Comparing Numerical Method for the Solution of Epidemic Model

Mat Salim Selamat

ABSTRACT

In this paper, the Adomian Decomposition Method (ADM) is applied to the epidemic model for non-fatal disease which is a three dimensional system of nonlinear ordinary differential equations. The size of population is assumed constant over the period of the epidemic. Comparison between the decomposition solutions and the classical Runge-Kutta (RK4) numerical solutions are made.

Introduction

Adomian decomposition method (ADM) (Adomian 1988; 1989; 1994) is widely used in a variety of problems in scientific models (Biazar 2005; Biazar & Montezeri 2005; Guellal et al. 1997; Hashim et al. 2006; Noorani et al. 2006; Olek 1994; Shawagfeh 1996; Shawagfeh & Kaya 2004). ADM provides, without linearization, perturbation, transformation or discretisation, an analytical solution in terms of rapidly convergences infinite power series with easily computable terms.

In this paper, we implemented the ADM for the solution of the spread of a non-fatal disease in a population, which assumes to have constant size over the period of the epidemic is considered. We note that, Biazar (2005) also demonstrated the ADM to solve this problem. However, differs from Biazar (2005), we will divide the time interval into several steps and successively apply the decomposition solution with three, four and five terms over the subinterval.

General epidemic model

The spreading of a non-fatal disease in a population, which is assumed to have constant size over the period of the epidemic, is considered in. At time t, individuals in the population are classified into one of the following: *susceptibles* who can catch the disease; *infectives* who can pass on the disease to others; *removals* who have recovered and therefore immune.

Assume a large population of fixed size, N in which the number of susceptibles, S, infectives, I, and removals, R, at some time t are changing smoothly as continuous variables with $N = S + I + R$. The rate of change of the number of individuals in the three classes is determined by the following assumptions

(1) *Susceptibles* join the infective class at a rate, which is proportional to the product of the numbers of suspectibles and infectives, i.e. βSI, where β is infection rate.

(2) *Infectives* are removed at rate proportional to their numbers, i.e. γI, where γ is the removal rate.

Combining the above assumptions give the net rate of infectives as $\beta SI - \gamma I$. Changes in the number of susceptibles (S), infectives (I) and removals (R) are then described by the epidemic model as follows (Brown & Rothery 1993);

$$\frac{dS}{dt} = -\beta SI \qquad (1)$$

$$\frac{dI}{dt} = \beta SI - \gamma I \qquad (2)$$

$$\frac{dR}{dt} = \gamma I \qquad (3)$$

With initial condition,

$$S(0) = N_1, \qquad I(0) = N_2, \qquad R(0) = N_3 \qquad (4)$$

S, I and R are the number of susceptibles, infectives and removals, β is the infection rate and γ is the removals rate.

Adomian Decomposition Method

In this section, we will present direct application of ADM, to the epidemic model (1) – (3). First, we note that the epidemic model is a case of more general system of ODEs where the nonlinear term occurs as product of two of the dependent variables. According to Olek (1994) (see also Hashim et al. 2006, Noorani et al. 2006 and Vadasz & Olek 2000), the explicit solution for the epidemic model (1) – (3) is

$$S = \sum_{m=0}^{\infty} a_m \frac{(t - t^*)^m}{m!}$$

(21)

$$I = \sum_{m=0}^{\infty} b_m \frac{(t - t^*)^m}{m!}$$

(22)

$$R = \sum_{m=0}^{\infty} c_m \frac{(t - t^*)^m}{m!}$$

(23)

where the coefficients are given by the recurrence relations,

$$a_0 = S(t^*), \qquad b_0 = I(t^*), \qquad c_0 = R(t^*)$$

(24)

$$a_m = -\beta(m-1)!\sum_{k=0}^{m-1} \frac{a_m b_{m-k-1}}{k!(m-k-1)!}, \quad m \geq 1$$

(25)

$$b_m = -\gamma b_{m-1} + \beta(m-1)!\sum_{k=0}^{m-1} \frac{a_m b_{m-k-1}}{k!(m-k-1)!}, \quad m \geq 1$$

(26)

$$c_m = \gamma b_{m-1}$$

(27)

As first hinted in Adomian (1989), we treat the ADM as and algorithm for approximating the dynamical response in a sequence of time intervals (i.e., time step) $[0, t_1), [t_1, t_2), \ldots, [t_{m-1}, T)$ such that the initial condition in $[t^*, t_{m+1})$ is taken to be the condition at t^*.

Results and discussion

The Adomian algorithm is coded in the computer algebra package Maple. The Maple environment variable digits controlling the numbers of significant digits is set to 16 in all calculations done in this paper. For comparison with Biazar (2005), we set the parameters $N_1 = 20, N_2 = 15, N_3 = 10, \beta = 0.01$ and $\gamma = 0.02$. The simulations done in this paper are for the time span $t \in [0,100]$ and time step $\Delta t = 1$.

