# Mathematical modelling and analysis of HIV/AIDS and trichomonas vaginalis co-infection

by

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# Declaration

I, Chibale Kachinda Mumba, declare that the dissertation, which I hereby submit for the degree Magister Scientiae at the University of Pretoria, is my own work and has not previously been submitted by me for a degree at this or any other tertiary institution.

SIGNATURE:

DATE:

# Dedication

*To my lovely parents*

# Acknowledgements

# Financial Assistance

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# List of Abbreviations

| Abbreviation | Meaning |
|---|---|
| TV | Trichomonas vaginalis |
| HIV | Human immunodeficiency virus |
| AIDS | Acquired immune deficiency syndrome |
| DFE | Disease-free equilibrium |
| EEP | Endemic equilibrium point |
| LAS | Locally-asymptotically stable |
| GAS | Globally-asymptotically stable |
| HAART | Highly active antiretroviral therapy |
| STI | Sexually transmitted infection |

**Abstract**

Deterministic models for the transmission dynamics of HIV/AIDS and trichomonas vaginalis (TV) in a human population are formulated and analysed. The models which assumed standard incidence formulations are shown to have globally asymptotically stable (GAS) disease-free equilibria whenever their associated reproduction number is less than unity. Furthermore, both models possess a unique endemic equilibrium that is GAS whenever the associated reproduction number is greater than unity. An extended model for the co-infection of TV and HIV in a human population is also designed and rigorously analysed. The model is shown to exhibit the phenomenon of backward bifurcation, where a stable disease-free equilibrium (DFE) co-exists with a stable endemic equilibrium whenever the associated reproduction number is less than unity. This phenomenon can be removed by assuming that the co-infection of individuals with HIV and TV is negligible. Furthermore, in the absence of co-infection, the DFE of the model is shown to be GAS whenever the associated reproduction number is less than unity. This study identifies a sufficient condition for the emergence of backward bifurcation in the model, namely TV-HIV co-infection. The endemic equilibrium point is shown to be GAS (for a special case) when the associated reproduction number is greater than unity. Numerical simulations of the model, using initial and demographic data, show that increased incidence of TV in a population increases HIV incidence in the population. It is further shown that control strategies, such as treatment, condom-use and counselling of individuals with TV symptoms, can lead to the effective control or elimination of HIV in the population if their effectiveness level is high enough.

# Chapter 1

# Introduction

## 1.1 Public Health Impact

HIV/AIDS is one of the most severe health problems globally, with over 6.1 million cases (as of July 2015) [25]. South Africa is one of the countries with a very high number of people living with HIV/AIDS. It is therefore of paramount interest to look into the factors leading/resulting in this high prevalence rate of HIV/AIDS.

In this study, we consider the co-infection of two sexually transmitted infection (STI) called Trichomonas Vaginalis (TV) and HIV/AIDS. TV is an infection very common in both men and women, it is also the most prevalent non-viral STI globally [51] with more than 276 million people worldwide being annually affected [55]. Condoms are effective at reducing, but not fully preventing the transmission of both HIV and TV. TV infection is treated and cured with metromidazole (7 days course) or tinidazole (2 days course) and can clear on its own after 3 months. HIV/AIDS on the other hand is treated using highly active antiretroviral therapy (HAART), however there is no cure.

In women, TV is associated with vaginal itching, vaginal discharge, pain when urinating, e.t.c. [31]. Most men do not show any symptoms related to TV infection, although some experience swelling of the scrotum, urethral discharge and pain when urinating [31]. Further complications in women (particularly pregnant women) resulting from lack of treatment include pre-term delivery, low birth weight, and increased mortality, premature rapture of membranes, cervical cancer e.t.c. [13, 35, 49]. TV is of interest to this study because of its susceptibility to HIV, for instance, it increases the chances of an infected woman acquiring HIV if she has sexual contact with an infected individual [32, 34, 52]. Also, a woman is more likely to transmit HIV to her sexual partners if she is infected with TV [28, 35].

TV is not recognised as a severe STI. It is one of the most prevalent non viral STI's and yet it receives the least public health attention [51]. Few papers have attempted a mathematical report of this topic [4, 11, 40], however, TV requires more attention due to the damage it causes to the vaginal epithelium which increases a woman's chances of acquiring HIV infection. Furthermore, the parasite causes lysis of epithelial cells in the vaginal area. This results in more inflammation and leads to the disruption of the protective barrier which is usually provided by the epithelium.

## 1.2 Replication cycle (staged-progression) of HIV/AIDS

HIV infects the CD4$^+$ T cells and it is here where it predominantly replicates. The virus enters the cells by fusion after binding to the CD4 glycoprotein together with a chemokine receptor. The virus also infects other CD4-bearing cells, such as monocytes, tissue macrophages and dendritic cells, that replicate HIV inefficiency relative to CD4$^+$ T cells. The typical course of HIV infection proceeds via the following three consecutive stages:

### 1.2.1 Primary stage

At the time of introduction into an individual, HIV infects both resting and activated CD4$^+$ T cells but integrates and multiplies only in activated CD4$^+$ T cells. At the beginning, such replication continues virtually unopposed by the immune system. Hence, the rate of HIV replication is far greater than that of its clearance. The viral influx provokes the immune system, eventually triggering the activation of HIV-specific B cells (antibody producing cells) and the clonal expansion and differentiation of CD8$^+$ T cells into anti-HIV cytotoxic T lymphocytes (CTLs). This increase in HIV concentration (viremia) triggers the next round of activation of HIV-specific memory and residual naive CD4$^+$ T, CD8$^+$ T and B cell populations, resulting in the appearance of anti-HIV CTLs in the blood of the HIV-infected individual within 1 to 4 weeks, and anti-HIV antibodies within 8 to 12 weeks of initial infection. Even though this anti-HIV immune response effectively suppresses HIV viremia, by reversing the rates of HIV replication and its clearance, it fails to completely eradicate HIV.

### 1.2.2 Asymptomatic (chronic) stage

In general, an HIV infection is characterized by the appearance of a vigorous anti-HIV immune response usually capable of suppressing HIV replication leading to a major decrease of HIV in circulation with a corresponding increase in the numbers of CD4$^+$ T cells. The anti-HIV CTLs play a critical role in this process. However, the immune response fails to block HIV replication completely. Such failure is characterized by the persistence of low levels of viral replication and a gradual, but steady, decline in the CD4$^+$ T cells in the absence of clinical disease. This asymptomatic phase may last for many years or over a decade. In this stage, the rate of clearance of HIV is consistently greater than that of its replication.

### 1.2.3 AIDS stage

Levels of HIV in circulation remain low during the asymptomatic phase, however, a gradual but steady decline in the numbers of CD4$^+$ T cells continues. Once the CD4$^+$ T cell numbers reach below a threshold, the HIV concentration in circulation starts to rise rapidly (reaching levels $> 10^6$ virions/$ml$ blood) and the patient exhibits a precipitous loss of immunity to many other pathogens. This last stage of HIV disease is referred to as AIDS. In this phase, the patient invariably acquires life-threatening opportunistic infections that lead to death. A noteworthy feature of this phase of disease is the persistence of high concentrations of HIV in circulation with minimal CD4$^+$ T cell counts. Additional information on modelling the immuno-pathogenesis of HIV can be found in [19, 36] and the references therein. The above stages are illustrated in Figure 1.1.
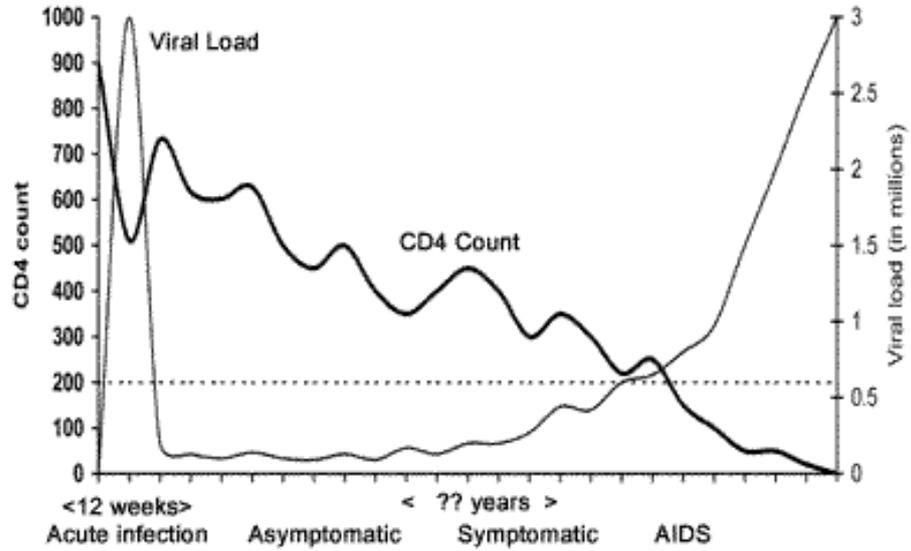
Figure 1.1: *Course of HIV infection in a typical adult.*

## 1.3 Staged Progression of trichomonas vaginalis (TV)

In women, trichomonas vaginalis is found in the lower female genital tract and in men it resides in the urethra and prostate. Here, it replicates by binary fission. The parasite does not survive well in the external environment and it does not appear to display a cyst form. Humans are the only known host for TV and it is mainly transmitted through sexual intercourse [10]. The progression stages of TV are depicted by Figure 1.2.
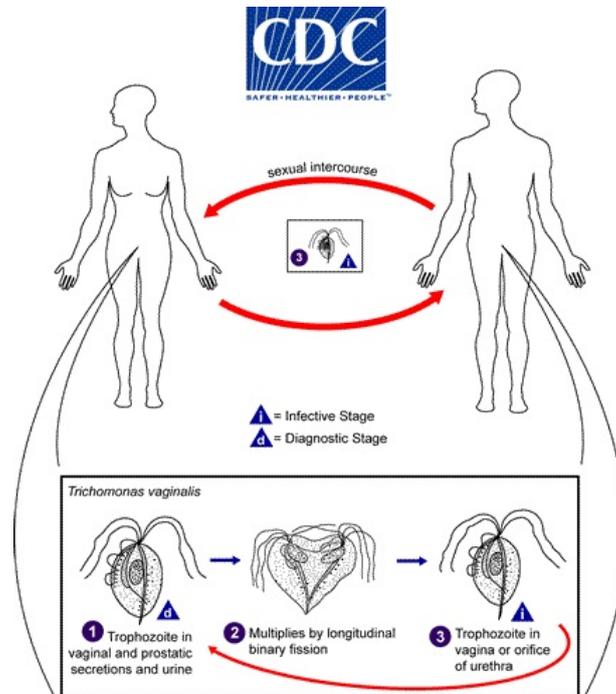


Figure 1.2: *Life Cycle of TV [10].*

The prevalence rate of TV among individuals with other STIs or multiple sexual partners is higher than in those without. In women, TV infection is commonly symptomatic. The prominent symptom is vaginitis with a purulent discharge. In addition to this, a woman may have vulvar and cervical lesions, dysuria and dyspareunia and abdominal pain. On the other hand, TV infection in men is frequently asymptomatic. Occasionally, there can be an occurrence of urethritis, epididymitis, and prostatitis. TV has an incubation period of 5 to 28 days [10].

## 1.4 Research Objectives

The objectives of this study are:

1. To design and rigorously analyse a model for the transmission dynamics of:

    (a) Trichomonas vaginalis (TV) only.

    (b) HIV/AIDS only.

    (c) TV and HIV/AIDS co-infection.

2. To gain insight into the transmission dynamics of TV and HIV/AIDS.

3. To assess the effectiveness of the control strategies available in reducing TV and HIV/AIDS prevalence.

4. To discuss some applications of the model for the purpose of managing the diseases.

## 1.5 Research Questions

The research questions are:

1. Will reducing TV infection substantially reduce HIV transmission?

2. What control interventions are necessary?

## 1.6 Dissertation Organization

This dissertation consists of five chapters. Chapter 1 gives an introduction of the study. Chapter 2 discuss some mathematical concepts applicable to the study. A TV-only model and an HIV/AIDS-only model are formulated and analysed in Chapter 3. Chapter 4 discusses the TV and HIV/AIDS co-infection model. It deals with the construction and analysis of this model as well as an assessment of control strategies. Numerical simulations of results obtained using mathematical tools (such as MATLAB and Maple) are displayed and the conclusion is given in Chapter 5.

# Chapter 2

# Mathematical Tools

In this chapter, the relevant literature used in the study is presented. First, mathematical and epidemiological preliminaries will be stated, and then a review of some co-infection models is presented.

## 2.1 Mathematical Preliminaries

In this section, some of the key mathematical theories and methodologies relevant to the analysis and understanding of the results presented in subsequent chapters are summarised. Throughout this section, for any $n \in \mathbb{N}$, we denote by $\mathbb{R}^n$ the Euclidean space of dimension $n$.

### 2.1.1 Equilibria of linear and non-linear autonomous systems

Consider the system of differential equation below,

$$\dot{x} = f(x, t), \quad x(0) = x_0. \tag{2.1.1}$$

Here $f : U \times \mathbb{R}_+ \to \mathbb{R}^n$ with $x \in U \subset \mathbb{R}^n$, $t \in \mathbb{R}_+$, $n \in \mathbb{N}$, and $U$ open in $\mathbb{R}^n$. The over dot in (2.1.1) represents the derivative with respect to time $(\frac{d}{dt})$ and (2.1.1) is referred to as a vector field on $\mathbb{R}^n$ or ordinary differential equation. Vector fields which explicitly depend on time are called non-autonomous, while vector fields that are independent of time are called autonomous. This dissertation only considers autonomous systems.

Consider the following general autonomous system
For $x \in U \subset \mathbb{R}^n$,

$$\dot{x} = f(x), \quad x(0) = X \in \mathbb{R}^n. \tag{2.1.2}$$

**Definition 2.1** *By a solution of (2.1.2), we mean a continuously differentiable function $x : I(X) \to \mathbb{R}^n$ such that $x(t)$ satisfies (2.1.2) [46].*

**Definition 2.2** *System (2.1.2) defines a dynamical system in a subset $E \subset \mathbb{R}^n$ if, for every $X \in E$, there exist a unique solution of (2.1.2) defined for all $t \in \mathbb{R}_+$ [46].*

**Definition 2.3** *Let $U$ be an open subset of $\mathbb{R}^n$. A function $f : U \to \mathbb{R}^n$ is Lipschitz if for all $x, y \in U$, there is a $K$ called Lipschitz constant such that*

$$||f(x) - f(y)|| \le K||x - y||.$$

Here $||\cdot||$ stands for the Euclidean norm in $\mathbb{R}^n$. If $f$ is Lipschitz on every bounded subset of $\mathbb{R}^n$, then $f$ is said to be globally Lipschitz [33].

**Theorem 2.1** *Let $f : \mathbb{R}^n \to \mathbb{R}^n$ be globally Lipschitz on $\mathbb{R}^n$. Then there exist a unique solution $x(t)$ to (2.1.2) for all $t \in \mathbb{R}_+$. Therefore (2.1.2) defines a dynamical system in $\mathbb{R}^n$ [46].*

**Definition 2.4** *An equilibrium (fixed) point of (2.1.2) is a point $\bar{x} \in \mathbb{R}$ such that $f(\bar{x}) = 0$.*

Clearly, the constant function $x(t) \equiv \bar{x}$ is a solution of (2.1.2) and by uniqueness of solutions, no other solution curve can pass through $\bar{x}$. If $U$ is the state space of some biological systems described by (2.1.2), then $\bar{x}$ is an equilibrium state such that when the system starts at $\bar{x}$ it will always be at $\bar{x}$ [54].

**Theorem 2.2** *Consider (2.1.1) where $f(x,t) \in C^r, r \geq 1$, on some open set $U \subseteq \mathbb{R}^n \times \mathbb{R}_+$, and let $(x_0, t_0) \in U$. Then there exist a local solution to the equation through the point $x_0$ at $t = t_0$ denoted by $x(t, t_0, x_0)$ with $x(t_0, t_0, x_0) = x_0$ for $| t - t_0 |$ sufficiently small. This solution is unique in the sense that any other solution through $x_0$ at $t = t_0$ must be the same as $x(t, t_0, x_0)$ on their common interval of existence. Moreover $x(t, t_0, x_0)$ is a $C^r$ function of $t, t_0$ and $x_0$ [54].*

**Theorem 2.3** *Let $C \subset U \subseteq \mathbb{R}^n \times \mathbb{R}_+$ be a compact set containing $(x_0, t_0)$. The solution $x(t, t_0, x_0)$ can be uniquely extended forward in $t$ up to the boundary of $C$ [24, 54].*

**Theorem 2.4** *(Gronwall Lemma) Let $x(t)$ satisfy*

$$\frac{dx}{dt} \leq px + q, \quad x(0) = x_0,$$

*for $p, q$ constants. Then for $t \geq 0$,*

$$x(t) \leq e^{pt}x_0 + \frac{q}{p}(e^{pt} - 1), \quad p \neq 0$$

*and*

$$x(t) \leq x_0 + qt, \quad p = 0 \quad [46].$$

### 2.1.2 Stability of solutions

Intuitively, we say that an equilibrium point $\bar{x}(t)$ of the differential equation (2.1.2) is stable if all solutions 'close' to $\bar{x}(t)$ at a given time remain close to $\bar{x}(t)$ for all time. It is asymptotically stable if it is stable and furthermore, all solutions starting near $\bar{x}(t)$ converge to $\bar{x}(t)$ as $t \longrightarrow \infty$. Formal definitions for these concepts is given below:

**Definition 2.5** *Let $\bar{x} \in \mathbb{R}^n$ be an equilibrium point of a dynamical system on $E$ defined by (2.1.2). Then $\bar{x}$ is said to be:*

1. *stable if for any $\epsilon > 0$, there exist $\delta = \delta(\epsilon) > 0$ such that if $||\bar{x}(0) - y(0)|| < \delta$, then, $||\bar{x}(t) - y(t)|| < \epsilon$ for all $t \geq 0$,*

2. *locally attractive if $||\bar{x}(t) - y(t)|| \to 0$ as $t \to \infty$ for all $||\bar{x} - y(0)||$ sufficiently small,*

3. *locally asymptotically stable if $\bar{x}$ is stable and locally attractive. For an asymptotically stable equilibrium point $\bar{x}$ of (2.1.2), the set of all initial data $x(0)$ such that*

$$\lim_{t\to\infty} \Phi(t)x(0) = \bar{x}$$

*is said to be the basin of attraction of $\bar{x}$,*

4. *globally attractive if (2) holds for any $x(0) \in E$, i.e. the basin of attraction of $\bar{x}$ is $E$,*

5. *globally asymptotically stable if (1) and (4) hold,*

6. *unstable if (1) fails*

### 2.1.3 Hartman-Grobman theorem

**Definition 2.6** *The Jacobian matrix of $f$ at the equilibrium $\bar{x}$, denoted by $Df(\bar{x})$, is the matrix*

$$
\begin{pmatrix}
\frac{\partial f_1}{\partial x_1}(\bar{x}) & . & . & . & \frac{\partial f_1}{\partial x_n}(\bar{x}) \\
. & . & & & . \\
. & & . & & . \\
. & & & . & . \\
\frac{\partial f_n}{\partial x_1}(\bar{x}) & . & . & . & \frac{\partial f_n}{\partial x_n}(\bar{x})
\end{pmatrix},
$$

*of partial derivatives of $f$ evaluated at $\bar{x}$ [33].*

To investigate the stability and asymptotic stability of an equilibrium solution of (2.1.2) consider the linearised form of (2.1.2) given by,

$$\dot{U} = JU, \tag{2.1.3}$$

near $\bar{x}(t)$ where $J$ is the Jacobian of the function $f$ at $\bar{x}$. It is assumed that $f$ is differentiable.

**Definition 2.7** *Let $x = \bar{x}$ be an equilibrium solution of (2.1.2). $\bar{x}$ is called a hyperbolic equilibrium point if none of the eigenvalues of $Df(\bar{x})$ have zero real part [54]. An equilibrium point that is not hyperbolic is called non hyperbolic.*

Let $X$ and $Y$ be two topological spaces.

**Definition 2.8** *A function $f : X \to Y$ is a homeomorphism if it is continuous, bijective with a continuous inverse [33].*

**Definition 2.9** *A function $h : X \to Y$ is a $C^1$ diffeomorphism if it is invertible and both $h$ and it's inverse $h^{-1}$ are $C^1$ maps [33].*

Consider two functions $f : \mathbb{R}^n \to \mathbb{R}^n$ and $g : \mathbb{R}^m \to \mathbb{R}^m$.

**Definition 2.10** *$f$ and $g$ are said to be conjugate if there exist a homeomorphism $h : \mathbb{R}^n \to \mathbb{R}^m$ such that, the composition $g \circ h = h \circ f$ (sometimes written as $g(h(x)) = h(f(x))$), $x \in \mathbb{R}^n$ [33].*

**Definition 2.11** *A $C^r (r \geq 1)$ function $\phi : U \times \mathbb{R}_+ \to \mathbb{R}^n$, $U \subset \mathbb{R}^n$ is called a flow for (2.1.2) if it satisfies the following properties*

- $\phi(x_0, 0) = x_0$

- $\phi(x_0, s + t) = \phi(\phi(x_0, s), t)$.

**Definition 2.12** *The set of all points in a flow $\phi(t, x_o)$ for (2.1.2) is called the orbit or trajectory of $f(x)$ with initial condition $x_0$, we write the orbit $\phi(x_0)$. When we consider $t \geq 0$, we say that, $\phi(t, x_o)$ is a forward orbit or forward trajectory.*

**Proposition 2.1** *If $f$ and $g$ are $C^k$ conjugate, then the orbits of $f$ maps to the orbits of $g$ under $h$.*

**Proposition 2.2** *If $f$ and $g$ are $C^k$ conjugate, $k \geq 1$, and $x_0$ is a fixed point of $f$, then the eigenvalues of $Df(x_0)$ are equal to the eigenvalues of $Dg(h(x_0))$.*

**Theorem 2.5** *(Hartman and Grobman) Assume that $f : \mathbb{R}^n \to \mathbb{R}^n$ is of class $C^1$ and consider a hyperbolic equilibrium point $\bar{x}$ of the dynamical system defined by (2.1.2). Then there exist $\delta > 0$, a neighbourhood $\mathcal{N} \subset \mathbb{R}^n$ of the origin and a homeomorphism $h$ defined from the ball $B = \{x \in R^n : ||x - \bar{x}|| < \delta\}$ onto $\mathcal{N}$ such that*

$$u(t) = h(x(t)) \text{ solves } (2.1.3) \text{ if and only if } x(t) \text{ solves } (2.1.2).$$

The direct application of the Hartman-Grobman theorem is that an orbit structure near a hyperbolic equilibrium solution is qualitatively the same as the orbit structure given by the associated linearised (around the zero equilibrium) dynamical system.

## 2.1.4 Linearisation

Determining the stability of an equilibrium (fixed) point $\bar{x}(t)$ requires the understanding of the nature of solutions near it. Let,

$$x = \bar{x}(t) + \epsilon, \ \epsilon \ \in \ \mathbb{R}^n. \tag{2.1.4}$$

If we substitute (2.1.4) in the general autonomous system (2.1.2) where $f$ is at least twice differentiable and apply Taylor's expansion at $\bar{x}$ we get,

$$\dot{x} = \dot{\bar{x}} + \dot{\epsilon} = f(\bar{x}(t)) + Df(\bar{x}(t))\epsilon + O(|\epsilon|^2),$$

where $|.|$ is the norm on $\mathbb{R}^n$. Hence,

$$\dot{\epsilon} = Df(\bar{x}(t))\epsilon + O(|\epsilon|^2). \tag{2.1.5}$$

Equation (2.1.5) describes the evolution of orbits near $\bar{x}$ [45, 18]. The behaviour of the solutions arbitrarily close to $\bar{x}$ is obtained by studying the associated linear system,

$$\dot{\epsilon} = Df(\bar{x}(t))\epsilon. \tag{2.1.6}$$

However, if $\bar{x}(t)$ is an equilibrium solution, i.e $f(\bar{x}) = 0$, then $Df(\bar{x})$ is a matrix with constant entries, and the solution of (2.1.6) through the point $\epsilon_0 \in \mathbb{R}^n$ at $t = 0$ is given by,

$$\epsilon(t) = \exp(Df(\bar{x}(t)))\epsilon_0. \tag{2.1.7}$$

It follows that $\epsilon(t)$ is asymptotically stable if all eigenvalues of $Df(\bar{x})$ have negative real parts. Then the Hartman-Grobman Theorem, (Theorem 2.5) leads to the following simple characterisation of the stability properties of $\bar{x}$.

**Theorem 2.6** *Suppose all of the eigenvalues of $Df(\bar{x})$ have negative real parts, then, the equilibrium solution $x = \bar{x}$ of the non-linear system (2.1.2) is asymptotically stable [8, 18, 54].*

Routh-Hurwitz stability criterion provides necessary and sufficient conditions for establishing the local stability of a dynamical system. Let

$$det(\lambda I - Df(\bar{x})) = 0,$$

be the characteristic equation of $Df(\bar{x})$. Then we obtain the following polynomial for $\lambda$.

$$a_0\lambda^n + a_1\lambda^{n-1} + ... + a_{n-1} + a_n = 0, \ a_0 > 0. \tag{2.1.8}$$

Then we define the Hurwitz matrix associated with the above polynomial as follows

$$H_n := (d_{2j-i})_{1 \le i,j \le n} = \begin{pmatrix} a_1 & a_3 & a_5 & a_7 & ... & 0 \\ a_0 & a_2 & a_4 & a_5 & ... & 0 \\ 0 & a_1 & a_3 & a_5 & ... & 0 \\ 0 & 0 & a_2 & a_4 & ... & 0 \\ \vdots & \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & 0 & 0 & ... & a_k \end{pmatrix},$$

where $a_k = 0$ for $k < 0$ or $k > 0$.

**Theorem 2.7** *(Routh-Hurwitz criterion [39, 41]) The roots of equation (2.1.8) have negative real parts if and only if $a_k > 0$ for all $k = 0, 1, ..., n$ and $detH_n[1, ..., n] > 0$ for all $k = 1, 2, ..., n$.*

For $n = 2, 3, \ and \ 4$, the roots of (2.1.8) have negative real parts if and only if
$n = 2 \ : \ a_0 > 0, \ a_1 > 0, \ a_2 > 0,$
$n = 3 \ : \ a_0 > 0, \ a_1 > 0, \ a_2 > 0, a_3 > 0$ and $a_1a_2 - a_0a_3 > 0,$
$n = 4 \ : \ a_i > 0,$ for $i = 0, 1, ...4, \ a_1a_2 - a_0a_3 > 0,$ and $a_1a_2a_3 - a_0a_3^2 - a_4a_1^2 > 0.$

## 2.1.5 Next generation method

The next generation method is a linearisation method that is used to establish the local asymptotic stability of the disease-free equilibrium (DFE) as well as the associated basic reproduction number. The method was first introduced by Diekmann and Hesterbeek [14] and improved for epidemiological models by van den Driessche and Watmough [50]. Below is the method by van den Driessche and Watmough [50]:

Suppose the disease transmission model, with non-negative initial conditions, can be written in terms of the following system:

$$\dot{x}_i = f_i(x_i) = \mathcal{F}_i(x) - \mathcal{V}_i(x), \ \text{for } i = 1, ..n, \tag{2.1.9}$$

where $\mathcal{V}_i = \mathcal{V}_i^- - \mathcal{V}_i^+$ and the function satisfy the following axioms listed below.
First, the disease-free states (non-infected state variables) of the model is defined by:

$$X_s = \{x \ge 0 | x_i = 0, i = 1, ..., m\},$$

where $x = (x_1, ..., x_n)^T$, $x_i \geq 0$ represents the number of individuals in each compartment and the first $m$ compartments corresponding to the infected individuals. Here, $\mathcal{F}_i(x)$ represents the rate of appearance of new infections in compartment $i$; $\mathcal{V}_i^+(x)$ represents the rate of transfer of individuals into compartment $i$ by all other means, and $\mathcal{V}_i^-(x)$ represents the rate of transfer of individuals out of compartment $i$. It is assumend that these functions are at least twice continuously differentiable in each variable [50].

Let $\bar{x}$ be the disease-free equilibrium of (2.1.9) and let $f_i(x)$ satisfy the following conditions:

**(A1)** if $x \geq 0$, then $\mathcal{F}_i(x)$, $\mathcal{V}_i^+(x)$, $\mathcal{V}_i^-(x) \geq 0$ for $i = 1, ..., n$.

**(A2)** if $x_i = 0$, then $\mathcal{V}_i^-(x) = 0$. In particular, if $x \in X_s$ then $\mathcal{V}_i^-(x) = 0$ for $i = 1, ..., m$.

**(A3)** $\mathcal{F}_i(x) = 0$ if $i > m$.

**(A4)** if $x \in X_s$, then $\mathcal{F}_i(x) = 0$ and $\mathcal{V}_i^+(x) = 0$ for $i = 1, ..., m$.

**(A5)** if $\mathcal{F}_i(x)$ is set to zero, then all eigenvalues of $Df(\bar{x})$ have negative real parts.

Then the derivatives $D\mathcal{F}(\bar{x})$ and $D\mathcal{V}(\bar{x})$ are partitioned as

$$D\mathcal{F}(\bar{x}) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix},$$

$$D\mathcal{V}(\bar{x}) = \begin{pmatrix} V & 0 \\ J_3 & J_4 \end{pmatrix},$$

where $F$ and $V$ are the $m \times n$ matrices given by
$F = \left[ \frac{\partial \mathcal{F}_i}{\partial x_j}(\bar{x}) \right]$ and $V = \left[ \frac{\partial \mathcal{V}_i}{\partial x_j}(\bar{x}) \right]$ with $1 \leq i, \ j \leq m$.
Further, $F$ is non-negative, $V$ is non-singular and $J_3$ and $J_4$ are matrices of the transition terms and all eigenvalues of $J_4$ have positive real parts.

**Theorem 2.8** *(van den Driessche and Watmough [50]) Consider the disease transmission model given by (2.1.9) with f(x) satisfying conditions A1-A5. If $\bar{x}$ is the disease-free equilibrium of the model, then $\bar{x}$ is locally asymptotically-stable if $\mathcal{R}_0 = \rho(FV^{-1}) < 1$ (where $\rho(A)$ is the spectral radius of a matrix A), but unstable if $\mathcal{R}_0 > 1$.*

An equilibrium point $\bar{x}$ of (2.1.2) is said to be globally asymptotically stable if all solutions converge to it. In epidemiology, it is important to know whether after an epidemic outbreak, an infectious disease will be established in a population over a period of time and whether this depends on the initial size of the population or not. Mathematically, this is determined by the global asymptotic stability of the endemic equilibrium. Furthermore, models of disease transmission may generally have solutions that differ from the calculated equilibrium solutions. These solutions affect the stability of the equilibria and are generally referred to as closed orbit.
In order to establish global properties of equilibria, it is often necessary to show the non-existence of closed orbits in the feasible region of the model.

