# Criteria for Annihilation of HIV-1 During HAART Therapy

Frank Nani and Mingxian Jin

Department of Mathematics and Computer Science Fayetteville State University, Fayetteville, NC 28301, USA

Abstract - HAART therapy of HIV-1 induced AIDS is modeled by a system of non-linear deterministic differential equations. The clinically plausible patho-physiological equations depict the dynamics of uninfected  $CD4^+$  T cells (x<sub>1</sub>), HIV-1 infected CD4+ T cells  $(x_2)$ , HIV-1 virions in the blood plasma  $(x_3)$ , HIV-1 specific CD8<sup>+</sup> T cells  $(x_4)$ , and the concentration of HAART drug molecules ( $x_5$ ). The criteria for the existence of clinically desirable therapeutic outcomes are presented. In particular, the necessary and sufficient conditions for the annihilation of HIV-1 virions are clearly exhibited in terms of the model physiological parameters. Computer simulations are presented illustrating patho-physiodynamics of HIV-1 induced AIDS. In this paper, HAART protocols with constant continuous or periodic transdermal and intravenous drug infusions are used in our mathematical model.

**Keywords:** HIV-1 patho-physiodynamics, mathematical modeling, HAART therapy, AIDS cure criteria, Michaelis-Menten kinetics

## **1** Introduction

HIV-1 virions induce AIDS by orchestrating an irreversible destruction of the CD4<sup>+</sup> T cells which then paralyze the immune system of the HIV-1 positive person. As a result of these physiological events, a host of opportunistic bacterial and viral infections overwhelm the HIV-1 positive person [12]. Highly active anti-retroviral therapy (HAART) protocols have been approved as an efficacious treatment of HIV-1 induced AIDS. This protocol consists of nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, protease inhibitors, anti-fungals /anti-bacterials and in future, integrase inhibitors. The reverse transcriptase inhibitors prevent reverse transcription of HIV-1 specific DNA. The protease inhibitors are antagonistic to maturation and formation of new HIV-1 virions. The possible role of integrase inhibitors is to prevent the integration of HIV-1 viral DNA into the patients' DNA [14].

HAART therapy is responsible for the reduction of viral load in CD4<sup>+</sup> T cells and production of measurable reconstitution of the patients' immune system [17]. However, HAART protocols have limited therapeutic efficacy due to extreme toxicity, non-compliance, intermittent scheduling, biochemical/clinical drug resistance, short drug half-life and low bio-availability. Many mathematical models of HAART therapy have been developed in an attempt to demonstrate the existence of efficacious and optimal therapies that will minimize side effects [8, 9, 10, 11, 13, 14, 15, 16]. Zaric et al. in 1998 presented a model which was focused on the simulation of protease inhibitors and role of drug resistant HIV-1 virions [18]. Stengel in [14] presented a mathematical model of HIV-1 infection and HAAART which demonstrated the efficacy of a mathematically optimal therapy. Using the LQR, Scheme, Caetano and Yoneyama in [2] constructed a HAART model which incorporated the roles of latently infected CD4<sup>+</sup> T cells, and discussed how the reverse transcriptase and protease inhibitors affected HIV-1 dynamics during HAART.

In this paper, an elaborate mathematical model will be constructed which will incorporate physiologically plausible effects such as Michaelis-Menten kinetics, role of HIV-1 latent viral reservoirs, continuous transdermal drug delivery, and the implicit lymphocyte proliferation induction by the  $CD4^+$  T cells. The activation and proliferation is accomplished by a paracrine and autocrine processes which are mediated by the cytokine interleukin-2, secreted by the  $CD4^+$  T cells. Several authors investigated the consequences of structured long-term and short-term treatment interruptions during HAART [1, 2, 4, 8]. The current model will discuss these consequences by means of simulations.

The current paper will be divided into five sections. The first section gives the introduction into HAART therapy and provides the basis for current research. This is followed by presentation and discussion of the model parameters in Section 2. In Section 3 the mathematical model of HAART therapy will be constructed. Also the necessary and sufficient criteria for annihilation of HIV-1 virions during HAART will be presented in this section. In Section 4, clinically plausible computer simulations will be exhibited. Section 5 will be the summary and discussion of the basic results of the paper.

## **2** Parameters

The model parameters, constants, and variables are listed as follows.

