Analysis and Optimal Control of an HIV Model with Immune Response

D. Bichara¹, A. Caicedo-Casso², D. Toro-Zapata³, S. Lee⁴

¹bichara@univ-metz.fr, ² caicedaa@mail.uc.edu, ³ hdtoro@uniquindio.edu.co, ⁴ mathever@gmail.com

¹University of Metz & INRIA NGE, ²University of Cincinnati, ³Universidad del Quindo,

⁴Arizona State University

July 28, 2011

Abstract

An HIV model incorporating immune response is considered. The basic reproduction number is exhibited. The global stability of the virus free equilibrium is proved and the stability of the endemic equilibrium in a special case is studied. Optimal control is applied to our model to maximize the healthy cells and minimize the cost of treatments.

1 Introduction

The human immunodeficiency virus (HIV) is the pathogen responsible for one of the world's killer disease, AIDS. The pathogen targets the immune response and then the infected person can be exposed to many opportunist diseases. The mathematical framework has been considered to model the dynamic of parasite within a host, in general and HIV in particular [1, 2, 7, 8, 14, 17, 18, 25, 29, 30, 32, 34, 35, 36, 41, 45, 46] and the references therein. A review has been done in [6].

Let us give a quick description of the dynamics of HIV within the host. When HIV invades the body, it targets the $CD4^+$ T-cells where the RNA of the virus is converted into DNA; thus, when they begin to multiply to fight this pathogen, they produce more of the virus. CD4⁺ T-cells are responsible for signal Cytotoxic T Lymphocyte cells (CTL) -other immune cells- that an invader is to be fought. The immune response cells respond to this message and set out to eliminate infection by killing infected cells; they act by lysing infected cells, causing them to explod, thus CTL remove infected cells from the system at constant rates, but they do not directly target free virus. Over the time, HIV is able to deplete the population of $CD4^+$ T-cells, causing that CTL cells are never deployed. $CD4^+$ T-cells in a healthy person is $1000mm^{-3}$, when the cell count reaches $200mm^{-3}$ or below in a HIV-patient, then the person is classified as having AIDS [8, 16] .

The simplest and most popular model for a virus within host is [5, 33, 36]:

$$
\begin{cases}\n\dot{T} = \sigma - \beta TV - \mu T \\
\dot{T}^* = \beta TV - \delta T^* \\
\dot{V} = \eta T^* - cV\n\end{cases}
$$
\n(1)

where T and T^* are respectively the concentration of healthy and infected cells. The variable V represents the load of virions. Many models derived from (1) have been mathematically studied in the literature [9, 12, 14, 22, 23, 43]. However this model does not take into account to immune response, which is a key phenomenon within the dynamics of HIV in the host. Nowak and Bangham have considered the immune response in [31]. The model is:

$$
\begin{cases}\n\dot{T} = \sigma - \beta TV - \mu T \\
\dot{T}^* = \beta TV - \delta T^* - \gamma T^* M \\
\dot{M} = \alpha T^* M - \delta M \\
\dot{V} = \eta T^* - cV\n\end{cases}
$$
\n(2)

The model of Nowak and Bangham is 4-dimensionnal. and studying its stability is difficult. Liu [24] proved the local asymptotic stability of equilibria by using a semisymbolic method. Liu proved also that a Hopf birfucation might occur under some conditions, as pointed out by Nowak and Bangham themselves for a 5-dimensional model proposed in the same paper. Murase et al. [28] have used Liu's technique to prove the local stability of the interior equilibrium of Nowak and Bangham's model by incorporating the absorption term, i.e: $-\beta T V$ virions lost by the infection process in the dynamic of virions. In Murase et al.'s model they consider that the immune response react on virions and not on infected cells. The global stability of equilibira of Nowak and Bangham's model has been done by Souza in [40].

Yet in Nowak and Bangham's model, the immune response decay goes to zero in the absence of infected cells T^* . However, even though small, immune response is expected during the infection [1]. In this paper, the model we consider is based on (2), but divide the immune response into two compartments where M and M^* denote the inactivated and activated immune response respectively. In this model the immune response never dies out. We prove the global stability of the virus free equilibrium (VFE) and prove there is a unique endemic equilibria. We prove also its global stability of a special case.

Optimal control has been applied to HIV models in order to find out conditions that would maximize the size of healthy cells and minimize the cost of treatment [44, 17, 16, 8]. Researches have suggested that treatment strategies must incorporate the action of Reverse Transcriptase (RT) inhibitors and Protease Inhibitors (PI) [1], which lead to a therapy based on drug cocktails of three or four medicaments taken in combination; indeed, the fact that HIV replicates rapidly (producing 10^{10} viral particles per day) shows that HIV is evolving so rapidly that treatment with a single drug was not effective [1, 36].

RT inhibitors based therapy inhibit reverse transcription by being incorporated into the newly synthesized viral DNA and prevent its further elongation or directly by binding to the enzyme and interfering with its function. On the other hand, PI based therapy cause infected cells to produce non-infectious virions. Virions created prior drug treatment remain infectious [36].

The aim of this paper is then double: the stability analysis and the optimal control formation which are in the literature. The paper is organized as follows: In the section 2 we analyze the model without treatment where the stability of equilibria is done. The section 3 is dedicated to the optimal control formulation. Numerical simulations are done in the last section.