**Definition 2.13** *A solution $x(t)$ is said to be a* periodic solution *if $x(t + T) = x(t)$ for all $t$, for some $T > 0$.*

## 2.1.6 Lyapunov functions and LaSalle's invariance principle

An efficient method for analysing the global stability of an equilibrium point is based on the use of Lyapunov functions [54]. Lyapunov functions are energy-like functions that decrease along trajectories [45]. If such a function exists then closed orbits are forbidden.

**Definition 2.14** *A function $V : \mathbb{R}^n \longrightarrow \mathbb{R}$ is said to be positive definite if,*

- *$V(x) > 0$, for all $x \neq 0$,*

- *$V(x) = 0$, if and only if $x = 0$,*

- *$V(x) \longrightarrow \infty$ as $x \longrightarrow \infty$.*

*The function $V$ is locally positive definite if there exists $U \subset \mathbb{R}^n$ containing a fixed point $x = \bar{x}$ such that*

- *$V(\bar{x}) = 0$,*

- *$V(x) > 0$ for all $x \in U \backslash \{\bar{x}\}$.*

**Definition 2.15** *[48] A function $V : \mathbb{R}^n \longrightarrow \mathbb{R}$ is said to be a Lyapunov-candidate if it is a positive definite function. That is, for $U$ in a neighbourhood around $x = 0$,*

- *$V(x) > 0$ for all $x \in U$,*

- *$V(x) = 0$ if and only if $x = \bar{x} = 0$.*

The general Lyapunov Function Theorem is given below.

**Theorem 2.9** *[54] Consider the vector field in (2.1.2) where $\bar{x}$ is an equilibrium solution of (2.1.2) and let $V : U \longrightarrow \mathbb{R}$ be a $C^1$ function defined on some neighbourhood $U$ of $\bar{x}$ such that,*
*i) $V$ is positive definite,*

*ii) if $\dot{V}(x) \leq 0$ in $U \backslash \{\bar{x}\}$, then $\bar{x}$ is stable.*

*iii) if $\dot{V}(x) < 0$ in $U \backslash \{\bar{x}\}$, then $\bar{x}$ is asymptotically stable.*

*iv) If $\dot{V}(x) < 0$ in $\mathbb{R}^n \backslash \{\bar{x}\}$, then $\bar{x}$ globally-asymptotically stable (GAS). whenever i) and ii) hold.*

*Any function $V$ that satisfies the above is called a* Lyapunov function.

**Example 1:** Consider the following vector field, with $\epsilon$ a real parameter,

$$\dot{x} = y,$$

$$\dot{y} = -x - \epsilon x^2 y.$$

The system has a non-hyperbolic equilibrium solution at $(x,y) = (0,0)$. Let $V(x,y) = \frac{(x^2+y^2)}{2}$. Clearly $V(0,0) = 0$ and $V(x,y) > 0$. Furthermore,

$$
\begin{aligned}
\dot{V}(x,y) &= x\dot{x} + y\dot{y}, \\
&= xy + y(-x - \epsilon x^2 y), \\
&= xy - xy - \epsilon x^2 y^2, \\
&= -\epsilon x^2 y^2 < 0, \\
&\text{for} \quad \epsilon > 0.
\end{aligned}
$$

Hence, $\dot{V} < 0$. Thus, by the Lyapunov Function Theorem 2.9 above, the equilibrium $(0,0)$ is stable for $\epsilon > 0$.

## 2.1.7 Limit sets and invariance principle

Since general epidemiology models deal with population of humans or animals, it is important to consider non negative populations, thus, epidemiological models should be considered in (feasible) regions where such property of non-negativity is preserved.

**Definition 2.16** *Let $x(t)$ be a solution of (2.1.2). A point $p$ is said to be a positive limit of $x(t)$, if there exists a sequence $\{t_n\}$ with $t_n \longrightarrow \infty$ as $n \longrightarrow \infty$, such that $x(t_n) \longrightarrow p$ as $n \longrightarrow \infty$. The set of all positive limit points of $x(t)$ is called the positive limit set of $x(t)$.*

**Definition 2.17** *[54] A point $x_0 \in \mathbb{R}^n$ is called*
*i) an $\omega$-limit point of $x \in \mathbb{R}^n$, denoted by $\omega(x)$, if there exists a sequence $\{t_n\}, t_n \longrightarrow \infty$ such that,*

$$\phi(t_n, x) \longrightarrow x_0.$$

*ii) an $\alpha$-limit point of $x \in \mathbb{R}^n$, denoted by $\alpha(x)$, if there exists a sequence $\{t_n\}, t_n \longrightarrow -\infty$ such that,*

$$\phi(t_n, x) \longrightarrow x_0.$$

**Definition 2.18** *The set of all $\omega$-limit points of a flow is called the $\omega$-limit set, while the set of all $\alpha$-limit points of a flow is called the $\alpha$-limit set [54].*

**Definition 2.19** *Let $S \subset \mathbb{R}^n$ be a set. Then, $S$ is said to be invariant under the vector field (2.1.2) if for any, $x(0) \in S$ we have $\phi_i(x_0) \in S$, $\forall t \in \mathbb{R}$. That is, if any trajectory starts in $S$, it will stay in $S$ for all time [45].*

If we restrict the region to positive times ($t \geq 0$), then $S$ is said to be positively invariant set. In other words, solutions in a positively invariant set remain there for all positive time. For negative time, the set is negatively invariant.

**Theorem 2.10** *(LaSalle's invariance principle [54])*
*Let $\bar{x}$ be an equilibrium point of (2.1.2) defined on $\Omega \subset \mathbb{R}^n$. Let $V$ be a positive definite Lyapunov function for $\bar{x}$ on the set $\Omega$. Furthermore let $\Omega_a = \{x \in \bar{\Omega} : \dot{V}(x) = 0\}$ and if*

$$S = \{the\ union\ of\ all\ trajectories\ that\ start\ and\ remain\ in\ \Omega_a\ for\ all\ t > 0\},$$

*(that is, $S$ is the largest positively invariant subset of $\Omega_a$ such that $S \subset \Omega$,) then $\bar{x}$ is globally asymptotically stable on $\Omega$ if and only if it is globally asymptotically stable on $S$.*

## 2.1.8 Bifurcation Theory

Mathematical models of phenomena in applied sciences like medicine, biology, physics or engineering typically lead to equations depending on one or more parameters, which are allowed to vary over a specified set (the parameter space).

**Definition 2.20** *Bifurcation can be defined as a qualitative change in dynamics of $\dot{x} = f(x, \mu)$ occurring upon a small change in the parameter ($\mu$).*

Bifurcation occurs at parameter values where the qualitative nature of the flow, such as the number of stationary points or periodic orbits change. If the stationary point ($\bar{x}$) is hyperbolic, a small perturbation of the system will not change the stability characteristics of the stationary point. Hyperbolic stationary points are structurally stable, so local bifurcations occur at points in parameter space where a stationary point is non hyperbolic [45].

**Definition 2.21** *Consider a one-parameter family of one-dimensional vector field $\dot{x} = f(x, \mu)$, an equilibrium solution given by $(\bar{x}, \mu) = (0, 0)$ is said to undergo bifurcation at $\mu = 0$ if the flow for $x$ near zero is not qualitatively the same as the flow near $x = 0$ at $\mu = 0$ [24].*

There are several types of bifurcations. In this dissertation we are interested in forward and backward bifurcation. The definitions follow in the next section.

## 2.1.9 Backward Bifurcation

Bifurcation analysis is the mathematical study of changes in the solutions of the system of differential equations when changing the parameters. The parameter values where they occur are called bifurcation points. By analysing the behaviour of the model at such points, one can derive much about the systems properties. It is well known in disease transmission modelling that a disease can be eradicated when the basic reproduction number $\mathcal{R}_0 < 1$. However, when a backward bifurcation occurs, stable endemic equilibria may also exist for $\mathcal{R}_0 < 1$, this means that the condition that $\mathcal{R}_0 < 1$ is only a necessity but not sufficient to guarantee the elimination of the disease. Indeed, the quantity $\mathcal{R}_0$ must be reduced further to avoid endemic states and guarantee eradication. The scenario is qualitatively described as follows: in the neighbourhood of 1, for $\mathcal{R}_0 < 1$, a stable disease-free equilibrium co-exists with stable endemic equilibrium. The endemic equilibrium disappears by saddle-node bifurcation when $\mathcal{R}_0$ is decreased below a critical value $\mathcal{R}_c < 1$ [5, 20].

**Definition 2.22** *Backward bifurcation happens when $\mathcal{R}_0$ is less than unity; a small positive unstable equilibrium appears while the disease-free equilibrium and a larger positive endemic equilibrium are locally-asymptotically stable [9]. Figure 2.1 depicts the backward bifurcation phenomenon.*
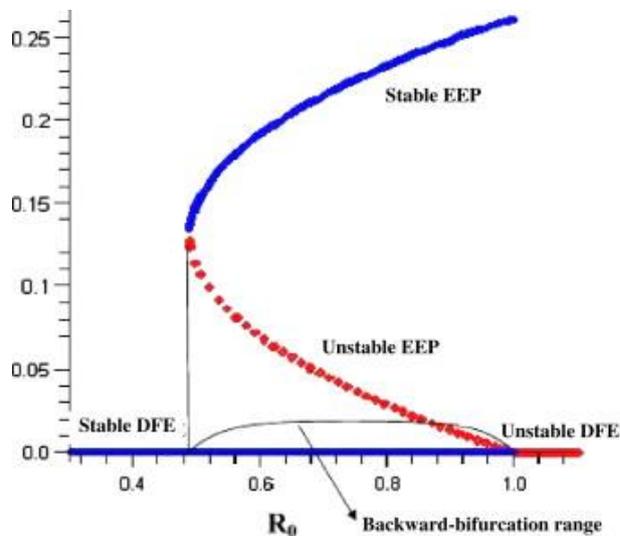


Figure 2.1: *Schematic diagram illustrating backward bifurcation [42].*

*A forward bifurcation occurs when $\mathcal{R}_0$ crosses unity from below; a small positive asymptotically-stable equilibrium appears and the disease-free equilibrium losses its stability [9]. This phenomenon is depicted in Figure 2.2.*
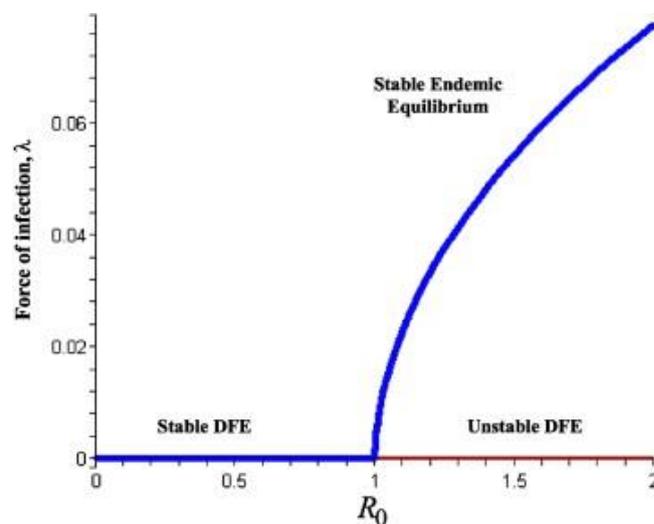


Figure 2.2: *Schematic diagram illustrating forward bifurcation [42].*

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**Theorem 2.11** *(Castillo-Chavez and Song [9])*
*Consider the following general system of ordinary differential equations with a parameter $\phi$,*

$$\frac{dX}{dt} = f(X, \phi), f : \mathbb{R}^n \times \mathbb{R} \longleftrightarrow \mathbb{R}^n, \text{ and } f \in C^2(\mathbb{R}^n \times \mathbb{R}). \qquad (2.1.10)$$

*Without loss of generality, it is assumed that $0$ is an equilibrium for system (2.1.10) for all values of the parameter $\phi$, (that is $f(0, \phi) \equiv 0$ for all $\phi$). Assume*

*A1: $A = D_X f(0, 0) = (\frac{fi}{xj}, 0, 0)$ is the linearised matrix of system (2.1.10) around the equilibrium $0$ with $\phi$ evaluated at $0$. Zero is a single eigenvalue of $A$ and all other eigenvalues of $A$ have negative real parts;*

*A2: Matrix $A$ has a non-negative right eigenvector $w$ and a left eigenvector $v$ corresponding to the zero eigenvalue.*

*Let $f_k$ be the kth component of $f$ and*

$$a = \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i x_j}(0, 0),$$

$$b = \sum_{k,i=1}^{n} v_k w_i \frac{\partial^2 f_k}{\partial x_i \phi}(0, 0).$$

*The local dynamics of system (2.1.10) around $0$ are totally determined by $a$ and $b$.*

*i. $a > 0, b > 0$. When $\phi < 0$ with $|\phi| \ll 1$, $0$ is locally asymptotically stable and there exists a positive unstable equilibrium; when $0 < \phi \ll 1$, $0$ is unstable and there exists a negative and locally asymptotically stable equilibrium.*
*ii. $a < 0, b < 0$. When $\phi < 0$ with $|\phi| \ll 1$, $0$ unstable; when $0 < \phi \ll 1$, $0$ is locally stable, and there exists a positive unstable equilibrium.*
*iii. $a > 0, b < 0$. When $\phi < 0$ with $|\phi| \ll 1$, $0$ unstable and there exists a locally asymptotically stable negative equilibrium; when $0 < \phi \ll 1$, $0$ is stable, and a positive unstable equilibrium appears.*
*iv. $a < 0, b > 0$. When $\phi < 0$ changes from negative to positive, $0$ changes its stability from stable to unstable. Correspondingly a negative unstable equilibrium becomes positive and locally asymptotically stable.*
*Particularly, if $a > 0$ and $b > 0$, then a backward bifurcation occurs at $\phi = 0$.*

## 2.2 Epidemiological preliminaries

In this section, some of the basic principles and methods associated with modelling in epidemiology are discussed. Epidemic models are used to study rapid outbreaks that occur in a short period of time, while endemic models are used for analysing diseases over long periods of time, during which there is renewal of susceptibles typically by birth or recovery from partial immunity [23].

## 2.2.1 Incidence functions

In this subsection, a short description of some of the most commonly used incidence functions is given, see [23, 47] for more details on various incidence functions in mathematical epidemiology.

Consider a community where the total population at time $t$ is denoted by $N(t)$, the susceptibles by $S(t)$ and the infectives by $I(t)$. Disease incidence is defined as the infection rate of susceptible individuals through their contact with infectives [50]. Incidence in disease models is generally characterized by an incidence function (a function that describes the mixing pattern within the community). Infections are transmitted through some kind of contact. The contact rate is defined as the number of times an infective individual comes into contact with other members per unit time. This often depends on the total number $N$ of individuals in the population, and it denoted by a function $C(N)$. If susceptible individuals are contacted by an infected individual they may get infected. Assuming that the probability of infection by every contact is $\beta_0$, then the product $\beta_0 C(N)$ is called the effective contact rate. It shows the capability of an infected individual infecting others (depending on the environment, the toxicity of the virus or bacterium, etc). Generally, apart from the susceptibles, individuals in other compartments of the population can not be infected when contact is made with the infectives. The fraction of the susceptible individuals in the total population is $\frac{S(t)}{N(t)}$, therefore, the mean adequate contact rate of an infective to the susceptibles is $\beta_0 C(N)\frac{S(t)}{N(t)}$, which is referred to as the infective rate. Furthermore, the total number of new infected individuals resulting per unit time, at time $t$, is denoted by $\beta_0 C(N)\frac{S(t)}{N(t)} I(t)$, and is called the incidence of the disease. When the contact rate is proportional to the size of the total population, that is $C(N) = kN$, the incidence given by $\beta_0 k S(t) I(t) = \beta S(t) I(t)$ (where $\beta_0 k = \beta$ is defined as the transmission coefficient) is called the bilinear incidence or simple mass-action incidence [47]. When the contact rate is a constant, that is $C(N) = k$, the incidence is given by $\beta_0 k \frac{S(t)}{N(t)} I(t) = \beta \frac{s(t)}{N(t)} I(t)$ (where $\beta_0 k = \beta$). This type of incidence function is referred to as the standard incidence [47].

Conventionally, it is assumed that new cases are generated through homogeneous mixing, yielding either the mass action incidence term (independent of the total population as described above) or the standard incidence term (dependent on the total population), this assumption may be inaccurate, for example where the incidence does not depend linearly on the number of currently infected individuals. That is, situations where a larger density of infected individuals decrease their per capita infectivity (saturation effect) and situations where multiple exposure to infected individuals are required for transmission to occur (threshold effect) [7]. Other forms of contact rates were also proposed, such as those with saturation as introduced by Dietz [47] and Heesterbeek and Metz [8], with contacts respectively given by,

$$C(N) = \frac{\alpha N}{1 + \omega N}, \quad \text{and} \quad C(N) = \frac{\alpha N}{1 + bN + \sqrt{1 + 2bN}},$$

satisfying,

$$C(0) = 0, \quad C'(N) \geq 0, \quad \left(\frac{C(N)}{N}\right)' \leq 0 \quad \lim_{N \to \infty} C(N) = C_0 \quad [47].$$

Moreover, other incidences for special cases such as $\beta S^p I^q$, $\frac{\beta S^p I^q}{N}$ were also introduced [47].

## 2.2.2 Reproduction number

One of the main results in mathematical epidemiology is that, mathematical epidemic models, exhibit a threshold behaviour. In epidemiological terms it can be said that: when the average number of secondary infections generated by an average infective individual during his or her period of infectiousness (referred to as the basic reproduction number) is less than unity and when this quantity exceeds unity, there is a difference in epidemic behaviour [12]. The basic reproduction number, denoted by $\mathcal{R}_0$, is defined as the number of secondary infections generated by a single infectious individual when introduced into a completely susceptible population over the duration of the infection of this single infectious individual [8]. The famous threshold criterion states that: The disease can invade the population if $\mathcal{R}_0 > 1$, whereas it can not invade the population if $\mathcal{R}_0 < 1$ [14, 50].

The course of the disease outbreak could be rapid enough that there are no significant demographic effects in the population, or there may be a flow of individuals into the population who may become infected. In either case, the disease will die out if the basic reproduction number is less than one, and if it is exceeds unity, there will be an epidemic. Mathematically, if $\mathcal{R}_0 < 1$, the disease-free equilibrium is approached by solutions of the model describing the situation. If $\mathcal{R}_0 > 1$, the disease-free equilibrium is unstable and solutions flow away from it. Furthermore, there is an endemic equilibrium with a positive number of infective individuals. In this case, the disease remains endemic in the population [12]. However, the situation may not be this straightforward, with more than one stable equilibrium when the basic reproduction number is less than one.

# 2.3 Impact of co-infection models

In this section, some co-infection models are discussed. The impact of the results obtained from co-infection models is vital for decision makers. In reality a single disease does not normally exist on its own. It is therefore worthwhile to study diseases that influence or encourage each other's existence. Diseases of special interest are those that tend to have devastating socio-economic implications. One particular importance of studying such models is to determine methods (control strategies) that can help in reducing their existence in the community.

Bhunu and Mushayabasa [4] formulated and analysed a sex structured model of TV and HIV co-infection to explore the impact of HIV on TV and vice-versa. The endemic equilibrium point was shown to exist whenever the corresponding reproduction number was greater than unity. They concluded that TV and HIV fuel each other.

Sharomi *et. al.* [44] designed a deterministic model to address the interaction between HIV and mycobacterium tuberculosis (TB). They evaluated the impact of various treatment strategies of HIV and TB and showed that the TB-Only treatment strategy saves less cases of the mixed infection than the HIV-Only strategy. Their study further showed that in the case where resources are limited, treatment of one of the diseases would be more beneficial in reducing new cases of the mixed infection than targeting the mixed

infection only diseases.

Mukandavire *et. al.* [37] formulated and analysed a deterministic model for the co-infection of HIV and malaria. Using centre manifold theory, they showed that the co-infection model exhibits the phenomenon of backward bifurcation. Simulations of their model showed that the two diseases co-exist whenever their reproduction numbers exceed unity. They also showed that a decrease in sexual activity of individuals with malaria symptoms reduces the number of new cases of HIV and the mixed HIV-malaria infection while increasing the number of malaria cases. They also showed that HIV-induced increase in susceptibility to malaria infection has marginal effect on the new cases of HIV and malaria but there is an increment in the number of new cases of the dual HIV-malaria infection.

Naresh and Tripathi [38] proposed a non-linear model for the transmission dynamics of HIV and TB within a population with varying sizes. They showed that their model possesses four equilibria (disease free, HIV free, TB free and a co-infection equilibrium) and showed that the co-infection equilibrium is always locally stable but may become globally stable under certain conditions which in turn shows that the disease becomes endemic due to constant migration of the population into the habitat.

# Chapter 3

# TV and HIV/AIDS Models

In this chapter, a TV and an HIV/AIDS model are formulated and rigorously analysed for their dynamical features. An analysis of the co-infection of these two diseases is also explored in Chapter 4.

The following are some of the assumptions made in the construction of the TV and the HIV/AIDS models:

1. Each individual in the population is susceptible to TV and HIV.

2. The population is homogeneously mixed, that is, the population interacts uniformly and interacts between time steps.

3. Individuals are equally likely to be infected by the infectious individuals (with TV or HIV) following effective contact.

4. Newborns and migrants are assumed to be susceptibles.

5. There is no vaccine or cure for HIV/AIDS. TV can be cured only after treatment.

## 3.1 Trichomonas Vaginalis (TV) Model

A deterministic model for the transmission dynamics of trichomonas vaginalis is considered and analysed. The total human population at time $t$, given by $N(t)$, is sub-divided into four mutually exclusive compartments consisting of Susceptible individuals $S(t)$, individuals infected with TV ($I_T$), and individuals receiving treatment for TV ($T_T$). So that,

$$N(t) = S(t) + I_T(t) + T_T(t).$$

The susceptible population is generated by the recruitment of individuals into the sexually-active population at (a rate $\Pi$) as well as from the the treatment of individuals with TV at (a rate $\nu$). These individuals acquire TV infection, following effective contact with infected individuals with TV at a rate $\lambda_T$, where

$$\lambda_T = \frac{\beta_1(I_T + \eta T_T)}{N},$$

and $\beta_1$ is the effective contact rate. The modification parameter $0 < \eta < 1$ accounts for the relative risk of infectiousness of individuals on treatment in comparison to those

not receiving treatment. The population of susceptible individuals is further decreased by natural death (at a rate $\mu$). It is assumed that natural deaths occur in all human compartments at the rate $\mu$. Therefore, the rate of change of the susceptible population is given by

$$\frac{dS}{dt} = \Pi + \nu T_T - (\lambda_T + \mu)S.$$

The population of individuals infected with TV is increased by the infection of susceptible individuals (at the rate $\lambda_T$). TV infection is diagnosed after random screening or voluntary testing. This population is decreased by the treatment of TV infected individuals (at a rate $\tau$) and natural death, so that,

$$\frac{dI_T}{dt} = \lambda_T S - (\tau + \mu)I_T.$$

The population of treated individuals is increased by the treatment of individuals with TV (at the rate $\tau$). This population is decreased by the recovery of treated individuals who return to the susceptible class (at a rate $\nu$). The population is further decreased by natural death. It is assumed that there is no partial or permanent immunity to TV and that individuals recover only after receiving treatment. Thus the rate of change of the treated population is given by

$$\frac{dT_T}{dt} = \tau I_T - (\nu + \mu)T_T.$$

Combining the aforementioned assumptions and derivations, it follows that the model for the transmission dynamics of TV takes the form of the following deterministic system of non linear differential equations (a schematic diagram is displayed in Figure 3.1 and a description of the parameters and variables is given in Tables 5.1 and 5.2):

$$\frac{dS}{dt} = \Pi + \nu T_T - (\lambda_T + \mu)S,$$

$$\frac{dI_T}{dt} = \lambda_T S - (\tau + \mu)I_T, \qquad\qquad (3.1.1)$$

$$\frac{dT_T}{dt} = \tau I_T - (\nu + \mu)T_T.$$

### 3.1.1 Qualitative Properties of the Model

In this subsection two basic properties of the model (3.1.1) are explored, namely the feasible solution (invariant region) and the positivity of solutions. The feasible solution depicts the region in which the solutions of the model are biologically plausible. All variables and parameter values are assumed to be non-negative because we are dealing with the human population. Thus, the positivity of the solution describes the non negativity of the solutions of the model.

**Feasible Solution**

**Lemma 3.1** *The feasible region given by*
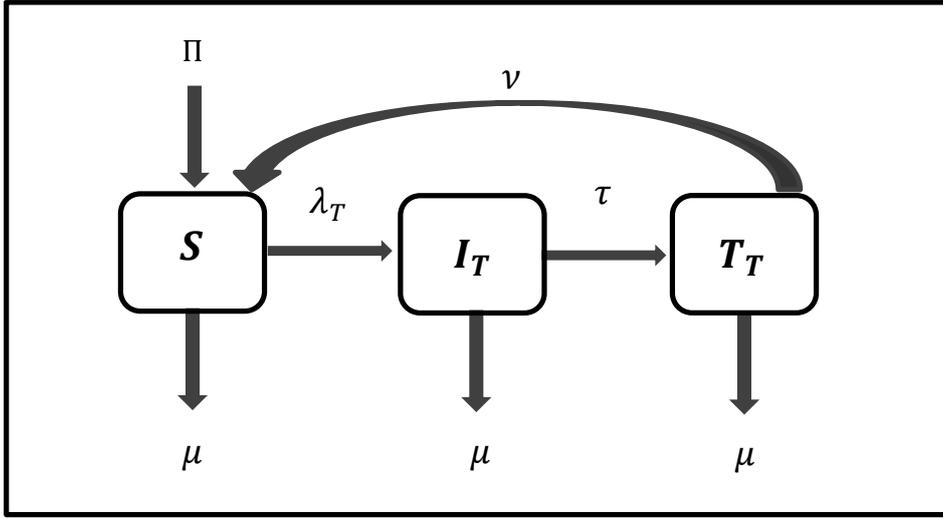
Figure 3.1: *Schematic diagram of the TV-only model (3.1.1).*

$$\mathcal{D} = \{(S, I_T, T_T) \in \mathbf{R}_+^3 : S + I_T + T_T \leq \tfrac{\Pi}{\mu}\},$$

*is positively invariant.*

### *Proof.*

Adding all the differential equations in the model (3.1.1) gives:

$$\frac{dN(t)}{dt} = \Pi - \mu N(t).$$

Thus, the solution becomes,

$$N(t) = N(0)e^{\mu t} + \tfrac{\Pi}{\mu}(1 - e^{-\mu t}).$$

If $N(0) \leq \tfrac{\Pi}{\mu}$, then $N(t) \leq \tfrac{\Pi}{\mu}$.

Therefore, the region $\mathcal{D}$ is positively invariant. This means that in this region the model (3.1.1) is well-posed epidemiologically and mathematically and it is sufficient to study the dynamics of the model (3.1.1) in $\mathcal{D}$. ∎

### Positivity of Solutions

**Lemma 3.2** *Let the initial data $S(0) > 0$, $I_T(0) > 0$, and $T_T(0) > 0$, then the solutions $S(t), I_T(t), T_T(t)$ of the TV-only model (3.1.1) are positive for all $t \geq 0$.*

### *Proof.*

The integrating factor for equation (1) of the TV-only model (3.1.1) is given by:

$$\rho(t) = e^{-(\mu t + \int_0^t \lambda_T(\psi)d\psi)} \geq 0.$$

Thus, using the first equation of system (3.1.1), we have,

$$\frac{d}{dt}\rho(t)S(t) = \rho(t)\Pi,$$

so that integrating both sides yields

$$\rho(t)S(t) = \rho(0)S(0) + \Pi \int_0^t \rho(\psi)d\psi \geq 0.$$

Hence $S(t) \geq 0$ for all $t \geq 0$. Similarly, it can be shown that $I_T(t) \geq 0$, and $T_T(t) \geq 0$ for all $t \geq 0$. ∎

## 3.1.2   Existence and Stability of Equilibria

**Local Stability of Disease-free Equilibrium (DFE)**

The TV-only model (3.1.1) has a unique DFE obtained by setting the right-hand sides of the equations in the model (3.1.1) to zero, given by,

$$\mathcal{E}_1 = (S^*, I_T^*, T_T^*) = \left(\frac{\Pi}{\mu}, 0, 0\right).$$

The linear stability of the DFE, $\mathcal{E}_1$, can be established using the next generation operator method on system (3.1.1) (Van den Driessche and Watmouth, 2002) [50]. The matrices $F$ (for the new infection terms) and $V$ (of the transition terms) are given, respectively by,

$$F = \begin{pmatrix} \beta_1 & \eta\beta_1 \\ 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \tau + \mu & 0 \\ -\tau & \nu + \mu \end{pmatrix}.$$

The associated reproduction number, denoted by $\mathcal{R}_T$ is then given by

$$\mathcal{R}_T = \rho(FV^{-1}) = \frac{\beta_1(K_2 + \eta\tau)}{K_1 K_2},$$

where $K_1 = \tau + \mu$ and $K_2 = \nu + \mu$.

**Lemma 3.3** *The DFE, $\mathcal{E}_1$, of the model (3.1.1) is locally-asymptotically stable (LAS) if $\mathcal{R}_T < 1$ and unstable if $\mathcal{R}_T > 1$.*

The threshold quantity, $\mathcal{R}_T$, is the associated reproduction number for TV [1, 2, 23]. It represents the average number of secondary infections that can be generated by one infected individual if introduced into a susceptible population where a fraction are receiving treatment. The epidemiological implication of Lemma 3.3, is that when $\mathcal{R}_T$ is less than one, introducing a small number of individuals infected with TV into the community would not produce large outbreaks, and the infection dies out in time.

