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Application of MADM in Identifying the Transmission Rate of Dengue fever: A Case Study of Shah Alam, Malaysia

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***Abstract*—**Identifying parameters in an epidemic model is one of the important aspect of modeling. In this paper, we suggest a method to identify the transmission rate by using the multistage Adomian decomposition method. As a case study, we use the data of the reported dengue fever cases in the city of Shah Alam, Malaysia. The result obtained fairly represents the actual situation. However, in the SIR model, this method serves as an alternative in parameter identification and enables us to make necessary analysis for a smaller interval.

***Keywords*—**dengue fever, multistage Adomian decomposition method, Shah Alam, SIR model

I. INTRODUCTION

DENGUE fever (DF) is now being classified as an endemic since it has affected populations in more than 100 tropical and sub-tropical countries throughout the world. Malaysia, a country located in Southeast Asia had its share of the reported DF cases. The increase from 41,486 cases of DF in 2009 to 46,171 in 2010 is quite alarming [1]. Out of 14 states in Malaysia, Selangor, which is located on the west coast of the peninsula, recorded the highest number, 18,676 in 2009 and 16,367 in 2010.

One of the methods in explaining the spread of any infectious disease is by using mathematical modeling. For diseases which are spread by infected human, the most comprehensive model is the Susceptible-Exposed-Infective-Recovered (*SEIR*) model [2]. However, in the transmission of DF, a vector is involved, namely the *Aedes* mosquitoes [2]. This type of infectious disease can be modeled using a vector-borne model. The model will have components of host (human) and vector (mosquito). Different combinations of classes of each component had been used by researchers in this area. The simplest vector-borne model comprises of the S-I-R for host and S-I for vector, as used by Esteva and Vargas [3] and Derouich, Boutayeb and Twizell [4]. However, for demonstration, in this paper, we will use the classic SIR model.

The Adomian decomposition method (ADM) is suitable in finding an infinite series solution to a differential equation, or a system of differential equations. However, the solution of the SIR model, or any system of differential equation, is only accurate for a small time *t* [9]. The multistage ADM (MADM) was developed to be used when a large time t is involved by applying ADM over successive time intervals [6]. The method was used to solve a predator-prey model [6], Lorenz system [7], and an epidemic model [5].

One important aspect of modeling is the parameter identification. For the classic SIR model, the most common method used is the numerical method by various curve-fitting techniques. Manseur and Messaoudi used a combination of ADM and Alienor method to identify parameter in an epidemic model for HIV [8]. In this paper, we will attempt to use the MADM to find the value of a parameter in the SIR model for DF.

This paper will describe the SIR model in the next section, followed by the MADM. The following section will demonstrate the use of proposed steps on the DF cases data of Shah Alam, Malaysia. The section on result and discussion, follows, with conclusion as the final section.

II. *SIR* EPIDEMIC MODEL

As mentioned earlier, the simplest epidemic model available is 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.

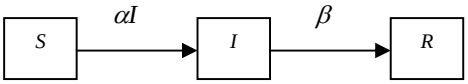

Fig. 1 Transfer diagram of the *SIR* model

Susceptible individuals become infected upon coming into contact with infectious individuals with α as the transmission rate while the infected individuals recover from the disease at rate of β, with $1/\beta$ as the average recovery time. The dynamics of each class can be represented as a system of first-

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order differential equation, known as the classic SIR model, as given by:

$$\begin{aligned} \frac{dS}{d\tau} &= -\alpha SI \,, \\ \frac{dI}{d\tau} &= \alpha SI - \beta I \,, \\ \frac{dR}{d\tau} &= \beta I \,. \end{aligned} \tag{1}$$

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

The threshold for most epidemic models is the basic reproduction number $\mathcal{R}_0$, 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* [2]. Hence, if $\mathcal{R}_0 > 1$, an epidemic will occur. For the system of differential equations (1), $\mathcal{R}_0$ is equal to $S_0\alpha/\beta$. Knowing the values of α and β will enable us to determine how serious the disease is spreading.

III. Identifying Parameters Using MADM

The most important part in a modeling process is to determine the values of parameters involved. Common method used in achieving this is by using the numerical method (curve fitting). Although MADM is normally used to find the solution to a differential equation or system of differential equations, we will attempt to use it to identify parameters.

