Parameter Estimation of The SIR Model Using The Multistage Adomian Decomposition Method (MADM)

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Abstract. In epidemiology, the classic Susceptible-Infective-Removed (SIR) model is often used to give a simple representation of the spread of an infectious disease. There are two parameters involved, namely the transmission rate and the removal rate. Identifying these parameters is crucial in modeling any infectious disease because they indicate the severity of the epidemic. Various methods are available in identifying these parameters and this paper will attempt to explore the use of MADM in estimating these values. The MADM will give the solution of the SIR model as a series solution in time for each small subinterval \([0,t_1), [t_1, t_2), \ldots, [t_{n-1}, T],\) over the period \([0,T].\) This method is tested on a set of influenza data used in many published articles and the result obtained is analyzed. It is found that this method gives a fairly good estimate in finding the values of the parameters of an SIR model.

1 Introduction

Epidemiology is a study of the spread of a disease by looking at how it is distributed in the population and factors affecting the spread. Before an infectious disease becomes an epidemic, studies need to be carried out to understand the why and how the spread occurs so that it can be contained.

Mathematical modeling is a powerful tool that can be used to analyze and explain the spread of infectious. The simplest model available is by classifying the population into the susceptible \((S),\) infective \((I)\) and the recovered/removed \((R)\) classes, thus the SIR model. Taking these classes as compartments in a transfer diagram, Fig. 1 can be used to represent the change in the number of the population in each class.

Fig. 1. Transfer diagram of the SIR model
Susceptible individuals become infected upon coming into contact with infectious individuals with $\alpha$ as the transmission rate while the infected individuals recover from the disease at rate of $\beta$, with $\frac{1}{\beta}$ as the average recovery time. The dynamics of each class can be represented as a system of first order differential equation, known as the classic SIR model, as given by:

$$\frac{dS}{dt} = -\alpha SI,$$
$$\frac{dI}{dt} = \alpha SI - \beta I,$$
$$\frac{dR}{dt} = \beta I. \quad (1)$$

The initial conditions at $t = 0$ for each class are $S_0$, $I_0$ and $R_0$, respectively. If $N$ is the total population, then $S(t) + I(t) + R(t) = N$.

The threshold for most epidemic models is the basic reproduction number $R_0$, and it is defined as the average number of secondary infections produced when one infected individual is introduced into a population where everyone is susceptible [8]. Hence, if $R_0 > 1$, an epidemic will occur. For the system of differential equation (1), $R_0$ is equal to $\frac{S_0 \alpha}{\beta}$. Knowing the values of $\alpha$ and $\beta$ will enable us to determine how serious the disease is spreading.

For any given set of data of infected individuals, several methods are available in determining the parameters $\alpha$ and $\beta$. In this paper, we will attempt to estimate them by using the multistage Adomian decomposition method (MADM). The procedures will be tested on a set of an influenza data and the result obtained will be analyzed to determine the suitability of using MADM for this purpose.

## 2 Materials and methods

### 2.1 Basic principles of the Adomian decomposition method (ADM)

The Adomian decomposition method was first introduced in the early 1980s to be used in solving stochastic and deterministic problems in basic and applied sciences. The ADM gives analytical solution in terms of an infinite series and it can be obtained without linearization, perturbation, transformation or discretization [7].
Any differential equation can be represented as

\[ Lu + Ru + Nu = g, \]  

(2)

where \( L \) is the highest order derivative (order \( n \)) which is easily invertible. This makes \( L^{-1} \) to be the \( n \)-fold integration. \( R \) is a linear differential operator (order \( < n \)) while \( Nu \) is the nonlinear term [1]. Solving equation (2) for \( Lu \), and applying the inverse operator \( L^{-1} \) to both sides, with the given conditions, we will obtain

\[ u = a + L^{-1}g - L^{-1}(Ru) - L^{-1}(Nu). \]  

(3)

The term, \( a \), resulted from the given conditions [6]. The decomposition of the nonlinear terms \( Nu \) can be given as the infinite series

\[ Nu = \sum_{n=0}^{\infty} A_n. \]  

(4)

In equation (4), \( A_n \) is the Adomian polynomials and can be obtained for various nonlinear terms, as discussed by Wazwaz [10]. If \( u = \sum_{n=0}^{\infty} u_n \), then, equation (3) can be written as

\[ \sum_{n=0}^{\infty} u_n = a + L^{-1}g - L^{-1}R \sum_{n=0}^{\infty} u_n - L^{-1} \sum_{n=0}^{\infty} A_n. \]  

(5)

Equation (5) can thus be used as an approximate solution to equation (2).

