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Research Article

Mathematical Model for Co-Infection of TB and HIV

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Abstract: A mathematical model of HIV/AIDS and TB including its co-infections is formulated. Basic reproduction numbersR_0^T, R_0^H, and R_0^{HT} are computed for sub-models of TB $SE_TI_TQ_TRV$, HIV/AIDS $SE_HI_HA_HQ_HRV$ and co-infection of AIDS and TB $SE_{HT}I_{HT}A_{HT}Q_{HT}RV$ respectively. We have shown that the model is locally and globally asymptotically stable when $R_0^T < 1$, $R_0^H < 1$, and $R_0^{HT} < 1$ for disease-free equilibrium points. Numerical simulations and sensitivity analysis with real value parameters are carried out. With the help of numerical simulation, we have shown that the sub-models of TB, HIV/AIDS and it's co-infections is globally stable when $R_0^T < 1$, $R_0^H < 1$, and$R_0^{HT} < 1$ respectively for endemic equilibrium points. Comparison between quarantined classes of TB, HIV/AIDS and it's co-infection versus recovered class is carried out.

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INTRODUCTION

Tuberculosis (TB) and human immunodeficiency virus/acquired immune deficiency syndrome (HIV/AIDS) are theleading causes of death from an infectious disease worldwide [1]. HIV infected humans are extremely probable to developTB disease due to their immunodeficiency, and the progression of HIVinfection is the most influential risk factor from TB infection to disease [2]. HIV infection increases the chance of activation of TB and TB increases the chance of HIV infection developing into AIDS. The relative risk of death and development of other opportunistic infections is higher in HIV-TB co-infected humans with respect to only one TB or HIV/AIDS [3].

According to World Health Organization (WHO), approximately33% population of the world is infected with TB and approximately 15% of TB patients are co-infected with HIV in all over the world. HIV patients are in more risk for getting primary TB infection and reactivation of exposed TB infection. HIV infection primarily affects those components of host immune system responsible for cell mediated immunity. These cells help us fight against various infections. Once they are destroyed our body's resistance to fight infections goes down. Thus, if a humanwith exposed TB infection gets HIV infection, then the immunity of human decreases and gets active TB.

The WorldHealth Organization (WHO) estimates that collaborative TB/HIV activities including TB preventive measures, ART therapy and HIV testing has recovered 1.3 million humans from 2005 to 2012.Thus, these collaborative activities are crucial for the reduction of TB-HIV co-infected humans. The reduction of TB related deaths among humans infectedwith HIV has decreased in recent years [4].

In past two and half decades, there are many epidemic models has been formulated for predicting the transmission of TB and HIV/AIDS.Few mathematicalmodels have also been formulated for co-infectionof TB and HIV/AIDS. Roeger [5] developed a population model for TB-HIV/AIDS co-infectiontransmission dynamics and assuming that TB-infected individualsin the active stage of the disease is too sick to remainsexually active and therefore they are unable to transmit HIV. Bhunu [6] formulated a TB-HIV co-infection model with both TB and HIV treatment. Kirschner [7] developed a cellular model for HIV-1 and TB co-infection inside a host.

Naresh and Tripathi [8] developed a model for TB-HIV co-infection in a variablesize population with only TB treatment. Sharomi [9] formulated the mathematical model and also included the treatment factor in it. Pawlowski [10] reviewed the available literature in order to highlight immunological events responsible for developing the one infection in the presence of the other. Escombe [11] analyzed how infectiousness of a co-infected person differs from the one having only TB. Baur[12] examined that how the latent TB

patient moves to active TB class if it catches HIV-1 infection too. Hove-Musekwaa and Nyabadzab formulated the dynamics of an HIV/AIDS model with screened disease carriers [13]. Naha and Dasari wrote review on HIV-Tuberculosis co-infection in an Indian scenario: the role of associated evidence of immune suppression [14].
N. Bacaer developed modeling the joint epidemic of TB and HIV in a South African township [15]. Wang formulated a mathematical model to show the global stability of an epidemic model for HIV-TB co-infection with infection-age [16].

In this paper, we have formulated a mathematical model for the co-infection of HIV/AIDS and TB. We assume that TB or HIV infected humans are exposed to the co-infection of both. We have divided the model into three sub-models including quarantined and vaccination classes to understand the co-infection of both HIV/AIDS and TB easily. The sub-model for TB is $SE_TI_TQ_TRV$ (Susceptible-Exposed-Infected-Quarantined-Recovered-Vaccination). Similarly, Sub-model for HIV/AIDS is $SE_HI_HA_HQ_HRV$ (Susceptible-Exposed-Infected-Quarantined-Recovered-Vaccination) and for co-infection of AIDS and TB is $SE_{HT}I_{HT}A_{HT}Q_{HT}RV$ (Susceptible-Exposed-Infected-Quarantined-Recovered-Vaccination).

The paper is organized as follows: Introduction is given in Section 1, the basic assumptions and parameters of the model is discussed and the epidemic model is developed in Section 2, Section 3 establishes the stability of the system developed, numerical simulations is given in Section 4, and finally conclusion in Section 5.

Model parameters and its formulation

We divided the human population into six classes $SEIQRV$ (Susceptible-Exposed-Infected-Quarantined-Recovered-Vaccinated) and the bird population into three classes $S_bE_bI_b$ (Susceptible-Exposed-Infected). Schematic flow of this model is shown in figure 1 and the state variables and associated parameters of this model are given in Table 1.

Table 1: The state variables and associated parameters of co-infected model of HIV and TB

