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Comments on "The Solution of a Mathematical Model for Dengue Fever Transmission Using Differential Transformation Method: J. Nig. Soc. Phys. Sci. **1** (2019) 82-87"

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Abstract

The mathematical model for dengue fever transmission studied by [1], has been re-investigated. The differential transformation method (DTM) is used to compute the semi-analytical solutions of the non-linear differential equations of the compartment (SIR) model of dengue fever. This epidemiology problem is well-posed. The effect of treatment as a control measure is studied through the growth equations of exposed and infected humans. The inadvertent errors in the recurrence relations (DTM) of equations for dengue disease transmission including initial conditions have been removed. Furthermore, the semi-analytic solutions of the model are obtained and verified with the built-in function `AsymptoticDSolveValue` of Wolfram Mathematica. It has been found that results obtained from the DTM are valid only for small-time t ($t < 1.5$), as t becomes large, the human population (exposed and recovered) and infected vector population become negative.

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1. Introduction

Dengue fever is a mosquito-borne flavivirus that is mostly found in tropical and sub-tropical regions of the world. The disease is spread by Aedes mosquito due to day-biting [2]. Dengue fever is the fastest-spreading vector-borne viral disease affecting 40 per cent of the world's population, and now endemic in over 100 countries. Over the last two decades, the number of dengue cases registered to WHO has increased from 505,430 cases in 2000 to over 2.4 million in 2010, and 4.2 million in 2019. Between 2000 and 2015, the number of registered deaths increased from 960 to 4032 [3]. A second potential vector, Aedes Albopictus, resides in temperate regions (North America and Europe), where it may give rise to occasional dengue outbreaks [4, 5].

The spread of infectious diseases is studied through various epidemiological models, including observational studies, interventional studies apart from mathematical modelling using the compartment model [6]. The pioneering work using the SIR model for contagious diseases is done by [7, 8, 9]. In the compartment model, the population is primarily divided into three distinct mutually exclusive compartments: susceptible $S(t)$, infected/infectious $I(t)$ and recovered $R(t)$ at any

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time t, based on the epidemiological status of the population [10].

For the first time, the DTM was used for solving electrical circuit problems [11]. The application of DTM in finding solutions for the set of non-linear ordinary differential equations obtained using the SIR model for various epidemiological diseases including Typhoid [12, 13], Malaria [14] and seasonal diseases [15] has been studied. In this SIR model for dengue disease, we consider two separate but dependent sets of non-linear ordinary differential equations related to human and vector population [16, 17]. The purpose of this paper is to find semi-analytical solutions to the dengue fever (SIR) model including the effect of treatment as a measure of control. The semi-analytic solutions are obtained by using the differential transform method (DTM) and are confirmed by using a built-in function: `AsymptoticDSolveValue` of Wolfram Mathematica and are discussed graphically also.

The paper is organized in the following sections: In section 2, the SIR model for dengue fever with model parameters including treatment is briefly described. The existence, uniqueness and positivity of the solution to the epidemiology problem are discussed in Section 3. Section 4 presents a theoretical concept and implementation of DTM. In Section 5, numerical solutions are obtained with a graphical discussion. Finally, concluding remarks in section 6.

2. Formulation of the Problem

Two sets of populations consisting of human and vector are considered in Figure 1. The population is divided into some mutually exclusive compartments as given below. The total human population is divided into the following mutually exclusive epidemiological classes: susceptible humans $S_h(t)$, humans with dengue in latent stage $E_h(t)$, humans infected with dengue $I_h(t)$, humans treated for dengue $R_h(t)$ (recovered), while the vector population is divided into three classes: susceptible vectors $S_v(t)$, vectors with dengue in latent stage $E_v(t)$, vectors with dengue $I_v(t)$. The class of treated vectors ($R_v(t)$) is not taken into consideration. Let $N_h(t)$ and $N_v(t)$ denote the total number of humans and vectors at time t, respectively. Hence, we have that, $N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$ and $N_v(t) = S_v(t) + E_v(t) + I_v(t)$, where $N_h(t) > 0, N_v(t) > 0, S_h(t) > 0, S_v(t) > 0, E_h(t) \geq 0, I_h(t) \geq 0, R_h(t) \geq 0, E_v(t) \geq 0, I_v(t) \geq 0$.

The susceptible humans are recruited at a rate Λ_h, while the susceptible vectors are recruited at a rate Λ_v. The susceptible humans' contract to dengue at a rate:

$$\lambda_{DV} = \frac{\beta_{vh}(\eta_v E_v + I_v)}{N_h}, \tag{1}$$

where $\eta_v < 1$, this accounts for the relative infectiousness of vectors with latent dengue E_v compared to vectors in the I_v class. Susceptible vectors acquire dengue infection from infected humans (infected blood is passed to a vector through a bite) at a rate:

$$\lambda_{DH} = \frac{\beta_{hv}(\eta_A E_h + \eta_B I_h)}{N_h}, \tag{2}$$

where $\eta_A < \eta_B$ this accounts for the relative infectiousness of humans with latent dengue E_h compared to humans in the I_h class [1].

