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Spread and Control of the Dynamics of HIV/AIDS-TB Co-infection in Ethiopia: A Mathematical Model Analysis

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Abstract

In this work we considered a nonlinear deterministic dynamical system to study the dynamics of HIV/AIDS-TB co-infection in Ethiopia. We found the system exhibit disease free equilibrium point and endemic equilibrium point. For the reproduction number $R_0 < 1$ the disease-free equilibrium point is locally asymptomatically stable and the endemic equilibrium point is locally asymptomatically unstable. We calculate basic reproduction number of the HIV/AIDS-TB co-infection dynamical system which depends on six parameters. Using real data collected from different sectors in Ethiopia we found that the numerical value of the basic reproduction number is 34.86. This shows that HIV/AIDS–TB co-infection spread in the society. Using sensitive analysis, we identify the most influential control parameter is the HIV/AIDS-TB co-infection transmission rate β_3. The HIV/AIDS-TB co-infection transmission rate $\beta_3 = \frac{Effective\ number\ of\ contact\ for\ HIV/AIDS-TB\ co-infection}{Total\ number\ of\ contact\ for\ HIV/AIDS-TB\ co-infection}$ which numerical value to be 0.021. But the real value of β_3 is 0.74, to be 0.74 in to 0.021 by fixing the number of contacts for HIV/AIDS-TB co-infection we decrease the effective number of contacts for HIV/AIDS-TB co-infection 74 to 21. We also perform numerical simulation based on real data collected from different health sectors in Ethiopia.

Keywords: Nonlinear dynamical system; HIV/AIDS-TB co-infection; Stability Analysis; Basic Reproduction Number; Sensitive Analysis; Numerical Simulation.

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1. Introduction

According with the World Health Organization (WHO), the human immunodeficiency virus (HIV) and mycobacterium tuberculosis are the first and second cause of death from a single infectious agent, respectively [1]. HIV/AIDS is transmitted primarily via unprotected sexual intercourse, contaminated blood transfusions, hypodermic needles, and from mother to child during pregnancy, delivery, or breastfeeding. There is no cure or vaccine to HIV/AIDS. However, antiretroviral treatment (ART) improves health, prolongs life, and substantially reduces the risk of HIV transmission [21]. To date, TB claims the second largest number of victims due to a single infectious agent right after HIV/AIDS [19]. Mycobacterium tuberculosis is the cause of most occurrences of tuberculosis (TB) and is usually acquired via airborne infection from someone who has active TB can coughs, sneezes, speaks, or sings. German Microbiologist Robert Koch discovered the causative organism Mycobacterium tuberculosis on 24th March 1882 [16]. The negative impact of synergic interactions between Tuberculosis (TB) and HIV has caused worldwide concern [12]. Tuberculosis (TB) and HIV infection have the effect of deeply on attack the immune system, since they can afford to weaken host immune response through a mechanism that has not been fully understood. Mycobacterium Tuberculosis and HIV are two pathogens in the same individual comes by co-infection and they giving increase the effect of one another, accelerating the deterioration of immunological functions and resulting in premature death if untreated [15]. Studying HIV/AIDS-TB coinfection is of significant importance because it may have negative effect both on the health of the coinfected individuals as well as on the public health in general [2].

Several numbers of mathematical models on co-infection have been formulated and analyzed. The studies discussed the HIV/AIDS-TB co-infection associated morbidity and mortality complications. Among those Mathematical models, the work done by [14], addressed the Analysis of HIV/AIDS and Tuberculosis coinfection Dynamics by considered two variants of a co epidemic model $SIxSI$ and $SIIxSEI$ of two diseases. Reference [20], addresses a mathematical analysis of the transmission dynamics of HIV/AIDS-TB co-infection in the presence of treatment. According to [17], a nonlinear mathematical model is proposed to study the effect of tuberculosis on the spread of HIV/AIDS infection in a logistically growing human population where the restricted growth is due to density dependence in both the birth and death. References [13], addresses Modeling Tuberculosis HIV/AIDS-TB Co-infections by consider a highly simplified deterministic model that incorporates the joint dynamics of Tuberculosis (TB) and HIV/AIDS. Reference [4] , a nonlinear mathematical model is proposed and analyzed to study the dynamics of HIV/AIDS, Tuberculosis (TB) and HIV/AIDS-TB co-infection by consider TB infected individuals are not HIV susceptible. Reference [10], Addressed risk of co-epidemic HIV/AIDS-TB is a major problem that must be faced by countries around the world by assumed that disease transmission occurs via random mixing between members in the susceptible, latent/exposed, and infected compartments. Reference [21], addresses a HIV/AIDS-TB co-infection population model and optimal control treatment by considered antiretroviral therapy for HIV/AIDS infection and treatments for latent and active tuberculosis. Reference [18], analyzed a Mathematical Modeling of Tuberculosis as an Opportunistic Respiratory Co-Infection in HIV/AIDS in the Presence of Protection. [9], develop a mathematical model to study the Threshold dynamic for quasi-endemic equilibrium from co-epidemic HIV/AIDS-TB model with re-infection TB in heterosexual population. Reference [15], addressed a Mathematical Modeling of Transmission dynamics of Co-infection Tuberculosis in HIV Community. Reference [11], addressed a non-linear

deterministic Mathematical model analysis of coinfection: HIV/AIDS and TB Perspective by consider simultaneous transmission of both pathogens to the susceptible. Reference [12], proposes a population Mathematical model for HIV/AIDS-TB co-infection and addresses the effect of treatment for HIV/AIDS infection, active tuberculosis and co-infection of HIV/AIDS-TB. In this paper we refer the initial HIV/AIDS-TB co-infection Mathematical Model done by Kelatlhegile Gosalamang Ricardo, Mathematical analysis of dual-infection HIV and TB perspective [11] and we extend it based on the Ethiopian context. We found disease free and endemic equilibrium points and we performed their local and global stability. Based on real data collected from different health sectors in Ethiopia we found that HIV/AIDS-TB co-infection has a strong impact on the spread of HIV/AIDS-TB co-infection. Finally we suggest some solutions based on our control parameters how to control the HIV/AIDS- TB co-infection.

2. Mathematical Model

2.1 Model assumptions of HIV/AIDS-TB Co-infection

Consider a nonlinear dynamical system in which the host population divides into eleven compartments, namely susceptible individuals both HIV/AIDS and TB $S(t)$, HIV-exposed individuals $E_H(t)$, HIV-infected individuals $I_H(t)$, HIV infected individuals with AIDS stage who are taking Antiretroviral treatment $A(t)$, TB-exposed individuals $E_T(t)$, TB-fast latently infected individuals $L_f(t)$, TB-slow latently infected individuals $L_s(t)$, active TB infected individuals $I_T(t)$, TB recovered or treated individuals $R_T(t)$, class of individuals infected with both HIV and active TB $I_{HT}(t)$, class of individuals infected with both HIV-infected with AIDS stage who are taking Antiretroviral treatment and active TB $A_T(t)$. The total population at time t, denoted by $N(t)$, is given by $N(t) = S(t) + E_H(t) + I_H(t) + A(t) + E_T(t) + L_f(t) + L_s(t) + I_T(t) + R_T(t) + I_{HT}(t) + A_T(t)$. Now in order to formulate the dynamics of the above system mathematically, the following assumptions have been adopted:

- We assume that all individuals in a given compartment are identically infectious.
- HIV infected class is considered susceptible to TB infection. However, TB infected population is not susceptible to HIV.
- The susceptible class, $S(t)$, containing individuals at risk of either HIV or TB or both HIV/AIDS-TB co-infection.
- The susceptible population is increased by the recruitment of individuals into the population by Λ.
- All individuals in different compartments suffer from natural death rate d.
- Susceptible individuals acquire TB infection from individuals with active TB at a rate λ_T given by $\lambda_T = \frac{\beta_1}{N}(I_T(t) + I_{HT}(t) + A_T(t))$, where β_1 is the transmission coefficient for TB infection.
- Susceptible individuals acquire HIV infection, following effective contact with people infected with HIV at a rate λ_H given by $\lambda_H = \frac{\beta_2}{N}[E_H(t) + I_H(t) + I_{HT}(t) + A(t) + A_T(t)]$, where β_2 is the transmission coefficient for HIV infection.
- And susceptible individuals acquire HIV/AIDS-TB co-infection, following effective contact with people infected with HIV/AIDS-TB co-infection at a rate λ_{TH} given by $\lambda_{TH} = \frac{\beta_3}{N}[I_{HT}(t) + A_T(t)]$,

where β_3 is the transmission coefficient for HIV/AIDS-TB co-infection.

- From the expression of λ_T, λ_H and λ_{HT} we can formulate another condition $\beta_3 = \kappa\beta_1\beta_2$ where $\kappa = \frac{(E_H(t)+I_H(t)+I_{HT}(t)+A(t)+A_T(t))(I_T(t)+I_{HT}(t)+A_T(t))\lambda_{TH}}{(I_{HT}(t)+A_T(t))\lambda_T\,\lambda_H}$ is a parameter. The parameter $\kappa < 1$, correspond to the assumption that the two pathogens are rarely transmitted simultaneously, while $\kappa > 1$ assumes high transmissibility of both pathogens.
- HIV-exposed individuals progress to the HIV-infected class at a rate δ, and progress to the AIDS class A at a rate μ.
- HIV-infected individuals with AIDS symptoms are suffer induced death at a rate d_H.
- Individuals in the class E_H are susceptible to TB infection and progress to individuals infected with both HIV and active TB $I_{HT}(t)$ by the rate λ_T.
- Individuals in the class I_H are susceptible to TB infection and progress to individuals infected with both HIV-infected with AIDS symptoms who are taking antiretroviral treatment and active TB $A_T(t)$ by the rate λ_T.
- Individuals in the class A are susceptible to TB infection and progress to individuals infected with both HIV-infected with AIDS symptoms who are taking antiretroviral treatment and active TB $A_T(t)$at a rate λ_T.
- Individuals in the class I_{HT} are progress to individuals infected with both HIV-infected with AIDS symptoms who are taking antiretroviral treatment and active TB $A_T(t)$at a rate φ.
- Individuals infected with both HIV-infected with AIDS symptoms who are taking antiretroviral treatment and active TB is suffering induced death at a rate d_{HT}.
- TB-exposed individuals are progress to either fast or slow latent infection by the rate $p\omega$ and $(1-p)\omega$ respactivly.
- The fast latent $L_f(t)$ and slow latent $L_s(t)$ infected classes are decreased by post exposure vaccination by the linear recovery rate ρ and ε respectively and inters into recovered class
- And if not get post exposure vaccination develop active TB infection at some time in the time of infection by the infection rate α and ϵ respectively and inter into $I(t)$ but we cannot consider pre-exposer vaccination.
- Individuals with active TB disease suffering induced death at a rate d_T.
- Individuals successfully treated at active TB infection stage develop immunity and go to recovery stage at a rate π.
- The recovered class is decrease by the rate θ which is the recurrence rate of successfully treated TB cases and inters into infected class. Based on the above assumptions we construct the following flow chart