$S(t)$:	Susceptible humans in time t
$E_T(t)$:	Exposed humans with TB in time t
$E_H(t)$:	Exposed humans with HIV+ in time t
$E_{HT}(t)$:	Exposed humans with TB and HIV+ in time t
$I_T(t)$:	Infectious humans with TB in time t
$I_H(t)$:	Infectious humans with HIV+ in time t
$I_{HT}(t)$:	Co-infectious humans with TB and HIV+ in time t
$A_H(t)$:	AIDS infected humans in time t
$A_{HT}(t)$:	AIDS and TB co-infected humans in time t
$Q_T(t)$:	Quarantined humans who are infected with TB in time t
$Q_H(t)$:	Quarantined humans who are infected with AIDS in time t
$Q_{HT}(t)$:	Quarantined humans who are co-infected with AIDS and TB in time t
$R(t)$:	Recovered humans in time t
$V(t)$:	Vaccinated humans in time t
$N(t)$:	Total human population in time t
B:	Birth rate of humans
β_T:	Infectivity of TB
β_H:	Infectivity of HIV+
β_{HT}:	Infectivity of both TB and HIV+
η:	Rate of transmission from Recovered to Susceptible humans
γ_T:	Rate of transmission from TB infected humans to Quarantined humans with TB infected
γ_H:	Rate of transmission from AIDS infected humans to Quarantined humans with AIDS infected
γ_{HT}:	Rate of transmission from TB and AIDS Co-infected humans to Quarantined humans with TB and AIDS co-infected
α_T:	Rate of transmission from Exposed with TB humans to Infected TB humans
α_H:	Rate of transmission from Exposed with HIV+ humans to Infected HIV+ humans
α_{HT}:	Rate of transmission from Co-exposed with TB and HIV+ humans to Co-infected with TB and HIV+ humans
σ_T:	Rate of transmission from Quarantined humans with TB infected to Recovered humans
σ_H:	Rate of transmission from Quarantined humans with AIDS infected to Recovered humans
σ_{HT}:	Rate of transmission from Quarantined humans with TB and AIDS co-infected to Recovered humans
ξ:	Rate of transmission from Vaccinated to Susceptible humans
ε:	Rate of transmission from Susceptible humans to Vaccinated humans
χ_T:	Rate of transmission from TB infected humans to co-infected humans with TB and HIV+
χ_H:	Rate of transmission from HIV+ infected humans to co-infected humans with TB and HIV+
θ:	Vertical transmission for HIV+
μ:	Natural death rate of humans

δ_H: Rate of transmission from HIV+ infected humans to AIDS infected humans
δ_{HT}: Rate of transmission from TB and HIV+ Co-infected humans to TB and AIDS Co-infected humans
d_T: Death rate due to TB
d_H: Death rate due to AIDS
d_{HT}: Death rate due to TB and AIDS.

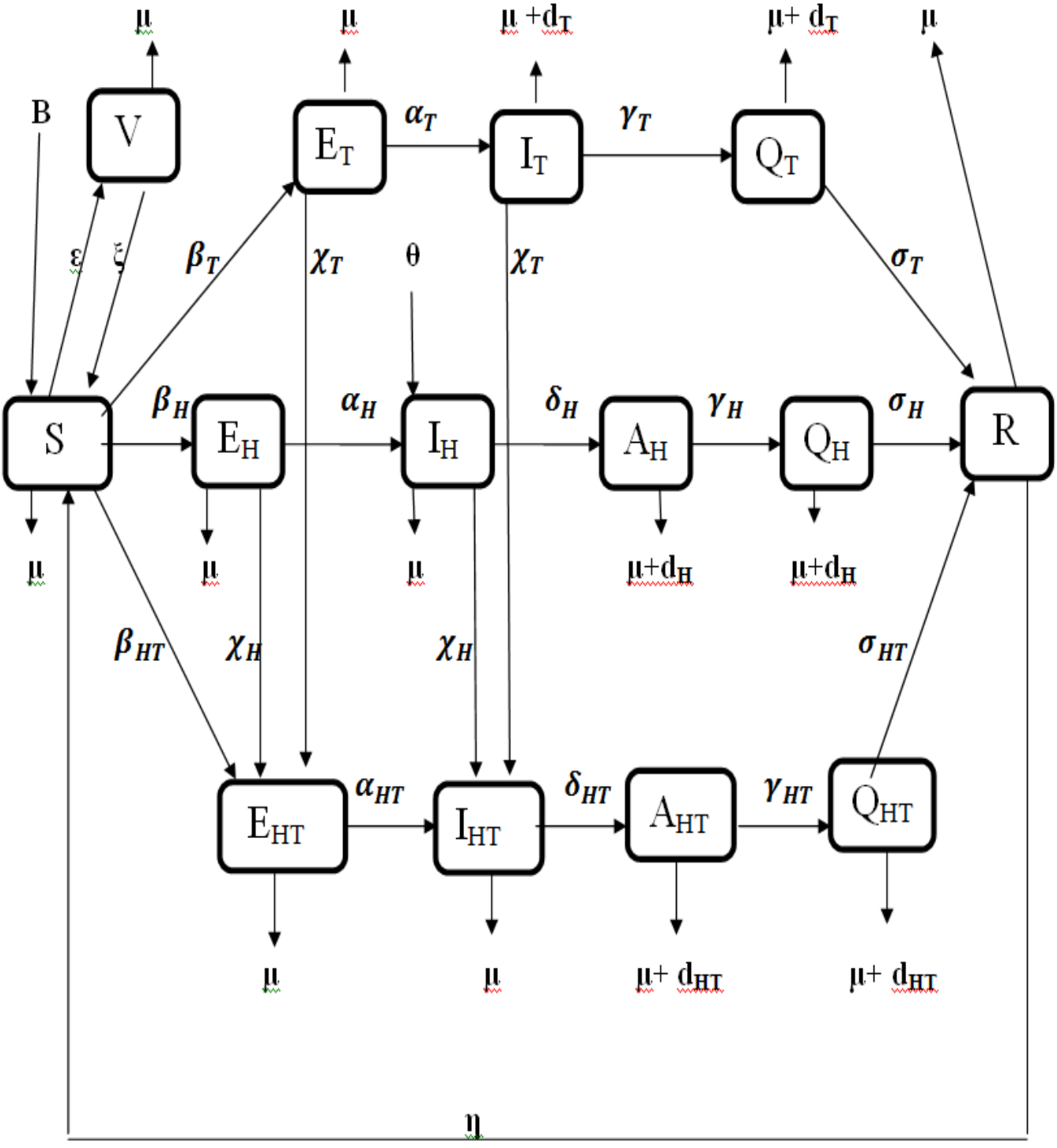

Figure 1: Schematic diagram for co-infected model of HIV and TB

MODEL EQUATIONS OF THE MODEL

Based on the flow of transmission of TB, HIV and it's co-infection in human population as depicted in figure 1, we have the following system of equations:

