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Numerical Solution of non-linear mathematical model of TB/HIV Co-infection

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ABSTRACT

To get a better understanding of HIV/TB co-infection, we've constructed and tested a mathematical model. This model includes a set of first order non-linear Ordinary Differential Equations with six exclusive compartments; for example, people infected with TB (TB-infected), HIV (HIV-infected), or people infected with both (co-infected) (A). Compartment transitions have been shown. It's worth pointing out that the paper mentions the existence of a positive invariant area and positive solution. The researchers were able to support their conclusions by employing MATLAB and in-depth computer simulations.

Key Words: Transmission rate, Death rate, Coinfection

1. Introduction:

HIV is known to be the most acute public health problem in the world today. Despite the fact that there have been few triumphs in containing HIV, it is spreading at alarming rates throughout the world, which is why the US has focused on it for so long. Despite considerable advancements in molecular biology research and medical developments throughout the second decade of the epidemic, this fact remains true. HIV, which used to be deadly but is now a manageable chronic illness if one can get access to antiretroviral medications. Dramatic decreases in the risk of death and sickness have resulted from these changes. But, unfortunately, treatment for the disease is still scarce, and the disease continues to spread. Millions of individuals have been devastated by it, and a great amount of money has been spent on research and therapy to remedy it. Though, in recent years, there have been a lot of breakthroughs in the medical field, unfortunately, there is still no cure or vaccine for HIV/AIDS. As such, we must thoroughly investigate the patterns of this deadly disease so that we can eventually stop its progression. In order to better understand the transmission patterns of HIV/AIDS, mathematical models have been employed to better regulate its spread.

McLean and Nowak (1992) described a model of HIV-CD4 T cell dynamics in the context of other diseases. The impact of HIV on tuberculosis has been debated; **West and Thompson (1997)** used models to simulate the transmission dynamics of HIV and TB and evaluated the influence of HIV on tuberculosis transmission. Using a model for the transmission of HIV and other infections across populations, Using equilibrium analysis, **Doyle et al. (1998)** constructed a model for HIV's propagation in a heterosexual population that accounts for contact tracking and group spread. **Greenhalgh et al. (2001)** examined the effects of condom use on HIV and AIDS transmissions within a heterogeneous group of men. **Moghadas and Gumel (2003)** discovered that, if an anti-therapy can reduce the transmission parameter of HIV below a specific threshold, then HIV eradication is possible. A theoretical framework of HIV/AIDS transmission in India was offered by **Srinivasa Rao (2003)**. **Naresh and Tripathi (2005)** put out a model of HIV-TB co-infection with constant new susceptibles while presenting findings showing TB eradication is possible if more than 90 percent TB infected individuals are treated, since it results in elimination of the disease. The nonlinear model introduced by **Tripathi et al. (2007)** to examine the impact of unassuming infectives being screened on the spread of HIV/AIDS in a uniform community with constant infections via immigration. Screening those who are infected, but aren't aware of it, has been demonstrated to reduce the spread of the AIDS epidemic.

Bhunu et al. (2009) found that HIV treatment had significant reductions in the numbers of people who progressed to tuberculosis. In addition, dealing with both latent and active tuberculosis cases leads in HIV's AIDS stage being delayed.

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According to **Naresh et al. (2009),** if TB is not linked to HIV infection, the number of people living with AIDS decreases. Additionally, a numerical analysis of the model is conducted to look into the impact of various model parameters on the disease's spread. **Roeger et al. (2009)** discovered that when people are co-infected with HIV and TB, they tend to develop active TB at a faster rate than those who are HIV-positive alone, which has led to a rise in the HIV/AIDS epidemic while simultaneously resulting in dampened oscillations in the system. The TB infection and HIV infection rates are both decreasing, moving the population towards TB-free equilibrium. Also, AIDS patients are found to live longer if TB and HIV aren't related. A computational study examines how critical characteristics affect the spreading of the disease. Nonlinear mathematical models were introduced by **Kaur et al. (2015)** to analyse the transmission dynamics of HIV-TB co-infection. The computations showed that only if the two diseases' basic reproduction numbers (that is, the number of people each infected person infects) are both under one can a disease-free equilibrium be stable.The mathematical model of HIV/TB co-infection was created by **Bolarin and Omatola (2016)**. They identified the stable equilibrium states and reached via a Bellman and Cooke theorem-based analysis. **Azeez et al. (2017)** has created a mathematical model focusing on the mechanism underlying the transmission of TB and HIV co-infection, analysing and enabling understanding and prediction of two infectious illnesses that spread and advance in distinct populations. The transmission of tuberculosis and HIV co-infection were examined using mathematical models by **Kabanikhin et al. (2017)**. Their sensitivity analysis included the use of the eigenvalue method to do the sensitivity matrix Hessian calculation. **Samad and Biswas (2020)** modelled the dynamic behaviours of HIV/AIDS and TB with quantitative analysis. This model is built using their biology and infection spreading characteristics. It's always important to make sure the model is stable, is healthy, has balance, and isn't plagued by disease.