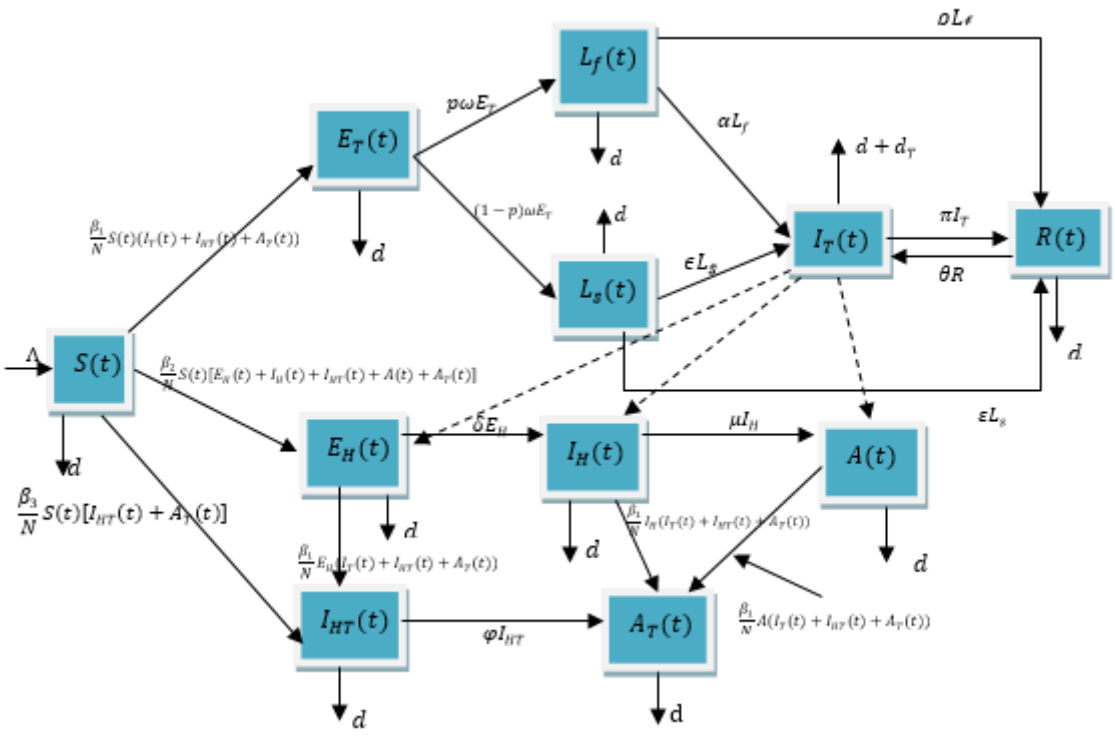

Figure 1: Flow diagram of HIV/AIDS-TB co-infection dynamical system

2.2 Model Equation

The corresponding dynamical system of the above flowchart

$$\frac{dS}{dt} = \Lambda - (\lambda_T + \lambda_H + \lambda_{HT})S - dS \quad (1)$$

$$\frac{dE_T}{dt} = \lambda_T S - (\omega + d)E_T \quad (2)$$

$$\frac{dL_f}{dt} = p\omega E_T - (\rho + \alpha + d)L_f \quad (3)$$

$$\frac{dL_s}{dt} = (1-p)\omega E_T - (\varepsilon + \epsilon + d)L_s \quad (4)$$

$$\frac{dI_T}{dt} = \alpha L_f + \epsilon L_s + \theta R - (\pi + d + d_T)I_T \quad (5)$$

$$\frac{dR}{dt} = \rho L_f + \varepsilon L_s + \pi I_T - (\theta + d)R \quad (6)$$

$$\frac{dE_H}{dt} = \lambda_H S - \lambda_T E_H - (\delta + d)E_H \quad (7)$$

$$\frac{dI_H}{dt} = \delta E_H - \lambda_T I_H - (\mu + d)I_H \quad (8)$$

$$\frac{dA}{dt} = \mu I_H - \lambda_T A - (d + d_H)A \quad (9)$$

$$\frac{dI_{HT}}{dt} = \lambda_{HT} S + \lambda_T E_H - (\varphi + d)I_{HT} \quad (10)$$

$$\frac{dA_T}{dt} = \lambda_T I_H + \lambda_T A + \varphi I_{HT} - (d + d_{HT})A_T \quad (11)$$

Where the total population size $N = S + E_T + L_f + L_s + I_T + R + E_H + I_H + A + I_{HT} + A_T$

2.3 Positivity of the Solution

Theorem 1: If $S(0) > 0, E_T(0) \geq 0, L_f(0) \geq 0, L_s(0) \geq 0, I_T(0) \geq 0, E_H(0) \geq 0, I_H(0) \geq 0, A(0) \geq 0, I_{HT}(0) \geq 0, A_T(0) \geq 0$ and $R(0) \geq 0$ then the solution region $(S(t), E_T(t), L_f(t), L_s(t), I_T(t), E_H(t), I_H(t), A(t), I_{HT}(t), A_T(t), R(t))$of the dynamical system (1) – (11) is positive for all time $t \geq 0$.

Proof: The dynamical system (1) – (11) is meaningful, when all solution of the state variables with nonnegative conditions is non-negative. To show this we have taken each differential equation of the dynamical system (1) – (11) as follow

1. From $\frac{dS}{dt} = \Lambda - (\lambda_T + \lambda_H + \lambda_{HT})S - dS$ its solution is $S(t) = e^{\int_0^t ((\lambda_T + \lambda_H + \lambda_{HT}) + d)d\tau}$ $\int_0^t \Lambda e^{-\int_0^t ((\lambda_T + \lambda_H + \lambda_{HT}) + d)d\tau} d\tau > 0$ since those model parameters and exponential functions are positive.
2. From $\frac{dE_T}{dt} = \lambda_T S - (\omega + d)E_T$ its solution is $E_T(t) = e^{\int_0^t (\omega + d)d\tau} \int_0^t \lambda_T S\, e^{-\int_0^t (\omega + d)d\tau} d\tau > 0$ since those model parameters and exponential functions are positive.
3. From $\frac{dL_f}{dt} = p\omega E_T - (\rho + \alpha + d)L_f$ its solution is $L_f(t) = e^{\int_0^t (\rho + \alpha + d)d\tau} \int_0^t p\omega E_T\, e^{-\int_0^t (\rho + \alpha + d)d\tau} d\tau > 0$ since those model parameters and exponential functions are positive.
4. From $\frac{dL_s}{dt} = (1 - p)\omega E_T - (\varepsilon + \epsilon + d)L_s$ its solution is $L_s(t) = e^{\int_0^t (\varepsilon + \epsilon + d)d\tau} \int_0^t (1 - p)\omega E_T\, e^{-\int_0^t (\varepsilon + \epsilon + d)d\tau} d\tau > 0$ since those model parameters and exponential functions are positive.
5. From $\frac{dI_T}{dt} = \alpha L_f + \epsilon L_s + \theta R - (\pi + d + d_T)I_T$ its solution is $L_T(t) = e^{\int_0^t (\pi + d + d_T)d\tau} \int_0^t (\alpha L_f + \epsilon L_s + \theta R)\, e^{-\int_0^t (\pi + d + d_T)d\tau} d\tau > 0$ since those model parameters and exponential functions are positive.
6. From $\frac{dR}{dt} = \rho L_f + \varepsilon L_s + \pi I_T - (\theta + d)R$ its solution is $R(t) = e^{\int_0^t (\theta + d)d\tau} \int_0^t (\rho L_f + \varepsilon L_s + \pi I_T)\, e^{-\int_0^t (\theta + d)d\tau} d\tau > 0$ since those model parameters and exponential functions are positive.
7. From $\frac{dE_H}{dt} = \lambda_H S - \lambda_T E_H - (\delta + d)E_H$ its solution is $E_H(t) = e^{\int_0^t (\lambda_T + (\delta + d))d\tau}$ $\int_0^t \lambda_H S\, e^{-\int_0^t (\lambda_T + (\delta + d))d\tau} d\tau > 0$ since those model parameters and exponential functions are positive.
8. From $\frac{dI_H}{dt} = \delta E_H - \lambda_T I_H - (\mu + d)I_H$ its solution is $I_H(t) = e^{\int_0^t (\lambda_T + (\mu + d))d\tau}$

$\int_0^{\mathrm{t}} \delta E_H \, e^{-\int_0^t (\lambda_T+(\mu+d))d\tau} \mathrm{d}\tau > 0$ since those model parameters and exponential functions are positive.

9. From $\frac{dA}{dt} = \mu I_H - \lambda_T A - (d + d_H)A$ its solution is $A(\mathrm{t}) = e^{\int_0^t (\lambda_T+(d+d_H))d\tau}$ $\int_0^{\mathrm{t}} \mu I_H \, e^{-\int_0^t (\lambda_T+(d+d_H))d\tau} \mathrm{d}\tau > 0$ since those model parameters and exponential functions are positive.
10. From $\frac{dI_{HT}}{dt} = \lambda_{HT} S + \lambda_T E_H - (\varphi + d) I_{HT}$ its solution is $I_{HT}(\mathrm{t}) = e^{\int_0^t (\varphi+d)d\tau} \int_0^{\mathrm{t}} (\lambda_{HT} S + \lambda_T E_H) \, e^{-\int_0^t (\varphi+d)d\tau} \mathrm{d}\tau > 0$ since those model parameters and exponential functions are positive.
11. From $\frac{dA_T}{dt} = \lambda_T I_H + \lambda_T A + \varphi I_{HT} - (d + d_{HT}) A_T$ its solution is $A_T(\mathrm{t}) = e^{\int_0^t (d+d_{HT})d\tau}$ $\int_0^{\mathrm{t}} (\lambda_T I_H + \lambda_T A + \varphi I_{HT}) \, e^{-\int_0^t (d+d_{HT})d\tau} \mathrm{d}\tau > 0$ since those model parameters and exponential functions are positive.

Hence all the parameters and state variables are positive.

2.4 Boundedness of the Solution

Theorem 2: If $\Omega = \{(S, E_T, L_f, L_s, I_T, R, E_H, I_H, A, I_{HT}, A_T) \in \mathbb{R}_+^{11} : S(t) + E_T(t) + L_f(t) + L_s(t) + I_T(t) + R(t) + E_H(t) + I_H(t) + A(t) + I_{HT}(t) + A_T(t) = N(t)\}$ is the feasible region of dynamical system (1) – (11) then the solution of the dynamical system (1) – (11) $\left((S, E_T, L_f, L_s, I_T, R, E_H, I_H, A, I_{HT}, A_T) \in \Omega\right)$ for all $t \geq 0$.

Proof: The total population in our model is denoted by N and divided in to eleven sub-classes which are denoted by S , E_T , $L_f, L_s, I_T, R, E_H, I_H, A,$ $I_{HT},$ A_T. From this we have $N(t) = S(t) + E_T(t) + L_f(t) + L_s(t) + I_T(t) + R(t) + E_H(t) + I_H(t) + A(t) + I_{HT}(t) + A_T(t)$.

And thus $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE_T}{dt} + \frac{dL_f}{dt} + \frac{dL_s}{dt} + \frac{dI_T}{dt} + \frac{dR}{dt} + \frac{dE_H}{dt} + \frac{dI_H}{dt} + \frac{dA}{dt} + \frac{dI_{HT}}{dt} + \frac{dA_T}{dt}$

That is $\frac{dN}{dt} = \Lambda - dN - d_T I_T - d_H A - d_{HT} A_T < \Lambda - dN$. After some calculation we gate

$N(t) \leq \frac{1}{d}(\Lambda - e^{\frac{-1}{d}(t+c)})$, for any constant $c = -d \ln(\Lambda - \mathrm{d}N_0)$ at any initial point $N(0) = N_0 \Longrightarrow N(t) \leq \frac{\Lambda}{d}\left(1 - e^{\frac{-t}{d}}\right) + N_0 e^{\frac{-t}{d}}$. This shows that all solutions in Ω remain in Ω for all time $t \geq 0$.

