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Homotopy perturbation method for solving viral dynamical model

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Abstract: In this article, homotopy perturbation method is implemented to give approximate and analytical solutions of nonlinear ordinary differential equation systems such as viral dynamical model. The proposed scheme is based on homotopy perturbation method (HPM), Laplace transform and Padé approximants. Some plots are presented to show the reliability and simplicity of the methods.

Keywords: Padé approximants; Homotopy perturbation method; viral dynamical model.

Viral Dinamik Model Çözümü için Homotopy Pertürbation Yöntemi

Özet: Bu makalede viral dinamik model gibi lineer olmayan adi diferensiyel denklem sisteminin yaklaşık analitik çözümünü bulmak için homotopy perturbation yöntemi uygulandı. Homotopy perturbation yöntemi temel alınarak, Laplace dönüşümü ve Padé yaklaşımları uygulandı. Yöntemleri doğruluğunu ve basitliğini göstermek için bazı grafikler sunuldu.

Anahtar kelimeler: **:** Padé yaklaşımı; Homotopy perturbation yöntemi; viral dinamik model

1. Introduction

On the behavior of solution of viral dynamic model is examined at the study [2]. The components of the basic three-component model are uninfected CD4+ T-cells, infected cells and free virus particles are denoted respectively by $x(t)$, $y(t)$ and $v(t)$. These quantities satisfy

$$\begin{cases} \dfrac{dx}{dt} = s - \mu x - \beta x v \\ \dfrac{dy}{dt} = \beta x v - \alpha y \\ \dfrac{dv}{dt} = c y - \gamma v \end{cases} \tag{1.1}$$

with initial conditions:

$$x(0) = M_1, \quad y(0) = M_2, \quad v(0) = M_3.$$

The motivation of this paper is to extend the application of the analytic homotopy-perturbation method (HPM) and variational iteration method [12–15] to solve the a three-species food chain model (1.1). The homotopy perturbation method (HPM) was first proposed by Chinese mathematician He [8-9,12-15]. The first connection between series solution methods such as an Adomian decomposition method and Padé approximants was established in. The transmission and dynamics of HTLV-I feature several biological characteristics that are of interest to epidemiologists, mathematicians, and biologists, see, for example, [10-11,16], etc. Like HIV, HTLV-I targets CD4+ T-cells, the most abundant white cells in the immune system, decreasing the body's ability to fight infection.

2 Padé approximaton

A rational approximation to $f(x)$ on $[a, b]$ is the quotient of two polynomials $P_N(x)$ and $Q_M(x)$ of degrees N and M, respectively. We use the notation $R_{N,M}(x)$ to denote this quotient. The $R_{N,M}(x)$ Padé approximations to a function $f(x)$ are given by [1]

$$R_{N,M}(x) = \frac{P_N(x)}{Q_M(x)} \quad \text{for } a \le x \le b. \tag{2.1}$$

The method of Padé requires that $f(x)$ and its derivative be continuous at $x = 0$. The polynomials used in (2.1) are

$$P_N(x) = p_0 + p_1 x + p_2 x^2 + ... + p_N x^N \tag{2.2}$$

$$Q_M(x) = 1 + q_1 x + q_2 x^2 + ... + q_M x^M \tag{2.3}$$

The polynomials in (2.2) and (2.3) are constructed so that $f(x)$ and $R_{N,M}(x)$ agree at $x = 0$ and their derivatives up to $N + M$ agree at $x = 0$. In the case $Q_0(x) = 1$, the approximation is just the Maclaurin expansion for $f(x)$. For a fixed value of $N + M$ the error is smallest when $P_N(x)$ and $Q_M(x)$ have the same degree or when $P_N(x)$ has degree one higher then $Q_M(x)$.

Notice that the constant coefficient of Q_M is $q_0 = 1$. This is permissible, because it notice be 0 and $R_{N,M}(x)$ is not changed when both $P_N(x)$ and $Q_M(x)$ are divided by the same constant. Hence the rational function $R_{N,M}(x)$ has $N + M + 1$ unknown coefficients. Assume that $f(x)$ is analytic and has the Maclaurin expansion

$$f(x) = a_0 + a_1 x + a_2 x^2 + ... + a_k x^k + ..., \tag{2.4}$$

and from the difference $f(x)Q_M(x) - P_N(x) = Z(x)$:

$$\left[\sum_{i=0}^{\infty} a_i x^i\right]\left[\sum_{i=0}^{M} q_i x^i\right] - \left[\sum_{i=0}^{N} p_i x^i\right] = \left[\sum_{i=N+M+1}^{\infty} c_i x^i\right], \tag{2.5}$$

The lower index $j = N + M + 1$ in the summation on the right side of (2.5) is chosen because the first $N + M$ derivatives of $f(x)$ and $R_{N,M}(x)$ are to agree at $x = 0$.