2. Mathematical Formulation:

At any one time, the entire population N(t) is classified into six categories: susceptible $S(t)$, those infected with active TB (I_T) and those infected with HIV (I_H), those who are dually infected (I_{HT}). Let R be TB recovered individuals and A be the percentage of AIDS patients.

The general consensus is that people with HIV are likely to become infected with TB through mingling with TB infectives. TB sufferers are known to be careful and remain away from HIV transmission. We think people who have both HIV and TB will be terribly unwell and won't be able to spread either disease. When everything is considered, the following equation summarizes it:

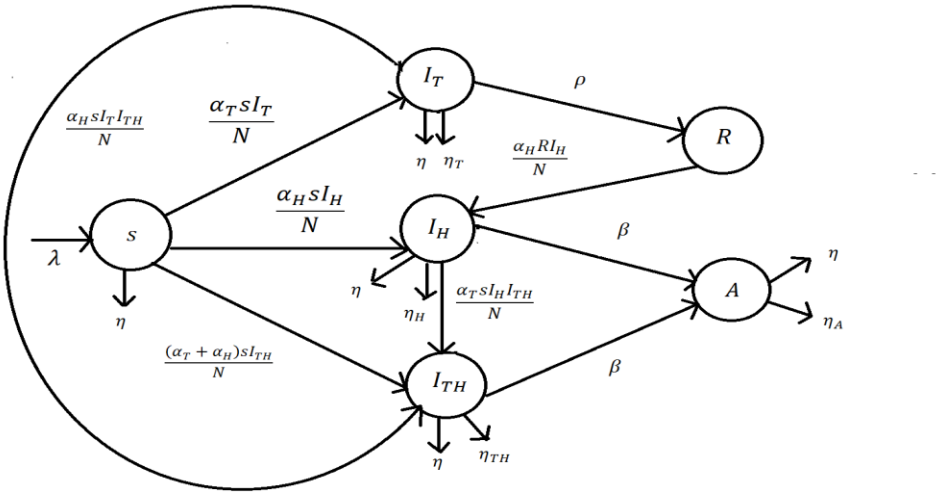

Fig.1: Flow diagram of TB/HIV Model

$$\frac{dS}{dt} = \lambda - \eta s - \frac{\alpha_T S I_T}{N} - \frac{\alpha_H S I_H}{N} - \frac{(\alpha_T + \alpha_H) S I_{TH}}{N} \quad (1)$$

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$$\frac{dI_T}{dt} = \frac{\alpha_T S I_T}{N} - \frac{\alpha_H I_T I_{TH}}{N} - (\eta + \eta_T + \rho) I_T \quad (2)$$

$$\frac{dI_H}{dt} = \frac{\alpha_H S I_H}{N} + \frac{\alpha_H R\, I_H}{N} - \frac{\alpha_T I_H I_{TH}}{N} - (\eta + \eta_H + \beta) I_H \quad (3)$$

$$\frac{dI_{TH}}{dt} = \frac{\alpha_T I_H I_{TH}}{N} + \frac{(\alpha_T + \alpha_H) S I_{TH}}{N} + \frac{\alpha_H I_T I_{TH}}{N} - (\eta + \eta_{TH} + \beta) I_{TH} \quad (4)$$

$$\frac{dR}{dt} = \rho I_T - \eta R - \frac{\alpha_H R\, I_H}{N} \quad (5)$$

$$\frac{dA}{dt} = \beta (I_H + I_{TH}) - (\eta + \eta_A) A \quad (6)$$

The following are the parameters used in TB/HIV Model.

