Parameter	Description	Value	Reference
Q	Rate of recruitment into population	100	
c_h	Per capita contact rate of HIV-infectious persons	1	
c_T	Per capita contact rate of TB-infectious persons	1	
β_h	HIV transmission probability per contact	Variable	
β_T	HIV transmission probability per contact	Variable	
σ	Rate of improvement to productive classes due to training and treatment of HIV-infected people	Variable	
δ	Rate of progression of HIV patients to AIDS	0.1	[24]
θ	Rate of progression from latent to active TB	0.03	[25]
r	Recovery rate from active TB infection	Variable	
τ_1	Modification parameter for increased rate of TB infection due to HIV	Variable	
f_1	Fraction of newly HIV-infected people who are productive	Variable	
f_2	Fraction of newly infected individuals with latent TB	Variable	
ρ	Modification parameter for reduced susceptibility to TB due to acquired partial immunity	Variable	
η_1, η_2	Modification parameters for increased progression to active TB for I_{nht} and I_{pht} classes	Variable	
ξ_1, ξ_2	Modification parameters for increased rate of HIV infection for E_p and I_{nt} classes	Variable	
$\kappa_1, \kappa_2, \kappa_3, \kappa_4$	Modification parameters for increased progression to AIDS for I_{nh}, I_{pht}, I_{nht} , and I_{nd} classes	Variable	
μ	Natural death rate of humans	0.02	
μ_h	AIDS-induced death rate in humans	0.1	
μ_T	TB-induced death rate in humans	0.2	[8]

The submodels are thus given by

$$\begin{array}{cc}
 \text{HIV-only Model (HOM)} & \text{TB-only Model (TOM)} \\
 \hline
 \frac{dS_p}{dt} = Q - (\lambda_{hh} + \mu)S_p & \frac{dS_p}{dt} = Q - (\lambda_{TT} + \mu)S_p; \\
 \frac{dI_{ph}}{dt} = \lambda_{hh}f_1S_p + \sigma I_{nh} - k_1I_{ph} & \frac{dE_p}{dt} = f_2\lambda_{TT}(S_p + \rho R_p) - k_3E_p; \\
 \frac{dI_{nh}}{dt} = (1 - f_1)S_p\lambda_{hh} - k_2I_{nh} & \frac{dI_{nt}}{dt} = (1 - f_2)(S_p + \rho R_p)\lambda_{TT} + \theta E_p - k_6I_{nt}; \\
 \frac{dA}{dt} = \delta(I_{ph} + \kappa_1I_{nh}) - k_8A & \frac{dR_p}{dt} = rI_{nt} - (\rho\lambda_{TT} + \mu)R_p,
 \end{array} \tag{4}$$

where λ_h, λ_T modify into $\lambda_{hh} = (\beta_h c_h (I_{ph} + I_{nh})/N_h)$ and $\lambda_{TT} = (\beta_T c_T I_{nt}/N_T)$, respectively, and the total population N modifies into $N_h = S_p + I_{ph} + I_{nh} + A$ and $N_T = S_p + E_p + I_{nt} + R_p$ for the HIV-only and TB-only models, respectively.

It is easy to show that the feasible regions of the HIV-only model and the TB-only are given by \mathcal{D}_H and \mathcal{D}_T , respectively, given as follows:

$$\begin{aligned}
 \mathcal{D}_H &= \left\{ (S_p, I_{ph}, I_{nh}, A) \in \mathbb{R}_+^4 \mid N_h < \frac{Q}{\mu} \right\}, \\
 \mathcal{D}_T &= \left\{ (S_p, E_p, I_{nt}, R_p) \in \mathbb{R}_+^4 \mid N_T < \frac{Q}{\mu} \right\}.
 \end{aligned} \tag{5}$$

The following theorem can then be established regarding the positive invariance of the feasible regions.

Theorem 1. (positive invariance of feasible regions).

- (1) If the initial conditions of the HIV-only model are in \mathcal{D}_H , then all its future solutions will remain in \mathcal{D}_H .
- (2) If the initial conditions of the TB-only model are in \mathcal{D}_T , then all its future solutions will remain in \mathcal{D}_T .

Proof. Adding all equations of the HIV-only model in equation (2) yields.

$dN_h/dt = Q - (S_p + I_{ph} + I_{nh} + A)\mu - A_{\mu h} \leq Q - \mu N_h$.
 Since (dN_h/dt) is bounded by $Q - \mu N_h$, a standard comparison theorem [26] shows that

$$N(t) \leq N(0)e^{-\mu t} + \frac{Q}{\mu}(1 - e^{-\mu t}). \tag{6}$$

Clearly, whenever $N(0) \leq (Q/\mu)$ then $N(t) \leq (Q/\mu)$, showing that every solution of the HIV-only model in

equation (4) starting in \mathcal{D}_H will remain in \mathcal{D}_H . This proves that \mathcal{D}_H is positive and attracting, completing the proof of the first part of the theorem.

Similar arguments can be applied on the TB-only model to prove the second part of the theorem. \square

Theorem 1 implies that it is sufficient to consider the dynamics of the submodels in equation (4) in their respective feasible regions, inside which the submodels are epidemiologically and mathematically well-posed [27].

3.1. Equilibrium Points of the Submodels

3.1.1. Disease-Free Equilibria and Local Stability. The submodels in equation (4) can be shown to each exhibit two equilibria, namely, the disease-free and endemic equilibrium points.

The infection-free equilibrium points of the HIV-only and TB-only submodels are given, respectively, by

$$\begin{aligned} \mathcal{E}_{H0} &= ((Q/\mu), 0, 0, 0), \\ \mathcal{E}_{T0} &= ((Q/\mu), 0, 0, 0). \end{aligned} \quad (7)$$

Using the next-generation matrix approach [28], the basic reproduction numbers of the submodels are obtained as given below.

$$\mathcal{R}_{H0} = \frac{\overbrace{\beta_h c_h [\sigma + (\kappa_1 f_1 + 1 - f_1)\delta + \mu]}^{\text{Basic Reproduction Number of HOM}}}{(\delta + \mu)(\sigma + \kappa_1 \delta + \mu)}, \quad (8)$$

$$\mathcal{R}_{T0} = \frac{\overbrace{\beta_T c_T (\theta + \mu(1 - f_2))}^{\text{Basic Reproduction Number of TOM}}}{(\theta + \mu)(r + \mu + \mu_T)}.$$

The following result concerns the local stability of the disease-free critical points of the submodels.

Lemma 1. (local stability of disease-free equilibria). *The disease-free equilibrium point \mathcal{E}_{H0} of the HIV-only model and \mathcal{E}_{T0} of the TB-only model are locally asymptotically stable whenever $\mathcal{R}_{H0} < 1$ and $\mathcal{R}_{T0} < 1$, respectively. The equilibria are unstable otherwise.*

Proof. The proof of this lemma is conducted using the second Lyapunov technique which states that a critical point of a given ode model is locally asymptotically stable if all eigenvalues of the Jacobian matrix of the model evaluated at the critical point have negative real part and unstable otherwise. The Jacobian matrices of the submodels at the disease-free critical points are given below:

$$\begin{aligned} &\text{HIV-only model I} \\ \mathcal{J}^H(\mathcal{E}_{H0}) &= \begin{bmatrix} -\mu & -\beta_a c_a & -\beta_a c_a & 0 \\ 0 & \beta_a c_a f_1 - k_1 & \beta_a c_a f_1 + \sigma & 0 \\ 0 & (1 - f_1)\beta_a c_a & (1 - f_1)\beta_a c_a - k_2 & 0 \\ 0 & \delta & \delta \kappa_1 & -k_8 \end{bmatrix}, \\ &\text{TB-only model I} \\ \mathcal{J}^T(\mathcal{E}_{T0}) &= \begin{bmatrix} -\mu & 0 & -\beta_T c_T & 0 \\ 0 & -k_3 & f_2 \beta_T c_T & 0 \\ 0 & \theta & (1 - f_2)\beta_T c_T - k_6 & 0 \\ 0 & 0 & r & -\mu \end{bmatrix}. \end{aligned} \quad (9)$$

Clearly, two of the eigenvalues of $\mathcal{J}^H(\mathcal{E}_{H0})$ (namely, $-\mu$ and $-k_8$) and also two of the eigenvalues of $\mathcal{J}^T(\mathcal{E}_{T0})$ (namely, $-\mu$, $-\mu$) are negative. The rest of the eigenvalues are roots of the polynomial equations

$$\mathfrak{X}_H^2 + \left(\frac{(k_2^2 f_1 + ((k_1 + k_2)\sigma + k_1^2)(1 - f_1) + k_1 k_2(1 - \mathcal{R}_{H0}))}{k_2 f_1 + (1 - f_1)(\sigma + k_1)} \right) \mathfrak{X}_H + k_1 k_2(1 - \mathcal{R}_{H0}) = 0, \quad (10)$$

$$\mathfrak{X}_T^2 + \left(k_3 + \frac{k_6 \theta f_2 + (1 - f_2) k_3 k_6 (1 - \mathcal{R}_{T0})}{\theta f_2 + (1 - f_2) k_3} \right) \mathfrak{X}_T + k_3 k_6 (1 - \mathcal{R}_{T0}) = 0. \quad (11)$$

Using the Routh–Hurwitz criterion, equations (10) and (11) will have all of their zeros in the left half of the plane if $\mathcal{R}_{H0} < 1$ and $\mathcal{R}_{T0} < 1$, concluding the proof. \square

3.1.2. Endemic Equilibria of Submodels. The HIV-only model can be shown to have an endemic equilibrium point $\mathcal{E}_H^* = (S_{ph}^*, I_{pah}^*, I_{nah}^*, A_h^*)$ of the HIV-only model (3), where

Endemic Equilibrium Point of HOM

$$\begin{aligned}
 S_p &= \frac{Q}{\lambda_{hh}^* + \mu}; \\
 I_{pa} &= \frac{Q\lambda_{hh}^*(k_2f_1 + (1 - f_1)\sigma)}{(\lambda_{hh}^* + \mu)k_2k_1}; \\
 I_{na} &= \frac{(1 - f_1)Q\lambda_{hh}^*}{(\lambda_{hh}^* + \mu)k_2}; \\
 A &= \delta \left(\frac{(1 - f_1)\kappa_1}{(\lambda_{hh}^* + \mu)k_2k_8} + \frac{(k_2f_1 + (1 - f_1)\sigma)}{(\lambda_{hh}^* + \mu)k_2k_1k_8} \right) Q\lambda_{hh}^*
 \end{aligned}$$

(12)