$$\begin{aligned}
\frac{dS}{dt} &= BN - \beta_T SI_T - \beta_H SI_H - \beta_{HT} SI_{HT} - (\xi + \mu)S - \varepsilon V - \eta R \\
\frac{dE_T}{dt} &= \beta_T SI_T - (\mu + \chi_T + \alpha_T)E_T \\
\frac{dE_H}{dt} &= \beta_H SI_H - (\mu + \chi_H + \alpha_H)E_H \\
\frac{dE_{HT}}{dt} &= \beta_{HT} SI_{HT} - (\mu + \alpha_{HT})E_{HT} + \chi_T E_T + \chi_H E_H \\
\frac{dI_T}{dt} &= \alpha_T E_T - (\mu + d_T + \psi_T + \gamma_T)I_T \\
\frac{dI_H}{dt} &= \alpha_H E_H - (\mu + \delta_H + \psi_H - \theta)I_H \\
\frac{dI_{HT}}{dt} &= \alpha_{HT} E_{HT} - (\mu + \delta_{HT} + d_T - \psi_T - \psi_H - \theta)I_H \\
\frac{dA_H}{dt} &= \delta_H I_H - (\mu + d_H + \gamma_H)A_H \\
\frac{dA_{HT}}{dt} &= \delta_{HT} I_{HT} - (\mu + d_{HT} + \gamma_{HT})A_{HT} \\
\frac{dQ_T}{dt} &= \gamma_T I_T - (\mu + d_T + \sigma_T)Q_T \\
\frac{dQ_H}{dt} &= \gamma_H A_H - (\mu + d_H + \sigma_H)Q_H \\
\frac{dQ_{HT}}{dt} &= \gamma_{HT} A_{HT} - (\mu + d_{HT} + \sigma_{HT})Q_{HT} \\
\frac{dR}{dt} &= \sigma_T Q_T + \sigma_H Q_H + \sigma_{HT} Q_{HT} - (\mu + \eta)R \\
\frac{dV}{dt} &= \xi S - (\varepsilon + \mu)V
\end{aligned} \tag{1}$$

And $N(t) = S(t) + E_H(t) + E_{HT}(t) + I_T(t) + I_H(t) + I_{HT}(t) + A_H(t) + A_{HT}(t) + Q_T(t) + Q_H(t) + Q_{HT} + R(t) + V(t)$.

STABILITY OF MODEL

In this section, we find the basic reproduction number and stability of the model. We prove that our model is locally and globally stable for disease-free-equilibrium.

Since all our model parameters are positive or non-negative, it is important to show that all state variables remain positive or non-negative for all positive initial conditions for $t \geq 0$. From our model equation, we have

$$\frac{dN}{dt} = B - \mu - (d_T I_T - \theta(I_H + I_{HT}) + d_H A_H + d_{HT} A_{HT} + d_T Q_T + d_H Q_H + d_{HT} Q_{HT})$$

$\leq B - \mu N$.

The closed set

$D = \left\{(S, V, E_T, E_H, E_{HT}, I_T, I_H, I_{HT}, A_H, A_{HT}, Q_T, Q_H, Q_{HT}, R) \in \mathbb{R}_+^{14}: N \leq \frac{B}{\mu}\right\}$is a feasible region of the model.

Theorem 1: The closed set D is bounded and positive invariant.

Proof: Since $\frac{dN}{dt} \leq B - \mu N$,

So$N$is bounded above by$\frac{B}{\mu}$.

Hence $\frac{dN}{dt} < 0$ whenever $(t) > \frac{B}{\mu}$.

On simplification, we have

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

As $t \to \infty$, $e^{-\mu t} \to 0$ and so $\lim_{t\to\infty} N(t) \leq \frac{B}{\mu}$.

Thus, D is bounded and positively invariant in $\mathbb{R}_+^{14}$.

BASIC REPRODUCTION NUMBER

For any epidemic model, the basic reproduction number is the average number of secondary infectious cases produced by a single infection in total susceptible population.
The basic reproduction number is calculated by $R_0=\rho(FV^{-1})$, where ρ is spectral radius of the matrix FV^{-1} and F & V are the matrices of new infection terms and the remaining transmission terms respectively [17].

For the system (1), the matrices F and V are as follows:

$$F=\begin{bmatrix} 0&0&0&\beta_T&0&0&0&0&0&0&0\\ 0&0&0&0&\beta_H&0&0&0&0&0&0\\ 0&0&0&0&0&\beta_{HT}&0&0&0&0&0\\ 0&0&0&0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0&0&0&0\\ 0&0&0&0&0&0&0&0&0&0&0 \end{bmatrix} \text{ and}$$

$$V=\begin{bmatrix} V_1&0&0&0&0&0&0&0&0&0&0\\ 0&V_2&0&0&0&0&0&0&0&0&0\\ -\chi_T&-\chi_H&V_3&0&0&0&0&0&0&0&0\\ -\alpha_T&0&0&V_4&0&0&0&0&0&0&0\\ 0&-\alpha_H&0&0&V_5&0&0&0&0&0&0\\ 0&0&-\alpha_{HT}&-\psi_T&-\psi_H&V_6&0&0&0&0&0\\ 0&0&0&0&-\delta_H&0&V_7&0&0&0&0\\ 0&0&0&0&0&-\delta_{HT}&0&V_8&0&0&0\\ 0&0&0&\gamma_T&0&0&0&0&V_9&0&0\\ 0&0&0&0&0&0&-\gamma_H&0&0&V_{10}&0\\ 0&0&0&0&0&0&0&-\gamma_{HT}&0&0&V_{11} \end{bmatrix},$$

where $V_1=\mu+\chi_T+\alpha_T, V_2=\mu+\chi_H+\alpha_H, V_3=\mu+\alpha_{HT},$

$V_4=\mu+d_T+\psi_T+\gamma_T,$

$V_5=\mu+\delta_H+\psi_H-\theta, V_6=\mu+\delta_{HT}+d_T-\theta,\ V_7=\mu+d_H+\gamma_H,$

$V_8=\mu+d_{HT}+\gamma_{HT}, V_9=\mu+d_T+\sigma_T, V_{10}=\mu+d_H+\sigma_H,$

$V_{11}=\mu+d_{HT}+\sigma_{HT}.$

The basic reproduction numbers for TB-only, HIV-only and co-infected with both sub-models are $R_0^T=\frac{\beta_T\alpha_T}{(\mu+d_T+\psi_T+\gamma_T)(\mu+\chi_T+\alpha_T)}$, $R_0^H=\frac{\beta_H\alpha_H}{(\mu+\delta_H+\psi_H-\theta)(\mu+\chi_H+\alpha_H)}$ and $R_0^{HT}=\frac{\beta_{HT}\alpha_{HT}}{(\mu+\delta_{HT}+d_T-\theta)(\mu+\alpha_{HT})}$ respectively.