- $x_1$ : the number density of non-HIV-1-infected CD4<sup>+</sup> helper T-lymphocytes per unit volume
- $x_2$ : the number density of HIV-1 infected CD4<sup>+</sup> helper T-lymphocytes per unit volume

- *x*<sub>3</sub>: the number density of HIV-1 virions in the blood plasma per unit volume
- x<sub>4</sub>: the number density of HIV-1 specific CD8<sup>+</sup> cytotoxicT-lymphocytes per unit volume
- *x*<sub>5</sub>: the concentration of drug molecules of the HAART treatment protocol
- $S_1$ : rate of supply of un-infected CD4<sup>+</sup> T<sub>4</sub>-lymphocytes
- $S_2$ : rate of supply of latently infected CD4<sup>+</sup> T<sub>4</sub>-lymphocytes
- S<sub>3</sub>: rate of supply of HIV-1 virions from macrophage, monocytes, microglial cells and other lymphoid tissue different from T<sub>4</sub>-lymphocytes
- $S_4$ : rate of supply of CD8<sup>+</sup> T<sub>8</sub> lymphocytes from the thymus
- D: rate of HAART drug infusion by transdermal delivery
- *a<sub>i</sub>*, *b<sub>i</sub>*: constant associated with activation of lymphocytes by cytokine interleukin-2 (IL-2) (*i* =1, 2, 3, 4)
- c: rate of HAART drug degradation and excretion
- $\alpha_i$ : constant associated with HIV-1 infection of CD4<sup>+</sup> T<sub>4</sub> helper cells (*i* =1, 2, 3)
- $\beta_{1:}$  the number of HIV-1 virions produced per day by replication and budding in CD4<sup>+</sup> T<sub>4</sub> helper cells
- $\beta_2$ : rate constant associated with replication and "budding" of HIV-1 in syncytia CD4<sup>+</sup> T<sub>4</sub> helper cells per day per microliter ( $\mu l$ ) and released into the blood plasma
- $\beta_{3:}$  the number of HIV-1 virions produced per day by replication and "budding" in non-syncytia CD4<sup>+</sup> T<sub>4</sub> helper cells and released into the blood plasma
- $\eta_i$ : constant depicting the rate of which HIV-1 virions incapacitate the CD8<sup>+</sup> T<sub>8</sub> cytotoxic cells (*i* =1, 2)
- $(\sigma_0, \lambda_0)$ : Michaelis-Menten metabolic rate constants associated with HAART drug elimination
- $(\sigma_i, \lambda_i)$ : Michaelis-Menten metabolic rate constants associated with HAART drug pharmacokinetics (*i* =2, 3)
- $\xi_i$ : cytotoxic coefficient where  $0 \le \xi_i \le 1$  (i = 2, 3)
- $q_i$ : constant depicting competition between infected and un-infected CD4<sup>+</sup> T<sub>4</sub> helper cells (i = 1, 2)
- $k_i$ : constant depicting degradation, loss of clonogenicity or "death" (i = 1, 2, 3, 4)
- $e_{i0}$ : constant depicting death or degradation or removal by apoptosis (programmed cell death) (i = 1, 2, 3, 4)
- $K_i$ : constant associated with the killing rate of infected CD4<sup>+</sup> T<sub>4</sub> cells by CD8<sup>+</sup> T<sub>8</sub> cytotoxic lymphocytes (*i* =1, 2) All the parameters are positive.

## **3** Model Equations and Analyses

#### **3.1 Model equations**

The HIV-1 patho-physiological dynamics during HAART therapy can be modeled using the following system of non-linear ordinary differential equations:

$$\begin{vmatrix} \dot{x}_{1} = S_{1} + a_{1}x_{1}^{2}e^{-b_{1}x_{1}} - \alpha_{1}x_{1}x_{3} - q_{1}x_{1}x_{2} - k_{1}x_{1} - e_{10} \\ \dot{x}_{2} = S_{2} + a_{2}x_{1}x_{2}e^{-b_{2}x_{1}} + \alpha_{2}x_{1}x_{3} - q_{2}x_{1}x_{2} - k_{2}x_{2} - \beta_{1}x_{3} \\ - K_{1}x_{2}x_{4} - e_{20} - \frac{\xi_{2}\sigma_{2}x_{2}x_{5}}{\lambda_{2} + x_{5}} \\ \dot{x}_{3} = S_{3} + \beta_{2}x_{2}x_{3} + \beta_{3}x_{3} - \alpha_{3}x_{1}x_{3} - \eta_{1}x_{3}x_{4} - k_{3}x_{3} - e_{30} \\ - \frac{\xi_{3}\sigma_{3}x_{3}x_{5}}{\lambda_{3} + x_{5}} \\ \dot{x}_{4} = S_{4} + a_{4}x_{1}x_{4}e^{-b_{4}x_{1}} - K_{2}x_{2}x_{4} - \eta_{2}x_{3}x_{4} - k_{4}x_{4} - e_{40} \\ \dot{x}_{5} = Df(t) - \frac{\sigma_{0}x_{5}}{\lambda_{0} + x_{5}} - \frac{\sigma_{2}x_{2}x_{5}}{\lambda_{2} + x_{5}} - \frac{\sigma_{3}x_{3}x_{5}}{\lambda_{3} + x_{5}} \\ f(t) = \begin{cases} 1 & \text{for constant continuous input} \\ || \left\lceil \sin nt \right\rceil || & \text{for periodic input} \\ x_{i}(t_{0}) = x_{i0} & for \quad i = \{1, 2, 3, 4, 5\} \end{cases}$$
(3.1)

The model includes the following clinical improvement:

- (i) The drug delivery uses transdermal, stealth-liposome encapsulated drug delivery, instead of the matrix tablet form because of improved therapeutic efficacy and reduced gastro-intestinal toxicity [6]. It is also assumed that elastic liposomes are formulated and selectively targeted such as to reduce toxicity to non-HIV-1-infected CD4<sup>+</sup> T cells ( $x_1$ ) and CD8<sup>+</sup> cytotoxic T cells ( $x_4$ ).
- (ii) The HAART drug is such that each renal excretion and body clearance rate follows Michaelis-Menten kinetics.
- (iii)  $g(x_1, x_j) = a_j x_1 x_j e^{-b_j x_1}$  for j=(1, 2, 4)This function depicts the process of lymphocyte activation which is mediated by  $x_1$  (CD 4<sup>+</sup>) T helper cells. These cells secrete a cytokine called interleukin-2.
- (iv) The periodic input function  $f(t) = |\text{ceil}(\sin(5 t))|$  can be depicted by the following plot:



#### **3.2** Criteria for Annihilation of HIV-1 Virions

In this subsection, the necessary and sufficient criteria will be presented for the cure of an AIDS patient through

annihilation of the HIV-1 infected CD4<sup>+</sup> T cells and plasma viremia. This criterion is derived for the scenario for which  $f(t) \equiv 1$ , which corresponds to constant continuous application of HAART drug either by transdermal delivery or intravenous infusion.

The desired physiological steady states during HAART therapy, are  $E_1 = [\hat{x}_1, 0, 0, 0, \hat{x}_5]$  and  $E_2 = [\bar{x}_1, 0, 0, \bar{x}_4, \bar{x}_5]$ . In each of these, the HIV-1 infected CD4<sup>+</sup> T cells  $(x_2)$  and plasma HIV-1 virions  $(x_3)$  are annihilated. In particular, E<sub>2</sub>=[ $\bar{x}_1$ , 0, 0,  $\bar{x}_4$ ,  $\bar{x}_5$ ] is plausibly physiologically easily attainable in an AIDS patient since some HIV-1 specific CD8<sup>+</sup> (cytotoxic T) cells usually persist during HAART as memory T cells.

Thus the criteria for annihilation of HIV-1 virions will be derived using  $E_2 = [\overline{x}_1, 0, 0, \overline{x}_4, \overline{x}_5]$  as a target steady state. In  $R_{+}^{x_1 x_4 x_5} = [x_1, x_4, x_5 | x_1 \ge 0, x_4 \ge 0, x_5 \ge 0]$ , the model equations reduce to (3.2).

