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MATHEMATICAL ANALYSIS OF ZIKA VIRUS TRANSMISSION: EXPLORING SEMI-ANALYTICAL SOLUTIONS AND EFFECTIVE CONTROLS

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Abstract. This paper examined the mathematical model of Zika virus transmission, focusing on the impact of the virus on humans and mosquitoes. Human and mosquito populations involved in Zika virus transmission are divided into two categories: susceptible and infected. In addressing the nonlinear differential equation that governing Zika virus transmission, the Taylor series method (TSM) and the new Homotopy perturbation method (NHPM) were employed to derive semi-analytical solutions. Furthermore, for a comprehensive assessment of the nonlinear

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2 DHARMALINGAM, JEEVA, NASIR, RIAD, FADUGBA, KEKANA, FIKADU, HESHAM, MAYSOON

system behavior and the accuracy of the obtained solutions, a comparative analysis was performed using numerical simulations. This comparative analysis enabled us to validate the results and to gain valuable insights into the behavior of the Zika virus transmission model under different conditions. Moreover, to decrease the number of infected human population, we analyzed the contact rate of Zika virus transmission between humans and mosquitoes, as well as between humans and humans.

Keywords: Zika virus transmission; Taylor series method (TSM); new homotopy perturbation method (NHPM);
system of nonlinear equation; semi-analytical solution; mathematical modeling; numerical simulation.
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1. INTRODUCTION

The primary mosquito that spreads the Zika virus is the Aedes species. In addition, the virus can be transferred from mother to children through blood transfusions, pregnancy, or soon after delivery. Recent studies have focused on the effectiveness and challenges associated with the Zika virus. It examines the stability of disease-free equilibrium, investigates the impact of significant variables on disease propagation, and conducts numerical simulations to evaluate strategies for control and the effect of delayed pregnancy on ZIKV transmission and microcephaly rates [1, 2, 3]. In epidemiology, the SIS model is a prominent tool for understanding the transmission dynamics of infectious diseases within a population via mathematical models. Over time, this model has undergone modifications, giving rise to variants such as the SIR model, the SEIR model, and more in the field of mathematics. The epidemiological model describes the dynamic interplay of the compartments across time using a set of differential equations, which provides crucial insights into illness transmission and growth [4, 5, 6]. Researchers have constructed mathematical models to understand Zika virus transmission dynamics. Mathematical models hypothesize that the virus primarily moves from mosquitoes to humans. Optimal control methods for a mathematical model of Zika virus (ZIKV) were developed by [7, 8]. In addition, [9] formulated and analyzed an innovative system of ordinary differential equations that encompassed both vector and sexual transmission pathways. [10] presented and scrutinized several SEIR models of Zika epidemics. [11, 12, 13, 14] contributed by developing a mathematical model of the Zika virus that incorporates nonlinear incidence, vertical transmission, and temperature considerations. A new mathematical model and Caputo derivative of the Zika virus transmission among humans and mosquitoes were developed by [15]. Semi-analytical

solutions are commonly utilized in cases where precise solutions to equations are unattainable [16, 17, 18, 19]. In a recent investigation [20] a hybrid approach incorporating the Shehu transform, Akbari-Ganji method, and Padé approximation was employed to obtain semi-analytical solutions for coffee berry disease. Furthermore, [21] utilized the Laplace-Adomian decomposition method to address a model related to SARS-CoV-2.

The main aim of this paper was to determine an semi-analytical solution for Zika virus transmission using the Taylor series method (TSM) and the new Homotopy perturbation method (NHPM). To validate these findings, the analytical results were compared with numerical simulations, offering valuable insights into the dynamics of Zika virus transmission.

Section 2 provides new mathematical model for the Zika virus transmission. The system of equations is analytically solved using the Taylor series method and a new Homotopy perturbation method in Sections 3 and 4, respectively. The numerical simulation of the model is presented in Section 5, followed by the discussion of results and the paper's conclusion in Sections 6 and 7.

