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Application of Chebyshev Polynomial-Exponential Method and Tamimi-Ansari Method in Dengue Transmission Dynamics: A Comparative Study

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Abstract. Dengue virus transmitted by mosquitoes, poses a significant global health threat, affecting millions of people annually. In this paper, we explore the dynamics of a dengue virus transmission model, structured as an epidemiological mathematical framework. The model divides the total population into seven compartments: susceptible humans $S(t)$, exposed humans $E(t)$, infected humans $I(t)$, recovered humans $R(t)$, susceptible mosquitoes $M(t)$, exposed mosquitoes $M_E(t)$, and infected mosquitoes $M_I(t)$. We employed the Chebyshev polynomial-exponential method (CPEM) and Tamimi-Ansari method (TAM) to conduct an in-depth semi-analytical examination of this model. The numerical simulation using MATLAB® *ode*45 solver was used to compare the results with CPEM and TAM, validating the accuracy and effectiveness of the obtained solutions. The comparison shows no significant differences between the CPEM with numerical results, which leads to a interesting findings. Additionally, by varying the sensitive parameters, we analyzed the behavior of the different compartments within the model. This investigation provides valuable insights into the responses of dengue transmission under various conditions, demonstrating the potential of novel semi-analytical methods for studying epidemiological models of infectious diseases, which is highly beneficial for researchers in the field.

1. Introduction

The dengue virus is a mosquito-borne infection spread mostly by Aedes aegypti and Aedes albopictus mosquitoes. It causes dengue fever, an illness that leads to high fever, severe headaches, eye pain, joint and muscle aches, rashes, and mild bleeding. In extreme cases, the condition can escalate to dengue hemorrhagic fever or shock syndrome, which can be fatal. There is no specific

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antiviral therapy for dengue; therefore, prevention focuses on controlling mosquito populations and avoiding bites, while supportive care can significantly improve recovery [1–4].

[5] presents a mathematical model for dengue fever transmission dynamics that includes a treatment function, analyzes the existence and stability of equilibria, demonstrates the possibility of backward bifurcation, and uses real data from six Indian states to estimate the key parameter corresponding to disease transmission. [6] describes an epidemiological model for dengue illness and conducts a sensitivity analysis to establish the relative impact of model parameters in disease transmission, as measured by the basic reproduction number R_0. [7] presents a mathematical model for the transmission of dengue fever in Medan, Indonesia, based on the SEIR (Susceptible-Exposed-Infected-Recovered) model, analyzing the stability of the equilibrium points and determining the disease's endemic nature. [8] develops a deterministic model for the transmission dynamics of a strain of dengue illness that permits transmission by exposed people and mosquitos, and then expands the model to include an incomplete vaccination against the dengue variant. [9] develops a host-vector SEIR-SEI mathematical model for dengue virus transmission dynamics, examines the stability of disease-free and endemic equilibrium points, and does a sensitivity analysis to find the most important model parameters. Recent studies by [10, 11] developed two mathematical models of dengue viral transmission, including the humoral immune response, and analyzed the stability of the equilibrium states (virus-free and endemic) using linearization and Lyapunov's direct technique.

[12] develops a SEIR-SEI mathematical model for dengue transmission, analyzing the dynamics of human and mosquito populations, and performs sensitivity analysis to assess the impact of key parameters on disease spread.

Analytical solutions in epidemiology are vital for understanding infectious disease dynamics and developing effective intervention strategies. By solving differential equations that model disease transmission, researchers can obtain explicit expressions for critical metrics such as infection rates, peak times, and equilibrium states. Various semi-analytical methods, including DTM, ADM, HPM, LADM, TSM, SAGPM, HOIPM and VIM, have been employed to address complex mathematical challenges. These solutions aid in predicting disease spread, assessing the impact of control measures, such as vaccination and quarantine, and optimizing resource allocation during outbreaks [13–23]. Over time, a variety of semi-analytical methods have been developed, with the Tamimi-Ansari method (TAM) being particularly notable for its efficiency in accurately solving complex differential equations. This method is recognized as a powerful tool for deriving approximate solutions for various mathematical models and systems [24–28].

Another noteworthy advancement is the innovative Chebyshev polynomial-exponential method (CPEM). Numerous combinations of semi-analytical methods have been developed to tackle initial value problems (IVPs), and it is crucial for these methods to demonstrate consistency, stability, zero stability, and convergence in order to effectively handle the non-linearity inherent in such models. [29] introduced CPEM as a solution approach for linear physical models in IVPs, utilizing the

first, second, third and fourth Chebyshev polynomials of the first kind combined with exponential functions that outperforms PJM [30].

The primary goal of this paper is to address a system of nonlinear differential equations within a dengue virus model utilizing both the Chebyshev polynomial-exponential method (CPEM) and the Tamimi-Ansari method (TAM). The structure of the paper is organized as follows: Section 2 presents the mathematical model of the dengue virus, while Section 3 details the application of CPEM to solve the dengue model. Section 4 outlines the methodology and solution of the dengue model using TAM. In Section 5, we provide the numerical solutions along with error estimates for the model, followed by a discussion of the results in Section 6. Finally, Section 7 concludes the paper.