2.5 Disease-Free Equilibrium

The disease-free equilibrium point is obtained by setting the right-hand sides of the dynamical system (1) – (11) equal to zero with assumption $I_T = I_H = I_{HT} = A_T = 0$ and obtained $E_{0TH} = (\frac{\Lambda}{d}, 0,0,0,0,0,0,0,0,0,0)$.

2.6 Basic Reproduction Number

The basic reproduction number R_0 is defined as the effective number of secondary infections produced by a single infectious individual introduced in a wholly susceptible population during his or her entire infectious period [3]. This definition is given for the models that represent spread of infection in a population. We calculate the basic reproduction number by using the next generation operator method on the dynamical system (1) – (11). In the dynamical system (1) – (11) the rate of appearance of new infections F and the transfer rate of individuals V at the disease-free steady state $E_{0TH} = (\frac{\Lambda}{d}, 0,0,0,0,0,0,0,0,0)$ is

$$F = \begin{pmatrix} 0 & 0 & \frac{\beta_1\Lambda}{Nd} & \frac{\beta_1\Lambda}{Nd} & 0 & 0 & \frac{\beta_1\Lambda}{Nd} & 0 & 0 & 0 \\ 0 & \frac{\beta_2\Lambda}{Nd} & \frac{\beta_2\Lambda}{dN} & \frac{\beta_2\Lambda}{Nd} & 0 & 0 & 0 & 0 & \frac{\beta_2\Lambda}{Nd} & \frac{\beta_2\Lambda}{Nd} \\ 0 & 0 & \frac{\beta_3\Lambda}{Nd} & \frac{\beta_3\Lambda}{Nd} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \omega + d & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \delta + d & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \varphi + d & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -\varphi & d + d_{HT} & 0 & 0 & 0 & 0 & 0 & 0 \\ -p\omega & 0 & 0 & 0 & \rho + \alpha + d & 0 & 0 & 0 & 0 & 0 \\ -(1-p)\omega & 0 & 0 & 0 & 0 & \varepsilon + \epsilon + d & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\alpha & -\epsilon & \pi + d + d_T & -\theta & 0 & 0 \\ 0 & 0 & 0 & 0 & -\rho & -\varepsilon & -\pi & (\theta + d) & 0 & 0 \\ 0 & -\delta & 0 & 0 & 0 & 0 & 0 & 0 & \mu + d & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\mu & d + d_H \end{pmatrix}$$

and

V^{-1}

$$= \begin{pmatrix} \frac{1}{\omega+d} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{1}{\delta+d} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \frac{1}{\varphi+d} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & a_{43} & \frac{1}{d+d_{HT}} & 0 & 0 & 0 & 0 & 0 & 0 \\ a_{51} & 0 & 0 & 0 & \frac{1}{\rho+\alpha+d} & 0 & 0 & 0 & 0 & 0 \\ a_{61} & 0 & 0 & 0 & 0 & \frac{1}{\varepsilon+\epsilon+d} & 0 & 0 & 0 & 0 \\ a_{71} & 0 & 0 & 0 & a_{75} & a_{76} & a_{77} & a_{78} & 0 & 0 \\ a_{81} & 0 & 0 & 0 & a_{85} & a_{86} & a_{87} & a_{88} & 0 & 0 \\ 0 & \frac{\delta}{(\delta+d)(\mu+d)} & 0 & 0 & 0 & 0 & 0 & 0 & \frac{1}{\mu+d} & 0 \\ 0 & a_{10\,2} & 0 & 0 & 0 & 0 & 0 & 0 & \frac{\mu}{(\mu+d)(d+d_H)} & \frac{1}{d+d_H} \end{pmatrix}$$

Where $a_{43} = \frac{\varphi}{(\varphi+d)(\ d+d_{HT})}$, $a_{51} = \frac{p\omega}{(\omega+d)(\rho+\alpha+d)}$, $a_{61} = \frac{(1-p)\omega}{(\omega+d)(\varepsilon+\epsilon+d)}$,

$a_{71} = \frac{p\omega(\varepsilon+\epsilon+d)[\alpha(\theta+d)+\rho\theta]+(1-p)\omega(\rho+\alpha+d)[\epsilon(\theta+d)+\theta\varepsilon]}{(\omega+d)(\rho+\alpha+d)(\varepsilon+\epsilon+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]}$,

$a_{81} = \frac{p\omega(\varepsilon+\epsilon+d)[\alpha\pi+\rho(\pi+d+d_T)]+(1-p)\omega(\rho+\alpha+d)[\epsilon\pi+\varepsilon(\pi+d+d_T)]}{(\omega+d)(\rho+\alpha+d)(\varepsilon+\epsilon+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]}$,

$a_{75} = \frac{\alpha(\theta+d)+\rho\theta}{(\rho+\alpha+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]}$, $a_{85} = \frac{\rho(\pi+d+d_T)+\alpha\pi}{(\rho+\alpha+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]}$,

$a_{76} = \frac{\epsilon(\theta+d)+\varepsilon\theta}{(\varepsilon+\epsilon+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]}$, $a_{77} = \frac{(\theta+d)}{(\pi+d+d_T)(\theta+d)-\pi\theta}$, $a_{86} = \frac{\epsilon\pi+\varepsilon(\pi+d+d_T)}{(\varepsilon+\epsilon+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]}$,

$a_{87} = \frac{\pi}{(\pi+d+d_T)(\theta+d)-\pi\theta}$, $a_{78} = \frac{\theta}{(\varepsilon+\epsilon+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]}$, $a_{88} = \frac{(\pi+d+d_T)}{(\pi+d+d_T)(\theta+d)-\theta\pi}$ and

$a_{10\,2} = \frac{\delta\mu}{(\delta+d)(\mu+d)(d+d_H)}$. Then

$$FV^{-1} = \begin{pmatrix} \frac{\beta_1\Lambda}{dN}a_{71} & 0 & \tau_4 & \frac{\beta_1\Lambda}{dN(d+d_{HT})} & \frac{\beta_1\Lambda}{dN}a_{75} & \frac{\beta_1\Lambda}{dN}a_{76} & \frac{\beta_1\Lambda}{dN}a_{77} & \frac{\beta_1\Lambda}{dN}a_{78} & 0 & 0 \\ 0 & \tau_1 & \tau_2 & \frac{\beta_2\Lambda}{dN(d+d_{HT})} & 0 & 0 & 0 & 0 & \tau_5 & \frac{\beta_2\Lambda}{dN(d+d_H)} \\ 0 & 0 & \tau_3 & \frac{\beta_3\Lambda\varphi}{dN(d+d_{HT})} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

where $\tau_1 = \frac{\beta_2\Lambda}{dN(\delta+d)} + \frac{\beta_2\Lambda\delta}{dN(\delta+d)(\mu+d)} + \frac{\beta_2\Lambda\delta\mu}{dN(\delta+d)(\mu+d)(d+d_H)}$, $\tau_2 = \frac{\beta_2\Lambda}{dN(\varphi+d)} + \frac{\beta_2\Lambda\varphi}{dN(\varphi+d)(d+d_{HT})}$, $\tau_3 = \frac{\beta_3\Lambda}{dN(\varphi+d)} + \frac{\beta_3\Lambda\varphi}{dN(\varphi+d)(d+d_{HT})}$, $\tau_4 = \frac{\beta_1\Lambda}{dN(\varphi+d)} + \frac{\beta_1\Lambda}{dN(\varphi+d)(d+d_{HT})}$ and $\tau_5 = \frac{\beta_2\Lambda}{dN(\mu+d)} + \frac{\beta_2\Lambda\mu}{dN(\mu+d)(d+d_H)}$.

From which, we obtain $FV^{-1}$and compute the reproduction numberof the dynamical system, as the spectral radius or the dominant Eigenvalue given by $\rho(FV^{-1}) = R_0 = max\{R_{0(TB)}, R_{0(HIV/AIDS)}, R_{0(HIV/AIDS-TB\ co-infection)}\}$, where, $R_{0(TB)} = \frac{p\omega\beta_1\Lambda(\varepsilon+\epsilon+d)[\alpha(\theta+d)+\rho\theta]+(1-p)\omega\beta_1\Lambda(\rho+\alpha+d)[\epsilon(\theta+d)+\theta\varepsilon]}{dN(\omega+d)(\rho+\alpha+d)(\varepsilon+\epsilon+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]}$, $R_{0(HIV/AIDS)} = \frac{\beta_2\Lambda}{dN(\delta+d)}\left(1 + \frac{\delta}{(\mu+d)} + \frac{\delta\mu}{(\mu+d)(d+d_H)}\right)$ and $R_{0(HIV/AIDS-TB\ co-infection)} = \frac{\beta_3\Lambda}{dN}\left(\frac{1}{\varphi+d} + \frac{\varphi}{(\varphi+d)(d+d_{HT})}\right)$. The threshold parameters $R_{0(TB)}, R_{0(HIV/AIDS)}$ and $R_{0(HIV/AIDS-TB\ co-infection)}$ are defined as the basic reproduction numbers due to TB, HIV/AIDS and HIV/AIDS-TB co-infection respectively.

2.7 Endemic Equilibrium Point

Endemic equilibrium point is steady-state solutions where the disease persists in the population and is obtained by setting the right hand side of the dynamical system (1) – (11) equal to zero. Thus we get the HIV/AIDS-TB co-infection endemic equilibrium point in terms of λ_T^*, λ_H^* and λ_{HT}^* are

$$E^{HT} = \left(\frac{\Lambda}{\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d}, \frac{\lambda_T^*\Lambda}{(\omega+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)}, \frac{\lambda_T^*\Lambda p\omega}{(\rho+\alpha+d)(\omega+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)}, \frac{\lambda_T^*\Lambda(1-p)\omega}{(\varepsilon+\epsilon+d)(\omega+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)},\right.$$
$$\frac{1}{(\pi+d+d_T)(\theta+d)-\theta\pi}\left[\frac{(\alpha(\theta+d)+\rho\theta)p\omega}{(\rho+\alpha+d)} + \frac{(\epsilon(\theta+d)+\theta\varepsilon)(1-p)\omega}{(\varepsilon+\epsilon+d)}\right]\frac{\lambda_T^*\Lambda}{(\omega+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)}, \frac{1}{(\theta+d)}\left[\frac{\rho p\omega}{(\rho+\alpha+d)} + \frac{\varepsilon(1-p)\omega}{(\varepsilon+\epsilon+d)} + \right.$$
$$\left.\left.\frac{\pi}{(\pi+d+d_T)(\theta+d)-\theta\pi}\left[\frac{(\alpha(\theta+d)+\rho\theta)p\omega}{(\rho+\alpha+d)} + \frac{(\epsilon(\theta+d)+\theta\varepsilon)(1-p)\omega}{(\varepsilon+\epsilon+d)}\right]\right]\frac{\lambda_T^*\Lambda}{(\omega+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)},\right.$$
$$\frac{\lambda_H^*\Lambda}{(\lambda_T^*+\delta+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)}, \frac{\lambda_H^*\Lambda\delta}{(\lambda_T^*+\mu+d)(\lambda_T^*+\delta+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)}, \frac{\lambda_H^*\Lambda\delta\mu}{(\lambda_T^*+d+d_H)(\lambda_T^*+\mu+d)(\lambda_T^*+\delta+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)},$$
$$\frac{1}{(\varphi+d)}\left(\frac{\lambda_{HT}^*\Lambda}{\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d} + \frac{\lambda_T^*\lambda_H^*\Lambda}{(\lambda_T^*+\delta+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)}\right), \frac{1}{(d+d_{HT})}\left(\frac{\lambda_T^*\lambda_H^*\Lambda\delta}{(\lambda_T^*+\mu+d)(\lambda_T^*+\delta+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)} + \right.$$
$$\left.\left.\frac{\lambda_T^*\lambda_H^*\Lambda\delta\mu}{(\lambda_T^*+d+d_H)(\lambda_T^*+\mu+d)(\lambda_T^*+\delta+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)} + \frac{\varphi}{(\varphi+d)}\left(\frac{\lambda_{HT}^*\Lambda}{\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d} + \frac{\lambda_T^*\lambda_H^*\Lambda}{(\lambda_T^*+\delta+d)(\lambda_T^*+\lambda_H^*+\lambda_{HT}^*+d)}\right)\right)\right)$$