2. GOVERNING SYSTEM OF EQUATION

Numerous mathematical models that study the spread of the Zika virus presume that mosquito-to-human transmission is the primary pathway. However, the World Health Organization recognizes that the Zika virus can also be spread via transfusion of infected blood and sexual contact with someone carrying the virus. [15] has developed a mathematical model including both transmission pathways. The Zika virus transmission model is based on the population of humans and mosquitoes, which are divided into two groups:

$$\frac{dN_h}{dt} = \wedge_h - k_1(S_h + I_h),$$

$$\frac{dN_m}{dt} = \wedge_m - k_2(S_m + I_m).$$

These two categories are divided into four sub-classes, where N_h represents the combined number of susceptible and infected humans ($N_h = S_h + I_m$), and N_m represents the combined number of susceptible and infected mosquitoes ($N_m = S_m + I_m$).

(1)
$$\frac{dS_h}{dt} = \wedge_h - \beta_1 S_h I_h - \beta_2 S_h I_m - k_1 S_h,$$
$$\frac{dI_h}{dt} = \beta_1 S_h I_h + \beta_2 S_h I_m - k_1 I_h,$$
$$\frac{dS_m}{dt} = \wedge_m - \mu_1 S_m I_h - k_2 S_m,$$
$$\frac{dS_m}{dt} = \mu_1 S_m I_h - k_2 I_m.$$

with initial conditions:

(2)
$$S_h(0) = S_{0h}, I_h(0) = I_{0h}, S_m(0) = S_{0m}, I_m(0) = I_{0m}.$$

where the recruitment rate of the human population is denoted by \wedge_h , and \wedge_m represents the recruitment rate of the mosquito population. β_1 indicates the effective contact rate from humans to humans, while β_2 denotes the effective contact rate from mosquitoes to humans. The effective contact rate between humans and mosquitoes is denoted by μ . k_1 and k_2 represent the natural death rates of humans and mosquitoes, respectively. The state variables S_h and I_h represent susceptible and infected individuals, respectively, in the human population, while S_m and I_m represent susceptible and infected mosquitoes. Variable *t* corresponds to time.

As equation (1) lacks an exact solution, we provide an semi-analytical solution by employing the Taylor series method (TSM) and new Homotopy perturbation method (NHPM). For computational purposes, systematic analysis was conducted using MATLAB.

3. Semi-Analytical Solution for Zika Virus Using Taylor Series Method (TSM)

In this section, we apply the Taylor series method to a system of nonlinear equation for Zika virus transmission. The basic concept and applications of TSM was discussed by researchers: [22] developed a Taylor series technique with numerical derivatives for initial value issues, [23] solved the Lane-Emden problem using the Taylor series approach, [24] implemented Taylor series approach in partial derivatives. This method has been successfully used to solve many differential problems in applied fields [25, 26, 27, 28, 29].

4

The Taylor series expansion (upto order four) for the Zika virus model is written as:

$$S_{h}(t) = \sum_{n=0}^{4} \frac{d^{n}S_{h}}{dt^{n}}\Big|_{t=0} \frac{t^{n}}{n!} = S_{h}(0) + \frac{S_{h}'(0)}{1!}t + \frac{S_{h}''(0)}{2!}t^{2} + \frac{S_{h}'''(0)}{3!}t^{3} + \frac{S_{h}''(0)}{4!}t^{4},$$

$$I_{h}(t) = \sum_{n=0}^{4} \frac{d^{n}I_{h}}{dt^{n}}\Big|_{t=0} \frac{t^{n}}{n!} = I_{h}(0) + \frac{I_{h}'(0)}{1!}t + \frac{I_{h}''(0)}{2!}t^{2} + \frac{I_{h}'''(0)}{3!}t^{3} + \frac{I_{h}''(0)}{4!}t^{4},$$

$$S_{m}(t) = \sum_{n=0}^{4} \frac{d^{n}S_{m}}{dt^{n}}\Big|_{t=0} \frac{t^{n}}{n!} = S_{m}(0) + \frac{S_{m}'(0)}{1!}t + \frac{S_{m}''(0)}{2!}t^{2} + \frac{S_{m}'''(0)}{3!}t^{3} + \frac{S_{m}''(0)}{4!}t^{4},$$

$$I_{m}(t) = \sum_{n=0}^{4} \frac{d^{n}I_{m}}{dt^{n}}\Big|_{t=0} \frac{t^{n}}{n!} = I_{m}(0) + \frac{I_{m}'(0)}{1!}t + \frac{I_{m}''(0)}{2!}t^{2} + \frac{I_{m}'''(0)}{3!}t^{3} + \frac{I_{m}''(0)}{4!}t^{4}.$$