A. Basic Principle of 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

$$Lu + Ru + Nu = g \,, \tag{2}$$

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 [9]. Solving (2) for Lu, and applying the inverse operator L^{-1} to both sides, with the given conditions, we will obtain

$$u = \varphi + L^{-1}g - L^{-1}(Ru) - L^{-1}(Nu). \tag{3}$$

The term, φ, arises from the given conditions [5]. The decomposition of the nonlinear terms Nu can be given as the infinite series

$$Nu = \sum_{n=0}^{\infty} A_n \,. \tag{4}$$

In (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, (3) can be written as

$$\sum_{n=0}^{\infty} u_n = a + L^{-1}g - L^{-1}R\sum_{n=0}^{\infty} u_n - L^{-1}\sum_{n=0}^{\infty} A_n \,. \tag{5}$$

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

B. Multistage ADM

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*. [11]. Generalizing these algorithms, Chowdhury *et al.* [6], Hashim *et al*. [7] and El-Tawil, *et al.* [12] 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 $[t^*, t_{k+1})$ is taken to be the condition at t^* [7]. As pointed out by Gonzalez-Parra *et al*. [5], 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:

$$X_i' = \sum_{j=1}^{n} a_{ij} X_{ij} + \sum_{p=1}^{n}\sum_{q=1}^{n} a_{ipq} X_p X_q \,, \quad i = 1,2,3,\ldots,n. \tag{6}$$

For all $t \geq t^*$, Chowdhury *et al*. [6] gives the general solution to (6) to be

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

The coefficients d_{im} are given as $d_{i0} = X_i(t^*)$, and

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

Referring to (1), we need to obtain the non-dimensionalized form of the equation by letting $u = \frac{S}{N}, v = \frac{I}{N}, w = \frac{R}{N}$ where N is ($S + I + R$) and $t = \beta\tau$. 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

$$\begin{aligned} \frac{du}{dt} &= -R_0 uv, \\ \frac{dv}{dt} &= R_0 uv - v = (R_0 u - 1)v, \\ \frac{dw}{dt} &= v. \end{aligned} \tag{9}$$

The solution obtained for (9), based on the principle of MADM mentioned earlier, is given by (10)-(12). For any $t \geq t^*$, we obtain

$$u(t) = a_0 - R_0 a_0 b_0 (t - t^*) - R_0 (a_1 b_0 + a_0 b_1) \frac{(t-t^*)^2}{2!} + \cdots, \tag{10}$$

$$v(t) = b_0 + (R_0 a_0 b_0 - b_0)(t - t^*) + [R_0 (a_1 b_0 + a_0 b_1) - b_1] \frac{(t-t^*)^2}{2!} + \cdots, \tag{11}$$

$$w(t) = c_0 + b_0 (t - t^*) + b_1 \frac{(t-t^*)^2}{2!} + \cdots. \tag{12}$$

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

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

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

C. Parameter Identification

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 α and β. 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 infective will be recorded. Hence, the equation that can be used to identify the parameters, specifically for the epidemic in reference, will be $v(t) = \frac{I}{N}$.

For the epidemic data available, in the interval [t^*, t_{m+1}), the points $v(t^*)$ and $v(t_{m+1})$ can be connected by a straight line, as given in Fig. 2.

If m is the slope of the line, the equation can be written as

$$v(t) = v(t^*) + m(t - t^*). \tag{13}$$

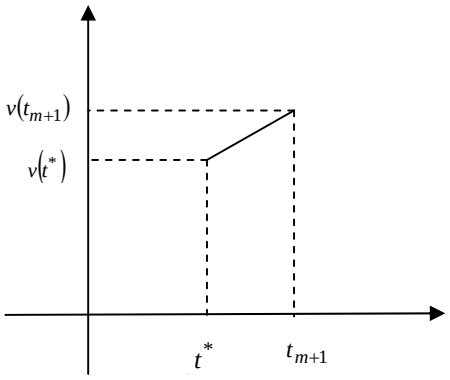

Fig. 2 Graph of data in subinterval [t^*, t_{m+1})

Comparing (11) and (13), we can see that

$$v(t^*) = b_0,$$

and,

$$m = R_0 a_0 b_0 - b_0. \tag{14}$$

Equation (14) can be rewritten and solved for R_0 to give us

$$R_0 = \frac{m + b_0}{a_0 b_0}. \tag{15}$$

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 with $u(t^*) = a_0$ and $v(t^*) = b_0$.