The model equations for dengue disease transmission including treatment as a control measure are:

$$\frac{dS_h}{dt} = \Lambda_h - \mu_h S_h - \lambda_{DV} S_h, \tag{3}$$

$$\frac{dE_h}{dt} = \lambda_{DV} S_h - (\gamma_h + \mu_h) E_h, \tag{4}$$

$$\frac{dI_h}{dt} = \gamma_h E_h - (\tau_h + \mu_h + \delta_{Dh}) I_h, \tag{5}$$

$$\frac{dR_h}{dt} = \tau_h I_h - \mu_h R_h, \tag{6}$$

$$\frac{dS_v}{dt} = \Lambda_v - \mu_v S_v - \lambda_{DH} S_v, \tag{7}$$

$$\frac{dE_v}{dt} = \lambda_{DH} S_v - (\gamma_v + \mu_v) E_v, \tag{8}$$

$$\frac{dI_v}{dt} = \gamma_v E_v - (\mu_v + \delta_{Dv}) I_v, \tag{9}$$

where Λ_h,Λ_v are the recruitment rates and μ_h, μ_v are natural death rates of susceptible human and vector population, respectively. β_{vh} and β_{hv} are the effective contact rate for dengue from vectors to humans and humans to vectors, respectively. The treatment rate for infected humans is τ_h. γ_h and γ_v are the progression rate of the human and vector population from the latent class (exposed) to the active dengue class, respectively. The disease induced deaths in human and vector are denoted by δ_{Dh} and δ_{Dv}. η_v, η_A, η_B are the modification parameters of E_v, E_h and I_h, respectively.

3. Existence, Uniqueness and Positivity of Solution

We will use the Lipchitz condition to verify the existence and uniqueness of solution [18] for the model equations (3)-(9):

$$\begin{aligned}
E_1 &= \Lambda_h - \mu_h S_h - \lambda_{DV} S_h,\\
E_2 &= \lambda_{DV} S_h - (\gamma_h + \mu_h) E_h,\\
E_3 &= \gamma_h E_h - (\tau_h + \mu_h + \delta_{Dh}) I_h,\\
E_4 &= \tau_h I_h - \mu_h R_h,\\
E_5 &= \Lambda_v - \mu_v S_v - \lambda_{DH} S_v,\\
E_6 &= \lambda_{DH} S_v - (\gamma_v + \mu_v) E_v,\\
E_7 &= \gamma_v E_v - (\mu_v + \delta_{Dv}) I_v.
\end{aligned}$$

Let B denote the region, $|t - t_0| \leq \delta, ||x - x_0|| \leq \alpha$, where $x = (x_1, x_2, \ldots x_n)$, $x_0 = (x_{10}, x_{20}, \ldots x_{n0})$ also suppose that $a(t, x)$ satisfies the Lipschitz condition:

$$||a(t, x_1) - a(t, x_2)|| \leq k||x_1 - x_2||$$

whenever the pairs $(t, x_1), (t, x_2)$ belong to B where k is a positive constant, then there is a positive constant $\delta \geq 0$, such that there exists a unique and continuous vector solution $x(t)$ of

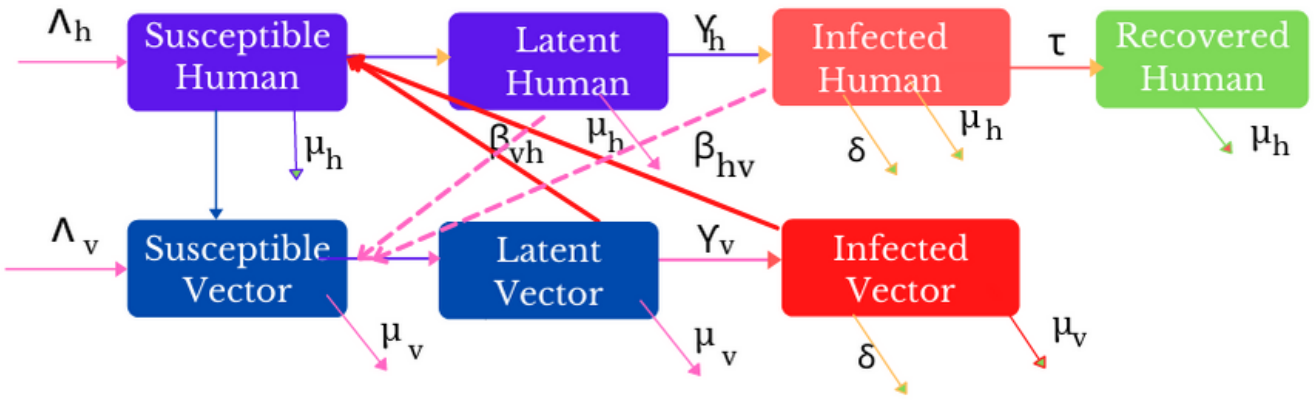

Figure 1: Dengue Fever Model

the system in the interval $|t-t_0|<\delta$. The condition is satisfied by the requirement that $\frac{\partial a_i}{\partial x_j}, i,j=1,2,3,..n$, be continuous and bounded in B. Considering the model equation (3)-(9), we are interested in the region $0 \le \alpha \le R$ [13].
Let B denote the region $0 \le \alpha \le R$, then equations (3) – (9) will have a unique solution if $\frac{\partial a_i}{\partial x_j}, i,j=1,2,3,..7$ are continuous and bounded in B.
For E_1:

$$\left|\frac{\partial E_1}{\partial S_h}\right| = |-(\mu_h+\lambda_{DV})| < \infty, \left|\frac{\partial E_1}{\partial E_h}\right| = 0 < \infty, \left|\frac{\partial E_1}{\partial I_h}\right| = 0 < \infty,$$
$$\left|\frac{\partial E_1}{\partial R_h}\right| = 0 < \infty, \left|\frac{\partial E_1}{\partial S_v}\right| = 0 < \infty, \left|\frac{\partial E_1}{\partial E_v}\right| = 0 < \infty, \left|\frac{\partial E_1}{\partial I_v}\right| = 0 < \infty.$$

For E_2:

$$\left|\frac{\partial E_2}{\partial S_h}\right| = |\lambda_{DV}| < \infty, \left|\frac{\partial E_2}{\partial E_h}\right| = |-(\gamma_h+\mu_h)| < \infty, \left|\frac{\partial E_2}{\partial I_h}\right| = 0 < \infty,$$
$$\left|\frac{\partial E_2}{\partial R_h}\right| = 0 < \infty, \left|\frac{\partial E_2}{\partial S_v}\right| = 0 < \infty, \left|\frac{\partial E_2}{\partial E_v}\right| = 0 < \infty, \left|\frac{\partial E_2}{\partial I_v}\right| = 0 < \infty.$$

For E_3:

$$\left|\frac{\partial E_3}{\partial S_h}\right| = 0 < \infty, \left|\frac{\partial E_3}{\partial E_h}\right| = |\gamma_h| < \infty,$$
$$\left|\frac{\partial E_3}{\partial I_h}\right| = |-(\tau_h+\mu_h+\delta_{Dh})| < \infty,$$
$$\left|\frac{\partial E_3}{\partial R_h}\right| = 0 < \infty, \left|\frac{\partial E_3}{\partial S_v}\right| = 0 < \infty, \left|\frac{\partial E_3}{\partial E_v}\right| = 0 < \infty, \left|\frac{\partial E_3}{\partial I_v}\right| = 0 < \infty.$$

For E_4:

$$\left|\frac{\partial E_4}{\partial S_h}\right| = 0 < \infty, \left|\frac{\partial E_4}{\partial E_h}\right| = 0 < \infty, \left|\frac{\partial E_4}{\partial I_h}\right| = |\tau_h| < \infty,$$
$$\left|\frac{\partial E_4}{\partial R_h}\right| = |-\mu_h| < \infty, \left|\frac{\partial E_4}{\partial S_v}\right| = 0 < \infty, \left|\frac{\partial E_4}{\partial E_v}\right| = 0 < \infty,$$
$$\left|\frac{\partial E_4}{\partial I_v}\right| = 0 < \infty.$$

These partial derivatives exist, are continuous and bounded, similarly for E_5, E_6, E_7. Hence the model has a unique solution. The positivity of the solution is presented in the following theorems:

Positivity of the Solution: We show that the model equations (3)–(9) are biologically and epidemiologically meaningful and well-posed as the solutions of all the stated variables are non-negative [16].
If $S_h(0)>0, E_h(0)\ge 0, I_h(0)\ge 0, R_h(0)\ge 0, S_v(0)>0, E_v(0)\ge 0$ and $I_v(0)\ge 0$, then the solution region $S_h(t)$, $E_h(t)$, $I_h(t)$, $R_h(t)$, $S_v(t)$, $E_v(t)$ and $I_v(t)$ of the system of equations (3)–(9) is always non-negative.
We consider each differential equation separately and show that its solution is positive.

Theorem 1: Positivity of susceptible human population: Consider the differential equation (3):

$$\frac{dS_h}{dt} = \Lambda_h - (\mu_h+\lambda_{DV})S_h(t) \ge -(\mu_h+\lambda_{DV})S_h(t),$$

$\Lambda_h > 0$ being recruitment rate of humans, we can write as:

$$\frac{dS_h}{S_h} = -(\mu_h+\lambda_{DV})dt$$

On integrating, the solution is $S_h = S_{h0}e^{-\int_0^t(\mu_h+\lambda_{DV})dt}$. It is clear from the solution that $S_h(t)$ is positive since $S_{h0}=S_h(0)>0$ and the exponential function is always positive.