## Global Stability of DFE

The global asymptotic stability of the DFE of the model (3.1.1) is now investigated. First define the invariant region:

$$\tilde{\mathcal{D}} = \{(S, I_T, T_T) \in \mathcal{D} : S \leq S^*\}.$$

**Theorem 3.1** *The DFE, $\mathcal{E}_1$, of the model (3.1.1) is globally-asymptotically stable (GAS) in $\tilde{\mathcal{D}}$ whenever $\mathcal{R}_T \leq 1$.*

***Proof.***
Consider the following Lyapunov function

$$\mathcal{F} = \mathcal{R}_T I_T + \frac{\beta_1 \eta}{K_2} T_T,$$

with the Lyapunov derivative given by

$$\dot{\mathcal{F}} = \mathcal{R}_T \dot{I}_T + \frac{\beta_1 \eta}{K_2} \dot{T}_T,$$

$$= \mathcal{R}_T(\lambda_T S - K_1 I_T) + \frac{\beta_1 \eta}{K_2}(\tau I_T - K_2 T_T),$$

$$= \mathcal{R}_T \lambda_T S - \frac{\beta_1 K_1}{K_1} I_T - \frac{\beta_1 \eta \tau K_1}{K_1 K_2} I_T + \frac{\beta_1 \eta \tau}{K_2} I_T - \frac{\beta_1 \eta K_2}{K_2} T_T,$$

$$= \mathcal{R}_T \lambda_T S - \frac{\beta_1}{K_1 K_2}(I_T + \eta T_T) K_1 K_2,$$

$$\quad (3.1.2)$$

$$= \mathcal{R}_T \lambda_T S - \frac{1}{K_1 K_2} \lambda_T N K_1 K_2,$$

$$= \lambda_T N \left[ \frac{\mathcal{R}_T \lambda_T S}{\lambda_T N} - 1 \right],$$

$$\leq \lambda_T N(\mathcal{R}_T - 1), \quad \text{since,} \quad S \leq S^* \text{ and } S^* \leq N \text{ in } \tilde{\mathcal{D}},$$

$$= \beta_1(I_T + \eta T_T)(\mathcal{R}_T - 1) \leq 0 \quad \text{for} \quad \mathcal{R}_T \leq 1.$$

Since all the model parameters are non-negative, it follows that $\dot{\mathcal{F}} \leq 0$ for $\mathcal{R}_T \leq 1$ with $\dot{\mathcal{F}} = 0$ if and only if $I_T = T_T = 0$. Hence, $\mathcal{F}$ is a Lyapunov function on $\tilde{\mathcal{D}}$. Furthermore, the largest compact invariant set in $\left\{(S, I_T, T_T) \in \tilde{\mathcal{D}} : \dot{\mathcal{F}} = 0\right\}$ is the singleton $\{\mathcal{E}_1\}$. It follows from LaSalle's Invariance principle, (Theorem 2.10), that every solution to the equation in the model (3.1.1) with initial conditions in $\tilde{\mathcal{D}}$, approaches $\mathcal{E}_1$ as $t \to \infty$, so

that $\mathcal{E}_1$ is GAS in $\tilde{\mathcal{D}}$ if $\mathcal{R}_T \leq 1$.

$\blacksquare$

The above mentioned result is very important to public health. The epidemiological implication is that it guarantees disease elimination provided $\mathcal{R}_T$ can be made to a value less than or equal to unity. This result is illustrated in Figure 3.2, showing convergence of solutions to DFE when $\mathcal{R}_T \leq 1$.
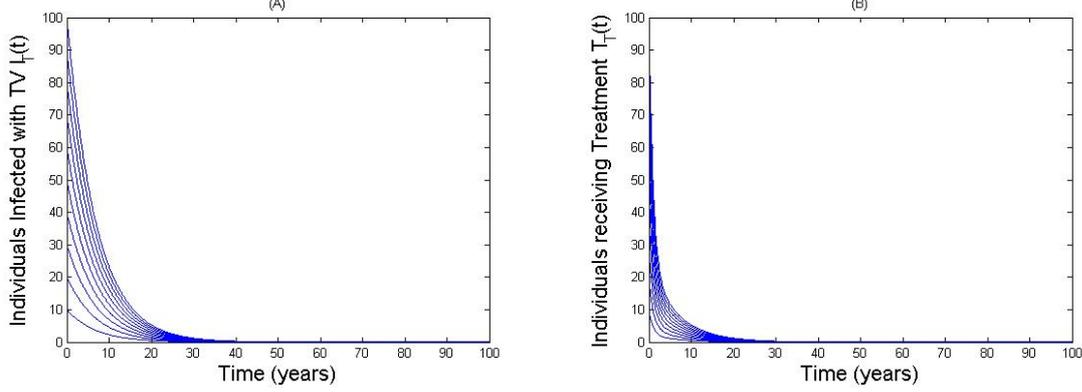


Figure 3.2: *Simulations of the TV-only model (3.1.1) showing that the disease dies out when $\mathcal{R}_T \leq 1$. The parameter values used are as given in Table 5.2.*

**Existence and Local Stability of Endemic Equilibrium Point (EEP)**

**Existence**   We find an equilibrium where at least one of $I_T^{**}$ or $T_T^{**}$ is non zero.
Let the EEP of the model (3.1.1) be denoted by,

$$\mathcal{E}_T = (S^{**}, I_T^{**}, T_T^{**}),$$

and consider the force of infection

$$\lambda_T^{**} = \frac{\beta_1(I_T^{**} + \eta T_T^{**})}{N^{**}}. \tag{3.1.3}$$

Solving the equations in system (3.1.1) in terms of the force of infection, by setting the right hand sides equations in (3.1.1) to zero, gives,

$$S^{**} = \frac{K_1 K_2 \Pi}{\mu[(K_1 + \nu)\lambda_T^{**} + K_1 K_2]}, \quad I_T^{**} = \frac{K_2 \lambda_T^{**} \Pi}{\mu[(K_1 + \nu)\lambda_T^{**} + K_1 K_2]},$$

$$T_T^{**} = \frac{\tau \lambda_T^{**} \Pi}{\mu[(K_1 + \nu)\lambda_T^{**} + K_1 K_2]}. \tag{3.1.4}$$

Substituting (3.1.4) in equation (3.1.3) gives,

$$\lambda_T^{**} = \frac{\beta_1(K_2 + \eta\tau)\lambda_T^{**}}{K_1 K_2 + K_2 \lambda_T^{**} + \tau \lambda_T^{**}}, \tag{3.1.5}$$

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multiplying out gives,

$$\lambda_T^{**}[K_1 K_2 + K_2 \lambda_T^{**} + \tau \lambda_T^{**}] = \beta_1(K_2 + \eta\tau)\lambda_T^{**},$$

$$K_1 K_2 + K_2 \lambda_T^{**} + \tau \lambda_T^{**} = \beta_1(K_2 + \eta\tau),$$

$$(K_2 + \tau)\lambda_T^{**} + K_1 K_2 - \beta_1(K_2 + \eta\tau) = 0,$$

$$(K_2 + \tau)\lambda_T^{**} + K_1 K_2 \left[1 - \frac{\beta_1(K_2 + \eta\tau)}{K_1 K_2}\right] = 0,$$

$$(K_2 + \tau)\lambda_T^{**} + K_1 K_2[1 - \mathcal{R}_T] = 0.$$

This shows that the non-zero (positive endemic) equilibrium of the model satisfy

$$a\lambda_T^{**} + b = 0. \qquad (3.1.6)$$

where,     $a = K_2 + \tau$ and $b = K_1 K_2(1 - \mathcal{R}_T)$.

It is clear that $a > 0$ and $b < 0$ when $\mathcal{R}_T > 1$. Thus the linear system (3.1.6) has a unique positive solution, given by $\lambda_T^{**} = -b/a$ whenever $\mathcal{R}_T > 1$. On the other hand, when $\mathcal{R}_T < 1$, $b > 0$. In this case, the force of infection at steady-state is negative. Hence the model has no positive equilibria in this case.

**Lemma 3.4** *The TV-only model (3.1.1) has a unique positive endemic equilibrium whenever $\mathcal{R}_T > 1$ and no positive endemic equilibrium whenever $\mathcal{R}_T < 1$.*

The local stability property of this endemic equilibrium is now explored.

**Theorem 3.2** *The unique endemic equilibrium of model (3.1.1) is LAS if $\mathcal{R}_T > 1$.*

***Proof.***
The proof is based on transforming the problem of analysing the stability of an equilibrium point to that of analysing the stability of a fixed point. Equation (3.1.5) gives a fixed point problem of the form

$$f(\lambda_T^{**}) = \frac{\beta_1(K_2 + \eta\tau)\lambda_T^{**}}{K_1 K_2 + (K_2 + \tau)\lambda_T^{**}}.$$

It follows that

$$f'(\lambda_T^{**}) = \frac{\beta_1(K_2 + \eta\tau)[K_1 K_2 + (K_2 + \tau)\lambda_T^{**}] - \beta_1(K_2 + \eta\tau)\lambda_T^{**}(K_2 + \tau)}{[K_1 K_2 + (K_2 + \tau)\lambda_T^{**}]^2},$$

$$= \frac{K_1 K_2 \beta_1 (K_2 + \eta\tau)}{[K_1 K_2 + (K_2 + \tau)\lambda_T^{**}]^2},$$

$$= \frac{(K_1 K_2)^2 \mathcal{R}_T)}{[K_1 K_2 + (K_2 + \tau)\lambda_T^{**}]^2}.$$

Evaluating $f'(\lambda_T^{**})$ at $\lambda_T^{**} = \frac{-b}{a}$ gives,

$$f'(\lambda_T^{**})|_{\lambda_T^{**} = \frac{-b}{a}} = \frac{(K_1 K_2)^2 \mathcal{R}_T}{[K_1 K_2 - K_1 K_2(1 - \mathcal{R}_T)]^2},$$

$$= \frac{(K_1 K_2)^2 \mathcal{R}_T}{(K_1 K_2 \mathcal{R}_T)^2},$$

$$= \frac{1}{\mathcal{R}_T}.$$

It is clear that

$$\left| f'(\lambda^{**})|_{\lambda^{**} = \frac{-b}{a}} \right| < 1,$$

whenever $\mathcal{R}_T > 1$. Thus, the unique endemic equilibrium is LAS if $\mathcal{R}_T > 1$. ∎

**Theorem 3.3** *The EEP of the model (3.1.1), is GAS whenever $\mathcal{R}_T > 1$ and $\nu = 0$.*

***Proof.***
Consider the following non-linear Lyapunov function

$$\mathcal{F} = S - S^{**} - S^{**} \ln \frac{S}{S^{**}} + I_T - I_T^{**} - I_T^{**} \ln \frac{I_T}{I_T^{**}} + \frac{\beta_1 \eta S^{**}}{\mu} \left[ T_T - T_T^{**} - T_T^{**} \ln \frac{T_T}{T_T^{**}} \right],$$

with Lyapunov derivative,

$$\dot{\mathcal{F}} = \dot{S} - \frac{S^{**}}{S} \dot{S} + \dot{I}_T - \frac{I_T^{**}}{I_T} \dot{I}_T + \frac{\beta_1 \eta S^{**}}{\mu} \left[ \dot{T}_T - \frac{T_T^{**}}{T_T} \dot{T}_T \right],$$

$$= \Pi - \lambda_T S - \mu S - \frac{S^{**}}{S}(\Pi - \lambda_T S - \mu S) + \lambda_T S - K_1 I_T - \frac{I_T^{**}}{I_T}(\lambda_T S - K_1 I_T)$$

$$+ \frac{\beta_1 \eta S^{**}}{\mu} \left[ \tau I_T - \mu T_T - \frac{T_T^{**}}{T_T}(\tau I_T - \mu T_T) \right].$$

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Let $\tilde{\beta} = \frac{\beta_1 \mu}{\Pi}$. Thus,

$$\dot{\mathcal{F}} = \Pi - \tilde{\beta}(I_T + \eta T_T)S - \mu S - \Pi \frac{S^{**}}{S} + \tilde{\beta} I_T S^{**} + \tilde{\beta} \eta T_T S^{**} + \mu S^{**} + \tilde{\beta}(I_T + \eta T_T)S - K_1 I_T$$

$$- \frac{I_T^{**}}{I_T} \tilde{\beta}(I_T + \eta T_T)S + K_1 I_T^{**} + \frac{\tilde{\beta} \eta S^{**}}{\mu} \tau I_T - \frac{\tilde{\beta} \eta S^{**}}{\mu} \mu T_T - \frac{\tilde{\beta} \eta S^{**}}{\mu} \tau \frac{T_T^{**}}{T_T} I_T + \frac{\tilde{\beta} \eta S^{**}}{\mu} \mu T_T^{**}.$$

It can be shown from the model (3.1.1) that at endemic steady-state,

$$\Pi = \tilde{\beta} I_T^{**} S^{**} + \tilde{\beta} \eta T_T^{**} S^{**} + \mu S^{**},$$

$$K_1 I_T^{**} = \tilde{\beta}(I_T^{**} + \eta T_T^{**})S^{**} \text{ and } \mu T_T^{**} = \tau I_T^{**}.$$

Substituting the above relations gives,

$$\dot{\mathcal{F}} = \tilde{\beta} I_T^{**} S^{**} + \tilde{\beta} \eta T_T^{**} S^{**} + \mu S^{**} - \mu S - (\tilde{\beta} I_T^{**} S^{**} + \tilde{\beta} \eta T_T^{**} S^{**} + \mu S^{**})\frac{S^{**}}{S} + \mu S^{**}$$

$$- \tilde{\beta} S I_T^{**} - \tilde{\beta} \eta \frac{I_T^{**}}{I_T} T_T S + \tilde{\beta}(I_T^{**} + \eta T_T^{**})S^{**} - \tilde{\beta} \eta T_T^{**} S^{**} \frac{I_T}{I_T^{**}} \frac{T_T^{**}}{T_T} + \tilde{\beta} \eta T_T^{**} S^{**},$$

which can be simplified to,

$$= \mu S^{**} \left[ 2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \right] + \tilde{\beta} I_T^{**} S^{**} \left[ 2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \right]$$

$$+ \tilde{\beta} \eta T_T^{**} S^{**} \left[ 3 - \frac{S^{**}}{S} - \frac{I_T T_T^{**}}{I_T^{**} T_T} - \frac{I_T^{**} T_T S}{I_T T_T^{**} S^{**}} \right].$$

Since the arithmetic mean exceeds the geometric mean, the following inequalities hold:

$$2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \leq 0,$$

$$3 - \frac{S^{**}}{S} - \frac{I_T T_T^{**}}{I_T^{**} T_T} - \frac{I_T^{**} T_T S}{I_T T_T^{**} S^{**}} \leq 0.$$

Thus, since all the model parameters are non-negative, it follows that $\dot{\mathcal{F}} \leq 0$ for $\mathcal{R}_T > 1$ and $\mathcal{F}$ is a Lyapunov function on $\mathcal{D}$. Furthermore, the largest compact invariant set in $\left\{ (S, I_T, T_T) \in \mathcal{D} : \dot{\mathcal{F}} = 0 \right\}$ is the singleton $\{\mathcal{E}_T\}$. Thus it follows by LaSalle's Invariance Principle (Theorem 2.10), that $(S(t), I_T(t), T_T(t)) \to (S^{**}, I_T^{**}, T_T^{**})$. Therefore, every solution of the equations of the model (3.1.1) with initial conditions in $\mathcal{D}$ approaches $\mathcal{E}_T$ as

$t \to \infty$ (whenever $\mathcal{R}_T > 1$) so that $\mathcal{E}_T$ is GAS if $\mathcal{R}_T > 1$. ∎

The epidemiological implication of the above result is that if $\mathcal{R}_T$ is greater than one, the infection will invade the community. The result is depicted in Figure 3.3, showing convergence of solutions to EEP when $\mathcal{R}_T > 1$.
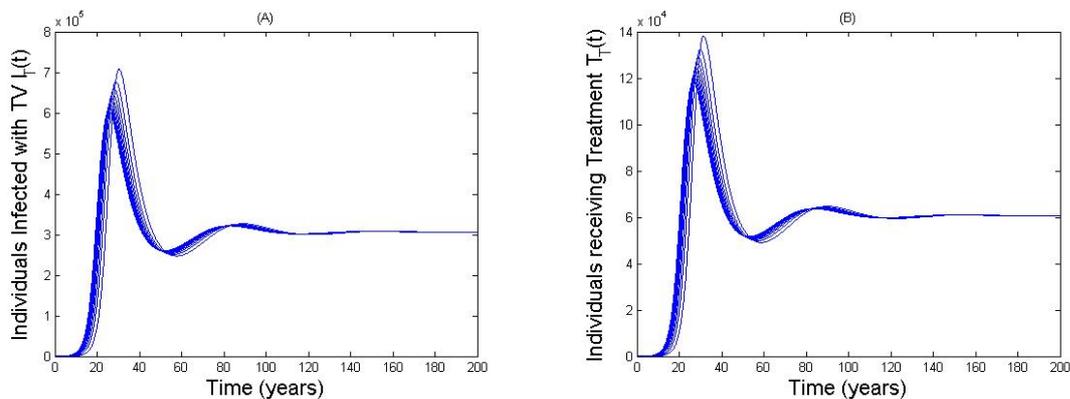


Figure 3.3: *Simulations of the TV-only model (3.1.1) showing that the disease is established when $\mathcal{R}_T > 1$. The parameter values used are as given in Table 5.2.*

## 3.2 HIV/AIDS Model

A deterministic model for HIV/AIDS is considered and analysed. The total human population at time $t$, given by $N(t)$, is divided into four classes, namely, the susceptible class ($S(t)$), individuals infected with HIV who do not possess any HIV-related illnesses ($I_H(t)$), individuals infected with AIDS who have clinical symptoms of AIDS ($A_H(t)$), individuals at HIV and AIDS class receiving treatment ($T_H(t)$), so that

$$N(t) = S(t) + I_H(t) + A_H(t) + T_H(t).$$

The susceptible population is generated by the recruitment of individuals into the sexually-active population at a rate $\Pi$. The individuals acquire HIV infection, following effective contact with infected individuals with HIV at a rate $\lambda_H$, where

$$\lambda_H = \frac{\beta_2(I_H + \eta_A A_H + \eta_T T_H)}{N}.$$

The effective contact rate is $\beta_2$. Here, $0 < \eta_A < 1$ and $0 < \eta_T < 1$ are modification parameters. They account for the relative risk of infectiousness of individuals in class $A_H$ and $T_H$, in comparison to those in class $I_H$. The susceptible population is further decreased by natural death (at a rate $\mu$). Natural deaths occur in all human compartments at the rate $\mu$. The rate of change for the susceptible individuals is given by

$$\frac{dS}{dt} = \Pi - (\lambda_H + \mu)S.$$

The population of individuals infected with HIV in the asymptomatic class is increased by the infection of susceptible individuals (at the rate $\lambda_H$). This population is decreased due to the progression of HIV infected individuals to AIDS class (at a rate $\alpha$), treatment of HIV infected individuals (at a rate $\theta$), and natural death. This gives

$$\frac{dI_H}{dt} = \lambda_H S - (\theta + \alpha + \mu)I_H.$$

The population of individuals infected with AIDS is increased by the progression of individuals with HIV to the AIDS class (at a rate $\alpha$). The population of individuals in class $A_H$ is reduced due to treatment (at a rate $\gamma$), disease induced death (at a rate $\delta_1$) and natural death. So that,

$$\frac{dA_H}{dt} = \alpha I_H - (\gamma + \mu + \delta_1)A_H.$$

The population of treated individuals is increased by the treatment of individuals in classes $I_H$ and $A_H$ (at the rate $\theta$ and $\gamma$, respectively). This population is decreased due to natural death and disease induced death (at a rate $\delta_2$). It is assumed that individuals infected with HIV do not fully recover. It follows that

$$\frac{dT_H}{dt} = \gamma A_H + \theta I_H - (\mu + \delta_2)T_H.$$

Combining the aforementioned assumptions and derivations, it follows that the model takes the form of the following non linear differential equations (a schematic diagram for

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the model is displayed in Figure 3.4 and a description of the parameters and variables is given in Tables 5.1 and 5.2):

$$\frac{dS}{dt} = \Pi - (\lambda_H + \mu)S,$$

$$\frac{dI_H}{dt} = \lambda_H S - (\theta + \alpha + \mu)I_H,$$

$$\frac{dA_H}{dt} = \alpha I_H - (\gamma + \mu + \delta_1)A_H,$$  \hfill (3.2.1)

$$\frac{dT_H}{dt} = \gamma A_H + \theta I_H - (\mu + \delta_2)T_H.$$
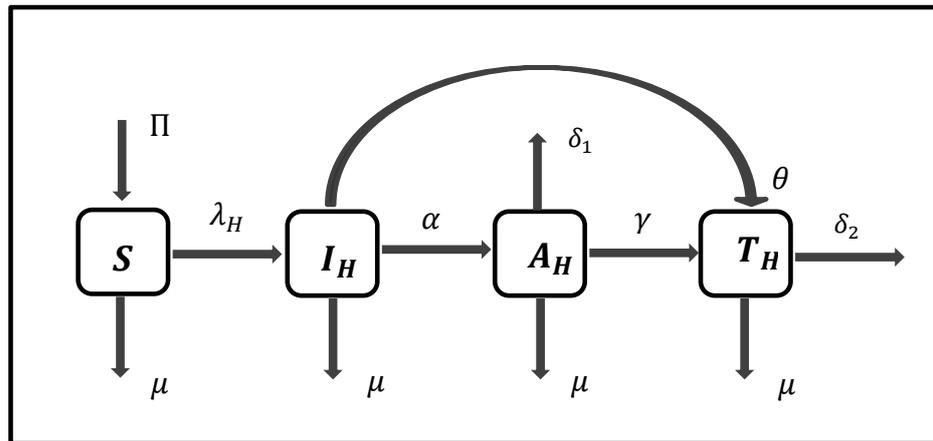


Figure 3.4: *Schematic diagram of the HIV/AIDS-only model (3.2.1).*

## 3.2.1  Qualitative Properties of the model

**Feasible Solution**

**Lemma 3.5** *The feasible region given by*

$$\mathcal{D} = \{(S, I_H, A_H, T_H) \in \mathbf{R}_+^4 : S + I_H + A_H + T_H \le \tfrac{\Pi}{\mu}\},$$

*is positively invariant.*

**Proof.**
Adding all the differential equations in the model (3.2.1) gives:

$$\frac{dN(t)}{dt} = \Pi - \mu N(t) - \delta_1 A_H(t) - \delta_2 T_H(t).$$

it follows that,

$$\frac{dN(t)}{dt} \le \Pi - \mu N(t).$$

Thus (using standard comparison theorem)[30],

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

In particular, $N(t) \leq \frac{\Pi}{\mu}$ if $N(0) \leq \frac{\Pi}{\mu}$.

Therefore, the region $\mathcal{D}$ is positively invariant. Thus, in the region $\mathcal{D}$, the model is well-posed epidemiologically and mathematically and it is sufficient to consider the dynamics of model (3.2.1) in this region. ∎

## Positivity of Solutions

**Lemma 3.6** : *Let the initial data $S(0) > 0$, $I_H(0) > 0$, $A_H(0) > 0$ and $T_H(0) > 0$, then the solutions $S(t), I_H(t), A_H(t), T_H(t)$ of the model (3.2.1) are positive for all $t \geq 0$.*

***Proof.***
The integrating factor of equation (1) of the model (3.2.1) is given by:

$$\rho(t) = e^{(\mu t + \int_0^t \lambda_H(\psi)d\psi)} \geq 0.$$

Thus, using the first equation of system (3.2.1), we have,

$$\frac{d}{dt}\rho(t)S(t) = \rho(t)\Pi,$$

so that integrating both sides yields

$$\rho(t)S(t) = \rho(0)S(0) + \Pi \int_0^t \rho(\psi)d\psi \geq 0.$$

Hence, $S(t) \geq 0$ for all $t \geq 0$. Similarly, it can be shown that $I_H(t) \geq 0, A_H(t) \geq 0$ and $T_H(t) \geq 0$ for all $t \geq 0$. ∎

## 3.2.2 Existence and Stability of Equilibria

### Local Stability of DFE

The HIV/AIDS-only model (3.2.1) has a DFE obtained by setting the right-hand sides of the equations in the model (3.2.1) to zero, given by

$$\mathcal{E}_2 = (S^*, I_H^*, A_H^*, T_H^*) = \left(\frac{\Pi}{\mu}, 0, 0, 0\right).$$

The linear stability of the DFE, $\mathcal{E}_2$, can be determined using the next generation operator method on system (3.2.1) [50]. The matrices $F$ (for the new infection terms) and $V$ (of the transition terms) are given, respectively by

$$F = \begin{pmatrix} \beta_2 & \eta_A\beta_2 & \eta_T\beta_2 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \theta + \alpha + \mu & 0 & 0 \\ -\alpha & \gamma + \mu + \delta_1 & 0 \\ -\theta & -\gamma & \mu + \delta_2 \end{pmatrix}.$$

The reproduction number, denoted by $\mathcal{R}_H$ is then given by

$$\mathcal{R}_H = \rho(FV^{-1}),$$

$$= \frac{\beta_2(K_2 K_3 + \eta_A \alpha K_3 + \eta_T \alpha \gamma + \eta_T K_2 \theta)}{K_1 K_2 K_3}, \tag{3.2.2}$$

$$= \frac{\beta_2[K_3(\eta_A \alpha + K_2) + \eta_T(\alpha \gamma + K_2 \theta)]}{K_1 K_2 K_3},$$

where, $K_1 = \theta + \alpha + \mu$, $K_2 = \gamma + \mu + \delta_1$ and $K_3 = \mu + \delta_2$.

**Lemma 3.7** *The DFE, $\mathcal{E}_2$, of the HIV/AIDS-only model (3.2.1) is LAS if $\mathcal{R}_H < 1$ and unstable if $\mathcal{R}_H > 1$ [50].*

The threshold quantity, $\mathcal{R}_H$, is the associated reproduction number of the HIV/AIDS [1, 2, 23]. It measures the average number of new HIV infections generated by a single HIV-infected individual if introduced into a population where a fraction of individuals are receiving treatment. The epidemiological implication of Lemma 3.7, is that when $\mathcal{R}_H$ is less than unity, a small introduction of infected individuals into the community would not produce an epidemic, and the disease dies out in time.

**Global Stability of DFE**

Here, the global asymptotic stability of the DFE of the model (3.2.1) is investigated. First define the invariant region:

$$\tilde{\mathcal{D}} = \{(S, I_H, A_H, T_H) \in \mathcal{D} : S \leq S^*\}.$$

**Theorem 3.4** *The DFE, $\mathcal{E}_2$, of the HIV/AIDS-only model (3.2.1) is GAS in $\tilde{\mathcal{D}}$ whenever $\mathcal{R}_H \leq 1$.*

***Proof.***
Consider the following Lyapunov function

$$\mathcal{F} = \mathcal{R}_H I_H + \frac{\beta_2(\eta_A K_3 + \eta_T \gamma)A_H}{K_2 K_3} + \frac{\beta_2 \eta_T T_H}{K_3},$$

with Lyapunov derivative,

$$\dot{\mathcal{F}} = \mathcal{R}_H \dot{I}_H + \frac{\beta_2(\eta_A K_3 + \eta_T \gamma)}{K_2 K_3} \dot{A}_H + \frac{\beta_2 \eta_T}{K_3} \dot{T}_H,$$

$$= \mathcal{R}_H[\lambda_H S - K_1 I_H] + \frac{\beta_2(\eta_A K_3 + \eta_T \gamma)}{K_2 K_3}[\alpha I_H - K_2 A_H] + \frac{\beta_2 \eta_T}{K_3}[\gamma A_H + \theta I_H - K_3 T_H],$$

$$= \mathcal{R}_H \frac{\beta_2(I_H + \eta_A A_H + \eta_T T_H)S}{N} - \beta_2(I_H + \eta_A A_H + \eta_T T_H) \qquad (3.2.3)$$

$$\leq \mathcal{R}_H \beta_2(I_H + \eta_A A_H + \eta_T T_H) - \beta_2(I_H + \eta_A A_H + \eta_T T_H), \text{ since. } S \leq S^* \text{ and } S^* \leq N \text{ in } \tilde{\mathcal{D}},$$

$$= \beta_2(I_H + \eta_A A_H + \eta_T T_H)[\mathcal{R}_H - 1] \leq 0, \qquad \text{where,} \qquad \mathcal{R}_H \leq 1.$$

Since all the model parameters are non-negative, it follows that $\dot{\mathcal{F}} \leq 0$ for $\mathcal{R}_H \leq 1$, with $\dot{\mathcal{F}} = 0$ if and only if $I_H = A_H = T_H = 0$. Hence, $\mathcal{F}$ is a Lyapunov function on $\tilde{\mathcal{D}}$. Further, the largest compact invariant set in $\left\{ (S, I_H, A_H, T_H) \in \tilde{\mathcal{D}} : \dot{\mathcal{F}} = 0 \right\}$ is the singleton $\{\mathcal{E}_2\}$. By LaSalle's Invariance principle (Theorem 2.10), every solution to the equations in the model (3.2.1) with initial conditions in $\tilde{\mathcal{D}}$, approaches $\mathcal{E}_2$ as $t \to \infty$ whenever $\mathcal{R}_H \leq 1$, so that $\mathcal{E}_2$ is GAS in $\tilde{\mathcal{D}}$ if $\mathcal{R}_H \leq 1$. ∎

The epidemiological implication of the above result is that it guarantees disease elimination provided $\mathcal{R}_H$ can be made to a value less than or equal to unity. The result is illustrated in Figure 3.5 showing convergence of solutions to DFE when $\mathcal{R}_H \leq 1$.

**Existence and local Stability of EEP**

**Existence**   We find an equilibrium where at least one of $I_H^{**}, A_H^{**}$ and $T_H^{**}$ is non zero. Let the EEP of the model (3.2.1) be denoted by,

$$\mathcal{E}_H = (S^{**}, I_H^{**}, A_H^{**}, T_H^{**}),$$

and consider the force of infection,

$$\lambda_H^{**} = \frac{\beta_2(I_H^{**} + \eta_A A_H^{**} + \eta_T T_H^{**})}{N^{**}}. \qquad (3.2.4)$$

Solving the equations in system (3.2.1) in terms of the force of infection, by setting the right hand sides of the equations in (3.2.1) to zero, gives,

$$S^{**} = \frac{\Pi}{\mu + \lambda_H^{**}}, \qquad I_H^{**} = \frac{\lambda_H^{**}\Pi}{K_1(\mu + \lambda_H^{**})},$$

$$A_H^{**} = \frac{\alpha\lambda_H^{**}\Pi}{K_1 K_2(\mu + \lambda_H^{**})}, \qquad T_H^{**} = \frac{(\gamma\alpha + \theta K_2)\lambda_H^{**}\Pi}{K_1 K_2 K_3(\mu + \lambda_H^{**})}. \qquad (3.2.5)$$

Substituting (3.2.5) into equation (3.2.4) yields,

$$\lambda_H^{**} = \frac{(K_2K_3 + \eta_A\alpha K_3 + \eta_T\gamma\alpha + \eta_T\theta K_2)\lambda_H^{**}\beta_2}{K_1K_2K_3 + \lambda_H^{**}K_2K_3 + \alpha\lambda_H^{**}K_3 + \lambda_H^{**}\gamma\alpha + \lambda_H^{**}\theta K_2}.$$

Multiplying out and collecting like terms gives,

$$(K_2K_3 + \alpha K_3 + \gamma\alpha + \theta K_2)\lambda_H^{**} - K_1K_2K_3 - K_1K_2K_3\mathcal{R}_H = 0,$$

$$(K_2K_3 + \alpha K_3 + \gamma\alpha + \theta K_2)\lambda_H^{**} + K_1K_2K_3(1 - \mathcal{R}_H) = 0.$$

This shows that the non-zero (positive) endemic equilibrium of the model satisfy

$$a\lambda_H^{**} + b = 0, \tag{3.2.6}$$

where
$a = K_2K_3 + \alpha K_3 + \gamma\alpha + \theta K_2$ and $b = K_1K_2K_3(1 - \mathcal{R}_H)$.