2 Analysis of the Model

2.1 The model

We divide the population as follows: T and T^* describe respectively the concentration of healthy CD^+T -cells and infected cells. M and M^* are respectively unactivated and activated immune response and V is the concentration of virions. Hence the model has the form:

$$
\begin{cases}\n\dot{T} = \sigma - \beta TV - \mu T \\
\dot{T}^* = \beta TV - \gamma T^* M^* - \delta T^* \\
\dot{M} = \lambda - \psi T^* M - \rho M \\
\dot{M}^* = \alpha T^* M^* - \rho M^* + \psi T^* M \\
\dot{V} = \eta T^* - cV\n\end{cases}
$$
\n(3)

In this model, σ is the constant recruitment of healthy cells from the thymus and bone marrow. A healthy cell becomes infected through contact with a HIV virion V with rate β . The parameter δ is the natural death rate of healthy CD⁺T-cells. The activated immune response M^* kills infected cells by quantity γT^*M^* . These killed infected cells produce αT^*M^* activated immune cells. It is biologically meaningful to consider $\gamma \geq \alpha$. This assumption means the immune cell kills more than it replicates itself by this process.The inactivated immune response is produced at constant rate λ . The infected cells stimulate the inactivated immune cells at rate ψ . Hence ψT^*M inactivated immune cells become activated. The natural death rate of both inactivated and activated immune cells is noted by ρ . The virion are produced by infected cells at rate ηT^* . This virions' production is usually proportional to the number of dead infected cells δT^* . That is why some authors (cite authors) consider the term $N\delta T^*$ as a virion's production quantity. In this model we neglect, as [25, 31, 36] the loss of virion during the infection $-\beta TV$ is neglected.

The positive orthant \mathbb{R}^5_+ is positively invariant for the system (3). The dynamic of healthy cells is:

$$
\dot{T} = \sigma - \beta TV - \mu T \le \sigma - \mu T
$$

Hence, we have

$$
\limsup_{t \to +\infty} T \le \frac{\sigma}{\mu}
$$

Similarly, $\limsup_{t\to+\infty} C \leq \frac{\sigma+\lambda}{\varepsilon}$ where $C = T + T^* + M + M^*$ and $\varepsilon = \max\{\mu, \delta, \rho\}.$ Hence, the set

$$
\Omega = \left\{ (C, V) \in \mathbb{R}_+^5 | T \leq \frac{\sigma}{\mu}; T + T^* + M + M^* \leq \frac{\sigma + \lambda}{\varepsilon}; V \leq \frac{\eta(\sigma + \lambda)}{c\varepsilon} \right\}
$$

is a compact attracting positively invariant for the system (3) since $\gamma - \alpha \geq 0$. Hence, all solutions of (3) with positive initial conditions remain positive and bounded.

2.2 Equilibria and basic reproduction number

The virus free equilibrium of (3) is given by:

$$
(T_0, 0, M_0, 0, 0) = \left(\frac{\sigma}{\mu}, 0, \frac{\lambda}{\rho}, 0, 0\right)
$$

and it belongs always in Ω .

The basic reproduction number ([10, 42])

$$
\mathcal{R}_0 = \frac{\eta}{\delta} \frac{\beta T_0}{c}
$$

denotes the number of secondary cases produced by an infected cell during its lifespan into a susceptible population. An infected cell produce $\eta \delta^{-1}$ virions during its lifespan. These virions infect during their lifespan $\eta \delta^{-1} c^{-1} \beta T_0$ on the whole healthy population. This dimensionless parameter is a key concept in mathematical epidemiology or immunology. In fact, it determines whether the disease/virus dies out or persists.

When $\mathcal{R}_0 > 1$, the infection becomes chronic. In this case, the equilibria are solutions of

the system:

$$
\begin{cases}\n\sigma - \beta \bar{T} \bar{V} - \mu \bar{T} = 0 \\
\beta \bar{T} \bar{V} - \gamma \bar{T}^* \bar{M}^* - \delta \bar{T}^* = 0 \\
\lambda - \psi \bar{T}^* \bar{M} - \rho \bar{M} = 0 \\
\alpha \bar{T}^* \bar{M}^* - \rho \bar{M}^* + \psi \bar{T}^* \bar{M} = 0 \\
\eta \bar{T}^* - c \bar{V} = 0\n\end{cases}
$$
\n(4)

We show that (4) supports a single "endemic" state. The endemic relations are given by:

$$
\overline{T} = \frac{\sigma c}{\beta \eta \overline{T}^* + \mu}, \quad \overline{V} = \frac{\eta}{c} \overline{T}^*, \quad \overline{M} = \frac{\lambda}{\psi \overline{T}^* + \rho}, \quad \overline{M}^* = \frac{\psi \lambda \overline{T}^*}{(\psi \overline{T}^* + \rho)(\rho - \alpha \overline{T}^*)} \quad [*]
$$

The term $\rho - \alpha \bar{T}^* \neq 0$ because otherwise, the fourth equation of (4) leads to $\psi \bar{T}^* \bar{M} = 0$ and then we reach the virus free equilibrium.