In the classic *SIR* model, the parameters are α, the transmission rate, and β, the recovery rate. The reciprocal of the recovery rate, $1/\beta$, is equivalent to the duration of recovery of that particular disease. Recall that $R_0 = \frac{\alpha N}{\beta}$. Equating the value obtained by (15) for each subinterval to $\alpha N/\beta$, an estimated value of α is obtained, based on the clinical or computed values of $1/\beta$ of the particular diseases, as published in the literature.

To check the suitability of the parameter values obtained, they are substituted back into the classic SIR model given by (1) and the system of equation is solved using Runge-Kutta (*rkf45*) package in Maple. Although this method does not give a very accurate result, it enables us to obtain a detailed threshold values in a smaller intervals as given in our earlier work [13].

IV. Application on DF Cases in Shah Alam, Malaysia

In this paper we concentrated on the identification of the transmission rate based on the reported DF cases in Shah Alam. The data was obtained from the Shah Alam City Council (*MBSA – Majlis Bandaraya Shah Alam*) for years 2006 until 2009. It was recorded weekly, from epidemic week 1 (first week of January) until epidemic week 52 (last week of December) for each year. The number of cases used is the total number of DF and dengue hemorrhagic fever (DHF), as recorded by the *MBSA*. The distribution of the new DF cases recorded for years 2006-2009 is given in Fig. 3.

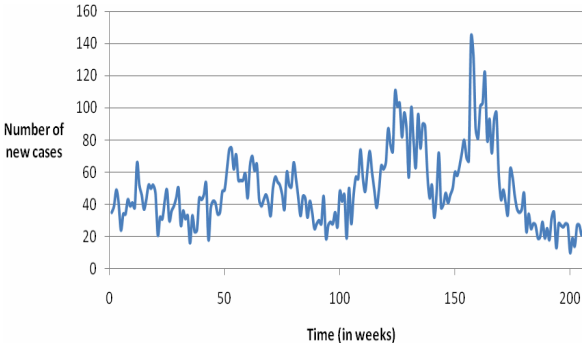

Fig. 3 Reported new DF cases in Shah Alam in 2006-2009

The total number of population of Shah Alam (N) is taken to be 500,000. In this study, we assume the population remains constant during these four years. We also assume that, once the population is infected and recovered, they will remain in the recovered class (R). For the value of β, which is the recovery rate of DF, we used the value 0.143, which is the accepted value as used in article by Burattini *et al.* [14],

We calculated α for each epidemic week using the steps outlined in the above section. Since we are using the non-dimensionalized form of the *SIR* model, the time unit is in days and the length of the interval was taken to be seven days (one week).

V. Result and Discussion

As pointed out earlier, DF is a vector-borne disease but in this paper, we are using the classic *SIR* model to demonstrate the use of MADM in finding the transmission rate. The result will be presented as two cases of α, a constant and a sine function.

A. α as a constant

When α was computed for the duration of four years, the values fluctuated each week, varying from 2.59×10^{-7} to 3.53×10^{-7}. The yearly average is given in Table 1.

TABLE I
AVERAGE OF TRANSMISSION RATE α

Year	Average α (10^{-7})
2006	2.89508
2007	2.89796
2008	2.91327
2009	2.94110

The overall average for the duration of four years is equal to 2.912×10^{-7}. Fig. 4 shows the comparison of the solution of the model using this average value for α with the actual data.