The basic reproduction number for the system (1) is $\max\{R_0^T, R_0^H, R_0^{HT}\}$.

Theorem 2: The system is locally asymptotically stable for disease-free equilibrium, when $R_0^T<1, R_0^H<1$, and $R_0^{HT}<1$.

Proof: Jacobian matrix of the system is as follows:

$$J=\begin{bmatrix} j_1 & 0 & 0 & 0 & -\beta_T & -\beta_H & -\beta_{HT} & 0 & 0 & 0 & 0 & 0 & \eta & \varepsilon \\ 0 & j_2 & 0 & 0 & \beta_T & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & j_3 & 0 & 0 & \beta_H & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \chi_T & \chi_H & j_4 & 0 & 0 & \beta_{HT} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha_T & 0 & 0 & j_5 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_H & 0 & 0 & j_6 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \alpha_{HT} & \psi_T & \psi_H & j_7 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \delta_H & 0 & j_8 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \delta_{HT} & 0 & j_9 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \gamma_T & 0 & 0 & 0 & 0 & j_{10} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_H & 0 & 0 & j_{11} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \gamma_{HT} & 0 & 0 & j_{12} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_T & \sigma_H & \sigma_{HT} & j_{13} & 0 \\ \xi & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & j_{14} \end{bmatrix},$$

Where, $j_1=-(\mu+\xi)$, $j_2=-(\mu+\chi_T+\alpha_T)$, $j_3=-(\mu+\chi_H+\alpha_H)$, $j_4=-(\mu+\alpha_{HT})$,
$j_5=-(\mu+\gamma_T+\psi_T+d_T)$, $j_6=-(\mu+\delta_H+\psi_H-\theta)$, $j_7=-(\mu+\delta_{HT}+d_T-\theta)$,
$j_8=-(\mu+d_H+\gamma_H)$, $j_9=-(\mu+d_{HT}+\gamma_{HT})$, $j_{10}=-(\mu+d_T+\sigma_T)$,
$j_{11}=-(\mu+d_H+\sigma_H)$, $j_{12}=-(\mu+d_{HT}+\sigma_{HT})$, $j_{13}=-(\mu+\eta)$, $j_{14}=-(\mu+\varepsilon)$.

Eigenvalues of the Jacobian matrix are as follows:

$\lambda_1=j_8, \lambda_2=j_9, \lambda_3=j_{10}, \lambda_4=j_{11}, \lambda_5=j_{12}, \lambda_6=j_{13},$

$\lambda_7=-\frac{2\mu+\delta_H+\chi_H+\alpha_H+\psi_H}{2}+\frac{1}{2}\sqrt{(\delta_H+\psi_H-\theta-\chi_H-\alpha_H)^2+4\alpha_H\beta_H},$

$\lambda_8=-\frac{2\mu+\delta_H+\chi_H+\alpha_H+\psi_H}{2}-\frac{1}{2}\sqrt{(\delta_H+\psi_H-\theta-\chi_H-\alpha_H)^2+4\alpha_H\beta_H},$

$\lambda_9=-\frac{2\mu+\varepsilon+\xi}{2}+\frac{1}{2}\sqrt{(\varepsilon-\xi)^2+4\varepsilon\xi}, \lambda_{10}=-\frac{2\mu+\varepsilon+\xi}{2}-\frac{1}{2}\sqrt{(\varepsilon-\xi)^2+4\varepsilon\xi},$

$\lambda_{11}=-\frac{2\mu+\alpha_{HT}+\delta_{HT}+d_T-\theta}{2}+\frac{1}{2}\sqrt{(\delta_{HT}+d_T-\alpha_{HT}-\theta)^2+4\alpha_{HT}\beta_{HT}},$

$\lambda_{12}=-\frac{2\mu+\alpha_{HT}+\delta_{HT}+d_T-\theta}{2}-\frac{1}{2}\sqrt{(\delta_{HT}+d_T-\alpha_{HT}-\theta)^2+4\alpha_{HT}\beta_{HT}},$

$\lambda_{13}=-\frac{2\mu+d_T+\chi_T+\alpha_T+\psi_T+\gamma}{2}+\frac{1}{2}\sqrt{(d_T+\psi_T+\gamma-\chi_T-\alpha_T)^2+4\alpha_T\beta_T},$

$\lambda_{14}=-\frac{2\mu+d_T+\chi_T+\alpha_T+\psi_T+\gamma}{2}-\frac{1}{2}\sqrt{(d_T+\psi_T+\gamma-\chi_T-\alpha_T)^2+4\alpha_T\beta_T}.$

Eigenvalues λ_1 , λ_2 , λ_3 , λ_4 , λ_5 λ_6 , λ_7 , λ_7 λ_{10}, λ_{12}, and λ_{14} have negative real value and on simplifying λ_7 is negative when $R_0^H < 1$. Similarly, on simplification eigenvalues λ_{11} and λ_{13} are negative when $R_0^{HT} < 1$ and $R_0^T < 1$ respectively.

Finally, for eigenvalue λ_9, we get a condition that the eigenvalue $\lambda_9 < 0$ when $\mu^2+\mu\varepsilon+\mu\xi > 0$, which is always true, because all parameters μ, ε and ξ are non-negative.

Hence all eigenvalues of Jacobian matrix J are negative when $R_0^T < 1$, $R_0^H < 1$, and $R_0^{HT} < 1$.

This proves that the system is locally asymptotically stable when $R_0^T < 1$, $R_0^H < 1$, and $R_0^{HT} < 1$.

GLOBAL STABILITY OF DISEASE-FREE EQUILIBRIUM

We show the global stability of the model using the method given by Kamgang and Sallet [18]. In this method, to show global stability, the model has to satisfy the five hypotheses, which has been summarized briefly as follows:

Consider the system
$\dot{Y}_1=M_1(Y)(Y_1-Y_1^*)+M_{12}(Y)Y_2$
$\dot{Y}_2=M_2(Y)Y_2$
on the positively invariant set $\Omega \subset \mathbb{R}_+^{n_1+n_2}$, and under following assumptions:
A_1 : The system is defined and dissipative on a positively invariant set Ω.
A_2 : The sub-system $\dot{Y}_1=M_1(Y_1,0)(Y_1-Y_1^*)$ is globally asymptotically stable at the equilibrium Y_1^* on the canonical projection of Ω on $\mathbb{R}_+^{n_1}$.
A_3 : The matrix $M_2(Y)$ is Metzler and irreducible for any given $Y \in \Omega$.
A_4 : There exists an upper-bound matrix $\bar{M}_2$ for $\Re=\{M_2(Y)/Y \in \Omega\}$ such that $\bar{M}_2=max_\Omega \Re$.
A_5 : $\alpha(\bar{M}_2) \leq 0$, where $\alpha(\bar{M}_2)$ is maximum real part of eigenvalues of $\bar{M}_2$.
If above assumptions A_1-A_5 are satisfied, the DFE is globally asymptotically stable for above system in $\bar{\Omega}$.