When the left side of (2.5) is multiplied out and the coefficients of the powers of x^i are set equal to zero for $k = 0,1,2,...,N + M$, the result is a system of $N + M + 1$ linear equations:

$$
\begin{aligned}
&a_0 - p_0 = 0\\
&q_1 a_0 + a_1 - p_1 = 0\\
&q_2 a_0 + q_1 a_1 + a_2 - p_2 = 0\\
&q_3 a_0 + q_2 a_1 + q_1 a_2 + a_3 - p_3 = 0\\
&q_M a_{N-M} + q_{M-1} a_{N-M+1} + a_N - p_N = 0
\end{aligned}
\tag{2.6}
$$

and

$$
\begin{aligned}
&q_M a_{N-M+1} + q_{M-1} a_{N-M+2} + \ldots + q_1 a_N + a_{N+2} = 0\\
&q_M a_{N-M+2} + q_{M-1} a_{N-M+3} + \ldots + q_1 a_{N+1} + a_{N+2} = 0\\
&. \qquad\qquad\qquad\qquad .\\
&. \qquad\qquad\qquad\qquad .\\
&. \qquad\qquad\qquad\qquad .\\
&q_M a_N + q_{M-1} a_{N+1} + \ldots + q_1 a_{N+M+1} + a_{N+M} = 0
\end{aligned}
\tag{2.7}
$$

Notice that in each equation the sum of the subscripts on the factors of each product is the same, and this sum increases consecutively from 0 to $N+M$. The M equations in (2.7) involve only the unknowns $q_1, q_2, q_3, ..., q_M$ and must be solved first. Then the equations in (2.6) are used successively to find $p_1, p_2, p_3, ..., p_N$ [1].

3.Homotopy perturbation method

To illustrate the homotopy perturbation method (HPM) for solving non-linear differential equations, He [8, 9] considered the following non-linear differential equation:

$$A(u) = f(r), \quad r \in \Omega \tag{3.1}$$

subject to the boundary condition

$$B\left(u, \frac{\partial u}{\partial n}\right) = 0, \quad r \in \Gamma \tag{3.2}$$

where A is a general differential operator, B is a boundary operator, f(r) is a known analytic function, Γ is the boundary of the domain Ω and $\frac{\partial}{\partial n}$ denotes differentiation along the normal vector drawn outwards from Ω. The operator A can generally be divided into two parts M and N. Therefore, (3.1) can be rewritten as follows:

$$M(u) + N(u) = f(r), \quad r \in \Omega \tag{3.3}$$

He [8, 9] constructed a homotopy $v(r, p) : \Omega x[0, 1] \to \Re$ which satisfies

$$H(v,p) = (1-p)\left[M(v) - M(u_0)\right] + p\left[A(v) - f(r)\right] = 0, \tag{3.4}$$

which is equivalent to

$$H(v,p) = M(v) - M(u_0) + pM(v_0) + p\left[N(v) - f(r)\right] = 0, \tag{3.5}$$

where $p \in [0,1]$ is an embedding parameter, and u_0 is an initial approximation of (3.5). Obviously, we have

$$H(v,0) = M(v) - M(u_0) = 0, \quad H(v,1) = A(v) - f(r) = 0. \qquad (3.6).$$

The changing process of p from zero to unity is just that of H(v,p) from $M(v) - M(v_0)$ to $A(v) - f(r)$. In topology, this is called deformation and $M(v) - M(v_0)$ and $A(v) - f(r)$ are called homotopic. According to the homotopy perturbation method, the parameter p is used as a small parameter, and the solution of Eq. (3.4) can be expressed as a series in p in the form

$$v = v_0 + pv_1 + p^2 v_2 + p^3 v_3 + ... \tag{3.7}$$

When $p \to 1$, Eq. (3.4) corresponds to the original one, Eqs. (3.3) and (3.7) become the approximate solution of Eq. (3.3), i.e.,

$$u = \lim_{p \to 1} v = v_0 + v_1 + v_2 + v_3 + ... \tag{3.8}$$

The convergence of the series in Eq. (3.8) is discussed by He in [8, 9].