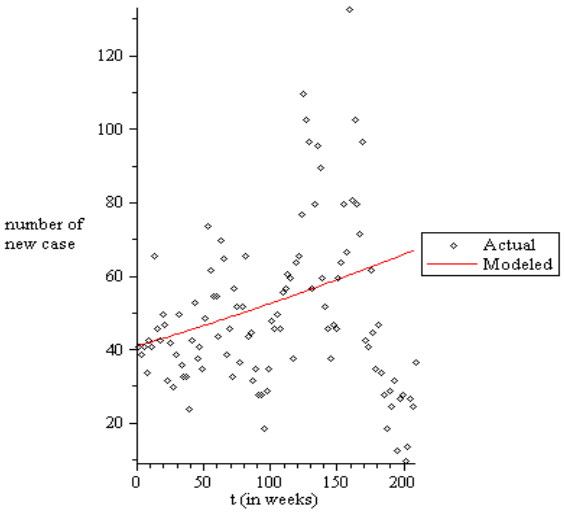

Fig. 4 Solution using α as a constant

With the average value of α, we find out that the modeled solution obtained indicates that the number of new cases increases as time increases. This does not agree with the actual data where the number of new cases decreases in the last 20 weeks.

For this average value of α, we obtain the basic reproduction number R_0 to be equal to 1.018. By taking this average value, the threshold value indicates that in Shah Alam dengue is an epidemic all year round. However, when α is at its lowest, R_0 is found to be 0.906, and this indicates that

dengue is not an epidemic.

B. α as a sine function

From the graph in Fig. 3 we can see that the occurrence of new dengue cases fluctuates a lot. One approach that we opted was to write α as a sine function. It will be of the form given by (16).

$$\alpha(t) = a + b_1 \sin(\omega t + \phi_1) \tag{16}$$

It will be referred to as the first harmonic sine function. Sine function representation for the values of α for each year was obtained. With this approach, we allow one peak and one trough in each year. The four sine functions of $\alpha(t)$ then was written as a piecewise function, substituted into (1) and solved using the Runge-Kutta (*rkf45*) package in Maple. The solution obtained, in comparison with the actual data, is shown in Fig. 5.

From the graph, the solution indicates the new cases increases, but not as fast as when we used α as a constant (the slope is smaller). In fact, the curve of the solution is sinusoidal although the peaks and troughs are not so distinct.

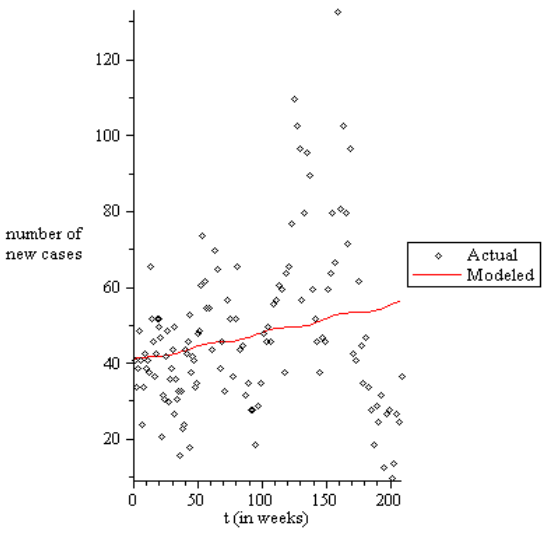

Fig. 5 Solution using α as first harmonic sine function

We are also interested to see if the solution will improve if we are to have two peaks and two troughs in one year. Hence, we need to write α in the form given by (17).

$$\alpha(t) = a + b_1 \sin(\omega t + \phi_1) + b_2 \sin(2\omega t + \phi_2) \tag{17}$$

Equation (17) is referred to as the second harmonic sine function. Repeating the steps used for the first harmonic, the solution is given in Fig. 6.

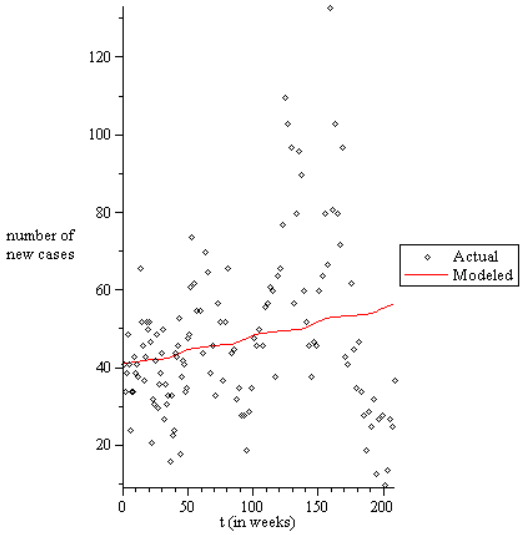

Fig. 6 Solution using α as second harmonic sine function

As shown by the graph in Fig. 6, increasing the peaks and troughs of α does not improve the solution. Again, the solution is sinusoidal with more peaks and trough, as compared to the solution when first harmonic sine function was used.