Theorem 2: Positivity of latent human population: Consider the differential equation (4):

$$\frac{dE_h}{dt} = \lambda_{DH}S_h(t) - (\gamma_h+\mu_h)E_h(t) \ge -(\gamma_h+\mu_h)E_h(t),$$

$S_h(t)$ is positive in time t and $\lambda_{DH}>0$ being humans' contract rate to dengue, we can write as:

$$\frac{dE_h}{E_h} = -(\gamma_h+\mu_h)dt.$$

On integrating, the solution is $E_h = E_{h0}e^{-\int_0^t(\gamma_h+\mu_h)dt}$. It is clear from the solution that $E_h(t)$ is positive since $E_{h0} = E_h(0) \geq 0$ and the exponential function is always positive.

Theorem 3: Positivity of infected human population: Consider the differential equation (5):

$$\frac{dI_h}{dt} = \gamma_h E_h(t) - (\tau_h + \mu_h + \delta_{Dh})I_h(t) \geq -(\tau_h + \mu_h + \delta_{Dh})I_h(t),$$

γ_h being the progression rate of humans from latent class to active dengue class and $E_h(t) \geq 0$, we can write as:

$$\frac{dI_h}{I_h} = -(\tau_h + \mu_h + \delta_{Dh})dt.$$

On integrating, the solution is $I_h = I_{h0}e^{-\int_0^t(\tau_h+\mu_h+\delta_{Dh})dt}$. So, it is clear from the solution that $I_h(t)$ is positive since $I_{h0} = I_h(0) \geq 0$ and exponential function is always positive.

Theorem 4: Positivity of recovered human population: Consider the differential equation (6):

$$\frac{dR_h}{dt} = \tau_h I_h(t) - \mu_h R_h(t) \geq -\mu_h R_h(t),$$

$\tau_h > 0$ being the treatment rate for infected humans and $I_h(t)$ is positive in time t, we can write as:

$$\frac{dR_h}{R_h} = -\mu_h dt.$$

On integrating, the solution is $R_h = R_{h0}e^{-\int_0^t \mu_h dt}$. It is clear from the solution that $R_h(t)$ is positive since $R_{h0} = R_h(0) \geq 0$ and the exponential function is always positive.

Theorem 5: Positivity of susceptible vector population: Consider the differential equation (7):

$$\frac{dS_v}{dt} = \Lambda_v - (\mu_v + \lambda_{DH})S_v(t) \geq -(\mu_v + \lambda_{DH})S_v(t),$$

$\Lambda_v > 0$ being recruitment rate of vectors, we can write as:

$$\frac{dS_v}{S_v} = -(\mu_v + \lambda_{DH})dt.$$

On integrating, the solution is $S_v = S_{v0}e^{-\int_0^t(\mu_v+\lambda_{DH})dt}$. It is clear from the solution that $S_v(t)$ is positive since $S_{v0} = S_v(0) > 0$ and the exponential function is always positive.

Theorem 6: Positivity of latent vector population: Consider the differential equation (8):

$$\frac{dE_v}{dt} = \lambda_{DH}S_v(t) - (\gamma_v + \mu_v)E_v(t) \geq -(\gamma_v + \mu_v)E_v(t),$$

$S_v(t)$ is positive in time t and $\lambda_{DH} > 0$ being vectors' contract rate to dengue due to infected humans, we can write as:

$$\frac{dE_v}{E_v} = -(\gamma_v + \mu_v)dt.$$

On integrating, the solution is $E_v = E_{v0}e^{-\int_0^t(\gamma_v+\mu_v)dt}$. It is clear from the solution that $E_v(t)$ is positive since $E_{v0} = E_v(0) \geq 0$ and the exponential function is always positive.

Theorem 7: Positivity of infected vector population: Consider the differential equation (9):

$$\frac{dI_v}{dt} = \gamma_v E_v(t) - (\mu_v + \delta_{Dv})I_v(t) \geq -(\mu_v + \delta_{Dv})I_v(t),$$

$\gamma_v > 0$ being the progression rate of vectors from latent class to active dengue class and $E_v(t) \geq 0$, we can write as:

$$\frac{dI_v}{I_v} = -(\mu_v + \delta_{Dv})dt.$$

On integrating, the solution is $I_v = I_{v0}e^{-\int_0^t(\mu_v+\delta_{Dv})dt}$. So, it is clear from the solution that $I_v(t)$ is positive since $I_{v0} = I_v(0) \geq 0$ and exponential function being positive always.
Hence, the stated problem is epidemiologically meaningful, well-posed and has a unique solution.