We consider the following numerical values [15] for the parameters in Zika virus transmission: $\wedge_h = 1.2$, $\wedge_m = 0.3$, $\beta_1 = 0.125 \times 10^{-4}$, $\beta_2 = 0.4 \times 10^{-4}$, $k_1 = 0.004$, $k_2 = 0.0014$, $\mu_1 = 0.475 \times 10^{-5}$ and initial conditions $S_h(0) = 800$, $I_h(0) = 200$, $S_m(0) = 600$ and $I_m(0) = 300$. Using the numerical values, equation (1) becomes:

(4)

$$S'_{h}(t) = 1.2 - (0.125 \times 10^{-4})S_{h}(t)I_{h}(t) - (0.4 \times 10^{-4})S_{h}(t)I_{m}(t) - (0.004)S_{h}(t),$$

$$I'_{h}(t) = (0.125 \times 10^{-4})S_{h}(t)I_{h}(t) - (0.4 \times 10^{-4})S_{h}(t)I_{m}(t) - (0.004)I_{h}(t),$$

$$S'_{m}(t) = 0.3 - (0.475 \times 10^{-5})S_{m}(t)I_{h}(t) - (0.0014)S_{m}(t),$$

$$I'_{m}(t) = (0.475 \times 10^{-5})S_{m}(t)I_{h}(t) - (0.0014)I_{m}(t).$$

Setting t = 0 in equation (4) and using initial conditions, one can obtain:

(5)
$$S'_h(0) = -13.6, I'_h(0) = 10.8, S'_m(0) = -1.11, I'_m(0) = 0.15.$$

To find the next derivative, differentiate equation (4) with respect to t, one can obtain:

$$S'_{h}(t) = -(0.125 \times 10^{-4})[S_{h}(t)I'_{h}(t) + S'_{h}(t)I_{h}(t)] - (0.4 \times 10^{-4})[S'_{h}(t)I_{m}(t) + S_{h}(t)I'_{m}(t)] - (0.004)S'_{h}(t),$$

$$I'_{h}(t) = (0.125 \times 10^{-4})[S_{h}(t)I'_{h}(t) + S'_{h}(t)I_{h}(t)] + (0.4 \times 10^{-4})[S'_{h}(t)I_{m}(t) + S_{h}(t)I'_{m}(t)] - (0.004)I'_{h}(t),$$

$$(6) \qquad -(0.004)I'_{h}(t),$$

$$S'_{h}(t) = -(0.475 \times 10^{-5})[S'_{h}(t)I_{h}(t) + S_{h}(t)I'_{h}(t)] - (0.0014)S'_{h}(t),$$

$$S'_{m}(t) = -(0.475 \times 10^{-5})[S'_{m}(t)I_{h}(t) + S_{m}(t)I'_{h}(t)] - (0.0014)S'_{m}(t),$$

$$I'_{m}(t) = (0.475 \times 10^{-5})[S'_{m}(t)I_{h}(t) + S_{m}(t)I'_{h}(t)] - (0.0014)I'_{m}(t).$$

6 DHARMALINGAM, JEEVA, NASIR, RIAD, FADUGBA, KEKANA, FIKADU, HESHAM, MAYSOON Setting t = 0 in equation (6) and using initial conditions and equation (5), one can obtain:

(7)
$$S''_h(0) = 0.1388, I''_h(0) = -0.1276, S''_m(0) = -0.0281715, I''_m(0) = 0.0295155.$$

Proceeding like this, the successive Taylor series derivatives are as follows: Third order:

(8)
$$S_{m}^{\prime\prime\prime}(0) = 0.001598904, I_{h}^{\prime\prime\prime}(0) = -0.001643704,$$
$$S_{m}^{\prime\prime\prime\prime}(0) = 0.000543749, I_{m}^{\prime\prime\prime\prime}(0) = -0.00054563.$$

Fourth order:

(9)

$$S_{h}^{i\nu}(0) = -0.0000713016, I_{h}^{i\nu}(0) = 0.00007148,$$

$$S_{m}^{i\nu}(0) = 5.724027041 \times 10^{-6}, I_{m}^{i\nu}(0) = -5.721392801 \times 10^{-6}$$