### 2.2 Multistage Adomian Decomposition Method (MADM)

In using the above principle to solve a system of differential equations, the solution can be obtained by iterating each equation individually as done by Biazar et al. [2]. Generalizing these algorithms, Chowdhury et al. [3], Hashim et al. [7] and El-Tawil, et al. [5] used the MADM to solve various systems of equations.

However, the solution obtained through ADM will not be convergent globally. To overcome this, ADM is applied over successive time intervals \([0, t_1), [t_1, t_2), \ldots, [t_{m-1}, T]\) by dividing the time interval \([0, T]\) into \( m \) equal
subintervals with the initial condition in \([t^*, t_{m+1})\) is taken to be the condition at \(t^*\) [7]. As pointed out by Gonzalez-Parra \textit{et al.} [6], the main advantage of splitting the domain is that fewer series terms are required to get a good approximation in a small time interval.

Consider the general form of a system of differential equations given as follows:

\[
\sum_{j=1}^{n} a_{ij} X_{ij} + \sum_{p=1}^{n} \sum_{q=1}^{n} a_{pq} X_p X_q, \quad i = 1, 2, 3, \ldots, n. \tag{6}
\]

For all \(t \geq t^*\), Chowdhury \textit{et al.} [3] gives the general solution to equation (6) to be

\[
X_i(t) = \sum_{m=0}^{\infty} d_{im} \left(\frac{(t-t^*)^m}{m!}\right), \quad i = 1, 2, \ldots, n. \tag{7}
\]

The coefficients \(d_{im}\) are given to be \(d_{i0} = X_i(t^*)\), and

\[
d_{im} = \sum_{j=1}^{n} a_{ij} d_{j(m-1)} + (m-1)! \sum_{p=1}^{n} \sum_{q=1}^{n} \sum_{k=0}^{m-1} a_{pq} \frac{d_{pq}}{k!} \frac{d_{p(m-k-1)}}{k!(m-k-1)!}, \quad m \geq 1. \tag{8}
\]

Referring to the system of equation (1), we need to obtain the non-dimensionalized form of the equation by letting \(N = \frac{S}{N}, v = \frac{I}{N}, w = \frac{R}{N}\) where \(N\) is \((S + I + R)\) and \(t = \beta t\). Taking \(R_0 = \frac{\alpha N}{\beta}\), and the initial conditions equal to \(u(0) = u_0 = \frac{S_0}{N}, v(0) = v_0 = \frac{I_0}{N}\) and \(w(0) = w_0 = \frac{R_0}{N}\), we will get

\[
\frac{du}{dt} = -R_0 uv, \tag{9}
\]

\[
\frac{dv}{dt} = R_0 uv - v = (R_0 u - 1)v, \tag{9}
\]

\[
\frac{dw}{dt} = v.
\]
The solution obtained for the system of differential equation (9), based on the principle of MADM mentioned earlier, is given by equation (10-12) below. For any \( t \geq t^* \), we obtain

\[
\begin{align*}
    u(t) &= a_0 - R_0 a_0 b_0 (t - t^*) - R_0 (a_1 b_0 + a_0 b_1) \left( \frac{t - t^*}{2!} \right)^2 + \cdots, \\
    v(t) &= b_0 + (R_0 a_0 b_0 - b_0) (t - t^*) + [R_0 (a_1 b_0 + a_0 b_1) - b_1] \left( \frac{t - t^*}{2!} \right)^2 + \cdots, \\
    w(t) &= c_0 + b_0 (t - t^*) + b_1 \left( \frac{t - t^*}{2!} \right)^2 + \cdots.
\end{align*}
\]

