

Backward Bifurcation and the Endemic Equilibrium for an HIV/AIDS - Tuberculosis Co infection Model

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Abstract

This study proposes a model that describes the dynamics of HIV/AIDS Co infection with Tuberculosis (TB) using systems of nonlinear ordinary differential equations. A characteristic of nonlinear oscillating systems is the sudden change in behavior which occurs as a parameter passes through a critical value called a bifurcation point. A bifurcation point is a point in parameter space where the number of equilibrium points, or their stability properties, or both, change. The results of the study shows that the Co infection model has a diseases-free equilibrium (DFE) which is globally asymptotically unstable implying that the stable endemic state co-exists with the DFE. Numerical simulations are carried out to illustrate the backward bifurcation phenomenon.

Keywords: Backward bifurcation, Equilibria, Co-infection, Stability .

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1.0 Introduction

A characteristic of nonlinear oscillating systems is the sudden change in behavior which occurs as a parameter passes through a critical value called a bifurcation point . An infectious disease does not invade a population of susceptibles when the basic reproduction number is less than unity. The epidemiological implication of backward bifurcation is that reducing the basic reproduction number to less than unity is not sufficient to control an epidemic (Lawi *et al.*, 2011). When the basic reproduction number is unity, each infectious individual causes one new infection, therefore, whether a disease invades with the basic reproduction number equal to unity will be determined by whether the basic reproduction number increases or decreases as the disease increases along the centre manifold. When backward bifurcation occurs, the DFE may not be globally asymptotically stable even if the basic reproduction number is less than unity and thus a stable endemic state co-exists with the DFE which poses a challenge to the design of effective control measures to be adopted.

2.0 The Model Equations

In this study, a deterministic model exploring the joint dynamics of HIV/AIDS and TB co infections at the population level within a single model is developed. The model is described by a system of ordinary differential equations. The total human population $N_H(t)$ is the sum of the following epidemiological classes: $S_H(t)$ -

Susceptible population at time t, $I_H(t)$ - HIV infected individuals at time t,

$I_A(t)$ - AIDS individuals at time t, $I_T(t)$ - TB infected individuals at time t, $I_{HT}(t)$ - Individuals co

infected with HIV and TB at time t, $I_{AT}(t)$ - Individuals co infected with TB and HIV and have progressed to

AIDS at time t .

$$\begin{aligned} \frac{dS_H(t)}{dt} &= \Lambda_H + r_t I_T(t) - \lambda_{ah} S_H(t) - \lambda_{th} S_H(t) - d_n S_H(t) \\ \frac{dI_H(t)}{dt} &= \lambda_{ah} S_H(t) + r_t I_{HT}(t) - (1 - \alpha) p I_H(t) - e_t^h \lambda_{th} I_H(t) \\ &\quad - d_n I_H(t) + \alpha I_A(t). \\ \frac{dI_A(t)}{dt} &= (1 - \alpha) p I_H(t) + r_t I_{AT}(t) - e_a^t \lambda_{th} I_A(t) - d_a I_A(t) \\ &\quad - d_n I_A(t) - \alpha I_A(t) \\ \frac{dI_T(t)}{dt} &= \lambda_{th} S_H(t) - e_t^h \lambda_{ah} I_T(t) - d_n I_T(t) - d_t I_T(t) - r_t I_T(t) \\ \frac{dI_{HT}(t)}{dt} &= e_t^h \lambda_{ah} I_T(t) + e_h^t \lambda_{th} I_H(t) - (1 - \alpha) \theta_1 p I_{HT}(t) \\ &\quad - d_n I_{HT}(t) - d_t I_{HT}(t) - r_t I_{HT}(t) + \alpha I_{AT}(t). \\ \frac{dI_{AT}(t)}{dt} &= e_a^t \lambda_{th} I_A(t) + (1 - \alpha) \theta_1 p I_{HT}(t) - \alpha I_{AT}(t) \\ &\quad - d_n I_{AT}(t) - d_a I_{AT}(t) - d_t I_{AT}(t) - r_t I_{AT}(t) - d_{at} I_{AT}. \end{aligned}$$

$$\frac{dN_H}{dt} = \Lambda_H - d_n N_H - (d_t A_{AT} + d_a B_{AT} + d_{at} I_{AT})$$

$$A_{AT} = (I_{AT} + I_T + I_{HT}), \text{ and } B_{AT} = (I_A + I_{AT}).$$

The forces of infection are given by:

$$\lambda_{ah} = \frac{\beta_a(1-\delta)c_1(I_H+I_{HT})}{N_H}, \quad \lambda_t = \frac{\beta_t c_2(I_T+I_{HT}+I_{AT})}{N_H}$$