2. Mathematical Modeling of Dengue Virus Transmission

In this section, we consider the dengue virus transmission model developed by N. Harshit and P. Harjule [12]. The human population is divided into four compartments: S represents those who are susceptible to the dengue virus, E includes individuals who have been exposed to the virus but are not yet infected, I denotes those who are currently infected, and R represents individuals who have recovered from the disease. Similarly, the mosquito population is categorized into three compartments: M represents susceptible mosquitoes, E_M includes exposed mosquitoes, and I_M refers to the infectious mosquito population. Equation (2.1) represents the $SEIRME_MI_M$ model, which incorporates the dynamics of both human and mosquito populations.

$$\begin{aligned}
\frac{dS}{dt} &= \Omega - \zeta SI - \varkappa S \\
\frac{dE}{dt} &= \zeta SI - (\sigma + \varkappa)E \\
\frac{dI}{dt} &= \sigma E - (\varsigma + \varkappa)I - \chi I \\
\frac{dR}{dt} &= (\varsigma + \varkappa)I - \varkappa R + \chi I \\
\frac{dM}{dt} &= \Upsilon - \rho M - \xi MI \\
\frac{dE_M}{dt} &= \xi MI - \varrho E_M - \eta E_M I \\
\frac{dI_M}{dt} &= \varrho E_M - \varphi I_M - \eta I_M I
\end{aligned} \tag{2.1}$$

The parameter Ω symbolizes the birth rate of the human population, ζ indicating the transmission rate from susceptible to infected human individuals. Human mortality is denoted by $\varkappa$ and σ describes the speed at which exposed individuals become infected. The recovery rate is represented by ς, while χ indicates the likelihood of death among those infected by the virus. Within the mosquito population, Υ signifies the birth rate, and ρ represents the death rate. ξ describes the rate at which mosquitoes become infected by humans, while ϱ reflects how exposed mosquitoes become infectious. The death rate of mosquitoes due to the virus is denoted by φ, and η reflects

the rate at which mosquitoes transmit the virus to humans. The dengue virus transmission model parameters and their values are listed in Table 1.

TABLE 1. Parameters and their numerical values [12]

Parameter	**Value**
Ω	0.0171
Υ	0.033
ζ	0.25
ρ	0.1299
σ	0.5
ξ	0.375
ς	0.2081
ϱ	0.5
χ	0.001493
φ	0.245
$\varkappa$	0.01666
η	0.25

3. Chebyshev Polynomial-Exponential Method (CPEM)

In this section, we solve the dengue transmission model using a novel approach. We utilize a combination of Chebyshev polynomials of the first kind along with an exponential function [29], represented in the following form:

$$G(\tau) = \beta_0 + \beta_1\tau + \beta_2(2\tau^2 - 1) + \beta_3(4\tau^3 - 3\tau) + \beta_4 e^{-2\tau} \tag{3.1}$$

Assuming that ω_n serves as the numerical approximation to the theoretical solution $\omega(\tau)$ and that $G_n = G(\tau_n, \omega_n)$, we define the mesh points as follows:

$$\tau_{n+1} - \tau_n = h \quad \text{for} \quad n = 0, 1, 2, 3, \ldots \tag{3.2}$$

Setting $\tau = \tau_n$ and $\tau = \tau_{n+1}$ in (3.1):

$$G(\tau_n) = \beta_0 + \beta_1\tau_n + \beta_2(2\tau_n^2 - 1) + \beta_3(4\tau_n^3 - 3\tau_n) + \beta_4 e^{-2\tau_n} \tag{3.3}$$

and

$$G(\tau_{n+1}) = \beta_0 + \beta_1\tau_{n+1} + \beta_2(2\tau_{n+1}^2 - 1) + \beta_3(4\tau_{n+1}^3 - 3\tau_{n+1}) + \beta_4 e^{-2\tau_{n+1}} \tag{3.4}$$

The derivatives correspond to g_n, g_n', g_n'', and g_n''' as follows: $G'(\tau_n) = g_n$, $G''(\tau_n) = g_n'$, $G'''(\tau_n) = g_n''$, and $G^{(4)}(\tau_n) = g_n'''$. By differentiating $G(\tau)$ and determining the constants, we arrive at the

following results:

$$\begin{aligned}
\beta_1 &= g_n - nhg_n' + \left(\frac{(nh)^2}{2} + \frac{1}{8}\right)g_n'' + \left(\frac{(nh)^2}{4} + \frac{nh}{4} + \frac{3}{16}\right)g_n''', \\
\beta_2 &= \frac{4g_n' - 4nhg_n'' - 2nhg_n''' - g_n'''}{16}, \\
\beta_3 &= \frac{2g_n'' + g_n'''}{48}, \\
\beta_4 &= \frac{g_n'''}{16e^{2\tau_n}}.
\end{aligned} \tag{3.5}$$