It is obvious that $a > 0$ and $b > 0$ when $\mathcal{R}_H < 1$. Thus the linear system (3.2.6) has a unique positive solution, given by $\lambda_H^{**} = -b/a$ whenever $\mathcal{R}_H > 1$. On the other hand, when $\mathcal{R}_H < 1$, the model has no positive equilibria because the force of infection at steady state is negative. These results are summarized below:

**Lemma 3.8** *The HIV/AIDS-only model (3.2.1) has a unique positive endemic equilibrium whenever $\mathcal{R}_H > 1$ and no positive endemic equilibrium whenever $\mathcal{R}_H < 1$.*

**Local Stability of the EEP**

**Theorem 3.5** *The unique endemic equilibrium of the HIV/AIDS-only model (3.2.1) is LAS if $\mathcal{R}_H > 1$.*

***Proof.***
The proof is based on transforming the problem of analysing the stability of an equilibrium point to that of analysing the stability of a fixed point. Equation (3.2.6) gives a fixed point problem of the form,

$$f(\lambda_H^{**}) = \frac{(K_2K_3 + \eta_A\alpha K_3 + \eta_T\gamma\alpha + \eta_T\theta K_2)\lambda_H^{**}\beta_2}{K_1K_2K_3 + \lambda_H^{**}K_2K_3 + \alpha\lambda_H^{**}K_3 + \lambda_H^{**}\gamma\alpha + \lambda_H^{**}\theta K_2}. \tag{3.2.7}$$

It follows that,

$$f'(\lambda_H^{**}) = \frac{(K_2K_3 + \eta_A\alpha K_3 + \eta_T\gamma\alpha + \eta_T\theta K_2)\beta_2}{K_1K_2K_3 + \lambda_H^{**}K_2K_3 + \alpha\lambda_H^{**}K_3 + \lambda_H^{**}\gamma\alpha + \lambda_H^{**}\theta K_2}$$

$$- \frac{(K_2K_3 + \eta_A\alpha K_3 + \eta_T\gamma\alpha + \eta_T\theta K_2)\lambda_H^{**}\beta_2((K_2K_3 + \alpha K_3 + \gamma\alpha + \theta K_2)}{(K_1K_2K_3 + \lambda_H^{**}K_2K_3 + \alpha\lambda_H^{**}K_3 + \lambda_H^{**}\gamma\alpha + \lambda_H^{**}\theta K_2)^2}.$$

Simplifying yields,

$$f'(\lambda_H^{**}) = \frac{(K_2 K_3 + \eta_A \alpha K_3 + \eta_T \gamma \alpha + \eta_T \theta K_2)\beta_2 K_1 K_2 K_3}{(K_1 K_2 K_3 + \lambda_H^{**} K_2 K_3 + \alpha \lambda_H^{**} K_3 + \lambda_H^{**} \gamma \alpha + \lambda_H^{**} \theta K_2)^2},$$

$$= \frac{(K_1 K_2 K_3)^2 \mathcal{R}_H}{(K_1 K_2 K_3 + \lambda_H^{**}(K_2 K_3 + \alpha K_3 + \gamma \alpha + \theta K_2))^2}.$$

Evaluating $f'(\lambda_H^{**})$ at $\lambda_H^{**} = \frac{-b}{a}$ gives,

$$f'(\lambda_H^{**})|_{\lambda_H^{**} = \frac{-b}{a}} = \frac{(K_1 K_2 K_3)^2 \mathcal{R}_H}{(K_1 K_2 K_3 + K_1 K_2 K_3 \mathcal{R}_H - K_1 K_2 K_3)^2} = \frac{1}{\mathcal{R}_H}.$$

It is clear that,

$$\left| f'(\lambda_H^{**})|_{\lambda_H^{**} = \frac{-b}{a}} \right| < 1,$$

whenever $\mathcal{R}_H > 1$. Thus, the unique endemic equilibrium is LAS if $\mathcal{R}_H > 1$. ∎

**Theorem 3.6** *The EEP of the HIV/AIDS-only model (3.2.1), is GAS whenever $\mathcal{R}_H > 1$ and $\eta_T = 0$.*

***Proof.***
Consider the following non-linear Lyapunov function

$$\mathcal{F} = S - S^{**} - S^{**} \ln \frac{S}{S^{**}} + I_H - I_H^{**} - I_H^{**} \ln \frac{I_H}{I_H^{**}} + \frac{\beta_2 \eta_A S^{**}}{K_2}\left[ A_H - A_H^{**} - A_H^{**} \ln \frac{A_H}{A_H^{**}} \right],$$

with Lyapunov derivative,

$$\dot{\mathcal{F}} = \dot{S} - \frac{S^{**}}{S}\dot{S} + \dot{I}_H - \frac{I_H^{**}}{I_H}\dot{I}_H + \frac{\beta_2 \eta_A S^{**}}{K_2}\left[ \dot{A}_H - \frac{A_H^{**}}{A_H}\dot{A}_H \right],$$

$$= \Pi - \lambda_H S - \mu S - \frac{S^{**}}{S}(\Pi - \lambda_H S - \mu S) + \lambda_H S - K_1 I_H - \frac{I_H^{**}}{I_H}(\lambda_H S - K_1 I_H)$$

$$+ \frac{\beta_2 \eta_A S^{**}}{K_2}\left[ \alpha I_H - K_2 A_H - \frac{A_H^{**}}{A_H}(\alpha I_H - K_2 A_H) \right].$$

Let $\tilde{\beta} = \frac{\beta_2 \mu}{\Pi}$. Thus,

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$$\dot{\mathcal{F}} = \Pi - \tilde{\beta}(I_H + \eta_A A_H)S - \mu S - \Pi \frac{S^{**}}{S} + \tilde{\beta}I_H S^{**} + \tilde{\beta}\eta_A A_H S^{**} + \mu S^{**}$$

$$+ \tilde{\beta}(I_H + \eta_A A_H)S - K_1 I_H - \frac{I_H^{**}}{I_H}\tilde{\beta}(I_H + \eta_A A_H)S + K_1 I_H^{**}$$

$$+ \frac{\tilde{\beta}\eta_A S^{**}}{K_2}\alpha I_H - \frac{\tilde{\beta}\eta_A S^{**}}{K_2}K_2 A_H - \frac{\tilde{\beta}\eta_A S^{**}}{K_2}\alpha I_H \frac{A_H^{**}}{A_H} + \frac{\tilde{\beta}\eta_A S^{**}}{K_2}K_2 A_H^{**}.$$

It can be shown from the HIV/AIDS-only model (3.2.1) that at endemic steady-state,

$$\Pi = \tilde{\beta}I_H^{**}S^{**} + \tilde{\beta}\eta_A A_H^{**}S^{**} + \mu S^{**},$$

$$K_1 I_H^{**} = \tilde{\beta}(I_H^{**} + \eta_A A_H^{**})S^{**}, \ K_2 A_H^{**} = \alpha I_H^{**}.$$

Substituting the above relations gives,

$$\dot{\mathcal{F}} = \tilde{\beta}I_H^{**}S^{**} + \tilde{\beta}\eta_A A_H^{**}S^{**} + \mu S^{**} - \mu S - (\tilde{\beta}I_H^{**}S^{**} + \tilde{\beta}\eta_A A_H^{**}S^{**} + \mu S^{**})\frac{S^{**}}{S}$$

$$+ \tilde{\beta}I_H S^{**} + \tilde{\beta}\eta_A A_H S^{**} + \mu S^{**} - K_1 I_H - \tilde{\beta}S I_H^{**} - \tilde{\beta}\eta_A \frac{I_H^{**}}{I_H}A_H S + \tilde{\beta}(I_H^{**} + \eta_A A_H^{**})S^{**}$$

$$+ \frac{\tilde{\beta}\eta_A S^{**}}{K_2}\alpha I_H^{**}\frac{I_H}{I_H^{**}} - \tilde{\beta}\eta_A S^{**}A_H - \frac{\tilde{\beta}\eta_A S^{**}}{K_2}\alpha I_H^{**}\frac{I_H}{I_H^{**}}\frac{A_H^{**}}{A_H} + \tilde{\beta}\eta_A S^{**}A_H^{**},$$

which can be simplified to,

$$= \mu S^{**}\left[2 - \frac{S^{**}}{S} - \frac{S}{S^{**}}\right] + \tilde{\beta}I_H^{**}S^{**}\left[2 - \frac{S^{**}}{S} - \frac{S}{S^{**}}\right]$$

$$+ \tilde{\beta}\eta_A A_H^{**}S^{**}\left[3 - \frac{S^{**}}{S} - \frac{I_H A_H^{**}}{I_H^{**}A_H} - \frac{S I_H^{**}A_H}{S^{**}I_H A_H^{**}}\right].$$

Since the arithmetic mean exceeds the geometric mean, the following inequalities hold:

$$2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \leq 0,$$

$$3 - \frac{S^{**}}{S} - \frac{I_H T_H^{**}}{I_H^{**}A_H} - \frac{I_H^{**}A_H S}{I_H A_H^{**}S^{**}} \leq 0.$$

Further, since all the model parameters are non-negative, it follows that $\dot{\mathcal{F}} \leq 0$ for $\mathcal{R}_H > 1$ and $\mathcal{F}$ is a Lyapunov function on $\mathcal{D}$.

Now we have that,

$$\lim_{t \to \infty} S(t) = S^{**}, \ \lim_{t \to \infty} I_H(t) = I_H^{**} \text{ and } \lim_{t \to \infty} A_H(t) = A_H^{**}.$$

Furthermore, at endemic steady-state, as $t \to \infty$,

$$\lim_{t \to \infty} T_H(t) = \lim_{t \to \infty} \frac{\theta I_H(t) + \gamma A_H}{K_3} = \frac{\theta I_H^{**}}{K_3} + \frac{\gamma A_H^{**}}{K_3} = T_H^{**}.$$

The largest compact invariant set in $\left\{ (S, I_H, A_H, T_H) \in \mathcal{D} : \dot{\mathcal{F}} = 0 \right\}$ is the singleton $\{\mathcal{E}_H\}$. Thus it follows by LaSalle's Invariance Principle (Theorem 2.10), that $(S(t), I_H(t), A_H(t), T_H(t)) \to (S^{**}, I_H^{**}, A_H^{**}, T_H^{**})$. Therefore, every solution of the equations of the model (3.2.1) with initial conditions in $\mathcal{D}$ approaches $\mathcal{E}_H$ as $t \to \infty$ (whenever $\mathcal{R}_H > 1$) so that $\mathcal{E}_H$ is GAS if $\mathcal{R}_H > 1$. ■

The epidemiological implication of the above theorem is that if $\mathcal{R}_H$ is greater than unity, HIV/AIDS will be established in the community when there is a small introduction of infected individuals. This result is depicted in Figure 3.6, showing convergence of solutions to EEP when $\mathcal{R}_H > 1$.

## Numerical Simulations
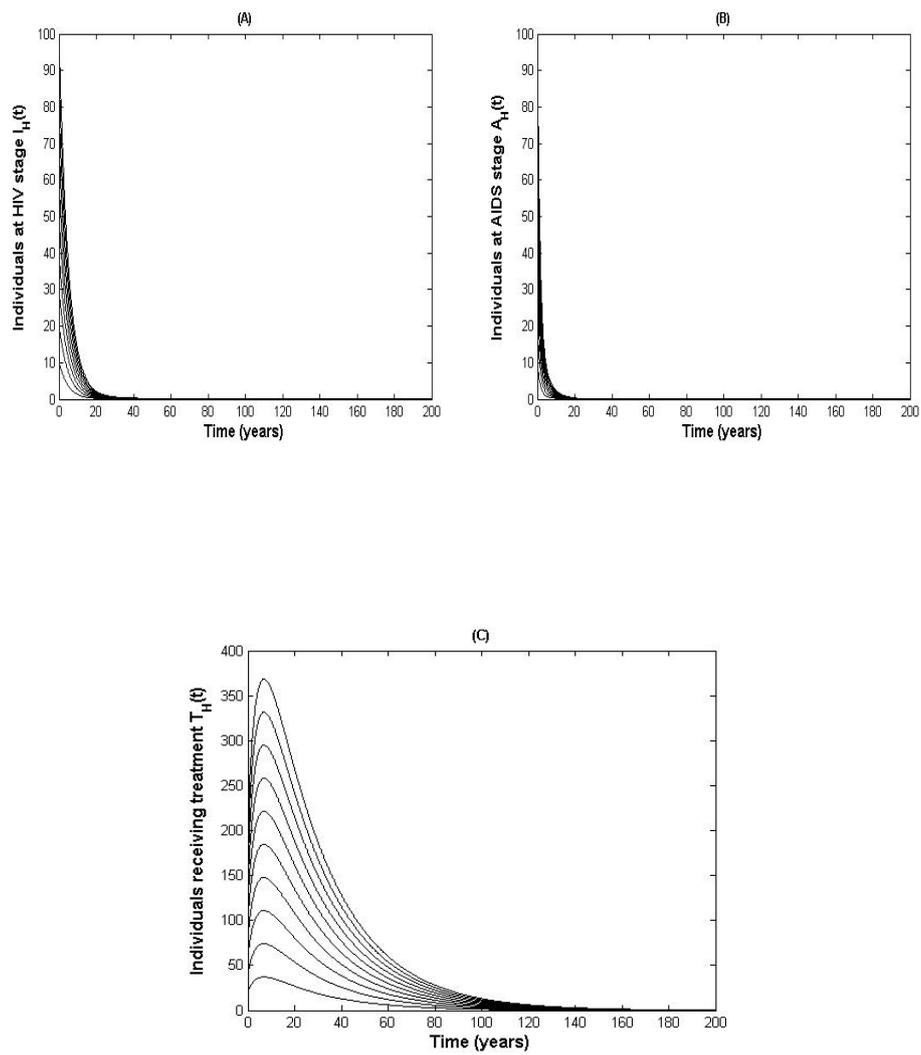


Figure 3.5: *Simulations of the HIV/AIDS-only model (3.2.1) showing that the disease dies out when $\mathcal{R}_H \leq 1$. The parameter values used are as given in Table 5.2, with $\beta_2 = 0.41$ so that $\mathcal{R}_H = 0.6754 < 1$.*
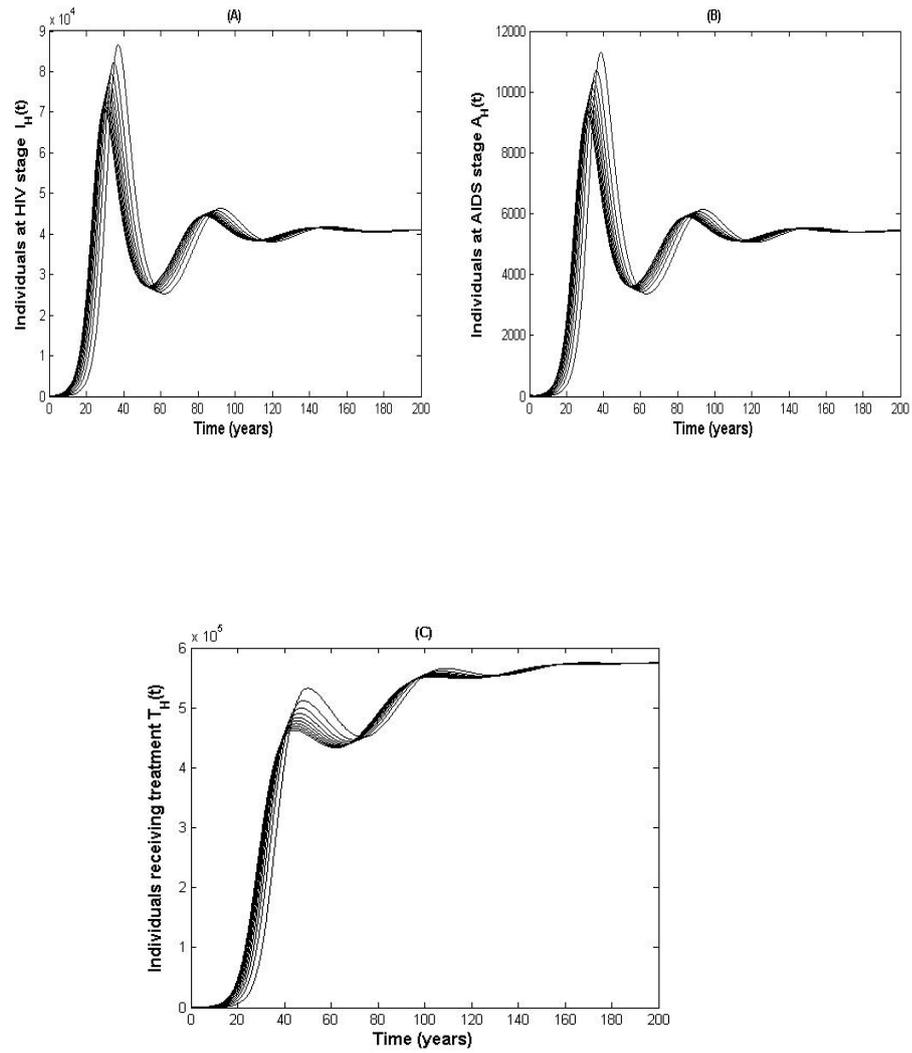
Figure 3.6: *Simulations of the HIV/AIDS-only model (3.2.1) showing that the disease is established when $\mathcal{R}_H > 1$. The parameter values used are as given in Table 5.2, with $\beta_2 = 0.91$, so that $\mathcal{R}_H = 1.4991 > 1$.*

# Chapter 4

# TV-HIV Co-infection Models

In this chapter, a co-infection model of TV and HIV/AIDS is formulated and analysed. This model is then extended to include control strategies for TV (condom-use and counselling) and an assessment of these control strategies is then investigated. Below are some of the assumptions made in the construction of the TV-HIV co-infection models:

1. Each individual in the population is susceptible to TV and/or HIV.

2. The population is homogeneously mixed, that is, the population interacts uniformly and interacts between time steps.

3. Individuals are equally likely to be infected by the infectious individuals (with TV or HIV) following effective contact.

4. Newborns and migrants are assumed to be susceptibles.

5. There is no vaccine or cure for HIV/AIDS, however TV is cured only after treatment.

6. Individuals do not get infected with TV and HIV during the same sexual encounter.

## 4.1 TV-HIV Co-infection Model (without Control)

A deterministic model for the transmission dynamics of HIV/AIDS and trichomonas vaginalis (TV) is considered and analysed. The total human population at time $t$, given by $N(t)$, is divided into eight mutually exclusive compartments, namely, the susceptible individuals ($S(t)$), individuals infected with HIV without clinical symptoms of HIV/AIDS ($I_H(t)$) (it is assumed in this study that individuals do not recover from HIV), individuals infected with AIDS with clinical symptoms ($A_H(t)$), individuals at HIV and AIDS classes receiving treatment ($T_H(t)$), individuals infected with TV ($I_T(t)$) and individuals receiving treatment for TV ($T_T(t)$), as well as individuals who previously only had TV (or HIV) but have acquired HIV (or TV) and now have both HIV and TV ($I_{TH}(t)$) and those with both diseases who are receiving treatment for TV ($T_{TH}(t)$), so that

$$N(t) = S(t) + I_T(t) + T_T(t) + I_H(t) + A_H(t) + T_H(t) + I_{TH}(t) + T_{TH}(t).$$

The susceptible population is increased by the introduction of individuals into the sexually active population at a rate $\Pi$. These individuals either acquire TV infection or HIV

infection, following effective contact with an infected individual in the $I_T$ or $I_H$ class, at a rate $\lambda_T$ or $\lambda_H$, respectively. Therefore, the force of infection is given by,

$$\lambda_1 = \lambda_T + \lambda_H$$

where,

$$\lambda_T = \frac{\beta_1(I_T + \eta T_T + \eta_{TH1}I_{TH} + \eta_{TH2}T_{TH})}{N} \quad \text{and}$$

$$\lambda_H = \frac{\beta_2(I_H + \eta_A A_H + \eta_T T_H + \eta_{HT1}I_{TH} + \eta_{HT2}T_{TH})}{N}.$$

The parameters $\beta_1$ and $\beta_2$ are the effective contact rates (contact capable of leading to infection) of TV and HIV, respectively. The modification parameters $0 < \eta < 1$, $\eta_{TH1} > 1$ and $0 < \eta_{TH2} < 1$ account for the relative risk of infectiousness of treated individuals, and individuals in the co-infection classes relative to infected individuals (with TV). Similarly, $0 < \eta_A < 1$, $0 < \eta_T < 1$, $\eta_{HT1} > 1$ and $0 < \eta_{HT2} < 1$ are modification parameters which account for the relative risk of infectiousness of individuals with AIDS symptoms, treated individuals and individuals in the co-infection classes in comparison to those in $I_H$ class, respectively. It is assumed that individuals in $A_H$ class are less infectious than those in $I_H$ class because they change/reduce their risky sexual behaviour as they are sick and aware that they are infected. Similarly, individuals in $T_H$ class are less infectious than those in $I_H$ class due to treatment (which significantly reduces their viral load). It is further assumed that individuals in $I_{TH}$ are more infectious that those in $I_T$ and $I_H$ class because they are infected with both TV and HIV which weakens their immune system. Similarly, individuals in $T_{TH}$ are less infectious that those in $I_{TH}$ class because they are receiving treatment for TV. The population of susceptible individuals is further decreased by natural death (at a rate $\mu$). It is assumed that natural deaths occur in all compartments at the rate $\mu$. The susceptible class is increased by the recovery of individuals in class $T_T$ (at a rate $\nu$). Thus the rate of change of the susceptible population is given by

$$\frac{dS}{dt} = \Pi + \nu T_T - (\lambda_H + \lambda_T)S - \mu S.$$

The population of individuals infected with trichomonas vaginalis ($I_T$) is generated by the infection of susceptible individuals (at the rate $\lambda_T$). This population is decreased by treatment (at a rate $\tau$), infection with HIV (at the rate $\sigma\lambda_H$, where $\sigma$ is a modification parameter that accounts for the increase in susceptibility to HIV of an TV infected individual i.e $\sigma > 1$) and due to natural death, so that

$$\frac{dI_T}{dt} = \lambda_T S - \sigma\lambda_H I_T - (\tau + \mu)I_T.$$

The population of treated individuals infected with TV is increased by the treatment of infected individuals with TV (at the rate $\tau$). The population is decreased by recovery (at the rate $\nu$) and natural death. The recovered individuals return to the susceptible class. Thus,

$$\frac{dT_T}{dt} = \tau I_T - (\nu + \mu)T_T.$$

Similarly, the population of individuals infected with HIV is generated by the infection of susceptible individuals (at the rate $\lambda_H$) and by recovery of individuals from TV in the $T_{TH}$ class (at a rate $\psi$). This population is decreased by the progression of HIV infected individuals to AIDS class ($A_H$) (at a rate $\alpha$), treatment (at a rate $\theta$), infection with

TV(at the rate $\sigma_1\lambda_T$, where $\sigma_1$ is a modification parameter that accounts for the increase in susceptibility to TV of an HIV infected individual i.e $\sigma_1 > 1$) and natural death. This gives

$$\frac{dI_H}{dt} = \lambda_H S + \psi T_{TH} - \sigma_1\lambda_T I_H - (\alpha + \theta + \mu)I_H.$$

Individuals infected with HIV progress to AIDS class $(A_H)$ (at the rate $\alpha$). The population of individuals in $A_H$ class is reduced due to treatment (at a rate $\gamma$), natural death and disease-induced death (at a rate $\delta_1$). So that,

$$\frac{dA_H}{dt} = \alpha I_H - (\gamma + \mu + \delta_1)A_H.$$

The population of treated individuals $(T_H)$ is increased by the treatment of individuals infected with HIV in the $I_H$ and $A_H$ classes (at the rate $\theta$ and $\gamma$, respectively). This population is decreased due to natural death and disease-induced death (at a rate $\delta_2$). It is assumed that individuals with HIV do not fully recover. Thus,

$$\frac{dT_H}{dt} = \theta I_H + \gamma A_H - (\mu + \delta_2)T_H.$$

The populations of individuals infected with both TV and HIV is generated due to infection with HIV (at the rate $\sigma\lambda_H$) and infection with TV (at the rate $\sigma_1\lambda_T$). It is reduced by treatment of TV (at the rate $\tau$) and natural death. So that

$$\frac{dI_{TH}}{dt} = \sigma\lambda_H I_T + \sigma_1\lambda_T I_H - (\tau + \mu)I_{TH}.$$

Finally, the population of treated individuals infected with TV and HIV is increased by the treatment of individuals in $I_{TH}$ class (at the rate $\tau$) and is decreased due to recovery from TV (at the rate $\psi$) and due to natural death. Individuals recover from TV and move to class $I_H$. Thus,

$$\frac{dT_{TH}}{dt} = \tau I_{TH} - (\psi + \mu)T_{TH}.$$

Combining the aforementioned assumptions and derivations, it follows that the model for the transmission dynamics of TV and HIV co-infection is given by the following system of non-linear differential equations (a flow chart for the model is illustrated in Figure 4.1 and a description of the parameters and variables is given in Tables 5.1 and 5.2):

$$\frac{dS}{dt} = \Pi + \nu T_T - (\lambda_H + \lambda_T)S - \mu S,$$

$$\frac{dI_T}{dt} = \lambda_T S - \sigma\lambda_H I_T - (\tau + \mu)I_T,$$

$$\frac{dT_T}{dt} = \tau I_T - (\nu + \mu)T_T,$$

$$\frac{dI_H}{dt} = \lambda_H S - \sigma_1\lambda_T I_H + \psi T_{TH} - (\alpha + \theta + \mu)I_H,$$

$$\frac{dA_H}{dt} = \alpha I_H - (\gamma + \mu + \delta_1)A_H, \tag{4.1.1}$$

$$\frac{dT_H}{dt} = \theta I_H + \gamma A_H - (\mu + \delta_2)T_H,$$

$$\frac{dI_{TH}}{dt} = \sigma\lambda_H I_T + \sigma_1\lambda_T I_H - (\tau + \mu)I_{TH},$$

$$\frac{dT_{TH}}{dt} = \tau I_{TH} - (\psi + \mu)T_{TH}.$$
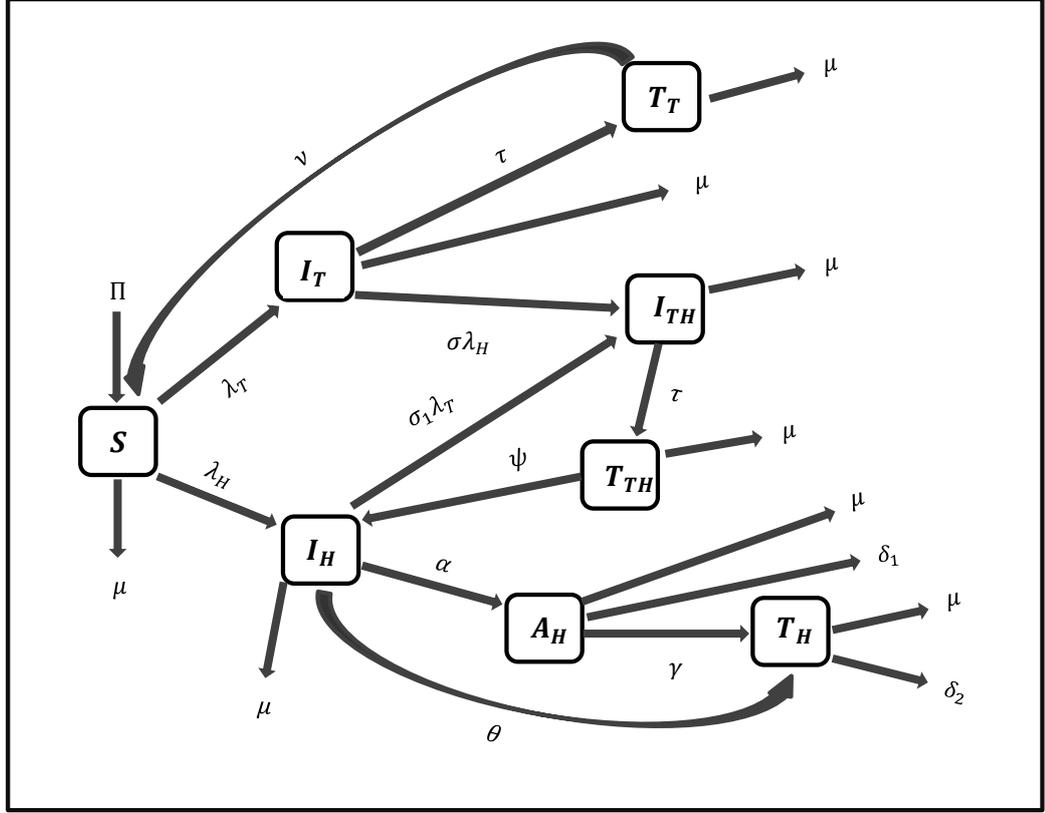
Figure 4.1: *Schematic Diagram for the TV-HIV model (4.1.1).*

The TV-HIV model (4.1.1) is fitted using parameter values obtained from UNAIDS website [25] as depicted in Figure 4.2, from which it is evident that the model fits the data reasonably well. The model (4.1.1) extends the models of transmission dynamics for TV and HIV such as those in [4], by allowing for TV transmission by treated individuals ($\eta \neq 0$).