By using endemic relations [*] and expressing all by \bar{T}^*, \bar{T}^* is/are the positive root(s) of the equation:

$$
A\xi^3 + B\xi^2 + C\xi + D = 0 \quad (\spadesuit)
$$

where:

$$
A = \beta \eta \psi \alpha \delta
$$

\n
$$
B = -\beta \eta \sigma \alpha \psi - \beta \eta \gamma \psi \lambda - \beta \eta \delta \rho (\psi - \alpha) + c \mu \psi \alpha \delta
$$

\n
$$
C = (\psi - \alpha) \beta \eta \sigma \rho - c \mu \gamma \psi \lambda - c \mu \delta \rho (\psi - \alpha) - \beta \eta \delta \rho^2
$$

\n
$$
D = \beta \eta \sigma \rho^2 - c \mu \delta \rho^2 = c \mu \delta \rho^2 (\mathcal{R}_0 - 1)
$$

Since $D > 0$, the equation (\spadesuit) has at least one negative root. We will apply the Descartes' rule of signs to determine the number of positive real zeros of (♠). According to the Descartes' rule of signs, there is no positive real root of (\spadesuit) if B and C are both positive. Let us prove this case is not possible if $\mathcal{R}_0 > 1$.

Lemma 1. If B and C are defined as above and $\mathcal{R}_0 > 1$ then $BC < 0$.

Proof.

$$
B = -\beta \eta \sigma \alpha \psi - \beta \eta \gamma \psi \lambda - \beta \eta \delta \rho (\psi - \alpha) + c \mu \psi \alpha \delta
$$

$$
< -\beta \eta \sigma \alpha \psi - \beta \eta \gamma \psi \lambda + \beta \eta \delta \rho (\alpha - \psi) + \beta \eta \sigma \psi \alpha \text{ because } \mathcal{R}_0 > 1
$$

$$
= -\beta \eta \gamma \psi \lambda + \beta \eta \delta \rho (\alpha - \psi)
$$

$$
< 0 \text{ if } (\alpha - \psi) < 0.
$$

If $(\alpha - \psi) > 0$, let's show that $C < 0$.

$$
C = (\psi - \alpha)\beta\eta\sigma\rho - c\mu\gamma\psi\lambda - c\mu\delta\rho(\psi - \alpha) - \beta\eta\delta\rho^2
$$

\n
$$
= -(\alpha - \psi)\beta\eta\sigma\rho - c\mu\gamma\psi\lambda - c\mu\delta\rho(\psi - \alpha) - \beta\eta\delta\rho^2
$$

\n
$$
< -(\alpha - \psi)c\mu\delta\rho - c\mu\gamma\psi\lambda - c\mu\delta\rho(\psi - \alpha) - \beta\eta\delta\rho^2
$$
 because $\mathcal{R}_0 > 1$
\n
$$
= -c\mu\gamma\psi\lambda - \beta\eta\delta\rho^2
$$

\n
$$
< 0.
$$

Hence, in any case, B and C cannot be both positive.

Let us assume the worst case where there are two positive roots and let set \bar{T}_1^* and \bar{T}_2^* the two positive roots of (\spadesuit) . Without lose of generality let's suppose that $\bar{T}_1^* < \bar{T}_2^*$. By the endemic relations defined above:

 \Box

 \bullet There are two corresponding endemic equilibria if and only if both \bar{T}_1^* and \bar{T}_2^* satisfy :

$$
\rho - \alpha \bar{T}_1^* > 0
$$
 and $\rho - \alpha \bar{T}_2^* > 0$ (conditions to get $\bar{M}^* > 0$)

or

$$
0 < \bar{T}_1^* < \bar{T}_2^* < \frac{\rho}{\alpha} \quad (*)
$$

 \bullet There's no corresponding endemic equilibrium if and only if both $\bar T_1^*$ and $\bar T_2^*$ satisfy :

$$
\frac{\rho}{\alpha} < \bar{T}_1^* < \bar{T}_2^* \quad (\star\star)
$$

 \bullet There's only corresponding endemic equilibrium if and only if both $\bar T_1^*$ and $\bar T_2^*$ satisfy :

$$
0 < \bar{T}_1^* < \frac{\rho}{\alpha} < \bar{T}_2^* \quad (\star \star \star)
$$

Let us consider the function:

$$
f(\xi) = A\xi^3 + B\xi^2 + C\xi + D
$$

Since $D > 0$, \bar{T}_1^* and \bar{T}_2^* are the two positive roots, the curve of $f(\xi)$ looks like:

Figure 1: The shape of f

According to this curve, to satisfy the two first above conditions (\star) and $(\star \star)$, we must

have $f(\frac{\rho}{\alpha})$ $\frac{\rho}{\alpha}$) > 0.

And to have $(\star \star \star)$: $0 < \bar{T}_1^* < \frac{\rho}{\rho}$ $\frac{\rho}{\alpha} < \bar{T}_2^*$, which leads to the uniqueness of the endemic equilibrium, we must have $f(\frac{\rho}{\rho})$ $\frac{\rho}{\alpha}$) < 0.

$$
A\frac{\rho^3}{\alpha^3} = \beta \eta \psi \alpha \delta \frac{\rho^3}{\alpha^3}
$$

= $\beta \eta \psi \delta \frac{\rho^3}{\alpha^2}$ (5)

$$
B\frac{\rho^2}{\alpha^2} = \left[-\beta \eta \sigma \alpha \psi - \beta \eta \gamma \psi \Lambda + \beta \eta \delta \rho (\alpha - \psi) + c\mu \delta \psi \alpha \right] \frac{\rho^2}{\alpha^2}
$$

$$
= \left[\alpha \psi (c\mu \delta - \beta \eta \sigma) - \beta \eta \gamma \psi \lambda + \beta \eta \delta \rho (\alpha - \psi) \right] \frac{\rho^2}{\alpha^2}
$$

$$
= \psi (c\mu \delta - \beta \eta \sigma) \frac{\rho^2}{\alpha} - \beta \eta \gamma \psi \lambda \frac{\rho^2}{\alpha^2} + \beta \eta \delta (\alpha - \psi) \frac{\rho^3}{\alpha^2}
$$
(6)

$$
C\frac{\rho}{\alpha} = \left[(\psi - \alpha)\beta\eta\sigma\rho - c\mu\gamma\psi\lambda - c\mu\delta\rho(\psi - \alpha) - \beta\eta\delta\rho^2 \right] \frac{\rho}{\alpha}
$$