2.1. Invariant Region

The HIV/AIDS-TB model is dissipative: All solutions are uniformly bounded in a proper subset $\{\Omega_{HT} \subset \mathbb{R}_+^6\}$. Let $(S_H, I_H, I_A, I_T, I_{AT}, I_{HT}) \in \mathbb{R}_+^6$ be any solution with non-negative initial conditions. It

can be easily shown that, all the feasible solutions of system enter the region $\left\{ \Omega_{HT} \subset \mathbb{R}_+^6 : N_H \leq \frac{\Lambda_H}{d_n} \right\}$.

Thus, Ω_{HT} is positively invariant and attracting and it is sufficient to consider its solutions in Ω_{HT} . Existence, uniqueness and continuation results for the system hold in this region. Therefore all solutions of the system starting in Ω_{HT} remain in Ω_{HT} for all $t \geq 0$. All parameters and state variables for the model are assumed to be non-negative for $t \geq 0$:

Parameter Values for the HIV/AIDS - TB Co Infection Model

Symbol	Parameter	Value (yr^{-1})	Source
Λ_H	Recruitment rate of humans	$0.4 \times 40 \times 10^4$	Kenya demographics profile (2014)
d_n	Natural death rate of humans	0.016667	Kenya demographics profile (2014)
α	Proportion of the HIV/AIDS victims treated	0.6	Kenya NACC report (2014)
p	Progression rate from HIV to AIDS (untreated)	0.1	Baryama and Mugisha (2007)
β_a	Transmission probability of HIV/AIDS	0.019	Baryama and Mugisha (2007)
c_1	Per capita number of sexual contacts	9	Kenya NACC report (2014)
δ	Effectiveness of counseling	Variable	
d_t	Death rate due to TB	0.02	Juan and Castillo (2009)
β_t	Transmission probability of TB in humans	0.027	Juan and Castillo (2009)
c_2	Contact rate of susceptible humans with the TB infected	15	Juan and Castillo (2009)
θ_2	Increased Progression rate from HIV to AIDS due to TB	2	Estimated
r_t	Proportion of TB victims treated	0.7	WHO report (2013)
d_a	HIV/AIDS-induced death rate	0.4	WHO report (2014)

2.0. Disease-Free Equilibrium Point of the Model

The DFE of the model is given by $\epsilon_{ht}^0 = S_H^0; I_H^0; I_A^0; I_T^0; I_{HT}^0; I_{AT}^0 = \left(\frac{\Lambda_H}{d_n}, 0, 0, 0, 0 \right)$. To study the stability of the DFE, the basic reproduction number (R_{HT}) which governs the qualitative dynamics of the model is first obtained. Define F_i as the rate of appearance of new infections in the class or compartment i and $v_i = v_i^- - v_i^+$, where v_i^- is the rate of transfer of individuals out of compartment i , and v_i^+ is the rate of

transfer of individuals into compartment i by all other means. Therefore the Jacobian of F_i and v_i at the DFE denoted by F and V respectively is given by:

$$F = \begin{pmatrix} \beta_a(1-\delta)c_1 & 0 & 0 & \beta_a(1-\delta)c_1 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \beta_t c_2 & \beta_t c_2 & \beta_t c_2 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} y_1 & -\alpha & 0 & -r_t & 0 \\ -(1-\alpha)p & y_2 & 0 & 0 & -r_t \\ 0 & 0 & y_3 & 0 & 0 \\ 0 & 0 & 0 & y_4 & -\alpha \\ 0 & 0 & 0 & -(1-\alpha)\theta_1 p & y_5 \end{pmatrix}$$