$$\begin{cases} \dot{x}_{1} = S_{1} + a_{1}x_{1}^{2}e^{-b_{1}x_{1}} - k_{1}x_{1} - e_{10} \\ \dot{x}_{4} = S_{4} + a_{4}x_{1}x_{4}e^{-b_{4}x_{1}} - k_{4}x_{4} - e_{40} \\ \dot{x}_{5} = Df(t) - \frac{\sigma_{0}x_{5}}{\lambda_{0} + x_{5}} \\ f(t) = 1 \\ x_{i}(t_{0}) = x_{i0} \quad for \quad i = \{1, 4, 5\} \end{cases}$$

$$(3.2)$$

Consider the Liapnnov functional:

$$V := \sum \frac{1}{2} c_i (x_i - \overline{x}_i)^2$$
where  $i = \{1, 4, 5\}$  and  $c_i \in R_+ = (0, \infty)$ 
(3.3)

The derivative of V along the solution curves of the model equations yields the result:

$$\overset{*}{V} = c_1(x_1 - \overline{x}_1)\dot{x}_1 + c_4(x_4 - \overline{x}_4)\dot{x}_4 + c_5(x_5 - \overline{x}_5)\dot{x}_5$$

At a steady state f(t) = 1, the following equations hold.

$$\begin{cases} S_{1} - e_{10} = k_{1}\overline{x}_{1} - a_{1}\overline{x}_{1}^{2}e^{-b_{1}\overline{x}_{1}} \\ S_{4} - e_{40} = k_{4}\overline{x}_{4} - a_{4}\overline{x}_{1}\overline{x}_{4}e^{-b_{4}\overline{x}_{1}} \\ D = \frac{\sigma_{0}\overline{x}_{5}}{\lambda_{0} + \overline{x}_{5}} \end{cases}$$
(3.4)

Thus

$$V = c_1 k_1 (x_1 - \overline{x}_1) (\overline{x}_1 - x_1) + a_1 c_1 (x_1 - \overline{x}_1) [G(\overline{x}_1) - G(x_1)] + c_4 k_4 (x_4 - \overline{x}_4) (\overline{x}_4 - x_4) + a_4 c_4 (x_4 - \overline{x}_4) [F(\overline{x}_1, \overline{x}_4) - F(x_1, x_4)] + c_5 \sigma_0 [L(\overline{x}_5) - L(x_5)] where$$

 $G(\mathbf{r}) - \mathbf{r}^2 e^{-b_1 x_1}$ 

$$F(x_1, x_4) = x_1 x_4 e^{-b_4 x_1}$$

$$L(x_5) = \frac{x_5}{\lambda_0 + x_5}$$
(3.5)

such that G, F, L are continuous, differentiable, and have bounded, derivatives.

$$u_{1} = x_{1} - \overline{x}_{1}$$

$$u_{2} = x_{4} - \overline{x}_{4}$$

$$u_{3} = x_{5} - \overline{x}_{5}$$
(3.6)

and let

Let

$$X = \begin{bmatrix} u_1 \\ u_2 \\ u_3 \end{bmatrix} \in R_+^3$$
(3.7)

such that  $X^T$  denotes the transpose of X. Define  $A \in M_{mn}(R)$ such that

$$A = \begin{bmatrix} a_{11} & \frac{1}{2}a_{12} & \frac{1}{2}a_{13} \\ \frac{1}{2}a_{12} & a_{22} & \frac{1}{2}a_{23} \\ \frac{1}{2}a_{13} & \frac{1}{2}a_{23} & \frac{1}{2}a_{33} \end{bmatrix}$$
(3.8)

Now

In particular, the  $[a_{ij}]_{3x3}$  are defined as follows:

$$\begin{cases} a_{11} \coloneqq -[c_1k_1 + a_1c_1(\frac{G(x_1) - G(\bar{x}_1)}{x_1 - \bar{x}_1})] \\ a_{12} \coloneqq -a_4c_4[\frac{F(x_1, x_4) - F(\bar{x}_1, \bar{x}_4)}{x_4 - \bar{x}_4}] = a_{21} \\ a_{13} = a_{31} = 0 \\ a_{22} = -c_4k_4 \\ a_{23} = a_{32} = 0 \\ a_{33} \coloneqq -c_5\sigma_0[\frac{L(x_5) - L(\bar{x}_5)}{x_5 - \bar{x}_5}] \end{cases}$$
(3.10)

As the flow associated with the model equations approaches  $E_2 = [\bar{x}_1, 0, 0, \bar{x}_4, \bar{x}_5]$ , the matrix entries  $[a_{ij}]_{3x3}$  have the following form:

$$a_{11} \rightarrow -[c_1k_1 + a_1c_1G'(\overline{x}_1)]$$

$$a_{12} \rightarrow -a_4c_4 \frac{\partial}{\partial x_1}[F(\overline{x}_1, \overline{x}_4)]$$

$$a_{22} = -c_4k_4$$

$$a_{33} \rightarrow -c_5\sigma_0L'(\overline{x}_5)$$
(3.11)

