Using Adomian Decomposition Method for Solving Vector-Host Model

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Abstract

In this paper, we use Adomian decomposition method (ADM) for solving vector-host model by using the alternate algorithm suggested by Biazar *et. al* [4]. Some of the first terms were generated and plotted against time and compared our results with the regular Runge-Kutta numerical methods by using Matlab `ode45` function.

Keywords: Adomian decomposition method, vector-host model, ODE solvers, numerical simulation, stability analysis.

1 Introduction

The vector-host model is a mathematical model (framework) for the spread of a disease that transmits from human to another human throw another carrier (vector). To formulate this model we consider the dynamics of the disease into two different populations, human population and vector population. We assumed that the human population is divided into three different subgroups, susceptible $s_h(t)$, infected (and infectious) $i_h(t)$ and recovered $r_h(t)$, and the vector population into two subgroups susceptible $s_v(t)$ and infected $i_v(t)$. It is assumed that susceptible individuals acquire infection following contacts with infected vectors at a per capita rate $ab\,i_v(t)$, where a is the per capita biting rate of vectors on humans, and b is the transmission probability per bite per human (as the case for malaria, [6, 8]). The per capita biting rate of vectors a is equal to the number of bites received per human from vectors due to conservation of bites mechanism [5, 7]. Infected humans recover and acquire permanent immunity

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at an average rate β. Susceptible vectors are acquire leishmaniasis infection following contacts with infected human at an average rate equal to $ac\,i_h(t)$, where a is the per capita biting rate, and c is the transmission probability for vector infection. It is also assumed that there is no demographic effects on the model. Then our model is given by

$$\begin{aligned} s_h' &= -ab\,s_h\,i_v \\ i_h' &= ab\,s_h\,i_v - \beta\,i_h \\ r_h' &= \beta\,i_h \\ s_v' &= -ac\,s_v\,i_h \\ i_h' &= ac\,s_v\,i_h \end{aligned} \tag{1}$$

with initial conditions:

$$s_h(0) = N_1, \quad i_h(0) = N_2, \quad r_h(0) = N_3, \quad s_v(0) = N_4, \quad i_v(0) = N_5.$$

2 Solving system (1) by Adomian decomposition method (ADM)

Adomian decomposition method (ADM) (see [1, 2]), considers s_h, i_h, r_h, s_v and i_v as the sums of the following series:

$$s_h = \sum_{i=0}^{\infty} s_h^i, \quad i_h = \sum_{i=0}^{\infty} i_h^i, \quad r_h = \sum_{i=0}^{\infty} r_h^i, \quad s_v = \sum_{i=0}^{\infty} s_v^i, \quad i_v = \sum_{i=0}^{\infty} i_v^i$$

By applying inverse of the operator $\frac{d(.)}{dt}$, which is the integration operator $\int_0^t (.)dt$ to each equation in the system (1) we have

$$\begin{aligned} s_h(t) &= s_h(t=0) - a\,b \int_0^t s_h(t)\,i_v(t)\,dt \\ i_h(t) &= i_h(t=0) + a\,b \int_0^t (s_h(t)\,i_v(t) - \beta\,i_h(t))\,dt \\ r_h(t) &= r_h(t=0) + \beta \int_0^t i_h(t)\,dt \\ s_v(t) &= s_v(t=0) - a\,c \int_0^t s_v(t)\,i_h(t)\,dt \\ i_v(t) &= i_v(t=0) + a\,c \int_0^t s_v(t)\,i_h(t)\,dt \end{aligned} \tag{2}$$