Where $y_1 = (1-\alpha)p + d_n$, $y_2 = d_a + d_n + \alpha$, $y_3 = d_a + d_t + r_t$
 $y_4 = (1-\alpha)\theta_1 p + d_n + d_t + r_t$, $y_5 = \alpha + d_n + d_a + d_t + d_{at} + r_t$.
 The TB reproduction number R_T (under treatment) is given by

$$R_T = \frac{\beta_t c_2}{d_n + d_t + r_t}.$$

The HIV/AIDS reproduction number (R_H) is given by:

$$R_H = \frac{\beta_a(1-\delta)c_1 \{d_n p(\alpha - 1) + (\alpha - 1)\alpha y_2 p \theta_1 + (y_4(y_5 y_2 + d_n r_t))\}}{\{(\alpha - 1)\alpha \pi_1 \theta_1 - d_n p r_t + \alpha p r_t + y_4(y_5 \pi_1 - d_n \pi_2)\}}$$

$$\pi_1 = \alpha d_n + d_a d_n + d_n^2 + d_a p - \alpha d_a p + d_n p - \alpha d_n p$$

$$\pi_2 = -d_n r_t - p r_t + \alpha p r_t.$$

The reproduction number for the system is given by $R_{HT} = \max\{R_T, R_H\}$. The reproduction number of TB (R_T) shows the number of secondary TB infectious cases produced by a TB infectious individual during his or her infectious period when introduced in a population of susceptibles. The HIV/AIDS reproduction number (R_H)

in the presence of TB, gives the number of secondary HIV/AIDS infections produced by an HIV/AIDS infectious individual during his or her infectious period when introduced in a population of susceptibles.

Lemma 1. *The DFE of the HIV/AIDS-TB model is locally asymptotically stable (LAS) if $R_{HT} < 1$, and unstable otherwise.*

Proof: Lemma 1 follows from Theorem 2 by Van and Watmough (2002).

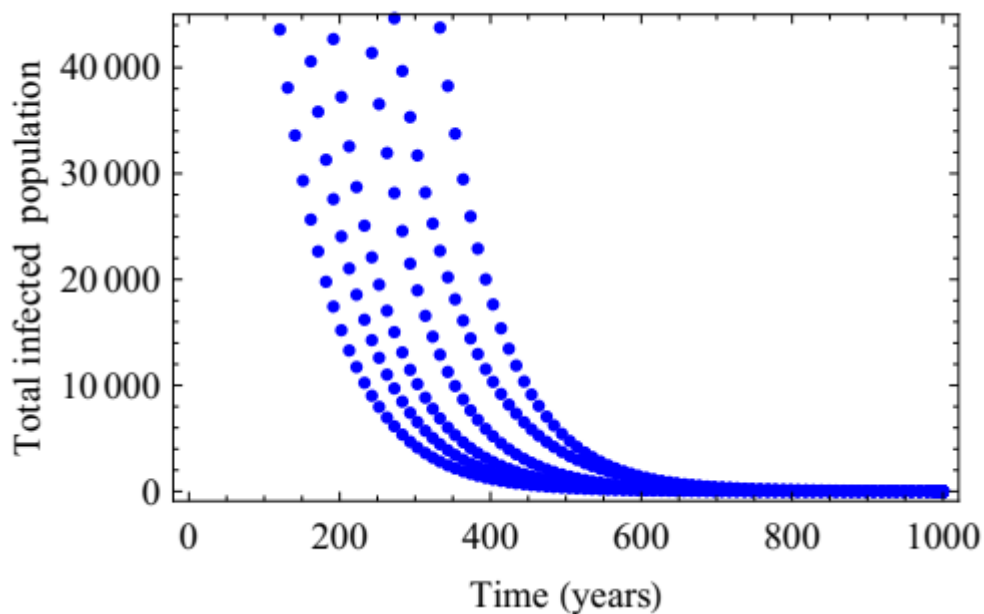


Figure 1: Local Disease Free Equilibrium with $R_H = 0.60610$ and $R_T = 0.7015$.

Figure 1 shows the graph of the total infected ($I_A + I_H + I_T + I_{AT} + I_{HT}$) against time in years. The TB reproduction number $R_T = 0.6061$ and the HIV/AIDS reproduction number $R_H = 0.7015$. The local DFE is stable and there is no possibility of further disease outbreaks in future.

