

## SBML Model Report

### Model name: “Perelson1993\_HIVinfection- \_CD4Tcells\_ModelA”



April 21, 2016

## 1 General Overview

This is a document in SBML Level 2 Version 4 format. This model was created by the following three authors: Ethan Choi<sup>1</sup>, Ethan Choi<sup>2</sup> and Ethan Choi<sup>3</sup> at June 25<sup>th</sup> 2010 at 1:37 p. m. and last time modified at June 25<sup>th</sup> 2010 at 1:37 p. m. Table 1 provides an overview of the quantities of all components of this model.

Table 1: Number of components in this model, which are described in the following sections.

Element	Quantity	Element	Quantity
compartment types	0	compartments	1
species types	0	species	0
events	0	constraints	0
reactions	0	function definitions	0
global parameters	14	unit definitions	7
rules	5	initial assignments	0

## Model Notes

This a model from the article:

### **Dynamics of HIV infection of CD4+ T cells.**

Perelson AS, Kirschner DE, De Boer R. Math Biosci 1993 Mar;114(1):81-125 [8096155](#) ,

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**Abstract:**

We examine a model for the interaction of HIV with CD4+ T cells that considers four populations: uninfected T cells, latently infected T cells, actively infected T cells, and free virus. Using this model we show that many of the puzzling quantitative features of HIV infection can be explained simply. We also consider effects of AZT on viral growth and T-cell population dynamics. The model exhibits two steady states, an uninfected state in which no virus is present and an endemically infected state, in which virus and infected T cells are present. We show that if  $N$ , the number of infectious virions produced per actively infected T cell, is less than a critical value,  $N_{crit}$ , then the uninfected state is the only steady state in the nonnegative orthant, and this state is stable. For  $N > N_{crit}$ , the uninfected state is unstable, and the endemically infected state can be either stable, or unstable and surrounded by a stable limit cycle. Using numerical bifurcation techniques we map out the parameter regimes of these various behaviors. Oscillatory behavior seems to lie outside the region of biologically realistic parameter values. When the endemically infected state is stable, it is characterized by a reduced number of T cells compared with the uninfected state. Thus T-cell depletion occurs through the establishment of a new steady state. The dynamics of the establishment of this new steady state are examined both numerically and via the quasi-steady-state approximation. We develop approximations for the dynamics at early times in which the free virus rapidly binds to T cells, during an intermediate time scale in which the virus grows exponentially, and a third time scale on which viral growth slows and the endemically infected steady state is approached. Using the quasi-steady-state approximation the model can be simplified to two ordinary differential equations that summarize much of the dynamical behavior. We compute the level of T cells in the endemically infected state and show how that level varies with the parameters in the model. The model predicts that different viral strains, characterized by generating differing numbers of infective virions within infected T cells, can cause different amounts of T-cell depletion and generate depletion at different rates. Two versions of the model are studied. In one the source of T cells from precursors is constant, whereas in the other the source of T cells decreases with viral load, mimicking the infection and killing of T-cell precursors. (ABSTRACT TRUNCATED AT 400 WORDS)

This model was taken from the [CellML repository](#) and automatically converted to SBML. The original model was: [Perelson AS, Kirschner DE, De Boer R. \(1993\) - version=1.0](#)  
The original CellML model was created by:

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To cite BioModels Database, please use: [Li C, Donizelli M, Rodriguez N, Dharuri H, Endler L, Chelliah V, Li L, He E, Henry A, Stefan MI, Snoep JL, Hucka M, Le Novre N, Laibe C \(2010\) BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. BMC Syst Biol., 4:92.](#)

## 2 Unit Definitions

This is an overview of eleven unit definitions of which four are predefined by SBML and not mentioned in the model.