By substituting the initial conditions, equations (5), (8) and (9) in equation (3), one can obtain the TSM solution for the Zika virus transmission:

(10)
$$S_h(t) = 800 - 13.6t + 0.0694t^2 + 0.000266484t^3 - 2.9709 \times 10^{-6}t^4,$$

(11)
$$I_h(t) = 200 + 10.8t - 0.0638t^2 - 0.00027395t^3 + 2.97836710^{-6}t^4,$$

(12)
$$S_m(t) = 600 - 1.11t - 0.01408575t^2 + 0.000090625t^3 + 2.385008333 \times 10^{-7}t^4,$$

(13)
$$I_m(t) = 300 + 0.15t + 0.01475775t^2 - 0.0000909383t^3 - 2.38391210^{-7}t^4.$$

4. SEMI-ANALYTICAL SOLUTION FOR ZIKA VIRUS USING NEW HOMOTOPY PER-TURBATION METHOD (NHPM)

In this section, we apply the NHPM to a system of nonlinear equation for Zika virus transmission. The basic concept and applications of the new Homotopy perturbation method (NHPM) was discussed by researchers: [30] solved prey-predator system of equation using NHPM, [31] applied for virus dynamics in computer network, [32] solved nonlinear parabolic equation in chemical sciences, [33] solved heat conduction equation. The new approach to the Homotopy perturbation method provides a simple semi solution in the zeroth iteration. This method employs a Homotopy transform to produce a series solution that converges to the differential equations.

We construct the Homotopy for the Equation (1) using initial conditions (2):

$$(1-p)\left[\frac{dS_{h}}{dt} - \wedge_{h} + \beta_{1}S_{h}I_{0h} + \beta_{2}S_{h}I_{0m} + k_{1}S_{h}\right] + p\left[\frac{dS_{h}}{dt} - \wedge_{h} + \beta_{1}S_{h}I_{h} + \beta_{2}S_{h}I_{m} + k_{1}S_{h}\right],$$

$$(14)$$

$$(14)$$

$$(1-p)\left[\frac{dI_{h}}{dt} - \beta_{1}S_{0h}I_{h} - \beta_{2}S_{0h}I_{0m} + k_{1}I_{h}\right] + p\left[\frac{dI_{h}}{dt} - \beta_{1}S_{h}I_{h} - \beta_{2}S_{h}I_{m} + k_{1}I_{h}\right],$$

$$(14)$$

$$(1-p)\left[\frac{dS_{m}}{dt} - \wedge_{m} + \mu_{1}S_{m}I_{0h} + k_{2}S_{m}\right] + p\left[\frac{dS_{m}}{dt} - \wedge_{m} + \mu_{1}S_{m}I_{h} + k_{2}S_{m}\right],$$

$$(1-p)\left[\frac{dI_{m}}{dt} - \mu_{1}S_{0m}I_{0h} + k_{2}I_{m}\right] + p\left[\frac{dS_{m}}{dt} - \mu_{1}S_{m}I_{h} + k_{2}I_{m}\right].$$

The approximate solutions of the equation (14) are given by

(15)

$$S_{h} = S_{h0} + pS_{h1} + p^{2}S_{h2} + ...,$$

$$I_{h} = I_{h0} + pI_{h1} + p^{2}I_{h2} + ...,$$

$$S_{m} = S_{m0} + pS_{m1} + p^{2}S_{m2} + ...,$$

$$I_{m} = I_{m0} + pI_{m1} + p^{2}I_{m2} +$$

Substituting the equation (15) in equation (14) and equating the coefficients of p_0 , one can obtain:

(16)
$$\frac{dS_{h0}}{dt} - \wedge_h + \beta_1 S_{h0} I_{0h} + \beta_2 S_{h0} I_{0m} + k_1 S_{h0} = 0,$$
$$\frac{dI_{h0}}{dt} - \beta_1 S_{0h} I_{h0} - \beta_2 S_{0h} I_{0m} + k_1 I_{h0} = 0,$$
$$\frac{dS_{m0}}{dt} - \wedge_m + \mu_1 S_{m0} I_{0h} + k_2 S_{m0} = 0,$$
$$\frac{dI_{m0}}{dt} - \mu_1 S_{0m} I_{0h} + k_2 I_{m0} = 0.$$

subject to the initial conditions for the equation (16):