3.0. Global Stability of Disease-Free Equilibrium

To ensure that elimination of the HIV/AIDS - TB co infections is independent of the initial sizes of the sub-populations, it is necessary to show that the DFE is globally asymptotically stable. The global asymptotic stability (GAS) of the disease-free state of the model is investigated using the theorem by Castillo-Chavez et al. (2002). The model is re written as follows:

$$\begin{aligned} \frac{dX}{dt} &= H(X, Z) \\ \frac{dZ}{dt} &= G(X, Z), \quad G(X, 0) = 0 \end{aligned}$$

where the components of the column-vector $X \in \mathbb{R}^m$ denote the uninfected population and the components

of $Z \in \mathbb{R}^n$ denote the infected population. Let $E_0^{ht} = (X^*, 0)$ denote the DFE of this system. The fixed point $E_0^{ht} = (X^*, 0)$ is a globally asymptotically stable equilibrium for this system provided that $R_0 < 1$ and the following two conditions satisfied:

(H1) For $\frac{dX}{dt} = H(X, 0)$: X^* is globally asymptotically stable

(H2) $G(X, Z) = PZ - \hat{G}(X, 0)$, $\hat{G}(X, 0) \geq 0$, for $(X, Z) \in \Omega_{HT}$,

where $P = D_Z G(X^*, 0)$ is an M-matrix (the off diagonal elements of P are non negative) and Ω_{HT} is

the region where the model makes biological sense. The DFE $E_0^{ht} = (X^*, 0)$, where $X^* = \left(\frac{\Lambda_H}{d_n} \right)$

Theorem 1. *The fixed point $E_0^{ht} = (X^*, 0)$ is a globally asymptotically stable equilibrium of the model provided that $R_{HT} < 1$ and the assumptions H1 and H2 are satisfied.*

Proof: From the system

$$H(X, 0) = \begin{pmatrix} \Lambda_H - d_n \\ \Lambda_V - d_v \end{pmatrix}$$

$$G(X, Z) = PZ - \hat{G}(X, Z)$$

$$P = \begin{pmatrix} \beta_1(1 - \delta)c_1 - y_1 & \alpha & 0 & r_t + \beta_1(1 - \delta)c_1 & 0 \\ (1 - \alpha)p & -y_2 & 0 & 0 & r_t \\ 0 & 0 & \beta_t c_2 - y_3 & \beta_t c_2 & \beta_t c_2 \\ 0 & 0 & 0 & -y_4 & \alpha \\ 0 & 0 & 0 & (1 - \alpha)\theta_1 p & -y_5 \end{pmatrix}$$

where: $y_1 = r_m + d_n + d_m$, $y_2 = \beta_a c_1 - (1 - \alpha)p + d_n$, $y_3 = d_a + d_n + \alpha$

$y_4 = r_m + d_m + (1 - \alpha)p\theta_1 - d_n$, $y_5 = r_m + d_m + \alpha + d_n + d_a$

$$\widehat{G} = \begin{pmatrix} G_1(X, Z) \\ G_2(X, Z) \\ G_3(X, Z) \\ G_4(X, Z) \\ G_5(X, Z) \end{pmatrix} = \begin{pmatrix} \lambda_{ah}(1 - \frac{S_H}{N_H}) + e_h^t \lambda_{th} I_H \\ e_a^t \lambda_t I_A \\ \lambda_{th}(1 - \frac{S_H}{N_H}) + e_t^a \lambda_{ah} I_T \\ -(e_t^a \lambda_{ah} I_T + e_h^t \lambda_{th} I_H) \\ -(e_a^t \lambda_{th} I_A) \end{pmatrix}$$

Notice that $G_4(X, Z) < 0$, $G_5(X, Z) < 0$ and so the conditions of **H1** and **H2** are not met so E_0^{ht} may not be globally asymptotically stable when $R_{HT} < 1$. This implies that there is the possibility of future disease outbreaks when the conditions favouring the outbreaks are prevailing leading to the backward bifurcation phenomenon. This result is numerically illustrated in figure 2 representing the graphs of the total infected population against time in years.