Using the alternate method for computing Adomian polynomials suggested by Biazar *et. al* [4], and substituting the initial conditions, we would have the following scheme

$$\begin{aligned}
s_h(t) &= N_1 - a\,b\int_0^t \sum_{i=0}^{n} s_h^{(i)}(t)\, i_v^{(n-i)}(t)\, dt \\
i_h(t) &= N_2 + a\,b\int_0^t \sum_{i=0}^{n} (s_h^{(i)}(t)\, i_v^{(n-i)}(t) - \beta\, i_h^{(n)}(t))\, dt \\
r_h(t) &= N_3 + \beta\int_0^t i_h^{(n)}(t)\, dt \qquad (3) \\
s_v(t) &= N_4 - a\,c\int_0^t \sum_{i=0}^{n} s_v^{(i)}(t)\, i_h^{(n-i)}(t)\, dt \\
i_v(t) &= N_5 + a\,c\int_0^t \sum_{i=0}^{n} s_v^{(i)}(t)\, i_h^{(n-i)}(t)\, dt
\end{aligned}$$

From the above method we can calculate some first few terms

$$\begin{aligned}
s_h^{(1)} &= -a\,b\,N_1\,N_5\,t \\
i_h^{(1)} &= (a\,b\,N_1\,N_5 - \beta\,N_2)\,t \\
r_h^{(1)} &= \beta\,N_2\,t \\
s_v^{(1)} &= -a\,c\,N_4\,N_2\,t \\
i_h^{(1)} &= a\,c\,N_4\,N_2\,t \\
s_h^{(2)} &= -\frac{1}{2}\,a\,b\Big[N_1(a\,c\,N_2\,N_4) - a\,b\,N_1\,N_5^2\Big]\,t^2 \\
i_h^{(2)} &= \frac{1}{2}\,a\,b\Big[N_1(a\,c\,N_2\,N_4) - a\,b\,N_1\,N_5^2 - \beta(a\,b\,N_1\,N_5 - \beta\,N_2)\Big]\,t^2 \\
r_h^{(2)} &= \frac{1}{2}\,\beta\Big[a\,b\,N_1\,N_5 - \beta\,N_2\Big]\,t^2 \\
s_v^{(2)} &= -\frac{1}{2}\,a\,c\Big[N_4(a\,b\,N_1\,N_5 - \beta\,N_2) - a\,c\,N_2^2\,N_4\Big]\,t^2 \\
i_v^{(2)} &= \frac{1}{2}\,a\,c\Big[N_4(a\,b\,N_1\,N_5 - \beta\,N_2) - a\,c\,N_2^2\,N_4\Big]\,t^2 \\
&\vdots
\end{aligned}$$

3 Convergence of the method

Since after the first step, applying the inverse operator $\int_0^t(.)dt$, we drive a system of Volterra integral equations of second kind, and the convergence of these systems is discussed in [3].

4 Numerical simulation and discussion

In this section we give numerical simulation for our model using (ADM) and the regular Runge-Kutta numerical method by applying Matlab® `ode45` function, and then we compare between the results.

The parameters values used are in Table 1.

parameter	parameter description	value
N_1	Initial value of population $s_h(t)$, susceptible individuals	100
N_2	Initial value of population $i_h(t)$, infected individuals	6
N_3	Initial value of population $r_h(t)$, recovered individuals	1
N_4	Initial value of population $s_v(t)$, susceptible vectors	80
N_5	Initial value of population $i_v(t)$, infected vectors	12
a	Biting rate of vectors	0.01
b	Progression rate of the disease in the vector	0.2
c	Progression rate of the disease in human	0.2
β	Human recovery rate	0.3

Table 1: Parameter values for the model simulation

We calculate three and four terms approximations for the variables are calculated and presented below.

Three terms approximation:

$$\begin{aligned} s_h^{(3)} &= 100 - 2.4\,t - 0.0672\,t^2 - 0.0007\,t^3 \\ i_h^{(3)} &= 6 - 0.6\,t - 0.0228\,t^2 + 0.003\,t^3 \\ r_h^{(3)} &= 1 + 1.8\,t + 0.09\,t^2 - 0.0023\,t^3 \\ s_v^{(3)} &= 80 - 0.96\,t - 0.0422\,t^2 + 0.0018\,t^3 \\ i_h^{(3)} &= 12 + 0.96\,t + 0.0422\,t^2 - 0.0018\,t^3 \end{aligned}$$