Symbols	Definition
N	Entire Population
S	Number of Susceptible
I_T	Individuals with active TB
I_H	Individuals with HIV Infection
I_{TH}	Individuals with coinfection (TB/HIV)
R	TB recovered individuals
A	Individuals with AIDS
λ	Constant recruitment rate
α_T	Rate of TB Transmission
α_H	Rate of HIV Transmission
η	Natural Death Rate
η_T	Death rate due to TB
η_H	Death rate due to HIV
η_{TH}	Death rate due to both HIV and TB
η_A	Death rate due to AIDS
β	Rate by which HIV infected or coinfected persons reaches to AIDS compartment
ρ	Rate by which TB patients recovered

3. Positive Invariant Region:

Since we have

$$N = S + I_T + I_H + I_{TH} + R + A \quad (7)$$

Adding equation (1) to (6) to obtain

$$\frac{dN}{dt} = \lambda - \eta N - \eta_T I_T - \eta_H I_H - \eta_{TH} I_{TH} - \eta_A A \quad (8)$$

We know this is the case, as shown in equation (8), in which there is no sickness.

$$\frac{dN}{dt} \leq \lambda - \eta N \quad (9)$$

Solving equation (9), we get

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$$N \leq \frac{\lambda}{\eta} + Ce^{-\eta t} \tag{10}$$

Applying initial condition $N(0) = N_0$ in equation (10), we get

$$N \leq \frac{\lambda}{\eta} + \left(N_0 - \frac{\lambda}{\eta}\right) e^{-\eta t} \tag{11}$$

$$\lim_{t \longrightarrow \infty} N(t) = \frac{\lambda}{\eta} (\text{Carrying Capacity})$$

Therefore, the human population model solutions (1) to (6) all enter the same region.

$$\mathcal{R} = \{(S, I_T, I_H, I_{TH}, R, A) \in \boldsymbol{R}^6\}$$

$$S > 0, I_T \geq 0, I_H \geq 0, I_{TH} \geq 0, R \geq 0, A \geq 0, N \leq \frac{\lambda}{\eta}$$

Therefore, the solution is positive in the region $\mathcal{R}$, and the equations (1) to (6) are both epidemiologically significant and mathematically well-posed. Thus, in this scenario, we may just use flow created by the model (1) to (6). Furthermore, the outcomes endure as the system continues.

There is an invariant region, called R, which makes the system equations (1) to (6) viable for t>0 if that point is in $\mathcal{R}$.

4. Positivity of Solution:

From equation (1), we have

$$\frac{dS}{dt} = \lambda - \left\{\eta + \frac{\alpha_T I_T}{N} + \frac{\alpha_H I_H}{N} + \frac{(\alpha_T + \alpha_H) I_{TH}}{N}\right\} S$$

$$\Longrightarrow \frac{dS}{dt} \geq -\left\{\eta + \frac{\alpha_T I_T}{N} + \frac{\alpha_H I_H}{N} + \frac{(\alpha_T + \alpha_H) I_{TH}}{N}\right\} S$$

$$\Longrightarrow \frac{dS}{S} \geq -\left\{\eta + \frac{\alpha_T I_T}{N} + \frac{\alpha_H I_H}{N} + \frac{(\alpha_T + \alpha_H) I_{TH}}{N}\right\} dt$$

Integrating on both Sides, We get

$$\Longrightarrow lnS \geq -\left[\eta + \frac{\alpha_T I_T}{N} + \frac{\alpha_H I_H}{N} + \frac{(\alpha_T + \alpha_H) I_{TH}}{N}\right] t + c$$

$$\Longrightarrow S \geq \exp\left[-\left\{\eta + \frac{\alpha_T I_T}{N} + \frac{\alpha_H I_H}{N} + \frac{(\alpha_T + \alpha_H) I_{TH}}{N}\right\} t + c\right]$$

$$\Longrightarrow S \geq K\exp\left[-\left\{\eta + \frac{\alpha_T I_T}{N} + \frac{\alpha_H I_H}{N} + \frac{(\alpha_T + \alpha_H) I_{TH}}{N}\right\} t\right] \qquad \text{where } e^c = K$$

Using initial condition $t = 0$, $S(0) \geq K$

$$\Longrightarrow S(t) \geq S(0)\exp\left[-\left\{\eta + \frac{\alpha_T I_T}{N} + \frac{\alpha_H I_H}{N} + \frac{(\alpha_T + \alpha_H) I_{TH}}{N}\right\} t\right] > 0 \tag{12}$$

