

A Comparison Between Adomian Decomposition Method and Differential Transformation Method in Solving SIR Epidemic Model with Constant Vaccination

Farahanie Fauzi^{1*}, Muhammad Hanif Ngadiman², Muhammad Nur Zikry Norhisham³, Wan Khairiyah Hulaini Wan Ramli⁴ and Rahaidah Muhammad⁵

^{1,2,3,4,5}Faculty of Computer and Mathematical Sciences, Universiti Teknologi MARA Kelantan, Bukit Ilmu, Machang, Kelantan, Malaysia

*farah244@uitm.edu.my

Abstract: The trend of susceptible, infected and recovered of an epidemic can be mathematically analyzed if the solution of its SIR model is obtained. Various analytical and numerical methods were used by previous researchers in order to solve the model. Adomian Decomposition is one of the methods. However, several studies discovered that ADM is tedious and time consuming in solving certain kinds of problems. In this project, another method was used and compared to ADM in solving SIR model with the coverage of vaccination. The method was Differential Transformation Method (DTM). The main objective of this project is to analyse the difference between these two methods in the process of getting the final solution. It was identified that to get only one term of the polynomial solution model of SIR, ADM requires many iterations unlike DTM which only requires one iteration for each term of the polynomial solution model. However, in terms of overall polynomial model, ADM gives a higher degree of polynomial model compared to DTM for the same number of iteration.

Keywords: ADM, DTM, SIR Model.

1 Introduction

In order to analyze the number of infected cases for an epidemic, it is crucial to formulate the epidemic into a mathematical model first. Mathematical model that formulate an epidemic is SIR model that was first introduced by Kermack and McKendrick [1]. Since then, the SIR model is widely used and extended to analyze various types of epidemic diseases [2-4]. SIR stand for Susceptible – Infected – Recovered if the epidemic is the first category diseases and Susceptible – Infected – Removed if the epidemic is the second category diseases. The second category diseases are those who were infected die and leave the population. The examples of first category diseases are chicken pox and flu while second category diseases are HIV or the Bubonic Plague where the infected can be considered removed from a population as many infected cannot survive.

The SIR model is a system of ordinary differential equations (ODE) and it can be solved either by using numerical or analytical techniques. Since some differential equations cannot be solved accurately (analytic or closed form solution), hence numerical techniques are used in solving the equation by providing approximation to the solution. There are several types of numerical techniques that are used in solving differential equation and one of the methods is Adomian Decomposition Methods (ADM). Adomian Decomposition Method is a semi-analytical technique for solving nonlinear differential equation without the need of linearizing the problem and it is also a popular

method among mathematicians [5]. In the meantime, previous researchers have come out with another semi-analytical numerical technique which is Differential Transformation Method (DTM) [6].

The main objective of this project is to analyze the differences between Adomian Decomposition Method and Differential Transformation Method in solving a system of ordinary differential equations. In order to do that, these two methods were applied in solving SIR epidemic model with constant vaccination. This project only focuses on the procedure of performing the algorithm of ADM and DTM in solving SIR epidemic model with constant vaccination which was obtained from Makinde [2017].

2 SIR model with constant vaccination

The SIR model with vaccination of a population of susceptible (S), infected (I) and recovered (R) is governed by the following system of ordinary differential equations [5]:

$$\begin{aligned}\frac{dS}{dt} &= (1-P)\pi N - \beta \frac{SI}{N} - \mu S \\ \frac{dI}{dt} &= \beta \frac{SI}{N} - (\gamma + \mu)I \\ \frac{dR}{dt} &= P\pi N + \gamma I - \mu R\end{aligned}\tag{1}$$

At time t , summation of susceptible, infected and recovered is the total population size.

$$S(t) + I(t) + R(t) = N(t)\tag{2}$$

where,

β : the rate of infection

γ : the rate of recovery

μ : the death rate

π : the birth rate

S : the number of susceptible individuals

I : the number of infected individuals

R : the number of recovered individuals with total immunity

N : total population

P : the fraction of citizens vaccinated at birth each year.