(17)
$$S_{h0}(0) = S_{0h}, I_{h0}(0) = I_{0h}, S_{m0}(0) = S_{0m}, I_{m0}(0) = I_{0m}.$$

Solving equation (16) using the initial conditions (17), one can obtained the following NHPM solutions for the Zika virus transmission:

(18)

$$S_{h}(t) = e^{-k_{1}t} [S_{0h} + \frac{\beta_{1}S_{0h}I_{0h} + \beta_{2}S_{0h}I_{0m} - \wedge_{h}}{k_{1}}] - [\frac{\beta_{1}S_{0h}I_{0h} + \beta_{2}S_{0h}I_{0m} - \wedge_{h}}{k_{1}}],$$

$$I_{h}(t) = e^{-k_{1}t} [I_{0h} - \frac{\beta_{1}S_{0h}I_{0h} + \beta_{2}S_{0h}I_{0m}}{k_{1}}] + [\frac{\beta_{1}S_{0h}I_{0h} + \beta_{2}S_{0h}I_{0m}}{k_{1}}],$$

$$S_{m}(t) = e^{-k_{2}t} [S_{0m} + \frac{\mu_{1}S_{0m}I_{0h} - \wedge_{m}}{k_{2}}] + [-\frac{\mu_{1}S_{0m}I_{0h} + \wedge_{m}}{k_{2}}],$$

$$I_m(t) = e^{-k_2 t} [I_{0m} - \frac{\mu_1 S_{0m} I_{0h}}{k_2}] + [\frac{\mu_1 S_{0m} I_{0h}}{k_2}]$$

Setting up the numerical values [15] for the obtained NHPM: $\wedge_h = 1.2$, $\wedge_m = 0.3$, $\beta_1 = 0.125 \times 10^{-4}$, $\beta_2 = 0.4 \times 10^{-4}$, $k_1 = 0.004$, $k_2 = 0.0014$, $\mu_1 = 0.475 \times 10^{-5}$, with initial conditions $S_h(0) = 800$, $I_h(0) = 200$, $S_m(0) = 600$ and $I_m(0) = 300$. Hence, the solution of system (1) by NHPM is as follows:

(19)
$$S_h(t) = 3400e^{-0.004t} - 2600,$$

(20)
$$I_h(t) = -2700e^{-0.004t} + 2900,$$

(21)
$$S_m(t) = 792.8571427e^{-0.0014t} - 192.8571429,$$

(22)
$$I_m(t) = -107.1428572e^{-0.0014t} + 407.1428572.$$

5. NUMERICAL SIMULATION

Using the *ode* solver, a system of first-order nonlinear differential equation (1) was numerically solved. The MATLAB software program was used to obtain numerical solutions. The accuracy of the solution was then determined by comparing the numerical results with the semianalytical solutions obtained using the TSM and NHPM. Visual representations of the analytical expressions for the concentrations S_h , I_h , S_m and I_m are shown in the figures along with the corresponding numerical results for the given parameter values. The comparison demonstrates satisfactory agreement between the analytical solution obtained through TSM, but there is a small deviation in the NHPM with the numerical results. To further illustrate the accuracy of the analytical solutions with the simulation, error estimation tables are provided. The maximum averages for the TSM and NHPM with the numerical simulation are noted as 0.0000001% and 0.0074546% respectively.

6. DISCUSSIONS

The Taylor series method (TSM) and the new Homotopy perturbation method (NHPM) are used to solve the system of equation for the concentration profiles S_h , I_h , S_m , I_m in Zika virus

transmission. The semi-analytical solutions of equations (10-13) and equations (19-22) are compared to the numerical simulation and figures were produced using the given parameters.

The concentration of susceptible human S_h is plotted in Figure 1.a using the equation (10) and equation (19). With the effect of these parameters, the concentration of the susceptible humans decreases. Table 1 provides the results of TSM and NHPM for susceptible humans. Similar to Figure 1.a in Figure 1.c, the concentration of susceptible mosquitoes S_m equation (12) and equation (21) is visually presented and decreases as a result of these parameters. It is clear that human and mosquito susceptibility rates fall over time due to impact of the infection rates. Table 3 provides the results of TSM and NHPM for susceptible mosquitoes.