=
$$
(\psi - \alpha)\beta\eta\sigma\frac{\rho^2}{\alpha} - c\mu\gamma\psi\lambda\frac{\rho}{\alpha} - c\mu\delta(\psi - \alpha)\frac{\rho^2}{\alpha} - \beta\eta\delta\frac{\rho^3}{\alpha}
$$
 (7)

Hence, we have:

$$
f(\frac{\rho}{\alpha}) = A\frac{\rho^3}{\alpha^3} + B\frac{\rho^2}{\alpha^2} + C\frac{\rho}{\alpha} + D
$$

= $-\beta\eta\gamma\psi\lambda\frac{\rho^2}{\alpha^2} - c\mu\gamma\psi\lambda\frac{\rho}{\alpha}$
< 0

Hence, we have proven the proposition

Proposition 1. If $\mathcal{R}_0 > 1$, there exists a unique endemic equilibrium of the system (3).

2.3 Stability of equilibria

Theorem 1. The virus free equilibrium is globally asymptotically stable if $\mathcal{R}_0 < 1$.

Proof. Let us consider the Lyapunov function

$$
\mathcal{L}=T^*+\frac{\delta}{\eta}V
$$

The derivative along trajectories of (3) is:

$$
\dot{\mathcal{L}} = \dot{T}^* + \frac{\delta}{\eta} \dot{V}
$$
\n
$$
= \beta T V - \gamma T^* M^* - \delta T^* + \frac{\delta}{\eta} (\eta T^* - cV)
$$
\n
$$
= \frac{\delta c}{\eta} \left(\frac{\beta \eta}{\delta c} T - 1 \right) V - \gamma T^* M^*
$$
\n
$$
= \frac{\delta c}{\eta} \left(\frac{\mathcal{R}_0}{T_0} T - 1 \right) V - \gamma T^* M^*
$$
\n
$$
\leq \frac{\delta c}{\eta} (\mathcal{R}_0 - 1) V
$$
\n
$$
\leq 0
$$

If $\dot{\mathcal{L}} = 0$ then $\left(\frac{\beta\eta}{\delta c}T - 1\right)V = 0$ and $T^*M^* = 0$. Hence, the largest invariant set included in $\{\dot{\mathcal{L}} = 0\}$ is reduced to the virus free equilibrium. Thus by LaSalle's invariance principle [19, 20], the VFE is globally asymptotically stable. \Box

We proved above that the system (3) has a unique endemic equilibrium if $\mathcal{R}_0 > 1$. However we do not have its explicit expression. Since (3) is a highly nonlinear 5-dimensional system, establishing the local stability by using Routh-Hurwitz criterion becomes almost impossible. Numerical simulations suggest that this unique endemic equilibrium seems to be asymptotically stable (see Fig 2). We study analytically a particular cases of model (3).

A Special Case: We consider that the proliferation of activated immune response M[∗] comes only from the process of killing infected cells. This means we neglect the activation of inactivated immune response by stimulation of infected cells, i.e. the term ψT^*M .

In this case, Model (3) becomes:

$$
\begin{cases}\n\dot{T} = \sigma - \beta TV - \mu T \\
\dot{T}^* = \beta TV - \gamma T^* M^* - \delta T^* \\
\dot{M} = \lambda - \psi T^* M - \rho M \\
\dot{M}^* = \alpha T^* M^* - \rho M^* \\
\dot{V} = \eta T^* - cV\n\end{cases}
$$
\n(8)

and Model (8) has three equilibria: The VFE E_0 , the activated immune free equilibria E_1 and another interior equilibria E_2 . We will study only on the interior equilibrium E_2 when it exists. In this case we can also easily get an explicit expression of this equilibrium. As in $[2, 14, 21, 40]$, we establish the global stability of E_2 using the same kind of Lyapunov function.

Proposition 2. If $\mathcal{R}_0 > 1$ and E_2 exists then E_2 is globally asymptotically stable.

Proof. Let us consider the Lyapunov function:

$$
\mathcal{L} = (T - \bar{T}\log T) + (T^* - \bar{T}^*\log T^*) + \frac{\beta \bar{T}}{c}(V - \bar{V}\log V) + \frac{\gamma}{\alpha}(M^* - \bar{M}^*\log M^*) + K
$$

where

$$
K = (\bar{T} - \bar{T}\log\bar{T}) + (\bar{T}^* - \bar{T}^*\log\bar{T}^*) + \frac{\beta\bar{T}}{c}(\bar{V} - \bar{V}\log\bar{V}) + \frac{\gamma}{\alpha}(\bar{M}^* - \bar{M}^*\log\bar{M}^*)
$$