Endemic Equilibrium Point of TOM

$$\begin{aligned}
 S_p &= \frac{Q}{\lambda_{TT}^* + \mu}; \\
 E_p &= \frac{f_2\lambda_{TT}^*(\rho\lambda_T + \mu)k_6Q}{(\lambda_{TT}^* + \mu)((\mu + \rho\lambda_{TT}^*)k_3k_6 - r\rho(\theta f_2 + (1 - f_2)k_3)\lambda_{TT}^*)}; \\
 I_{nT} &= \frac{(\theta f_2 + (1 - f_2)k_3)(\rho\lambda_{TT}^* + \mu)Q\lambda_{TT}^*}{(\lambda_{TT}^* + \mu)((\mu + \rho\lambda_{TT}^*)k_3k_6 - r\rho(\theta f_2 + (1 - f_2)k_3)\lambda_{TT}^*)}; \\
 R_p &= \frac{r(\theta f_2 + (1 - f_2)k_3)Q\lambda_{TT}^*}{(\lambda_{TT}^* + \mu)((\mu + \rho\lambda_{TT}^*)k_3k_6 - r\rho(\theta f_2 + (1 - f_2)k_3)\lambda_{TT}^*)}.
 \end{aligned}$$

Substituting the expressions in equation (12) into λ_{hh} and λ_{TT} and simplifying leads to the following equations.

$$[\mathcal{K}_1\lambda_{hh}^* - k_1\mu k_2(\mathcal{R}_{H0} - 1)k_8]\lambda_{hh}^* = 0, \quad (13)$$

$$[\mathcal{K}_2(\lambda_{TT}^*)^2 + \mathcal{K}_3\lambda_T - \mu^2k_3k_6(\mathcal{R}_{T0} - 1)]\lambda_{TT}^* = 0, \quad (14)$$

where

$$\begin{aligned}
 \mathcal{K}_1 &= k_1k_2k_8 - ((1 - f_1)k_1\kappa_1 \\
 &\quad + k_2f_1 + (1 - f_1)\sigma)\delta\mu_a > 0; \\
 \mathcal{K}_2 &= \rho\mu((r + \mu_T)f_2 + \mu + \theta); \\
 \mathcal{K}_3 &= \mu(\rho k_3k_6(1 - \mathcal{R}_{T0}) \\
 &\quad - (\theta f_2 + (1 - f_2)k_3)(r\rho + \mu_T) + k_3k_6).
 \end{aligned} \quad (15)$$

Equation (12) has two solutions, namely, $\lambda_{hh}^* = 0$ (corresponding to the disease-free equilibrium point \mathcal{E}_{H0}) and $\lambda_{hh}^* = \kappa_1/\mu k_1 k_2 (\mathcal{R}_{H0-1})k_8$ (corresponding to the endemic equilibrium point \mathcal{E}_H^*), which are positive only when $\mathcal{R}_{H0} > 1$. The following theorem is thus established.

Theorem 2. (existence of endemic equilibria of the HIV-only model). For the HIV-only model,

- (i) Only the disease-free equilibrium exists whenever $\mathcal{R}_{H0} \leq 1$.

- (ii) The endemic equilibrium \mathcal{E}_H^* exists only when $\mathcal{R}_{H0} > 1$.

It can be observed that whenever $\mathcal{R}_{T0} > 1$, then the last term of equation (13) will be negative and the equation will have a unique positive root. Also, whenever $\mathcal{R}_{T0} \leq 1$, then equation (13) will have a positive root if $\mathcal{K}_3 < 0$. The following theorem is thus easily established.

Theorem 3. (existence of endemic equilibria of the TB-only model).

- (i) The TB-only submodel has a unique endemic equilibrium point when $\mathcal{R}_{T0} > 1$.
- (ii) The TB-only submodel may still have an endemic equilibrium even if $\mathcal{R}_{T0} \leq 1$.

Theorem 3 suggests the existence of backward bifurcation in the TB-only submodel. This will be explored later.

3.2. Global Stability of Infection-Free Equilibria. In this section, we adopt the first Lyapunov technique to study the global stability of the disease-free equilibria of the HIV-only and TB-only submodels.

To do this, we define the Lyapunov functions

$$\begin{aligned} \text{HIV-only Model} \\ \mathcal{L}_h &= k_2 k_8 I_{pa} + k_8 (\sigma + k_1) I_{na}, \\ \text{TB-only Model} \\ \mathcal{L}_T &= \theta E_p + k_3 I_{nT}. \end{aligned} \quad (16)$$

$$\begin{aligned} \text{HIV-only Model I} \\ \frac{d\mathcal{L}_h}{dt} &= k_2 k_8 \frac{dI_{pa}}{dt} + k_8 (\sigma + k_1) \frac{dI_{na}}{dt} \\ &= k_2 k_8 [\lambda_{hh} f_1 S_p + \sigma I_{nh} - k_1 I_{ph}] \\ &\quad + k_8 (\sigma + k_1) [(1 - f_1) S_p \lambda_{hh} - k_2 I_{nh}], \\ &\leq k_1 k_2 (\mathcal{R}_{H0} - 1) (I_{pa} + I_{na}) \end{aligned}$$

Therefore, $(d\mathcal{L}_h/dt) \leq 0$ if $\mathcal{R}_{H0} \leq 1$; $(d\mathcal{L}_h/dt) = 0$ if and only if $I_{pa} = I_{na} = 0$ and the largest compact invariant set in $\{(S_p, I_{pa}, I_{na}, A) \in \mathcal{D}_H \mid (d\mathcal{L}_h/dt) = 0\}$ is the singleton set \mathcal{E}_{H0} . From LaSalle's invariance principle [29], we can conclude that all solutions of the HIV-only model with initial conditions in \mathcal{D}_H will eventually converge to \mathcal{E}_{H0} , showing that \mathcal{E}_{H0} is globally asymptotically stable whenever $\mathcal{R}_{H0} \leq 1$.

As for the TB-only model, we observe that $\mathcal{R}_{T0} \leq 1$ does not guarantee that $(d\mathcal{L}_T/dt) \leq 0$. This suggests the presence of backward bifurcation, which we shall explore in the next section. However, we note that when $\rho = 0$, then $\mathcal{R}_{T0} \leq 1$ will guarantee that $(d\mathcal{L}_T/dt) \leq 0$. Therefore, the TB-only model has a globally asymptotically stable (GAS) disease-free equilibrium whenever $\mathcal{R}_{T0} \leq 1$ and there is no reinfection. The following result is thus established.

Theorem 4. (global stability of infection-free equilibria of submodels).

- (1) The HIV-only model has a GAS disease-free equilibrium whenever $\mathcal{R}_{H0} < 1$.
- (2) The infection-free equilibrium of the TB-only model is GAS whenever $\mathcal{R}_{T0} < 1$ and $\rho \leq \rho^*$ such that $\rho^* R_p + S_p \leq N_T$.

The essence of the result in Theorem 4 is that HIV only can be eradicated by keeping the basic reproduction number below unity, but TB only may be difficult to be eradicated even after keeping the basic reproduction number below unity.

The time derivatives of the above Lyapunov functions are given as follows.

$$\begin{aligned} \text{HIV-only Model} \\ \frac{d\mathcal{L}_h}{dt} &= k_2 k_8 \frac{dI_{pa}}{dt} + k_8 (\sigma + k_1) \frac{dI_{na}}{dt} \\ &= \theta [f_2 \lambda_{TT} f_1 (S_p + R_p) - k_3 E_p] \\ &\quad + k_3 [(1 - f_2) (S_p + R_p) \lambda_{TT} \theta E_p - k_6 I_{nT}], \\ &= k_3 k_6 \left(\frac{\mathcal{R}_{T0} (R_p + S_p)}{N_T} - 1 \right) I_{nT} \end{aligned} \quad (17)$$

3.3. Bifurcation Analysis of Submodels. The center manifold theory described in [25] is used here to study the directions of bifurcation of the submodels. We note that this theory can be used to determine the direction of bifurcation if the Jacobian of the respective models evaluated at the disease-free equilibrium has a simple eigenvalue. The Jacobian of the submodels evaluated at the disease-free equilibria is given by

$$\begin{aligned} \text{HIV-only Model} \\ \mathcal{J}_H &= \begin{bmatrix} -\mu & -\beta_h c_h & -\beta_h c_h & 0 \\ 0 & \beta_h c_h f_1 - k_1 & \beta_h c_h f_1 + \sigma & 0 \\ 0 & (1 - f_1) \beta_h c_h & (1 - f_1) \beta_h c_h - k_2 & 0 \\ 0 & \delta & \delta k_1 & -k_8 \end{bmatrix}, \\ \text{TB-only Model} \\ \mathcal{J}_T &= \begin{bmatrix} -\mu & 0 & -\beta_T c_T & 0 \\ 0 & -k_3 & f_2 \beta_T c_T & 0 \\ 0 & \theta & (1 - f_2) \beta_T c_T - k_6 & 0 \\ 0 & 0 & r & -\mu \end{bmatrix}. \end{aligned} \quad (18)$$

It is easy to show that each of the Jacobians has a simple eigenvalue when the associated basic reproduction number equals unity, which then allows us to employ the center manifold theory to study the direction of bifurcation for the submodels.

Now, the right and left eigenvector pairs (corresponding to the simple eigenvalues) for the HIV-only and TB-only submodels $(\mathbf{w}^H, \mathbf{v}^H)$ and $(\mathbf{w}^T, \mathbf{v}^T)$ are such that

$$\begin{aligned}
 & \text{HIV-only Model} \\
 & \overline{w_1^H = \frac{-k_1 k_2 k_8}{\delta(k_2 f_1 + (1 - f_1)(k_1 \kappa_1 + \sigma))\mu}, v_1^H = 0;} \\
 & \overline{w_2^H = \frac{k_8(k_2 f_1 + (1 - f_1)\sigma)}{\delta(k_2 f_1 + (1 - f_1)(k_1 \kappa_1 + \sigma))}, v_2^H = \frac{(k_2 f_1 + (1 - f_1)(k_1 \kappa_1 + \sigma))\delta k_2}{k_8(k_2^2 f_1 + (\sigma(k_1 + k_2) + k_1^2)(1 - f_1))};} \\
 & \overline{w_3^H = \frac{k_8(1 - f_1)k_1}{\delta(k_2 f_1 + (1 - f_1)(k_1 \kappa_1 + \sigma))}, v_3^H = \frac{(\sigma + k_1)}{k_2} v_2^H;} \\
 & \overline{w_4^H = 1, v_4^H = 0;} \\
 & \text{TB-only Model} \\
 & \overline{w_1^T = -\frac{k_3 k_6}{(\theta f_2 + (1 - f_2)k_3)r}, v_1^T = 0;} \\
 & \overline{w_2^T = \frac{f_2 k_6 \mu}{r(\theta f_2 + (1 - f_2)k_3)}, v_2^T = \frac{r\theta(\theta f_2 + (1 - f_2)k_3)}{(\theta(k_3 + k_6)f_2 + (1 - f_2)k_3^2)\mu};} \\
 & \overline{w_3^T = \frac{\mu}{r}, v_3^T = \frac{r(\theta f_2 + (1 - f_2)k_3)k_3}{(\theta(k_3 + k_6)f_2 + (1 - f_2)k_3^2)\mu};} \\
 & \overline{w_4^T = 1, v_4^T = 0}
 \end{aligned} \tag{19}$$