To show the existence of the interior endemic equilibrium point we can use the normalization techniques by letting $s = \frac{S}{N}, e_T = \frac{E_T}{N}, l_f = \frac{L_f}{N}, l_s = \frac{L_s}{N}, i_T = \frac{I_T}{N}, r = \frac{R}{N}$, $e_H = \frac{E_H}{N}, i_H = \frac{I_H}{N}, a = \frac{A}{N}, i_{HT} = \frac{I_{HT}}{N}, a_T = \frac{A_T}{N}$, $\lambda_{T_*} = \beta_1(i_T + i_{HT} + a_T)$, $\lambda_{H_*} = \beta_2(e_H + i_H + a + i_{HT} + a_T)$, $\lambda_{(HT)_*} = \beta_3(i_{HT} + a_T)$, then the normalized system are

$$\frac{de_T}{dt} = \lambda_{T_*}(1 - g_4 - i_{HT} - a_T) - (\omega + d)e_T \quad (12)$$
$$\frac{dl_f}{dt} = p\omega e_T - (\rho + \alpha + d)l_f \quad (13)$$
$$\frac{dl_s}{dt} = (1-p)\omega e_T - (\varepsilon + \epsilon + d)l_s \quad (14)$$
$$\frac{di_T}{dt} = \alpha l_f + \epsilon l_s + \theta r - (\pi + d_T + d)I_T \quad (15)$$
$$\frac{dr}{dt} = \rho l_f + \varepsilon l_s + \pi i_T - (\theta + d)r \quad (16)$$

$$\frac{de_H}{dt} = \lambda_{H_*}(1 - g_4 - i_{HT} - a_T) - (\delta + \lambda_{T_*} + d)e_H \quad (17)$$

$$\frac{di_H}{dt} = \delta e_H - (\lambda_{T_*} + \mu + d)i_H \quad (18)$$

$$\frac{da}{dt} = \mu i_H - (\lambda_{T_*} + d_H + d)a \quad (19)$$

$$\frac{di_{HT}}{dt} = \lambda_{(HT)_*}(1 - g_4 - i_{HT} - a_T) + \lambda_{T_*}e_H - (\varphi + \mathrm{d})i_{HT} \quad (20)$$

$$\frac{da_T}{dt} = \lambda_{T_*}i_H + \lambda_{T_*}a + \varphi i_{HT} - (\mathrm{d} + d_{HT})a_T \quad (21)$$

With $\frac{dN}{dt} = \Lambda - \mathrm{d}N - d_T I_T - d_H A - d_{HT}A_T \Longrightarrow \frac{dN}{dt} = \frac{N}{N}\left(\frac{\Lambda}{N} - \mathrm{d}N - d_T I_T - d_H A - d_{HT}A_T\right)$

$\left(\frac{\Lambda}{N} - \mathrm{d} - d_T i_T - d_H a - d_{HT}a_T\right)N = 0.$

$\frac{\Lambda}{N} = \mathrm{d} + d_T i_T + d_H a + d_{HT}a_T$ and $s = 1 - \left(e_T + l_f + l_s + i_T + r + e_H + i_H + a\right) - i_{HT} - a_T.$

By equating equation (20) and (21) equals to zero and solving i_{HT}^* , we gate

From $\frac{di_{HT}}{dt} = \beta_3(i_{HT} + a_T)\left(\left(1 - e_T - l_f - l_s - i_T - r - e_H - i_H - a\right) - i_{HT} - a_T\right) + \beta_1(i_T + i_{HT} + a_T)e_H - (\varphi + \mathrm{d})i_{HT} = 0$

$((1 - g_4)\beta_3 + \beta_1 e_H - (\varphi + \mathrm{d}))\, i_{HT} - 2\beta_3 i_{HT}a_T + \left((1 - g_4)\beta_3 + \beta_1 e_H\right)a_T - \beta_3(i_{HT})^2 - \beta_3(a_T)^2 + \beta_1 e_H i_T = 0 \quad (22)$

From $\frac{da_T}{dt} = \lambda_{T_*}i_H + \lambda_{T_*}a + \varphi i_{HT} - (\mathrm{d} + d_{HT})a_T = 0$

$\beta_1 i_H i_T + \beta_1 i_H i_{HT} + \beta_1 i_H a_T + \beta_1 a i_T + \beta_1 a i_{HT} + \beta_1 a a_T + \varphi i_{HT} - (\mathrm{d} + d_{HT})a_T = 0$

$$\Rightarrow a_T = \frac{\beta_1 i_H i_T + \beta_1 a i_T + (\beta_1 i_H + \beta_1 a + \varphi)i_{HT}}{-\beta_1 i_H - \beta_1 a + (\mathrm{d} + d_{HT})} \quad (23)$$

Substitute (23) into (22) we gate

$((1 - g_4)\beta_3 + \beta_1 e_H - (\varphi + \mathrm{d}))\, i_{HT} - 2\beta_3 i_{HT}\frac{\beta_1 i_H i_T + \beta_1 a i_T + (\beta_1 i_H + \beta_1 a + \varphi)i_{HT}}{-\beta_1 i_H - \beta_1 a + (\mathrm{d} + d_{HT})} + \left(\left(1 - e_T - l_f - l_s - i_T - r - e_H - i_H - a\right)\beta_3 + \beta_1 e_H\right)\frac{\beta_1 i_H i_T + \beta_1 a i_T + (\beta_1 i_H + \beta_1 a + \varphi)i_{HT}}{-\beta_1 i_H - \beta_1 a + (\mathrm{d} + d_{HT})} - \beta_3(i_{HT})^2 - \beta_3\left(\frac{\beta_1 i_H i_T + \beta_1 a i_T + (\beta_1 i_H + \beta_1 a + \varphi)i_{HT}}{-\beta_1 i_H - \beta_1 a + (\mathrm{d} + d_{HT})}\right)^2 + \beta_1 e_H i_T = 0$

$g_3(i_{HT})^2 + g_1 i_{HT} + g_2 = 0$

$g_1 = -\Big(\left[\left((1 - g_4)\beta_3 + \beta_1 e_H\right)\left(\beta_1 i_H + \beta_1 a - (\mathrm{d} + d_{HT})\right) + 2\beta_3\beta_1(i_H i_T + a i_T)\right][\mathrm{d} + d_{HT} + \varphi] + (\varphi + \mathrm{d})\left(\beta_1 i_H + \beta_1 a - (\mathrm{d} + d_{HT})\right)^2\Big),$

$g_2 = -[(1-g_4)(i_H+a)\beta_3 + (\mathrm{d}+d_{HT})e_H]\big(\beta_1 i_H + \beta_1 a - (\mathrm{d}+d_{HT})\big)\beta_1 i_T - \beta_3(\beta_1 i_H i_T + \beta_1 a i_T)^2$, $g_3 = \beta_3\big(\beta_1 i_H + \beta_1 a - (\mathrm{d}+d_{HT})\big)[3\beta_1 i_H + 3\beta_1 a + 2\varphi - (\mathrm{d}+d_{HT})\,] - \beta_3(\beta_1 i_H + \beta_1 a + \varphi)^2$ and $g_4 = e_T + l_f + l_s + i_T + r + e_H + i_H + a$.

Then for the case $\frac{-g_1}{2g_3} > 0$, $(g_1)^2 - 4g_3g_2 = 0$, the unique interior endemic equilibrium point i_{HT} exists which is , $i^*_{HT} = \frac{[((1-g_4)\beta_3+\beta_1 e_H)(\beta_1 i_H+\beta_1 a-(\mathrm{d}+d_{HT}))+2\beta_3\beta_1(i_H i_T+a i_T)][\mathrm{d}+d_{HT}+\varphi]+(\varphi+\mathrm{d})(\beta_1 i_H+\beta_1 a-(\mathrm{d}+d_{HT}))^2}{2\beta_3((\beta_1 i_H+\beta_1 a)-(\mathrm{d}+d_{HT}))[(3\beta_1 i_H+3\beta_1 a+2\varphi)-(\mathrm{d}+d_{HT})\,]-2\beta_3(\beta_1 i_H+\beta_1 a+\varphi)^2}$, when $e_T > 0,\ l_f > 0,\ l_s > 0,\ i_T > 0, r > 0, e_H > 0, i_H > 0$ and $a > 0$, that is for the cases when $R_{0(TB)} > 1$, $R_{0(HIV/AIDS)} > 1$ and $R_{0(\mathrm{HIV/AIDS-TB}\ co-infection)} > 1$. An endemic equilibrium $i^*_{HT} > 0$ exists provided $R_0 > 1$, where R_0 is the number of secondary TB or HIV/AIDS or HIV/AIDS-TB co-infections due to a single TB or a single HIV/AIDS or HIV/AIDS-TB co-infective individual. The basic reproduction number R_0 is given by $R_0 = \max\{R_{0(T\boldsymbol{B})}, R_{0(HIV/AIDS)},\ R_{0(\mathrm{HIV/AIDS-TB}\ co-infection)}\}$.

2.8 Local Stability of the Disease Free Equilibrium

Theorem 3: The disease free equilibrium point $E_{0TH} = (\frac{\Lambda}{d}, 0,0,0,0,0,0,0,0,0)$ of the dynamical system (1) – (11) is locally asymptotically stable if $R_0 < 1$ whereas unstable.