## 4.1.1   Feasible Solution

**Lemma 4.1** *: The feasible region given by*

$$\mathcal{D} = \{(S, I_T, T_T, I_H, A_H, T_H, I_{TH}, T_{TH}) \in \mathbf{R}_+^8 : S + I_T + T_T + I_H + A_H + T_H + I_{TH} + T_{TH} \leq \frac{\Pi}{\mu}\},$$

*is positively-invariant.*

**Proof.**
Adding all the differential equations in the model (4.1.1) gives:

$$\frac{dN(t)}{dt} = \Pi - \mu N(t) - \delta_1 A_H(t) - \delta_2 T_H(t).$$
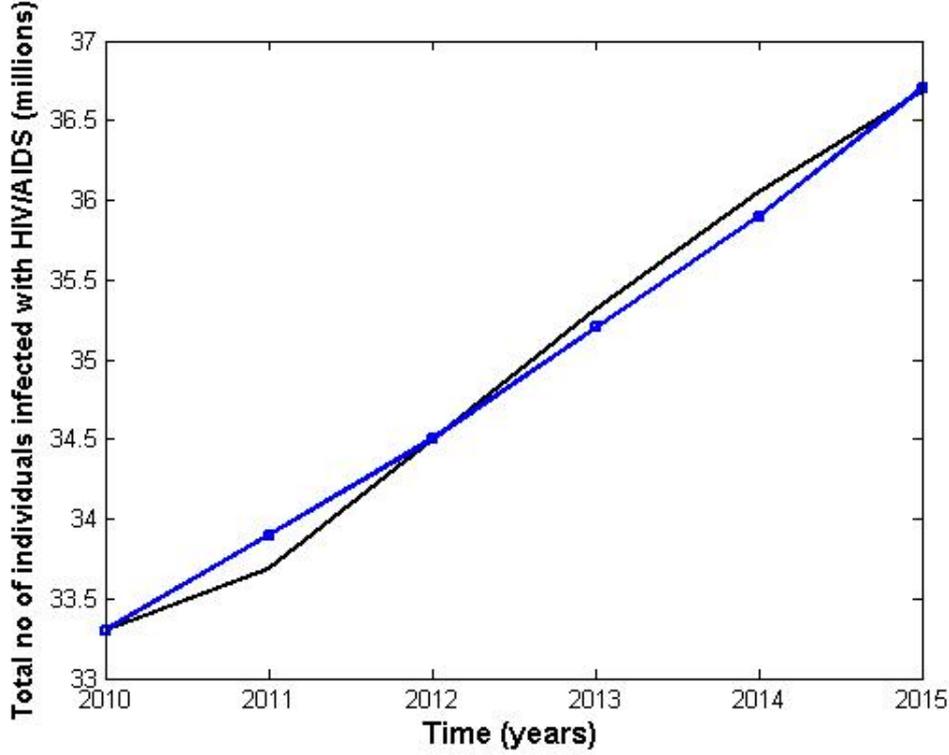
Figure 4.2: *Data fitting of the simulation for the model (4.1.1) using HIV/AIDS data from literature [25]. Parameter values used are as given in Table 5.2. ($\mathcal{R}_2 = 1.0049$).*

Thus,

$$\frac{dN(t)}{dt} \leq \Pi - \mu N(t), \tag{4.1.2}$$

and so $\frac{dN(t)}{dt} < 0$ if $N(t) > \frac{\Pi}{\mu}$. It follows from (4.2.2), and Gronwall's inequality that

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

Hence, $N(t) \leq \frac{\Pi}{\mu}$ if $N(0) \leq \frac{\Pi}{\mu}$. Therefore, the region $\mathcal{D}$ is positively-invariant. Thus, in the region $\mathcal{D}$ the model is well-posed epidemiologically and mathematically. ∎

### 4.1.2 Positivity of Solutions

**Lemma 4.2** *Let the initial data $S(0) > 0$, $I_T(0) > 0$, $T_T(0) > 0$, $I_H(0) > 0$, $A_H(0) > 0$, $T_H(0) > 0$, $I_{TH}(0) > 0$ and $T_{TH}(0) > 0$ then the solutions $S(t), I_T(t), T_T(t), I_H(t), A_H(t), T_H(t), I_{TH}(t), T_{TH}(t)$ of the model (4.1.1) are positive for all $t \geq 0$.*

***Proof.***
Suppose $S(t)$ is not positive, then there exists a first time, say $t^* > 0$, such that $S(t) > 0$ for $t \in [0, t^*)$ and $S(t^*) = 0$. By inspection of the equation of $I_T(t)$, we obtain that

$$\frac{dI_T}{dt} \geq -(\sigma \lambda_H + K_1)I_T(t), \text{ for } t \in [0, t^*),$$

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from which one can deduce that $I_T(t) > 0$ for $t \in [0, t^*)$. Thus it is clear from equation (4.1.1) that

$$\frac{dS}{dt} \geq -(\lambda_T + \lambda_H + \mu)S(t), \text{ for } t \in [0, t^*).$$

It follows that $S(t^*) > 0$, which contradicts that $S(t^*) = 0$. Therefore $S(t)$ is positive. Using a similar approach as that for $S(t)$ it is easy to show that $I_T(t) > 0$, $T_T(t) > 0$, $I_H(t) > 0$, $A_H(t) > 0$, $T_H(t) > 0$, $I_{TH}(t) > 0$ and $T_{TH}(t) > 0$.

It follows that if we begin with positive parameters, they will remain positive for all time.

$\blacksquare$

### 4.1.3 Local Asymptotic Stability of Disease-free Equilibrium (DFE)

The TV-HIV model (4.1.1) has a DFE obtained by setting the right-hand sides of the equations in the model (4.1.1) to zero, given by,

$$\mathcal{E}_3 = (S^*, I_T^*, T_T^*, I_H^*, A_H^*, T_H^*, I_{TH}^*, T_{TH}^*) = \left(\frac{\Pi}{\mu}, 0, 0, 0, 0, 0, 0, 0\right).$$

The linear stability of the DFE, $\mathcal{E}_3$, can be established using the next generation operator method on system (4.1.1). Using the notation in [50], the matrices $F$ (for the new infection terms) and $V$ (for the transition terms) are given, respectively, by

$$F = \begin{pmatrix} \beta_1 & \eta\beta_1 & 0 & 0 & 0 & \eta_{TH1}\beta_1 & \eta_{TH2}\beta_1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \beta_2 & \eta_A\beta_2 & \eta_T\beta_2 & \eta_{HT1}\beta_2 & \eta_{HT2}\beta_2 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} Q_1 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\tau & Q_2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & Q_3 & 0 & 0 & 0 & -\psi \\ 0 & 0 & -\alpha & Q_4 & 0 & 0 & 0 \\ 0 & 0 & -\theta & -\gamma & Q_5 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & Q_1 & 0 \\ 0 & 0 & 0 & 0 & 0 & -\tau & Q_6 \end{pmatrix},$$

where, $Q_1 = \tau + \mu$, $Q_2 = \nu + \mu$, $Q_3 = \theta + \alpha + \mu$, $Q_4 = \gamma + \mu + \delta_1$, $Q_5 = \mu + \delta_2$, and $Q_6 = \psi + \mu$.

The basic reproduction number, denoted by $\mathcal{R}_0$ is then given by

$$\mathcal{R}_0 = \rho(FV^{-1}) = \max\{\mathcal{R}_1, \mathcal{R}_2\},$$

where $\mathcal{R}_1$ and $\mathcal{R}_2$ are the associated reproduction numbers for TV and HIV/AIDS, respectively, given by

$$\mathcal{R}_1 = \frac{\beta_1(Q_2 + \eta\tau)}{Q_1 Q_2} \text{ and } \mathcal{R}_2 = \frac{\beta_2[Q_4(Q_5 + \theta\eta_T) + \alpha(\eta_A Q_5 + \gamma\eta_T)]}{Q_3 Q_4 Q_5}. \tag{4.1.3}$$

Therefore, applying Theorem 2 of [50], the following result is established.

**Lemma 4.3** *The DFE, $\mathcal{E}_3$, of the model (4.1.1) is LAS if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$.*

The threshold quantity $\mathcal{R}_0 = \max\{\mathcal{R}_1, \mathcal{R}_2\}$, is the associated reproduction number [1, 2, 23, 50]. It represents the average number of secondary TV (or HIV) cases that are generated as a result of introducing one TV (or HIV) infected individual into a susceptible population where some individuals are treated. The epidemiological implication of Lemma 4.3 is that when $\mathcal{R}_0$ is less than unity, a small influx of individuals infected with TV or HIV into the community will not generate large outbreaks (of TV and/or HIV) and the disease dies out in time. In the next section we show that the disease may still persist in the community even though $\mathcal{R}_0 < 1$. This is owing to the existence of backward bifurcation.

## 4.1.4   Backward bifurcation analysis

The existence of backward bifurcation will be explored using Centre Manifold Theory [9, 50]. To apply this theory we first carry out the following change of variables. Let $S = x_1, I_T = x_2, T_T = x_3, I_H = x_4, A_H = x_5, T_H = x_6, I_{TH} = x_7$, and $T_{TH} = x_8$ so that $N = x_1 + x_2 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8$. In addition, by using vector notation $X = (x_1, x_2, x_2, x_3, x_4, x_5, x_6, x_7, x_8)^T$, the TV-HIV model (4.1.1) can be written in the form $\frac{dX}{dt} = F(X)$, with $(f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8)^T$ as follows,

$$\frac{dx_1}{dt} = f_1 = \Pi + \nu x_3 - (\lambda_H + \lambda_T)x_1 - \mu x_1,$$

$$\frac{dx_2}{dt} = f_2 = \lambda_T x_1 - \sigma\lambda_H x_2 - (\tau + \mu)x_2,$$

$$\frac{dx_3}{dt} = f_3 = \tau x_2 - (\nu + \mu)x_3,$$

$$\frac{dx_4}{dt} = f_4 = \lambda_H x_1 + \psi x_8 - \sigma_1\lambda_T x_4 - (\alpha + \theta + \mu)x_4,$$

$$\frac{dx_5}{dt} = f_5 = \alpha x_4 - (\gamma + \mu + \delta_1)x_5, \tag{4.1.4}$$

$$\frac{dx_6}{dt} = f_6 = \theta x_4 + \gamma x_5 - (\mu + \delta_2)x_6,$$

$$\frac{dx_7}{dt} = f_7 = \sigma\lambda_H x_2 + \sigma_1\lambda_T x_4 - (\tau + \mu)x_7,$$

$$\frac{dx_8}{dt} = f_8 = \tau x_7 - (\psi + \mu)x_8,$$

with the forces of infection given by,

$$\lambda_T = \frac{\beta_1(x_2 + \eta x_3 + \eta_{TH1}x_7 + \eta_{TH2}x_8)}{x_1 + x_2 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8} \text{ and}$$

$$\lambda_H = \frac{\beta_2(x_4 + \eta_A x_5 + \eta_T x_6 + \eta_{HT1} x_7 + \eta_{HT2} x_8)}{x_1 + x_2 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8}.$$

Consider the case when $\mathcal{R}_0 = 1$ (that is $\mathcal{R}_0 = \max\{\mathcal{R}_1, \mathcal{R}_2\} = 1$). Also suppose that $\beta_2 = \beta_2^*$ is chosen as the bifurcation parameter. Solving for $\beta_2 = \beta_2^*$ from $\mathcal{R}_0 = 1$ in (4.1.3) gives

$$\beta_2^* = \frac{Q_3 Q_4 Q_5}{Q_4(Q_5 + \theta \eta_T) + \alpha(\eta_A Q_5 + \gamma \eta_T)}.$$

The Jacobian of the system (4.1.4) evaluated at the DFE, $\mathcal{E}_3$, with $\beta_2 = \beta_2^*$ and denoted by $J^*$, is given by

$$J^* = \begin{pmatrix} M_1 & M_2 \\ M_3 & M_4 \end{pmatrix},$$

where,

$$M_1 = \begin{pmatrix} -\mu & -\beta_1 & -\beta_1 \eta + \nu & -\beta_2^* \\ 0 & \beta_1 - Q_1 & \beta_1 \eta & 0 \\ 0 & \tau & -Q_2 & 0 \\ 0 & 0 & 0 & \beta_2^* - Q_3 \end{pmatrix},$$

$$M_2 = \begin{pmatrix} -\beta_2^* \eta_A & -\beta_2^* \eta_T & -(\beta_2^* \eta_{HT1} + \beta_1 \eta_{TH1}) & -(\beta_2^* \eta_{HT2} + \beta_1 \eta_{TH2}) \\ 0 & 0 & -(\beta_2^* \eta_{HT1} + \beta_1 \eta_{TH1}) & -(\beta_2^* \eta_{HT1} + \beta_1 \eta_{TH2}) \\ 0 & 0 & 0 & 0 \\ \beta_2^* \eta_A & \beta_2^* \eta_T & \beta_2^* \eta_{HT1} & \beta_2^* \eta_{HT2} + \psi \end{pmatrix},$$

$$M_3 = \begin{pmatrix} 0 & 0 & 0 & \alpha \\ 0 & 0 & 0 & \theta \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$M_4 = \begin{pmatrix} -Q_4 & 0 & 0 & 0 \\ \gamma & -Q_5 & 0 & 0 \\ 0 & 0 & -Q_1 & 0 \\ 0 & 0 & \tau & -Q_6 \end{pmatrix}.$$

The Jacobian has a simple zero eigenvalue (with all other eigenvalues having negative real part), therefore the Centre Manifold Theory can be used to analyse the dynamics of the system (4.1.4).

**Eigenvectors of $\mathbf{J}^*(\mathcal{E}_3)|_{\beta_2 = \beta_2^*}$** For the case when $\mathcal{R}_0 = 1$, it can be shown that $J^*$ has a left eigenvector (corresponding to the zero eigenvalue), given by $\bar{v} = [v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8]$, where

$v_1 = 0,$

$v_2 > 0,$

$$v_3 = \frac{\beta_1 \eta}{Q_2} v_2,$$

$$v_4 > 0,$$

$$v_5 = \frac{\beta_2^*(\eta_A Q_5 + \gamma \eta_T)}{Q_4 Q_5} v_4,$$

$$v_6 = \frac{\beta_2^* \eta_T}{Q_5} v_4,$$

$$v_7 = \frac{\beta_1 \eta_{TH1}(Q_6 + \tau)}{Q_1 Q_6} v_2 + \frac{\beta_2 \eta_{HT2}(Q_6 + \tau) + \beta_2^* \tau \psi}{Q_1 Q_6} v_4,$$

$$v_8 = \frac{\beta_1 \eta_{TH1}}{Q_6} v_2 + \frac{\beta_2^*(\eta_{HT2} + \psi)}{Q_6} v_4.$$

Similarly, the components of the right eigenvector of $J^*(\mathcal{E}_3)|_{\beta_2 = \beta_2^*}$ (corresponding to the zero eigenvalue), denoted by $\bar{w} = [w_1, w_2, w_3, v, w_4, w_5, w_6, w_7, w_8]^T$ are

$$w_1 = -\frac{1}{\mu}\left[\left(\frac{\beta_1(Q_2 + \eta\tau) - \nu\tau}{Q_2}\right) w_2 + \left(\frac{\beta_2^*(Q_4 Q_5 + \eta_A \alpha Q_5 + \eta_T \theta Q_4 + \eta_T \alpha\gamma)}{Q_4 Q_5}\right) w_4\right],$$

$$w_2 > 0,$$

$$w_3 = \frac{\tau}{Q_2} w_2,$$

$$w_4 > 0,$$

$$w_5 = \frac{\alpha}{Q_4} w_4,$$

$$w_6 = \frac{(\theta Q_4 + \alpha\gamma)}{Q_4 Q_5} w_4,$$

$$w_7 = 0,$$

$$w_8 = 0.$$

In addition, $\bar{v} \cdot \bar{w} = 1$. That is,

$$\bar{v} \cdot \bar{w} = v_2 w_2 + v_3 w_3 + v_4 w_4 + v_5 w_5 + v_6 w_6,$$

$$= \frac{Q_2^2 + \beta_1 \eta\tau}{Q_2^2} v_2 w_2 + \frac{Q_4^2 Q_5^2 + \beta_2^*[\alpha(\eta_A Q_5^2 + \eta_T \gamma Q_5 + \eta_T \gamma Q_4) + \eta_T \theta Q_4^2]}{Q_4^2 Q_5^2} v_4 w_4,$$

$$= 1.$$

It is worth noting that the free left components $v_2$ and $v_4$, and free right components $w_2$ and $w_4$ are chosen to be

$$v_2 = v_4 = \frac{1}{2}, \qquad w_2 = \frac{Q_2^2}{Q_2^2 + \beta_1 \eta\tau}, \quad \text{and}$$

$$w_4 = \frac{Q_4^2 Q_5^2}{Q_4^2 Q_5^2 + \beta_2[\alpha(\eta_A Q_5^2 + \eta_T \gamma Q_5 + \eta_T \gamma Q_4) + \eta_T \theta Q_4^2]},$$

in order to achieve the above result.

**Computation of a**  For the transformed TV-HIV model (4.1.4), the associated non-zero partial derivatives of $F$ (evaluated at the DFE) are given by

$$\frac{\partial^2 f_1}{\partial x_2 \partial x_2} = \frac{2\beta_1 \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_2 \partial x_3} = \frac{\mu(\beta_1 + \beta_1 \eta)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_2 \partial x_4} = \frac{\mu(\beta_1 + \beta_2)}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_2 \partial x_5} = \frac{\mu(\beta_1 + \beta_2 \eta_A)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_2 \partial x_6} = \frac{\mu(\beta_1 + \beta_2 \eta_T)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_2 \partial x_7} = \frac{-(\beta_2 \eta_{HT1} + \beta_1 + \beta_1 \eta_{TH1})\mu}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_2 \partial x_8} = \frac{-(\beta_2 \eta_{HT2} + \beta_1 + \beta_1 \eta_{TH2})\mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_3 \partial x_7} = \frac{-(\beta_2 \eta_{HT1} + \beta_1 \eta + \beta_1 \eta_{TH1})\mu}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_3 \partial x_3} = \frac{2\beta_1 \eta \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_3 \partial x_4} = \frac{\mu(\beta_1 \eta + \beta_2)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_3 \partial x_5} = \frac{\mu(\beta_1 \eta + \beta_2 \eta_A)}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_3 \partial x_6} = \frac{\mu(\beta_1 \eta + \beta_2 \eta_T)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_4 \partial x_7} = \frac{-(\beta_2 \eta_{HT1} + \beta_2 + \beta_1 \eta_{TH1})\mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_4 \partial x_4} = \frac{2\beta_2 \mu}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_4 \partial x_5} = \frac{\mu(\beta_2 + \beta_2 \eta_A)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_4 \partial x_6} = \frac{\mu(\beta_2 + \beta_2 \eta_T)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_4 \partial x_8} = \frac{-(\beta_2 \eta_{HT2} + \beta_2 + \beta_1 \eta_{TH2})\mu}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_5 \partial x_7} = \frac{-(\beta_2 \eta_{HT1} + \beta_2 \eta_A + \beta_1 \eta_{TH1})\mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_5 \partial x_8} = \frac{-(\beta_2 \eta_{HT2} + \beta_2 \eta_A + \beta_1 \eta_{TH2})\mu}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_5 \partial x_5} = \frac{2\beta_2 \eta_A \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_5 \partial x_6} = \frac{\mu(\beta_2 \eta_A + \beta_2 \eta_T)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_6 \partial x_7} = \frac{-(\beta_2 \eta_{HT1} + \beta_2 \eta_T + \beta_1 \eta_{TH1})\mu}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_6 \partial x_6} = \frac{2\beta_2 \eta_T \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_6 \partial x_8} = \frac{-(\beta_2 \eta_{HT2} + \beta_2 \eta_T + \beta_1 \eta_{TH2})\mu}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_2 \partial x_2} = -\frac{2\beta_1 \mu}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_2 \partial x_3} = -\frac{\mu(\beta_1 + \beta_1 \eta)}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_2 \partial x_4} = -\frac{\mu(\beta_1 + \sigma \beta_2)}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_2 \partial x_8} = \frac{-(\sigma \beta_2 \eta_{HT2} + \beta_1 + \beta_1 \eta_{TH2})\mu}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_2 \partial x_7} = \frac{-(\beta_1 + \sigma \beta_2 \eta_{HT1} + \beta_1 \eta_{TH1})\mu}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_2 \partial x_5} = -\frac{\mu(\beta_1 + \sigma \beta_2 \eta_A)}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_2 \partial x_6} = -\frac{\mu(\beta_1 + \sigma \beta_2 \eta_T)}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_3 \partial x_7} = -\frac{(\beta_1 \eta + \beta_1 \eta_{TH1})\mu}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_3 \partial x_3} = -\frac{2\beta_1 \eta \mu}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_3 \partial x_4} = \frac{\partial^2 f_2}{\partial x_3 \partial x_5} = \frac{\partial^2 f_2}{\partial x_3 \partial x_6} = -\frac{\beta_1 \eta \mu}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_3 \partial x_8} = -\frac{(\beta_1 \eta + \beta_1 \eta_{TH2})\mu}{\Pi},$$

$$\frac{\partial^2 f_4}{\partial x_2 \partial x_4} = -\frac{(\sigma_1 \beta_1 + \beta_2)\mu}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_4 \partial x_4} = -\frac{2\beta_2 \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_3 \partial x_8} = \frac{-(\beta_2 \eta_{HT2} + \beta_1 \eta + \beta_1 \eta_{TH2})\mu}{\Pi},$$

$$\frac{\partial^2 f_4}{\partial x_2 \partial x_5} = \frac{\partial^2 f_4}{\partial x_3 \partial x_5} = -\frac{\beta_2 \eta_A \mu}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_4 \partial x_5} = -\frac{\mu(\beta_2 + \beta_2 \eta_A)}{\Pi},$$

$$\frac{\partial^2 f_4}{\partial x_4 \partial x_7} = -\frac{(\beta_2 + \beta_2 \eta_{HT1} + \sigma_1 \beta_1 \eta_{TH1})\mu}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_4 \partial x_8} = -\frac{(\beta_2 + \beta_2 \eta_{HT2} + \sigma_1 \beta_1 \eta_{TH2})}{\Pi},$$

$$\frac{\partial^2 f_4}{\partial x_5 \partial x_7} = -\frac{(\beta_2 \eta_A + \beta_2 \eta_{HT1})\mu}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_5 \partial x_8} = -\frac{(\beta_2 \eta_A + \beta_2 \eta_{HT2})}{\Pi},$$

$$\frac{\partial^2 f_4}{\partial x_6 \partial x_7} = -\frac{(\beta_2 \eta_T + \beta_2 \eta_{HT1})\mu}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_6 \partial x_8} = -\frac{(\beta_2 \eta_T + \beta_2 \eta_{HT2})}{\Pi},$$

$$\frac{\partial^2 f_4}{\partial x_3 \partial x_6} = -\frac{\beta_2 \eta_T \mu}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_3 \partial x_4} = -\frac{\mu(\beta_2 + \sigma_1 \beta_1 \eta)}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_4 \partial x_6} = -\frac{\mu(\beta_2 + \beta_2 \eta_T)}{\Pi},$$

$$\frac{\partial^2 f_4}{\partial x_5 \partial x_5} = -\frac{2\beta_2 \eta_A \mu}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_6 \partial x_6} = -\frac{2\beta_2 \eta_T \mu}{\Pi}, \quad \frac{\partial^2 f_4}{\partial x_5 \partial x_6} = -\frac{\mu(\beta_2 \eta_A + \beta_2 \eta_T)}{\Pi},$$

$$\frac{\partial^2 f_7}{\partial x_2 \partial x_4} = \frac{(\sigma_1 \beta_1 + \sigma \beta_2)\mu}{\Pi}, \quad \frac{\partial^2 f_7}{\partial x_2 \partial x_5} = \frac{\sigma \beta_2 \eta_A \mu}{\Pi}, \quad \frac{\partial^2 f_7}{\partial x_2 \partial x_6} = \frac{\sigma \beta_2 \eta_T \mu}{\Pi},$$

$$\frac{\partial^2 f_7}{\partial x_2 \partial x_7} = \frac{\sigma \beta_2 \eta_{HT1} \mu}{\Pi}, \quad \frac{\partial^2 f_7}{\partial x_2 \partial x_8} = \frac{\sigma \beta_2 \eta_{HT2} \mu}{\Pi}, \quad \frac{\partial^2 f_7}{\partial x_4 \partial x_7} = \frac{\sigma_1 \beta_1 \eta_{TH1} \mu}{\Pi}, \quad \frac{\partial^2 f_7}{\partial x_4 \partial x_8} = \frac{\sigma_1 \beta_1 \eta_{TH2} \mu}{\Pi}.$$

Using the expressions above, it follows that

$$a = \sum_{k,i,j}^{8} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0),$$

$$= \frac{2\mu}{\Pi}[v_7 w_2 \sigma \beta_2^* w_4 + v_7 w_2 \sigma \beta_2^* w_5 \eta_A + v_7 w_2 \sigma \beta_2 w_6 \eta_T - v_2 w_2 \sigma \beta_2^* w_4 - v_2 w_2 \sigma \beta_2^* w_5 \eta_A$$

$$+ v_7 w_4 \sigma_1 \beta_1 (w_2 + \eta w_3) - v_4 w_4 \sigma_1 \beta_1 (w_2 + \eta w_3)$$

$$- v_2 w_2 \sigma \beta_2^* w_6 \eta_T - \beta_1 (v_2 w_2 w_2 + v_2 w_2 w_3 + v_2 w_2 w_4 + v_2 w_2 w_5 + v_2 w_2 w_6 + v_2 w_3 \eta w_2 + w_3 v_2 w_3 \eta)$$

$$- \beta_1 (w_4 v_2 w_3 \eta w_5 + w_6 v_2 w_3 \eta) - \beta_2^* (w_2 v_4 w_4 + w_3 v_4 w_4 + w_4 v_4 w_4 + w_5 v_4 w_4 + w_6 v_4 w_4)$$

$$- \beta_2^* (w_2 v_4 w_5 \eta_A + w_3 v_4 w_5 \eta_A + w_4 v_4 w_5 \eta_A + w_5 v_4 w_5 \eta_A + w_6 v_4 w_5 \eta_A + w_2 v_4 w_6 \eta_T + w_3 v_4 w_6 \eta_T)$$

$$- \beta_2^* (w_4 v_4 w_6 \eta_T + w_5 v_4 w_6 \eta_T + w_6 v_4 w_6 \eta_T)],$$

which can be simplified to the following,

$$a = \sum_{k,i,j}^{8} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0),$$

$$= \frac{2\mu}{\Pi}[v_7 w_4 \sigma_1 \beta_1 (w_2 + \eta w_3) + v_7 w_2 \sigma \beta_2^* (w_4 + w_5 \eta_A + w_6 \eta_T)$$

$$- v_2 w_2 \sigma \beta_2^* (w_4 + w_5 \eta_A + w_6 \eta_T) - v_4 w_4 \sigma_1 \beta_1 (w_2 + \eta w_3)$$

$$- \beta_1 (v_2 w_2 + v_2 w_3 \eta)(w_2 + w_3 + w_4 + w_5 + w_6)$$

$$- \beta_2^* (v_4 w_4 + v_4 w_5 \eta_A + v_4 w_6 \eta_T)(w_2 + w_3 + w_4 + w_5 + w_6)].$$

(4.1.5)

**Computation of b**  Substituting the vectors $\bar{v}$ and $\bar{w}$ and the respective partial derivatives (evaluated at the DFE) into the expression of $b$ yields,

$$b = \sum_{k,i,j}^{8} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta_2}(0,0) = v_4 w_4 + v_4 w_5 \eta_A + v_4 w_6 \eta_T > 0.$$

Since the coefficient $b$ is automatically positive, it follows that the model (4.1.1) will undergo backward bifurcation if the coefficient $a$, given by (4.1.5), is positive.

The above results can be summarised by the following theorem.

**Theorem 4.1** *The TV-HIV model (4.1.1) exhibits backward bifurcation whenever the bifurcation parameter a, given by (4.1.5), is positive.*

It is worth mentioning that in the absence of co-infection, that is for the case when $\sigma = \sigma_1 = 0$, the bifurcation parameter $a < 0$. This rules out the existence of backward bifurcation when $\sigma = \sigma_1 = 0$. To further rule out the existence of backward bifurcation, a global stability of the DFE when $\sigma = \sigma_1 = 0$ is proven below.