In particular, it can be shown that

$$\frac{\partial}{\partial x_1} F(\overline{x}_1, \overline{x}_4) \Big|_{x_1 = \overline{x}_1} = \overline{x}_4 e^{-b_4 \overline{x}_1} (1 - \overline{x}_1 b_4)$$

$$G'(\overline{x}_1) = \overline{x}_1 e^{-b_1 \overline{x}_1} (2 - \overline{x}_1 b_1)$$

$$L'(\overline{x}_5) = \frac{\lambda_0}{(\lambda_0 + \overline{x}_5)^2} > 0$$
(3.12)

Thus

$$F_{x_{1}}(\overline{x}_{1}, \overline{x}_{4}) = \begin{cases} > 0 \ if \ \overline{x}_{1} < \frac{1}{b_{4}} \\ = 0 \ if \ \overline{x}_{1} = \frac{1}{b_{4}} \\ < 0 \ if \ \overline{x}_{1} > \frac{1}{b_{4}} \end{cases}$$
(3.13)

Similarly,

$$G'(\overline{x}_{1}) = \begin{cases} > 0 \ if \ \overline{x}_{1} < \frac{2}{b_{2}} \\ = 0 \ if \ \overline{x}_{1} = \frac{2}{b_{2}} \\ < 0 \ if \ \overline{x}_{1} > \frac{2}{b_{2}} \end{cases}$$
(3.14)

Since F(x<sub>1</sub>, x<sub>4</sub>), G(x<sub>1</sub>), and L(x<sub>5</sub>) are continuous and differentiable functions in each variable, the matrix entries a<sub>11</sub>, a<sub>12</sub>, a<sub>22</sub>, a<sub>33</sub> exist and remain bounded in the space:  $R_{+}^{x_1x_4x_5}$ , as  $[x_1, 0, 0, x_4, x_5] \rightarrow [\overline{x}_1, 0, 0, \overline{x}_4, \overline{x}_5]$ .

Hence, V can be written in the form

The matrix A is negative definite if the following criteria hold:

$$A = \det a_{11} < 0 \quad or \quad a_{11} < 0$$

$$A_{2} = \det \begin{vmatrix} a_{11} & \frac{1}{2}a_{12} \\ \frac{1}{2}a_{12} & a_{22} \end{vmatrix} > 0 \quad or \quad a_{11}a_{22} - \frac{1}{4}(a_{12})^{2} > 0$$

$$A_{3} = \det \begin{vmatrix} a_{11} & \frac{1}{2}a_{12} & 0 \\ \frac{1}{2}a_{12} & a_{22} & 0 \\ 0 & 0 & a_{33} \end{vmatrix} < 0 \text{ or } a_{33}[a_{11}a_{22} - \frac{1}{4}(a_{12})^{2}] < 0$$

$$(3.16)$$

Theorem 3.1: Suppose

(i) 
$$G'(\bar{x}_1) > 0$$
  
(ii)  $c_4 k_4 [c_1 k_1 + a_1 G'(\bar{x}_1)] < \frac{1}{4} [a_4 c_4 F_{x_1}(\bar{x}_1, \bar{x}_4)]^2$ 

Then the physiological steady state  $E_2=[\bar{x}_1, 0, 0, \bar{x}_4, \bar{x}_5]$  is globally asymptotically stable, and hence the HIV-1 virions are annihilated in the CD4<sup>+</sup> T cells and the blood plasma. Thus  $E_2=[\bar{x}_1, 0, 0, \bar{x}_4, \bar{x}_5]$  is a global attractor.

<u>*Proof.*</u> The result follows immediately from the negative definite criteria on  $A_1$ ,  $A_2$ , and  $A_3$ . It is noted that  $a_{33}<0$ , and  $a_{11}<0$  if  $G'(\bar{x}_1) > 0$ . If  $a_{11}$  and  $a_{33}$  are both negative, then the restriction on  $A_3$  is satisfied if condition (ii) of the theorem holds. Thus V is negative definite and the theorem holds.  $\Box$ 

### 4 Simulation results and discussion

In this section, the simulation results are presented. The computer programming code for the simulations was written in C++. Transdermal delivery was simulated as a rectangular periodic function f(t) such that  $f := |\text{ceil}(\sin(5 t))|$ .