For this paper, we only attempted until the second harmonic. The threshold values are not computed for these cases due to the complexity of the piecewise functions of both the first and second harmonic sine function of the α values.

VI. Conclusion

In this paper we have given the detailed steps taken on how we use the MADM to identify the transmission rate of the dengue fever, taking Shah Alam, Malaysia as the case study. The results obtained were not as accurate as we like them. The reason of the inaccuracy is due the classic *SIR* model used, instead of the vector-borne epidemic model.

Part of our future work will be to see whether there will be any improvement in the result if higher harmonic terms are used for the sine function in representing the transmission rate. We will also attempt to identify the transmission rate for this same case by using the vector-borne epidemic model.

References

[1] Ministry of Health, Malaysia. (2011, January 06). Dengue Fever and Chikugunya situation in Malaysia. Retrieved January 25, 2011, from Ministry of Health, Malaysia: http://www.moh.gov.my/press_release/96

[2] H. Hethcote, "The Mathematics of Infectious Diseases," SIAM Review, vol. 42, no. 4, pp. 599-653, 2000.

[3] L. Esteva and C. Vargas, "Coexistence of different serotypes of dengue virus," Journal of Mathematical Biology , vol. 46, pp. 31-47, 2003.

[4] M. Derouich, A. Boutayeb, and E. Twizell, " A model of dengue fever," BioMedical Engineering OnLine, vol. 2:4, pp. 1-10, Feb. 2003.

[5] G. Gonzalez-Parra, A. J. Arenas, and L. Jodar, " Piecewise Finite Series Solutions of Seasonal Disease Models using Multistage Adomian Method," Communications in Nonlinear Science and Numerical Simulation , vol. 14, pp. 3967-3977, 2009.

[6] M. Chowdhury, I. Hashim, and S. Mawa, " Solution of prey-predator problem by numeric-analytic technique," Nonlinear Science and Numerical Simulation , vol. 14, pp. 1008-1012, 2009.

[7] I. Hashim, M. Noorani, R. Ahmad, S. Bakar, E. Ismail, and A. Zakaria, "Accuracy of the Adomian decomposition method applied to the Lorenz system," Chaos, Soliton and Fractals , vol. 28, pp. 1149-1159, 2006.
[8] S. Manseur, N. Messaoudi, and Y. Cherrualt, " Parameter identification of an HIV model by the combined Adomian/Alienor method," Kybernetes , vol. 35 (10), pp. 1725-1734, 2006.
[9] G. Adomian, Solving frontier problems of physics: The decomposition method. Boston: Kluwer Academic Publishers, 1994.
[10] A. M. Wazwaz, " A new algorithm for calculating Adomian polynomials for nonlinear operators," Applied Mathematics and Computation , vol. 111, pp. 53-69, 2000.
[11] J. Biazar, " Solution of the epidemic model by Adomian decomposition method," Applied Mathematics and Computation , vol. 173, pp.1101-1106, 2006.
[12] M. A. El-Tawil, A. A. Bahnasawi, and A. Abdel-Naby, " Solving Riccati differential equation using Adomian's decomposition method," Applied Mathematics and Computation , vol. 157, pp. 503-514, 2004.N. Yusoff, H. Budin, ans S. Ismail, "Parameter estimation of the SIR model using the multistage Adomian decomposition method (MADM)" in Proceedings of the 6th IMT-GT International Conference on Mathematics, Statistics and its Applications (ICMSA 2010), 2010, pp.635-645
[13] M. Burattini, M. Chen, A. Chow, F. Coutinho, K. Goh, Lopez, et al., "Modelling the control strategies against dengue in Singapore," Epidemiology and Infection , vol. 136, pp. 309-319, 2008.

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