Theorem 3: The system (1) is globally stable for disease-free equilibrium when $R_0^T \leq 1$, $R_0^H \leq 1$, and $R_0^{HT} \leq 1$.

Proof: We have shown above that $D = \left\{(S, V, E_T, E_H, E_{HT}, I_T, I_H, I_{HT}, A_H, A_{HT}, Q_T, Q_H, Q_{HT}, R) \in \mathbb{R}_+^{14}: N \leq \frac{B}{\mu}\right\}$ is bounded and positively invariant in $\mathbb{R}_+^{14}$, where the hypotheses A_1 and A_2 are satisfied.

In our model, $X_1 = (S, V, A_H, A_{HT}, Q_T, Q_H, Q_{HT}, R)$ and $X_2 = (E_T, I_T, E_H, I_H, E_{HT}, I_{HT})$.
The matrix $A_2(x)$ is given by

$$\begin{bmatrix} -(\mu+\chi_T+\alpha_T) & \beta_T S & 0 & 0 & 0 & 0 \\ \alpha_T & -(\mu+\gamma_T+\psi_T+d_T) & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\mu+\chi_H+\alpha_H) & \beta_H S & 0 & 0 \\ 0 & 0 & \alpha_H & -(\mu+\delta_H+\psi_H-\theta) & 0 & 0 \\ \chi_T & 0 & \chi_H & 0 & -(\mu+\alpha_{HT}) & \beta_{HT} S \\ 0 & 0 & 0 & 0 & \alpha_{HT} & -(\mu+d_{HT}+\gamma_{HT}) \end{bmatrix}.$$

As required by hypothesis A_3, for any $x \in \mathbb{R}_+^{14}$ the matrix is irreducible.

Now, for hypothesis A_4, there is a maximum and uniquely realized in $\mathbb{R}_+^8$ if $S = 1$at DFE. This maximum matrix is J_2, the block of the Jacobian at DFE, corresponding to the matrix $A_2(x)$ is given by J_2=

$$\begin{bmatrix} -(\mu+\chi_T+\alpha_T) & \beta_T & 0 & 0 & 0 & 0 \\ \alpha_T & -(\mu+\gamma_T+\psi_T+d_T) & 0 & 0 & 0 & 0 \\ 0 & 0 & -(\mu+\chi_H+\alpha_H) & \beta_H & 0 & 0 \\ 0 & 0 & \alpha_H & -(\mu+\delta_H+\psi_H-\theta) & 0 & 0 \\ \chi_T & 0 & \chi_H & 0 & -(\mu+\alpha_{HT}) & \beta_{HT} \\ 0 & 0 & 0 & 0 & \alpha_{HT} & -(\mu+d_{HT}+\gamma_{HT}) \end{bmatrix}.$$

For the hypothesis A_4 the diagonal block matrix A_{11}^2, A_{22}^2 and A_{33}^2 are bounded by the matrices

$$\bar{A}_{11}^2 = \begin{bmatrix} -(\mu+\chi_T+\alpha_T) & \beta_T \\ \alpha_T & -(\mu+\gamma_T+\psi_T+d_T) \end{bmatrix}, \bar{A}_{22}^2 = \begin{bmatrix} -(\mu+\chi_H+\alpha_H) & \beta_H \\ \alpha_H & -(\mu+\delta_H+\psi_H-\theta)) \end{bmatrix} \text{ and}$$

$$\bar{A}_{33}^2 = \begin{bmatrix} -(\mu+\alpha_{HT}) & \beta_{HT} \\ \alpha_{HT} & -(\mu+d_{HT}+\gamma_{HT}) \end{bmatrix}, \text{ which are maximum.}$$

This maximum is realized at each point of manifold$\mathcal{M}_1$ $(E_T = 0, I_T = 0, E_H = 0, I_H = 0, E_{HT} = 0, I_{HT} = 0)$. This implies that these points belong to the manifold with equations

$E_T = I_T = E_H = I_H = E_{HT} = I_{HT} = 0$. Thus, the hypothesis A_4 is satisfied.

Now for the hypothesis A_5 , the condition $\alpha(\bar{A}_{11}^2) \leq 0$, $\alpha(\bar{A}_{22}^2) \leq 0$ and $\alpha(\bar{A}_{33}^2) \leq 0$ can be expressed as:

$\frac{\beta_T \alpha_T}{(\mu+d_T+\psi_T+\gamma_T)(\mu+\chi_T+\alpha_T)} \leq 1$, $\frac{\beta_H \alpha_H}{(\mu+\delta_H+\psi_H-\theta)(\mu+\chi_H+\alpha_H)} \leq 1$ and $\frac{\beta_{HT} \alpha_{HT}}{(\mu+\delta_{HT}+d_T-\theta)(\mu+\alpha_{HT})} \leq 1$. Thus the hypothesis A_5 is equivalent to $R_0^T \leq 1$, $R_0^H \leq 1$, and $R_0^{HT} \leq 1$.

This proves that the model is globally stable for disease-free equilibrium when $R_0^T \leq 1$, $R_0^H \leq 1$, and $R_0^{HT} \leq 1$.

NUMERICAL SIMULATIONS

In this section, using Runge-kutta-Fehlberg method of order 4 and 5, we numerically simulate our system (1) with real parametric values as given in Table 2 and also establish the stability of models by taking different examples. MATLAB is used to simulate the systems.

Example 1: In this example, we have shown the global stability of system (2) at disease-free equilibrium. We consider the global dynamics of the co-infectious class of AIDS & TB and recovered class of AIDS & TB plane with the parametric values given in Table 2 to show the global stability of disease-free equilibrium point when $R_0^T < 1$, $R_0^H < 1$, and $R_0^{HT} < 1$. We have basic reproduction numbers for TB, HIV/AIDS and co-infection of TB & HIV are$R_0^T = 0.0315 < 1$, $R_0^H = 0.4611 < 1$, and $R_0^{HT} = 0.1953 < 1$ respectively. As observe from figure 2, we find that the nature of trajectory from any initial point finally tends to disease-free equilibrium point, which clearly indicate the global stability of disease-free equilibrium. Figure 3 also shows the global stability of system (1) in infected-quarantined class of TB plane.