In equations (10-12), \( a_0 = u(t^*) \), \( b_0 = v(t^*) \) and \( c_0 = w(t^*) \), while, for \( m \geq 1 \), we have

\[
\begin{align*}
    a_m &= -R_0 (m-1)! \sum_{k=0}^{m-1} \frac{a_k b_{(m-k-1)}}{k!(m-k-1)!}, \\
    b_m &= -b_{m-1} + R_0 (m-1)! \sum_{k=0}^{m-1} \frac{a_k b_{(m-k-1)}}{k!(m-k-1)!}, \\
    c_m &= b_{m-1}.
\end{align*}
\]

In the next section, we will use the solution obtained above to estimate the parameters in the SIR model.

### 2.3 Parameter estimation

One of the main results expected from the modeling process is the estimation of the parameter values. In the case of (1), the parameters are \( \alpha \) and \( \beta \). To simplify the estimation of these values, the non-dimensionalized form will be used with only one parameter, that is, \( R_0 \). In all cases of epidemics, the number of infectives will be recorded. Hence, the equation that can be used to identify the parameters, specifically for the epidemic in reference, will be the \( I(t) \) or \( v(t) \) (non-dimensionalized).

For the epidemic data available, in the interval \([t^*, t_{m+1}]\), the points \( I(t^*) \) and \( I(t_{m+1}) \) can be connected by a straight line. If \( m \) is the slope of the line, the equation can be written as

\[
I(t) - I(t^*) = m(t - t^*)
\]
or,
\[ I(t) = I(t^*) + m(t - t^*) . \]  
\( (13) \)

Comparing equations (11) and (13), we can see that
\[ I(t^*) = b_0 \text{ and } m = R_0a_0b_0 - b_0 . \]  
\( (14) \)

Equation (14) can be rewritten and solving for \( R_0 \) gives
\[ R_0 = \frac{m + b_0}{a_0b_0} . \]  
\( (15) \)

The data set available might be a daily data set, or weekly, or monthly. The length of the subinterval will then either be one day, or one week, or one month, respectively. For each of this subinterval, the slope of the line connecting the two consecutive points will be computed. Taking \( t^* \) to be the left end point of the subinterval, the values of \( R_0 \) can be computed for each subinterval.

In the classic SIR model, there are two parameters. They are \( \alpha \), the transmission rate, and \( \beta \), the recovery rate. The reciprocal of the recovery rate, \( \frac{1}{\beta} \), is equivalent to the duration of recovery of that particular disease. Equating the value obtained by equation (15) for each subinterval to \( \frac{\alpha N}{\beta} \), the first estimated value of \( \alpha \) can be obtained, based on the clinical or computed values of \( \frac{1}{\beta} \) of certain diseases published in the literature. Further simulation can be done to find a better \( \beta \), and thus \( \alpha \), for the particular set of data.

2.4 Application to an influenza data

In validating this proposed method, we used the set of data as provided by the Communicable Disease Surveillance Centre which is published in the British Medical Journal, 4 March 1978 [4]. It was regarding an influenza case which occurred in a boarding school of 763 students. It was reported that it started with one student who contacted the flu and the school recorded the progress of the spread for two weeks.

This set of data has been used by several articles to demonstrate an application of an SIR model. Murray stated that for this set of data, the values of parameter \( \alpha \) and \( \beta \) are 0.00218 and 0.44036, respectively [9]. These values will be used as a basis for comparison later.
The number of infective available was recorded daily and can be represented by the Fig. 2.

Fig. 2. Number of influenza cases in a boarding school
(Source: Communicable Disease Surveillance Centre, 1978)

For this set of data, the length of subinterval used will be one day and the slopes of straight lines in each subinterval are computed. To start the estimation of \( \alpha \), an assumed value of \( \beta \) will be used.

However, in using MADM, we discover that the values of \( \alpha \) fluctuate daily and on certain days, very drastically. To overcome this problem, the \( \alpha \) values over the period of 14 days is fitted to the sine function of the form

\[
\alpha(t) = a + b \sin(\alpha t + \phi).
\]  

(16)

The sine function is found to give a better fit when compared to the linear or quadratic fit.