Proof: The Jacobean matrix of the dynamical system (1) – (11) at the DFE point $E_{0TH} = (\frac{\Lambda}{d}, 0,0,0,0,0,0,0,0,0)$ is:

$$J(E_{0TH}) = \begin{pmatrix} -d & 0 & 0 & 0 & -\frac{\beta_1\Lambda}{dN} & 0 & -\frac{\beta_2\Lambda}{Nd} & -\frac{\beta_2\Lambda}{Nd} & -\frac{\beta_2\Lambda}{Nd} & \tau_6 & \tau_7 \\ 0 & -(\omega+d) & 0 & 0 & \frac{\beta_1\Lambda}{Nd} & 0 & 0 & 0 & 0 & \frac{\beta_1\Lambda}{Nd} & \frac{\beta_1\Lambda}{Nd} \\ 0 & p\omega & \tau_8 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & (1-p)\omega & 0 & \tau_9 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha & \epsilon & \tau_{10} & \theta & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \rho & \varepsilon & \pi & -(\theta+d) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \tau_{12} & \frac{\beta_2\Lambda}{Nd} & \frac{\beta_2\Lambda}{Nd} & \frac{\beta_2\Lambda}{Nd} & \frac{\beta_2\Lambda}{Nd} \\ 0 & 0 & 0 & 0 & 0 & 0 & \delta & -(\mu+d) & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \mu & -(d+d_H) & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \tau_{11} & \frac{\beta_3\Lambda}{Nd} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \varphi & -(d+d_{HT}) \end{pmatrix}$$

Where $\tau_6 = -(\frac{\beta_1}{N} + \frac{\beta_2}{N} + \frac{\beta_3}{N})\frac{\Lambda}{d}$, $\tau_7 = -(\frac{\beta_1}{N} + \frac{\beta_2}{N} + \frac{\beta_3}{N})\frac{\Lambda}{d}$, $\tau_8 = -(\rho+\alpha+d)$, $\tau_9 = -(\varepsilon+\epsilon+d)$, $\tau_{10} = -(\pi + d + d_T)$, $\tau_{11} = \frac{\beta_3\Lambda}{Nd} - (\varphi+d)$ and $\tau_{12} = \frac{\beta_2\Lambda}{dN} - (\delta+d)$

The corresponding characteristic equation of the above Jacobian matrix

$$\begin{vmatrix} -d-\lambda & 0 & 0 & 0 & -\frac{\beta_1\Lambda}{dN} & 0 & -\frac{\beta_2\Lambda}{Nd} & -\frac{\beta_2\Lambda}{Nd} & -\frac{\beta_2\Lambda}{Nd} & \tau_6 & \tau_7 \\ 0 & -(\omega+d)-\lambda & 0 & 0 & \frac{\beta_1\Lambda}{Nd} & 0 & 0 & 0 & 0 & \frac{\beta_1\Lambda}{Nd} & \frac{\beta_1\Lambda}{Nd} \\ 0 & p\omega & \tau_8-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & (1-p)\omega & 0 & \tau_9-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha & \epsilon & \tau_{10}-\lambda & \theta & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \rho & \varepsilon & \pi & -(\theta+d)-\lambda & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \tau_{12}-\lambda & \frac{\beta_2\Lambda}{Nd} & \frac{\beta_2\Lambda}{Nd} & \frac{\beta_2\Lambda}{Nd} & \frac{\beta_2\Lambda}{Nd} \\ 0 & 0 & 0 & 0 & 0 & 0 & \delta & \tau_{13} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \mu & \tau_{14} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \tau_{11}-\lambda & \frac{\beta_3\Lambda}{Nd} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \varphi & \tau_{15} \end{vmatrix} =$$

0 , where $\tau_{13} = -(\mu+d)-\lambda\ \tau_{14} = -(d+d_H)-\lambda$ and $\tau_{15} = -(d+d_{HT})-\lambda$

After some calculations and using Routh Hurwitz stability criteria we get all the root of the characteristics equation are negative if $R_0 < 1$ and some of the eigenvalues are positive if $R_0 > 1$. Therefore the disease free equilibrium point of the dynamical system (1) – (11) is stable if $R_0 < 1$ and unstable if $R_0 > 1$.

2.9 Global Stability of the Disease Free Equilibrium

Theorem 4: If the disease-free equilibrium point $E_{0TH} = \left(\frac{\Lambda}{d}, 0,0,0,0,0,0,0,0,0\right)$ of the dynamical system (1) – (11) is globally asymptotically stable when

$$\left\{\begin{matrix}\left(1-\frac{\mathrm{S}(0)}{S}\right)\Lambda + \frac{p\omega}{(\omega+d)}\lambda_T S + \frac{\alpha p\omega}{(\rho+\alpha+d)}E_T + \frac{\epsilon(1-p)\omega}{(\varepsilon+\epsilon+d)}E_T + \frac{\pi}{(\pi+d+d_T)}\left(\alpha L_f + \epsilon L_s + \theta R\right) + \frac{\theta}{(\theta+d)}\left(\rho L_f + \varepsilon L_s + \pi I_T\right) + \\ \frac{\delta}{(\delta+d)}\lambda_H S + \frac{\mu\delta}{(\mu+d)}E_H + \frac{\mu}{(d+d_H)}I_H + \frac{\varphi\lambda_{HT}}{(\varphi+d)}S + \frac{\varphi\lambda_T}{(\varphi+d)}E_H + \frac{\lambda_T}{(d+d_{HT})}I_H + \frac{\lambda_T}{(d+d_{HT})}A + \frac{\varphi}{(d+d_{HT})}I_{HT}\end{matrix}\right\}$$

$$< \left\{\begin{matrix}\left(1-\frac{\mathrm{S}(0)}{S}\right)(\lambda_T + \lambda_H + \lambda_{HT} + d)S + p\omega E_T + \alpha L_f + \epsilon L_s + \pi I_T + \theta R + \\ \frac{\delta\lambda_T}{(\delta+d)}E_H + \delta E_H + \frac{\mu\lambda_T}{(\mu+d)}I_H + \mu I_H + \frac{\lambda_T}{(d+d_H)}A + A + \varphi I_{HT} + A_T\end{matrix}\right\}$$

Proof: We define the Lyapunov function $V: R_+^{11} \to R_+$ by:

$$L = \left\{\begin{matrix}u_1\left(S - \mathrm{S}(0) - \mathrm{S}(0)\ln\frac{\mathrm{S}}{\mathrm{S}(0)}\right) + u_2\frac{p\omega}{(\omega+d)}E_T + u_3\frac{\alpha}{(\rho+\alpha+d)}L_f + u_4\frac{\epsilon}{(\varepsilon+\epsilon+d)}L_s + u_5\frac{\pi}{(\pi+d+d_T)}I_T + \\ u_6\frac{\theta}{(\theta+d)}R + u_7\frac{\delta}{(\delta+d)}E_H + u_8\frac{\mu}{(\mu+d)}I_H + u_9\frac{1}{(d+d_H)}A + u_{10}\frac{\varphi}{(\varphi+d)}I_{HT} + u_{11}\frac{1}{(d+d_{HT})}A_T\end{matrix}\right\}$$

Thus we get L is continuous function for all $\left(S, E_T, L_f, L_s, I_T, R, E_H, I_H, A, I_{HT}, A_T\right) \in \Re_+^{11}$ and has 1st order partial derivatives and L has minimum at E_0 , finally we calculate the time derivative of $L\left(S, E_T, L_f, L_s, I_T, R, E_H, I_H, A, I_{HT}, A_T\right)$ along the solution path yields

$$\frac{dL}{dt} = \left\{\begin{matrix}u_1\left(\frac{dS}{dt} - \frac{\mathrm{S}(0)}{S}\frac{dS}{dt}\right) + u_2\frac{p\omega}{(\omega+d)}\frac{dE_T}{dt} + u_3\frac{\alpha}{(\rho+\alpha+d)}\frac{dL_f}{dt} + u_4\frac{\epsilon}{(\varepsilon+\epsilon+d)}\frac{dL_s}{dt} + u_5\frac{\pi}{(\pi+d+d_T)}\frac{dI_T}{dt} + \\ u_6\frac{\theta}{(\theta+d)}\frac{dR}{dt} + u_7\frac{\delta}{(\delta+d)}\frac{dE_H}{dt} + u_8\frac{\mu}{(\mu+d)}\frac{dI_H}{dt} + u_9\frac{1}{(d+d_H)}\frac{dA}{dt} + u_{10}\frac{\varphi}{(\varphi+d)}\frac{dI_{HT}}{dt} + u_{11}\frac{1}{(d+d_{HT})}\frac{dA_T}{dt}\end{matrix}\right\}$$

After some calculation we gate $\frac{dL}{dt} = L_1 - L_2$ where

$$L_1 = \left\{\begin{array}{c}\left(1-\frac{S(0)}{S}\right)\Lambda+\frac{p\omega}{(\omega+d)}\lambda_T S+\frac{\alpha p\omega}{(\rho+\alpha+d)}E_T+\frac{\epsilon(1-p)\omega}{(\varepsilon+\epsilon+d)}E_T+\frac{\pi}{(\pi+d+d_T)}\left(\alpha L_f+\epsilon L_s+\theta R\right)+\frac{\theta}{(\theta+d)}\left(\rho L_f+\varepsilon L_s+\pi I_T\right)+\\ \frac{\delta}{(\delta+d)}\lambda_H S+\frac{\mu\delta}{(\mu+d)}E_H+\frac{\mu}{(d+d_H)}I_H+\frac{\varphi\lambda_{HT}}{(\varphi+d)}S+\frac{\varphi\lambda_T}{(\varphi+d)}E_H+\frac{\lambda_T}{(d+d_{HT})}I_H+\frac{\lambda_T}{(d+d_{HT})}A+\frac{\varphi}{(d+d_{HT})}I_{HT}\end{array}\right\} >$$

0 and $L_2 = \left\{\begin{array}{c}\left(1-\frac{S(0)}{S}\right)(\lambda_T+\lambda_H+\lambda_{HT}+d)S+p\omega E_T+\alpha L_f+\epsilon L_s+\pi I_T+\theta R+\\ \frac{\delta\lambda_T}{(\delta+d)}E_H+\delta E_H+\frac{\mu\lambda_T}{(\mu+d)}I_H+\mu I_H+\frac{\lambda_T}{(d+d_H)}A+A+\varphi I_{HT}+A_T\end{array}\right\} > 0.$

Therefore we conclude that if $L_1 < L_2$ then, $\frac{dL}{dt} < 0$ which implies the diseases free equilibrium point of the dynamical system (1) – (11) is globally asymptotically stable.

2.10 Local Stability of the HIV/AIDS-TB co-infection Equilibrium Point

Theorem 5: If the HIV/AIDS-TB coinfection endemic equilibrium point E^{TH} of the dynamical system (1) – (11) is locally asymptotically stable then $R_0 > 1$.

Proof: The Jacobean matrix of the dynamical system (1) – (11) at the HIV/AIDS-TB coinfection equilibrium point E^{TH} is

$$J(E^{TH}) = \begin{pmatrix} -(\lambda_H^*+d) & 0 & 0 & 0 & -d_1 & 0 & -d_2 & -d_2 & -d_2 & -d_5 & -d_5 \\ \lambda_T^* & -b_1 & 0 & 0 & d_1 & 0 & 0 & 0 & 0 & d_1 & d_1 \\ 0 & p\omega & -b_2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & (1-p)\omega & 0 & -b_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha & \epsilon & -b_4 & \theta & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \rho & \varepsilon & \pi & -b_5 & 0 & 0 & 0 & 0 & 0 \\ \lambda_H^* & 0 & 0 & 0 & -e_1 & 0 & d_2-f_1 & d_3 & d_4 & d_3-f_5 & d_4 \\ 0 & 0 & 0 & 0 & -e_2 & 0 & \delta & -f_2 & 0 & -e_2 & -f_5 \\ 0 & 0 & 0 & 0 & -e_3 & 0 & 0 & \mu & -f_3 & -e_3 & -e_3 \\ \lambda_{HT}^* & 0 & 0 & 0 & e_1 & 0 & \lambda_T & 0 & 0 & b_8-d_7 & b_8 \\ 0 & 0 & 0 & 0 & f_4 & 0 & 0 & \lambda_T & \lambda_T & f_4+\varphi & f_4-b_9 \end{pmatrix}$$

Where $d_1 = \frac{\beta_1}{N}S^*,\ d_2 = \frac{\beta_2}{N}S^*,\ d_5 = \left(\frac{\beta_1}{N}+\frac{\beta_2}{N}+\frac{\beta_3}{N}\right)S^*, f_1 = \lambda_T+\delta+d,\ d_7 = \varphi+d,\ b_1 = \omega+d,\ b_2 = \rho+\alpha+d,\ b_3 = \varepsilon+\epsilon+d,\ b_4 = \pi+d+d_T,\ b_5 = \theta+d,\ f_2 = \lambda_T+\mu+d,\ f_3 = \lambda_T+d+d_H,\ b_8 = \frac{\beta_3}{N}S^*, f_4 = (I_H^*+A^*)\frac{\beta_1}{N}, f_5 = \frac{\beta_1}{N}I_H^*, e_1 = \frac{\beta_1}{N}E_H^*, e_2 = \frac{\beta_1}{N}I_H^*, e_3 = \frac{\beta_1}{N}A^*$ and $b_9 = (d+d_{HT})$ are positive parameter.