4. Differential Transform Method (DTM)

The differential transformation of the k^{th} derivative of $f(x)$ is defined as:

$$F(k) = \frac{1}{k!}\left[\frac{d^k f(x)}{dx^k}\right]_{x_0}. \tag{10}$$

We obtain,

$$f(x) = \sum_{k=0}^{\infty} F(k)(x - x_0)^k, \tag{11}$$

is called the inverse differential transformation of F(k). In real applications, the function f(x) can be expressed as a finite series and equation (11) can be expressed as:

$$f(x) = \sum_{k=0}^{n} F(k)(x - x_0)^k. \tag{12}$$

So, we have

$$f(x) = \sum_{k=0}^{n} (x - x_0)^k \frac{1}{k!}\left[\frac{d^k f(x)}{dx^k}\right]_{x_0}. \tag{13}$$

From equations (10) and (11), the following properties are obtained:

1. If $z(x) = f(x) \pm g(x)$, then $Z(k) = F(k) \pm G(k)$.
2. If $z(x) = \alpha F(x)$, then $Z(k) = \alpha F(k)$.
3. If $z(x) = f'(x)$, then $Z(k) = (k+1)F(k+1)$.
4. If $z(x) = f''(x)$, then $Z(k) = (k+1)(k+2)F(k+2)$.
5. If $z(x) = f^{(l)}(x)$, then $Z(k) = (k+1)(k+2)...(k+l)F(k+l)$.
6. If $z(x) = u(x)v(x)$, then $Z(k) = \sum_{l=0}^{k} F(l)G(k-l)$.
7. If $z(x) = \alpha x^l$, then $Z(k) = \alpha\delta(k-l)$, where Kronecker delta, $\delta(k-l) = \begin{cases}1, k=l\\0, k\neq l\end{cases}$

Using the fundamental operations of differential transformation method, let $S_h(k)$,$E_h(k)$, $I_h(k)$, $R_h(k)$, $S_v(k)$, $E_v(k)$ and $I_v(k)$ denote the differential transformations of $S_h(t)$, $E_h(t)$,

$I_h(t)$, $R_h(t)$, $S_v(t)$,$E_v(t)$ and $I_v(t)$ respectively, the recurrence relation to each equation of the system (3)–(9) is:

$$S_h(k+1) = \frac{1}{k+1}\left\{\Lambda_h\delta(k) - \mu_h S_h(k) - \frac{\beta_{vh}\eta_v}{N_h}\sum_{m=0}^{k} S_h(m)E_v(k-m) - \frac{\beta_{vh}}{N_h}\sum_{m=0}^{k} S_h(m)I_v(k-m)\right\} \tag{14}$$

$$E_h(k+1) = \frac{1}{k+1}\left\{\frac{\beta_{vh}\eta_v}{N_h}\sum_{m=0}^{k} S_h(m)E_v(k-m) + \frac{\beta_{vh}}{N_h}\sum_{m=0}^{k} S_h(m)I_v(k-m) - (\gamma_h+\mu_h)E_h(k)\right\} \tag{15}$$

$$I_h(k+1) = \frac{1}{k+1}\{\gamma_h E_h(k) - (\tau_h+\mu_h+\delta_{Dh})I_h(k)\} \tag{16}$$

$$R_h(k+1) = \frac{1}{k+1}\{\tau_h I_h(k) - \mu_h R_h(k)\} \tag{17}$$

$$S_v(k+1) = \frac{1}{k+1}\left\{\Lambda_v\delta(k) - \mu_v S_v(k) - \frac{\beta_{hv}\eta_A}{N_h}\sum_{m=0}^{k} S_v(m)E_h(k-m) - \frac{\beta_{hv}\eta_B}{N_h}\sum_{m=0}^{k} S_v(m)I_h(k-m)\right\} \tag{18}$$

$$E_v(k+1) = \frac{1}{k+1}\left\{\frac{\beta_{hv}\eta_A}{N_h}\sum_{m=0}^{k} S_v(m)E_h(k-m) + \frac{\beta_{hv}\eta_B}{N_h}\sum_{m=0}^{k} S_v(m)I_h(k-m) - (\gamma_v+\mu_v)E_v(k)\right\} \tag{19}$$

$$I_v(k+1) = \frac{1}{k+1}\left\{\gamma_v E_v(k) - (\mu_v+\delta_{Dv})I_v(k)\right\} \tag{20}$$

The recurrence relations (14), (15), (18) and (19) are the rectified forms of (8), (9), (12) and (13) of the study [1]. The semi-analytical solutions and numerical solutions have significantly changed due to these corrections.

5. Numerical and Graphical Simulation of the Model Equations

With the initial conditions $S_h(0) = 3503$, $E_h(0) = 490$, $I_h(0) = 390$, $R_h(0) = 87$, $S_v(0) = 390$,$E_v(0) = 100$, $I_v(0) = 130$, we compute the semi-analytical solutions for $k = 4$ using following values of the parameters: $N_h = 4470$, $N_v = 620$, $\Lambda_h = 500$, $\Lambda_v = 1,000,000$, $\mu_h = 0.02041$, $\mu_v = 0.5$, $\beta_{vh} = 0.5$, $\beta_{hv} = 0.4$, $\gamma_h = 0.3254$, $\gamma_v = 0.03$, $\delta_{Dh} = 0.365$, $\delta_{Dv} = 0$, $\eta_v = 0.4$, $\eta_A = 0.2$, $\eta_B = 0.5$ [5].