A detailed description of the model and its dynamics can be found in Fred [7] and Sumera [3]. The population is assumed to has a constant size hence (2) can be normalized into $s + i + r = 1$ making the SIR model (1) converts to:

$$\begin{aligned}\frac{dS}{dt} &= (1-P)\pi - \beta si - \mu s \\ \frac{dI}{dt} &= \beta si - (\gamma + \mu)i \\ \frac{dR}{dt} &= P\pi + \gamma i - \mu r\end{aligned}\quad (3)$$

In analyzing the trends of susceptible, infected and recovered with the effect of vaccination, the solution for the above system is required. In the next subsection, the detailed procedure of solving the system using ADM and DTM will be explained.

3 Methodology

A Adomian Decomposition Method

Before solving the SIR model, it is crucial to transform the model into a form that match the ADM algorithm. As explained by Biazar et al. [8], Biazar [9] and Adomian [10], the equivalent canonical form of the SIR model is as follows:

$$\begin{aligned}s(t) &= s(0) + (1-P)\pi t - \beta \int_0^t si \, dt - \pi \int_0^t s \, dt \\ i(t) &= i(0) + \beta \int_0^t si \, dt - (\gamma + \pi) \int_0^t i \, dt \\ r(t) &= r(0) + P\pi t + \gamma \int_0^t i \, dt - \pi \int_0^t r \, dt\end{aligned}\quad (4)$$

The solutions of Eq. (4) are considered to be the following series

$$s = \sum_{n=0}^{\infty} s_n, \quad i = \sum_{n=0}^{\infty} i_n, \quad r = \sum_{n=0}^{\infty} r_n \quad (5)$$

$$si = \sum_{n=0}^{\infty} F_n(s_0, \dots, s_n, i_0, \dots, i_n) \quad (6)$$

where

and

$$F_n = \frac{1}{n!} \left[\frac{d^n \left(\sum_{k=0}^{\infty} s_k \lambda^k \right) \left(\sum_{k=0}^{\infty} i_k \lambda^k \right)}{d\lambda^n} \right]_{\lambda=0} \quad (7)$$

The non-linear function F_n is called Adomian's polynomial. Substituting (5)-(7) into (4) gives the solution of the SIR model as follows:

$$\begin{aligned} \sum_{n=0}^{\infty} s_n &= s(0) + (1-P)\pi t - \beta \int_0^t \sum_{n=0}^{\infty} F_n dt - \pi \int_0^t \sum_{n=0}^{\infty} s_n dt \\ \sum_{n=0}^{\infty} i_n &= i(0) + \beta \int_0^t \sum_{n=0}^{\infty} F_n dt - (\gamma + \pi) \int_0^t \sum_{n=0}^{\infty} i_n dt \\ \sum_{n=0}^{\infty} r_n &= r(0) + P\pi t + \gamma \int_0^t \sum_{n=0}^{\infty} i_n dt - \pi \int_0^t \sum_{n=0}^{\infty} r_n dt \end{aligned} \quad (8)$$

with initial conditions and iteration functions given in Eq. (9)

$$\begin{aligned} s_0 &= s(0) + (1-p)\pi t \\ i_0 &= i(0) \\ r_0 &= r(0) + P\pi t \\ s_{n+1} &= -\beta \int_0^t F_n dt - \pi \int_0^t s_n dt \\ i_{n+1} &= \beta \int_0^t F_n dt - (\gamma + \pi) \int_0^t i_n dt \\ r_{n+1} &= \gamma \int_0^t i_n dt - \pi \int_0^t r_n dt \end{aligned} \quad (9)$$

From (8) and (9), it can be seen that to obtain the final solution of the SIR model, many iterations are required to reduce the truncation error of the final solution. In order to reduce the calculation time, (8) and (9) are solved using *Maple* software. The final solution of SIR model with vaccination using ADM will be explained in the next section.

B Differential Transformation Method

According to Ibrahim and Moftah Ismail [2012] a differential transformation $y'(x)$ of function $y(x)$ is defined as follows:

$$y'(x) = \frac{1}{n!} \left[\frac{d^n y(x)}{dx^n} \right]_{x=0} \quad (10)$$

In Eq. (10), the original function $y(x)$ and the transformed function is $y'(x)$. The differential inverse transformation of $y'(x)$ is defined as follows:

$$y(x) = \sum_{n=0}^{\infty} x^n y'(x) \quad (11)$$

In fact, Eq. (12) can be obtained from equation (10) and (11)

$$y(x) = \sum_{n=0}^{\infty} \frac{x^n}{n!} \left[\frac{d^n y(x)}{dx^n} \right]_{x=0} \quad (12)$$

The concept of differential transformation is derived from Taylor series expansion implies on Eq. (12) above.