Similarly

From equation (2),

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$$\frac{dI_T}{dt} = \frac{\alpha_T S I_T}{N} - \frac{\alpha_H I_T I_{TH}}{N} - (\eta + \eta_T + \rho) I_T$$

$$\Longrightarrow \frac{dI_T}{dt} \geq -\left\{\frac{\alpha_H I_{TH}}{N} + (\eta + \eta_T + \rho)\right\} I_T$$

$$\Longrightarrow \frac{dI_T}{I_T} \geq -\left\{\frac{\alpha_H I_{TH}}{N} + (\eta + \eta_T + \rho)\right\} dt$$

Integrating on both sides, we get

$$\Longrightarrow \ln I_T \geq -\left\{\frac{\alpha_H I_{TH}}{N} + (\eta + \eta_T + \rho)\right\} t + c$$

$$\Longrightarrow I_T \geq exp\left[-\left\{\frac{\alpha_H I_{TH}}{N} + (\eta + \eta_T + \rho)\right\} t + c\right]$$

$$\Longrightarrow I_T \geq Kexp\left[-\left\{\frac{\alpha_H I_{TH}}{N} + (\eta + \eta_T + \rho)\right\} t\right]$$

Using initial condition $t = 0$, $I_T(0) \geq K$

$$\Longrightarrow I_T \geq I_T(0) exp\left[-\left\{\frac{\alpha_H I_{TH}}{N} + (\eta + \eta_T + \rho)\right\} t\right] \geq 0 \qquad (13)$$

Using equations (3)-(6), we can see that we know $I_H \geq 0, I_{TH} \geq, R \geq 0, A \geq 0$

5. Numerical Results and Discussion:

We conducted out numerical simulations of the coinfection model helps to demonstrate the findings of the previous qualitative research. Variables and parameters were employed to create the coinfection modelling simulation. For the sake of illustrating our assumptions, we took some of the parameter values as given. By using MATLAB to programme the values for the compartments and parameters, the numerical solutions of the model were performed using language.

$\beta = 0.05,0.1$, $\alpha_T = 0.2,0.3$, $\alpha_H = 0.2,0.3$,$\eta = 0.070, 0.075$, $\eta_T = 0.09,0.2$, $\eta_H = 0.5,0.8$

$\eta_{TH} = 0.15,0.2$, $\rho = 2,5$, $\eta_A = 0.2,0.3$

The secondary data taken as all the beginning values and parameters values include:

$S(0) = 1000, I_T(0) = 500, I_H(0) = 400, I_{TH}(0) = 350, R(0) = 200, A(0) = 100$

In Figure (2), we can see the results of the transmission rates of TB and HIV on the susceptible population (S) together with how HIV and HIV/TB population reaches the AIDS compartment. Increasing β values and increasing numbers of sensitive individuals have been recorded. The rate of infection from TB rises, causing the vulnerable population to decline. The risk of transmitting HIV is increasing, while the number of susceptible people is going down. **In figure 3**, the susceptible population is affected by the natural death rate (η), death rate from TB (η_T), and death rate from HIV (η_H). It is discovered that natural death rates and vulnerable populations are on the rise. As TB deaths rise, there is also no significant change in the number of people vulnerable to it. Since more people die from HIV, the population expands, as more of them are exposed to the disease. **Figure (4)** illustrates the influence of the death rate from HIV/TB and TB recuperation rate on the susceptible population. The death rate and vulnerable population are both expected to rise with the spread of HIV/TB. The ability to recover from TB is getting better, and the amount of the population who are susceptible to the disease is increasing slowly. In **figure (5),** the rate at which HIV and HIV/TB populations (β) reach the AIDS compartment has been illustrated and is presented with respect to TB and HIV transmission rates from the TB and HIV infected populations $(\alpha_T \; and \; \alpha_H)$. It is discovered that β rises, whereas the HIV-positive population falls. Higher transmission of TB leads to lower levels of HIV infection. There is a rise in both the

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spread of HIV (α_H) and the number of HIV infected people. It can be shown in **figure (6)** that the transmission rates from TB and HIV $(\alpha_T \; and \; \alpha_H)$ on coinfectious population is represented. It has been noticed that the coinfectious population has reduced, while β has increased. In time, the coinfectious population grows at an increased rate as transmission (α_T) increases. Rate of transmission from HIV (α_H) increases, The coinfectious population exhibits no noticeable increasing trend.