The derivative of $\mathcal L$ along the trajectories of (3) is given by:

$$
\begin{split}\n\dot{\mathcal{L}} &= \left(1 - \frac{\bar{T}}{\bar{T}}\right)\dot{T} + \left(1 - \frac{\bar{T}^*}{\bar{T}^*}\right)\dot{T}^* + \frac{\beta \bar{T}}{c}\left(1 - \frac{\bar{V}}{V}\right)\dot{V} + \frac{\gamma}{\alpha}\left(1 - \frac{\bar{M}}{M}\right)\dot{M} \\
&= \mu \bar{T}\left(2 - \frac{\bar{T}}{\bar{T}} - \frac{T}{\bar{T}}\right) + \beta \bar{T}\bar{V}\left(3 - \frac{\bar{T}}{\bar{T}} - \frac{T^*}{\bar{T}^*}\frac{\bar{V}}{V} - \frac{\bar{T}^*}{\bar{T}^*}\frac{T}{\bar{V}}V\right) - \gamma T^*M^* - \delta T^* + \gamma \bar{T}^*M^* - \gamma \bar{T}^*\bar{M}^* \\
&+ \beta \bar{T}\bar{V}\frac{T^*}{\bar{T}^*} + \frac{\gamma}{\alpha}\left(\alpha T^*M^* - \rho M^* - \alpha T^*\bar{M}^* + \rho \bar{M}^*\right) \\
&= C_1 + C_2 - \gamma T^*M^* - \delta T^* + \gamma \bar{T}^*M^* - \gamma \bar{T}^*\bar{M}^* + \beta \bar{T}\bar{V}\frac{T^*}{\bar{T}^*} + \frac{\gamma}{\alpha}\left(\alpha T^*M^* - \rho M^* - \alpha T^*\bar{M}^* + \rho \bar{M}^*\right) \\
&= C_1 + C_2 - \gamma T^*M^* - \delta T^* + \gamma \bar{T}^*M^* - \gamma \bar{T}^*\bar{M}^* + \beta \bar{T}\bar{V}\frac{T^*}{\bar{T}^*} \\
&+ \frac{\gamma}{\alpha}\left(\alpha T^*M^* - \rho M^* - \frac{\bar{M}^*}{M^*}(\alpha T^*M^* - \rho M^*)\right) \\
&= C_1 + C_2 - \gamma T^*M^* - \delta T^* + \gamma \bar{T}^*M^* - \gamma \bar{T}^*\bar{M}^* + \beta \bar{T}\bar{V}\frac{T^*}{\bar{T}^*} \\
&+ \frac{\gamma}{\alpha}\left(\alpha T^*M^* - \rho M^* - \alpha T^*\bar{M}^* + \rho \bar{M}^*\right) \\
&= C_1 + C_2 - \gamma T^*M^* - \delta T^* +
$$

 ${\{\dot{V} = 0\}} = \{(T, T^*, V, M, M^*) \mid T = \overline{T}, T^* = \overline{T}^*, V = \overline{V}\}.$ Hence the invariant subset of $\{\dot{V} = 0\}$ included in Ω is reduced to the E_2 . By the LaSalle's invariance principle, the equilibrium E_2 is globally asymptotically stable. \Box

3 Optimal Control Formulation

The main purpose of formulating an optimal control problem is to determine optimal control functions u_1 and u_2 that maximize the uninfected CD4+ T-cell count and minimize the cost of treatment. With this idea in mind, let us consider the following functional

$$
J(u_1, u_2) = \int_0^{\tau} \left(T - \frac{\alpha_1}{2} u_1^2 - \frac{\alpha_2}{2} u_2^2 \right) dt
$$

The goal is to obtain a pair $(\tilde{u}_2, \tilde{u}_1) \in \Gamma$ such that $J(\tilde{u}_1, \tilde{u}_2) \geq J(u_1, u_2)$, for all $(u_1, u_2) \in \Gamma$, where,

$$
\Gamma = \{(u_1, u_2) | (u_1, u_2) \in L^2([0, \tau]), 0 \le u_1, u_2 \le 1\}
$$

In other words, we want to maximize the functional J over Γ subject to the dynamical system,

$$
\begin{cases}\n\dot{T} = \sigma - \beta (1 - u_1) T V - \mu T \\
\dot{T}^* = \beta (1 - u_1) T V - \gamma T^* M^* - \delta T^* \\
\dot{M} = \Lambda - \psi T^* M - \rho M \\
\dot{M}^* = \alpha T^* M^* - \rho M^* + \psi T^* M \\
\dot{V} = \eta (1 - u_2) T^* - cV \\
\dot{W} = \eta u_2 T^* - cW\n\end{cases}
$$
\n(9)

Notice that for the rest of the paper, we use Λ instead of λ to avoid any confusion with the adjoint system. We define the Hamiltoninan function given by,

$$
\mathcal{H}(\cdot) = T - \frac{\alpha_1}{2}u^2 - \frac{\alpha_2}{2}v^2 + \lambda_1(\sigma - \beta(1 - u_1)TV - \mu) + \lambda_2(\beta(1 - u_1)TV - \gamma T^*M^* - \delta T^*)
$$

$$
+ \lambda_3(\Lambda - \psi T^*M - \rho M) + \lambda_4(\alpha T^*M^* - \rho M^* + \psi T^*M) + \lambda_5(\eta(1 - u_2)T^* - cV)
$$

$$
+ \lambda_6(\eta u_2 T^* - cW) + z_1 u_1 + z_2(1 - u_1) + z_3(u_2) + z_4(1 - u_2)
$$

Where $z_i \geq 0$ for $i = 1, ..., 4$ and,

$$
z_1u_1 = 0, \ z_2(1 - u_1) = 0, \ z_3(u_2) = 0, \ z_4(1 - u_2) = 0 \tag{10}
$$