5.1. Low Dengue Treatment($\tau_h = 0.25$)

$$s_h(t) = \sum_{k=0}^{4} S_h(k)t^k = 3503 + 361.8919131767338t + 8.365058543813413t^2 - 686.2825200034454t^3 + 197.4722799192922t^4,$$

$$e_h(t) = \sum_{k=0}^{4} E_h(k)t^k = 490 - 102.83504317673376t + 5.722527622691168t^2 + 685.5659739627513t^3 - 253.23941572498939t^4,$$

$$i_h(t) = \sum_{k=0}^{4} I_h(k)t^k = 390 - 88.3639t + 11.342391324645417t^2 - 1.7816527943897462t^3 + 56.05381198239061t^4,$$

$$r_h(t) = \sum_{k=0}^{4} R_h(k)t^k = 87 + 95.72433t - 12.02235428765t^2 + 1.026991360724097t^3 - 0.11659352306745382t^4,$$

$$s_v(t) = \sum_{k=0}^{4} S_v(k)t^k = 390 + 999794.7744966443t - 263054.4930350626t^2 + 48072.332846142934t^3 - 6858.820737023293t^4,$$

$$e_v(t) = \sum_{k=0}^{4} E_v(k)t^k = 100 - 42.774496644295304t + 13117.134652512259t^2 - 6547.277795576331t^3 + 1717.2934391692909t^4,$$

$$i_v(t) = \sum_{k=0}^{4} I_v(k)t^k = 130 - 62.t + 14.85838255033557t^2 + 128.69494943339998t^3 - 65.19145214599749t^4$$

These solutions are the same as obtained from the in-built function `AsymptoticDSolveValue` of Wolfram Mathematica 13. Following is the program:

$$\begin{aligned} &AsymptoticDSolveValue[\\ &\{S_h'[t] - \Lambda_h + \mu_h S_h[t] + (\beta_{vh}\eta_v/N_h)S_h[t]\\ &E_v[t] + (\beta_{vh}/N_h)S_h[t]I_v[t] == 0,\\ &E_h'[t] - (\beta_{vh}\eta_v/N_h)S_h[t]\\ &E_v[t] - (\beta_{vh}/N_h)S_h[t]I_v[t] + (\gamma_h+\mu_h)E_h[t] == 0,\\ &I_h'[t] - \gamma_h E_h[t] + (\tau_h+\mu_h+\delta_{Dh})I_h[t] == 0,\\ &R_h'[t] - \tau_h I_h[t] + \mu_h R_h[t] == 0,\\ &S_v'[t] - \Lambda_v + \mu_v S_v[t] + (\beta_{hv}\eta_A/N_h)S_v[t]\\ &E_h[t] + (\beta_{hv}\eta_B/N_h)S_v[t]I_h[t] == 0,\\ &E_v'[t] - (\beta_{hv}\eta_A/N_h)S_v[t]E_h[t] - (\beta_{hv}\eta_B/N_h)\\ &S_v[t]I_h[t] + (\gamma_v+\mu_v)E_v[t] == 0,\\ &I_v'[t] - \gamma_v E_v[t] + (\mu_v+\delta_{Dv}) \end{aligned}$$

$$I_v[t] == 0, S_h[0] == Sh[0], E_h[0] == E_h[0],$$
$$I_h[0] == Ih[0], R_h[0] == Rh[0], S_v[0] == Sv[0], E_v[0] == Ev[0],$$
$$I_v[0] == Iv[0]\},$$
$$\{S_h[t], E_h[t], I_h[t], R_h[t], S_v[t], E_v[t], I_v[t]\}, \{t, 0, 4\}]$$

5.2. Moderate Dengue Treatment($\tau_h = 0.50$)

$$s_h(t) = \sum_{k=0}^{4} S_h(k)\,t^k = 3503 + 361.8919131767338\,t + 8.365058543813413\,t^2 - 686.2380770354108\,t^3 + 254.42405449756384\,t^4$$

$$e_h(t) = \sum_{k=0}^{4} E_h(k)\,t^k = 490 - 102.83504317673376\,t + 5.722527622691168\,t^2 + 685.5215309947168\,t^3 - 310.1875748678114\,t^4,$$

$$i_h(t) = \sum_{k=0}^{4} I_h(k)\,t^k = 390 - 185.8639\,t + 65.55161632464 54\,t^2 - 18.725982040526862\,t^3 + 59.912219486045935\,t^4,$$

$$r_h(t) = \sum_{k=0}^{4} R_h(k)\,t^k = 87 + 193.22433\,t - 48.43782928765\,t^2 + 11.25480808602788\,t^3 - 2.3981754133248154\,t^4,$$

$$s_v(t) = \sum_{k=0}^{4} S_v(k)\,t^k = 390 + 999794.7744966443\,t - 263053.6423639217\,t^2 + 49525.708598154626\,t^3 - 7943.074169380729\,t^4,$$

$$e_v(t) = \sum_{k=0}^{4} E_v(k)\,t^k = 100 - 42.774496644295304\,t + 13116.28398137132\,t^2 - 8000.645040876618\,t^3 + 2812.4460625275524\,t^4,$$

$$i_v(t) = \sum_{k=0}^{4} I_v(k)\,t^k = 130 - 62.t + 14.85838255033557\,t^2 + 128.6864427219906\,t^3 - 76.09064314682345\,t^4$$