The corresponding characteristic equation of the above Jacobian matrix

$$\begin{vmatrix} \tau_{16} & 0 & 0 & 0 & -d_1 & 0 & -d_2 & -d_2 & -d_2 & -d_5 & -d_5 \\ \lambda_T^* & -b_1-\lambda & 0 & 0 & d_1 & 0 & 0 & 0 & 0 & d_1 & d_1 \\ 0 & p\omega & -b_2-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & (1-p)\omega & 0 & -b_3-\lambda & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha & \epsilon & -b_4-\lambda & \theta & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \rho & \varepsilon & \pi & -b_5-\lambda & 0 & 0 & 0 & 0 & 0 \\ \lambda_H^* & 0 & 0 & 0 & -e_1 & 0 & \tau_{17} & d_3 & d_4 & d_3-f_5 & d_4 \\ 0 & 0 & 0 & 0 & -e_2 & 0 & \delta & -f_2-\lambda & 0 & -e_2 & -f_5 \\ 0 & 0 & 0 & 0 & -e_3 & 0 & 0 & \mu & -f_3-\lambda & -e_3 & -e_3 \\ \lambda_{HT}^* & 0 & 0 & 0 & e_1 & 0 & \lambda_T & 0 & 0 & \tau_{18} & b_8 \\ 0 & 0 & 0 & 0 & f_4 & 0 & 0 & \lambda_T & \lambda_T & f_4+\varphi & \tau_{19} \end{vmatrix} = 0$$

Where $\tau_{16} = -(\lambda_H^* + d) - \lambda\ \tau_{17} = d_2 - f_1 - \lambda$, $\tau_{18} = b_8 - d_7 - \lambda$ and $\tau_{19} = f_4 - b_9 - \lambda$

After some calculations and using Routh Hurwitz stability criteria we get all the root of the characteristics equation are negative if $R_0 > 1$. Therefore the HIV/AIDS-TB co-infection endemic equilibrium point of the dynamical system (1) – (11) is stable if $R_0 > 1$.

2.11 Global Stability analysis of Interior Equilibrium Point

Theorem 6: The HIV/AIDS-TB co-infection endemic equilibrium point E^{TH} of the dynamical system (1) – (11) is globally asymptotically stable

$$\text{if} \left\{ \begin{array}{c} \left(1-\frac{S^*}{S}\right)\Lambda + \left(1-\frac{{E_T}^*}{E_T}\right)\lambda_T S + \left(1-\frac{{L_f}^*}{L_f}\right)p\omega E_T + \left(1-\frac{{L_s}^*}{L_s}\right)(1-p)\omega E_T + \\ \left(1-\frac{{I_T}^*}{I_T}\right)(\alpha L_f + \epsilon L_s + \theta R) + \left(1-\frac{R^*}{R}\right)(\rho L_f + \varepsilon L_s + \pi I_T) + \left(1-\frac{{E_H}^*}{E_H}\right)\lambda_H S + \\ \left(1-\frac{I_H^*}{I_H}\right)\delta E_H + \left(1-\frac{A^*}{A}\right)\mu I_H + \left(1-\frac{I_{HT}^*}{I_{HT}}\right)[\lambda_{HT} S + \lambda_T E_H] + \left(1-\frac{{A^*}_T}{A_T}\right)[\lambda_T I_H + \lambda_T A + \varphi I_{HT}] \end{array} \right\} <$$

$$\left\{ \begin{array}{c} \left(1-\frac{S^*}{S}\right)[(\lambda_T + \lambda_H + \lambda_{HT})S + dS] + \left(1-\frac{{E_T}^*}{E_T}\right)(\omega + d)E_T + \left(1-\frac{{L_f}^*}{L_f}\right)(\rho + \alpha + d)L_f + \\ \left(1-\frac{{L_s}^*}{L_s}\right)(\varepsilon + \epsilon + d)L_s + \left(1-\frac{{I_T}^*}{I_T}\right)(\pi + d + d_T)I_T + \left(1-\frac{R^*}{R}\right)(\theta + d)R + \\ \left(1-\frac{{E_H}^*}{E_H}\right)[\lambda_T E_H - (\delta + d)E_H] + \left(1-\frac{{I_H}^*}{I_H}\right)[\lambda_T I_H + (\mu + d)I_H] + \\ \left(1-\frac{A^*}{A}\right)[\lambda_T A + (d + d_H)A] + \left(1-\frac{I_{HT}^*}{I_{HT}}\right)(\varphi + d)I_{HT} + \left(1-\frac{{A^*}_T}{A_T}\right)(d + d_{HT})A_T \end{array} \right\}$$

Proof: We define the Lyapunov function $L: R_+^{11} \to R_+$

$$L(E^{TH}) = \left\{ \begin{array}{c} u_1\left(S - S^* - S^* \ln\left(\frac{S}{S^*}\right)\right) + u_2\left(E_T - {E_T}^* - {E_T}^* \ln\left(\frac{E_T}{{E_T}^*}\right)\right) + u_3\left(L_f - {L_f}^* - {L_f}^* \ln\left(\frac{L_f}{{L_f}^*}\right)\right) + \\ u_4\left(L_s - {L_s}^* - {L_s}^* \ln\left(\frac{L_s}{{L_s}^*}\right)\right) + u_5\left(I_T - {I_T}^* - {I_T}^* \ln\left(\frac{I_T}{{I_T}^*}\right)\right) + u_6\left(R - R^* - R^* \ln\left(\frac{R}{R^*}\right)\right) + \\ u_7\left(E_H - {E_H}^* - {E_H}^* \ln\left(\frac{E_H}{{E_H}^*}\right)\right) + u_8\left(I_H - {I_H}^* - {I_H}^* \ln\left(\frac{I_H}{{I_H}^*}\right)\right) + u_9\left(A - A^* - A^* \ln\left(\frac{A}{A^*}\right)\right) + \\ u_{10}\left(I_{HT} - I_{HT}^* - I_{HT}^* \ln\left(\frac{I_{HT}}{I_{HT}^*}\right)\right) + u_{11}\left(A_T - {A^*}_T - {A^*}_T \ln\left(\frac{A_T}{{A^*}_T}\right)\right) \end{array} \right\}$$

Thus we get L is continuous function for all $E^{TH} \in \Re_+^{11}$ and has 1st order partial derivatives and L has minimum

at E^{TH}, finally we calculate the time derivative of $L(E^{TH})$ along the solution path yields $\frac{dL}{dt} = L_3 - \mathrm{L}_4$

Where

$$L_3 = \left\{ \begin{array}{c} \left(1-\frac{\mathrm{S}^*}{S}\right)\Lambda + \left(1-\frac{{E_T}^*}{E_T}\right)\lambda_T S + \left(1-\frac{{L_f}^*}{L_f}\right)p\omega E_T + \left(1-\frac{{L_S}^*}{L_s}\right)(1-p)\omega E_T + \\ \left(1-\frac{{I_T}^*}{I_T}\right)(\alpha L_f + \epsilon L_s + \theta R) + \left(1-\frac{R^*}{R}\right)(\rho L_f + \varepsilon L_s + \pi I_T) + \left(1-\frac{{E_H}^*}{E_H}\right)\lambda_H S + \\ \left(1-\frac{{I_H}^*}{I_H}\right)\delta E_H + \left(1-\frac{A^*}{A}\right)\mu I_H + \left(1-\frac{\mathrm{I}^*_{HT}}{I_{HT}}\right)[\lambda_{HT} S + \lambda_T E_H] + \left(1-\frac{{A^*}_T}{A_T}\right)[\lambda_T I_H + \lambda_T A + \varphi I_{HT}] \end{array} \right\} > 0 \quad ,$$

and so

$$L_4 = \left\{ \begin{array}{c} \left(1-\frac{\mathrm{S}^*}{S}\right)[(\lambda_T + \lambda_H + \lambda_{HT})S + dS] + \left(1-\frac{{E_T}^*}{E_T}\right)(\omega + d)E_T + \left(1-\frac{{L_f}^*}{L_f}\right)(\rho + \alpha + d)L_f + \\ \left(1-\frac{{L_s}^*}{L_s}\right)(\varepsilon + \epsilon + d)L_s + \left(1-\frac{{I_T}^*}{I_T}\right)(\pi + d + d_T)I_T + \left(1-\frac{R^*}{R}\right)(\theta + d)R + \\ \left(1-\frac{{E_H}^*}{E_H}\right)[\lambda_T E_H - (\delta + d)E_H] + \left(1-\frac{{I_H}^*}{I_H}\right)[\lambda_T I_H + (\mu + d)I_H] + \\ \left(1-\frac{A^*}{A}\right)[\lambda_T A + (d + d_H)A] + \left(1-\frac{\mathrm{I}^*_{HT}}{I_{HT}}\right)(\varphi + d)I_{HT} + \left(1-\frac{{A^*}_T}{A_T}\right)(d + d_{HT})A_T \end{array} \right\} > 0$$

Therefore we conclude that if $L_3 < L_4$ then, $\frac{dL(\mathrm{E}^{TH})}{dt} < 0$ which implies the HIV/AIDS-TB co-infection endemic equilibrium point is globally asymptotically stable.

3. Parameter Estimation

In this section we give numerical simulation for the dynamical system (1) – (11) for the purpose of verifying the analytical results. This is done by using a set of parameter values whose sources are obtained from WHO, CDC and Minister of health of Ethiopia

Parameter Estimation for Numerical Simulation

To perform numerical simulation and sensitivity analysis we collect the following parameter values obtained from different sources.