4. Applications

In this section, we will apply the homotopy perturbation method to nonlinear ordinary differential equation systems (1.1).

4.1 Homotopy perturbation method to viral dynamic model

According to homotopy perturbation method, we derive a correct functional as follows:

$$\begin{aligned}
&(1-p)(\dot{v}_1 - \dot{x}_0) + p(\dot{v}_1 - s + \mu v_1 + \beta v_1 v_3) = 0,\\
&(1-p)(\dot{v}_2 - \dot{y}_0) + p(\dot{v}_2 - \beta v_1 v_3 + \alpha v_2) = 0,\\
&(1-p)(\dot{v}_3 - \dot{v}_0) + p(\dot{v}_3 - c v_2 + \gamma v_3) = 0,
\end{aligned} \tag{4.1}$$

where “dot” denotes differentation with respect to t, and the initial approximations are as follows:

$$
\begin{aligned}
&v_{1,0}(t) = x_0(t) = x(0) = M_1, \\
&v_{2,0}(t) = y_0(t) = y(0) = M_2, \\
&v_{3,0}(t) = v_0(t) = v(0) = M_3.
\end{aligned} \tag{4.2}
$$

and

$$
\begin{aligned}
&v_1 = v_{1,0} + p v_{1,1} + p^2 v_{1,2} + p^3 v_{1,3} + \ldots, \\
&v_2 = v_{2,0} + p v_{2,1} + p^2 v_{2,2} + p^3 v_{2,3} + \ldots, \\
&v_3 = v_{3,0} + p v_{3,1} + p^2 v_{3,2} + p^3 v_{3,3} + \ldots,
\end{aligned} \tag{4.3}
$$

Where $v_{i,j}, i, j = 1,2,3,\ldots$ are functions yet to be determined. Substituting Eqs.(4.2) and (4.3) into Eq. (4.1) and arranging the coefficients of “p” powers, we have

$$
\begin{aligned}
&\left(\dot{v}_{1,1} - s + \mu M_1 + \beta M_1 M_3\right) p + \left(\dot{v}_{1,2} + \mu v_{1,1} + \beta\left(v_{3,1} M_1 + v_{1,1} M_3\right)\right) p^2 \\
&+\left(\dot{v}_{1,3} + \mu v_{1,2} + \beta(v_{3,2} M_1 + v_{1,2} M_3 + v_{1,1} v_{3,1})\right) p^3 + \ldots = 0, \\
&\left(\dot{v}_{2,1} - \beta M_1 M_3\right) p + \left(\dot{v}_{2,2} - \beta\left(v_{3,1} M_1 + v_{1,1} M_3\right) + \alpha v_{2,1}\right) p^2 \\
&\quad +\left(\dot{v}_{2,3} - \beta(v_{3,2} M_1 + v_{1,2} M_3 + v_{1,1} v_{3,1}) + \alpha v_{2,2}\right) p^3 + \ldots = 0, \\
&\left(\dot{v}_{3,1} - c M_2 + \gamma M_3\right) p + \left(\dot{v}_{3,2} - c v_{2,1} + \gamma v_{3,1}\right) p^2 \\
&\quad +\left(\dot{v}_{3,3} - c v_{2,2} + \gamma v_{3,2}\right) p^3 + \ldots = 0,
\end{aligned} \tag{4.4}
$$

In order to obtain the unknowns $v_{i,j}(t), i, j = 1,2,3,$ we must construct and solve the following system which includes nine equations with nine unknowns, considering the initial conditions