5.3. High Dengue Treatment($\tau_h = 0.75$)

$$s_h(t) = \sum_{k=0}^{4} S_h(k)\,t^k = 3503 + 361.8919131767338\,t + 8.365058543813413\,t^2 - 686.1936340673763\,t^3 + 311.3702737048312\,t^4,$$

$$e_h(t) = \sum_{k=0}^{4} E_h(k)\,t^k = 490 - 102.83504317673376\,t + 5.722527622691168\,t^2 + 685.4770880266824\,t^3 - 367.13017863962915\,t^4,$$

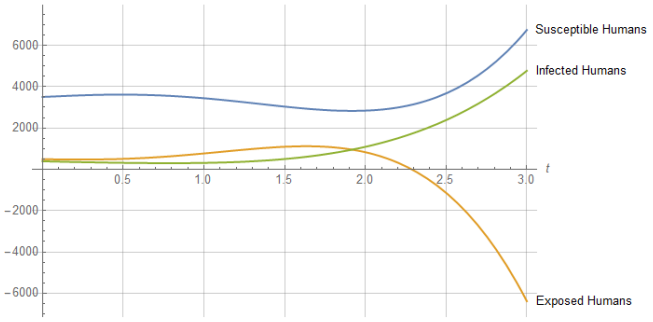

Figure 2: Susceptible, Exposed, Infected Human ($\tau = 0.5$)

$$i_h(t) = \sum_{k=0}^{4} I_h(k)\,t^k = 390 - 283.3639\,t + 144.13584132464 54\,t^2 - 53.93038836999731\,t^3 + 71.07183667576527\,t^4,$$

$$r_h(t) = \sum_{k=0}^{4} R_h(k)\,t^k = 87 + 290.72433\,t - 109.22830428765\,t^2 + 36.777076894665\,t^3 - 10.299602854229525\,t^4,$$

$$s_v(t) = \sum_{k=0}^{4} S_v(k)\,t^k = 390 + 999794.7744966443\,t - 263053.6423639217\,t^2 + 50978.94257164284\,t^3 - 9299.8224883176 48\,t^4,$$

$$e_v(t) = \sum_{k=0}^{4} E_v(k)\,t^k = 100 - 42.774496644295304\,t + 13115.43331023038\,t^2 - 9453.870507653413\,t^3 + 4180.0925091263725\,t^4,$$

$$i_v(t) = \sum_{k=0}^{4} I_v(k)\,t^k = 130 - 62.t + 14.85838255033557\,t^2 + 128.6779360105812\,t^3 - 86.98877080872326\,t^4.$$

The graph of susceptible, exposed, infected human population with moderate treatment and exposed, infected vectors is plotted against time t Figures 2 and 3. It is found that the susceptible and infected human population grows with time t while the exposed human population becomes negative after $t = 2.25$, being population graph, it can't be negative (limitation of DTM). Similarly, the graph of the infected vectors becomes negative.

The effect of the treatment as a control measure can be studied from Figures 4 and 5, where the effect of better treatment on infected population is found positive initially, the recovered population also increases initially and then consequently decreases (after $t = 1.70$, for high treatment rate) due to fast growth of infected population.

6. Conclusions

The compartmental model for dengue fever with treatment control measure [1] has been re-investigated and the

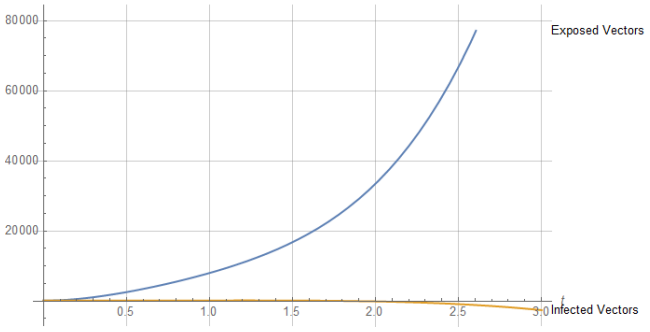

Figure 3: Exposed and Infected Vectors

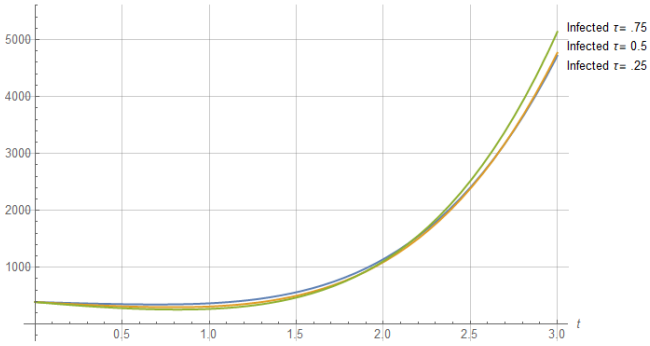

Figure 4: Infected Human with different Treatment (τ)