The results of a coinfected population after removing the influence of natural death rate (η), death rate from TB (η_T), death rate from HIV (η_H), and death rate from TB/HIV can be shown **in figure (7).** It's discovered that the death rate is increasing and the coinfected population is shrinking. The population that has both TB and coinfections has a huge rise in death rate. The coinfected population grows a little as death rates due to HIV increase. Coinfected populations suffer death rates because to increases in TB/HIV deaths. **In Figure (8),** the rate at which the HIV and HIV/TB population β reaches the AIDS compartment is illustrated, with transmission rates from TB and HIV α_T and α_H given, which indicates the rates at which individuals who've recovered from TB are likely to transmit HIV and/or TB. It is discovered that β levels increased, reducing the incidence of TB by some margin. The proportion of TB transmission is climbing, and the TB-infected population is expanding. The number of TB survivors is shrinking, while HIV transmission rates are increasing. **Figure (9)** shows the influence of TB casualty rate (η_T), and HIV fatality rate (η_H), and TB recovery rate on the number of TB patients who are cured. It has been shown that TB fatalities are increasing, and those infected are becoming less numerous. There has been a slow rise in the people who have recovered from TB, whereas HIV-related deaths have risen considerably. More people have recovered from TB, and they're able to do so at a consistent rate. **Figure (10)** shows the impact of HIV and HIV/TB population growth rate (β) on AIDS compartment population, HIV and TB transmission rates (α_T and α_H) on AIDS population from TB. According to the source, there are indications that β is increasing, which means the number of AIDS patients is also rising. Slightly, the AIDS population has grown due to an increase in the transmission rate of TB α_T. AIDS continues to expand in size because transmission rate (α_H) is increasing. **Figure (11)** shows the influence of the mortality rate from natural causes (η), tuberculosis-related deaths (η_T), and HIV-related deaths (η_H), on the AIDS population. Natural death rates are rising, and the AIDS population is falling. TB fatalities rise while the AIDS population grows indistinctly. More people die from HIV, although the AIDS population is decreasing. The **figure (12)** demonstrates the impact of TB/HIV mortality rates on the population. It is discovered that TB/HIV deaths and AIDS rates are on the rise. The number of people who with AIDS increases, whereas the number of people who die from AIDS drops.

Fig. 2: Variation in Susceptible population with time t for different values of β, α_T and α_H

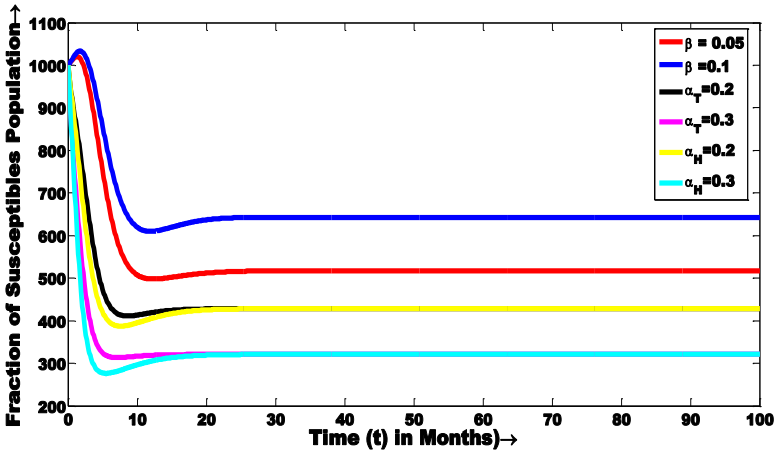

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Fig. 3: Variation in Susceptible population with time t for different values of η, η_T and η_H

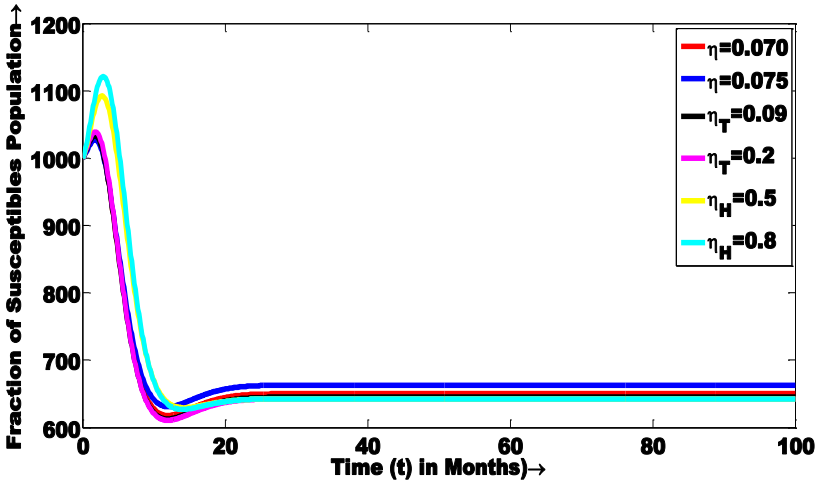

Fig. 4: Variation in Susceptible population with time t for different values of η_{TH} and ρ