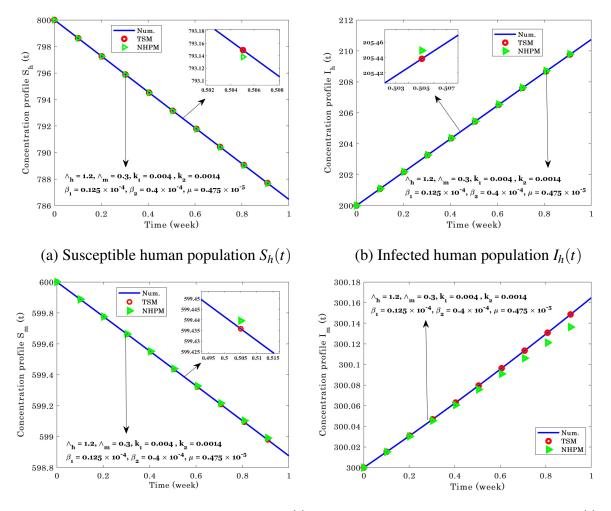
The concentration of the infected human I_m is plotted in Figure 1.b using equation (11) and equation (20). With the effects of these parameters, the concentration of infected humans is increasing. Table 2 provides the results of TSM and NHPM for infected humans. Similar to Figure 1.b in Figure 1.d, concentration of infected mosquitoes I_m equation (13) and equation (22) is visually presented and increases as a result of these parameters. It is evident that the rates of human and mosquito infections are growing over time, as the contact rate is on high. Table 4 provides the results of TSM and NHPM for infected mosquitoes.

From the simulation computed using MATLAB, we can conclude that TSM provides a better approximation than NHPM in solving the system of nonlinear equation in Zika virus transmission. It should be noted that within a small time internal, TSM and NHPM provide better approximation with simulation, but NHPM diverges as the average error % increases over the time. The convergence of the TSM with numerical simulation for time $t, t \in [0, 100]$ is shown in Figure 2.

In Figure 3.a, when β_1 is increased [$0.1 \times 10^{-4} - 0.7 \times 10^{-4}$] while keeping other parameters fixed, the susceptible human population decreases. Figure 3.b illustrates that with an increase in β_1 [$0.1 \times 10^{-4} - 0.7 \times 10^{-4}$] and fixed parameters, the infected human population also increases. In Figure 4.a, as β_2 is increased [$0.1 \times 10^{-4} - 0.9 \times 10^{-4}$] while other parameters remain fixed, the susceptible mosquito population decreases. Figure 4.b illustrates that with an increase in β_2 [$0.1 \times 10^{-4} - 0.9 \times 10^{-4}$] and fixed parameters, the infected mosquito population also increases.

10 DHARMALINGAM, JEEVA, NASIR, RIAD, FADUGBA, KEKANA, FIKADU, HESHAM, MAYSOON

Figures 5.a-5.c illustrates the impact of the human-to-human contact rate β_1 , on the concentrations of susceptible humans S_h , and infected humans I_h . It is evident that a decrease in β_1 values $[1.25 \times 10^{-4}, 1.25 \times 10^{-5}, 1.25 \times 10^{-6}]$ leads to an increase in the number of susceptible humans and a decrease in the number of infected humans. Similarly, Figures 6.a-6.c demonstrates the effect of the mosquito-to-human contact rate β_2 , on S_h and I_h concentrations. The graphs show that a decrease in β_2 values $[0.4 \times 10^{-3}, 0.4 \times 10^{-4}, 0.4 \times 10^{-5}]$ results in an increase in the number of susceptible humans and a decrease in the number of infected humans.



(c) Susceptible mosquitoes population $S_m(t)$ (d) Infected mosquitoes population $I_m(t)$ FIGURE 1. Comparison of semi-analytical expressions obtained by TSM and NHPM with numerical simulation for the Zika virus transmisson.