To determine the optimality conditions, it is necessary to solve the first order condition ∂H $\frac{\partial H}{\partial u_1} = 0$ and $\frac{\partial H}{\partial u_2} = 0$ to obtain,

$$
u_1 = \frac{\beta T V(\lambda_1 - \lambda_2) - z_1 + z_2}{\alpha_1}
$$
 and $u_2 = \frac{\eta T^*(\lambda_6 - \lambda_5) - z_3 + z_4}{\alpha_2}$

The next step is to use the penalty functions z_i and (10) to determine the optimal expressions for $\widetilde{u_1}$ and $\widetilde{u_2}$ to finally have,

$$
\widetilde{u}_1 = \begin{cases}\n0 & \frac{\beta TV(\lambda_1 - \lambda_2)}{\alpha_1} \leq 0 \\
\frac{\beta TV(\lambda_1 - \lambda_2)}{\alpha_1} & 0 < \frac{\beta TV(\lambda_1 - \lambda_2)}{\alpha_1} < 1 \\
1 & \frac{\beta TV(\lambda_1 - \lambda_2)}{\alpha_1} \geq 1 \\
\frac{\beta TV(\lambda_1 - \lambda_2)}{\alpha_1} < 0\n\end{cases}
$$
\n
$$
\widetilde{u}_2 = \begin{cases}\n0 & \frac{\eta T^*(\lambda_6 - \lambda_5)}{\alpha_2} \leq 0 \\
\frac{\eta T^*(\lambda_6 - \lambda_5)}{\alpha_2} < 0 < \frac{\eta T^*(\lambda_6 - \lambda_5)}{\alpha_2} < 1 \\
1 & \frac{\eta T^*(\lambda_6 - \lambda_5)}{\alpha_2} \geq 1\n\end{cases}
$$

However, a better way to express this functions is,

$$
\widetilde{u}_1 = \max\left(0, \min\left(\frac{\beta TV(\lambda_1 - \lambda_2)}{\alpha_1}, 1\right)\right)
$$
 and $\widetilde{u}_2 = \max\left(0, \min\left(\frac{\eta T^*(\lambda_6 - \lambda_5)}{\alpha_2}, 1\right)\right)$

Now, it is necessary to determine the adjoint equations for this problem to be solved. Pontryagin's Maximum Principle [38] establishes the adjoint equations are given by,

$$
\frac{d\lambda_1}{dt} = -\frac{\partial H}{\partial T} \qquad \frac{d\lambda_2}{dt} = -\frac{\partial H}{\partial T^*} \qquad \frac{d\lambda_3}{dt} = -\frac{\partial H}{\partial M}
$$

$$
\frac{d\lambda_4}{dt} = -\frac{\partial H}{\partial M^*} \qquad \frac{d\lambda_5}{dt} = -\frac{\partial H}{\partial V} \qquad \frac{d\lambda_6}{dt} = -\frac{\partial H}{\partial W}
$$

By doing so we get the following adjoint system of equations

$$
\begin{cases}\n\frac{d\lambda_1}{dt} = -(1 - \lambda_1 \beta (1 - u_1)V + \lambda_2 \beta (1 - u_1)V - \mu \lambda_1) \\
\frac{d\lambda_2}{dt} = -(-\lambda_2 \gamma M^* - \lambda_2 \delta + \lambda_3 \psi M + \lambda_4 \alpha M + \lambda_4 \psi M + \lambda_5 \eta (1 - u_2) + \lambda_6 \eta u_2) \\
\frac{d\lambda_3}{dt} = -(\lambda_3 \psi T^* - \lambda_3 \rho + \lambda_4 \psi T^*) \\
\frac{d\lambda_4}{dt} = -(-\lambda_2 \gamma T^* + \lambda_4 \alpha T^* - \lambda_4 \rho) \\
\frac{d\lambda_5}{dt} = -(-\lambda_1 \beta (1 - u_1)T + \lambda_2 \beta (1 - u_1)T - \lambda_5 c) \\
\frac{d\lambda_6}{dt} = c\lambda_6\n\end{cases}
$$
\n(11)

subject to the transversality condition $\lambda_i(\tau) = 0$, for $i = 1, \ldots, 6$.

4 Numerical simulations

4.1 Model without Control

Figures (2) and (??) show the behavior of a patient in his initial stage of infection. The initial conditions considered were $T_0 = 1000$; $T_0^* = 0$, $M_0 = 0$, $M_0^* = 1$, $V_0 = 10$, and the parameters were $\sigma = 15, \beta = 0.000024, \mu = 0.02, \eta = 500, c = 2.4, \delta = 0.26, \Lambda = 0.1,$ $\psi = 0.01, \ \rho = 0.05$ and $\alpha = 0.005$. In figure (2) it is considered $\gamma = 0.01$ and in figure (??) $\gamma = 1$. It is easy to see how a bigger γ has a bigger impact on reducing the effects of infection, leading to higher levels in the uninfected $CD4^+$ T-cell counts.

In both cases of the value of $\mathcal{R}_0 = 14.42$ and $T^* = 9.84$ in the figure (2) and $T^* = 4.19$ in the figure (??).

Figure 2: Graph without control

4.2 Model with Constant Control

Figure (3) exibits the behavior of the HIV dynamics considering different constant values for the control u_1 and with $u_2 = 0$ (only RTI control). The values of the initial condition and parameters are as before with $\gamma = 1$. In figure (4) is almost the same situation with $u_1 = 0$ and different constant values for u_2 (only PI control).