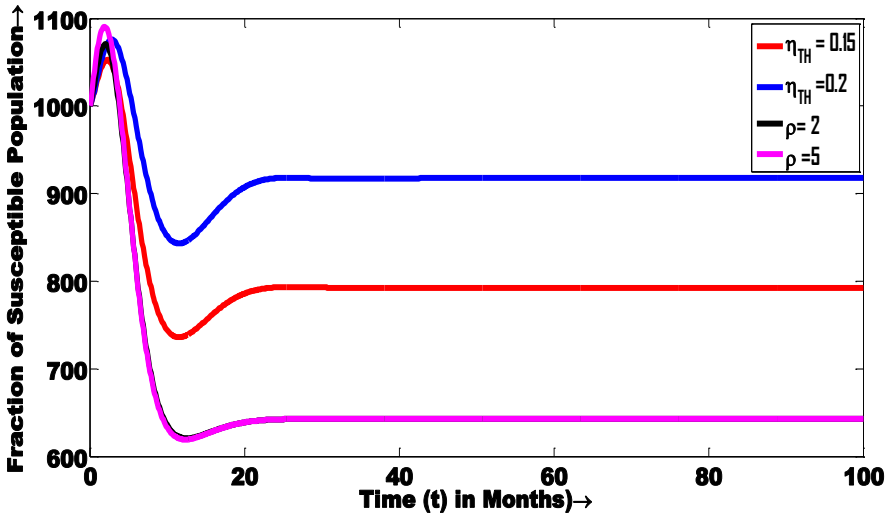

Fig. 5: Variation in HIV infectious population with time t for different values of β, α_T and α_H

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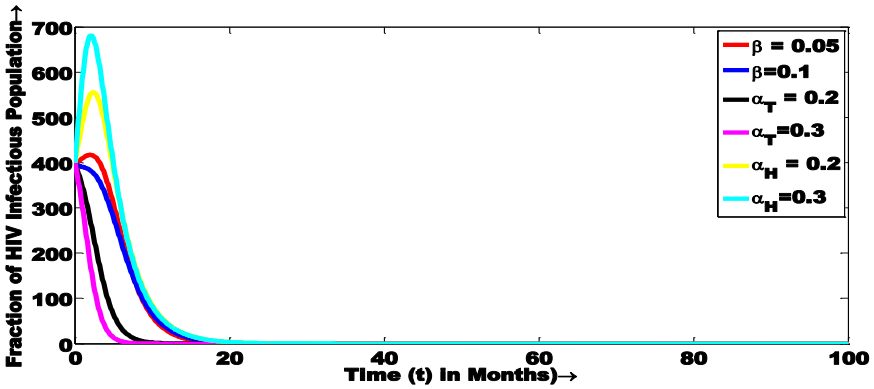

Fig. 6: Variation in coinfectious population with time t for different values of β, α_T and α_H

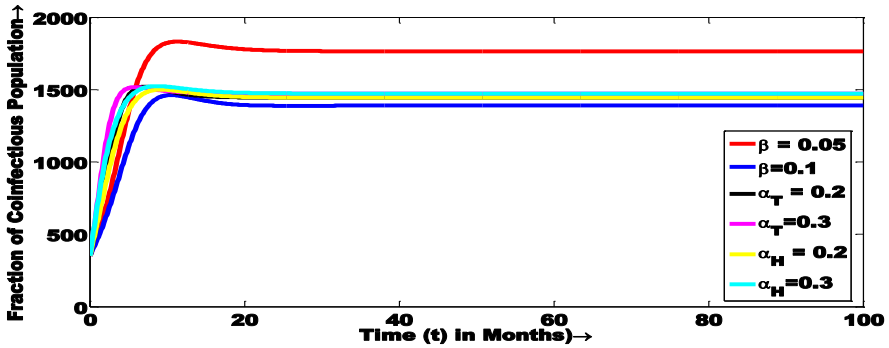

Fig. 7: Variation in coinfectious population with time t for different values of η, η_T, η_H and η_{TH}

