



Application of the homotopy analysis method for solving a model for HIV infection of CD4⁺ T-cells

M. Ghoreishi^a, A.I.B.Md. Ismail^a, A.K. Alomari^{b,*}

^a School of Mathematical Sciences, Universiti Sains Malaysia, 11800, Penang, Malaysia

^b Department of Mathematics, Faculty of Science, Hashemite University, 13115, Al-Zarqa, Jordan

ARTICLE INFO

Article history:

Received 23 March 2011

Received in revised form 23 May 2011

Accepted 20 July 2011

Keywords:

HIV infection model

Homotopy analysis method

h-curve

Analytical solution

ABSTRACT

In this paper, the homotopy analysis method (HAM) is investigated to give an approximate solution of a model for HIV infection of CD4⁺ T-cells. This method allows for the solution of the governing differential equation to be calculated in the form of an infinite series with components which can be easily calculated. The HAM utilizes a simple method to adjust and control the convergence region of the infinite series solution by using an auxiliary parameter. The results obtained are presented, and six terms are sufficient to obtain an approximation solution that is very accurate.

© 2011 Elsevier Ltd. All rights reserved.

1. Introduction

Many nonlinear mathematical models have been developed to describe infection by the human immunodeficiency virus (HIV). In 1989, a model for the infection of the human immune system by HIV was developed by Perelson [1]. This model of virus spread has three variables: the population sizes of uninfected cells, infected cells, and free virus particles. Perelson et al. [2] extended the model described in [1] and developed a new model by considering four variables:

1. cells that are uninfected,
2. cells that are latently infected,
3. cells that are actively infected, and
4. free virus particles.

Their model is described by a system of four ordinary differential equations. It was noted that the model can replicate many of the symptoms of AIDS observed clinically. Culshaw and Ruan [3] reduced the model described in [2] to a system of three ordinary differential equations by assuming that all the infected cells are capable of producing the virus.

In this paper, the homotopy analysis method (HAM) is introduced and developed for approximately solving the model for HIV infection of CD4⁺ T-cells of Culshaw and Ruan described above. The model is [3]

$$\begin{aligned} \frac{dT}{dt} &= s - \mu_T T + rT \left(1 - \frac{T+I}{T_{\max}}\right) - k_1 VT, \\ \frac{dI}{dt} &= k_1 VT - \mu_I I, \\ \frac{dV}{dt} &= N\mu_b I - k_1 VT - \mu_V V, \end{aligned} \quad (1)$$

* Corresponding author.

E-mail addresses: mkgghoreishi@gmail.com (M. Ghoreishi), izani@cs.usm.my (A.I.B.Md. Ismail), abdomari2008@yahoo.com (A.K. Alomari).