## 4.1.5 Global-asymptotic Stability of DFE when $\sigma = \sigma_1 = 0$

First of all notice that be setting $\sigma = \sigma_1 = 0$ in (4.1.1) the equation of $\frac{dI_{TH}}{dt} \to 0$ as $t \to \infty$, thus $\frac{dT_{TH}}{dt} \to 0$ as $t \to \infty$. Hence, it follows that the system (4.1.1) can be simplified to

$$\frac{dS}{dt} = \Pi + \nu T_T - (\lambda_H + \lambda_T)S - \mu S,$$

$$\frac{dI_T}{dt} = \lambda_T S - (\tau + \mu)I_T,$$

$$\frac{dT_T}{dt} = \tau I_T - (\nu + \mu)T_T,$$

$$\frac{dI_H}{dt} = \lambda_H S - (\alpha + \theta + \mu)I_H, \tag{4.1.6}$$

$$\frac{dA_H}{dt} = \alpha I_H - (\gamma + \mu + \delta_1)A_H,$$

$$\frac{dT_H}{dt} = \theta I_H + \gamma A_H - (\mu + \delta_2)T_H.$$

Next define the invariant region

$$\tilde{\mathcal{D}} = \{(S, I_T, T_T, I_H, A_H, T_H, I_{TH}, T_{TH}) \in \mathcal{D} : S \le S^*\}.$$

We claim the following:

**Theorem 4.2** *The DFE, $\mathcal{E}_3$, of the model (4.1.1) with $\sigma = \sigma_1 = 0$ (or equivalently (4.1.6)), in the absence of co-infection ($\sigma = \sigma_1 = 0$), is globally-asymptotically stable (GAS) in $\tilde{\mathcal{D}}$ whenever $\mathcal{R}_0 \le 1$.*

***Proof.***
Consider the following Lyapunov function

$$\mathcal{F} = \mathcal{R}_1 I_T + \frac{\beta_1 \eta}{Q_2}T_T + \mathcal{R}_2 I_H + \frac{\beta_2(\eta_A Q_5 + \eta_T \gamma)}{Q_4 Q_5}A_H + \frac{\beta_2 \eta_T}{Q_5}T_H,$$

with Lyapunov derivative given by,

$$\dot{\mathcal{F}} = \mathcal{R}_1 \dot{I}_T + \frac{\beta_1 \eta}{Q_2} \dot{T}_T + \mathcal{R}_2 \dot{I}_H + \frac{\beta_2(\eta_A Q_5 + \eta_T \gamma)}{Q_4 Q_5} \dot{A}_H + \frac{\beta_2 \eta_T}{Q_3} \dot{T}_H,$$

$$= \mathcal{R}_1(\lambda_T S - Q_1 I_T) + \frac{\beta_1 \eta}{Q_2}(\tau I_T - Q_2 T_T) + \mathcal{R}_2[\lambda_H S - Q_3 I_H]$$

$$+ \frac{\beta_2(\eta_A Q_5 + \eta_T \gamma)}{Q_4 Q_5}[\alpha I_H - Q_4 A_H] + \frac{\beta_2 \eta_T}{Q_5}[\theta I_H + \gamma A_H - Q_5 T_H],$$

$$= \mathcal{R}_1 \lambda_T S - \beta_1(I_T + \eta T_T) + \mathcal{R}_2 \lambda_H S - \beta_2(I_H + \eta_A A_H + \eta_T T_H), \qquad (4.1.7)$$

$$= \mathcal{R}_1 \lambda_T S - \lambda_T N + \mathcal{R}_2 \lambda_H S - \lambda_H N,$$

$$= \lambda_T N \left[ \frac{\mathcal{R}_1 \lambda_T S}{\lambda_T N} - 1 \right] + \lambda_H N \left[ \frac{\mathcal{R}_2 \lambda_H S}{\lambda_H N} - 1 \right],$$

$$\leq \lambda_T N[\mathcal{R}_1 - 1] + \lambda_H N^*[\mathcal{R}_2 - 1], \quad \text{since } S \leq S^* \text{ in } \tilde{\mathcal{D}} \text{ and } S \leq N,$$

$$= \beta_1(I_T + \eta T_T)[\mathcal{R}_1 - 1] + \beta_2(I_H + \eta_A A_H + \eta_T T_H)[\mathcal{R}_2 - 1] \leq 0 \quad \text{when} \quad \mathcal{R}_0 \leq 1.$$

Since all the parameters and variables of the model (4.1.6) are non-negative (Lemma 4.2), it follows that $\dot{\mathcal{F}} \leq 0$ for $\mathcal{R}_0 \leq 1$ (i.e. $\mathcal{R}_1 \leq 1$ and $\mathcal{R}_2 \leq 1$) with $\dot{\mathcal{F}} = 0$ if and only if $I_T = T_T = I_H = A_H = T_H = 0$. Hence $\mathcal{F}$ is a Lyapunov function on $\tilde{\mathcal{D}}$. Further, the largest compact invariant set in $\left\{ (S, I_T, T_T, I_H, A_H, T_H) \in \tilde{\mathcal{D}} : \dot{\mathcal{F}} = 0 \right\}$ is the singleton $\{\mathcal{E}_3\}$. Therefore, it follows by LaSalle's Invariance Principle (Theorem 2.10), that $(I_T(t), T_T(t), I_H(t), A_H(t), T_H(t)) \to (0, 0, 0, 0, 0)$ as $t \to \infty$. Thus, every solution of the equations of the model (4.1.6) with initial conditions in $\tilde{\mathcal{D}}$ approaches $\mathcal{E}_3$ as $t \to \infty$ (whenever $\mathcal{R}_0 \leq 1$), so that $\mathcal{E}_3$ is GAS in $\tilde{\mathcal{D}}$ if $\mathcal{R}_0 \leq 1$. ∎

The epidemiological implication of this Theorem is that if $\mathcal{R}_0$ can be made to a value less than unity, a small influx of individuals into the community will not generate large outbreaks of the disease and it will die out in time. This result is depicted in Figure 4.3, showing convergence to DFE when $\mathcal{R}_0 < 1$.

### 4.1.6 Existence and local Stability of EEP

**Existence** We find an equilibrium where at least one of the infected components ($I_T^{**}$, $T_T^{**}$, $I_H^{**}$, $A_H^{**}$, $T_H^{**}$, $I_{TH}^{**}$ and $T_{TH}^{**}$) is non zero.
Let the EEP of the model (4.1.1) be denoted by

$$\mathcal{E}_{TH} = (S^{**}, I_T^{**}, T_T^{**}, I_H^{**}, A_H^{**}, T_H^{**}, I_{TH}^{**}, T_{TH}^{**}),$$

and consider the force of infection

$$\lambda_{TH}^{**} = \frac{\beta_1(I_T^{**} + \eta T_T^{**} + \eta_{TH1} I_{TH}^{**} + \eta_{TH2} T_{TH}^{**}) + \beta_2(I_H^{**} + \eta_A A_H^{**} + \eta_T T_H^{**} + \eta_{HT1} I_{TH}^{**} + \eta_{HT2} T_{TH}^{**})}{N^{**}}.$$

$$(4.1.8)$$

Solving the equations in system (4.1.1) at the endemic equilibrium point in terms of the force of infection, by setting the right hand sides of the equations in (4.1.1) to zero, gives

$$S^{**} = \frac{Q_2(Q_1 + \sigma\lambda_H^{**})\Pi}{\mu Q_1 Q_2 + \mu(\nu + Q_1)\lambda_T^{**} + Q_2[Q_1 + \sigma(\lambda_T^{**} + \lambda_H^{**} + \mu)]\lambda_H^{**}},$$

$$I_T^{**} = \frac{Q_2\lambda_T^{**}\Pi}{\mu Q_1 Q_2 + \mu(\nu + Q_1)\lambda_T^{**} + Q_2[Q_1 + \sigma(\lambda_T^{**} + \lambda_H^{**} + \mu)]\lambda_H^{**}},$$

$$T_T^{**} = \frac{\tau\lambda_T^{**}\Pi}{\mu Q_1 Q_2 + \mu(\nu + Q_1)\lambda_T^{**} + Q_2[Q_1 + \sigma(\lambda_T^{**} + \lambda_H^{**} + \mu)]\lambda_H^{**}},$$

$$I_H^{**} = \frac{Q_2\lambda_H^{**}\Pi(Q_1^2 Q_6 + \psi\tau\sigma\lambda_T^{**} + Q_1 Q_6\sigma\lambda_H^{**})}{(\mu Q_1 Q_2 + \mu(\nu + Q_1)\lambda_T^{**} + Q_2[Q_1 + \sigma(\lambda_T^{**} + \lambda_H^{**} + \mu)]\lambda_H^{**})(\sigma_1\lambda_T^{**}\mu(Q_1 + \psi) + Q_1 Q_3 Q_6)},$$

$$A_H^{**} = \frac{\alpha Q_2\lambda_H^{**}\Pi(Q_1^2 Q_6 + \psi\tau\sigma\lambda_T^{**} + Q_1 Q_6\sigma\lambda_H^{**})}{Q_4(\mu Q_1 Q_2 + \mu(\nu + Q_1)\lambda_T^{**} + Q_2[Q_1 + \sigma(\lambda_T^{**} + \lambda_H^{**} + \mu)]\lambda_H^{**})(\sigma_1\lambda_T^{**}\mu(Q_1 + \psi) + Q_1 Q_3 Q_6)},$$

$$T_H^{**} = \frac{Q_2\lambda_H^{**}\Pi(\gamma\alpha + \theta Q_4)(Q_1^2 Q_6 + \psi\tau\sigma\lambda_T^{**} + Q_1 Q_6\sigma\lambda_H^{**})}{Q_4 Q_5(\mu Q_1 Q_2 + \mu(\nu + Q_1)\lambda_T^{**} + Q_2[Q_1 + \sigma(\lambda_T^{**} + \lambda_H^{**} + \mu)]\lambda_H^{**})(\sigma_1\lambda_T^{**}\mu(Q_1 + \psi) + Q_1 Q_3 Q_6)},$$

$$I_{TH}^{**} = \frac{Q_2 Q_6\lambda_T^{**}\lambda_H^{**}\Pi(\sigma\sigma_1\lambda_T^{**} + \sigma Q_3 + \sigma\sigma_1\lambda_H^{**} + Q_1\sigma_1)}{(\mu Q_1 Q_2 + \mu(\nu + Q_1)\lambda_T^{**} + Q_2[Q_1 + \sigma(\lambda_T^{**} + \lambda_H^{**} + \mu)]\lambda_H^{**})(\sigma_1\lambda_T^{**}\mu(Q_1 + \psi) + Q_1 Q_3 Q_6)},$$

$$T_{TH}^{**} = \frac{\tau Q_2\lambda_T^{**}\lambda_H^{**}\Pi(\sigma\sigma_1\lambda_T^{**} + \sigma Q_3 + \sigma\sigma_1\lambda_H^{**} + Q_1\sigma_1)}{(\mu Q_1 Q_2 + \mu(\nu + Q_1)\lambda_T^{**} + Q_2[Q_1 + \sigma(\lambda_T^{**} + \lambda_H^{**} + \mu)]\lambda_H^{**})(\sigma_1\lambda_T^{**}\mu(Q_1 + \psi) + Q_1 Q_3 Q_6)}.$$

$$(4.1.9)$$

**Theorem 4.3** *The EEP of the TV-HIV model (4.1.1), is GAS whenever $\mathcal{R}_0 > 1$ and $\eta_T = \nu = \sigma = \sigma_1 = 0$.*

### *Proof.*
The proof is based on using non-linear Lyapunov function of Goh-Volterra type (functions of this type have been used in ecology and mathematical epidemiology literature, see for instance [16, 17]). Consider the following non-linear Lyapunov function

$$\mathcal{F} = S - S^{**} - S^{**}\ln\frac{S}{S^{**}} + I_T - I_T^{**} - I_T^{**}\ln\frac{I_T}{I_T^{**}} + \frac{\beta_1\eta S^{**}}{Q_2}\left[T_T - T_T^{**} - T_T^{**}\ln\frac{T_T}{T_T^{**}}\right]$$

$$+ I_H - I_H^{**} - I_H^{**}\ln\frac{I_H}{I_H^{**}} + \frac{\beta_2\eta_A S^{**}}{Q_4}\left[A_H - A_H^{**} - A_H^{**}\ln\frac{A_H}{A_H^{**}}\right],$$

with Lyapunov derivative,

$$\dot{\mathcal{F}} = \dot{S} - \frac{S^{**}}{S}\dot{S} + \dot{I}_T - \frac{I_T^{**}}{I_T}\dot{I}_T + \frac{\beta_1\eta S^{**}}{Q_2}\left[\dot{T}_T - \frac{T_T^{**}}{T_T}\dot{T}_T\right] + \dot{I}_H - \frac{I_H^{**}}{I_H}\dot{I}_H + \frac{\beta_2\eta_A S^{**}}{Q_4}\left[\dot{A}_H - \frac{A_H^{**}}{A_H}\dot{A}_H\right],$$

$$= \Pi - \lambda_H S - \lambda_T S - \mu S - \frac{S^{**}}{S}(\Pi - \lambda_H S - \lambda_T S - \mu S) + (\lambda_T S - Q_1 I_T) - \frac{I_T^{**}}{I_T}((\lambda_T S - Q_1 I_T)$$

$$+ \frac{\beta_1\eta S^{**}}{Q_2}\left[\tau I_T - Q_2 T_T - \frac{T_T^{**}}{T_T}(\tau I_T - Q_2 T_T)\right] + \lambda_H S - Q_3 I_H - \frac{I_H^{**}}{I_H}(\lambda_H S - Q_3 I_H)$$

$$+ \frac{\beta_2\eta_A S^{**}}{Q_4}\left[\alpha I_H - Q_4 A_H - \frac{A_H^{**}}{A_H}(\alpha I_H - Q_4 A_H)\right].$$

Let $\tilde{\beta} = \frac{\beta\mu}{\Pi}$. Applying this and simplifying yields,

$$\dot{\mathcal{F}} = \Pi - \mu S - \Pi\frac{S^{**}}{S} + \tilde{\beta}_1(I_T + \eta T_T)S^{**} + \tilde{\beta}_2(I_H + \eta_A A_H)S^{**} + \mu S^{**} - Q_1 I_T$$

$$- \frac{I_T^{**}}{I_T}\tilde{\beta}_1(I_T + \eta T_T)S + Q_1 I_T^{**} + \frac{\tilde{\beta}_1\eta S^{**}}{Q_2}\tau I_T - \tilde{\beta}_1\eta S^{**}T_T - \frac{\tilde{\beta}_1\eta S^{**}}{Q_2}\frac{T_T^{**}}{T_T}\tau I_T + \tilde{\beta}_1\eta S^{**}T_T^{**}$$

$$- Q_3 I_H - \frac{I_H^{**}}{I_H}\tilde{\beta}_2(I_H + \eta_A A_H)S + Q_3 I_H^{**}$$

$$+ \frac{\tilde{\beta}_2\eta_A S^{**}}{Q_4}\alpha I_H - \tilde{\beta}_2\eta_A S^{**}A_H - \frac{\tilde{\beta}_2\eta_A S^{**}}{Q_4}\alpha I_H\frac{A_H^{**}}{A_H} + \tilde{\beta}_2\eta_A S^{**}A_H^{**}.$$

It can be shown from the model (4.1.1) that at endemic steady-state,

$$\Pi = \tilde{\beta}_1 I_T^{**} S^{**} + \tilde{\beta}_1\eta T_T^{**} S^{**} + \tilde{\beta}_2 I_H^{**} S^{**} + \tilde{\beta}_2\eta_A A_H^{**} S^{**} + \mu S^{**},$$

$$Q_1 I_T^{**} = \tilde{\beta}_1 I_T^{**} S^{**} + \tilde{\beta}_1\eta T_T^{**} S^{**}, \qquad Q_2 T_T^{**} = \tau I_T^{**},$$

$$Q_3 I_H^{**} = \tilde{\beta}_2 I_H^{**} S^{**} + \eta_A A_H^{**} S^{**}, \qquad Q_4 A_H^{**} = \alpha I_H^{**}.$$

Substituting the above relations gives,

$$\dot{\mathcal{F}} = \tilde{\beta}_1 I_T^{**} S^{**} + \tilde{\beta}_1 \eta T_T^{**} S^{**} + \tilde{\beta}_2 I_H^{**} S^{**} + \tilde{\beta}_2 \eta_A A_H^{**} S^{**} + \mu S^{**} - \mu S$$

$$- (\tilde{\beta}_1 I_T^{**} S^{**} + \tilde{\beta}_1 \eta T_T^{**} S^{**} + \tilde{\beta}_2 I_H^{**} S^{**} + \tilde{\beta}_2 \eta_A A_H^{**} S^{**} + \mu S^{**}) \frac{S^{**}}{S} + \mu S^{**} - \tilde{\beta}_1 I_T^{**} S^{**} \frac{S}{S^{**}}$$

$$- \tilde{\beta}_1 \eta T_T^{**} S^{**} \frac{S I_T^{**} T_T}{S^{**} I_T T_T^{**}} + \tilde{\beta}_1 I_T^{**} S^{**} + \tilde{\beta}_1 \eta T_T^{**} S^{**} - \tilde{\beta}_1 \eta T_T^{**} S^{**} \frac{I_T T_T^{**}}{I_T^{**} T_T} + \tilde{\beta}_1 \eta T_T^{**} S^{**}$$

$$- \tilde{\beta}_2 I_H^{**} S^{**} \frac{S}{S^{**}} - \tilde{\beta}_2 \eta_A A_H^{**} S^{**} \frac{S I_H^{**} A_H}{S^{**} I_H A_H^{**}} + \tilde{\beta}_2 I_H^{**} S^{**} + \tilde{\beta}_2 \eta_A A_H^{**} S^{**}$$

$$- \tilde{\beta}_2 \eta_A A_H^{**} S^{**} \frac{I_H A_H^{**}}{I_H^{**} A_H} + \tilde{\beta} \eta_A A_H^{**} S^{**},$$

which can be simplified to,

$$= \mu S^{**} \left[ 2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \right] + \tilde{\beta}_1 I_T^{**} S^{**} \left[ 2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \right] + \tilde{\beta}_2 I_H^{**} S^{**} \left[ 2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \right]$$

$$+ \tilde{\beta}_1 \eta T_T^{**} S^{**} \left[ 3 - \frac{S^{**}}{S} - \frac{I_T T_T^{**}}{I_T^{**} T_T} - \frac{S I_T^{**} T_T}{S^{**} I_T T_T^{**}} \right] + \tilde{\beta}_2 \eta_A A_H^{**} S^{**} \left[ 3 - \frac{S^{**}}{S} - \frac{I_H A_H^{**}}{I_H^{**} A_H} - \frac{S I_H^{**} A_H}{S^{**} I_H A_H^{**}} \right].$$

Since the arithmetic mean exceeds the geometric mean, the following inequalities hold:

$$2 - \frac{S^{**}}{S} - \frac{S}{S^{**}} \leq 0,$$

$$3 - \frac{S^{**}}{S} - \frac{I_T T_T^{**}}{I_T^{**} T_T} - \frac{S I_T^{**} T_T}{S^{**} I_T T_T^{**}} \leq 0,$$

$$3 - \frac{S^{**}}{S} - \frac{I_H T_H^{**}}{I_H^{**} A_H} - \frac{S I_H^{**} A_H}{S^{**} I_H A_H^{**}} \leq 0.$$

Further, since all the model parameters are non-negative, it follows that $\dot{\mathcal{F}} \leq 0$ for $\mathcal{R}_0 > 1$ and $\mathcal{F}$ is a Lyapunov function on $\mathcal{D}$.
Now we have that,

$$\lim_{t \to \infty} S(t) = S^{**}, \ \lim_{t \to \infty} I_T(t) = I_T^{**}, \ \lim_{t \to \infty} T_T(t) = T_T^{**},$$

$$\lim_{t \to \infty} I_H(t) = I_H^{**} \text{ and } \lim_{t \to \infty} A_H(t) = A_H^{**}.$$

Furthermore, at endemic steady-state, as $t \to \infty$,

$$\lim_{t \to \infty} T_H(t) = \lim_{t \to \infty} \frac{\theta I_H(t) + \gamma A_H}{Q_5} = \frac{\theta I_H^{**}}{Q_5} + \frac{\gamma A_H^{**}}{Q_5} = T_H^{**},$$

$$\lim_{t\to\infty} I_{TH}(t) = \lim_{t\to\infty} \frac{\sigma \lambda_{TH} I_T(t)}{Q_1} = \frac{\sigma \lambda_{TH}^{**} I_T^{**}(t)}{Q_1} = I_{TH}^{**},$$

$$\lim_{t\to\infty} T_{TH}(t) = \lim_{t\to\infty} \frac{\tau I_{TH}(t)}{Q_6} = \frac{\tau I_{TH}^{**}(t)}{Q_6} = T_{TH}^{**}.$$

Thus, $\dot{\mathcal{F}} \leq 0$ for $\mathcal{R}_0 > 1$. Hence $\mathcal{F}$ is a Lyapunov function on $\mathcal{D}$. The proof is completed using similar arguments as in the proof of Theorem 4.2. ∎

The biological implication of this theorem is that when $\mathcal{R}_0$ is greater than unity a small influx of infected individuals into a community will generate large outbreaks of the disease and it will invade the population provided $\eta_T = \nu = \sigma = \sigma_1 = 0$. Simulations of the model showing convergence to EEP when $\mathcal{R}_0 > 1$ is depicted in Figure 4.4.

### 4.1.7 Numerical Simulations
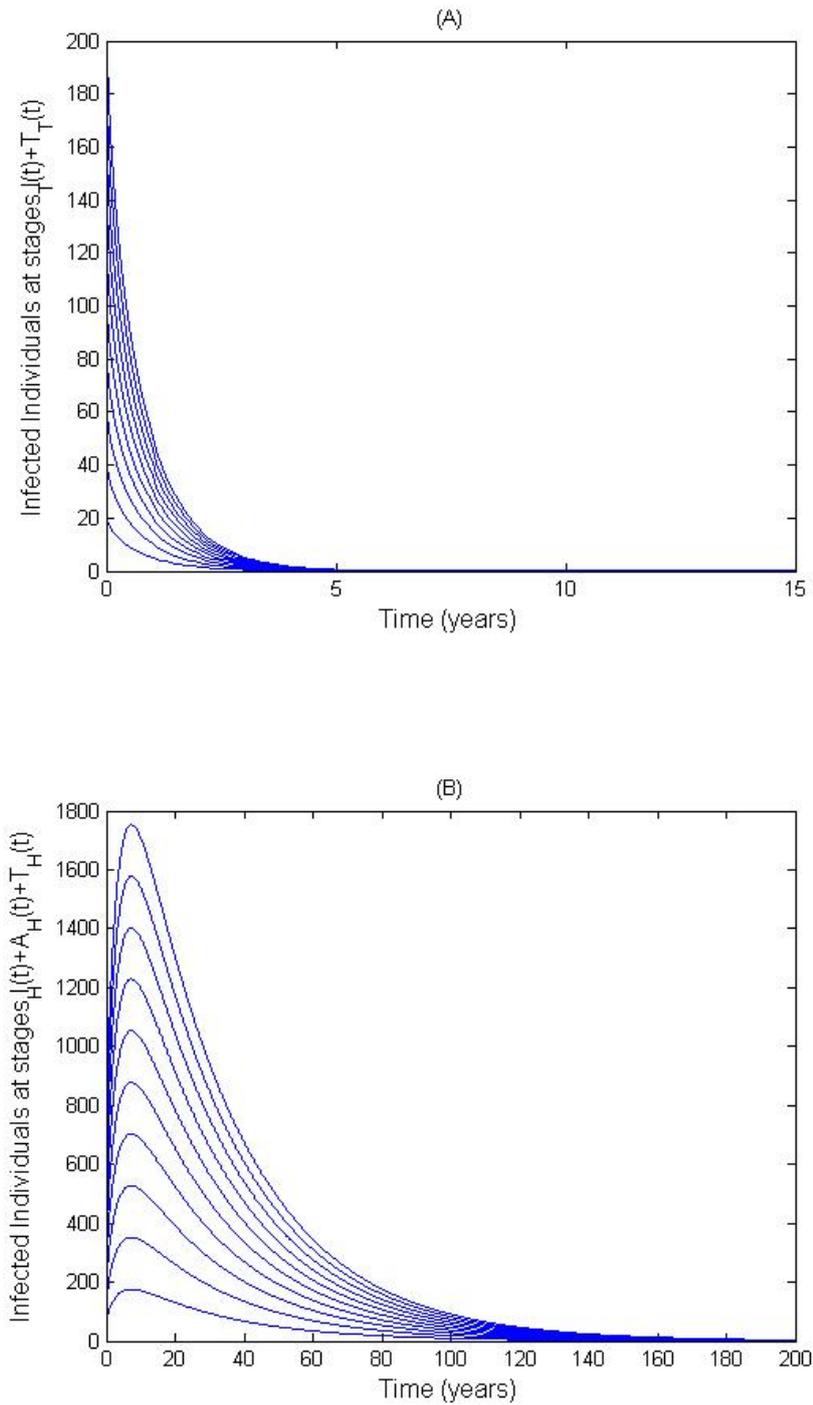


Figure 4.3: *Simulations of the model (4.1.1), using various initial conditions, showing individuals infected with (A)TV and (B)HIV/AIDS when $\sigma = \sigma_1 = 0$, $\beta_1 = 0.709$ and $\beta_2 = 0.65$. Other parameter values used are as given in Table 5.2 with moderate treatment effectiveness used for TV (so that $\mathcal{R}_0 = 0.7298 < 1$).*
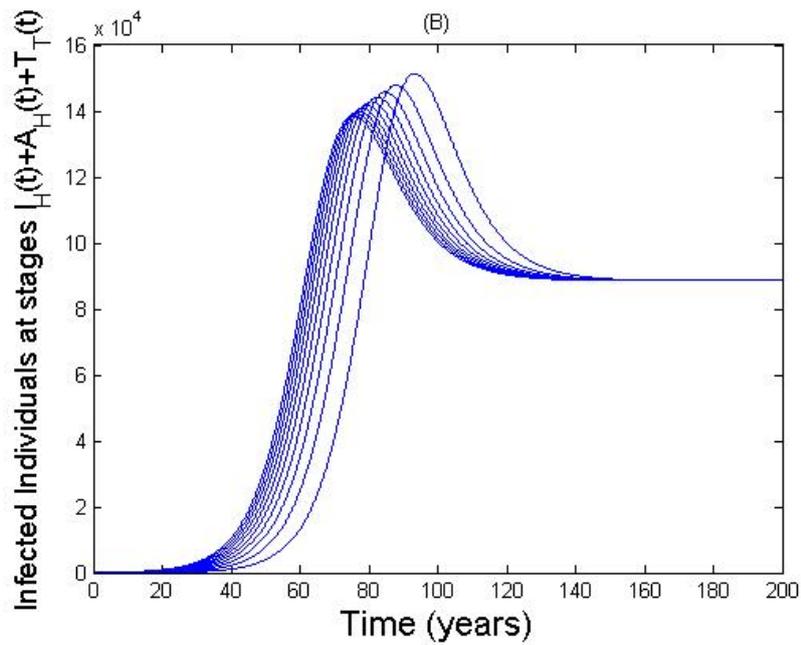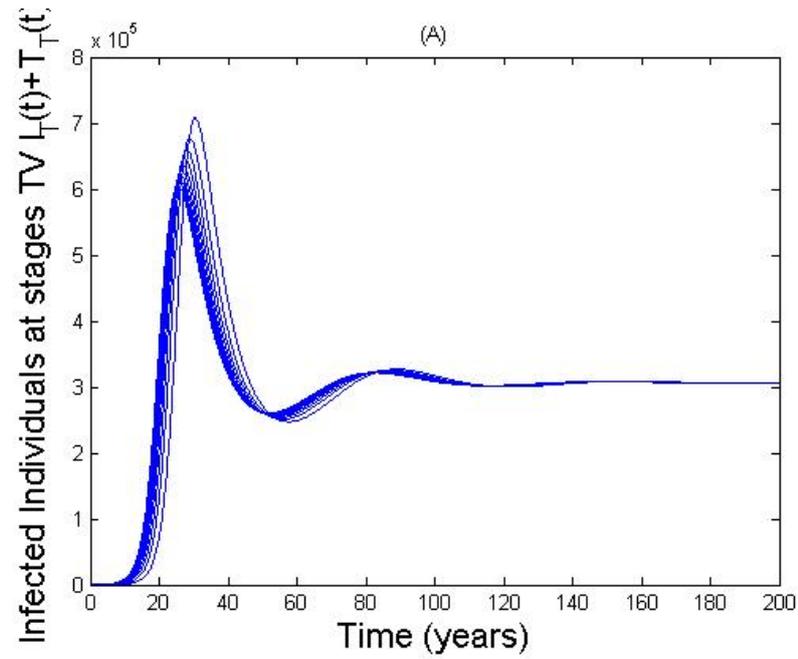
Figure 4.4: *Simulations of the model (4.1.1), using various initial conditions, showing individuals infected with (A)TV and (B)HIV/AIDS when $\sigma = \sigma_1 = 0$, $\beta_1 = 3.651$ and $\beta_2 = 1.65$. Other parameter values used are as given in Table 5.2 with moderate treatment effectiveness used for TV (so that $\mathcal{R}_0 = 1.8526 > 1$).*

## Effect of TV on Dynamics of HIV

The TV-HIV model (4.1.1) is simulated using parameter values presented in Table 5.2 (unless otherwise stated), to evaluate the effect of the dynamics of TV on the spread of HIV in the human population. The effect of TV on the transmission of HIV by individuals infected with TV is monitored by simulating the model (4.1.1), using varying values of the parameter for the increased likelihood of individuals infected with TV acquiring co-infection with HIV. The simulation results illustrated in Figure 4.5 show that the total number of new HIV infections decreases with decreasing values of $\sigma$. That is, a reduction in the TV incidence in the population reduces the HIV incidence in the same population. This could be due to the fact that an individual's susceptibility to HIV is increased due to TV infection. In particular, it could be due to a woman's increased susceptibility to HIV by two or three-fold by TV infection.
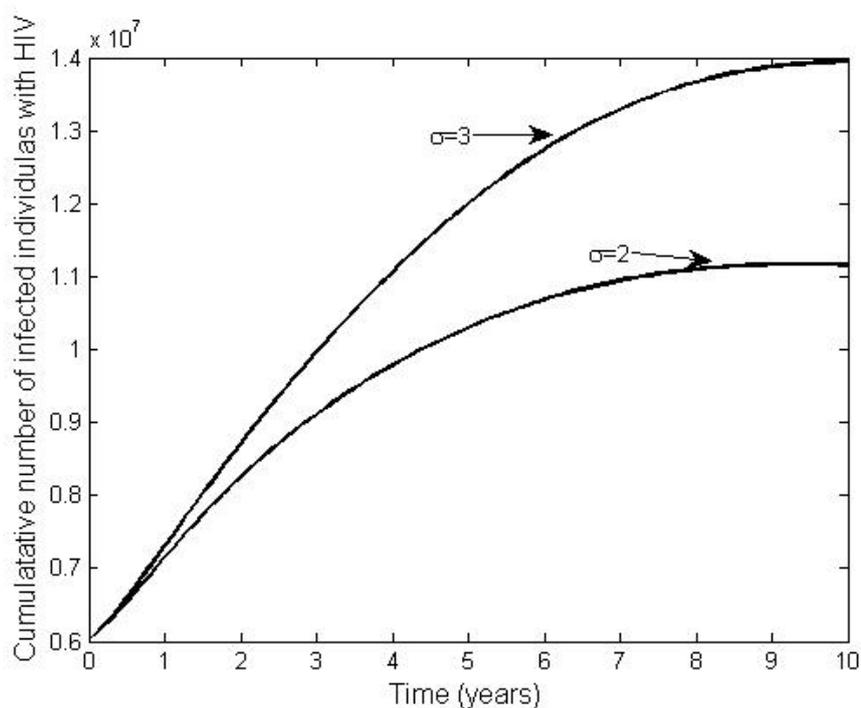


Figure 4.5: *Simulations of the model (4.1.1) showing the cumulative number of individuals infected with HIV/AIDS with varying values of $\sigma$.*

## 4.2 TV-HIV Co-infection Model (with Control)

In this section, the TV-HIV model (4.1.1) is extended to incorporate the dynamics of counselling and condom use (for the purpose of assessing these control strategies) in the population by sub-dividing the infective class ($I_T$) into two compartments consisting of new infected individuals unaware of their TV status (non-counselled),($I_T^U(t)$), counselled individuals infected with TV, ($I_T^C(t)$), so that

$$N(t) = S(t) + I_T^U(t) + I_T^C(t) + T_T(t) + I_H(t) + A_H(t) + T_H(t) + I_{TH}(t) + T_{TH}(t).$$

In this extended model, susceptible individuals acquire TV infection, following effective contact with an infected individuals in the $I_T^U(t)$, $I_T^C(t)$ or $T_T$ classes, at a rate $\lambda_T^1$, where

$$\lambda_T^1 = \frac{\beta_1(1 - \epsilon\kappa)(I_T^U + \eta_1 I_T^C + \eta_2 T_T + \eta_{TH1} I_{TH} + \eta_{TH2} T_{TH})}{N}$$

is the force of infection.