Choosing $\beta_h^* = (k_1 k_2 / c_h (k_2 f_1 + (1 - f_1)(\sigma + k_1)))$ and $\beta_T^* = (k_3 k_6 / (\theta f_2 + (1 - f_2)k_3) c_T)$ as the bifurcation

parameters for the HIV-only and TB-only models, the bifurcation co-coefficients of the submodels are obtained as

$$\begin{aligned}
 & \text{HIV-only Model} \\
 & \overline{\mathbf{a}^H = -\frac{2c_h \mu \beta_h^*}{Q} (v_2 f_1 + (1 - f_1)v_3)(w_2 + w_3 + w_4)(w_3 + w_2); \mathbf{b}^H = (v_2 f_1 + (1 - f_1)v_3)c_h(w_3 + w_2);} \\
 & \text{TB-only Model} \\
 & \overline{\mathbf{a}^T = 2\left(\frac{\beta_T^* c_T (f_2 v_2 + (1 - f_2)v_3)\mu^2}{rQ}\right)\left[\rho - 1 - \frac{\mu(\theta f_2 + (1 - f_2)k_3 + f_2 k_6)}{r(\theta f_2 + (1 - f_2)k_3)}\right]; \mathbf{b}^T = \frac{c_T(\theta f_2 + (1 - f_2)k_3)\mu}{\theta r} v_2^T.}
 \end{aligned} \tag{20}$$

Clearly, $\mathbf{a}^H < 0$ and $\mathbf{b}^H > 0$ and hence by Theorem 2 (item (iv)) of [25], the following theorem is established.

Theorem 5. (bifurcation of the HIV-only model). *The unique endemic equilibrium point \mathcal{E}_H^* of the HIV-only model is locally asymptotically stable when R_{H0} is close to 1. Specifically, the HIV-only submodel exhibits forward bifurcation at $\mathcal{R}_{H0} = 1$.*

Obviously, $\mathbf{b}^T > 0$, and the sign of \mathbf{a}^T depends on the sign of $\rho - 1 - (\mu(\theta f_2 + (1 - f_2)k_3 + f_2 k_6) / r(\theta f_2 + (1 - f_2)k_3))$. The following theorem is thus obtained.

Theorem 6. (bifurcation of TB-only model). *The TB-only model undergoes a backward bifurcation when the following condition holds.*

$$\rho > 1 + \frac{\mu(\theta f_2 + (1 - f_2)k_3 + f_2 k_6)}{r(\theta f_2 + (1 - f_2)k_3)}. \tag{21}$$

Proof. We note that whenever $\rho > 1 + (\mu(\theta f_2 + (1 - f_2)k_3 + f_2 k_6) / r(\theta f_2 + (1 - f_2)k_3))$, then $\mathbf{a}^T > 0$, so that by Theorem 2 of [25], the TB-only model will exhibit backward bifurcation. This concludes the proof. \square

Theorem 6 suggests that the control of the spread of TB requires more effort beyond getting the basic reproduction below 1. This phenomenon has been identified in several other studies, especially of diseases in which there is relapse and exogenous re-infection.

3.4. Sensitivity Analysis. In this section, the normalized forward sensitivity index is employed to study the effect of marginal changes in model parameters on the spread of the two diseases. This is done to determine the parameters that

drive the spread of these infections. Parameters with positive sensitivity indices drive the spread of the contagion and the parameters with negative indices inhibit the spread of the diseases. The sensitivity index of a function ζ that differentially depends on a variable ϑ is given by

$$\mathcal{S}_{\zeta}^{\vartheta} = \frac{\partial \zeta}{\partial \vartheta} \times \frac{\vartheta}{\zeta}. \quad (22)$$

To this end, the sensitivity indices are presented as follows:

$$\begin{array}{c} \text{HIV-only Model I} \\ \hline \mathcal{S}_{\mathcal{R}_{H0}}^{\beta_h} = 1, \\ \mathcal{S}_{\mathcal{R}_{H0}}^{c_h} = 1, \\ \mathcal{S}_{\mathcal{R}_{H0}}^{\kappa_1} = -\frac{\delta \kappa_1 (1 - f_1) (\sigma + \delta + \mu)}{(\delta \kappa_1 + \mu + \sigma) (\mu + (f_1 \kappa_1 + 1 - f_1) \delta + \sigma)}, \\ \mathcal{S}_{\mathcal{R}_{H0}}^{f_1} = -\frac{\delta (1 - \kappa_1) f_1}{\mu + (f_1 \kappa_1 + 1 - f_1) \delta + \sigma}, \\ \mathcal{S}_{\mathcal{R}_{H0}}^{\delta} = -\frac{\delta [\kappa_1 (f_1 \kappa_1 + 1 - f_1) \delta^2 + (\mu + \sigma) ((1 - f_1) \kappa_1 + f_1) \mu + 2\delta \kappa_1 + \sigma]}{(\delta + \mu) (\delta \kappa_1 + \mu + \sigma) (\delta f_1 \kappa_1 + (1 - f_1) \delta + \mu + \sigma)}, \\ \mathcal{S}_{\mathcal{R}_{H0}}^{\sigma} = \frac{\delta \sigma (1 - \kappa_1) (1 - f_1)}{(\delta \kappa_1 + \mu + \sigma) (\mu + (f_1 \kappa_1 + 1 - f_1) \delta + \sigma)}, \\ \mathcal{S}_{\mathcal{R}_{H0}}^{\mu} = -\frac{((f_1 \kappa_1^2 + 1 - f_1) \delta^2 + ((f_1 \kappa_1 + 1 - f_1) (2\mu + \sigma) + \sigma \kappa_1) \delta + (\mu + \sigma)^2) \mu}{(\delta + \mu) (\delta \kappa_1 + \mu + \sigma) ((1 + (\kappa_1 - 1) f_1) \delta + \mu + \sigma)}. \\ \hline \text{TB-only Model I} \\ \mathcal{S}_{\mathcal{R}_{T0}}^{\beta_T} = 1, \\ \mathcal{S}_{\mathcal{R}_{T0}}^{c_T} = 1, \\ \mathcal{S}_{\mathcal{R}_{T0}}^{f_2} = -\frac{f_2 \mu}{(1 - f_2) \mu + \theta}, \\ \mathcal{S}_{\mathcal{R}_{T0}}^{\theta} = \frac{\theta f_2 \mu}{(\theta + \mu) ((1 - f_2) \mu + \theta)}, \\ \mathcal{S}_{\mathcal{R}_{T0}}^{\mu_T} = -\frac{\mu_T}{r + \mu + \mu_T}, \\ \mathcal{S}_{\mathcal{R}_{T0}}^r = -\frac{r}{r + \mu + \mu_T}, \\ \mathcal{S}_{\mathcal{R}_{T0}}^{\mu} = -\frac{\mu [(1 - f_2) \mu^2 + \theta (\theta + 2\mu + f_2 (r + \mu_T))]}{(\theta + \mu) (r + \mu + \mu_T) ((1 - f_2) \mu + \theta)}. \end{array} \quad (23)$$

The parameters $\beta_h, c_h, \beta_T, c_T, \theta$ have positive sensitivity indices, which implies that an increase (a decrease) in each of these parameters will cause an increase (a decrease) in the

corresponding basic reproduction number and subsequently drive (inhibit) the spread of the diseases. Also, the parameters $\kappa_1, f_1, f_2, \delta, \sigma, \mu, r,$ and μ_T have negative sensitivity

indices, which implies that an increase (decrease) in these parameters will cause a decrease (increase) in the respective basic reproduction numbers and subsequently inhibit (drive) the spread of the contagion.

3.5. *The Impact of HIV on TB.* In order to study the impact of HIV on TB progression and vice versa, we relate the basic reproduction numbers of the two submodels. To do this, use the expression of \mathcal{R}_{T_0} to obtain μ^2 and substitute it into the expression of \mathcal{R}_{H_0} to obtain

$$\mathcal{R}_{H_0} = \frac{\beta_h c_h [(\delta \kappa_1 + \mu + \sigma) f_1 + (1 - f_1)(\sigma + \delta + \mu)] \mathcal{R}_{T_0}}{\beta_T c_T [\theta f_2 + (1 - f_2)(\theta + \mu)] + [(\sigma - \theta)\mu + (\delta + \mu)(\delta \kappa_1 + \sigma) - (\theta + \mu)(r + \mu_T)] \mathcal{R}_{T_0}}. \quad (24)$$

With \mathcal{R}_{H_0} now expressed in terms of \mathcal{R}_{T_0} and other model parameters, it is then possible to analytically study the

impact of the model parameters on \mathcal{R}_{H_0} and subsequently the spread of HIV/AIDS.

Now, we have the following:

$$\left. \begin{aligned} \frac{\partial \mathcal{R}_{H_0}}{\partial \mathcal{R}_{T_0}} &= \beta_T c_T [(1 - f_2)\mu + \theta] \mathcal{Z}_1, \\ \frac{\partial \mathcal{R}_{H_0}}{\partial c_T} &= -\beta_T [(1 - f_2)\mu + \theta] \mathcal{Z}_1 \mathcal{R}_{T_0}, \\ \frac{\partial \mathcal{R}_{H_0}}{\partial \beta_T} &= -c_T [(1 - f_2)\mu + \theta] \mathcal{Z}_1 \mathcal{R}_{T_0}, \\ \frac{\partial \mathcal{R}_{H_0}}{\partial \theta} &= [(r + \mu + \mu_T) \mathcal{R}_{T_0} - \beta_T c_T] \mathcal{Z}_1 \mathcal{R}_{T_0}, \\ \frac{\partial \mathcal{R}_{H_0}}{\partial r} &= (\theta + \mu) \mathcal{Z}_1 \mathcal{R}_{T_0}^2, \\ \frac{\partial \mathcal{R}_{H_0}}{\partial f_2} &= \beta_T c_T \mu \mathcal{Z}_1 \mathcal{R}_{T_0}, \\ \frac{\partial \mathcal{R}_{H_0}}{\partial \mu_T} &= (\theta + \mu) \mathcal{Z}_1 \mathcal{R}_{T_0}^2 \end{aligned} \right\} \text{HIV - only model} \quad (25)$$