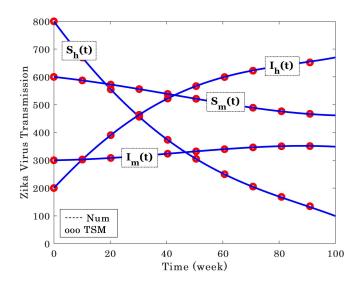


FIGURE 2. The accuracy of TSM with numerical simulation over time $t \in [0, 100]$

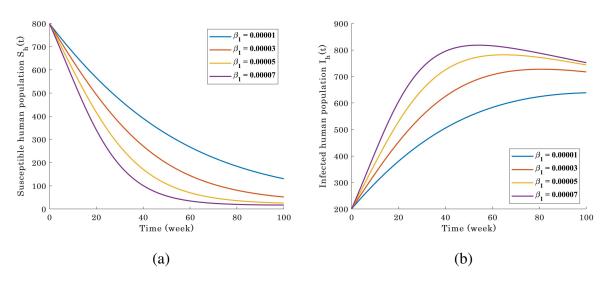


FIGURE 3. Impact of varying β_1 values on susceptible human population $S_h(t)$ and infected human population $I_h(t)$

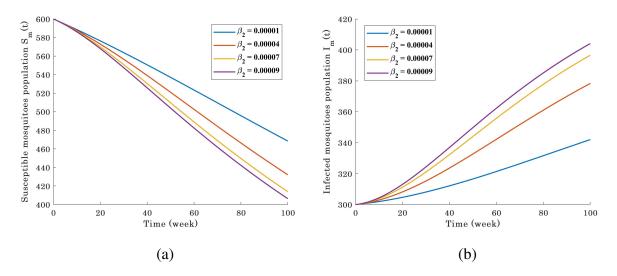


FIGURE 4. Impact of varying β_2 values on susceptible mosquitoes population $S_m(t)$ and infected mosquitoes population $I_m(t)$

TABLE 1. Comparison of TSM and NHPM with numerical results for the concentration susceptible human S_h

Susceptible human S _h					
t	Num.	TSM	NHPM	TSM	NHPM
				Error%	Error%
0	800.000000	800.000000	800.000000	0.000000	0.000000
0.2	797.282778	797.282778	797.281088	0.000000	0.000211
0.4	794.571121	794.571121	794.564350	0.000000	0.000852
0.6	791.865041	791.865041	791.849784	0.000000	0.001926
0.8	789.164551	789.164551	789.137389	0.000000	0.003441
1	786.469664	786.469663	786.427164	0.000001	0.005403
Ave	Average Error				0.0019721

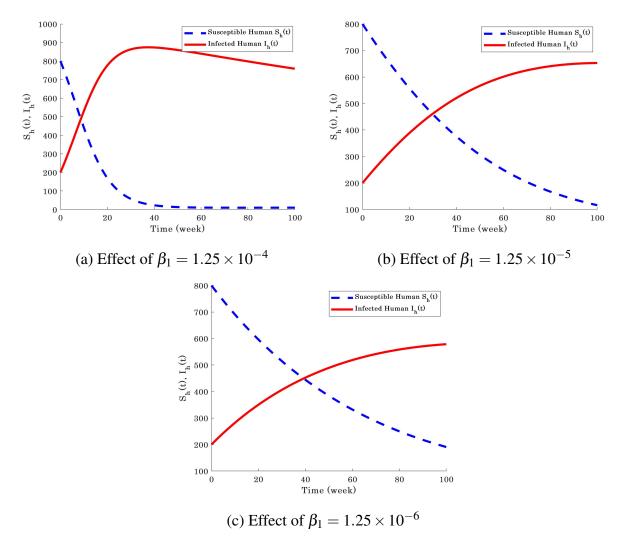


FIGURE 5. Graphical representation of the susceptible and infected human population when varying the contact rate of humans to humans β_1