The undetermined coefficients β_1, β_2, β_3, and β_4 are defined in equation (3.5). According to this definition, the mesh points τ_n and τ_{n+1} are represented as $\tau_n = \tau_0 + nh$ and $\tau_{n+1} = \tau_0 + (n+1)h$. Let $\tau_0 = 0$, we obtain:

$$\tau_n = nh, \quad \tau_{n+1} = (n+1)h$$

Thus,

$$\tau_{n+1} - \tau_n = (n+1)h - nh = h \tag{3.6}$$

$$\tau_{n+1}^2 - \tau_n^2 = ((n+1)h)^2 - (nh)^2 = h^2(2n+1) \tag{3.7}$$

$$\tau_{n+1}^3 - \tau_n^3 = ((n+1)h)^3 - (nh)^3 = h^3(3n^2 + 3n + 1) \tag{3.8}$$

Subtracting (3.4) from (3.3), we obtain:

$$G(\tau_{n+1}) - G(\tau_n) = \beta_1(\tau_{n+1} - \tau_n) + \beta_2(2\tau_{n+1}^2 - 2\tau_n^2) + \beta_3(4\tau_{n+1}^3 - 4\tau_n^3 - 3\tau_{n+1} + 3\tau_n) + \beta_4\left(e^{-2\tau_{n+1}} - e^{-2\tau_n}\right) \tag{3.9}$$

Substituting (3.6), (3.7), and (3.8) into (3.9), we get:

$$\implies \beta_1 h + 2\beta_2 h^2(2n+1) + \beta_3 4h^3(3n^2 + 3n + 1) - 3h + \beta_4 h\left(e^{-2(n+1)h} - e^{-2nh}\right) \tag{3.10}$$

From (3.5) with $\tau_n = nh$, we have:

$$\begin{aligned}
\beta_4 &= \frac{g_n'''}{16e^{-2nh}} \\
\beta_3 &= \frac{2g_n'' + g_n'''}{48} \\
\beta_2 &= \frac{4g_n' - 4nhg_n'' - 2nhg_n''' - g_n'''}{16} \\
\beta_1 &= g_n - nhg_n' + \left(\frac{(nh)^2}{2} + \frac{1}{8}\right)g_n'' + \left(\frac{(nh)^2}{4} + \frac{nh}{4} + \frac{3}{16}\right)g_n'''
\end{aligned} \tag{3.11}$$

By substituting equation (3.11) and setting $G(\tau_{n+1}) - G(\tau_n) = \omega_{n+1} - \omega_n$, we obtain the CPEM approach for solving the dengue model can be expressed as:

$$\omega_{n+1} = \omega_n + hg_n + h^2\left(g_n' - \frac{g_n'''}{8}\right) + h^3\left(\frac{g_n''}{6} + \frac{g_n'''}{12}\right) + \left(\frac{h}{8} + \frac{e^{-2h}}{16} - \frac{1}{16}\right)g_n''' \tag{3.12}$$

with initial conditions:

$$\omega(\tau_0) = \omega_0$$

The semi-analytical solution for the dengue model (2.1) has been obtained using a novel semi-analytical method that combines the exponential function with Chebyshev polynomials of the first kind, where ω_i denotes the various compartments in the dengue transmission $SEIRMM_EM_I$ model. This method (3.12) demonstrates fourth order accuracy, as evidenced by the local truncation error. A comprehensive comparative analysis was performed to assess the performance of the CPEM (3.12) in linear physical models [29]. The results demonstrate that the CPEM is more efficient, necessitating less computational time and fewer gradient evaluations per iteration. However, the accuracy of this method has yet to be evaluated with nonlinear physical models and real-world applications. Therefore, this paper examines its accuracy and efficiency in the context of dengue virus transmission.

4. Tamimi-Ansari Method (TAM)

4.1. **TAM Methodology.** Consider the following nonlinear differential equation [27]:

$$L(W) + N(W) + f = 0, \tag{4.1}$$

with the initial condition

$$W(0) = m, \tag{4.2}$$

where L is a linear operator, N represents a nonlinear operator, f is a known function, and W is the unknown function.
Let W_0 be the initial approximation, determined by solving the initial problem:

$$L(W_0) + f = 0 \quad \text{and} \quad W_0 = m, \tag{4.3}$$

The subsequent approximate solution is obtained by solving the following equation:

$$L(W_1) + f + N(W_0) = 0 \quad \text{with} \quad W_1 = m, \tag{4.4}$$

This leads to a straightforward iterative procedure for solving a series of nonlinear problems:

$$L(W_{n+1}) + f + N(W_n) = 0 \quad \text{with} \quad W_n = m, \tag{4.5}$$

Here, W_n serves as an approximate solution to (4.5), and the overall solution to the problem is expressed as [26, 28]:

$$W = \lim_{n\to\infty} W_n. \tag{4.6}$$

4.2. **Semi-analytical solution using TAM.** To solve the dengue transmission model using the Tamimi-Ansari method (TAM), we start by defining the model equations in terms of the linear and nonlinear operators, as well as the corresponding functions. First, consider the nonlinear differential equation provided in Equation (4.1), subject to the initial condition in Equation (4.2). The method begins by identifying an initial approximation W_0, which is found by solving the linearized problem in Equation (4.3). This serves as the foundation for the iterative process, where subsequent approximations are determined by solving Equation (4.4). Next, we apply this approach to our model, which is designed to capture the dynamics of dengue transmission. The dengue virus model (2.1) is composed of several compartments representing the human and mosquito populations, each governed by a specific differential equation.
We define the linear operators for each compartment in the model as follows:

$$\begin{aligned} L_1(S(t)) &= \frac{dS(t)}{dt} \\ L_2(E(t)) &= \frac{dE(t)}{dt} \\ L_3(I(t)) &= \frac{dI(t)}{dt} \\ L_4(R(t)) &= \frac{dR(t)}{dt} \\ L_5(M(t)) &= \frac{dM(t)}{dt} \\ L_6(E_M(t)) &= \frac{dE_M(t)}{dt} \\ L_7(I_M(t)) &= \frac{dI_M(t)}{dt} \end{aligned} \tag{4.7}$$

The nonlinear interactions in the model are represented by the following operators:

$$\begin{aligned} N_1(S(t)) &= -\zeta S(t)I(t) - \varkappa S(t) \\ N_2(E(t)) &= \zeta S(t)I(t) - (\sigma + \varkappa)E(t) \\ N_3(I(t)) &= \sigma E(t) - (\varsigma + \varkappa)I(t) - \chi I(t) \\ N_4(R(t)) &= (\varsigma + \varkappa)I(t) - \varkappa R(t) + \chi I(t) \\ N_5(M(t)) &= -\rho M(t) - \xi M(t)I(t) \\ N_6(E_M(t)) &= \xi M(t)I(t) - \varrho E_M(t) - \eta E_M(t)I(t) \\ N_7(I_M(t)) &= \varrho E_M(t) - \varphi I_M(t) - \eta I_M(t)I(t) \end{aligned} \tag{4.8}$$

The functions associated with each compartment are defined as:

$$\begin{aligned} f_1(t) &= \Omega \\ f_2(t) &= 0 \\ f_3(t) &= 0 \end{aligned} \tag{4.9}$$

$$f_4(t) = 0$$
$$f_5(t) = \Upsilon$$
$$f_6(t) = 0$$
$$f_7(t) = 0$$

By iteratively applying the TAM approach, we can progressively refine the solution for each compartment of the dengue virus transmission model, leading to a more accurate representation of the dynamics involved in the spread of the virus within both human and mosquito populations. The final solution to the problem in Equation (4.6) is given by the limit of the sequence of approximations as n approaches infinity, as shown in Equation (4.10).

$$\begin{aligned}
L_1(S_{n+1}(t)) + N_1(S_n(t)) + f_1(t) = 0, &\quad S_{n+1}(0) = m_1 \\
L_2(E_{n+1}(t)) + N_2(E_n(t)) + f_2(t) = 0, &\quad E_{n+1}(0) = m_2 \\
L_3(I_{n+1}(t)) + N_3(I_n(t)) + f_3(t) = 0, &\quad I_{n+1}(0) = m_3 \\
L_4(R_{n+1}(t)) + N_4(R_n(t)) + f_4(t) = 0, &\quad R_{n+1}(0) = m_4 \\
L_5(M_{n+1}(t)) + N_5(M_n(t)) + f_5(t) = 0, &\quad M_{n+1}(0) = m_5 \\
L_6(E_{M(n+1)}(t)) + N_6(E_{Mn}(t)) + f_6(t) = 0, &\quad E_{M(n+1)}(0) = m_6 \\
L_7(I_{M(n+1)}(t)) + N_7(I_{Mn}(t)) + f_7(t) = 0, &\quad I_{M(n+1)}(0) = m_7
\end{aligned} \tag{4.10}$$

The initial problem for each variable must be solved to get the initial approximation, and by integrating, we get:

$$\begin{aligned}
S_0(t) &= m_1 + \Omega t \\
E_0(t) &= m_2 \\
I_0(t) &= m_3 \\
R_0(t) &= m_4 \\
M_0(t) &= m_5 + \Upsilon t \\
E_{M0}(t) &= m_6 \\
I_{M0}(t) &= m_7
\end{aligned} \tag{4.11}$$

In the first step, solve the following problem:

$$\begin{aligned}
S_1'(t) = N_1(S_0(t)), &\quad S_1(0) = m_1 \\
E_1'(t) = N_2(E_0(t)), &\quad E_1(0) = m_2 \\
I_1'(t) = N_3(I_0(t)), &\quad I_1(0) = m_3 \\
R_1'(t) = N_4(R_0(t)), &\quad R_1(0) = m_4 \\
M_1'(t) = N_5(M_0(t)), &\quad M_1(0) = m_5 \\
E_{M1}'(t) = N_6(E_{M0}(t)), &\quad E_{M1}(0) = m_6 \\
I_{M1}'(t) = N_7(I_{M0}(t)), &\quad I_{M1}(0) = m_7
\end{aligned} \tag{4.12}$$