$$\left. \begin{aligned} \frac{\partial \mathcal{R}_{T_0}}{\partial \mathcal{R}_{H_0}} &= \mathcal{Z}_2 \beta_h ((1 + (\kappa_1 - 1) f_1) \delta + \mu + \sigma) c_h \\ \frac{\partial \mathcal{R}_{T_0}}{\partial \beta_h} &= -\mathcal{Z}_2 \mathcal{R}_{H_0} ((1 + (\kappa_1 - 1) f_1) \delta + \mu + \sigma) c_h \\ \frac{\partial \mathcal{R}_{T_0}}{\partial c_h} &= -\mathcal{Z}_2 \mathcal{R}_{H_0} \beta_h ((1 + (\kappa_1 - 1) f_1) \delta + \mu + \sigma); \\ \frac{\partial \mathcal{R}_{T_0}}{\partial \sigma} &= \mathcal{R}_{H_0} ((\delta + \mu) \mathcal{R}_{H_0} - \beta_h c_h) \mathcal{Z}_2 \\ \frac{\partial \mathcal{R}_{T_0}}{\partial \delta} &= [((\kappa_1 + 1)\mu + 2\delta \kappa_1 + \sigma) \mathcal{R}_{H_0} - (f_1 \kappa_1 - f_1 + 1) c_h \beta_h] \mathcal{Z}_2 \mathcal{R}_{H_0} \\ \frac{\partial \mathcal{R}_{T_0}}{\partial f_1} &= -\delta \mathcal{R}_{H_0} c_h \beta_h (\kappa_1 - 1) \mathcal{Z}_2 \\ \frac{\partial \mathcal{R}_{T_0}}{\partial \kappa_1} &= \delta \mathcal{R}_{H_0} ((\delta + \mu) \mathcal{R}_{H_0} - f_1 \beta_h c_h) \mathcal{Z}_2 \end{aligned} \right\} \text{TB - only Model 1}$$

where

$$\mathcal{E}_1 = \frac{\beta_h c_h [\mu + (f_1 \kappa_1 + 1 - f_1) \delta + \sigma]}{\{\beta_T c_T [\theta f_2 + (1 - f_2) (\theta + \mu)] + [(\sigma - \theta) \mu + (\delta + \mu) (\delta \kappa_1 + \sigma) - (\theta + \mu) (r + \mu_T)] \mathcal{R}_{T0}\}^2} > 0;$$

$$\mathcal{E}_2 = \frac{\beta_T c_T [\theta + \mu (1 - f_2)]}{((-\delta \kappa_1 + \delta + \sigma) \mu - \delta (\delta \kappa_1 + \sigma) + (\theta + r + \mu_T) \mu + \theta (r + \mu_T)) \mathcal{R}_{H0} + ((\delta \kappa_1 + \mu + \sigma) f_1 + (1 - f_1) (\sigma + \delta + \mu)) c_h \beta_h}^2 > 0 \quad (26)$$

We observe that \mathcal{R}_{H0} is an increasing function of \mathcal{R}_{T0} , r , f_2 , and μ_T since its derivatives with respect to these parameters are positive, showing that these parameters drive the spread of HIV/AIDS. Also, \mathcal{R}_{H0} is a decreasing function of β_T and c_T , indicating that these two parameters inhibit the spread of HIV/AIDS. We observe that since β_T and c_T drive TB which in turn drives HIV/AIDS, it is expected that these two parameters would transitively drive HIV. Therefore, this result is counter-intuitive.

4. Qualitative Analysis of the Full Model

It is easy to show that the biologically feasible region of the full model given by

$$\mathcal{D} = \left\{ (S_p, I_{ph}, I_{nh}, E_p, I_{pht}, I_{nht}, I_{nt}, R_p, I_{nd}, A) \in \mathbb{R}_+^{10} \mid N \leq \frac{Q}{\mu} \right\}, \quad (27)$$

is a positively invariant and attracting set. Therefore, all analyses are carried out inside this set.

4.1. Equilibrium Points of the Full Model. The disease-free equilibrium point of the full model is given by $\mathcal{E}_0 = ((Q/\mu), 0, 0, 0, 0, 0, 0, 0, 0, 0)$.

Using the next-generation matrix approach [28], the basic reproduction number of the full HIV-TB model (2) is obtained as

$$\mathcal{R}_0 = \max \{ \mathcal{R}_{H0}, \mathcal{R}_{T0} \}. \quad (28)$$

The following is obtained.

Lemma 2. *The disease-free equilibrium point \mathcal{E}_0 of the full HIV-TB model (2) is locally asymptotically stable whenever $\mathcal{R}_0 < 1$ and unstable otherwise.*

Proof. The proof of this result is similar to that of Theorem 2. \square

Next, we present some result on the global stability of the disease-free equilibrium point of the full model. To do this, refer to [30] and rewrite the model as follows:

$$\begin{aligned} \frac{dU}{dt} &= F(U, I) \\ \frac{dI}{dt} &= G(U, I), \end{aligned} \quad (29)$$

where $U = (S_p, R_p)$ and $I = (I_{ph}, I_{nh}, E_p, I_{pht}, I_{nht}, I_{nt}, I_{nd}, A)$ denote the uninfected and infected compartments, respectively. Based on [30], the disease-free equilibrium point \mathcal{E}_0 is globally stable if the following conditions hold.

(H1) $dU/dt = F(U, 0)$ is globally stable.

(H2) $G(U, I) = \mathbb{A}I - \widehat{G}(U, I)$, $\widehat{G}(U, I) \geq 0 \forall (U, I) \in \Omega$, where $\mathbb{A} = (\partial G / \partial I)(U_0, 0)$ is an M -matrix.

In the full model, we note that

$$F(U, I) = \begin{pmatrix} Q - (\lambda_h + \lambda_T + \mu) S_p \\ r I_{nt} - (\rho \lambda_T + \lambda_h + \mu) R_p \end{pmatrix},$$

$$G(U, I) = \begin{pmatrix} f_1 \lambda_h (S_p + R_p) + \sigma I_{nh} - (\tau_1 \lambda_T + k_1) I_{ph} \\ (1 - f_1) \lambda_h (S_p + R_p) - (\tau_1 \lambda_T + k_2) I_{nh} \\ f_2 \lambda_T (S_p + \rho R_p) - (\xi_1 \lambda_h + k_3) E_p \\ \tau_1 f_2 \lambda_T I_{ph} + \sigma I_{nht} - k_4 I_{pht} \\ \tau_1 (1 - f_2) \lambda_T I_{nh} + \xi_1 \lambda_h E_p + \tau_2 r I_{nd} - k_5 I_{nht} \\ (1 - f_2) \lambda_T (S_p + \rho R_p) + \theta E_p - (\xi_2 \lambda_h + k_6) I_{nt} \\ \xi_2 \lambda_h I_{nt} + \tau_1 \lambda_T [f_2 I_{nh} + (1 - f_2) I_{ph}] + \theta (\eta_1 I_{nht} + \eta_2 I_{pht}) - k_7 I_{nd} \\ \delta (I_{ph} + \kappa_1 I_{nh} + \kappa_2 I_{pht} + \kappa_3 I_{nht} + \kappa_4 I_{nd}) - k_8 A \end{pmatrix}. \quad (30)$$

We observe that $F(U, 0) = \begin{pmatrix} Q - \mu S_p \\ -\mu R_p \end{pmatrix}$ has \mathcal{E}_0 as a globally stable critical point, satisfying condition (H1). To test condition (H2), we find $\widehat{G}(U, I) = \mathbb{A}I - G(U, I)$.

Now, $\mathbb{A} = [\mathbb{A}_1, \mathbb{A}_2]$ where

$$\begin{aligned} \mathbb{A}_1 &= \begin{bmatrix} f_1\beta_a c_a - k_1 & f_1\beta_a c_a + \sigma & 0 & f_1\beta_a c_a \\ (1-f_1)\beta_a c_a & (1-f_1)\beta_a c_a - k_2 & 0 & (1-f_1)\beta_a c_a \\ 0 & 0 & -k_3 & 0 \\ 0 & 0 & 0 & -k_4 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & \theta & 0 \\ 0 & 0 & 0 & \eta_2\theta \\ \delta & \delta\kappa_1 & 0 & \delta\kappa_2 \end{bmatrix}, \\ \mathbb{A}_2 &= \begin{bmatrix} f_1\beta_a c_a & 0 & f_1\beta_a c_a & 0 \\ (1-f_1)\beta_a c_a & 0 & (1-f_1)\beta_a c_a & 0 \\ 0 & f_2\beta_T c_T & f_2\beta_T c_T & 0 \\ \sigma & 0 & 0 & 0 \\ -k_5 & 0 & \tau_2 r & 0 \\ 0 & (1-f_2)\beta_T c_T - k_6 & (1-f_2)\beta_T c_T & 0 \\ \eta_1\theta & 0 & -k_7 & 0 \\ \delta\kappa_3 & 0 & \delta\kappa_4 & -k_8 \end{bmatrix}, \\ \widehat{G}(U, I) &= \begin{pmatrix} -f_1(N - S_p - R_p)\lambda_h - I_{pa}\tau_1\lambda_T \\ -(1-f_1)(N - S_p - R_p)\lambda_h - \tau_1\lambda_T I_{na} \\ -f_2(N - S_p - \rho R_p)\lambda_{TT} - \xi_1\lambda_h E_p \\ \tau_1 f_2 \lambda_{TT} I_{pa} \\ I_{na}\tau_1(1-f_2)\lambda_{TT} + \xi_1\lambda_h E_p \\ -(1-f_2)(N - S_p - \rho R_p)\lambda_{TT} - \xi_2\lambda_h I_{nT} \\ \tau_1((1-f_2)I_{pa} + f_2 I_{na})\lambda_{TT} + \\ \xi_2\lambda_h I_{nT} \\ 0 \end{pmatrix}. \end{aligned} \tag{31}$$

It can be clearly seen that $\widehat{G}(U, I) \not\equiv 0$, and hence condition (H2) does not hold. Therefore, the disease-free equilibrium \mathcal{E}_0 of the full model is not globally asymptotically stable.