In particular, the drug input is continuous for 6 months and off for another 6 months until HAART is discontinued. Figure 1 presents an unsuccessful HAART therapy for a hypothetical AIDS patient with the patho-physiological parametric configuration  $P_1$  in Table 1. In this HAART scenario, the plasma HIV-1 virions ( $x_3$ ) completely overwhelmed the non-infected CD4<sup>+</sup> T helper cells ( $x_1$ ) and the HIV-1 specific CD8<sup>+</sup> cytotoxic T cells ( $x_4$ ). The HIV-1 infected CD4<sup>+</sup> T cells ( $x_2$ ) exhibit periodic dynamics and the prognosis for the hypothetical patient is unwholesome. Figure 2 depicts a successful HAART outcome in which the plasma HIV-1 virions  $(x_3)$  are annihilated using the hypothetical patient parameter configuration  $P_2$  in Table 2. Also the HIV-1 infected CD4<sup>+</sup> T helper cells  $(x_2)$  are

drastically reduced to below 100 cells/ $\mu l$ . The non-infected CD4<sup>+</sup> T helper cells ( $x_1$ ) are repopulated in this simulation. This outcome has been clinically observed and discussed by Ye et al. [17].

TABLE 1. Hypothetica	l AIDS Patient Parametric	Configuration $P_1$
----------------------	---------------------------	---------------------

$S_{1} = 400 / day/\mu l$ $a_{1} = 0.09 / day/cell/\mu l$ $b_{1} = 0.01 / cell/\mu l$ $a_{1} = 0.5 / day/virion/\mu l$ $k_{1} = 0.0005 / day/\mu l$ $q_{1} = 0.00045 / day/\mu l/cell$ $e_{10} = 0.0025 cells/day/\mu l$ $x_{10} = 800 cells/\mu l$	$S_{2} = 800 / day/\mu l$ $a_{2} = 0.03 / day/cell/\mu l$ $b_{2} = 0.004/cell/\mu l$ $a_{2} = 0.5 / day/virion/\mu l$ $k_{2} = 0.005 / day/\mu l$ $q_{2} = 0.00001 / day/\mu l/cell$ $\beta_{1} = 1.5 virons/CD4^{+}/day$ $K_{1} = 0.0001 / day/\mu l$ $e_{20} = 0.0005 cells/day/\mu l$ $\xi_{2} = 0.85$ $r_{1} = 400 cells/\mu l$	$S_{3} = 10 / day/\mu l$ $\beta_{2} =$ 0.0015virons/CD4 <sup>+</sup> /day/\mu l $\beta_{3} = 1.05 virons/CD4+/day$ $\alpha_{3} = 0.027 / day/virion/\mu l$ $k_{3} = 0.0001 / day$ $q_{1} = 0.25$ $\xi_{3} = 0.001$ $x_{30} = 500 cells/\mu l$	$S_{4} = 10 / day/\mu l$ $a_{4} = 0.35 / day/cell/\mu l$ $b_{4} = 0.01/cell/\mu l$ $K_{2} = 0.0024 / day/\mu l$ $k_{4} = 0.08 / day/\mu l$ $e_{40} = 0.0002 cells/day/\mu l$ $\eta_{2} = 0.45$ $x_{40} = 730 cells/\mu l$	D = 3000  units $\sigma_0 = 0.5 \text{ mg/day}$ $\sigma_2 = 30 \text{ mg/day}$ $\sigma_3 = 5 \text{ mg/day}$ $\lambda_0 = 5 \text{ mg/L}$ $\lambda_2 = 10 \text{ mg/L}$ $\lambda_3 = 0.025 \text{ mg/L}$ $x_{50} = 1500 \text{ cells/}\mu l$ n = 5
$\chi_{10}$ 500 certs $\mu$	$z_2 = 0.83$ $x_{20} = 400 \text{ cells}/\mu l$	30 500 <b>co</b> ns, <i>µ</i>		





Figure 1 Simulation results using parametric configuration  $P_1$ 

TABLE 2. Hy	vpothetical A	AIDS P	atient Pa	arametric (	Configurati	on P <sub>2</sub>
· _	/ · · · · · ·					- 4