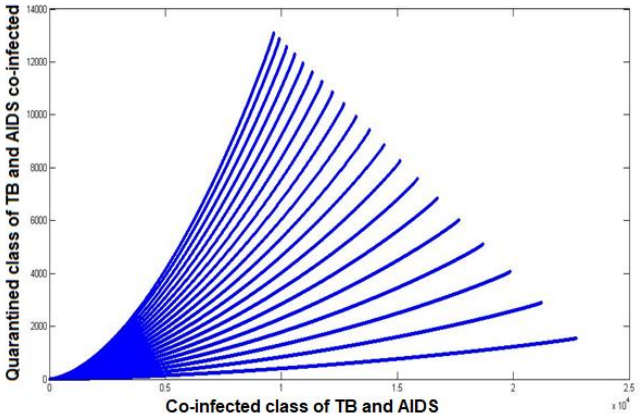

Figure 2 : Global stability in co-infected and Quarantined of AIDS and TB plane when $R_0^T < 1$, $R_0^H < 1$, and $R_0^{HT} < 1$.

Table 2: Parametric values for co-infected model of HIV and TB

Parameter	Value	Parameter	Value
N	1,00,000	χ_H	0.3
B	0.8	δ_H	0.6
β_T	0.8	δ_{HT}	0.7
β_H	0.85	γ_T	0.64
β_{HT}	0.75	γ_H	0.3
α_T	0.65	γ_{HT}	0.4
α_H	0.7	d_T	0.1
α_{HT}	0.02	d_H	0.5
χ_T	0.2	d_{HT}	0.6
σ_T	0.8	ψ_T	0.08
σ_H	0.4	ψ_H	0.2
σ_{HT}	0.1	μ	0.03
ε	0.05	η	0.6
ξ	0.08	θ	0.001

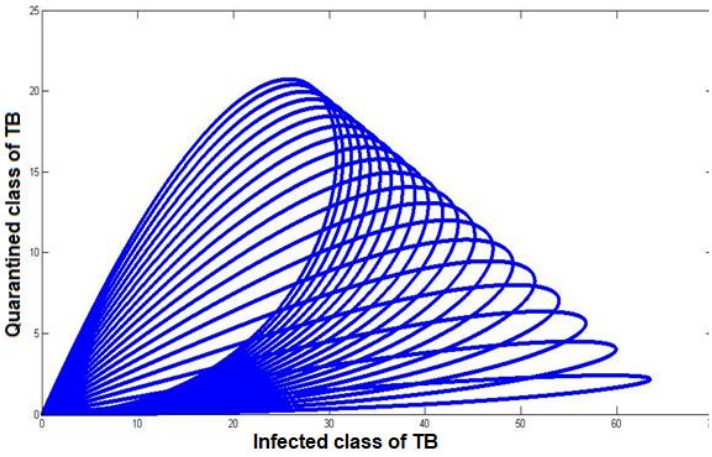

Figure 3: Global stability in Infected and Quarantined plane of TB when $R_0^T < 1$, $R_0^H < 1$, and $R_0^{HT} < 1$.

Example 2: In this example, we have shown the global stability of TB-only sub-model $SE_TI_TQ_TRV$ at endemic equilibrium points when $R_0^T < 1$. We consider the initial conditions $S(0) = 93000, E_T(0) = 2000, I_T(0) = 2000, Q_T(0) = 2000,\ R(0) = 1000, V(0) = 0$ for figure 3, and $S(0) = 89000, E_T(0) = 10000, I_T(0) = 10000, Q_T(0) = 8000,\ R(0) = 0, V(0) = 1000$ for figure 4 with parametric values given in Table 2. We have the basic reproduction number is $R_0^T = 0.5649 < 1$.As observe from figure 4 & 5, we find that the nature of trajectory from any initial point finally tends to endemic equilibrium point, which clearly indicate the global stability of endemic equilibrium when $R_0^T < 1$. Figure 5 also shows the more recovered TB population by using vaccination with compared to figure 4.

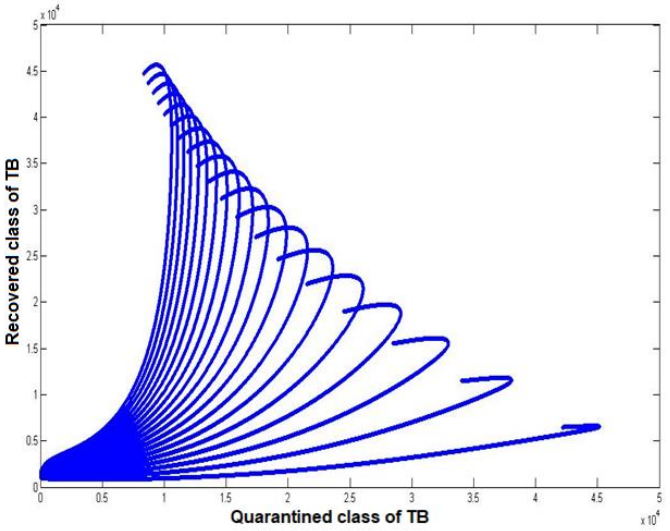

Figure 4: Global stability in Quarantined and Recovered class of TB plane when $R_0^T < 1$ and no vaccination.

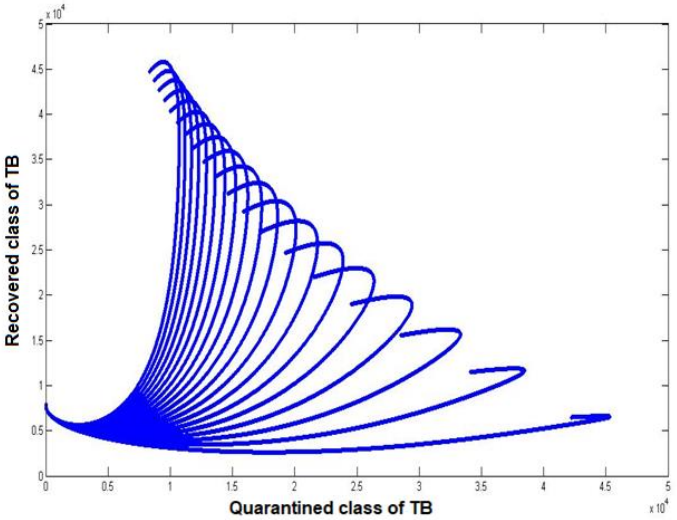

Figure 5: Global stability in Quarantined and Recovered class of TB plane when $R_0^T < 1$ with vaccination.