This solution represents the first iteration of the model: $S_1(t), E_1(t), I_1(t), R_1(t), M_1(t), E_{M1}(t)$, and $I_{M1}(t)$. Similarly, we solve the following problem:

$$\begin{aligned}
S_2'(t) &= N_1(S_1(t)), & S_2(0) &= m_1 \\
E_2'(t) &= N_2(E_1(t)), & E_2(0) &= m_2 \\
I_2'(t) &= N_3(I_1(t)), & I_2(0) &= m_3 \\
R_2'(t) &= N_4(R_1(t)), & R_2(0) &= m_4 \\
M_2'(t) &= N_5(M_1(t)), & M_2(0) &= m_5 \\
E_{M2}'(t) &= N_6(E_{M1}(t)), & E_{M2}(0) &= m_6 \\
I_{M2}'(t) &= N_7(I_{M1}(t)), & I_{M2}(0) &= m_7
\end{aligned} \tag{4.13}$$

This solution represents the second iteration of the model: $S_2(t), E_2(t), I_2(t), R_2(t), M_2(t), E_{M2}(t)$, and $I_{M2}(t)$. This process continues to obtain the approximations at $n \to \infty$ for $S_n(t), E_n(t), I_n(t), R_n(t), M_n(t), E_{Mn}(t)$, and $I_{Mn}(t)$.

Thus, the semi-analytical solution for the dengue virus transmission model (2.1) using the Tamimi-Ansari method (TAM) is obtained as follows:

$$\begin{aligned}
S(t) = 10 &- 5.14950t + 0.02090283500t^2 - 0.1740987485t^3 + 0.1794810978t^4 \\
&- 0.02420660426t^5 - 0.01397161503t^6 - 0.00001914226826t^7 - 6.439281423 \times 10^{-9}t^8 \ldots
\end{aligned} \tag{4.14}$$

$$\begin{aligned}
E(t) = 3 &+ 3.45002t - 0.8692511666t^2 + 0.3236851040t^3 - 0.1231058406t^4 \\
&+ 0.02423552455t^5 + 0.01397161503t^6 + 0.00001914226826t^7 + 6.439281423 \times 10^{-9}t^8 \ldots
\end{aligned} \tag{4.15}$$

$$\begin{aligned}
I(t) = 2 &+ 1.047494t + 0.7440056700t^2 - 0.2009863661t^3 + 0.05182908005t^4 \\
&- 0.009757880322t^5 + 0.002020717596t^6 + 0.0009979725020t^7 + 1.196391766 \times 10^{-6}t^8 \\
&+ 3.577378569 \times 10^{-10}t^9 \ldots
\end{aligned} \tag{4.16}$$

$$\begin{aligned}
R(t) = 1 &+ 0.435846t + 0.1148687328t^2 + 0.05547326729t^3 - 0.01159948821t^4 \\
&- 0.002552838023t^5 - 1.090550074 \times 10^{-6}t^6 \ldots
\end{aligned} \tag{4.17}$$

$$\begin{aligned}
M(t) = 5 &- 4.3665t + 0.9390160500t^2 - 0.1686816323t^3 + 0.08531374807t^4 \\
&- 0.09766629570t^5 - 0.02691906061t^6 - 0.00007881179105t^7 - 4.761746066 \times 10^{-8}t^8 \ldots
\end{aligned} \tag{4.18}$$

$$\begin{aligned}
E_M(t) = 2 &+ 1.750t - 3.667285375t^2 - 0.1081185410t^3 - 0.07952868529t^4 \\
&+ 0.1823356616t^5 + 0.05280600143t^6 + 0.0001330439770t^7 + 7.531534960 \times 10^{-8}t^8 \ldots
\end{aligned} \tag{4.19}$$

$$I_M(t) = 1 + 0.255t + 1.149075750t^2 - 0.3207818229t^3 - 0.1260229600t^4 - 0.006946361196t^5 + 0.0006198227896t^6 + 5.139350928 \times 10^{-7}t^7 \ldots \tag{4.20}$$

5. Numerical Simulation

In this section, we numerically solve the dengue virus transmission model using CPEM and TAM. A numerical simulation of the system of Equations (2.1) was developed using the *ode*45 solver. In this analysis, we assumed the initial human populations of 10 individuals in the susceptible human class, 3 in the exposed human class, 2 in the infected human class, and 1 in the recovered human class. For the mosquito population, we assumed 5 individuals in the susceptible mosquito class, 2 in the exposed mosquito class, and 1 in the infected mosquito class. This establishes the initial conditions of the system (2.1) as $S(0) = 10$, $E(0) = 3$, $I(0) = 2$, $R(0) = 1$, $M(0) = 5$, $M_E(0) = 2$, and $M_I(0) = 1$. Solutions for the susceptible human $S(t)$, exposed human $E(t)$, infected human $I(t)$, recovered human $R(t)$, susceptible mosquitoes $M(t)$, exposed mosquitoes $M_E(t)$, and infected mosquitoes $M_I(t)$ compartments are calculated at specific time points: $t = 0$, 0.01, 0.04, 0.08, 0.1, 0.4, 0.7 and 1.