$S_{1} = 800 / day / \mu l$ $a_{1} = 0.15 / day / cell / \mu l$ $b_{1} = 0.01 / cell / \mu l$ $a_{1} = 0.5 / day / virion / \mu l$ $k_{1} = 0.0005 / day / \mu l$ $a_{2} = 0.00045 / day / \mu l$	$S_{2} = 800 / day/\mu l$ $a_{2} = 0.03 / day/cell/\mu l$ $b_{2} = 0.004 / cell/\mu l$ $\alpha_{2} = 0.5 / day/virion/\mu l$ $k_{2} = 0.005 / day/\mu l$ $a_{3} = 0.00001 / day/\mu l$	$S_3 = 10 / day/\mu l$ $\beta_2 = 0.0015$ virons/CD4 <sup>+</sup> /day/\mu l $\beta_3 = 1.05 \text{ virons/CD4+/day}$ $\alpha_3 = 0.027 / day/virion/\mu l$ $k_{-} = 0.0001 / day$	$S_{4} = 10 / day/\mu l$ $a_{4} = 0.35 / day/cell/\mu l$ $b_{4} = 0.01/cell/\mu l$ $K_{2} = 0.0024 / day/\mu l$ $k_{4} = 0.08/day/\mu l$ $a_{4} = 0.0022 cells/day/\mu l$	D = 4000 units $\sigma_0 = 0.5 mg/day$ $\sigma_2 = 30 mg/day$ $\sigma_3 = 5 mg/day$ $\lambda_0 = 5 mg/L$ $\lambda_0 = 10 mg/L$
$e_{10} = 0.0025 \text{ cells/day/}\mu l$ $x_{10} = 500 \text{ cells/}\mu l$	$\beta_{1} = 1.5 \text{ virons/CD4}^{+}/\text{day}$ $K_{1} = 0.0001/\text{day}/\mu l$ $e_{20} = 0.0005 \text{ cells/day}/\mu l$ $\xi_{2} = 0.85$ $x_{20} = 400 \text{ cells}/\mu l$	$e_{30} = 0.0001 / day$ $\eta_1 = 0.25$ $\xi_3 = 0.001$ $x_{30} = 500 \text{ cells}/\mu l$	$\eta_2 = 0.45$ $x_{40} = 730 \text{ cells}/\mu l$	$\lambda_3 = 0.025 mg/L$ $x_{50} = 1500 \text{ cells/}\mu l$ n = 5





Figure 2 Simulation results using parametric configuration  $P_2$ 

## **5** Summarizing remarks

In this research, we presented a mathematical model which describes the patho-physiological dynamics of HIV-1 induced AIDS during HAART therapy. This model incorporates several physiological aspects of HIV-1 patho-physiology. These include the recruitment of virions from latent HIV-1 reservoirs ( $S_3$ ) such as macrophages, microglial cells and lymphoid tissues. The model also includes autocrine and paracrine activation of CD4<sup>+</sup> and

CD8<sup>+</sup> T cells. Michaelis-Menten pharmacokinetics is used to describe the dynamics of the HAART drug in the AIDS patient. The simulations used a blend of estimated and literature based [3, 10, 13] hypothetical patient parametric configurations. The simulation results depict respectively scenarios for efficacious and non-efficacious HAART therapeutic outcomes.

The necessary conditions for existence of a plausible physiological outcome  $E_2 = [\bar{x}_1, 0, 0, \bar{x}_4, \bar{x}_5]$  are

$$\begin{cases} S_1 + a_1 \overline{x_1}^2 e^{-b_1 \overline{x_1}} - k_1 \overline{x_1} - e_{10} = 0 \\ S_2 - e_{20} = 0 \\ S_4 + a_4 \overline{x_1} \overline{x_4} e^{-b_4 \overline{x_1}} - k_4 \overline{x_4} - e_{40} = 0 \\ D - \frac{\sigma_0 \overline{x_5}}{\lambda_0 + \overline{x_5}} = 0 \end{cases}$$
(5.1)

The sufficient conditions for successful HAART therapy and cure of AIDS are

$$\begin{cases} G'(\overline{x}_{1}) > 0 \\ c_{4}k_{4}[c_{1}k_{1} + a_{1}G'(\overline{x}_{1})] < \frac{1}{4}[a_{4}c_{4}F_{x_{1}}(\overline{x}_{1}, \overline{x}_{4})]^{2} \end{cases} (5.2)$$

It is possible to refine (5.2) to

$$\overline{x}_1 = K_m^{CD8+} < 2K_m^{CD4+}$$

where  $K_m$  denotes the Michaelis-Menten constant. In a future publication, more necessary and sufficient criteria for the cure of HIV-1 induced AIDS will be presented and discussed.