The endemic equilibrium of the full HIV-TB model $\mathcal{E}^* = (S_p^*, I_{ph}^*, I_{nh}^*, E_p^*, I_{plt}^*, I_{nht}^*, I_{nt}^*, R_p^*, I_{nd}^*, A^*)$ is such that we have the following:

$$\begin{aligned}
S_p^* &= \frac{Q}{(\lambda_h^* + \lambda_T^* + \mu)} \\
I_{ph}^* &= \frac{1}{(\tau_1 \lambda_T^* + k_1)} \left(f_1 + \frac{\sigma(1-f_1)}{(\tau_1 \lambda_T^* + k_2)} \right) (S_p^* + R_p^*) \lambda_h^* I_{nh}^* = \frac{(1-f_1)}{(\tau_1 \lambda_T^* + k_2)} (S_p^* + R_p^*) \lambda_h^* \\
E_p^* &= \frac{f_2}{(\xi_1 \lambda_h^* + k_3)} (S_p^* + \rho R_p^*) \lambda_T^* \\
I_{pht}^* &= \left[\frac{\tau_1 f_2}{k_4 (\tau_1 \lambda_T^* + k_1)} \left(f_1 + \frac{\sigma(1-f_1)}{(\tau_1 \lambda_T^* + k_2)} \right) + \frac{\sigma \tau_1 (1-f_2)(1-f_1)}{k_4 k_5 (\tau_1 \lambda_T^* + k_2)} \right] (S_p^* + R_p^*) \lambda_h^* \lambda_T^* \\
&\quad + \frac{\sigma \xi_1 f_2}{k_4 k_5 (\xi_1 \lambda_h^* + k_3)} (S_p^* + \rho R_p^*) \lambda_h^* \lambda_T^* + \frac{\sigma \tau_2 r}{k_4 k_5} I_{nd}^* \\
I_{nht}^* &= \lambda_h^* \lambda_T^* \left[\frac{\tau_1 (1-f_2)(1-f_1)}{k_5 (\tau_1 \lambda_T^* + k_2)} (S_p^* + R_p^*) + \frac{\xi_1 f_2}{k_5 (\xi_1 \lambda_h^* + k_3)} (S_p^* + \rho R_p^*) \right] + \frac{\tau_2 r}{k_5} I_{nd}^* \\
I_{nt}^* &= \frac{1}{\xi_2 \lambda_h^* + k_6} \left[(1-f_2) + \frac{\theta f_2}{(\xi_1 \lambda_h^* + k_3)} \right] (S_p^* + \rho R_p^*) \lambda_T^* R_p^* = \frac{\mathcal{X} S_p^* \lambda_T^*}{(1-\rho \mathcal{X} \lambda_T^*)} \\
I_{nd}^* &= \frac{\lambda_h^* \lambda_T^*}{\mathcal{E}_1} \left\{ \left[\frac{\xi_2}{\xi_2 \lambda_h^* + k_6} \left((1-f_2) + \frac{\theta f_2}{(\xi_1 \lambda_h^* + k_3)} \right) + \frac{\theta \xi_1 f_2}{k_5 (\xi_1 \lambda_h^* + k_3)} \left(\eta_1 + \frac{\eta_2 \sigma}{k_4} \right) \right] (S_p^* + \rho R_p^*) \right. \\
&\quad \left. + \frac{1}{(\tau_1 \lambda_T^* + k_2)} \left[\mathcal{E}_2 + \frac{\mathcal{E}_3}{(\tau_1 \lambda_T^* + k_1)} [f_1 (\tau_1 \lambda_T^* + k_2) + \sigma(1-f_1)] \right] (S_p^* + R_p^*) \right\} \\
A^* &= \frac{\delta}{k_8} (I_{ph}^* + \kappa_1 I_{nh}^* + \kappa_2 I_{pht}^* + \kappa_3 I_{nht}^* + \kappa_4 I_{nd}^*),
\end{aligned} \tag{32}$$

where

$$\begin{aligned}
\mathcal{E}_1 &= \left(k_7 - \frac{\theta \tau_2 r}{k_5} \left(\eta_1 + \frac{\eta_2 \sigma}{k_4} \right) \right); \mathcal{E}_2 = \tau_1 (1-f_1) \left(\theta \left(\eta_1 + \frac{\eta_2 \sigma}{k_4} \right) \frac{(1-f_2)}{k_5} + f_2 \right); \\
\mathcal{E}_3 &= \tau_1 \left(\frac{\eta_2 \theta f_2}{k_4} + (1-f_2) \right); \mathcal{X} = \frac{r [(1-f_2)(\xi_1 \lambda_h + k_3) + \theta f_2]}{(\rho \lambda_T + \lambda_h + \mu)(\xi_1 \lambda_h + k_3)(\xi_2 \lambda_h + k_6)}.
\end{aligned} \tag{33}$$

Substituting (32) into the infection force functions λ_h and λ_T yields the following set of nonlinear equations.

$$\begin{pmatrix} \lambda_h^* \\ \lambda_T^* \end{pmatrix} = \begin{pmatrix} F_1(\lambda_h^*, \lambda_T^*) \\ F_2(\lambda_h^*, \lambda_T^*) \end{pmatrix}. \tag{34}$$

The equilibrium point of the full HIV-TB model is characterized by the fixed points of equation (34).

4.2. Bifurcation of the Full Model. Considering \mathcal{R}_0 as the basic reproduction number of the model, we observe that when $\mathcal{R}_{H0} = 1$, the Jacobian of the model possesses a simple eigenvalue, which allows the application of the center manifold theory [25] to study the existence and direction of bifurcation for the full model. The eigenvectors associated with the simple eigenvalues are then given by $\mathbf{w} = (w_1, w_2, w_3, w_4, w_5, w_6, w_7, w_8, w_9, w_{10})^T$ and $\mathbf{v} = (v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8, v_9, v_{10})$ where

$$\begin{aligned}
 w_1 &= \frac{c_a(\sigma + k_1)\beta_a w_3}{(f_1\beta_a c_a - k_1)\mu} + \frac{(-\beta_T\beta_a c_T c_a f_1 + \beta_T c_T k_1)w_7}{(f_1\beta_a c_a - k_1)\mu} \\
 w_2 &= -\frac{w_3(f_1\beta_a c_a + \sigma)}{f_1\beta_a c_a - k_1}; \\
 w_4 &= \frac{f_2\beta_T c_T w_7}{k_3}; \\
 w_5 &= w_6 = w_9 = 0; \\
 w_8 &= \frac{r w_7}{\mu} \\
 w_{10} &= -\frac{\delta(-c_a f_1(\kappa_1 - 1)\beta_a + k_1\kappa_1 + \sigma)w_3}{(f_1\beta_a c_a - k_1)k_8}; \\
 v_1 &= v_8 = v_{10} = 0; \\
 v_2 &= \frac{(1 - f_1)\beta_a c_a v_3}{-f_1\beta_a c_a + k_1}; \\
 v_4 &= \frac{\theta v_7}{k_3}; \\
 v_5 &= \frac{\beta_a c_a k_1(1 - f_1)v_3}{(-f_1\beta_a c_a + k_1)k_4} + \frac{\eta_2 \theta v_9}{k_4}; \\
 v_6 &= \frac{\beta_a c_a k_1(1 - f_1)(\sigma + k_4)v_3}{(-f_1\beta_a c_a + k_1)k_4 k_5} + \frac{\theta(\sigma\eta_2 + \eta_1 k_4)v_9}{k_4 k_5}; \\
 v_9 &= \frac{((\theta - k_3)f_2 + k_3)c_T\beta_T k_5 k_4 v_7}{(\tau_2 r\theta(\sigma\eta_2 + \eta_1 k_4) - k_7 k_4 k_5)k_3} - \frac{c_a k_1 \beta_a v_3(-1 + f_1)(r(\sigma + k_4)\tau_2 + k_4 k_5)}{(\tau_2 r\theta(\sigma\eta_2 + \eta_1 k_4) - k_7 k_4 k_5)(f_1\beta_a c_a - k_1)}; \\
 \text{with } w_7 = v_7 = 0, w_3 \neq 0, v_3 \neq 0 &\text{ when } \mathcal{R}_0 = \mathcal{R}_{H0} = 1; \\
 \text{and } w_7 \neq 0, v_7 \neq 0, w_3 = v_3 = 0 &\text{ when } \mathcal{R}_0 = \mathcal{R}_{T0} = 1.
 \end{aligned} \tag{35}$$

The eigenvectors are chosen such that $\mathbf{w} \bullet \mathbf{v} = 1$ or equivalently

$$\left[\frac{(1 - f_1)\beta_a c_a (f_1\beta_a c_a + \sigma)}{(f_1\beta_a c_a - k_1)^2} + 1 \right] v_3 w_3 + \left(\frac{\theta f_2 \beta_T c_T + k_3^2}{k_3^2} \right) w_7 v_7 = 1. \tag{36}$$

Now, when β_a is taken as bifurcation parameter with $\mathcal{R}_0 = \mathcal{R}_{H0} = 1$, we obtain the following bifurcation coefficients:

$$\mathbf{a} = \mathbf{a}^{\beta_a^*} = \frac{2\beta_a(\sigma + k_1)(f_1\delta c_a(1 - \kappa_1)\beta_a + (\delta\kappa_1 + k_8)k_1 + \sigma(k_8 + \delta))c_a(1 - f_1)\mu k_1 w_3^2 v_3}{(k_1 - f_1\beta_a c_a)^3 k_8 Q},$$

$$\mathbf{b} = \mathbf{b}^{\beta_a^*} = \frac{(1 - f_1)c_a k_1(\sigma + k_1)v_3 w_3}{(f_1\beta_a c_a - k_1)^2}.$$

Further, when β_T is taken as bifurcation parameter with $\mathcal{R}_0 = \mathcal{R}_{T0} = 1$, we obtain the following bifurcation coefficients:

$$\mathbf{a} = \mathbf{a}^{\beta_T^*} = \frac{2\beta_T c_T((\mu + (1 - \rho)r)k_3 + f_2\mu c_T \beta_T)((1 - f_2)k_3 + f_2\theta)w_7^2 v_7}{k_3^2 Q}$$

$$\mathbf{b} = \mathbf{b}^{\beta_T^*} = \frac{((1 - f_2)k_3 + f_2\theta)w_7 v_7 c_T}{k_3}.$$

Now, clearly, $\mathbf{b}^{\beta_a^*} > 0$, $\mathbf{b}^{\beta_T^*} > 0$, and hence the presence and direction of bifurcation in the model depend on the signs of $\mathbf{a}^{\beta_a^*}$ and $\mathbf{a}^{\beta_T^*}$. The following result of bifurcation is thus established.

Theorem 7. (bifurcation of the full model).

- (i) If $\mathcal{R}_0 = \mathcal{R}_{H0}$, then the HIV-TB model exhibits backward bifurcation at $\mathcal{R}_0 = 1$ whenever $k_1 < \beta_a c_a f_1$; otherwise, the direction of the bifurcation is forward.
- (ii) If $\mathcal{R}_0 = \mathcal{R}_{T0}$, then the HIV-TB model exhibits backward bifurcation at $\mathcal{R}_0 = 1$ whenever $\rho > 1 + (\mu/r) + (f_2\mu c_T \beta_T / rk_3)$; otherwise, the direction of the bifurcation is forward.