### 2.1 Unit `day`

**Name** `day`

**Definition** 86400 s

### 2.2 Unit `per_day`

**Name** `per_day`

**Definition**  $(86400 \text{ s})^{-1}$

### 2.3 Unit `mm3`

**Name** `mm3`

**Definition**  $\text{mm}^3$

### 2.4 Unit `per_mm3`

**Name** `per_mm3`

**Definition**  $\text{mm}^{-3}$

### 2.5 Unit `per_day_mm3`

**Name** `per_day_mm3`

**Definition**  $(86400 \text{ s})^{-1} \cdot \text{mm}^{-3}$

### 2.6 Unit `mm3_per_day`

**Name** `mm3_per_day`

**Definition**  $\text{mm}^3 \cdot (86400 \text{ s})^{-1}$

## 2.7 Unit time

**Name** time

**Definition** 86400 s

## 2.8 Unit substance

**Notes** Mole is the predefined SBML unit for substance.

**Definition** mol

## 2.9 Unit volume

**Notes** Litre is the predefined SBML unit for volume.

**Definition** l

## 2.10 Unit area

**Notes** Square metre is the predefined SBML unit for area since SBML Level 2 Version 1.

**Definition** m<sup>2</sup>

## 2.11 Unit length

**Notes** Metre is the predefined SBML unit for length since SBML Level 2 Version 1.

**Definition** m

# 3 Compartment

This model contains one compartment.

Table 2: Properties of all compartments.

Id	Name	SBO	Spatial Dimensions	Size	Unit	Constant	Outside
COMPartment			3	1		<input checked="" type="checkbox"/>	

## 3.1 Compartment COMPartment

This is a three dimensional compartment with a constant size of one litre.

## 4 Parameters

This model contains 14 global parameters.

Table 3: Properties of each parameter.

Id	Name	SBO	Value	Unit	Constant
s	s		10.000		<input checked="" type="checkbox"/>
r	r		0.030		<input checked="" type="checkbox"/>
T_max	T_max		1500.000		<input checked="" type="checkbox"/>
mu_T	mu_T		0.020		<input checked="" type="checkbox"/>
T	T		1000.000		<input type="checkbox"/>
k_1	k_1		$2.4 \cdot 10^{-5}$		<input checked="" type="checkbox"/>
T_1	T_1		0.000		<input type="checkbox"/>
k_2	k_2		0.003		<input checked="" type="checkbox"/>
mu_b	mu_b		0.240		<input checked="" type="checkbox"/>
T_2	T_2		0.000		<input type="checkbox"/>
mu_V	mu_V		2.400		<input checked="" type="checkbox"/>
N	N		1400.000		<input checked="" type="checkbox"/>
V	V		0.001		<input type="checkbox"/>
T_tot	T_tot		0.000		<input type="checkbox"/>

## 5 Rules

This is an overview of five rules.

### 5.1 Rule T

Rule T is a rate rule for parameter T:

$$\frac{d}{dt}T = s - \text{mu\_T} \cdot T + r \cdot T \cdot \left(1 - \frac{T + T_1 + T_2}{T_{\text{max}}}\right) - k_1 \cdot V \cdot T \quad (1)$$

### 5.2 Rule T\_1

Rule T\_1 is a rate rule for parameter T\_1:

$$\frac{d}{dt}T_1 = k_1 \cdot V \cdot T - \text{mu\_T} \cdot T_1 - k_2 \cdot T_1 \quad (2)$$

### 5.3 Rule T\_2

Rule T\_2 is a rate rule for parameter T\_2:

$$\frac{d}{dt}T_2 = k_2 \cdot T_1 - \text{mu\_b} \cdot T_2 \quad (3)$$

## 5.4 Rule $V$

Rule  $V$  is a rate rule for parameter  $V$ :

$$\frac{d}{dt}V = N \cdot \mu_b \cdot T_2 - k_1 \cdot V \cdot T - \mu_V \cdot V \quad (4)$$

## 5.5 Rule $T_{\text{tot}}$

Rule  $T_{\text{tot}}$  is an assignment rule for parameter  $T_{\text{tot}}$ :

$$T_{\text{tot}} = T + T_1 + T_2 \quad (5)$$

SBML2<sup>A</sup>TeX was developed by Andreas Dräger<sup>a</sup>, Hannes Planatscher<sup>a</sup>, Dieudonné M Wouamba<sup>a</sup>, Adrian Schröder<sup>a</sup>, Michael Hucka<sup>b</sup>, Lukas Endler<sup>c</sup>, Martin Golebiewski<sup>d</sup> and Andreas Zell<sup>a</sup>. Please see <http://www.ra.cs.uni-tuebingen.de/software/SBML2LaTeX> for more information.

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