It is easy to see that the principal difference between both treatment is the appearance of the non-infectious viral particles because the application of PI treatment in figure (4) but this apparently do not have a big impact on cellular or viral levels compared to corresponding in figure (3). Both graphs show how increasing the effectiveness of control has a positive effect on uninfected CD4+ T-cells and a negative effect on viral loads, as expected.

Figure 3: Graph with no control (black), control at $u_1 = 0.4$ (blue), $u_1 = 0.6$ (red) and $u_1 = 0.9$ (magenta). For the set of parameters we have $u_c=0.931.$

Figure 4: Graph with no control (black), control at $u_2 = 0.4$ (blue), $u_2 = 0.6$ (red) and $u_2 = 0.9$ (magenta). For the set of parameters we have $u_c=0.931.$

Figure 5: Graph with no control (black), control at $u_1 = u_2 = 0.4$ (blue), $u_1 = u_2 = 0.6$ (red) and $u_1 = u_2 = 0.7$ (magenta). For the set of parameters we have $u_c = 0.931$.

Figure (5) show the scenario with both control strategies and the same parameters as above. It is possible to see how lower levels on each control are needed to increase the uninfected cell count.

Figure (6) show the dynamic of the system (9) in both cases: without control and optimal controls.

5 Acknowledgments

The authors would like thanks E. McKiernan, E. Thomas, E.Soho and Baojun Song for valuable discussions on the subject. This research was conducted in the Mathematical and Theoretical Biology Institute (MTBI) at the Mathematical, Computational and Modeling Sciences Center (MCMSC). This project has been partially supported by grants from the

Figure 6: Graph with optimal control (green) using weight constants $\alpha_1 = \alpha_2 = 1$ and without control (black).

National Science Foundation (NSF - Grant DMPS-0838705), the National Security Agency (NSA - Grant H98230-11-1-0211), the Alfred P. Sloan Foundation and the Office of the Provost of Arizona State University. D. Bichara has been partially supported by INRIA MASAIE Team.