The results for 3, 4 and 5 terms are plotted on Figure 1, 2 and 3 respectively.

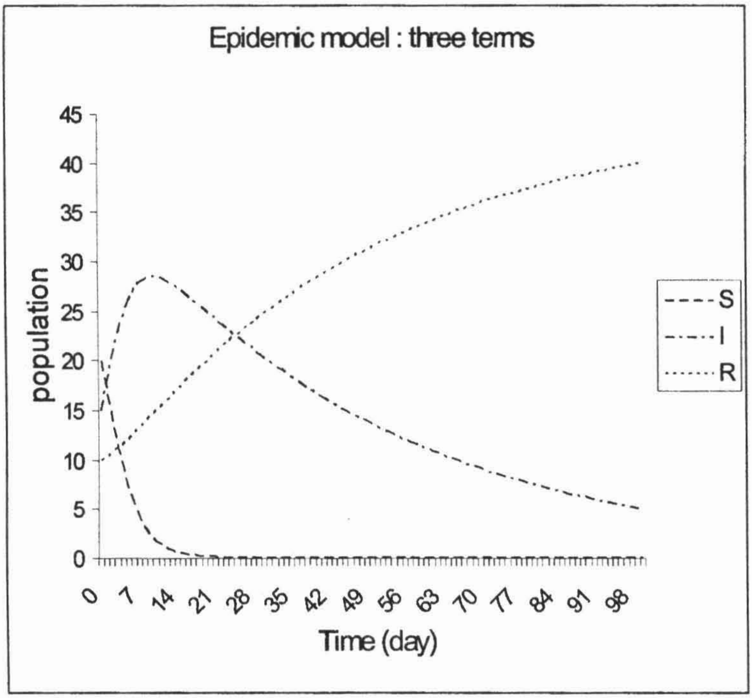

Fig.1: Plots of three terms approximations for *S*(*t*), *I*(*t*), *R*(*t*) versus time

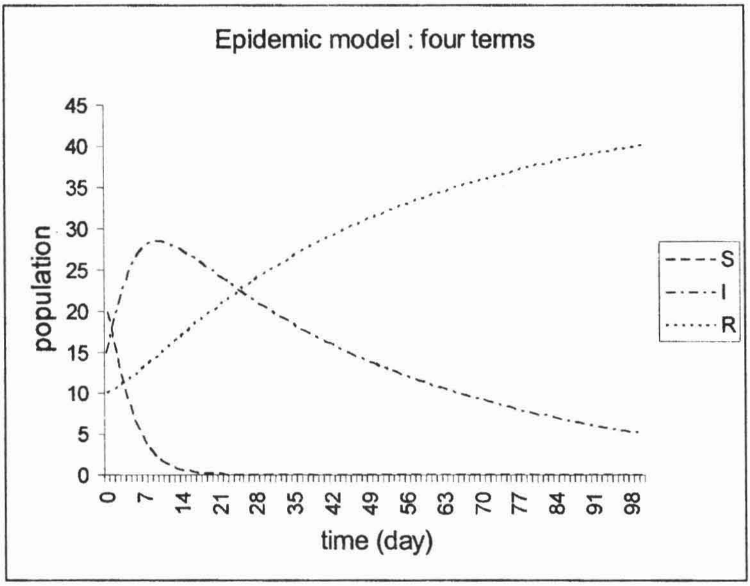

Fig.2: Plots of four approximations for *S*(*t*), *I*(*t*), *R*(*t*) versus time

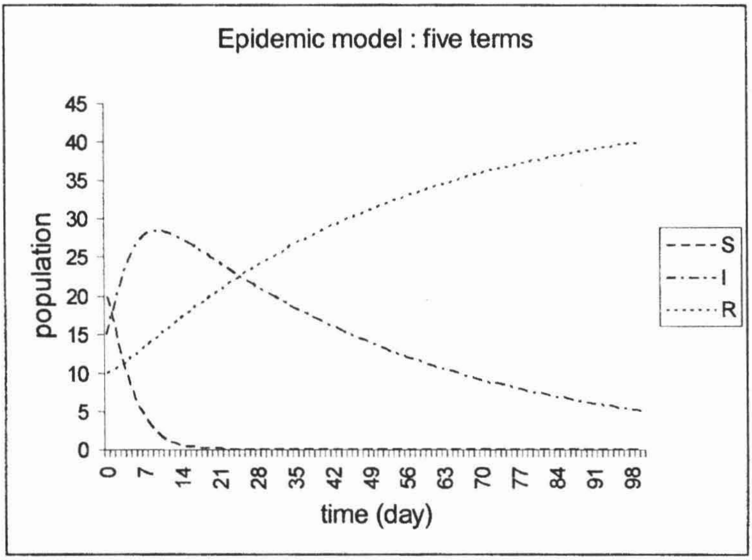

Fig.3: Plots of five approximations for *S*(*t*), *I*(*t*), *R*(*t*) versus time

As the plots show, the numbers of infectives increased until all the population caught by the disease and then decreased to zero. Meanwhile the number of the immune population increased. The results are more possible compare to Biazar (2005) because the number of susceptibles decreased to zero and never increased, which is agree with the earlier assumption.