Example 3: In this example, we have shown the global stability of HIV/AIDS-only sub-model $SE_HI_HQ_HRV$ at endemic equilibrium points when $R_0^H < 1$. We consider the initial conditions $S(0) = 93000, E_H(0) = 2000, I_H(0) = 2000, Q_H(0) = 2000,\ R(0) = 1000, V(0) = 0$ for figure 3, and $S(0) = 89000, E_H(0) = 10000, I_H(0) = 10000, Q_H(0) = 8000,\ R(0) = 0, V(0) = 1000$ for figure 4 with parametric values given in Table 2. We have the basic reproduction

number is $R_0^H = 0.7385 < 1$. As observe from figure 5 & 6, we find that the nature of trajectory from any initial point finally tends to endemic equilibrium point, which clearly indicate the global stability of endemic equilibrium when $R_0^T < 1$. Figure 7 also shows the more recovered TB population by using vaccination with compared to figure 6.

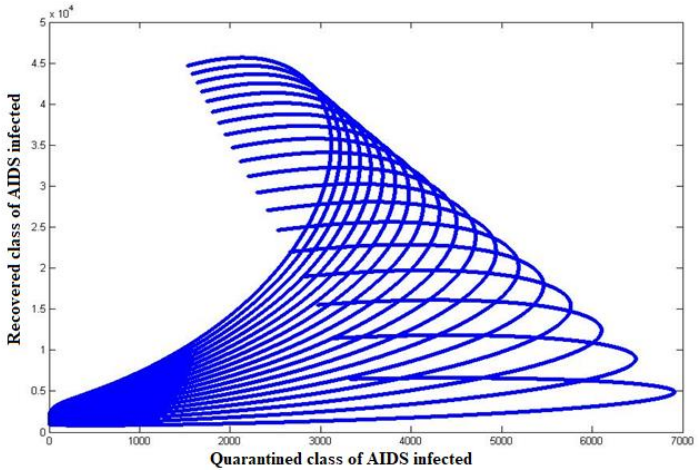

Figure 6: Global stability in Quarantined and Recovered class of HIV/AIDS plane when$R_0^H < 1$ and no vaccination.

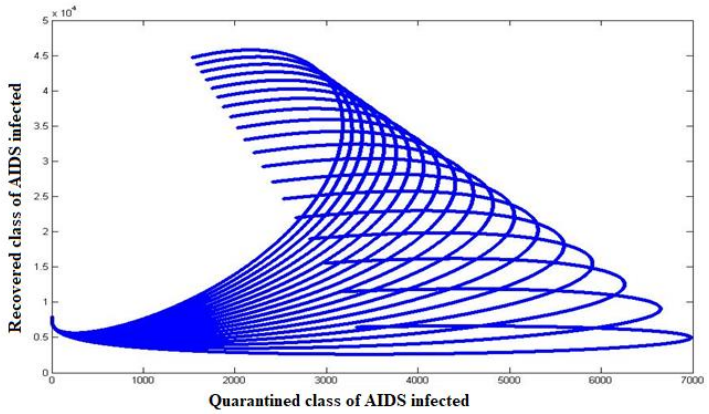

Figure 7: Global stability in Quarantined and Recovered class of AIDS plane when$R_0^H < 1$ with vaccination.

Example 4: In this example, we have shown the global stability of co-infected TB & HIV/AIDS sub-model $SE_{HT}I_{HT}Q_{HT}RV$ at endemic equilibrium points when $R_0^{HT} < 1$. We consider the initial conditions $S(0) = 93000, E_{HT}(0) = 2000, I_{HT}(0) = 2000, Q_{HT}(0) = 2000,\ R(0) = 1000, V(0) = 0$ for figure 3, and $S(0) = 89000, E_{HT}(0) = 10000, I_{HT}(0) = 10000, Q_{HT}(0) = 8000,\ R(0) = 0, V(0) = 1000$ for figure 4 with parametric values given in Table 2. We have the basic reproduction number is $R_0^{HT} = 0.7113 < 1$. As observe from figure 8 & 9, we find that the nature of trajectory from any initial point finally tends to endemic equilibrium point, which clearly indicate the global stability of endemic equilibrium when $R_0^{HT} < 1$. Figure 9 also shows the more recovered TB population by using vaccination with compared to figure 8.

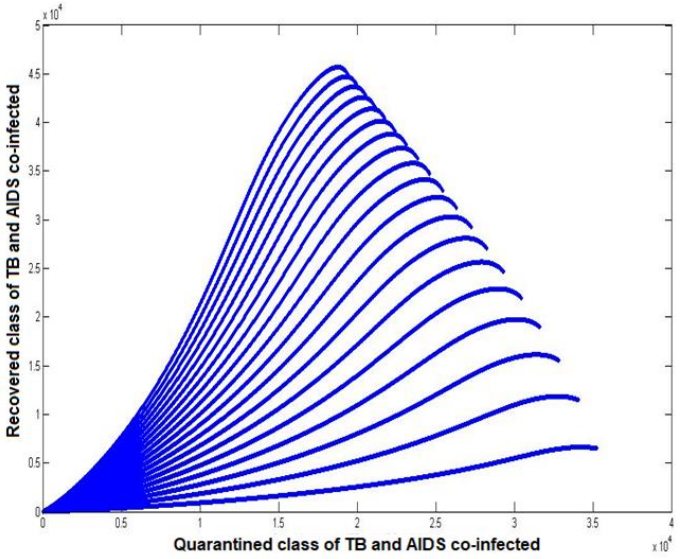

Figure 8: Global stability in Quarantined and Recovered class of TB &AIDS plane when$R_0^{HT} < 1$ and no vaccination.