$v_{i,j}(0) = 0, i, j = 1,2,3,$

$$
\begin{aligned}
&\dot{v}_{1,1} - s + \mu M_1 + \beta M_1 M_3 = 0, \\
&\dot{v}_{1,2} + \mu v_{1,1} + \beta\left(v_{3,1} M_1 + v_{1,1} M_3\right) = 0, \\
&\dot{v}_{1,3} + \mu v_{1,2} + \beta(v_{3,2} M_1 + v_{1,2} M_3 + v_{1,1} v_{3,1}) = 0, \\
&\dot{v}_{2,1} - \beta M_1 M_3 + \alpha M_2 = 0, \\
&\dot{v}_{2,2} - \beta\left(v_{3,1} M_1 + v_{1,1} M_3\right) + \alpha v_{2,1} = 0, \\
&\dot{v}_{2,3} - \beta(v_{3,2} M_1 + v_{1,2} M_3 + v_{1,1} v_{3,1}) + \alpha v_{2,2} = 0, \\
&\dot{v}_{3,1} - c M_2 + \gamma M_3 = 0, \\
&\dot{v}_{3,2} - c v_{2,1} + \gamma v_{3,1} = 0, \\
&\dot{v}_{3,3} - c v_{2,2} + \gamma v_{3,2} = 0.
\end{aligned} \tag{4.5}
$$

From Eq. (3.8), if the three terms approximations are sufficient, we will obtain:

$$
\begin{aligned}
x(t) &= \lim_{p\to 1} v_1(t) = \sum_{k=0}^{3} v_{1,k}(t),\\
y(t) &= \lim_{p\to 1} v_2(t) = \sum_{k=0}^{3} v_{2,k}(t),\\
v(t) &= \lim_{p\to 1} v_3(t) = \sum_{k=0}^{3} v_{3,k}(t),
\end{aligned} \tag{4.6}
$$

therefore

$$
\begin{aligned}
x(t) &= M_1 + \left(s - \mu M_1 - \beta M_1 M_3\right)t \\
&+ \frac{1}{2}\left[-\mu\left(s-\mu M_1-\beta M_1M_3\right)-\beta M_1\left(cM_2-\gamma M_3\right)+\beta M_3\left(s-\mu M_1-\beta M_1M_3\right)\right]t^2 \\
&+ \frac{1}{6}\begin{bmatrix}
\mu^2\left(s-\mu M_1-\beta M_1M_3\right)+\beta\mu M_1\left(cM_2-\gamma M_3\right)+\beta\mu M_3\left(s-\mu M_1-\beta M_1M_3\right)\\
-\beta cM_1\left(\beta M_1M_3-\alpha M_2\right)+\beta\gamma M_1\left(cM_2-\gamma M_3\right)-\mu M_3\left(s-\mu M_1-\beta M_1M_3\right)\\
-\beta M_1M_3\left(cM_2-\gamma M_3\right)-\beta M_3^2\left(s-\mu M_1-\beta M_1M_3\right)\\
+2\left(s-\mu M_1-\beta M_1M_3\right)\left(cM_2-\gamma M_3\right)
\end{bmatrix}t^3 \\
y(t) &= M_2 + \left(\beta M_1M_3-\alpha M_2\right)t \\
&+ \frac{1}{2}\left[\beta M_1\left(cM_2-\gamma M_3\right)+\beta M_3\left(s-\mu M_1-\beta M_1M_3\right)-\alpha\left(\beta M_1M_3-\alpha M_2\right)\right]t^2 \\
&+ \frac{1}{6}\begin{bmatrix}
\beta cM_1\left(\beta M_1M_3-\alpha M_2\right)-\beta\gamma M_1\left(cM_2-\gamma M_3\right)-\beta\mu M_3\left(s-\mu M_1-\beta M_1M_3\right)\\
-\beta^2M_1M_3\left(cM_2-\gamma M_3\right)-\beta^2M_3^2\left(s-\mu M_1-\beta M_1M_3\right)-\alpha\beta M_1\left(cM_2-\gamma M_3\right)\\
+2\left(s-\mu M_1-\beta M_1M_3\right)\left(cM_2-\gamma M_3\right)\beta-\alpha\beta M_3\left(s-\mu M_1-\beta M_1M_3\right)\\
\alpha^2\left(\beta M_1M_3-\alpha M_2\right)
\end{bmatrix}t^3 \\
v(t) &= M_3 + \left(cM_2-\gamma M_3\right)t \\
&+ \frac{1}{2}\left[c\left(\beta M_1M_3-\alpha M_2\right)-\gamma\left(cM_2-\gamma M_3\right)\right]t^2 \\
&+ \frac{1}{6}\begin{bmatrix}
\beta cM_1\left(cM_2-\gamma M_3\right)+c\beta M_3\left(s-\mu M_1-\beta M_1M_3\right)-c\alpha\left(\beta M_1M_3-\alpha M_2\right)\\
-\gamma c\left(\beta M_1M_3-\alpha M_2\right)+\gamma^2\left(cM_2-\gamma M_3\right)
\end{bmatrix}t^3,
\end{aligned} \tag{4.7}
$$