Like ADM, in order to solve a system, the system needs to be transformed into the form that DTM can recognize. By using fundamental operations of differential transformation method [11], the following recurrence relations of the SIR model with respect to time t are obtained.

$$\begin{aligned} S(n+1) &= \frac{1}{n+1} \left\{ (1-P)\pi\delta(n) - \beta \sum_{l=0}^n S(l)I(n-l) - \pi S(n) \right\} \\ I(n+1) &= \frac{1}{n+1} \left\{ \beta \sum_{l=0}^n S(l)I(n-l) - (\gamma + \pi)I(n) \right\} \\ R(n+1) &= \frac{1}{n+1} \left\{ P\pi\delta(n) + \gamma I(n) - \pi R(n) \right\} \end{aligned} \quad (13)$$

The recurrence relations (13) are the solutions for each population of susceptible, infected and recovered. In order to minimize the time required for calculating each iterations, the recurrence relations are solved using *Matlab* software.

C Analyzed Case

As for the constant parameters involved in the SIR model, the parameters vary depending on various measles situations in a population and vaccination coverage. In this project, all the parameter values were obtained from Makinde [2017]. According to Makinde [2017], $s(0)$ is the initial population of susceptible, $i(0)$ is initial population of the infected and $r(0)$ is initial population of the recovered. It is assumed that the population is in the early stage of being infected. The initial number of infected is assumed to be 20% of the total population that makes the initial number of susceptible with 80% of total population. The assumed rates of change from susceptible to infected and infected to recovered are 0.8 and 0.03, respectively. The birth rate of the population is assumed to be 0.4 ($\pi = 0.4$) and the fraction of citizens vaccinated each year is assumed to be 0.9 ($P = 0.9$) [5].

Table 1: The Value of Parameters

$s(0)$	$i(0)$	$r(0)$	β	γ	π	P
0.8	0.2	0	0.8	0.03	0.4	0.9

4 Results and Discussion

Adomian Decomposition Method gives a higher degree of polynomial solution compared to Differential Transformation Method for the same number of iteration. However, ADM needs several

iterations to get the coefficient for every term of the polynomial solution unlike DTM that only needs one iteration for each term. Each iteration of DTM works to calculate the coefficient for each term of the polynomial solution.

Table 2: The First 3 Iterations of ADM and DTM

Iteration	ADM	DTM
Initial condition	$S_0 = 0.8 + 0.04t$ $I_0 = 0.2$ $R_0 = 0.36t$	$S_0 = 0.8$ $I_0 = 0.2$ $R_0 = 0$
1 st iteration	$S_1 = 0.8 - 0.408t + 0.02t^2$ $I_1 = 0.2 - 0.086t$ $R_1 = 0.366t - 0.072t^2$	$S_1 = 0.8 - 0.408t$ $I_1 = 0.2 + 0.042t$ $R_1 = 0.366t$
2 nd iteration	$S_2 = 0.8 - 0.408t + 0.1008t^2 + 0.002667t^3$ $I_2 = 0.2 + 0.042t - 0.03698t^2$ $R_2 = 0.366t - 0.07257t^2 + 0.0096t^3$	$S_2 = 0.8 - 0.408t + 0.1008t^2$ $I_2 = 0.2 + 0.042t - 0.02823t^2$ $R_2 = 0.366t - 0.07257t^2$

From Table 2, it can be seen that for each iteration, ADM gives a higher degree of solution compared to DTM. It can be concluded that to achieve a certain accuracy in solving SIR model with vaccination, ADM is one step ahead of DTM. But in terms of method of solution, DTM is simpler than ADM because each iteration of ADM involves Adomian Polynomial which requires several integrations of polynomial. Here are the solutions obtained by using 4 iterations of ADM and DTM.

Solution given by ADM:

$$\begin{aligned}
 S(t) &= 0.8 - 0.408t + 0.1008t^2 - 0.008223999996t^3 + 0.0004602933334t^4 \\
 &\quad + 0.4846933334 \times 10^{-5}t^5 \\
 I(t) &= 0.2 + 0.042t - 0.02823t^2 - 0.001169699999t^3 - 0.00056432t^4 \\
 R(t) &= 0.366t - 0.07257t^2 + 0.0093937t^3 - 0.00096264t^4 + 1.536 \times 10^{-7}t^5
 \end{aligned} \tag{14}$$

Solution given by DTM:

$$\begin{aligned}
 S(t) &= 0.8 - 0.408t + 0.1008t^2 - 0.008223999996t^3 - 0.001811776t^4 \\
 I(t) &= 0.2 + 0.042t - 0.02823t^2 - 0.001169699999t^3 - 0.00275991875t^4 \\
 R(t) &= 0.366t - 0.07257t^2 + 0.0093937t^3 - 0.00094814275t^4
 \end{aligned} \tag{15}$$

Because ADM and DTM are both semi-analytical techniques, big number of iterations is required to increase the accuracy of the solution.