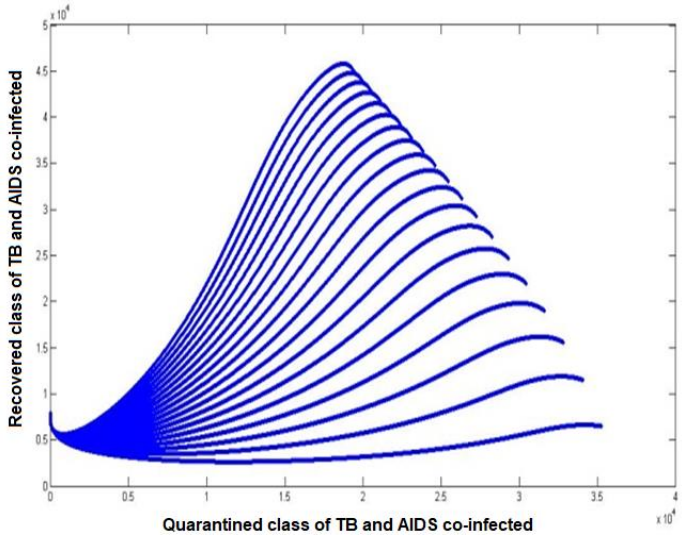

Figure 9: Global stability in Quarantined and Recovered class of TB &AIDS plane when$R_0^T < 1$ with vaccination.

Example 5: In this example, we have shown the comparision of different classes of system (1). Figure 10 shows comparision between quaratined classes of TB, HIV/AIDS and co-infected of both vesus Recovered class. It shows that as the quarantined population infected with TB or HIV/AIDS increased, the recovered population also increased and whenthe quarantined population infected with TB or HIV/AIDS decreased, the recovered population also decreased, but when the quarantined population co-infected with both TB and HIV/AIDS increased, the recovered population increased for short period and after that it decreased even when the quarantined population co-infected with both TB and HIV/AIDS increased.

Figure 11 shows the comparision between infected classes of TB, HIV/AIDS and it's co-infected class versus time in years.

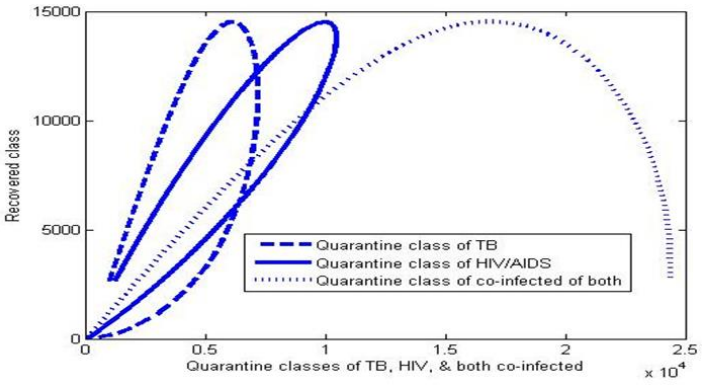

Figure 10: Comparison between Quarantined classes of TB, AIDS and it's co-infections.

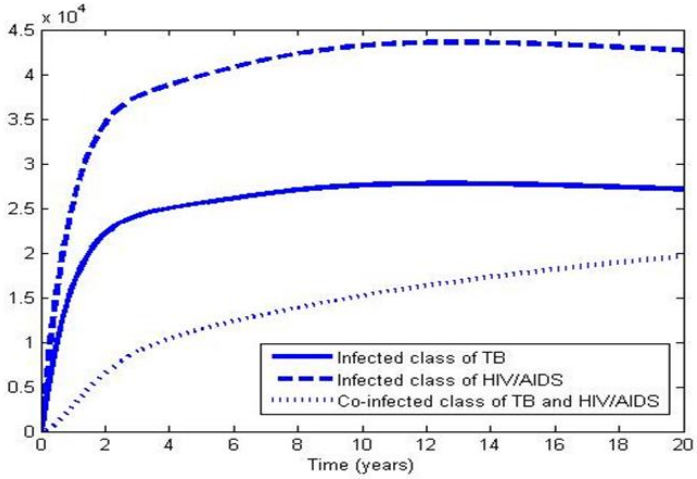

Figure 11: Comparison between Infected classes of TB, AIDS and it's co-infections.

CONCLUSIONS

We have developed a mathematical model for TB, HIV/AIDS and it's co-infections. We calculated the basic reproduction numbers $R_0^T = \frac{\beta_T \alpha_T}{(\mu+d_T+\psi_T+\gamma_T)(\mu+\chi_T+\alpha_T)}$, $R_0^H = \frac{\beta_H \alpha_H}{(\mu+\delta_H+\psi_H-\theta)(\mu+\chi_H+\alpha_H)}$ and $R_0^{HT} = \frac{\beta_{HT} \alpha_{HT}}{(\mu+\delta_{HT}+d_T-\theta)(\mu+\alpha_{HT})}$ for sub-models of TB $(SE_T I_T Q_T RV)$, HIV/AIDS $(SE_H I_H A_H Q_H RV)$ and co-infection of AIDS and TB $(SE_{HT} I_{HT} A_{HT} Q_{HT} RV)$ respectively. We have shown that the model is locally and globally asymptotically stable when $R_0^T < 1$, $R_0^H < 1$, and $R_0^{HT} < 1$ for disease-free equilibrium points. Figure (2) and (3) shows the global stability of disease-free equilibrium of system (1) when basic reproduction numbers for TB, HIV/AIDS and co-infection of TB & HIV are $R_0^T = 0.0315 < 1$, $R_0^H = 0.4611 < 1$, and $R_0^{HT} = 0.1953 < 1$ respectively. Figure (4) and (5) shows the global stability of TB-only sub-model $SE_T I_T Q_T RV$ at endemic equilibrium points when $R_0^T = 0.5649 < 1$. Figure (6) and (7) shows the global stability of HIV/AIDS-only sub-model $SE_H I_H Q_H RV$ at endemic equilibrium points when $R_0^H = 0.7385 < 1$. Figure (8) and (9) shows the global stability of co-infected TB & HIV/AIDS sub-model $SE_{HT} I_{HT} Q_{HT} RV$ at endemic equilibrium points $R_0^{HT} = 0.7113 < 1$.Figure 10 shows that as the quarantined population infected with TB or HIV/AIDS increased, the recovered population also increased and when the quarantined population infected with TB or HIV/AIDS decreased, the recovered population also decreased, but when the quarantined population co-infected with both TB and HIV/AIDS increased, the recovered population increased for short period and after that it decreased even when the quarantined population co-infected with both TB and HIV/AIDS increased.Figure 11 indicates that as the TB and HIV infected class increases, the co-infected class of both TB and HIV also increases.

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CONFLICT OF INTEREST: None

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