5.1. **Numerical solution by CPEM.** Table 2 presents the numerical values obtained using the Chebyshev polynomial-exponential method (3.12).

Table 2. Numerical values of (2.1) using CPEM

t	$S(t)$	$E(t)$	$I(t)$	$R(t)$	$M(t)$	$E_M(t)$	$I_M(t)$
0.00	10.00000	3.00000	2.00000	1.00000	5.00000	2.00000	1.00000
0.01	9.94851	3.03442	2.01055	1.00437	4.95643	2.01732	1.00257
0.04	9.79404	3.13664	2.04307	1.01762	4.82682	2.06717	1.01051
0.08	9.58809	3.27061	2.08845	1.03563	4.65660	2.12877	1.02153
0.10	9.48511	3.33662	2.11198	1.04479	4.57258	2.15752	1.02719
0.40	7.94123	4.25220	2.52606	1.19598	3.39986	2.43485	1.11087
0.70	6.42208	5.01998	3.03518	1.37783	2.40161	2.44892	1.15922
1.00	4.98670	5.60594	3.60941	1.59563	1.59822	2.24350	1.14087

5.2. **Numerical solution by TAM.** Table 3 presents the numerical values obtained using the Tamimi-Ansari method (4.14)-(4.20).

TABLE 3. Numerical values of (2.1) using TAM

t	$S(t)$	$E(t)$	$I(t)$	$R(t)$	$M(t)$	$E_M(t)$	$I_M(t)$
0.00	10.00000	3.00000	2.00000	1.00000	5.00000	2.00000	1.00000
0.01	9.94851	3.03441	2.01055	1.00437	4.95643	2.01713	1.00266
0.04	9.79404	3.13663	2.04308	1.01762	4.82683	2.06413	1.01202
0.08	9.58809	3.27060	2.08846	1.03563	4.65661	2.11647	1.02758
0.10	9.48510	3.33662	2.11199	1.04479	4.57258	2.13821	1.03666
0.40	7.93669	4.25880	2.52641	1.19594	3.39392	2.10636	1.26203
0.70	6.38326	5.07627	3.03999	1.37719	2.34661	1.40872	1.60017
1.00	4.83859	5.81957	3.63560	1.59203	1.36448	0.13034	1.95094

5.3. **Numerical solution by** *ode*45 **solver.** Table 4 presents the numerical values obtained using the *ode*45 solver, the simulations were performed using MATLAB®.

TABLE 4. Numerical values of (2.1) using *ode*45 solver

t	$S(t)$	$E(t)$	$I(t)$	$R(t)$	$M(t)$	$E_M(t)$	$I_M(t)$
0.00	10.00000	3.00000	2.00000	1.00000	5.00000	2.00000	1.00000
0.01	9.94851	3.03441	2.01056	1.00437	4.95644	2.01730	1.00257
0.04	9.79404	3.13661	2.04310	1.01762	4.82686	2.06711	1.01052
0.08	9.58810	3.27050	2.08854	1.03565	4.65672	2.12856	1.02155
0.10	9.48512	3.33643	2.11213	1.04481	4.57278	2.15716	1.02721
0.40	7.94126	4.25210	2.52611	1.19599	3.39996	2.43471	1.11086
0.70	6.42213	5.01982	3.03525	1.37787	2.40179	2.44873	1.15916
1.00	4.98687	5.60563	3.60949	1.59570	1.59851	2.24329	1.14075

5.4. **Error estimation.** In this subsection, we will analyze the error percentages of CPEM and TAM by comparing them with results from the *ode*45 solver for validation purposes. Since the dengue virus transmission model in Equation (2.1) does not have an exact solution, the *ode*45 solver is employed as a benchmark to estimate the errors in the numerical solutions. The difference between the two sets of results is evaluated using the following error estimation formula:

$$\text{Error estimation } \% = \left|\frac{\text{Num} - \text{SA}}{\text{Num}}\right| \times 100 \tag{5.1}$$

In this context, **Num** refers to the results obtained from the *ode*45 solver, while **SA** corresponds to the outcomes from the semi-analytical methods CPEM (3.12) and TAM (4.14)-(4.20). This formula is utilized to estimate the errors based on the data presented in Tables 5 and 6.