5. Optimal Control of the Industrial HIV-TB

In this section, the basic HIV-TB co-infection model (2) is extended incorporating time-dependent controls to study the impact of those controls on the dynamics of the diseases. The goal here is study how public health interventions could be employed on a dynamical basis to eradicate or to drive the spread of the diseases to acceptable levels. One very important

strategy for controlling the spread of diseases is to adopt strategies aimed at reducing the contact and/or transmission rate of the disease. To incorporate this strategy into our basic model, we introduce controls $u_1(t)$ and $u_2(t)$ such that as these controls increase, the transmission rates of HIV and TB respectively are reduced. We define $u_1(t)$ and $u_2(t)$ as the respective preventative strategies for reduction of HIV and TB transmission. These include abstinence, use of condoms in the case of HIV, and use of nose masks and isolation in the case of TB. Another very important strategy that is useful in curtailing the spread of HIV is administration of antiretroviral therapy, which helps in reducing the viral load in infected persons. We introduce this strategy as the control $u_3(t)$ such that as $u_3(t)$ increases, the viral load reduces and subsequently helps in reducing the progressing of infected persons into the AIDS stage. Since treatment is available for TB-infected persons, we introduce the control $u_4(t)$ such that a timely application of the control will increase the recovery rate of the TB-infected persons. Finally, in order to improve productivity, human resource departments will often implement in-service training to increase the capacity of the employees. We introduce a control $u_5(t)$ to measure the capacity building strategy adopted to increase productivity. The extended model with controls is thus given by

$$\left. \begin{aligned}
 \frac{dS_p}{dt} &= Q - ((1 - u_1)\lambda_a + (1 - u_2)\lambda_T + \mu)S_p \\
 \frac{dI_{ph}}{dt} &= f_1\lambda_h(1 - u_1)(S_p + R_p) + \sigma u_5 I_{nh} - (\tau_1(1 - u_2)\lambda_T + \delta(1 - u_3) + \mu)I_{ph} \\
 \frac{dI_{nh}}{dt} &= (1 - f_1)(S_p + R_p)(1 - u_1)\lambda_h - (\tau_1(1 - u_2)\lambda_T + \sigma u_5 + \kappa_1\delta(1 - u_3) + \mu)I_{nh} \\
 \frac{dE_p}{dt} &= f_2(1 - u_2)\lambda_T(S_p + \rho R_p) - (\xi_1(1 - u_1)\lambda_h + \theta + \mu)E_p \\
 \frac{dI_{pht}}{dt} &= \tau_1 f_2(1 - u_2)\lambda_T I_{ph} + \sigma u_5 I_{nht} - (\eta_2\theta + \kappa_2\delta(1 - u_3) + \mu)I_{pht} \\
 \frac{dI_{nht}}{dt} &= \tau_1(1 - f_2)(1 - u_2)\lambda_T I_{nh} + \xi_1(1 - u_1)\lambda_h E_p + \tau_2 r u_4 I_{nd} \\
 &\quad - (\eta_1\theta + \kappa_3\delta(1 - u_3) + \sigma u_5 + \mu)I_{nht} \\
 \frac{dI_{nt}}{dt} &= (1 - f_2)(S_p + \rho R_p)(1 - u_2)\lambda_T + \theta E_p - (\xi_2(1 - u_1)\lambda_h + r u_4 + \mu + \mu_T)I_{nt} \\
 \frac{dR_p}{dt} &= r u_4 I_{nt} - (\rho(1 - u_2)\lambda_T + (1 - u_1)\lambda_h + \mu)R_p \\
 \frac{dI_{nd}}{dt} &= \xi_2(1 - u_1)\lambda_h I_{nt} + \tau_1 f_2(1 - u_2)\lambda_T I_{nh} + \tau_1(1 - f_2)(1 - u_2)\lambda_T I_{ph} \\
 &\quad + \eta_1\theta I_{nht} + \eta_2\theta I_{pht} - (\tau_2 r u_4 + \kappa_4\delta(1 - u_3) + \mu + \mu_T)I_{nd} \\
 \frac{dA}{dt} &= \delta(1 - u_3)(I_{ph} + \kappa_1 I_{nh} + \kappa_2 I_{pht} + \kappa_3 I_{nht} + \kappa_4 I_{nd}) - (\mu + \mu_a)A
 \end{aligned} \right\} \tag{39}$$

The main goal of incorporating the time-depended controls into the basic model is to help minimize the number of infections and improve productivity at minimal cost. Thus, an objective functional defined by

$$J = \min_{u_i} \int_0^T \left(b_1 I_{nh} + b_2 I_{nht} + b_3 I_{nt} + b_4 I_{nd} + \sum_{j=1}^5 \omega_j u_j^2 \right) dt, \tag{40}$$

can be considered as a proxy of the main goal. The constants b_i s are positive weights associated with the corresponding populations and $\omega_i u_i^2$ s are the costs associated with implementing the controls u_i s. Thus, $\omega_1 u_1^2$ is the cost of implementing measures to prevent transmission of HIV. The objective function J is chosen in line with previous studies concerning optimal control of infectious diseases [9]. The main aim in setting up the optimal control problem is to minimize the number of nonproductive infectives in subclasses I_{nh} , I_{nht} , and I_{nd} and the costs of implementing the

controls. Thus, an optimal tuple $(u_1^*, u_2^*, u_3^*, u_4^*, u_5^*)$ is sought such that

$$J(u_1^*, u_2^*, u_3^*, u_4^*, u_5^*) = \text{Min}\{J(u_1, u_2, u_3, u_4, u_5) \mid u_i \in \mathcal{U}\}, \tag{41}$$

where \mathcal{U} is the set of admissible controls with $0 \leq u_i \leq 1$ for $t \in [0, t_j]$. Pontryagin's maximum principle [31] provides the conditions necessary for existence of an optimal tuple. With this principle, the problem of solving equations (39) and (40) is converted to one of a point-wise minimization with respect to the controls of a Hamiltonian, H , function given by

$$H = b_1 I_{nh} + b_2 I_{nht} + b_3 I_{nt} + b_4 I_{nd} + \sum_{j=1}^5 \omega_j u_j^2 + \sum_{i=1}^{10} \lambda_i \frac{dX_i}{dt}, \tag{42}$$

where $X = \{S_p, I_{ph}, I_{nh}, E_p, I_{pht}, I_{nht}, I_{nt}, R_p, I_{nd}, A\}$. λ_i s are the co-state or adjoint variables associated with the state

variables. The following theorem follows from application of Pontryagin's maximum principle [31] and the existence result for optimal control from [32].

Theorem 8. Let $x^* = (S_p^*, I_{ph}^*, I_{nh}^*, E_p^*, I_{phT}^*, I_{nhT}^*, I_{nT}^*, R_p^*, I_{nd}^*, A^*)$ be the solution of the state equation (39) and $u^* = (u_1^*, u_2^*, u_3^*, u_4^*, u_5^*)$ be the corresponding optimal control tuple. Then, there exist adjoint variables $\ell_i, i \in [1, 10]$ satisfying the following set of differential equations.

$$\frac{d\ell}{dt} = \mathfrak{F}(x, \ell, t), \quad (43)$$

with transversality conditions $\ell_i(t_f) = 0, \forall i = 1, 2, \dots, 10$, $\mathfrak{F} = (\mathfrak{F}_1, \mathfrak{F}_2, \dots, \mathfrak{F}_{10})^T$, where $\mathfrak{F}_i = -(\partial H / \partial x_i)$.
The optimal controls are also shown to be given by

$$\left. \begin{aligned} u_1^* &= \frac{\lambda_h}{2\omega_1} [((\ell_2 - \ell_3)f_1 + \ell_3 - \ell_1)S_p + ((\ell_2 - \ell_3)f_1 + \ell_3 - \ell_8)R_p \\ &\quad + (\ell_6 - \ell_4)\xi_1 E_p + (\ell_9 - \ell_7)\xi_2 I_{nT}]; \\ u_2^* &= \frac{\lambda_{TT}}{2\omega_2} [((\ell_6 - \ell_9)f_2 + \ell_3 - \ell_6)I_{na} + ((\ell_9 - \ell_5)f_2 + \ell_2 - \ell_9)I_{pa}] \tau_1 \\ &\quad - ((\ell_4 - \ell_7)f_2 + \ell_7)(\rho R_p + S_p) + \rho R_p \ell_8 + S_p \ell_1]; \\ u_3^* &= \frac{-\delta}{2\omega_3} [(\ell_2 - \ell_{10})I_{pa} + \kappa_1(\ell_3 - \ell_{10})I_{na} + \kappa_2(\ell_5 - \ell_{10})I_{pa1} \\ &\quad + \kappa_3(\ell_6 - \ell_{10})I_{na1} + \kappa_4(\ell_9 - \ell_{10})I_{nd}]; \\ u_4^* &= \frac{r}{2\omega_4} [\tau_2(\ell_9 - \ell_6)I_{nd} + (\ell_7 - \ell_8)I_{nT}]; \\ u_5^* &= \frac{\sigma}{2\omega_5} [(\ell_6 - \ell_5)I_{na1} + I_{na}(\ell_3 - \ell_2)]. \end{aligned} \right\} \quad (44)$$

The control is bounded as follows:

$$\begin{aligned} \tilde{u}_1 &= \begin{cases} 0 & \text{if } u_1^* \leq 0 \\ u_1^* & \text{if } 0 < u_1^* < 1 \\ 1 & \text{if } u_1^* \geq 1 \end{cases}, \quad \tilde{u}_2 = \begin{cases} 0 & \text{if } u_2^* \leq 0 \\ u_2^* & \text{if } 0 < u_2^* < 1 \\ 1 & \text{if } u_2^* \geq 1 \end{cases}, \quad \tilde{u}_3 = \begin{cases} 0 & \text{if } u_3^* \leq 0 \\ u_3^* & \text{if } 0 < u_3^* < 1 \\ 1 & \text{if } u_3^* \geq 1 \end{cases}, \\ \tilde{u}_4 &= \begin{cases} 0 & \text{if } u_4^* \leq 0 \\ u_4^* & \text{if } 0 < u_4^* < 1 \\ 1 & \text{if } u_4^* \geq 1 \end{cases}, \quad \tilde{u}_5 = \begin{cases} 0 & \text{if } u_5^* \leq 0 \\ u_5^* & \text{if } 0 < u_5^* < 1 \\ 1 & \text{if } u_5^* \geq 1 \end{cases}. \end{aligned} \quad (45)$$

Proof. Due to the convexity of the function under the integral in J with respect to $u_i, \forall i = 1 \dots 5$, a priori boundedness of the state solutions, and the Lipschitz property of the state system with respect to the state variables, the existence of the optimal control tuple is established using Corollary 4.1 of Fleming and Rishel [32]. The adjoint system (43) is obtained by differentiating the Hamiltonian H with respect to the state variables. The characterizations in equation (44) are obtained by solving the stationarity conditions $(\partial H / \partial u_i) = 0$ for u_i . This completes the proof. \square

6. Numerical Experimentation

This section presents a numerical analysis of the optimal control problem (39) resulting from incorporation of the control efforts into model equation (2). The solution process involves the solution of the optimality system consisting of the state system (39) and the adjoint system (43). Following [33], the following iterative scheme is employed:

- (i) Make a guess on the control profiles u_i , usually $u_i = 0$

TABLE 2: Costs and health benefits of various intervention strategies.

Strategies	Total infections averted	Cost (\$)
1	488263.887	10440.182
2	56.033	50015.728
3	488263.925	10433.573
4	488263.887	10440.151
5	56.242	49950.050

TABLE 3: Comparing cost and benefit of strategies 1 and 2.