Estimation of basic reproduction number R_0

$R_{0(TB)} = \frac{p\omega\beta_1\Lambda(\varepsilon+\epsilon+d)[\alpha(\theta+d)+\rho\theta]+(1-p)\omega\beta_1\Lambda(\rho+\alpha+d)[\epsilon(\theta+d)+\theta\varepsilon]}{dN(\omega+d)(\rho+\alpha+d)(\varepsilon+\epsilon+d)[(\pi+d+d_T)(\theta+d)-\theta\pi]} = 0.00012441,$

$R_{0(HIV/AIDS)} = \frac{\beta_2\Lambda}{dN(\delta+d)}\left(1+\frac{\delta}{(\mu+d)}+\frac{\delta\mu}{(\mu+d)(d+d_H)}\right) = 11.1847$ and

$R_{0(\mathrm{HIV/AIDS-TB}\ co-infection)} = \frac{\beta_3\Lambda}{dN}\left(\frac{1}{\varphi+d}+\frac{\varphi}{(\varphi+d)(d+d_{HT})}\right) = 34.8648$

From this value of basic reproduction number $R_{0(TB)} = 0.00012441 < 1, R_{0(HIV/AIDS)} = 11.1847 > 1$ and

$R_{0(\text{HIV/AIDS}-\text{TB } co-infection)} = 34.86475 > 1$ which implies that the individuals infected by HIV/AIDS-TB co-infection disease are increased in the community and HIV/AIDS-TB co-infection is influenced the HIV/AIDS dynamics than TB dynamics.

Table 1: Parameter estimation

Parameter	Symbol	Value	Source
recruitment of individuals to the susceptible class	Λ	3013010	Calculated
Transmission coefficients for TB	β_1	0.00151	[5]
Transmission coefficients for HIV	β_2	0.24	[5]
Transmission coefficients for HIV-TB	β_3	0.74	[22]
progress rate from HIV-exposed to the HIV-infected class	δ	0.021978	Calculated
progress rate from HIV-infected to the HIV-infected with AIDS stage	μ	0.62097	[6]&[8]
progression rate from exposed to latent infection	ω	0.0238095	Calculated
Probability of progression rate from exposed to fast latent infection	$p\omega$	0.02142855	Calculated
Probability of progression rate from exposed to slow latent infection	$(1-p)\omega$	0.00238095	Calculated
Linear recovery rate from fast latent to recovered by post exposer vaccination	ρ	0.99474	Calculated
Linear recovery rate from slow latent to recovered by post exposer vaccination	ε	0.000365297	Calculated
Infectious rate from fast latent to infection	α	0.0052632	Calculated
Infectious rate from slow latent to infection	ϵ	0.9996347	Calculated
Treatment rate from infectious to recovered	π	0.96	[5]
progress rate from HIV-infected co-infected with active TB to the HIV-infected with AIDS stage co-infected with active TB	φ	0.88	[5]
recurrence rate from recovered TB to infectious TB	θ	0.000014	[5]
Natural death rate	d	0.077	[7]
TB induced death rate	d_T	0.00024	[6]
HIV/AIDS induced death rate	d_H	0.015942	[8]
HIV-TB induced death rate	d_{HT}	0.002	[5]
The parameter	K	2041.94	Calculated

4. Numerical Analysis

The numerical analysis is obtained from the graphs of basic reproduction number with respect to the parameters obtained and given in Table-1. Transmission coefficients for HIV/AIDS-TB co-infection β_3

Case 1: Graphical representation of the basic reproduction number $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)}$ versus transmission coefficients for HIV/AIDS-TB co-infection β_3 and keeping other parameters constant, $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)}(\beta_3) = 47.114523568 * \beta_3$

Case 2: Graphical representation of the basic reproduction number $R_{0(HIV/AIDS)}$ versus transmission coefficients for HIV/AIDS-TB co-infection β_3 and keeping other parameters constant, $R_{0(HIV/AIDS)} = 15.56671\beta_3$

For these two cases (1 and 2) the graphical representation of the basic reproduction number in $(R_{0(\text{HIV/AIDS-TB } co-infection)}, \beta_3)$ and $(R_{0(HIV/AIDS)}, \beta_3)$, -plans shown below in figure-2 and figure-3 respectively.

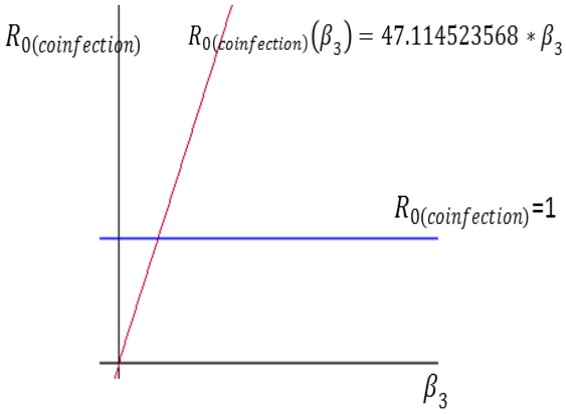

Figure 2: Basic reproduction number $R_{0(\text{HIV/AIDS-TB } co-infection)}$ versus Transmission coefficients for HIV/AIDS-TB co-infection β_3

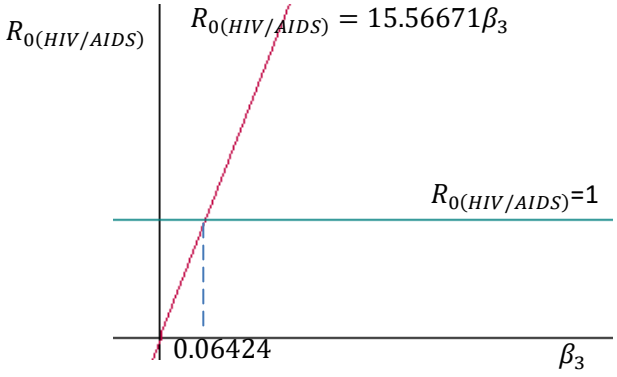

Figure 3: Basic reproduction number $R_{0(HIV/AIDS)}$ versus Transmission coefficients for HIV/AIDS-TB co-infection β_3

Figure-2 shows that the basic reproduction number $R_{0(\text{HIV/AIDS-TB } co-infection)} < 1$ when $\beta_3 < 0.0212249$ and $R_{0(\text{HIV/AIDS-TB } co-infection)} > 1$ when $\beta_3 > 0.0212249$ and figure-3 shows that the basic reproduction number $R_{0(HIV/AIDS)} < 1$ when $\beta_3 < 0.06424$ and $R_{0(HIV/AIDS)} > 1$ when $\beta_3 > 0.06424$

Case 3: Graphical representation of the basic reproduction number $R_{0(TB)}$ versus transmission coefficients for HIV/AIDS-TB co-infection β_3 and keeping other parameters constant, $R_{0(TB)} = 0.000168117\beta_3$

Case4: Graphical representation of the basic reproduction number $R_{0(\text{HIV/AIDS-TB } coinfection)}$ versus Progress rate from individuals infected both HIV and TB to individuals infected both HIV with AIDS who are taking Antiretroviral treatment and active TB φ and keeping other parameters constant,

$$R_{0(\text{HIV/AIDS-TB } co-infection)} = 0.274857090678\left(\frac{1}{0.077+\varphi} + \frac{\varphi}{(0.077+\varphi)(0.079)}\right)$$

For these two cases (3 and 4) the graphical representation of the basic reproduction number in $(R_{0(TB)}, \beta_3)$ and $(R_{0(\text{HIV/AIDS-TB } co-infection)}, \varphi)$, -plans shown below in figure-4 and figure-5 respectively.

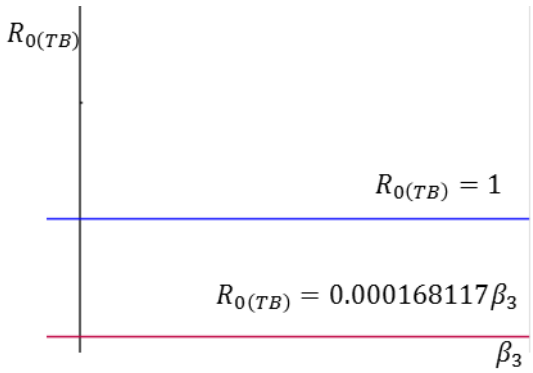

Figure 4: Basic reproduction number $R_{0(TB)}$versus Transmission coefficients for HIV/AIDS-TB co-infection β_3

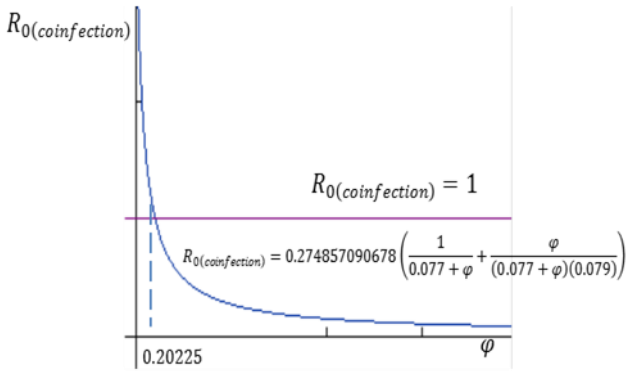

Figure 5: Basic reproduction number $R_{0(\text{HIV/AIDS−TB } co-infection)}$versus progress rate φ

Figure-4 shows that the basic reproduction number $R_{0(TB)} < 1$ for any value of β_3 and Figure-5 shows that the basic reproduction number $R_{0(\text{HIV/AIDS−TB } co-infection)} < 1$ when $\varphi > 0.20225$ and $R_{0(\text{HIV/AIDS−TB } co-infection)} > 1$ when $\varphi < 0.20225$

Case-5: Graphical representation of the basic reproduction number $R_{0(\text{HIV/AIDS−TB } co-infection)}$ versus natural death rate d and keeping other parameters constant,

$$R_{0(\text{HIV/AIDS−TB } co-infection)} = \frac{2229627.4}{d*105350020}\left(\frac{1}{d+0.88}+\frac{0.88}{(0.88+d)(0.002+d)}\right)$$

Case-6: Graphical representation of the basic reproduction number $R_{0(\text{HIV/AIDS−TB } co-infection)}$ versus HIV/AIDS-TB co-infection induced death rate d_{HT} and keeping other parameters constant, $R_{0(\text{HIV/AIDS−TB } co-infection)} = 0.27485709068\left(1.1363636364+\frac{0.9195402299}{(0.077+d_{HT})}\right)$

For these two cases (5 and 6) the graphical representation of the basic reproduction number in $\left(R_{0(\text{HIV/AIDS−TB } co-infection)}, d\right)$ and $\left(R_{0(\text{HIV/AIDS−TB } co-infection)}, d_{HT}\right)$, -plans shown below in figure-6 and figure-7 respectively.

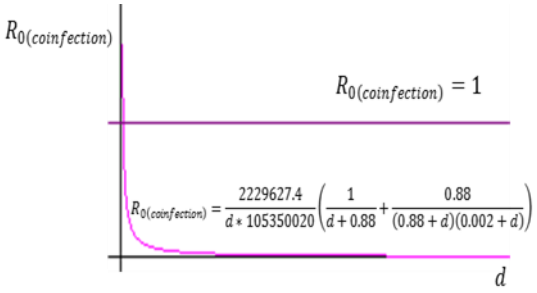

Figure 6: Basic reproduction number $R_{0(\text{HIV/AIDS-TB } co-infection)}$ versus natural death rate d

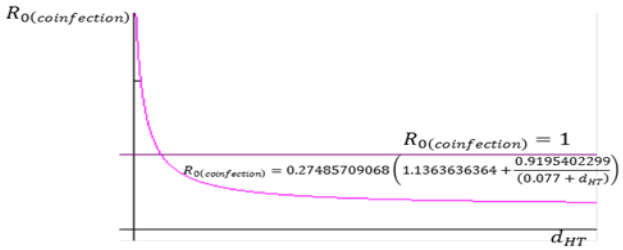

Figure 7: Basic reproduction number $R_{0(\text{HIV/AIDS-TB } co-infection)}$ versus HIV/AIDS-TB co-infection induced death rate d_{HT}

5. Sensitivity Analysis

To determine how best we can do in order to reduce human mortality and morbidity due to HIV/AIDS-TB co-infection, it is necessary to know the relative importance of different factors responsible for its transmission and prevalence. Sensitivity indices allow us to measure the relative change in a state variable when a parameter changes.