The parameter $\beta_1$ is the effective contact rate, $0 < \epsilon < 1$ is the condom efficacy, $0 < \kappa < 1$ measures compliance in condom use, while $\eta_1$ and $\eta_2$ are modification parameters accounting for the reduction in the transmission rates of counselled ($I_T^C$) and treated individuals ($T_T$), in relation to infected non-counselled individuals ($I_T^C$). Since treatment reduces infectiousness of treated individuals, it is plausible to set $0 < \eta_2 < 1$. It is similarly assumed that counselled individuals modify their risky sexual behaviour positively, so that $0 < \eta_1 < 1$. Individuals in the $I_T^C$ class are detected via random screening or voluntary testing, and are counselled (at a rate $\xi$). Individuals in class $I_T^C$ receive treatment (at a rate $\tau$) and move to class $T_T$. It is assumed that all treated individuals recover (at a rate $\nu$). It is also assumed that only individuals in class $I_T^U$ acquire HIV (at a rate $\sigma\lambda_H$) and that only individuals in class $I_H$ acquire TV (at a rate $\sigma_1\lambda_T^1$). The other compartments and variables remain the same as in the model (4.1.1).

In summary, the model takes the form of the following deterministic system of non linear differential equations (a flow chart is depicted in Figure 4.6 and a description of parameters and variables in Tables 5.1 and 5.2):
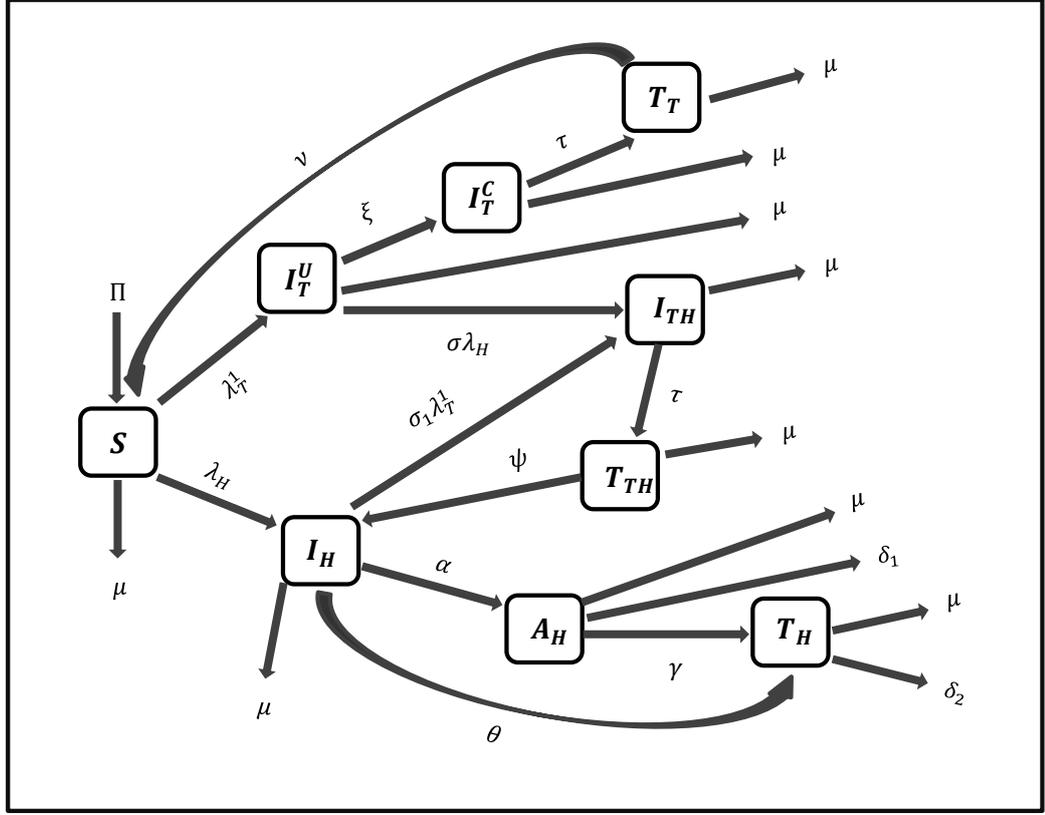
Figure 4.6: *Schematic Diagram for the extended TV-HIV model (4.2.1).*

$$\frac{dS}{dt} = \Pi + \nu T_T - (\lambda_H + \lambda_T^1)S - \mu S,$$

$$\frac{dI_T^U}{dt} = \lambda_T^1 S - \sigma \lambda_H I_T^U - (\xi + \mu)I_T^U,$$

$$\frac{dI_T^C}{dt} = \xi I_T^U - (\tau + \mu)I_T^C,$$

$$\frac{dT_T}{dt} = \tau I_T^C - (\nu + \mu)T_T,$$

$$\frac{dI_H}{dt} = \lambda_H S - \sigma_1 \lambda_T^1 I_H + \psi T_{TH} - (\alpha + \theta + \mu)I_H, \qquad (4.2.1)$$

$$\frac{dA_H}{dt} = \alpha I_H - (\gamma + \mu + \delta_1)A_H,$$

$$\frac{dT_H}{dt} = \theta I_H + \gamma A_H - (\mu + \delta_2)T_H,$$

$$\frac{dI_{TH}}{dt} = \sigma \lambda_H I_T^U + \sigma_1 \lambda_T^1 I_H - (\tau + \mu)I_{TH},$$

$$\frac{dT_{TH}}{dt} = \tau I_{TH} - (\psi + \mu)T_{TH}.$$

The TV-HIV model (4.2.1) extends the models of transmission dynamics for TV and

HIV, and is to the author's knowledge the first to incorporate control strategies of TV and HIV co-infection in a population. In addition, it extends numerous TV models in the literature such as those in [3, 4, 6] by (*inter alia*):

1. Allowing for TV transmission by treated individuals ($\eta_2 \neq 0$),

2. Sub-dividing the infected population with TV into counselled and non-counselled individuals,

3. Assessing various control strategies for TV (counselling, treatment and condom-use).

### 4.2.1   Qualitative Properties of the model

The extended TV-HIV model (4.2.1) will now be rigorously analysed for its dynamical features. This model monitors human population, therefore it is important that all the variables and parameters of the model are non-negative as well as the region to be considered is biologically feasible. This is proved below.

**Feasible Solution**

**Lemma 4.4** : *The biologically-feasible region given by*

$$\mathcal{D} = \left\{ (S, I_T^U, I_T^C, T_T, I_H, A_H, T_H, I_{TH}, T_{TH}) \in \mathbf{R}_+^9 \; : \; S + I_T^U + I_T^C + T_T + I_H + A_H + \right.$$

$$\left. T_H + I_{TH} + T_{TH} \leq \frac{\Pi}{\mu} \right\},$$

*is positively-invariant.*

***Proof.***
Adding all the differential equations in the model (4.2.1) gives:

$$\frac{dN(t)}{dt} = \Pi - \mu N(t) - \delta_1 A_H(t) - \delta_2 T_H(t).$$

Thus,

$$\frac{dN(t)}{dt} \leq \Pi - \mu N(t), \tag{4.2.2}$$

and so   $\frac{dN(t)}{dt} < 0$ if $N(t) > \frac{\Pi}{\mu}$.
It follows from (4.2.2), and Gronwall's inequality that

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

Hence, $N(t) \leq \frac{\Pi}{\mu}$ if $N(0) \leq \frac{\Pi}{\mu}$. Therefore, the region $\mathcal{D}$ is positively-invariant. Thus, in the region $\mathcal{D}$ the model is well-posed epidemiologically and mathematically and it is sufficient to consider the dynamics of the flow generated by (4.2.1) in $\mathcal{D}$. ■

**Positivity of Solutions**

**Lemma 4.5** *Let the initial data $S(0) > 0$, $I_T^U(0) > 0$, $I_T^C(0) > 0$, $T_T(0) > 0$, $I_H(0) > 0$, $A_H(0) > 0$, $T_H(0) > 0$, $I_{TH}(0) > 0$ and $T_{TH}(0) > 0$ then the solutions $S(t), I_T^U(t), I_T^C(t)$, $T_T(t), I_H(t), A_H(t), T_H(t), I_{TH}(t), T_{TH}(t)$ of the model (4.2.1) are positive for all $t \geq 0$.*

***Proof.***
Suppose $S(t)$ is not positive, then there exists a first time, say $t^* > 0$, such that $S(t) > 0$ for $t \in [0, t^*)$ and $S(t^*) = 0$. By inspection of the equation of $I_T^U(t)$, we obtain that

$$\frac{dI_T^U(t)}{dt} \geq -(\sigma\lambda_H + \xi + \mu)I_T^U(t), \text{ for } t \in [0, t^*),$$

from which one can deduce that $I_T^U(t) > 0$ for $t \in [0, t^*)$. Thus it is clear from equation (4.2.1) that

$$\frac{dS(t)}{dt} \geq -(\lambda_T^1 + \lambda_H + \mu)S(t), \text{ for } t \in [0, t^*).$$

It follows that $S(t^*) > 0$, which contradicts that $S(t^*) = 0$. Therefore $S(t)$ is positive. Using a similar approach as that for $S(t)$ it is easy to show that $I_T^U(t) > 0$, $I_T^C(t) > 0$, $T_T(t) > 0$, $I_H(t) > 0$, $A_H(t) > 0$, $T_H(t) > 0$, $I_{TH}(t) > 0$ and $T_{TH}(t) > 0$. ∎

### 4.2.2 Local Asymptotic Stability of DFE

The TV-HIV model (4.2.1) has a unique DFE obtained by setting the right-hand sides of the equations in the model (4.1.1) to zero, given by,

$$\mathcal{E}_4 = (S^*, I_T^{U*}, I_T^{C*}, T_T^*, R^*, I_H^*, A_H^*, T_H^*, I_{TH}^*, T_{TH}^*) = \left(\frac{\Pi}{\mu}, 0, 0, 0, 0, 0, 0, 0, 0, 0\right).$$

The linear stability of the DFE, $\mathcal{E}_4$, can be established using the next generation operator method on system (4.1.1). Using the notation in [50], the matrices $F$ (for the new infection terms) and $V$ (for the transition terms) are given, respectively, by

$$F = \begin{pmatrix} \beta_1(1-\epsilon\kappa) & \eta_1\beta_1(1-\epsilon\kappa) & \eta_2\beta_1(1-\epsilon\kappa) & 0 & 0 & 0 & \eta_{TH1}\beta_1(1-\epsilon\kappa) & \eta_{TH2}\beta_1(1-\epsilon\kappa) \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_2 & \eta_A\beta_2 & \eta_T\beta_2 & \eta_{HT1}\beta_2 & \eta_{HT2}\beta_2 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} K_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -\xi & K_2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\tau & K_3 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & K_4 & 0 & 0 & 0 & -\psi \\ 0 & 0 & 0 & -\alpha & K_5 & 0 & 0 & 0 \\ 0 & 0 & 0 & -\theta & -\gamma & K_6 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & K_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\tau & K_7 \end{pmatrix},$$

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where, $K_1 = \xi + \mu$, $K_2 = \tau + \mu$, $K_3 = \nu + \mu$, $K_4 = \theta + \alpha + \mu$, $K_5 = \gamma + \mu + \delta_1$, $K_6 = \mu + \delta_2$ and $K_7 = \psi + \mu$.

The associated reproduction number, denoted by $\mathcal{R}_T$ is then given by

$$\mathcal{R}_T = \rho(FV^{-1}) = \max\{\mathcal{R}_{01}, \mathcal{R}_{02}\},$$

where $\mathcal{R}_{01}$ and $\mathcal{R}_{02}$ are the associated reproduction numbers for TV and HIV/AIDS, respectively, given by

$$\mathcal{R}_{01} = \frac{\beta_1(1 - \epsilon\kappa)(K_2K_3 + \eta_1\xi K_3 + \eta_2\tau\xi)}{K_1K_2K_3} \text{ and } \mathcal{R}_{02} = \frac{\beta_2[K_5(K_6 + \theta\eta_T) + \alpha(\eta_A K_6 + \gamma\eta_T)]}{K_4K_5K_6}.$$

Therefore, applying Theorem 2 of [50], the following result is established.

**Lemma 4.6** *The DFE, $\mathcal{E}_4$, of the model (4.2.1) is LAS if $\mathcal{R}_T < 1$ and unstable if $\mathcal{R}_T > 1$*
.

The threshold quantity, $\mathcal{R}_T = \max\{\mathcal{R}_1, \mathcal{R}_2\}$, is the associated reproduction number [1, 2, 23, 50]. It represents the average number of secondary cases generated by a typically TV or HIV infected individual in a susceptible population where the aforementioned control strategies (condom-use, counselling and treatment) are used. The epidemiological implication of Lemma 4.6 is that when $\mathcal{R}_T$ is less than unity, a small influx of infected individuals into the community would not generate large outbreaks, and the disease dies out in time (since the DFE is LAS). However, we show in the next subsection that the disease may still persist even when $\mathcal{R}_T < 1$ (this is owing to the existence of backward bifurcation).

### 4.2.3 Backward bifurcation analysis

The existence of backward bifurcation will be explored using Centre Manifold Theory [9, 50]. To apply this theory we first carry out the following change of variables. Let $S = x_1, I_T^U = x_2, I_T^C = x_3, T_T = x_4, I_H = x_5, A_H = x_6, T_H = x_7, I_{TH} = x_8$, and $T_{TH} = x_9$ so that $N = x_1 + x_2 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8 + x_9$. In addition, by using vector notation $X = (x_1, x_2, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9)^T$, the TV-HIV model (4.2.1) can be written in the form $\frac{dX}{dt} = F(X)$, with $(f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8, f_9)^T$ as follows,

$$\frac{dx_1}{dt} = f_1 = \Pi + \nu x_4 - (\lambda_H + \lambda_T^1)x_1 - \mu x_1,$$

$$\frac{dx_2}{dt} = f_2 = \lambda_T^1 x_1 - \sigma \lambda_H x_2 - (\xi + \mu)x_2,$$

$$\frac{dx_3}{dt} = f_3 = \xi x_2 - (\tau + \mu)x_3,$$

$$\frac{dx_4}{dt} = f_4 = \tau x_3 - (\nu + \mu)x_4,$$

$$\frac{dx_5}{dt} = f_5 = \lambda_H x_1 + \psi x_9 - \sigma_1 \lambda_T^1 x_5 - (\alpha + \theta + \mu)x_5, \qquad (4.2.3)$$

$$\frac{dx_6}{dt} = f_6 = \alpha x_5 - (\gamma + \mu + \delta_1)x_6,$$

$$\frac{dx_7}{dt} = f_7 = \theta x_5 + \gamma x_6 - (\mu + \delta_2)x_7,$$

$$\frac{dx_8}{dt} = f_8 = \sigma \lambda_H x_2 + \sigma_1 \lambda_T^1 x_5 - (\tau + \mu)x_8,$$

$$\frac{dx_9}{dt} = f_9 = \tau x_8 - (\psi + \mu)x_9.$$

with the forces of infection given by

$$\lambda_T^1 = \frac{\beta_1 c(x_2 + \eta_1 x_3 + \eta_2 x_4 + \eta_{TH1} x_8 + \eta_{TH2} x_9)}{x_1 + x_2 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8 + x_9} \quad \text{and}$$

$$\lambda_H = \frac{\beta_2(x_5 + \eta_A x_6 + \eta_T x_7 + \eta_{HT1} x_8 + \eta_{HT2} x_9)}{x_1 + x_2 + x_2 + x_3 + x_4 + x_5 + x_6 + x_7 + x_8 x_9},$$

with $c = 1 - \epsilon \kappa$.

Consider the case when $\mathcal{R}_T = 1$ (that is $\mathcal{R}_T = \max\{\mathcal{R}_{01}, \mathcal{R}_{02}\} = 1$). Also suppose that $\beta_2 = \beta_2^*$ is chosen as the bifurcation parameter. Solving for $\beta_2 = \beta_2^*$ from $\mathcal{R}_T = 1$ in (4.2.2) gives

$$\beta_2^* = \frac{K_4 K_5 K_6}{K_5(K_6 + \theta \eta_T) + \alpha(\eta_A K_5 + \gamma \eta_T)}.$$

The Jacobian of the system (4.2.3) evaluated at the DFE, $\mathcal{E}_4$, with $\beta_2 = \beta_2^*$ and denoted by $J^*$, is given by

$$J^* = \begin{pmatrix} M_1 & M_2 \\ M_3 & M_4 \end{pmatrix},$$

where,

$$M_1 = \begin{pmatrix} -\mu & -\beta_1 c & -\beta_1 c \eta_1 & -\beta_1 c \eta_2 + \nu & -\beta_2^* \\ 0 & \beta_1 c - K_1 & -\beta_1 c \eta_1 & \beta_1 c \eta_2 & 0 \\ 0 & \xi & -K_2 & 0 & 0 \\ 0 & 0 & \tau & -K_2 & 0 \\ 0 & 0 & 0 & 0 & \beta_2^* - K_4 \end{pmatrix},$$

$$M_2 = \begin{pmatrix} -\beta_2^*\eta_A & -\beta_2^*\eta_T & -(\beta_2^*\eta_{HT1} + \beta_1 c\eta_{TH1}) & -(\beta_2^*\eta_{HT2} + \beta_1 c\eta_{TH2}) \\ 0 & 0 & -(\beta_2^*\eta_{HT1} + \beta_1 c\eta_{TH1}) & -(\beta_2^*\eta_{HT1} + \beta_1 c\eta_{TH2}) \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ \beta_2^*\eta_A & \beta_2^*\eta_T & \beta_2^*\eta_{HT1} & \beta_2^*\eta_{HT2} + \psi \end{pmatrix},$$

$$M_3 = \begin{pmatrix} 0 & 0 & 0 & 0 & \alpha \\ 0 & 0 & 0 & 0 & \theta \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

$$M_4 = \begin{pmatrix} -K_5 & 0 & 0 & 0 \\ \gamma & -K_6 & 0 & 0 \\ 0 & 0 & -K_2 & 0 \\ 0 & 0 & \tau & -K_7 \end{pmatrix}.$$

The Jacobian has a simple zero eigenvalue (with all other eigenvalues having negative real part), therefore the Centre Manifold Theory can be used to analyse the dynamics of the system (4.1.4).

**Eigenvectors of $\mathbf{J}^*(\mathcal{E}_4)|_{\beta_2=\beta_2^*}$** For the case when $\mathcal{R}_T = 1$, it can be shown that $J^*$ has a left eigenvector (corresponding to the zero eigenvalue), given by $\bar{v} = [v_1, v_2, v_3, v_4, v_5, v_6, v_7, v_8]$, where
$v_1 = 0$,

$v_2 > 0$,

$v_3 = \dfrac{\beta_1 c(\tau\eta_2 + \eta_1 K_3)}{K_2 K_3} v_2$,

$v_4 = \dfrac{\beta_1 c\eta_2}{K_3} v_2$,

$v_5 > 0$,

$v_6 = \dfrac{\beta_2^*(\eta_A K_6 + \gamma\eta_T)}{K_5 K_6} v_5$,

$v_7 = \dfrac{\beta_2^*\eta_T}{K_6} v_5$,

$v_8 = \dfrac{\beta_1 c(\eta_{TH1} Q_7 + \tau\eta_{TH2})}{Q_2 Q_7} v_2 + \dfrac{\beta_2^*(\eta_{HT1} Q_7 + \tau\eta_{HT2}) + \tau\psi}{K_2 K_7} v_5$,

$v_9 = \dfrac{\beta_1 c\eta_{TH2}}{Q_7} v_2 + \dfrac{\beta_2^*\eta_{HT2} + \psi}{K_7} v_5$.

Similarly, the components of the right eigenvector of $J^*(\mathcal{E}_4)|_{\beta_2=\beta_2^*}$ (corresponding to the zero eigenvalue), denoted by $\bar{w} = [w_1, w_2, w_3, v, w_4, w_5, w_6, w_7, w_8, w_9]^T$ are

$$w_1 = -\frac{1}{\mu}\left[\left(\frac{\beta_1 c(K_2 K_4 + \eta_1\xi K_4 + \eta_2\tau\xi) - \nu\tau\xi}{K_2 K_4}\right) w_2 + \left(\frac{\beta_2^*(K_5 K_6 + \eta_A\alpha K_6 + \eta_T\theta K_5 + \eta_T\alpha\gamma)}{K_5 K_6}\right) w_5\right],$$

$$w_2 > 0,$$

$$w_3 = \frac{\xi}{K_2} w_2,$$

$$w_4 = \frac{\tau \xi}{K_2 K_3} w_2,$$

$$w_5 > 0,$$

$$w_6 = \frac{\alpha}{K_5} w_5,$$

$$w_7 = \frac{(\theta K_5 + \alpha \gamma)}{K_5 K_6} w_5,$$

$$w_8 = 0,$$

$$w_9 = 0.$$

In addition, $\bar{v} \cdot \bar{w} = 1$. That is,

$$\bar{v} \cdot \bar{w} = v_2 w_2 + v_3 w_3 + v_4 w_4 + v_5 w_5 + v_6 w_6 + v_7 w_7,$$

$$= \frac{K_2^2 K_3^2 + \beta_1 c (K_3^2 \eta_1 \xi + K_3 \tau \eta_2 \xi + \tau \xi \eta_2 K_2)}{K_2^2 K_3^2} v_2 w_2$$

$$+ \frac{K_5^2 K_6^2 + \beta_2^* [\alpha(\eta_A K_6^2 + \eta_T \gamma K_6 + \eta_T \gamma K_5) + \eta_T \theta K_5^2]}{K_5^2 K_6^2} v_5 w_5,$$

$$= 1.$$

It is worth noting that the free left components $v_2$ and $v_4$, and free right components $w_2$ and $w_4$ are chosen to be

$$v_2 = v_5 = \frac{1}{2}, \quad w_2 = \frac{K_2 K_3^2}{K_2 K_3^2 + \beta_1 c (K_3 \eta_1 + K_3 \tau \eta_2 + \tau \xi \eta_2)}, \quad \text{and}$$

$$w_5 = \frac{K_5^2 K_6^2}{K_5^2 K_6^2 + \beta_2^* [\alpha(\eta_A K_6^2 + \eta_T \gamma K_6 + \eta_T \gamma K_5) + \eta_T \theta K_5^2]},$$

in order to achieve the above result.

**Computation of a**  For the transformed TV-HIV model (4.1.4), some of the associated non-zero partial derivatives of $F$ (evaluated at the DFE) are given by

$$\frac{\partial^2 f_1}{\partial x_2 \partial x_2} = \frac{2\beta_1 c \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_2 \partial x_3} = \frac{\mu c (\beta_1 + \beta_1 \eta_1)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_2 \partial x_4} = \frac{\mu (\beta_1 c + \beta_2 \eta_2)}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_2 \partial x_5} = \frac{\mu (\beta_1 c + \beta_2)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_2 \partial x_6} = \frac{\mu (\beta_1 c + \beta_2 \eta_A)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_2 \partial x_7} = \frac{\mu (\beta_1 c + \beta_2 \eta_T)}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_3 \partial x_3} = \frac{2\beta_1 c\eta_1 \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_3 \partial x_4} = \frac{\mu(\beta_1 c\eta_1 + \beta_1 c\eta_2)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_4 \partial x_4} = \frac{2\beta_1 c\eta_2 \mu}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_3 \partial x_5} = \frac{\mu(\beta_1 c\eta_1 + \beta_2)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_3 \partial x_6} = \frac{\mu(\beta_1 c\eta_1 + \beta_2 \eta_A)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_3 \partial x_7} = \frac{\mu(\beta_1 c\eta_1 + \beta_2 \eta_T)}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_4 \partial x_5} = \frac{\mu(\beta_2 + \beta_1 c\eta_2)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_4 \partial x_6} = \frac{\mu(\beta_1 c\eta_2 + \beta_2 \eta_A)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_4 \partial x_7} = \frac{\mu(\beta_1 c\eta_2 + \beta_2 \eta_T)}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_5 \partial x_5} = \frac{2\beta_2 \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_5 \partial x_6} = \frac{\mu(\beta_2 + \beta_2 \eta_A)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_5 \partial x_7} = \frac{\mu(\beta_2 + \beta_2 \eta_T)}{\Pi},$$

$$\frac{\partial^2 f_1}{\partial x_6 \partial x_6} = \frac{2\beta_2 \eta_A \mu}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_6 \partial x_7} = \frac{\mu(\beta_2 \eta_A + \beta_2 \eta_T)}{\Pi}, \quad \frac{\partial^2 f_1}{\partial x_7 \partial x_7} = \frac{2\beta_2 \eta_T \mu}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_2 \partial x_2} = -\frac{2\beta_1 c\mu}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_2 \partial x_3} = -\frac{\mu(\beta_1 c + \beta_1 c\eta_1)}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_2 \partial x_5} = -\frac{\mu(\beta_1 c + \sigma\beta_2)}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_2 \partial x_6} = -\frac{\mu(\beta_1 c + \sigma\beta_2 \eta_A)}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_2 \partial x_7} = -\frac{\mu(\beta_1 c + \sigma\beta_2 \eta_T)}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_3 \partial x_4} = -\frac{\mu(\beta_1 c\eta_1 + \beta_1 c\eta_2)}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_3 \partial x_3} = -\frac{2\beta_1 c\eta_1 \mu}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_3 \partial x_5} = \frac{\partial^2 f_2}{\partial x_3 \partial x_6} = \frac{\partial^2 f_2}{\partial x_3 \partial x_7} = -\frac{\beta_1 \eta_1 \mu}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_4 \partial x_4} = -\frac{2\beta_1 c\eta_2 \mu}{\Pi}, \quad \frac{\partial^2 f_2}{\partial x_4 \partial x_5} = \frac{\partial^2 f_2}{\partial x_4 \partial x_6} = \frac{\partial^2 f_2}{\partial x_4 \partial x_7} = -\frac{\beta_1 c\eta_2 \mu}{\Pi},$$

$$\frac{\partial^2 f_5}{\partial x_4 \partial x_5} = \frac{\partial^2 f_5}{\partial x_3 \partial x_5} = -\frac{\beta_2 \mu}{\Pi}, \quad \frac{\partial^2 f_5}{\partial x_3 \partial x_5} = \frac{\partial^2 f_5}{\partial x_4 \partial x_6} = -\frac{\beta_2 \eta_A \mu}{\Pi},$$

$$\frac{\partial^2 f_2}{\partial x_2 \partial x_4} = -\frac{\mu(\beta_1 c + \beta_1 c\eta_2)}{\Pi}, \quad \frac{\partial^2 f_5}{\partial x_4 \partial x_7} = \frac{\partial^2 f_5}{\partial x_3 \partial x_7} = -\frac{\beta_2 \eta_T \mu}{\Pi}.$$

Computation of $a$ using the expressions above results in the following expression,

$$a = \sum_{k,i,j}^{9} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0),$$

$$= \frac{2\mu}{\Pi}[v_8 w_2 \sigma \beta_2 w_5 + v_8 w_2 \sigma \beta_2 w_6 \eta_A + v_8 w_2 \sigma \beta_2 w_7 \eta_T - v_2 w_2 \sigma \beta_2 w_5 - v_2 w_2 \sigma \beta_2 w_6 \eta_A$$

$$+ v_8 w_5 \sigma_1 \beta_1 c(w_2 + w_3 \eta_1 + w_4 \eta_2) - v_5 w_5 \sigma_1 \beta_1 c(w_2 + w_3 \eta_1 + w_4 \eta_2)$$

$$- v_2 w_2 \sigma \beta_2 w_7 \eta_T - \beta_1 c(v_2 w_2 w_2 + v_2 w_2 w_3 + v_2 w_2 w_4 + v_2 w_2 w_5 + v_2 w_2 w_6 + v_2 w_2 w_7)$$

$$- \beta_1 c(v_2 w_3 \eta_1 w_2 + w_3 v_2 w_3 \eta_1 + w_4 v_2 w_3 \eta_1 + v_2 w_3 \eta_1 w_5 + w_6 v_2 w_3 \eta_1 + v_2 w_3 \eta_1 w_7)$$

$$- \beta_1 c(v_2 w_4 \eta_2 w_2 + w_3 v_2 w_4 \eta_2 + w_4 v_2 w_4 \eta_2 + v_2 w_4 \eta_2 w_5 + w_6 v_2 w_4 \eta_2 + v_2 w_4 \eta_2 w_7))$$

$$- \beta_2(w_2 v_5 w_5 + w_3 v_5 w_5 + w_4 v_5 w_5 + w_5 v_5 w_5 + w_6 v_5 w_5 + w_7 v_5 w_5)$$

$$- \beta_2(w_2 v_5 w_6 \eta_A + w_3 v_5 w_6 \eta_A + w_4 v_5 w_6 \eta_A + w_5 v_5 w_6 \eta_A + w_6 v_5 w_6 \eta_A + +w_7 v_5 w_6 \eta_A)$$

$$- \beta_2(w_2 v_5 w_7 \eta_T + w_3 v_5 w_7 \eta_T + w_4 v_5 w_7 \eta_T + w_5 v_5 w_7 \eta_T + w_6 v_5 w_7 \eta_T + w_7 v_5 w_7 \eta_T)],$$

which can be simplified to the following,

$$a = \sum_{k,i,j}^{9} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0),$$

$$= \frac{2\mu}{\Pi}[v_8 w_5 \sigma_1 \beta_1 c(w_2 + w_3 \eta_1 + w_4 \eta_2) + v_8 w_2 \sigma \beta_2^*(w_5 + w_6 \eta_A + w_7 \eta_T)$$

$$- v_5 w_5 \sigma_1 \beta_1 c(w_2 + w_3 \eta_1 + w_4 \eta_2) - v_2 w_2 \sigma \beta_2^*(w_4 + w_5 \eta_A + w_6 \eta_T) \qquad (4.2.4)$$

$$- \beta_1 c(v_2 w_2 + v_2 w_3 \eta_1 + v_2 w_4 \eta_2)(w_2 + w_3 + w_4 + w_5 + w_6 + w_7)$$

$$- \beta_2^*(v_4 w_4 + v_4 w_5 \eta_A + v_4 w_6 \eta_T)(w_2 + w_3 + w_4 + w_5 + w_6 + w_7)].$$

**Computation of b** Substituting the vectors $\bar{v}$ and $\bar{w}$ and the respective partial derivatives (evaluated at the DFE) into the expression of $b$ yields,

$$b = \sum_{k,i,j}^{8} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta_2}(0,0) = v_5 w_5 + v_5 w_6 \eta_A + v_5 w_7 \eta_T > 0.$$

Since the coefficient $b$ is automatically positive, it follows that the model (4.2.1) will undergo backward bifurcation if the coefficient $a$ given by (4.2.4), is positive.

The above results can be summarised by the following theorem.

**Theorem 4.4** *The TV-HIV model (4.2.1) exhibits backward bifurcation whenever the bifurcation parameter $a$, given by (4.2.4), is positive.*

In the absence of co-infection, that is for the case when $\sigma = \sigma_1 = 0$, the bifurcation parameter $a < 0$. This rules out the existence of backward bifurcation when $\sigma = \sigma_1 = 0$. To further rule out the existence of backward bifurcation, a global stability of the DFE when $\sigma = \sigma_1 = 0$ is proven below.