TABLE 5. Error estimation values of the CPEM (3.12)

t	$S(t)$	$E(t)$	$I(t)$	$R(t)$	$M(t)$	$E_M(t)$	$I_M(t)$
0.00	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
0.01	0.000000	0.000330	0.000497	0.000000	0.000202	0.000991	0.000000
0.04	0.000000	0.000956	0.001468	0.000000	0.000829	0.002903	0.000990
0.08	0.000104	0.003363	0.004309	0.001931	0.002577	0.009866	0.001958
0.10	0.000105	0.005695	0.007102	0.001914	0.004374	0.016689	0.001947
0.40	0.000378	0.002351	0.001979	0.000836	0.002941	0.005750	0.000900
0.70	0.000779	0.003188	0.002306	0.002903	0.007494	0.007759	0.005176
1.00	0.003409	0.005530	0.002216	0.004387	0.018142	0.009361	0.010519
Average	0.000597	0.002676	0.002484	0.001392	0.004202	0.005695	0.002573

TABLE 6. Error estimation values of the TAM (4.14)-(4.20)

t	$S(t)$	$E(t)$	$I(t)$	$R(t)$	$M(t)$	$E_M(t)$	$I_M(t)$
0.00	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
0.01	0.000000	0.000000	0.000497	0.000000	0.000202	0.008427	0.008977
0.04	0.000000	0.000638	0.000979	0.000000	0.000622	0.144163	0.148438
0.08	0.000104	0.003058	0.003830	0.001931	0.002362	0.567990	0.590279
0.10	0.000211	0.005695	0.006628	0.001914	0.004374	0.878470	0.919968
0.40	0.057548	0.157569	0.011876	0.004181	0.177649	13.486206	13.608375
0.70	0.605251	1.124542	0.156165	0.049352	2.297453	42.471404	38.045654
1.00	2.973408	3.816520	0.723371	0.229993	14.640509	94.189784	71.022573
Average	0.454564	0.622985	0.093273	0.035921	2.139849	17.282602	13.841989

6. DISCUSSION OF RESULTS

The individual populations S, E, I, R, M, M_E, and M_I in the dengue virus transmission model (2.1) were determined by solving the system of equations using the Chebyshev polynomial-exponential method (CPEM) and Tamimi-Ansari method (TAM). The parameter values listed in Table 1 and assumed initial conditions were used in the analysis, and Tables 2 and 3 gives the numerical values of our semi-analytical expressions for concentrations S, E, I, R, M, M_E, and M_I. Using *ode*45 solver, a comparison of the CPEM and TAM with numerical simulation (Table 4) was performed. Table 5 provides the error estimates for CPEM, showing that the overall error is less than 0.006%. Similarly, Table 6 presents the error estimates for TAM, where the overall error remains below 18%. The tables clearly show that CPEM consistently provides a more accurate approximation, even within

a limited time interval.

Figure 1 presents the combined effects of varying the transmission rate ζ on both the susceptible and exposed human populations. Increasing the transmission rate ζ results in a decrease in the susceptible human population, and rise in the exposed human population, indicating that the disease transmission impacts cause individuals to move to the exposed class. Figure 2 shows the combined effects of varying the infection rate σ on the exposed and infected human populations. This indicates that the spread of dengue disease accelerates as the infection rate increases. Figure 3 illustrates the combined effects of varying the rate χ of infectious people dying due to dengue on both the infected and recovered human populations. Figure 4 depicts the combined effects of varying the recovery rate ς on the infected and recovered human populations. This indicates that dengue transmission slows down as early vaccination or effective treatment leads to an increase in the recovery rate, helping the population recover through measures such as vaccines and other interventions. Figure 5 shows the combined effects of varying the transmission rate η of the virus from mosquitoes to humans on the populations of exposed and infected mosquitoes. This indicates that an increase in η leads to a rise in both E_M and I_M classes. Finally, Figure 6 illustrates the overall dynamics of the dengue virus transmission model (2.1) as determined by the newly proposed CPEM (3.12). These figures enable us to analyze the model's behavior and suggest potential preventive measures for controlling the transmission of the dengue virus.

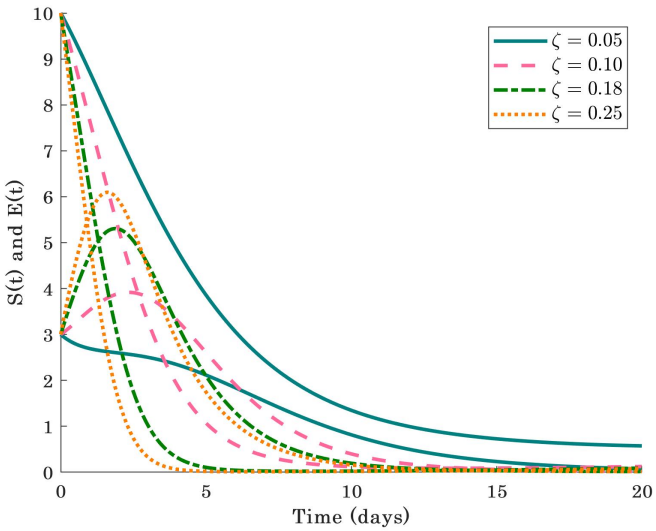

FIGURE 1. Combined effects of varying transmission rate ζ on susceptible and exposed human populations