Four terms approximation:

$$\begin{aligned}
s_h^{(4)} &= 100 - 2.4\,t - 0.0672\,t^2 - 0.0007\,t^3 + 0.0002\,t^4 \\
i_h^{(4)} &= 6 - 0.6\,t - 0.0228\,t^2 + 0.003\,t^3 - 0.0004\,t^4 \\
r_h^{(4)} &= 1 + 1.8\,t + 0.09\,t^2 - 0.0023\,t^3 + 0.0002\,t^4 \\
s_v^{(4)} &= 80 - 0.96\,t - 0.0422\,t^2 + 0.0018\,t^3 - 0.0001\,t^4 \\
i_h^{(4)} &= 12 + 0.96\,t + 0.0422\,t^2 - 0.0018\,t^3 + 0.0001\,t^4
\end{aligned}$$

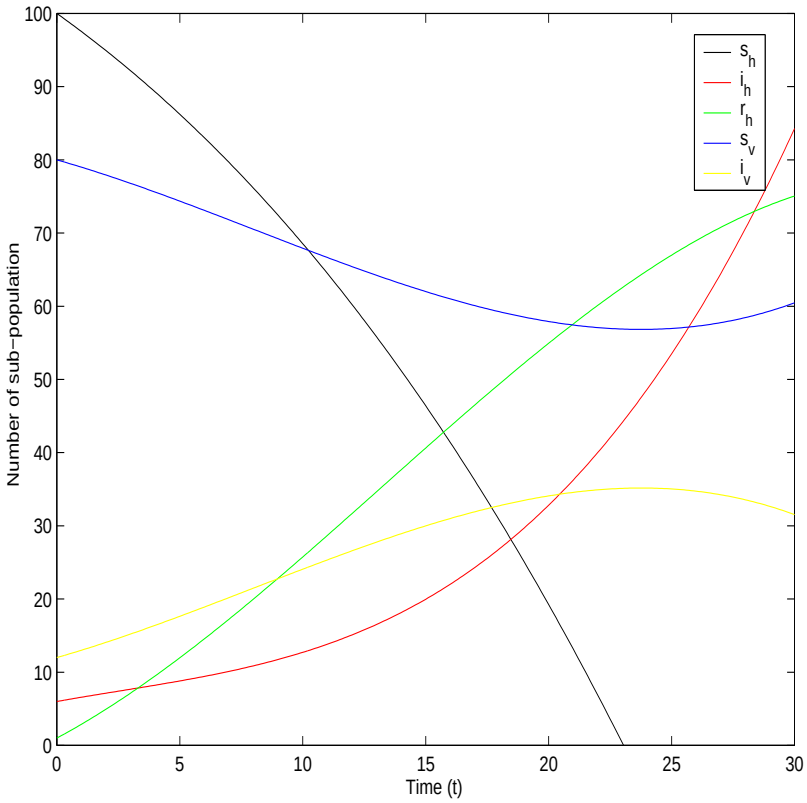

Figure 1: Simulation results using three terms approximation

We noticed that the three terms approximation of Adomian decomposition method is very similar to the simulation results generated using Matlab® `Ode45` function, which is reasonable compared to reality because it is clear that the number of susceptible (humans and vectors) decrease as the number of infected (humans and vectors) increase, and the number of recovered humans increases, as seen from Figures 1,3. However, as seen from Figure 2, using four terms approximation we found that the number of susceptible humans decrease first and then increase again, which coincide with reality, and this case needs further investigation, and it may happens due to the use of alternate method for computing Adomian polynomials.