### 4.2.4 Global-asymptotic Stability of DFE when $\sigma = \sigma_1 = 0$

First of all notice that by setting $\sigma = \sigma_1 = 0$ in (4.2.1) the equation of $\dfrac{dI_{TH}}{dt} \to 0$ as $t \to \infty$, thus $\dfrac{dT_{TH}}{dt} \to 0$ as $t \to \infty$. Hence, it follows that the system (4.2.1) can be simplified to

$$
\begin{aligned}
\frac{dS}{dt} &= \Pi + \nu T_T - (\lambda_H + \lambda_T^1)S - \mu S, \\
\frac{dI_T^U}{dt} &= \lambda_T^1 S - (\xi + \mu)I_T^U, \\
\frac{dI_T^C}{dt} &= \xi I_T^U - (\tau + \mu)I_T^C, \\
\frac{dT_T}{dt} &= \tau I_T - (\nu + \mu)T_T, \\
\frac{dI_H}{dt} &= \lambda_H S - (\alpha + \theta + \mu)I_H, \\
\frac{dA_H}{dt} &= \alpha I_H - (\gamma + \mu + \delta_1)A_H, \\
\frac{dT_H}{dt} &= \theta I_H + \gamma A_H - (\mu + \delta_2)T_H.
\end{aligned}
\tag{4.2.5}
$$

Next, define the invariant region

$$
\tilde{\mathcal{D}}_{\prime} = \{(S, I_T^U, I_T^C, T_T, I_H, A_H, T_H, I_{TH}, T_{TH}) \in \mathcal{D} : S \le S^*\}.
$$

We claim the following:

**Theorem 4.5** *The DFE, $\mathcal{E}_4$, of the model (4.2.5), is GAS in $\tilde{\mathcal{D}}_{\prime}$ whenever $\mathcal{R}_T \le 1$.*

***Proof.***
Consider the following Lyapunov function

$$
\mathcal{F} = \mathcal{R}_{01}I_T^U + \frac{\beta_1 c(\eta_1 K_3 + \eta_2 \tau)}{K_2 K_3}I_T^C + \frac{\beta_1 c\eta_2}{K_3}T_T + \mathcal{R}_{02}I_H + \frac{\beta_2(\eta_A K_6 + \eta_T \gamma)}{K_5 K_6}A_H + \frac{\beta_2 \eta_T}{K_6}T_H
$$

with Lyapunov derivative given by,

$$\dot{\mathcal{F}} = \mathcal{R}_{01}\dot{I}_T^U + \frac{\beta_1 c(\eta_1 K_3 + \eta_2 \tau)}{K_2 K_3}\dot{I}_T^C + \frac{\beta_1 c\eta_2}{K_3}\dot{T}_T + \mathcal{R}_{02}\dot{I}_H + \frac{\beta_2(\eta_A K_6 + \eta_T \gamma)}{K_5 K_6}\dot{A}_H + \frac{\beta_2 \eta_T}{K_6}\dot{T}_H,$$

$$= \mathcal{R}_{01}(\lambda_T^1 S - K_1 I_T^U) + \frac{\beta_1 c(\eta_1 K_3 + \eta_2 \tau)}{K_2 K_3}(\xi I_T^U - K_2 I_T^C) + \frac{\beta_1 c\eta_2}{K_3}(\tau I_T^C - K_3 T_T)$$

$$+ \mathcal{R}_{02}[\lambda_H S - K_4 I_H] + \frac{\beta_2(\eta_A K_6 + \eta_T \gamma)}{K_5 K_6}[\alpha I_H - K_5 A_H] + \frac{\beta_2 \eta_T}{K_6}[\theta I_H + \gamma A_H - K_6 T_H],$$

$$= \mathcal{R}_{01}\lambda_T^1 S - \beta_1 c(I_T^U + \eta_1 I_T^C + \eta_2 T_T) + \mathcal{R}_{02}\lambda_H S - \beta_2(I_H + \eta_A A_H + \eta_T T_H),$$

$$= \mathcal{R}_{01}\lambda_T^1 S - \lambda_T^1 N + \mathcal{R}_{02}\lambda_H S - \lambda_H N,$$

$$= \lambda_T^1 N\left[\frac{\mathcal{R}_{01}\lambda_T^1 S}{\lambda_T^1 N} - 1\right] + \lambda_H N\left[\frac{\mathcal{R}_{02}\lambda_H S}{\lambda_H N} - 1\right],$$

$$\leq \lambda_T^1 N^*[\mathcal{R}_{01} - 1] + \lambda_H N^*[\mathcal{R}_{02} - 1], \quad \text{since } S \leq S^* \text{ in } \tilde{\mathcal{D}}, \text{ and } N \leq N^*,$$

$$= \beta_1 c(I_T^U + \eta_1 I_T^C + \eta_2 T_T)[\mathcal{R}_{01} - 1] + \beta_2(I_H + \eta_A A_H + \eta_T T_H)[\mathcal{R}_{02} - 1] \leq 0$$

(4.2.6)

when $\mathcal{R}_T \leq 1$, where $c = 1 - \epsilon\kappa$.

Since all the parameters and variables of the model (4.2.5) are non-negative (Lemma 4.5), it follows that $\dot{\mathcal{F}} \leq 0$ for $\mathcal{R}_T \leq 1$ (i.e. $\mathcal{R}_{01} \leq 1$ and $\mathcal{R}_{02} \leq 1$) with $\dot{\mathcal{F}} = 0$ if and only if $I_T^U = I_T^C = T_T = I_H = A_H = T_H = 0$. Hence $\mathcal{F}$ is a Lyapunov function on $\tilde{\mathcal{D}}$. Further, the largest compact invariant set in $\left\{(S, I_T^U, I_T^C, T_T, I_H, A_H, T_H) \in \tilde{\mathcal{D}} : \dot{\mathcal{F}} = 0\right\}$ is the singleton $\{\mathcal{E}_4\}$. Thus, it follows by LaSalle's Invariance Principle (Theorem 2.10), that
$(I_T^U(t), I_T^C(t), T_T(t), I_H(t), A_H(t), T_H(t)) \to (0, 0, 0, 0, 0, 0)$ as $t \to \infty$ and that every solution of the equations of the model (4.2.5) with initial conditions in $\tilde{\mathcal{D}}$ approaches $\mathcal{E}_4$ as $t \to \infty$ (whenever $\mathcal{R}_T \leq 1$). ∎

## 4.3 Assessment of conrol strategies for TV

An assessment of control strategies for HIV/AIDS is fully considered by Garba and Gumel [16], therefore, in this section, only the main control strategies for TV are considered. This is of interest to this study because infection with TV increases susceptibility to HIV. The control strategies considered include:

1. using condoms by sexually active individuals (condom-only strategy);

2. counselling of infected individuals (counselling-only strategy);

3. treatment of infected individuals (treatment-only strategy);

4. using condoms and receiving different levels of counselling for TV (condom and counselling strategy);

5. Counselling and treatment of infected individuals who have tested positive for TV at varying levels (counselling and treatment strategy);

6. using condoms, receiving counselling and treatment for TV (condom, counselling and treatment strategy);

### 4.3.1 Condom-only strategy

Since not all the sexually-active individuals in a population are expected to strictly comply to the use of condoms consistently and correctly during every sexual encounter, it is therefore informative to determine whether or not the use of condoms as a sole intervention strategy will offer a beneficial population-level impact. This is done by setting all the treatment and counselling related parameters and state variables of the model (4.2.1) to zero (i.e. $I_T^C = T_T = T_{TH} = \xi = \tau = \nu = \eta_1 = \eta_2 = 0$), which produces a reduced model with the following associated reproduction number,

$$\mathcal{R}_{c1} = \frac{\beta_1(1 - \epsilon\kappa)}{\mu}.$$

Firstly, the effect of condom use on TV transmission dynamics can be assessed qualitatively, by differentiating the expression for $\mathcal{R}_{c1}$ partially with respect to $\kappa$ (condom compliance). This gives

$$\frac{\partial \mathcal{R}_{c1}}{\partial \kappa} = -\frac{\beta_1 \epsilon}{\mu} < 0.$$

Since $\mathcal{R}_{c1}$ is a decreasing function of $\kappa$, an increase in condom compliance ($\kappa$) results in a decrease of $\mathcal{R}_{c1}$. This result is depicted in Table 4.1. Thus, the above analysis shows that condom use will always have a positive population-level impact (even for small efficacy and compliance level) by reducing the disease burden. In this study, condom efficacy is fixed at 0.8, unless otherwise stated.

A contour plot of the associated reproduction threshold $\mathcal{R}_{c1}$ (as a function of condom efficacy ($\epsilon$) and compliance ($\kappa$)), is shown in Figure 4.7. This figure, generated by using $\beta_1 = 0.045$ as well as the set of parameter values in Table 5.2 (where all parameters related to counselling and treatment are set to zero), shows a decrease in $\mathcal{R}_{c1}$ with increasing $\epsilon$ and $\kappa$. It is clear that significantly high condom efficacy and compliance is needed to effectively

| Compliance Level | $\mathcal{R}_{c1}$ |
|---|---|
| Low ($\kappa = 0.25$) | 31.7632 |
| Moderate ($\kappa = 0.5$) | 23.8824 |
| High ($\kappa = 0.75$) | 15.8816 |

Table 4.1: *Reproduction numbers ($\mathcal{R}_{c1}$) of the model (4.2.1) for the condom-only strategy.*

control TV, that is, to attain $\mathcal{R}_{c1} < 1$ so that TV/HIV can be eliminated as guaranteed by Lemma 4.6. In particular, even if the condom efficacy level is 80% ($\epsilon = 0.8$), at least 75% ($\kappa = 0.75$) of sexually-active individuals would still be required to use condoms consistently and correctly in order to effectively control the spread of TV in a population.



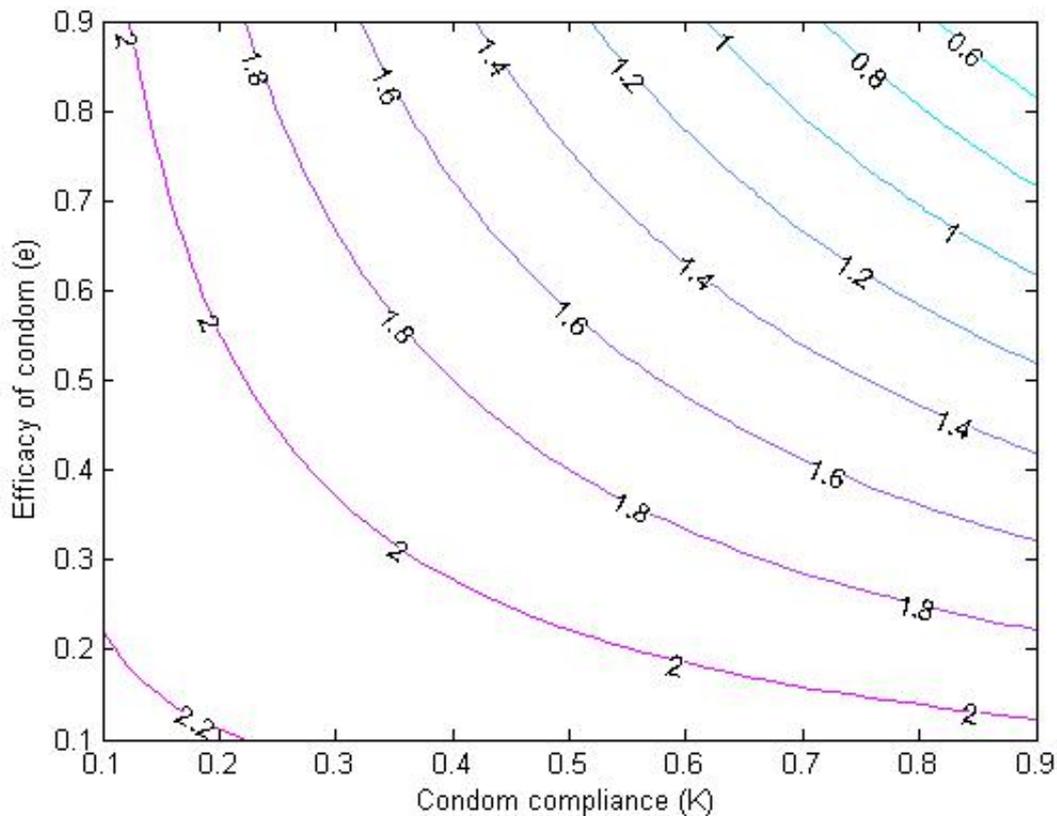Figure 4.7: *Simulatins of the model (4.2.1) showing a contour plot of $\mathcal{R}_{c1}$ where $\beta_1 = 0.045$*

### 4.3.2 Counselling-only Strategy

In this case, all the parameters and state variables of the model (4.2.1), related to condom-use and treatment, are set to zero. This gives a reduced model with the following associated reproduction number

$$\mathcal{R}_{c2} = \frac{\beta_1(1 + \eta_1\xi)}{K_1},$$

where $K_1 = \xi + \mu$. Differentiating $\mathcal{R}_{c2}$ partially with respect to the counselling rate $\xi$ gives,

$$\frac{\partial \mathcal{R}_{c2}}{\partial \xi} = \frac{\beta_1 \eta_1}{K_1} - \frac{\beta_1(1 + \eta_1 \xi)}{K_1^2} = \frac{\beta_1(\mu \eta_1 - 1)}{K_1^2}.$$

Thus, $\frac{\partial \mathcal{R}_{c2}}{\partial \xi} < 0$ since $0 < \mu < 1$ and $0 < \eta_1 < 1$.

Therefore, counselling individuals infected with TV will reduce the reproduction number $\mathcal{R}_{c2}$ and thus reduce the TV burden, if the relative risk of infectiousness of counselled infected individuals ($\eta_1$) does not exceed unity (that is, if counselled individuals infected with TV reduce their risky sexual behaviour).

Simulations are carried out to further assess the impact of counselling individuals infected with TV using the following levels of counselling:

I) Low counselling effectiveness: $\xi = 0.05$;

II) Moderate counselling effectiveness: $\xi = 0.5$;

III) High counselling effectiveness: $\xi = 5$.

Table 4.2 shows that an increase in the level of effectiveness for counselling results in a decrease in the reproduction number. Thus, counselling individuals infected with TV results in a reduction of the burden of the disease. A high counselling effectiveness level is enough to get $\mathcal{R}_{c2} < 1$, which is enough to eradicate TV.

| Level | $\mathcal{R}_{c2}$ |
|---|---|
| Low $\xi = 0.05$ | 10.4484 |
| Moderate $\xi = 0.5$ | 1.3691 |
| High $\xi = 5$ | 0.1413 |

Table 4.2: *Reproduction numbers ($\mathcal{R}_{c2}$) of the model (4.2.1) for the counselling-only strategy.*

### 4.3.3   Treatment-only Strategy

The singular effect of treatment of individuals with TV is assessed using the TV-HIV model (4.1.1) (where counselling and condom-use related variables are not incorporated) by first of all differentiating the threshold quantity

$$\mathcal{R}_{c3} = \frac{\beta_1(Q_2 + \tau \eta)}{Q_1 Q_2},$$

(where $Q_1 = \tau + \mu$ and $Q_2 = \nu + \mu$), partially with respect to $\tau$ yields,

$$\frac{\partial \mathcal{R}_{c3}}{\partial \tau} = \frac{\beta_1 \eta}{Q_1 Q_2} - \frac{\beta_1(Q_2 + \tau \eta)}{Q_1^2 Q_2} = \frac{\beta_1(\mu \eta - Q_2)}{Q_1^2 Q_2}.$$

It follows that $\frac{\partial \mathcal{R}_{c3}}{\partial \tau} < 0$ whenever $\eta < \eta_\tau$, where $\eta_\tau = \frac{Q_2}{\mu}$.

Therefore, the treatment of non-counselled individuals will reduce the reproduction number and therefore the TV burden if the relative infectiousness of treated individuals ($\eta$) does not exceed the threshold quantity $\eta_\tau$. On the other hand, if $\eta > \eta_\tau$, then the use of treatment will increase the $\mathcal{R}_{c3}$ and as a result increase the burden of TV.

**Lemma 4.7** *The treatment of infected individuals will have a positive population-level impact if $\eta < \eta_\tau$.*

Numerical simulations of the model are carried out to further assess the impact of the Treatment-only Strategy on TV in a population. The following arbitrarily chosen levels of treatment effectiveness are considered:

I) Low treatment effectiveness: $\tau = 0.5$;

II) Moderate treatment effectiveness: $\tau = 2$;

III) High treatment effectiveness: $\tau = 50$.

The simulation results depicted in Figure 4.8 shows that an increase in treatment of individuals infected with TV results in a decrease in the total number of individuals infected with TV. Furthermore, Table 4.3 shows that an increase in the level of effectiveness for treatment of individuals infected with TV results in a reduction of the reproduction number. Therefore, treating individuals infected with TV results in a decline of the burden of TV in the community.

| Level | $\mathcal{R}_{c3}$ |
|---|---|
| Low $\tau = 0.5$ | 7.4015 |
| Moderate $\tau = 2$ | 2.1699 |
| High $\tau = 50$ | 0.4367 |

Table 4.3: *Reproduction numbers ($\mathcal{R}_{c3}$) of the model (4.1.1) for the treatment-only strategy.*

## 4.3.4 Condom and Counselling Strategy

Here, we study the combined impact of condom-use and counselling. The following counselling effectiveness levels will be used:

I) Low counselling effectiveness: $\xi = 0.05$ coupled with different condom compliance levels: low ($\kappa = 0.25$), moderate ($\kappa = 0.5$) and high ($\kappa = 0.75$);

II) Moderate counselling effectiveness: $\xi = 0.5$ coupled with different condom compliance levels: low ($\kappa = 0.25$), moderate ($\kappa = 0.5$) and high ($\kappa = 0.75$);

III) High counselling effectiveness: $\xi = 5$ coupled with different condom compliance levels: low ($\kappa = 0.25$), moderate ($\kappa = 0.5$) and high ($\kappa = 0.75$);
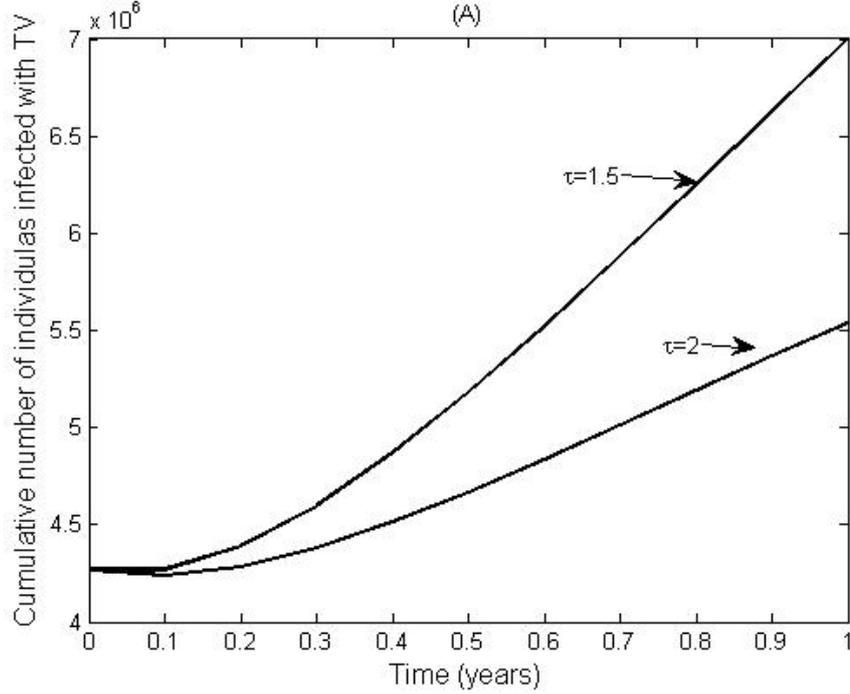
Figure 4.8: *Simulations of the model (4.1.1) showing the cumulative number of individuals infected with TV for various levels of treatment. Parameter values used are as given in Table 5.2.*

We first set all the treatment-related parameters and state variables of the model (4.2.1) to zero, (i.e. $T_T = T_{TH} = \tau = \nu = \psi = 0$).

The associated reproduction number of the reduced model is given by

$$\mathcal{R}_{c4} = \beta_1(1 - \epsilon\kappa)\frac{\mu + \eta_1\xi}{\mu K_1}.$$

Table 4.4 shows a decrease in $\mathcal{R}_{c4}$ with increasing condom compliance and counselling effectiveness. This strategy reduces the burden of the disease (an increase in counselling and condom use reduces the reproduction number).

| Condom compliance level | Low counselling | Moderate counselling | High counselling |
|---|---|---|---|
| Low ($\kappa = 0.25$) | 8.3587 | 1.0983 | 0.1130 |
| Moderate ($\kappa = 0.5$) | 6.2691 | 0.8215 | 0.0848 |
| High ($\kappa = 0.75$) | 4.1794 | 0.5476 | 0.0565 |

Table 4.4: *Reproduction numbers ($\mathcal{R}_{c4}$) of the model (4.2.1) for the condom use and counselling strategy.*

### 4.3.5 Counselling and Treatment Strategy

Next, we study the combined impact of counselling and treating of individuals infected with TV.

The following levels of effectiveness will be used:

I) Low counselling and treatment effectiveness: $\xi = 0.05$ and $\tau = 0.5$;

II) Moderate counselling and treatment effectiveness: $\xi = 0.5$ and $\tau = 2$;

III) High counselling and treatment effectiveness: $\xi = 5$ and $\tau = 50$.

Setting the condom-use related parameter values of model (4.2.1) to zero ($\kappa = \epsilon = 0$) gives a reduced model with the following reproduction number,

$$\mathcal{R}_{c5} = \frac{\beta_1(K_2 K_3 + \eta_1 \xi K_3 + \eta_2 \tau \xi)}{K_1 K_2 K_3},$$

where, $K_1 = \xi + \mu$, $K_2 = \tau + \mu$, $K_3 = \nu + \mu$.

Table 4.5 shows that $\mathcal{R}_{c5}$ decreases with increasing counselling and treatment effectiveness. As expected, high levels of treatment and counselling reduces the burden of the disease in the population.

| Treatment | Counselling | | |
|---|---|---|---|
| | **Low** | **Moderate** | **High** |
| Low | 10.7007 | 1.6997 | 0.4825 |
| Moderate | 10.5132 | 1.4541 | 0.2290 |
| High | 10.4511 | 1.3727 | 0.1450 |

Table 4.5: *Reproduction numbers ($\mathcal{R}_{c5}$) of the model (4.2.1) for the counselling and treatment strategy.*

### 4.3.6 Condom, Counselling and Treatment strategy

Finally, we explore the condom, counselling and treatment strategy. The following levels of effectiveness will be used:

I) Low counselling and treatment effectiveness: $\xi = 0.05$ and $\tau = 0.5$. Coupled with different condom compliance levels: low ($\kappa = 0.25$), moderate ($\kappa = 0.5$) and high ($\kappa = 0.75$);

II) Moderate counselling and treatment effectiveness: $\xi = 0.5$ and $\tau = 2$. Coupled with different condom compliance levels: low ($\kappa = 0.25$), moderate ($\kappa = 0.5$) and high ($\kappa = 0.75$);

III) High counselling and treatment effectiveness: $\xi = 5$ and $\tau = 50$. Coupled with different condom compliance levels: low ($\kappa = 0.25$), moderate ($\kappa = 0.5$) and high ($\kappa = 0.75$).

It follows from Table 4.6 that using a moderate effective counselling and treatment strategy, together with moderate and high condom compliance (subject to 80% condom efficacy) can reduce the burden of TV in the population. Table 4.6 also shows a decrease in the reproduction number $\mathcal{R}_{c6}$ with an increase in counselling and treatment, coupled with increasing levels of condom compliance.

| Condom compliance level | Counsel. and Treat. | | |
|---|---|---|---|
| | Low Level | Moderate Level | High Level |
| Low ($\kappa = 0.25$) | 8.5606 | 1.1632 | 0.1160 |
| Moderate ($\kappa = 0.5$) | 6.4204 | 0.8720 | 0.0870 |
| High ($\kappa = 0.75$) | 4.2803 | 0.5816 | 0.0580 |

Table 4.6: *Reproduction numbers ($\mathcal{R}_{c6}$) of the model (4.2.1) for the condom, counselling and treatment strategy.*

It should be noted that the best strategy for the eradication of TV in the population is the one that includes all three interventions. Here, a low counselling and treatment effectiveness level coupled with high condom compliance level is enough to control the disease in the population.

# Chapter 5

# Conclusion

1. New trichomonas vaginalis (TV) and HIV/AIDS models are formulated and analysed. Some of the findings include:

i) The DFE of each model is GAS whenever the associated reproduction number is less than unity and unstable when greater than unity. This result guarantees disease elimination when the associated reproduction number is less than one.

ii) The TV-only and HIV-only models both have unique endemic equilibria which are GAS whenever the associated reproduction number is greater than unity. The implication of this result is that each disease will invade the population if the associated reproduction number is greater than one.

2. A new model for the transmission dynamics of the co-infection of TV and HIV/AIDS co-infection is constructed and analysed. This model includes the treatment of individuals infected with TV and those infected with HIV/AIDS. An extension of this model is considered, which incorporates condom-use and counselling of individuals with clinical symptoms of TV.

Some of the main theoretical findings of the study are summarized below:

i) Both of the TV-HIV co-infection models undergo the phenomenon of backward bifurcation. It is established that co-infection of TV with HIV is the condition for the emergence of this phenomenon.

ii) Backward bifurcation can be removed by assuming the co-infection of TV and HIV is negligible. In the absence of co-infection of TV with HIV/AIDS, the DFE of the TV-HIV model (and the extended model) is shown to be globally-asymptotically stable whenever the associated reproduction number is less than unity. Hence the elimination of TV and HIV in this case.

iii) The endemic equilibrium of the sub-model is shown to be GAS for a special case. Meaning that TV and HIV co-exist in the population whenever the associated reproduction number is greater than unity.

Numerical simulations of the models show the following:

i) In the absence of co-infection, the DFE of the resulting model is GAS whenever the associated reproduction number is less than unity.

ii) A reduction in the TV incidence in the population reduces HIV incidence in the same population. Therefore, it would be worthwhile to focus some more resources towards the elimination TV in a population.

iii) An increase in the treatment effectiveness level of individuals infected with TV results in a decline in the burden of TV in the community.

iv) An increase in the level of treatment effectiveness of individuals infected with HIV/AIDS results in a reduction of the burden of the disease in the community.

An assessment of control strategies for TV resulted in the following results:

i) Condom-use has a positive population level impact on TV. This means that an increase in condom use will result in a decline in the burden of TV. An increase in the compliance of condom-use results in a decrease in the value of the associated reproduction number of TV.

ii) Counselling has a positive population level impact on TV. Thus, an increase in counselling of individuals infected with TV will result in a decrease of TV in a population.

iii) Treatment of individuals infected with TV also has a positive population level impact. An increase in the level of effectiveness of treatment results in a decline of the associated reproduction number. The higher the treatment effectiveness level of TV in a population, the lower the burden of the disease.

iv) If control strategies are implemented at a high level of effectiveness, the burden of TV will be reduced in that population. This will result in the reduction of HIV/AIDS incident in the population.

HIV/AIDS has very harsh implications to individuals infected and affected as well as to the economy. Many lives are lost leaving thousands of children orphaned and without breadwinners, there is a loss of the young skilled labour force and the cost of antiretroviral drugs (used for HIV treatment) in developing countries is very high. Taking into account the contribution TV infections have on the transmission of HIV, implementing control interventions of TV (such as treatment, condom-use and counselling) may (to some extent) help in the fight against HIV/AIDS.

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| Variables | Description |
|---|---|
| $N$ | Total population |
| $S$ | Susceptible individuals |
| $I_T$ | Population of individuals infected with TV |
| $T_T$ | Population of individuals receiving treatment for TV |
| $I_H$ | Population of individuals infected with HIV |
| $A_H$ | Population of infected individuals with AIDS symptoms |
| $T_H$ | Population of individuals receiving treatment |
| $I_{TH}$ | Population of individuals infected with TV and HIV |
| $T_{TH}$ | Population of individuals receiving treatment for TV |
| $\lambda_T, \lambda_T^1$ | Force of infection for TV |
| $\lambda_H$ | Force of infection for HIV |

| Parameters | Description |
|---|---|
| $\Pi$ | Recruitment rate of humans |
| $\mu$ | Natural mortality rate |
| $\beta_1$ | Effective contact rate for TV |
| $\beta_2$ | Effective contact rate for HIV |
| $\eta$ | Modification parameter |
| $\eta_1$ | Modification parameter |
| $\eta_2$ | Modification parameter |
| $\eta_A$ | Modification parameter |
| $\eta_T$ | Modification parameter |
| $\xi$ | Counselling rate for TV |
| $\sigma$ | Co-infection parameter |
| $\tau$ | Treatment rate for TV |
| $\nu$ | Recovery rate for TV |
| $\psi$ | Progression rate from class $T_{TH}$ to class $I_H$ |
| $\alpha$ | Progression rate from class $I_H$ to class $A_H$ |
| $\theta$ | Treatment rate for class $I_H$ |
| $\gamma$ | Treatment rate for class $A_H$ |
| $\phi$ | Progression rate from class $I_{TH}$ to class $T_{TH}$ |
| $\delta_1$ | Disease-induced mortality rate for class $A_H$ |
| $\delta_2$ | Disease-induced mortality rate for class $T_H$ |

Table 5.1: *Description of Variables and Parameters of the models.*

| Parameters | Nominal Value | Reference |
|---|---|---|
| $\Pi$ | 500000 | Assumed |
| $\mu$ | 0.02 | [16, 44] |
| $\beta_1$ | 0.709 | [6] |
| $\beta_2$ | variable | |
| $\eta$ | 0.5 | Assumed |
| $\eta_1$ | 0.5 | Assumed |
| $\eta_2$ | 0.2 | Assumed |
| $\eta_A$ | 0.05 | Assumed |
| $\eta_T$ | 0.001 | [44] |
| $\xi$ | variable | |
| $\sigma$ | 2 | Assumed |
| $\tau$ | variable | |
| $\nu$ | 0.9 | [6] |
| $\psi$ | 0.7 | Assumed |
| $\alpha$ | 0.2 | [37] |
| $\theta$ | 0.8 | Assumed |
| $\gamma$ | 0.4 | Assumed |
| $\delta_1$ | 0.01 | [44] |
| $\delta_2$ | 0.04 | Assumed |

Table 5.2: *Parameter values of the models.*