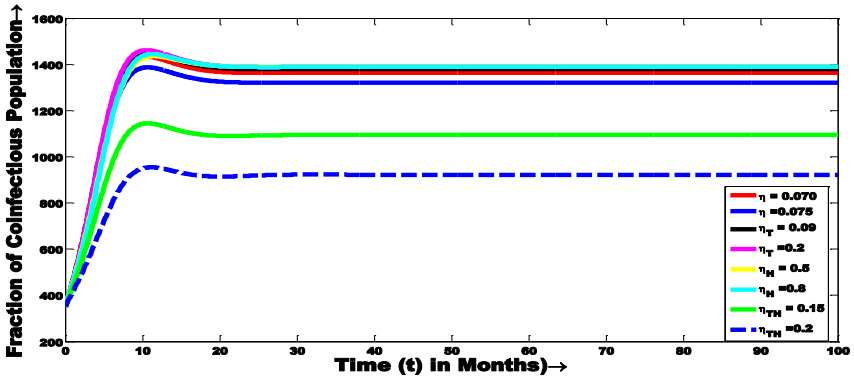

Fig. 8: Variation in Population recovered from TB with time t for different values of β, α_T and α_H

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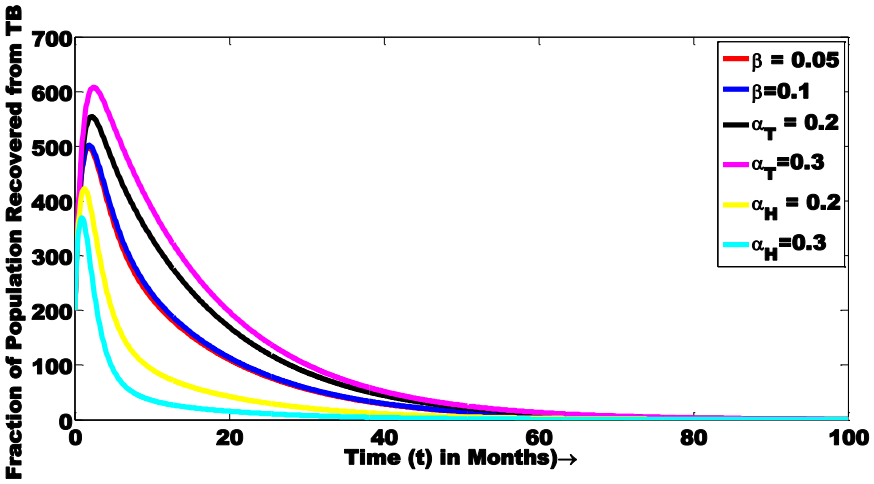

Fig. 9: Variation in Population recovered from TB with time t for different values of η_T, η_H and ρ

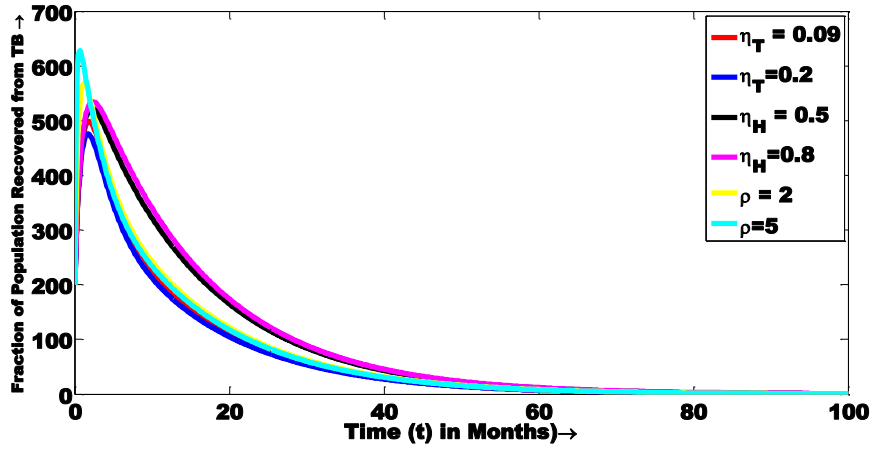

Fig. 10: Variation in AIDS population with time t for different values of β, α_T and α_H