References

- [1] B. M. Adams, H. T. Banks, M. Davidian, H. dae Kwon, H. T. Tran, S. N. WYNNE, AND E. S. ROSENBERG, Hiv dynamics: modeling, data analysis, and optimal treatment protocols, J. Comput. Appl. Math, 184 (2005), pp. 10–49.
- [2] P. Adda, J. L. Dimi, A. Iggidr, J. C. Kamgang, G. Sallet, and J. J. Tewa, General models of host-parasite systems. Global analysis, Discrete Contin. Dyn. Syst. Ser. B, 8 (2007), pp. 1–17 (electronic).
- [3] C. Althaus and R. J. De Boer, Implications of ctl-mediated killing of hiv-infected cells during the non-productive stage of infection, PLoS ONE, 6 (2011).
- [4] N. Bacaer, R. Ouifki, C. Pretorius, R. Wood, and B. Williams, Modeling the joint epidemic of TB and HIV in a South African township, J. Math. Biol., 57 (2008), pp. 557–593.
- [5] S. Bonhoeffer, R. May, G. Shaw, and M. Nowak, Virus dynamics and drug therapy, Proc Natl Acad Sci U S A, 94 (1997), pp. 6971–6976.
- [6] D. Covert and D. Kirschner, Revisiting early models of the host-pathogen interactions in hiv infection, Comments Theor. Biol., 5 (2000).
- [7] R. V. Culshaw and S. Ruan, A delay-differential equation model of hiv infection of $cd+4$ t-cells, Math. Biosci., 165 (2000), pp. 27–39.
- [8] R. V. Culshaw, S. Ruan, and R. J. Spiteri, Optimal hiv treatment by maximising immune response., J Math Biol, 48 (2004), pp. 545–62.
- [9] P. De Leenheer and H. L. Smith, Virus dynamics: A global analysis., SIAM J. Appl. Math., 63 (2003), pp. 1313–1327.
- [10] O. Diekmann, J. A. P. Heesterbeek, and J. A. J. Metz, On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations, J. Math. Biol., 28 (1990), pp. 365–382.
- [11] M. Fishman and A. Perelson, Lymphocytes memory and affinity selection, J. Theoret. Biol., 173 (1996).
- [12] H. Gomez-Acevedo and M. Y. Li, Global dynamics of a mathematical model for HTLV-I infection of T cells, Canad. Appl. Math. Quart., 10 (2003), pp. 71–86.
- [13] H. W. Hethcote and J. Van Ark, Modeling HIV transmission and AIDS in the united states, vol. 95 of Lect. Notes Biomath., Springer-Verlag, 1994.
- [14] A. IGGIDR, J. MBANG, AND G. SALLET, Stability analysis of within-host parasite models with delays, Math. Biosci., 209 (2007).
- [15] J. A. Jacquez, C. P. Simon, J. Koopman, L. Sattenspiel, and T. Perry, modeling and analyzing HIV transmission : the effect of contact patterns, Math. Biosci., 92 (1988).
- [16] H. R. Joshi, Optimal control of an hiv immunology model, Optimal control applications and methods, 23 (2002), pp. 199–213.
- [17] D. KIRSCHNER, G. F. WEBB, AND M. CLOYD, *Model of hiv-1 disease progression* based on virus-induced lymph node homing and homing-induced apoptosis of $c d4$ + lymphocytes., J Acquir Immune Defic Syndr, 24 (2000), pp. 352–62.
- [18] D. E. Kirschner, R. Mehr, and A. S. Perelson, Role of the thymus in pediatric HIV-1 infection., J Acquir Immune Defic Syndr Hum Retrovirol, 18 (1998), pp. 95– 109.
- [19] J. LaSalle, Stability theory for ordinary differential equations. stability theory for ordinary differential equations., J. Differ. Equations, 41 (1968), pp. 57–65.
- [20] J. P. LaSalle, The stability of dynamical systems, Society for Industrial and Applied Mathematics, Philadelphia, Pa., 1976. With an appendix: "Limiting equations and stability of nonautonomous ordinary differential equations" by Z. Artstein, Regional Conference Series in Applied Mathematics.
- [21] A. KOROBEINIKOV, *Global properties of basic virus dynamics models*, Bull. Math. Biol., 66 (2004).
- [22] M. Y. Li AND S. HONGYING, Impact of intracellular delays and target-cell dynamics on in vivo viral infections, SIAM J. Appl. Math., 70 (2010), pp. 2434–2448.
- [23] M. Y. Li and H. Shu, Global dynamics of an in-host viral model with intracellular delay, Bull Math Biol, 72 (2010), pp. 1492–1505.
- [24] W.-m. Lui, Nonlinear oscillation in models of immune responses to persistent viruses, Theor Popul Biol, 52 (1997), pp. 224–230.
- [25] R. M. May and R. M. Anderson, Transmission dynamics of hiv infection., Nature, 326 (1987), pp. 137–142.
- [26] C. McCluskey, A model of HIV/AIDS with staged progression and amelioration., Math. Biosci., 181 (2003), pp. 1–16.
- [27] J. E. Mittler, B. Sulzer, A. U. Neumann, and A. S. Perelson, Influence of delayed viral production on viral dynamics in HIV-1 infected patients., Math. Biosci., 152 (1998), pp. 143–163.
- [28] A. Murase, T. Sasaki, and T. Kajiwara, Stability analysis of pathogen-immune interaction dynamics, J. Math. Biol. Math, 51 (2005), pp. 247–267.
- [29] P. W. Nelson, J. Murray, and A. S. Perelson, A model of hiv-1 pathogenesis that includes an intracellular delay., Math. Biosci., 163 (2000), pp. 201–215.
- [30] P. W. NELSON AND A. S. PERELSON, Mathematical analysis of delay differential equation models of HIV-1 infection., Math. Biosci., 179 (2002), pp. 73–94.
- [31] M. A. Nowak and R. Bangham, Population dynamics of immune responses to persistent viruses., Science, 272 (1996), pp. 74–79.
- [32] M. A. Nowak AND R. M. MAY, *Mathematical biology of hiv infections: antigenic* variation and diversity threshold., Math Biosci, 106 (1991), pp. 1–21.
- [33] $____\$, virus dynamics. Mathematical principles of immunology and virology, Oxford University Press, 2000.
- [34] A. PERELSON, *Modeling the interaction of the immune system with hiv*, in Mathematical and statistical approaches to AIDS epidemiology with HIV, C. Castillo-Chavez, ed., Springer-Verlag, 1989, pp. 350–370.
- [35] A. S. Perelson, D. E. Kirschner, and R. De Boer, Dynamics of HIV infection of $CD4+T$ cells., Math Biosci, 114 (93), pp. 81–125.
- [36] A. S. Perelson and P. W. Nelson, Mathematical analysis of HIV-1 dynamics in vivo, SIAM Rev., 41 (1999), pp. 3–44 (electronic).
- $[37]$, *Modeling viral infections*, in An introduction to mathematical modeling in physiology, cell biology, and immunology (New Orleans, LA, 2001), vol. 59 of Proc. Sympos. Appl. Math., Amer. Math. Soc., Providence, RI, 2002, pp. 139–172.
- [38] L. Pontryagin, V. Boltyanskii, R. Gamkrelidze, and E. Mishchenko, The mathematical theory of optimal processes, Wiley, New Jersey, 1962.
- [39] R. R. Regoes, D. Wodarz, and M. A. Nowak, Virus dynamics : the effect of target cell limitation and immune responses on virus evolution, J. Theoret. Biol., 191 (1998), pp. 451–462.
- [40] M. SOUZA AND J. P. ZUBELLI, Global analysis of a class of hiv models with immune response and antigenic variation, arXiv:0810.4364v1 [q-bio.PE], (2008).
- [41] N. STILIANAKIS AND D. SCHENZLE, On the intra-host dynamics of hiv-1 infections, Math. Biosci., 199 (2006), pp. 1–25.
- [42] P. van den Driessche and J. Watmough, reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci., 180 (2002), pp. 29–48.
- [43] L. WANG AND M. Y. LI, Mathematical analysis of the global dynamics of a model for HTLV-I infection and of $cd4^+$ t cells, Math. Biosci., 200 (2006), pp. 44–57.
- [44] L. M. Wein, S. A. Zenios, and M. A. Nowak, Dynamic multidrug therapies for hiv: a control theoretic approach., J Theor Biol, 185 (1997), pp. 15–29.
- [45] D. WODARZ, A. LLOYD, A. JANSEN, AND M. A. NOWAK, Dynamics of macrophage and t cell infection by hiv, J. Theoret. Biol., 196 (1999).
- [46] D. WODARZ AND M. A. NOWAK, *Mathematical models of hiv pathogenesis and treat*ment., Bioessays, 24 (1999), pp. 1178–87.