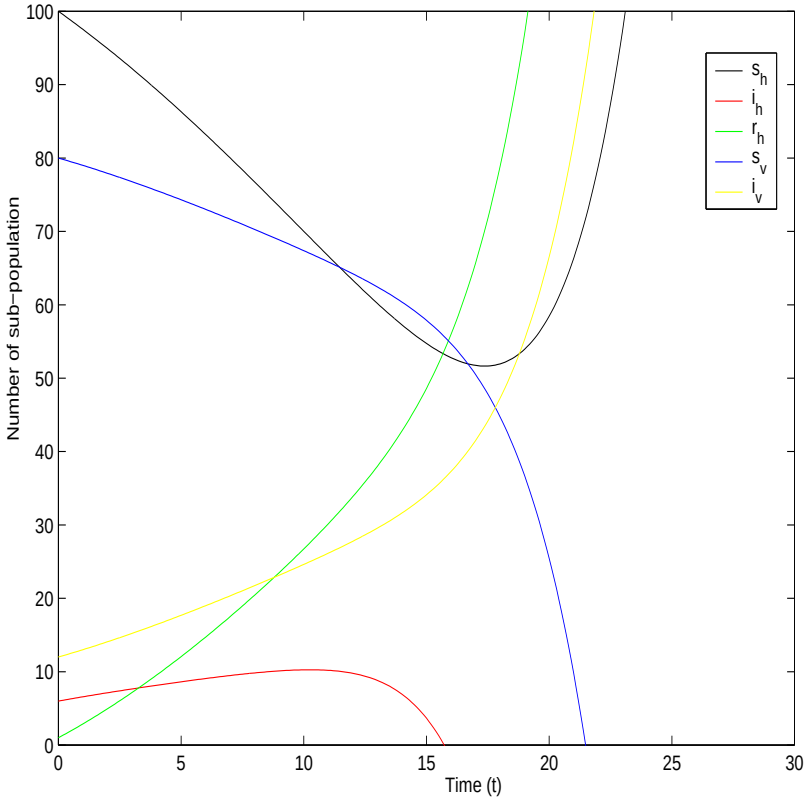

Figure 2: Simulation results using four terms approximation

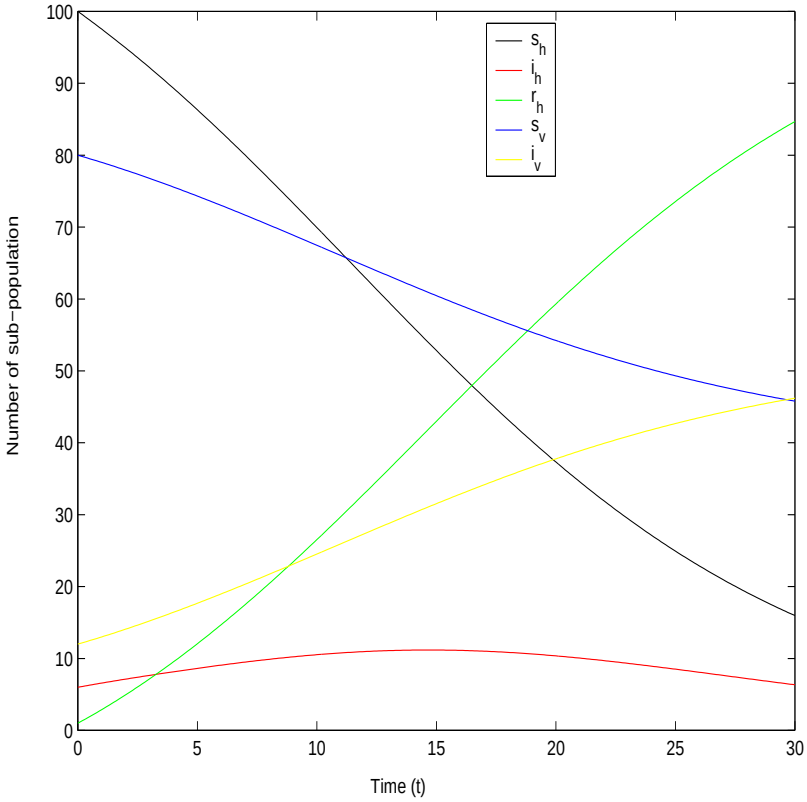

Figure 3: Simulation results using ode45

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