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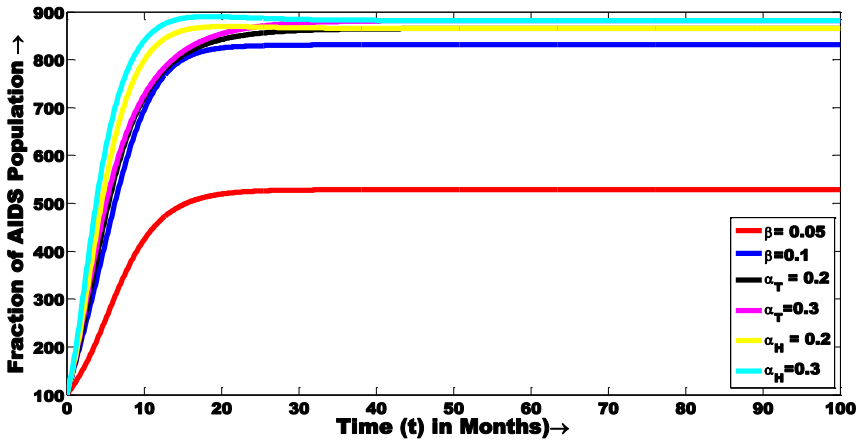

Fig.11: Variation in AIDS population with time t for different values of η, η_T, η_H

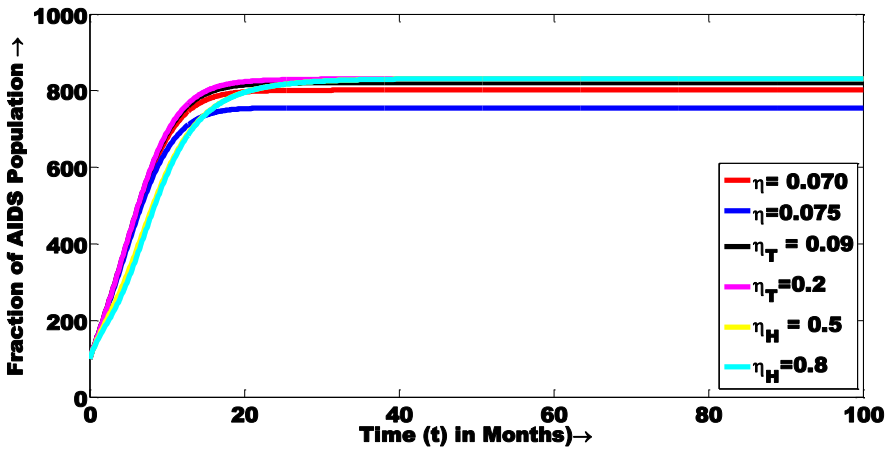

Fig.12: Variation in AIDS population with time t for different values of η_{TH}, η_A

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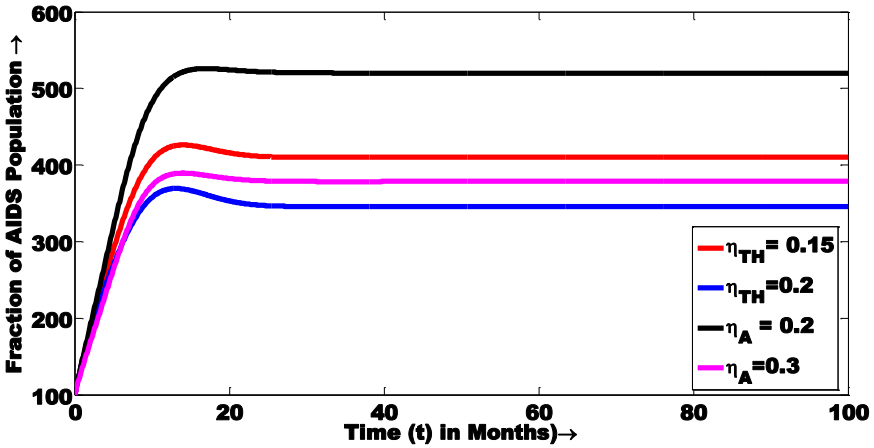

6. Closing Comments:

Infectives with many diseases have harder therapy than infectives that have a single ailment. Therefore, if we can stop co-infected individuals from entering the population, it will allow us to design better plans to keep the numbers of both HIV and TB infections down.

Our model highlights the necessity of adequate counseling of the TB infectives such that, over time, there are no co-infected individuals. It's vital to remember that about 14 million people globally are afflicted with both HIV and hepatitis C. In turn, therapy of both HIV and TB can significantly impact the dynamics of these diseases, and hence is a major parameter. It is also critical to understand how HIV is spread, as well as to educate the public. Regarding our model, we would want to emphasize that treatment and knowledge of HIV-TB co-infection were not considered. We should research the impact of treatment and education for HIV/TB co-infection on the model in the future, and we are looking into it at the moment.

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