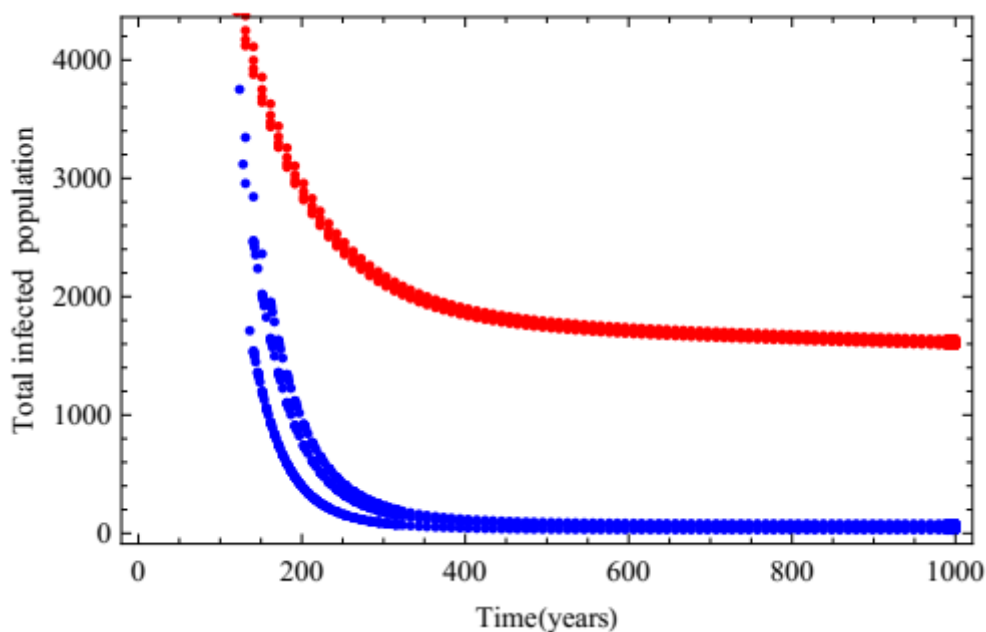


Figure 2: Backward Bifurcation ($R_T = 0.954717$ and $R_H = 0.997300$).

Figure 2 depicts the phenomenon of backward bifurcation, where multiple stable equilibria co-exists when $R_{HT} \leq 1$. The TB reproduction number (R_T) = 0.954717 and the HIV/AIDS reproduction number (R_H) = 0.997303.

5. Conclusion

It is noted that the DFE co exist with the endemic equilibrium resulting into the backward bifurcation phenomenon which implies that the classical epidemiological requirement for the eradication of the disease

whenever $R_{HT} < 1$ is no longer sufficient, though necessary which poses a challenge to the design of effective control measures to be adopted.

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REFERENCES

- Baryama, F. and Mugisha, T. (2007). Comparison of single - stage and staged progression models for HIV/AIDS models. *International Journal of Mathematics and Mathematical Sciences*, 12(4): 399 - 417.
- Juan, P. and Castillo, C. (2009). Mathematical modeling of tuberculosis epidemics. *Mathematical Biosciences and Engineering*, (6) 2: 209 - 237.
- Kenya demographics profile. (2014). Accessed on 3rd August 2015 at www.indexmundi.com/kenya/demographicsprofile 2014.
- Kenya National AIDS Control Council (NACC) Report.(2014). Accessed on 03/08/ 2015 at <http://www.kaisernetwork.org>.
- Lawi, G. O., Mugisha, J. Y. and Omolo - Ongati, N. (2011), Mathematical model for malaria and meningitis co-infection among children. *Applied Mathematical Sciences*, Vol. 5: 47, 2337 – 2359
- Van, P. and Watmough, J. (2002). Reproduction numbers and the sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences*, 180(200): 29-48.
- World Health Organization (WHO). (2013). HIV - Associated TB facts: Challenges and key issues. <http://www.who.int/tb/challenges/hiv/>, Accessed on 13th, August, 2013.
- World Health Organization (WHO). (2014a). The World Health Report; HIV/AIDS global maps, Global prevalence of HIV/AIDS, malaria and tuberculosis. <http://www.google.com/imgres?>, Accessed on 5th, February, 2014.
- World Health Organization (WHO). (2014b). World Malaria Report 2013; Country profiles. <http://www.google.com/imgres?>, Accessed on 5th, February, 2014.