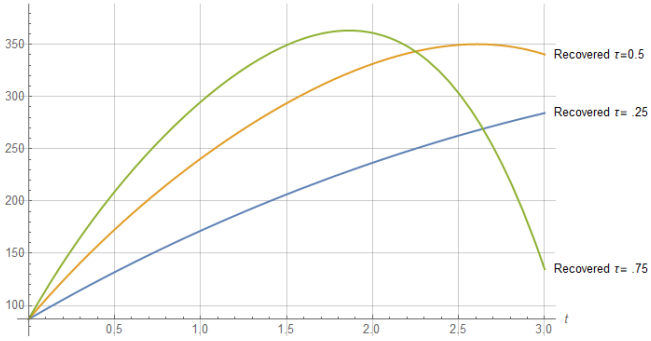

Figure 5: Recovered Human with different Treatment (τ)

inadvertent errors have been removed from the recurrence relations of the model equations due to DTM. The existence, uniqueness and positivity of the solutions have been established. The semi-analytical solutions of the model equations are re-computed using the DTM and built-in function AsymptoticDSolveValue of Wolfram Mathematica and are found to be the same. It has been found that results obtained from the DTM are valid only for a small interval of time $t(t < 1.5)$, as t becomes large, the exposed, recovered human population and infected vector population becomes negative. For smaller t, the better the treatment is, recovery will be faster

Figure 5.

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References

[1] F. Y. Eguda, A. James & S. Babuba, "The Solution of a Mathematical Model for Dengue Fever Transmission Using Differential Transformation Method", Journal of Nigerian Society of Physical Sciences **1** (2019) 82.

[2] Dengue. Retrieved from World Health Organization: https://www.who.int/immunization/diseases/dengue/en/(2021)

[3] Dengue-and-Severe-Dengue. Retrieved from World Health Organization: https://www.who.int/news-room/fact-sheets/detail/dengue-and-severe-dengue (2021).

[4] A. Mathieu, N Hens, C Marais & B P Beutels, "Dynamic Epidemiological Models for Dengue" PLOSONE **7** (2012) 1.

[5] Messina, J. P., Brady, O. J., Golding, N., Kraemer .et.al. The current and future global distribution and the population at risk of dengue. Nature Microbiology **4** (2019), 1508–1515.

[6] V Capasso & G Serio, "A generalization of the Kermack-McKendrick deterministic epidemic model", Mathematical Biosciences **42** (1978) 43.

[7] W. O. Kermack & MA. G. McKendrick, "Contribution to the Mathematical Theory of Epidemics" (Part 1). Proceedings of Royal Society London **138A** (1932) 55.

[8] W. O. Kermack & MA. G. McKendrick, "Contribution to the Mathematical Theory of Epidemics (Part II)", Proceedings of Royal Society London **141** (1932) 94.

[9] W. O. Kermack & MA. G. McKendrick, "A contribution to the mathematical theory of epidemics", Proceedings of the Royal Society of London A: Mathematical, Physical and Engineering Science **115** (1927), 700.

[10] H Hethcote, "The Mathematics of Infectious Diseases", SIAM Review, **42** (2000) 599.

[11] J K Zhou, "Differential Transformation and Its Applications for Electrical Circuits", Huazhong University Press, China 1986.

[12] P Olumuyiwa et. al. "Direct and Indirect Transmission Dynamics of Typhoid Fever Model by Differential Transform Method", ATBU Journal of Science, Technology and Education, **6** (2018) 167.

[13] P. Olumuyiwa & M O. Ibrahim, "Application of Differential Transform Method in Solving a Typhoid Fever Model", International Journal Of Mathematical Analysis And Optimization: Theory And Applications **1** (2017) 250.

[14] A. Abioye, M. O. Ibrahim, O. Peter, A. Sylvanus & F. Abiodun, "Differential Transform Method for Solving Mathematical Model of SEIR and SEI Spread of Malaria", International Journal of Sciences: Basic and Applied Research **40** (2018) 197.

[15] J. A. Abraham, G. P. Gilberto & Benito M. Chen-Charpentier, "Dynamical analysis of the transmission of seasonal diseases using the differential transformation method", Mathematical and Computer Modelling **50** (2009), 765.

[16] M. Derouich & A. Boutayeb, "Dengue fever: Mathematical modelling and computer simulation", Applied Mathematics and Computation **177** (2006) 528.

[17] Z. N. Meksianis, N Anggriani & A. K. Supriatna, "Application of differential transformation method for solving dengue transmission mathematical model", AIP Conference Proceedings 2018.

[18] N. R. Derrick & S. L. Grossman, "Differential Equation with applications", Addison Wesley Publishing Company Inc., Philippines 1976.