Table 1

Variables and parameters for contagion

s	the (assumed constant) rate of production of CD4+ T-cells	0.272
μ	their per capita death rate	0.00136
βxy	the rate of infection of CD4+ T-cells by virus	0.00027
α	the per capita rate of disappearance of infected cells	0.33
c	the rate of production of virions by infected cells	50
γ	the death rate of virus particles	2

This was done with the standard parameter values given above and initial values $M_1 = 100$, $M_2 = 0$ and $M_3 = 1$ for the three-component model.

A few first approximations for $x(t)$, $y(t)$ and $v(t)$ are calculated and presented below:

Three terms approximations:

$$\begin{aligned} x(t) &= 100 - 0.109t + 0.026911165t^2 - 0.02407000173t^3 \\ y(t) &= 0.027t - 0.031440285t^2 + 0.02751623336t^3, \\ v(t) &= 1 - 2t + 2.675t^2 - 2.307338083t^3, \end{aligned} \tag{4.8}$$

Four terms approximations:

$$\begin{aligned} x(t) &= 100 - 0.109t + 0.026911165t^2 - 0.02407000173t^3 + .01556829228t^4 \\ y(t) &= 0.027t - 0.031440285t^2 + 0.02751623336t^3 - 0.01783019773t^4, \\ v(t) &= 1 - 2t + 2.675t^2 - 2.307338083t^3 + 1.497621958t^4, \end{aligned} \tag{4.9}$$

Five terms approximations:

$$\begin{aligned} x(t) &= 100 - 0.109t + 0.026911165t^2 - 0.02407000173t^3 + .01556829228t^4 \\ &\quad - 0.008085139722t^5, \\ y(t) &= 0.027t - 0.031440285t^2 + 0.02751623336t^3 - 0.01783019773t^4 \\ &\quad + 0.009257698196t^5, \\ v(t) &= 1 - 2t + 2.675t^2 - 2.307338083t^3 + 1.497621958t^4 - 0.7773507604t^5, \end{aligned} \tag{4.10}$$

Six terms approximations:

$$\begin{aligned} x(t) &= 100 - 0.109t + 0.026911165t^2 - 0.02407000173t^3 + .01556829228t^4 \\ &\quad - 0.008085139722t^5 + .003500021813t^6, \\ y(t) &= 0.027t - 0.031440285t^2 + 0.02751623336t^3 - 0.01783019773t^4 \\ &\quad + 0.009257698196t^5 - 0.004007362583t^6, \\ v(t) &= 1 - 2t + 2.675t^2 - 2.307338083t^3 + 1.497621958t^4 - 0.7773507604t^5 \\ &\quad + 0.3362644052t^6, \end{aligned} \tag{4.11}$$

In this section, we apply Laplace transformation to (4.11), which yields

$$\begin{aligned} L\left(x(s)\right) &= \frac{100}{s} - \frac{.109}{s^2} + \frac{.05382233}{s^3} - \frac{.1444200104}{s^4} + \frac{.3736390147}{s^5} \\ &\quad - \frac{.9702167666}{s^6} + \frac{2.520015705}{s^7} \end{aligned}$$

$$L\left(y(s)\right)=\frac{.027}{s^2}-\frac{.06288057}{s^3}+\frac{.1650974002}{s^4}$$
$$-\frac{.4279247455}{s^5}+\frac{1.110923784}{s^6}-\frac{2.88530106}{s^7} \qquad (4.12)$$

$$L\left(v(s)\right)=\frac{1}{s}-\frac{2}{s^2}+\frac{5.35}{s^3}-\frac{13.8440285}{s^4}$$
$$+\frac{35.94292699}{s^5}-\frac{93.28209125}{s^6}+\frac{242.1103717}{s^7}$$