Definition: The normalized forward sensitivity index of a variable, u, that depends differentially on a parameter, p is defined as:

$\psi_p^u = \frac{p}{u} x \frac{\partial u}{\partial p}$. From the analysis in the previous section, we can see that the basic reproductive number $R_{0(\text{HIV/AIDS-TB } co-infection)}$ plays an important role in predicting HIV/AIDS-TB co-infection transmission and it prevalence. Therefore, we perform a sensitivity analysis to determine how $R_{0(\text{HIV/AIDS-TB } co-infection)}$ varies due to the uncertainty in the estimation of parameters used in the dynamical system. Since we have calculated a formula for $R_{0(\text{HIV/AIDS-TB } co-infection)}$, we now derive an analytical expression for the sensitivity of $R_{0(\text{HIV/AIDS-TB } co-infection)}$ to each of the parameters using

$$\boldsymbol{\psi}_{\boldsymbol{q}}^{R_{0(\text{HIV/AIDS-TB } coinfection)}} = \frac{\boldsymbol{q}}{R_{0(\text{HIV/AIDS-TB } co-infection)}} \boldsymbol{x} \frac{\boldsymbol{\partial}\, R_{0(\text{HIV/AIDS-TB } coinfection)}}{\boldsymbol{\partial q}}$$

If the result is negative, than the relationship between the parameters and $R_{0(\text{HIV/AIDS-TB } co-infection)}$ is

inversely proportional that is negative sensitivity index having larger modulus corresponds with small $R_{0(\text{HIV/AIDS–TB } co-infection)}$. On the one hand, a positive sensitivity index means that an increase in the value of a parameter would increase $R_{0(\text{HIV/AIDS–TB } co-infection)}$. So the sensitivity indexes of the HIV/AIDS-TB co-infection reproduction number $R_{0(\text{HIV/AIDS–TB } co-infection)} = \frac{\beta_3 \Lambda}{dN}\left(\frac{1}{\varphi+d} + \frac{\varphi}{(\varphi+d)(d+d_{HT})}\right)$ are

1. $\psi_{\beta_3}^{R_{0(\text{HIV/AIDS–TB } co-infection)}} = \frac{\beta_3}{R_{0(\text{HIV/AIDS–TB } co-infection)}} x \frac{\Lambda}{dN}\left(\frac{1}{\varphi+d} + \frac{\varphi}{(\varphi+d)(d+d_{HT})}\right) = 0.26923237$
2. $\psi_{\varphi}^{R_{0(\text{HIV/AIDS–TB } co-infection)}} = \frac{\varphi}{R_{0(\text{HIV/AIDS–TB } co-infection)}} x \frac{\beta_3 \Lambda}{dN}\left(\frac{-d}{(\varphi+d)^2} + \frac{(\varphi+d)(d+d_{HT}) - \varphi(d+d_{HT})}{((\varphi+d)(d+d_{HT}))^2}\right) = 0.018307$
3. $\psi_{d}^{R_{0(\text{HIV/AIDS–TB } co-infection)}} = \frac{d}{R_{0(\text{HIV/AIDS–TB } co-infection)}} x \frac{\beta_3 \Lambda}{dN}\left(-\frac{(d\varphi+d^2)}{(\varphi+d)^2} - \frac{\varphi\left((\varphi+d)(d^2+dd_{HT})+(d\varphi+d^2)(d+d_{HT})\right)}{\left((\varphi+d)(d^2+dd_{HT})\right)^2}\right) = -0.49422156$
4. $\psi_{d_{HT}}^{R_{0(\text{HIV/AIDS–TB } co-infection)}} = \frac{d_{HT}}{R_{0(\text{HIV/AIDS–TB } co-infection)}} x \frac{-\beta_3 \Lambda \varphi(\varphi+d)}{dN\left((\varphi+d)(d+d_{HT})\right)^2} = -0.00625447829$

So that we have the following sensitivity index table

Table 2: Sensitivity analysis

Parameters	Values of sensitivity index
β_3	0.26923237
φ	0.018307
d	−0.49422156
d_{HT}	−0.00625447829

6. Results

We discussed on the system of non-linear ordinary differential equation to study the dynamics of HIV/AIDS, TB and HIV/AIDS-TB co-infection. Under this we take an appropriate mathematical model on the epidemic of HIV/AIDS, TB and HIV/AIDS-TB co-infection and we found that an important aspect of mathematical epidemiology which is known as basic reproduction number $R_{0(TB)}, R_{0(HIV/AIDS)}$ and $R_{0(\text{HIV/AIDS–TB } co-infection)}$ is determining how to spread and control HIV/AIDS, TB and HIV/AIDS-TB co-infection. We observed that when the HIV/AIDS-TB co-infection basic reproduction number $R_0 = \max\{R_{0(TB)}, R_{0(HIV/AIDS)}, R_{0(\text{HIV/AIDS–TB } co-infection)}\} < 1$, the disease free equilibrium point is locally asymptotically stable. When $R_0 = \max\{R_{0(TB)}, R_{0(HIV/AIDS)}, R_{0(\text{HIV/AIDS–TB } co-infection)}\} > 1$, the disease free equilibrium point is locally asymptotically unstable and the endemic equilibrium point is asymptotically stable.

7. Discussions

In this study we adopted and extended the appropriate mathematical model on the dynamics of HIV/AIDS –TB co-infection and we found that an important aspect of mathematical epidemiology which is known to be basic reproduction number R_0 which determines how HIV/AIDS-TB co-infection spreads in the country and how to

control it. In our modified model we have derived the basic reproduction number $R_0 = \frac{\beta_3 \Lambda}{dN}\left(\frac{1}{\varphi+d} + \frac{\varphi}{(\varphi+d)(d+d_{HT})}\right)$ which depends on six parameters. We also found that the numerical value of the basic reproduction number based on some collected data from Ministry of health of Ethiopia and standard data taken from different sources like WHO and CDC is $R_0 = 34.8648$. From the result and numerical analysis figure 2, 3 and 4 shows the transmission coefficient for HIV/AIDS-TB co-infection β_3 has positive effect on the basic reproduction number $R_{0(HIV/AIDS)}$ and $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)}$ but have no significant effect on basic reproduction number $R_{0(TB)}$. We discuss about these control parameters in detail as follows. Figure-2 shows that the basic reproduction number $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)} < 1$ when transmission coefficient for HIV/AIDS-TB co-infection $\beta_3 < 0.0212249$ and $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)} > 1$ when transmission coefficient for HIV/AIDS-TB co-infection $\beta_3 > 0.0212249$ and figure-3 shows that the basic reproduction number $R_{0(HIV/AIDS)} < 1$ when transmission coefficient for HIV/AIDS-TB co-infection $\beta_3 < 0.06424$ and $R_{0(HIV/AIDS)} > 1$ when transmission coefficient for HIV/AIDS-TB co-infection $\beta_3 > 0.06424$. Figure-4 shows that the basic reproduction number $R_{0(TB)} < 1$ for any value of transmission coefficient for HIV -TB co-infection β_3. From figure 5 Progress rate from the class of individuals infected both HIV and TB to the class of individuals infected both HIV with AIDS stage who are taking antiretroviral treatments and active TB φ is negative effect on the basic reproduction number $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)}$. This implies that from figure-5 the basic reproduction number $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)} < 1$ when progress rate from the class of individuals infected both HIV and TB to the class of individuals infected both HIV with AIDS stage who are taking antiretroviral treatments and active TB $\varphi > 0.20225$ and $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)} > 1$ when progress rate from the class of individuals infected both HIV and TB to the class of individuals infected both HIV with AIDS stage who are taking antiretroviral treatments and active TB $\varphi < 0.20225$. This implies that if the progress rate from the class of individuals infected both HIV and TB to the class of individuals infected with both HIV with AIDS stage who are taking antiretroviral treatments and active TB φ increases then the reproduction number $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)}$ decreases. Using real data collected from different sectors in Ethiopia we found that the numerical value of the basic reproduction number is 34.86. This shows that HIV/AIDS–TB co-infection spread in the society. Using sensitive analysis, we identify the most influential control parameter is the HIV/AIDS-TB co-infection transmission rate β_3. The HIV/AIDS-TB co-infection transmission rate $\beta_3 = \frac{Effective\ number\ of\ contact\ for\ HIV/AIDS-TB\ co-infection}{Total\ number\ of\ contact\ for\ HIV/AIDS-TB\ co-infection}$ which numerical value to be 0.021. But the real value of β_3 is 0.74, to be 0.74 in to 0.021 by fixing the number of contacts for HIV/AIDS-TB co-infection we decrease the effective number of contacts for HIV/AIDS-TB co-infection 74 to 21. We also perform numerical simulation based on real data collected from different health sectors in Ethiopia.

8. Conclusions

The purpose of this study was to develop a mathematical model for HIV/AIDS-TB co-infection dynamics. Based on the data we have obtained unstable disease free equilibrium point, stable endemic equilibrium point for both HIV/AIDS-TB co-infection dynamic and HIV/AIDS dynamic and the basic reproduction number $R_{0(TB)} = 0.00012441 < 1, R_{0(HIV/AIDS)} = 11.1847 > 1$ and $R_{0(\text{HIV/AIDS}-\text{TB } co-infection)} =$

$34.86475 > 1$, shows that the HIV/AIDS-TB co-infection influencing HIV/AIDS dynamics. We have shown that the positivity and boundedness of the dynamical system, the existence, uniqueness, local stability and global stability of the disease free equilibrium points of the HIV/AIDS-TB co-infection dynamical system. The existence, uniqueness, local stability and global stability of the endemic equilibrium points of the HIV/AIDS-TB co-infection dynamical system were analyzed. We have provided rigorous simulations to determine important parameters and effective control strategies without necessarily carrying out clinical trials.

9. Recommendations

From the above results and discussion, we would like to recommend the following to control the spread of HIV/AIDS - TB co-infection. To control the HIV/AIDS-TB co-infection disease in the community we make the control parameter $\beta_3 < 0.021$. The HIV/AIDS-TB co-infection transmission rate $\beta_3 = \frac{Effective\ number\ of\ contact\ for\ HIV/AIDS-TB\ co-infection}{Total\ \ number\ of\ contact\ for\ HIV/AIDS-TB\ co-infection}$ which numerical value to be 0.021. But the real value of β_3 is 0.74, to be 0.74 in to 0.021 by fixing the number of contact for HIV/AIDS-TB co-infection we decrease the effective number of contact for HIV/AIDS-TB co-infection 74 to 21 and make progress rate from the class of individuals infected both HIV/AIDS-TB to the class of individuals infected both HIV/AIDS with AIDS stage and active TB $\varphi > 0.20225$. Models which incorporate other protective measures such as vaccination for TB infection, education of population and using condom for HIV/AIDS infection may be considered for further research.

10. Limitations

There was a problem to get well registered data on HIV/AIDS-TB co-infection, TB infection and HIV/AIDS infection.

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