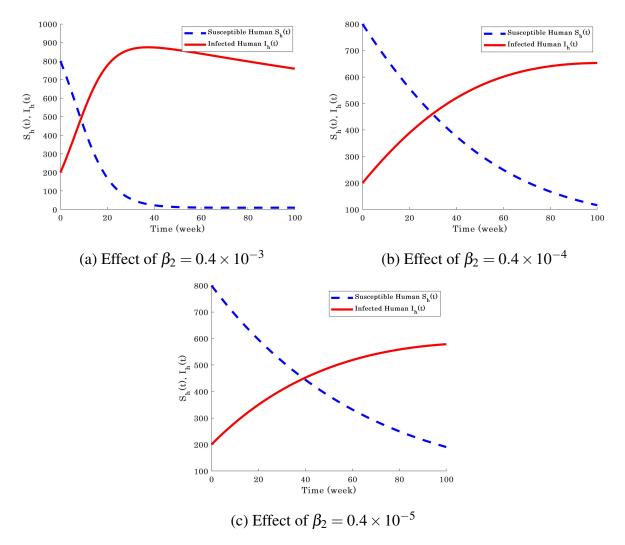


FIGURE 6. Graphical representation of the susceptible and infected human population when varying the contact rate of mosquitoes to humans β_2

TABLE 2. Comparison of TSM and NHPM with numerical results for the con	-
centration infected human I_h	

Infected human I_h					
t	Num.	TSM	NHPM	TSM	NHPM
				Error%	Error%
0	200.000000	200.000000	200.000000	0.000000	0.000000
0.2	202.157446	202.157445	202.159136	0.000001	0.000836
0.4	204.309775	204.309774	204.316546	0.000001	0.003314
0.6	206.456973	206.456973	206.472230	0.000000	0.007390
0.8	208.599029	208.599028	208.626191	0.000001	0.013021
1	210.735929	210.735929	210.778429	0.000000	0.020167
Ave	Average Error				0.0074546

TABLE 3. Comparison of TSM and NHPM with numerical results for the concentration susceptible mosquitoes S_m

Susceptible mosquitoes S_m					
t	Num.	TSM	NHPM	TSM	NHPM
				Error%	Error%
0	600.000000	600.000000	600.000000	0.000000	0.000000
0.2	599.777437	599.777437	599.778030	0.000000	0.000099
0.4	599.553751	599.553752	599.556123	0.000001	0.000396
0.6	599.328947	599.328948	599.334278	0.000001	0.000889
0.8	599.103029	599.103031	599.112496	0.000001	0.001580
1	598.876001	598.876005	598.890775	0.000001	0.002467
Ave	Average Error				0.0009051

16 DHARMALINGAM, JEEVA, NASIR, RIAD, FADUGBA, KEKANA, FIKADU, HESHAM, MAYSOON TABLE 4. Comparison of TSM and NHPM with numerical results for the concentration infected mosquitoes I_m

Infected mosquitoes I_m					
t	Num.	TSM	NHPM	TSM	NHPM
				Error%	Error%
0	300.000000	300.000000	300.000000	0.000000	0.000000
0.2	300.030590	300.030589	300.029995	0.000001	0.000198
0.4	300.062356	300.062355	300.059983	0.000001	0.000791
0.6	300.095294	300.095293	300.089962	0.000001	0.001777
0.8	300.129400	300.129398	300.119932	0.000001	0.003155
1	300.164669	300.164666	300.149895	0.000001	0.004922
Ave	Average Error				0.0018071

7. CONCLUSION

In this paper, we derived a solution for a system of nonlinear equations describing Zika virus transmission dynamics. By utilizing the Taylor series method and new Homotopy perturbation method (NHPM), we obtained semi-analytical expressions for the populations of susceptible humans, infected humans, susceptible mosquitoes, and infected mosquitoes. The analytical solutions were compared with numerical simulations, and the results showed that the Taylor series method demonstrated excellent agreement with the numerical outcomes. Figures and Tables emphasize the accuracy and efficiency of the Taylor series method in addressing strongly nonlinear equations. The behavior of the different population compartments was distinct under the Taylor series method, new Homotopy perturbation method, and numerical approaches. Specifically, the number of susceptible humans and mosquitoes declined, while the infected populations of both humans and mosquitoes increased. A key part of the analysis focused on reducing the infected human population by decreasing the mosquito-to-human and human-to-human contact rates. The results indicated that when both contact rates were reduced, the number of infected humans diminished over time, thereby illustrating an effective strategy for controlling the spread of Zika. These semi-analytical methods offer powerful computational

tools in the field of epidemiology, aiding in the understanding of disease transmission and providing insights into infectious disease management within populations.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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18 DHARMALINGAM, JEEVA, NASIR, RIAD, FADUGBA, KEKANA, FIKADU, HESHAM, MAYSOON

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