Strategies	Total infections averted	Total cost (\$)	ICER
2	56.03259	50015.72772	892.61856
1	488263.88729	10440.18163	-0.08106

- (ii) Using the guess in step (i) above, solve the state system forward using a fourth-order Runge–Kutta method.
- (iii) Using the guessed u_i s and the values of the state variables in step (ii) above, solve the adjoint system (43) backward using a fourth-order Runge–Kutta scheme.
- (iv) With the current state and adjoint variables values, update the control using the characterizations (44) and bounds.
- (v) With the current adjoint variables values and updated controls, repeat step (ii) and continue the process until the current iteration’s values are closer to the previous iteration’s values.

To determine the most efficient strategy that can be employed to fight the spread of the diseases and also improve productivity, we seek to compare the following possible strategies:

- (1) Fighting only HIV and skills training (i.e., $u_1 \neq 0, u_3 \neq 0, u_5 \neq 0, u_2 = u_4 = 0$).
- (2) Fighting only TB and skills training (i.e., $u_2 \neq 0, u_4 \neq 0, u_5 \neq 0, u_1 = u_3 = 0$).
- (3) Fighting both diseases and skills training (i.e., $u_1 \neq 0, u_2 \neq 0, u_3 \neq 0, u_4 \neq u_5 \neq 0$).

- (4) Implementing only preventive controls and skills training (i.e., $u_1 \neq 0, u_2 \neq 0, u_3 = u_4 = 0, u_5 \neq 0$).
- (5) Implementing only curative controls and skills training (i.e., $u_1 = u_2 = 0, u_3 \neq 0, u_4 \neq 0, u_5 \neq 0$).

The comparison of the above strategies is achieved using the numerical simulation results, which are computed using the same initial state values and the model parameter values in Table 1. The number of infections averted is used as a proxy for the benefits of interventions. The total number of infections averted is calculated as the difference in the total number of infectives at final time between the controlled and uncontrolled problems. Table 2 presents the health benefit of various intervention strategies.

To compare the various strategies, use is made of the incremental cost-effectiveness ratio (ICER) which is one of three ratios used to measure effectiveness of different interventions. The ICER is used to compare the differences between the cost and health benefits of two alternative intervention strategies that compete for same resources. The ICER is defined as the extra cost incurred for an extra benefit. The ICER between two intervention strategies is the ratio of differences in cost to differences in health outcomes. Thus, for our case, the ICER between strategies 1 and 2 is given by

$$ICER(1) = \frac{\text{ost of strategy 1} - \text{ost of strategy 2}}{\text{otal infections saved by strategy 1} - \text{otal infections saved by strategy 2}} \tag{46}$$

Thus, we carry out the comparisons as follows. Comparing strategies 1 and 2, we have the following (see Table 3).

The cost-effectiveness ratio of strategy 1 over 2 is calculated as follows:

$$ICER(1) = \frac{10440.18163 - 50015.72772}{488263.88729 - 56.03259} = -0.08106. \tag{47}$$

Thus, a comparison between strategies 1 and 2 reveals that a cost saving of \$0.08106 is made by preferring strategy 1

over strategy 2. Hence, we conclude that strategy 1 should be preferred to strategy 2.

Next, we compare strategies 1 and 3 as follows (see Table 4).

A comparison between strategies 1 and 3 reveals that a cost saving of \$176.36800 is made by preferring strategy 3 over strategy 1. Hence, we conclude that strategy 3 should be preferred to strategies 1 and 2.

Next, we compare strategies 3 and 4 as follows (see Table 5).

A comparison between strategies 3 and 4 reveals that a cost saving of \$175.98549 is made by preferring strategy 3

TABLE 4: Comparing cost and benefit of strategies 1 and 3.

Strategies	Total infections averted	Total cost (\$)	ICER
1	488263.88729	10440.18163	0.02138
3	488263.92476	10433.57277	-176.36800

TABLE 5: Comparing cost and benefit of strategies 3 and 4.

Strategies	Total infections averted	Total cost (\$)	ICER
4	488263.88738	10440.15149	0.02138
3	488263.92476	10433.57277	-175.98549

TABLE 6: Comparing cost and benefit of strategies 3 and 5.

Strategies	Total infections averted	Total cost (\$)	ICER
5	56.24200	49950.04995	888.127182
3	488263.92476	10433.57277	-0.08094

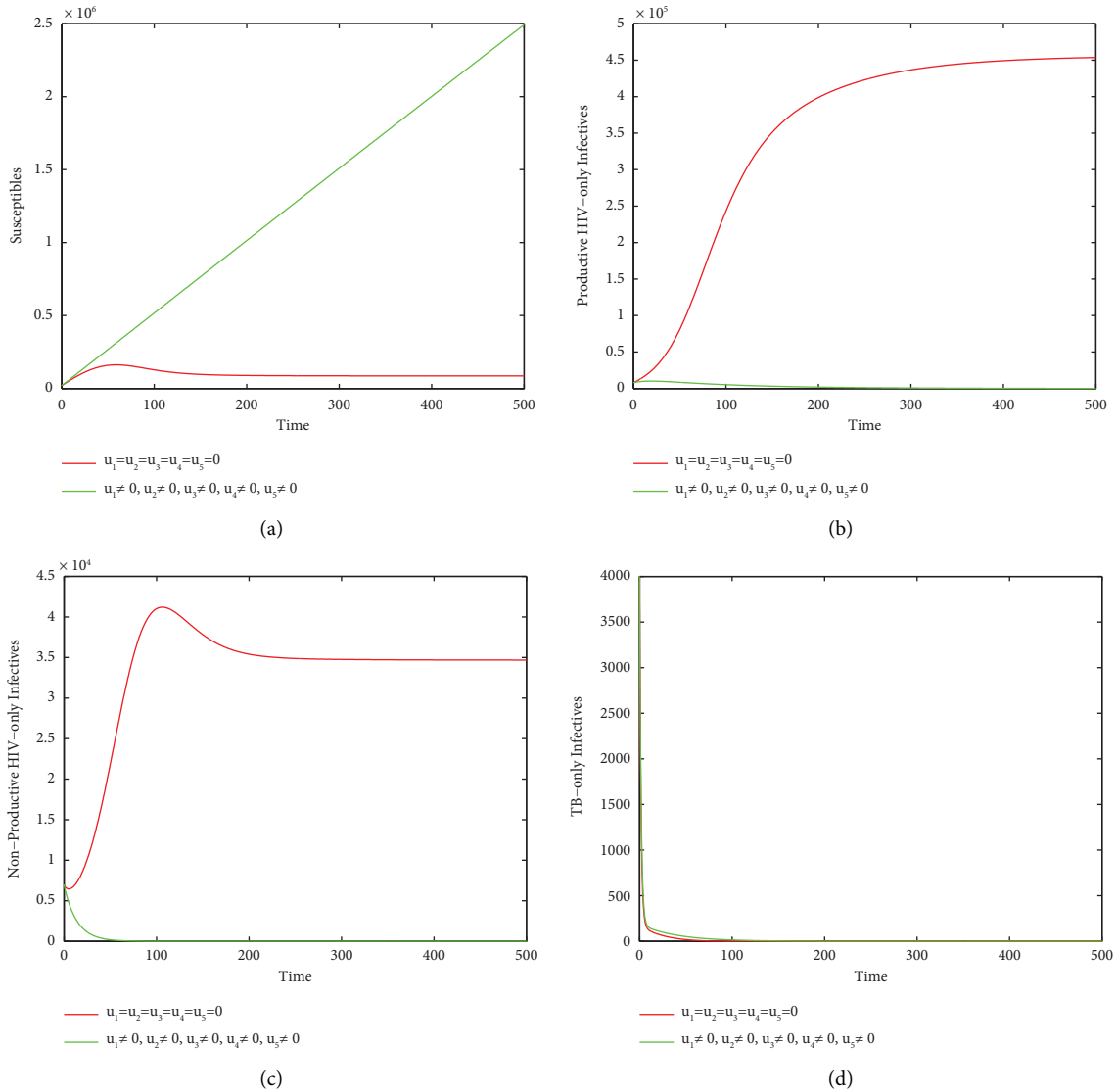


FIGURE 2: Continued.

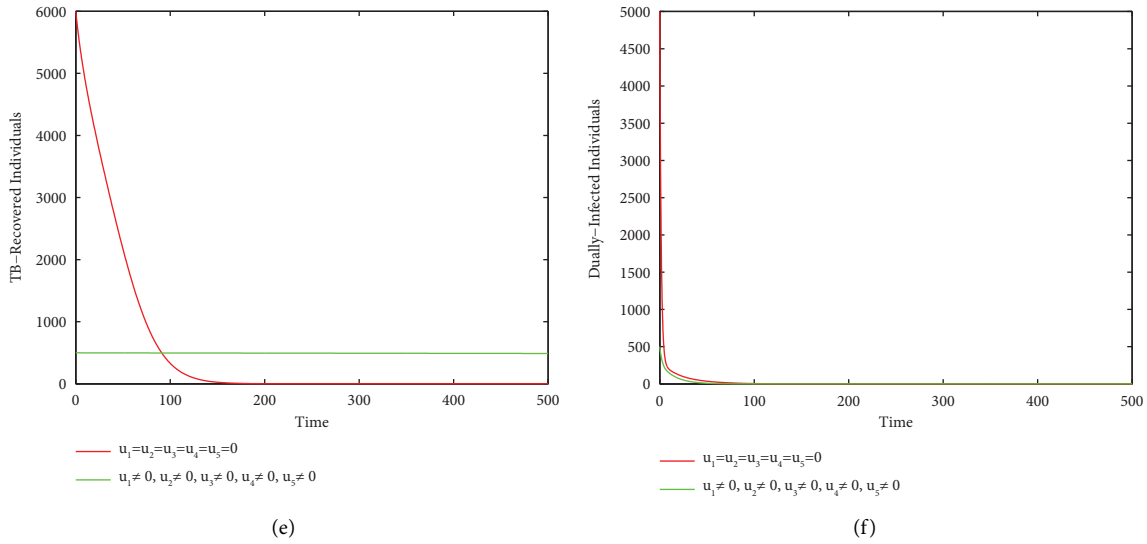


FIGURE 2: Simulation results for the implementation of both preventative and curative measures along with skills training in combating the spread of HIV-TB co-infection.