These computed values of \( \alpha(t) \) and \( \beta \) are then used to solve equation (9) (modeled) using Runge-Kutta \((rkf45)\) package in Maple. These modeled values of infectives, \( v(t) \), are then compared to the actual set of data. The ones with the smaller mean square error (MSE) will be taken as a better estimate.

3 Result

In presenting the result obtained, we will first solve the non-dimensionalized SIR model, equation (9), using the values given in [9]. As mentioned earlier, MSE will be used in the analysis. Then, we will present the results obtained
when several assumed $\beta$ are used in MADM, and the transmission rate obtained is written as the sine function given by equation (16).

### 3.1 Case $\alpha = 0.00218$ and $\beta = 0.441$

Recall that, this parameter values are taken from [9] but the method used was not mentioned specifically, probably it is some form of curve fitting. Since this parameter values will be used as the basis for comparison, we will present the solution of equation (9) as in Fig. 3.

![Fig.3. Solution for the case $\alpha = 0.00218$ and $\beta = 0.441$](image)

The MSE value for this case is 0.0005175.

### 3.2 Case $\beta = 0.441$ and $\alpha$ as a sine function

In this case, we used the same value of $\beta$ as previously stated, but $\alpha$ is written as a sine function. For this case, with this value of $\beta$, we obtained a set of $\alpha$ values daily. As mentioned in the previous section, this set of values was written in the form given in equation (16). The function obtained is

$$\alpha(t) = 0.001196 + 0.002248 \sin(0.4488t - 0.0903). \quad (17)$$
The line graph in Fig. 4 represents the solution of $v(t)$ of equation (9) with $\beta$ equals 0.441 and the transmission rate is given as in equation (17), while the point plot represent the actual data. From the graph we can see that the estimate obtained when we use the MADM is not as good as the one obtained by Murray [9], but it will be an alternative method besides the curve fitting. The MSE value for this case is 0.002446.

### 3.3 Other values of $\beta$

The next step is to use several values of $\beta$ which are close enough to the one used by Murray. As above, using the MADM, the $\alpha$ values obtained are written as in equation (16). Table 1 below tabulates the different $\beta$ values used, and the MSE values.

<table>
<thead>
<tr>
<th>$\beta$</th>
<th>0.420</th>
<th>0.43</th>
<th>0.441</th>
<th>0.445</th>
<th>0.45</th>
</tr>
</thead>
<tbody>
<tr>
<td>MSE</td>
<td>0.002236</td>
<td>0.002201</td>
<td>0.002446</td>
<td>0.0036374</td>
<td>0.004043</td>
</tr>
</tbody>
</table>

From Table 1 we can see that, with MADM and $\alpha(t)$ as a sine function, we obtain 0.43 to be the best estimate for the value of $\beta$. Refining the values of $\beta$ to be in between 0.43 and 0.441 (3 decimal places) did not improve the estimates.
3.4 The basic reproduction number

As mentioned earlier, these parameter values are indicators of the severity of the epidemic and in epidemiology, the basic reproduction number $R_0 = \frac{S_0 \alpha}{\beta}$ is normally used. For the result obtained in section 3.3, the basic reproduction number for this influenza case is

$$R_0 = \frac{762}{0.43}(0.001194 + 0.002199 \sin(0.4488t - 0.0379)) .$$

The numerical values of $R_0$ can be simplified as follows:

$$R_0 = \begin{cases} 
1 & , t \leq 7 \\
0.5 & , t = 8 \\
<1 & , t \geq 9 
\end{cases}$$

Indirectly, the MADM method makes it possible to obtain $R_0$ for a smaller time interval.

4 Conclusion

The MADM is a decomposition method used in approximating solution of a system of ordinary differential equations. In this paper, we presented the possibility of this method being used to estimate the parameters in an SIR model. Although the estimates did not give accurate results yet it provides the detailed values for a smaller time interval. This method also serves as an alternative method in approximating parameters, besides the numerical and curve fitting methods.

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References