We also employ the Maple's built-in fourth-order Runge-Kutta procedure `rk4` with time step $\Delta t = 0.01$, in our attempt to demonstrate the accuracy of the ADM solution. We choose this time step because from our previous calculation the time step $\Delta t = 0.01$ is sufficiently enough for our comparison purpose.

In tables 1 – 3, we present the absolute error between 3, 4 and 5-term ADM solutions at time step $\Delta t = 1.0$ and the RK4 solutions on time step $\Delta t = 0.01$. We can see that the maximum difference between the ADM solution and RK4 is in order of magnitude of 10^{-2}, which is still not accurate enough. Obviously, further improvement can be made on the ADM solution by taking a smaller time step and increasing the number of terms in the series solution. As shown in Table 4 the 10-term decomposition solutions on time step $\Delta t = 0.01$ agree with the RK4 solutions to at least 3 decimal places, which is more accurate from previous results. However, we note that, increasing the number of terms and taking smaller time step will increase the computational efforts.

Table 1: Differences between 3-term decomposition and RK4$_{0.01}$

	$\Delta = \lvert ADM_{1.0} - RK4_{0.01} \rvert$		
t	ΔS	ΔI	ΔR
10	-4.2490E-03	2.5193E-02	6.8094E-03
20	-8.3411E-04	6.5578E-03	9.3364E-03
30	-1.2097E-04	4.1436E-03	1.0348E-02
40	-2.1983E-05	3.2628E-03	1.1083E-02
50	-5.2258E-06	2.6514E-03	1.1672E-02
60	-1.5860E-06	2.1662E-03	1.2153E-02
70	-5.9323E-07	1.7719E-03	1.2546E-02
80	-2.6431E-07	1.4499E-03	1.2868E-02
90	-1.3612E-07	1.1865E-03	1.3131E-02
100	-7.9003E-08	9.7106E-04	1.3347E-02

Table 2: Differences between 4-term decomposition and RK4$_{0.01}$

	$\Delta = \lvert ADM_{1.0} - RK4_{0.01} \rvert$		
t	ΔS	ΔI	ΔR
10	-5.6847E-03	1.8770E-02	6.3310E-03
20	-4.4722E-04	9.5866E-04	7.6393E-03
30	-4.6348E-05	-9.6718E-05	7.6851E-03
40	-7.2462E-06	-1.5123E-04	7.6575E-03
50	-1.5928E-06	-1.3272E-04	7.6289E-03
60	-4.6172E-07	-1.1023E-04	7.6047E-03
70	-1.6768E-07	-9.0615E-05	7.5846E-03
80	-7.3200E-08	-7.4296E-05	7.5682E-03
90	-3.7142E-08	-6.0866E-05	7.5547E-03
100	-2.1314E-08	-4.9848E-05	7.5437E-03

Table 3: Differences between 5-term decomposition and $RK4_{0.01}$

	$\Delta = \lvert ADM_{1.0} - RK4_{0.01} \rvert$	
t	ΔS	ΔI
10	-5.4845E-03	1.8766E-02
20	-4.5645E-04	1.0707E-03
30	-4.9072E-05	-1.5686E-05
40	-7.8031E-06	-8.7049E-05
50	-1.7290E-06	-8.0572E-05
60	-5.0333E-07	-6.7621E-05
70	-1.8324E-07	-5.5755E-05
80	-8.0116E-08	-4.5765E-05
90	-4.0695E-08	-3.7512E-05
100	-2.3372E-08	-3.0730E-05

Table 4. Differences between 10-term $ADM_{0.01}$ and $RK4_{0.01}$

	$\Delta = \lvert ADM_{0.01} - RK4_{0.01} \rvert$	
t	ΔS	ΔI
10	-5.582E-05	1.918E-04
20	-4.966E-06	1.446E-05
30	-5.582E-07	2.667E-06
40	-9.096E-08	1.395E-06
50	-2.044E-08	1.040E-06
60	-6.001E-09	8.323E-07
70	-2.197E-09	6.764E-07
80	-9.643E-10	5.519E-07
90	-4.912E-10	4.510E-07
100	-2.827E-10	3.687E-07

Conclusion

In this work, the ADM was applied to the solution of epidemic model. Comparison between the decomposition solutions and the fourth-order Runge-Kutta numerical solutions were made. We conclude that, the ADM with diving subinterval will give more reliable solution compare to the standard ADM solutions (Biazar 2005). The accuracy of the decomposition solutions improve by taking smaller time step and increasing the term of the series.

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MAT SALIM SELAMAT, Mathematics and Statistics Department, Universiti Teknologi MARA Pahang.
matsalim@pahang.uitm.edu.my