For simplicity, let $s=\frac{1}{t}$; then

$$L(x(t)) = 100t\text{-}.109t^2 + .05382233t^3 \text{-}.1444200104t^4 + .3736390147t^5$$
$$\text{-}.9702167666t^6 + 2.520015705t^7$$

$$L(y(t)) = 0.027t^2 \text{-}.06288057t^3 + .1650974002t^4 \text{-}.4279247455t^5$$
$$+1.110923784t^6 \text{-}2.88530106t^7 \qquad (4.13)$$

$$L(v(t)) = t-2t^2 + 5.35t^3 \text{-}13.8440285t^4 + 35.94292699t^5$$
$$\text{-}93.28209125t^6 + 242.1103717t^7$$

Padé approximant $[4/4]$ of (4.13) and substituting $t=\frac{1}{s}$, we obtain $[4/4]$ in terms of s. By using the inverse Laplace transformation, we obtain

$$x(t) = .008231687905e^{-2.595814579t} + 100.0178711e^{-.0008093617298t}$$
$$\text{-}.02610282415e^{.2559676681t} + .0003377192999e^{4102.105793t}$$
$$y(t) = \text{-}.009436126942e^{-2.595127407t} + .009436126831e^{.2662158241t}$$
$$+.1127264179*10^{-9}e^{18.37622499t} \qquad (4.14)$$
$$v(t) = .8066611297e^{-2.593466302t} \text{-}.01482572078e^{-2.46958404t}$$
$$+.2081645911e^{.266304151t} \text{-}.0001952110838e^{37173.86307t}$$

These results obtained by Padé approximations for $x(t)$, $y(t)$ and $v(t)$ are calculated and presented follow.

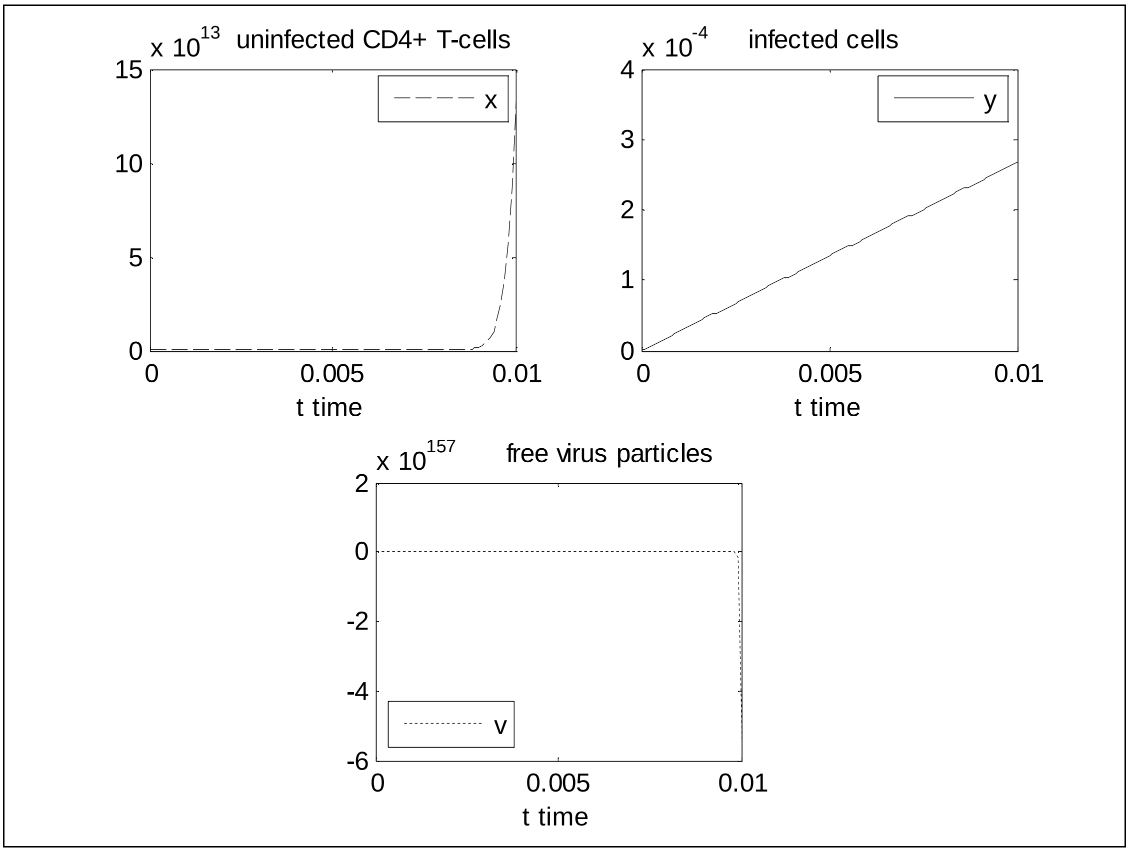

Figure. 1. Plots of Padé approximations for viral dynamical model

These results obtained by homotopy perturbation method, three, four, five and six terms approximations for $x(t)$, $y(t)$ and $v(t)$ are calculated and presented follow.