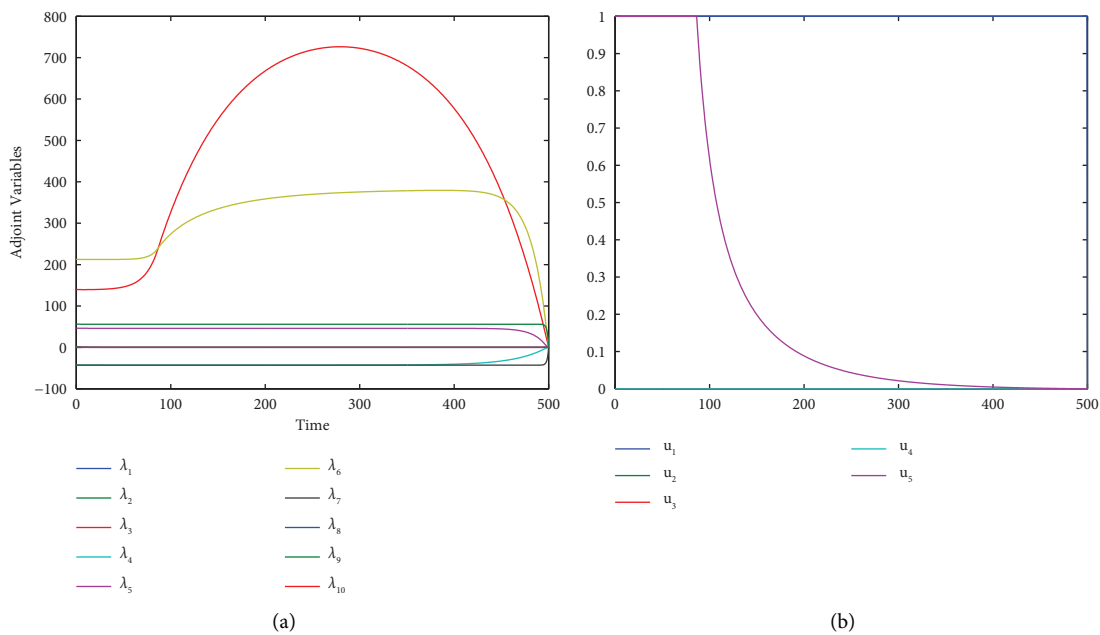


FIGURE 3: Plots of adjoint variables and control profiles for the best strategy in combating spread of HIV-TB co-infection.

over strategy 4. Hence, we conclude that strategy 3 should be preferred to strategies 1, 2, and 4.

Next, we compare strategies 3 and 5 as follows (see Table 6).

A comparison between strategies 3 and 5 reveals that a cost saving of \$0.08094 is made by preferring strategy 3 over strategy 5. Hence, we conclude that strategy 3 should be preferred to strategies 1, 2, 4, and 5.

These results imply that strategy 3, which is the implementation of all control strategies, strongly dominates over all other combinations of controls. Thus, the most cost-effective combination of our chosen controls is the one that involves all the controls, namely, prevention, treatment, and

skills training. This goes to imply that multiple strategies in the combat against the spread of the two diseases should be adopted if cost-effectiveness is desired. The simulation results of the best strategy are presented in Figures 2 and 3.

7. Conclusion

In this paper, a deterministic mathematical model that describes the spread and effects of HIV-TB co-infection on workforce evolution has been proposed and analyzed. The basic model is split into two submodels, namely, the HIV-only and TB-only models, which are qualitatively analyzed

for boundedness and stability of disease-free equilibrium states. The local stability and global stability of the disease-free equilibrium points of the submodels and the full model together with other qualitative properties are discussed. The full model is modified by incorporating time-dependent control variables into it, and an optimal control problem is formed by considering a minimization of a quadratic objective functional, which is chosen in line with extant literature on epidemic models due to the nonlinearity of the cost associated with implementation of controls, subject to the modified model. The optimal control problem is qualitatively analyzed using Pontryagin's maximum principle, and numerical simulations are carried out considering various implementations of the interventions aimed at fighting the spread of the co-infection and improving productivity. Through the cost-effectiveness analysis, it was observed that combining preventive and curative measures together with skills training/improvement is the most cost-effective strategy that should be adopted in the fight against the spread of HIV-TB co-infection within the workforce.

Data Availability

The data used to support the findings of this study are included within the article.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

References

- [1] WHO, *Global Tuberculosis Report*. Technical Report, World Health Organization, Geneva, Switzerland, 2014.
- [2] Y. Honda, L. Rogers, and K. Nakata, "Type I interferon induces inhibitory 16-kD CCAAT/enhancer binding protein (C/EBP) β , repressing the HIV-1 long terminal repeat in macrophages: pulmonary tuberculosis alters C/EBP expression, enhancing HIV-1 replication," *Journal of Experimental Medicine*, vol. 188, no. 7, pp. 1255–1265, 1998.
- [3] D. Kirschner, "Using mathematics to understand HIV immune dynamics," *AMS notices*, vol. 43, no. 2, 1996.
- [4] A. S. Perelson and P. W. Nelson, "Mathematical analysis of HIV-1 dynamics in vivo," *SIAM Review*, vol. 41, no. 1, pp. 3–44, 1999.
- [5] N. I. Stilianakis, K. Dietz, and D. Schenzle, "Analysis of a model for the pathogenesis of AIDS," *Mathematical Biosciences*, vol. 145, no. 1, pp. 27–46, 1997.
- [6] A. Gumel, P. N. Shivakumar, and B. M. Sahai, "A mathematical model for the dynamics of HIV-1 during the typical course of infection," *Nonlinear Analysis: Theory, Methods & Applications*, vol. 47, no. 3, pp. 1773–1783, 2001.
- [7] T. Jean, W. Garira, A. Gumel, and Z. Mukandavire, "Mathematical analysis of a model for HIV-malaria co-infection," *MBE*, vol. 6, no. 2, pp. 333–362, 2009.
- [8] O. Sharomi, C. Podder, A. Gumel, and B. Song, "Mathematical analysis of the transmission dynamics of HIV/TB coinfection in the presence of treatment," *Mathematical Biosciences and Engineering*, vol. 5, no. 1, p. 145, 2008.
- [9] B. Seidu and D. Oluwole, "Makinde. "Optimal control of HIV/AIDS in the workplace in the presence of careless individuals," *Computational and Mathematical Methods in Medicine*, vol. 2014, Article ID 831506, 2014.
- [10] R. Jan, M. A. Khan, and J. F. GomezAguilar, "Asymptomatic carriers in transmission dynamics of dengue with control interventions," *Optimal Control Applications and Methods*, vol. 41, no. 2, pp. 430–447, 2019.
- [11] M. Ibrahim Daabo and B. Seidu, "Modelling the effect of irresponsible infective immigrants on the transmission dynamics of HIV/AIDS," *Advances in Applied Mathematical Biosciences*, vol. 3, pp. 31–40, 2012.
- [12] B. Seidu, O. D. Makinde, and I. Y. Seini, "Mathematical analysis of the effects of HIV-malaria Co-infection on workplace productivity," *Acta Biotheoretica*, vol. 63, no. 2, pp. 151–182, 2015.
- [13] U. Saif, K. M. Altaf, F. Muhammad, and T. Gul, "Modeling and analysis of tuberculosis (tb) in khyber pakhtunkhwa, Pakistan," *Mathematics and Computers in Simulation*, vol. 65, Article ID S0378475419301089, 2019.
- [14] R. Webster West and J. R. Thompson, "Modeling the impact of hiv on the spread of tuberculosis in the United States," *Mathematical Biosciences*, vol. 143, no. 1, pp. 35–60, 1997.
- [15] R. Naresh and A. Tripathi, "Modelling and analysis of HIV-TB co-infection in a variable size population," *Mathematical Modelling and Analysis*, vol. 10, no. 3, pp. 275–286, 2005.
- [16] R. Naresh, D. Sharma, and A. Tripathi, "Modelling the effect of tuberculosis on the spread of hiv infection in a population with density-dependent birth and death rate," *Mathematical and Computer Modelling*, vol. 50, no. 7-8, pp. 1154–1166, 2009.
- [17] C. P. Bhunu, W. Garira, and Z. Mukandavire, "Modeling hiv/aids and tuberculosis coinfection," *Bulletin of Mathematical Biology*, vol. 71, no. 7, pp. 1745–1780, 2009.
- [18] S. Kumar and S. Jain, "Assessing the effects of treatment in HIV-TB co-infection model," *The European Physical Journal Plus*, vol. 133, no. 8, p. 294, 2018.
- [19] A. Mallela, S. Lenhart, and N. K. Vaidya, "Hiv-tb co-infection treatment: modeling and optimal control theory perspectives," *Journal of Computational and Applied Mathematics*, vol. 307, pp. 143–161, 2016.
- [20] R. A. Tanvi, R. Aggarwal, and T. Kovacs, "Assessing the effects of Holling Type-II treatment rate on HIV-TB co-infection," *Acta Biotheoretica*, vol. 69, no. 1, pp. 1–35, 2020.
- [21] R. A. Tanvi and R. Aggarwal, "Dynamics of HIV-TB co-infection with detection as optimal intervention strategy," *International Journal of Non-linear Mechanics*, vol. 120, Article ID 103388, 2020.
- [22] K. O. Okosun, O. D. Makinde, and I. Takaidza, "Analysis of recruitment and industrial human resources management for optimal productivity in the presence of the HIV/AIDS epidemic," *Journal of Biological Physics*, vol. 39, no. 1, pp. 99–121, 2013.
- [23] B. Seidu, O. D. Makinde, and C. S. Bornaa, "Mathematical analysis of an industrial HIV/AIDS model that incorporates carefree attitude towards sex," *Acta Biotheoretica*, vol. 69, no. 3, pp. 257–276, 2021.
- [24] A. Tripathi, R. Naresh, and D. Sharma, "Modeling the effect of screening of unaware infectives on the spread of HIV infection," *Applied Mathematics and Computation*, vol. 184, no. 2, pp. 1053–1068, 2007.
- [25] C. Castillo-Chavez and B. Song, "Dynamical models of tuberculosis and their applications," *Mathematical Biosciences and Engineering*, vol. 1, no. 2, pp. 361–404, 2004.

- [26] V. Lakshmikanthan, S. Leela, and A. Anatolii Andreevich Martyniuk, *Stability Analysis of Nonlinear Systems*, CRC Press, Boca Raton, FL, USA, 1989.
- [27] H. W. Hethcote, "The mathematics of infectious diseases," *SIAM Review*, vol. 42, no. 4, pp. 599–653, 2000.
- [28] P. van den Driessche and J. Watmough, "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission," *Mathematical Biosciences*, vol. 180, no. 1-2, pp. 29–48, 2002.
- [29] J. P. La Salle, *An Invariance Principle in the Theory of Stability*, Technical report, Center for Dynamical Systems, Providence, RI, USA, 1966.
- [30] C. Castillo-Chavez, Z. Feng, and W. Huang, "On the computation of r_0 and its role on global stability," in *Mathematical Approaches for Emerging and Reemerging Infectious Diseases: An Introduction*, pp. 229–250, Springer, Berlin, Germany, 2002.
- [31] L. S. Pontryagin, *The mathematical theory of optimal processes*, CRC Press, Boca Raton, FL, USA, 1962.
- [32] W. H. Fleming and R. W. Rishel, *Deterministic and stochastic optimal control*, Springer-Verlag, Berlin, Germany, 1975.
- [33] S. M. Lenhart and J. T. Workman, *Optimal control applied to biological models*, CRC Press, Boca Raton, FL, USA, 2007.