## **6** References

- S.H. Bajaria, G. Webb, D.E. Kirschner, "Predicting differential responses to structured treatment interruptions during HAART", Bulletin of Mathematical Biology, 66, pp. 1093–1118, 2004
- [2] M.A.L. Caetano, T. Yoneyama, "Short and long period optimization of drug doses in the treatment of AIDS", Anais de Academia Brasileira de Ciências, September año/vol 74, número 003, pp. 379-392, 2002
- [3] M.S. Ciupe, B.L. Bivort, D.M. Bortz. P.W. Nelson, "Estimating kinetics parameters from HIV primary infection data through the eyes of three different mathematical models", Mathematical Biosciences 200, 1–27, 2006
- [4] L.K. Doepel, "International HIV/AIDS trial finds continuous antiretroviral therapy superior to episodic Therapy", NIH News, National Institute of Health, at <u>http://www.nih.gov/news/pr/jan2006/niald-18.htm</u>, Jan 18, 2006
- [5] C. Hess et al., "HIV-1 specific CD8+ T cells with an effector phenotype and control of viral replication", Lancet 362, pp. 863-866, 2004
- [6] S. Jain, A. K. Tiwary, N. K. Jain, "Transdermal delivery of an anti-HIV agent using elastic liposomes: mechanism of action", Current Drug Delivery, vol. 3(2), pp. 57-166, 2006
- [7] X. Jin et al., "An antigenic threshold for maintaining human immunodeficiency virus type 1-specific

cytotoxic T lymphocytes", Mol. Med. 6, pp.803-809, 2000

- [8] J. Lisziewicz and F. Lori, "Structured treatment interruptions in HIV/AIDS therapy", Microbes and Infection, 4, pp.207-214, 2002
- [9] S. H. Lowe, J.M. Prins, J.M. Lange, "Anti-retroviral therapy in previously untreated adults infected with the human immunodeficiency virus type 1: established and potential determinants of virological outcome", Neth. J. Med., 62, pp.424-440, 2004
- [10] F. Nani and M. Jin, "Mathematical modeling and simulation of latency phase HIV-1 dynamics", Int'l Conf. Bioinformatics and Computational Biology (BIOCOMP'10), vol. II, pp. 428-434, July 2010
- [11] M.A. Nowak, S. Bonhoeffer, G. M. Shaw, R.M. May, "Anti-viral drug treatment: dynamics of resistance of free virus and infected cell population", J. Theor. Biol. 184, pp. 203-217, 1997
- [12] G. Pantaleo, A.S. Fauci, "New concepts in the immunopathogenesis of HIV infection" Annual Review of Immunology, vol. 13, pp. 487-512, 1995
- [13] A. S. Perelson et al., "Decay characteristics of HIV-1 infected compartments during combination therapy", Nature, vol. 387, pp. 188-191, 1997
- [14] R. F. Stengel, "Mutation and control of the human immunodeficiency virus", Mathematical Biosciences, vol. 231, pp. 93-102, 2008
- [15] W.Y. Tan, Z. Xiang, "Some state space models of HIV pathogenesis under treatment by anti-viral drugs in HIV-infected individuals", Mathematical Biosciences, 156, pp.69-94, 1999
- [16] D. Wodarz, M.A. Nowak, "Specific therapy regimes could lead to long-term immunological control of HIV", Proc. National Acad. Sci. USA, 96, pp. 14464-14469, 1999
- [17] P. Ye, A. P. Kourtis, and D. E. Kirschner, "Reconstitution of thymic function in HIV-1 patients treated with highly active antiretroviral therapy", Clinical Immunology, vol. 106, pp. 95-105, 2003
- [18] G.S. Zaric, A. M. Bayoumi, ML Brandean, and DK Owens, "Effects of protease inhibitors on the spread of HIV strains, A simulation study", Simulation, pp.262-275, 1998