5 Conclusion and Recommendation

The Adomian Decomposition Method and Differential Transformation Method developed by previous researchers were tested on several examples. In this paper, these two methods were tested on SIR model with vaccination which is a set of ordinary differential equations. The obtained results show that both approaches can solve the equation effectively. It can be summarized that in order to solve this particular model, both methods have their own pros and cons characteristics.

Although ADM's solution is slightly different from the solution given by DTM, both solutions show that vaccination does contribute to the decreasing number of infected. This is proven by plotting Eq. (14) and (15) using the help of *Maple* software.

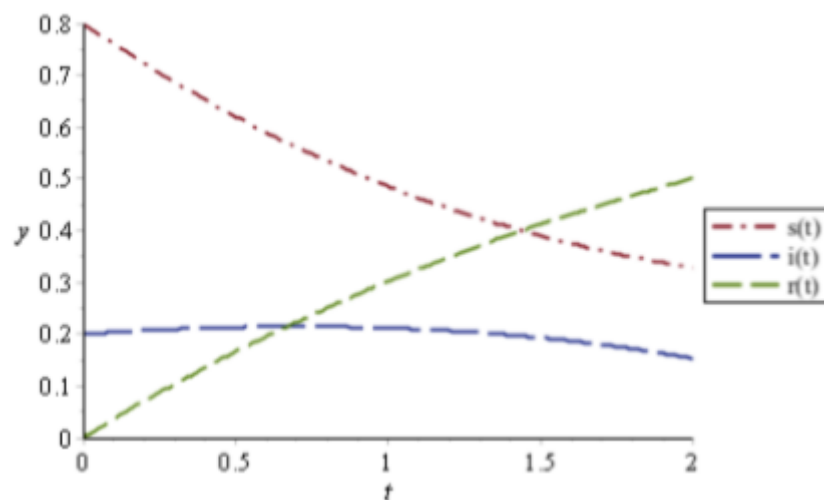


Figure 1: Solution given by ADM

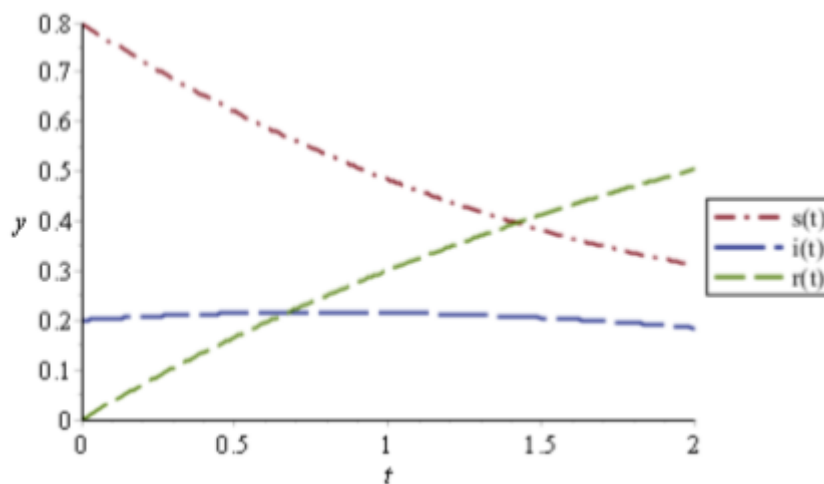


Figure 2: Solution given by DTM

When using numerical methods in finding approximate solutions of mathematical models, it is crucial to do analysis of error. The measurement of error gives the accuracy and precision of the approximate solution. Precision refers to how close the approximate values to the actual values. In order to determine the precision of both ADM and DTM's solutions, an experimental data is required to

analyse how close both solutions are to the actual situation. Therefore, it is recommended to conduct an analysis of error on both ADM and DTM's solutions for the next project.

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