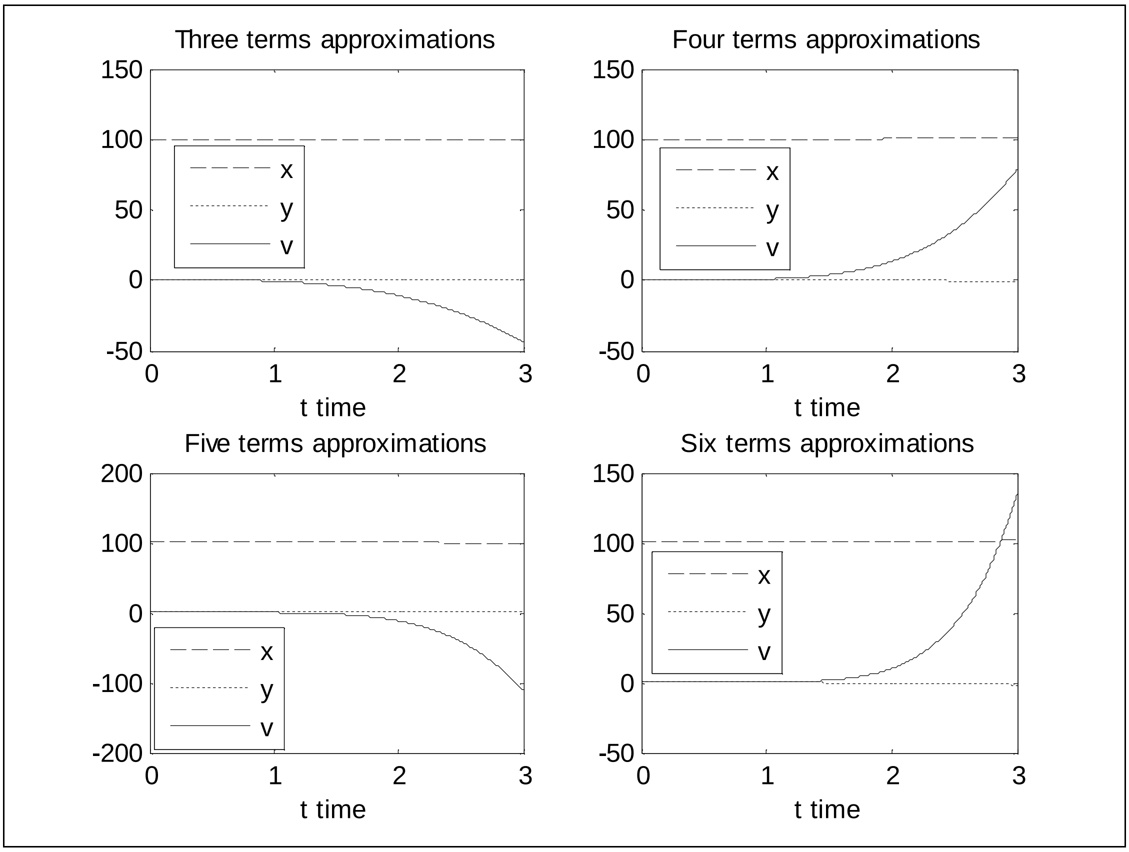

Figure. 2. Plots of three, four, five and six terms approximations for viral dynamic model

5. Conclusions

In this paper, homotopy perturbation method was used for finding the solutions of nonlinear ordinary differential equation systems such as viral dynamical model. We demonstrated the accuracy and efficiency of these methods by solving some ordinary differential equation systems. We use Laplace transformation and Padé approximant to obtain an analytic solution and to improve the accuracy of homotopy perturbation method. We apply He's homotopy perturbation method to calculate certain integrals. It is easy and very beneficial tool for calculating certain difficult integrals or in deriving new integration formula.

The computations associated with the examples in this paper were performed using Maple 7 and Matlab 7

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