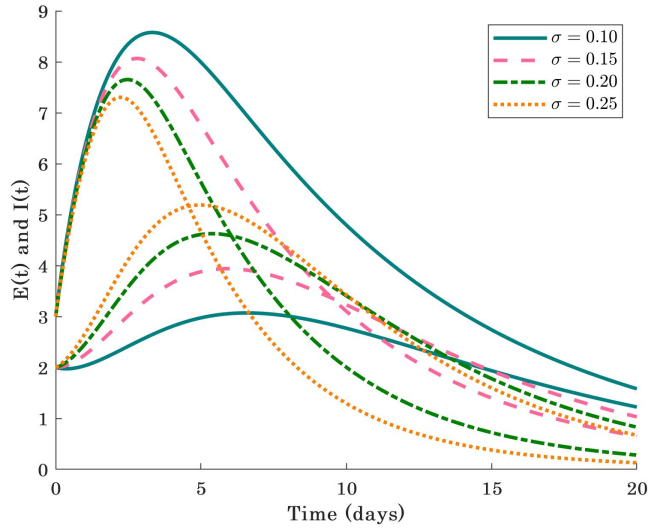

FIGURE 2. Combined effects of varying rate of exposed people becoming infected σ on exposed and infected human populations

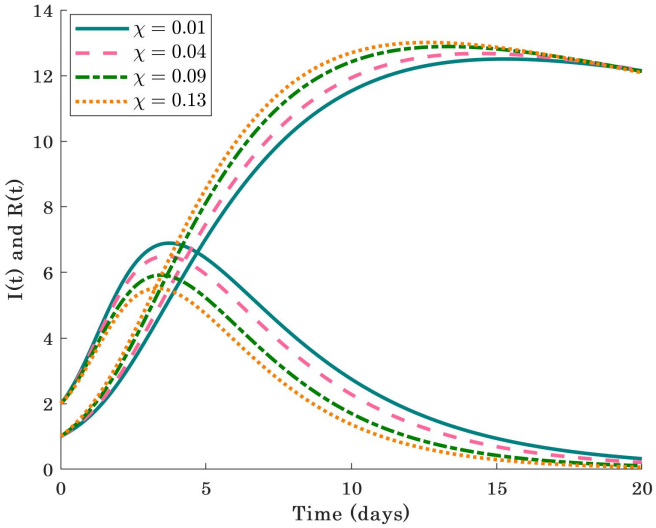

FIGURE 3. Combined effects of varying rate of infectious people dying due to dengue virus χ on infected and recovered human populations

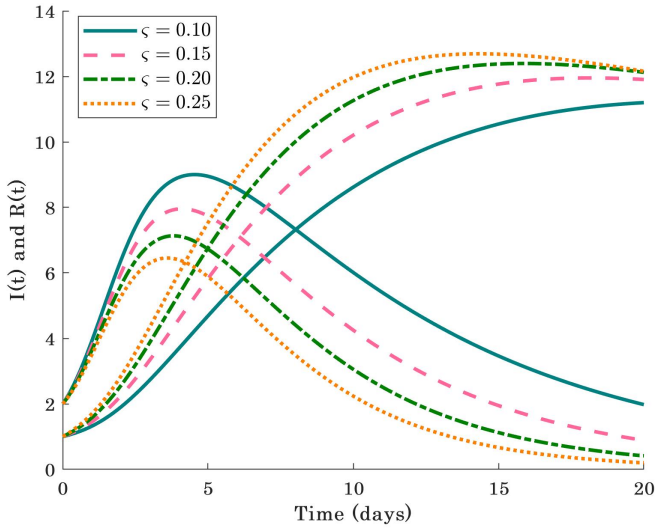

FIGURE 4. Combined effects of varying rate at which infectious people recover from illness ς on infected and recovered human populations

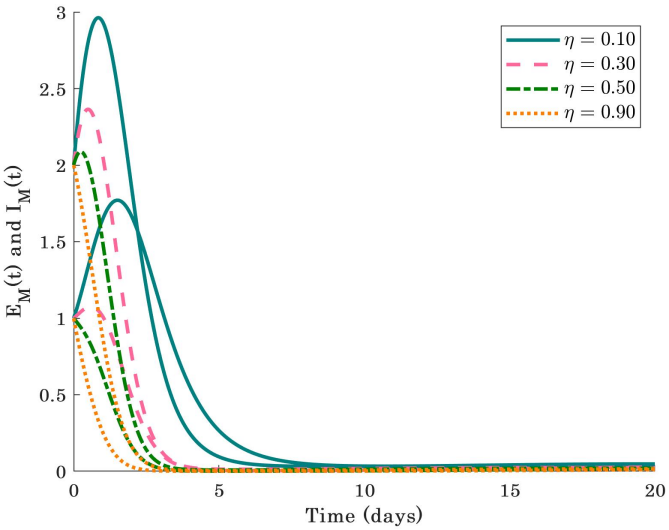

FIGURE 5. Combined effects of varying rate at which mosquitoes transmit the virus to humans η on exposed and infected mosquitoes

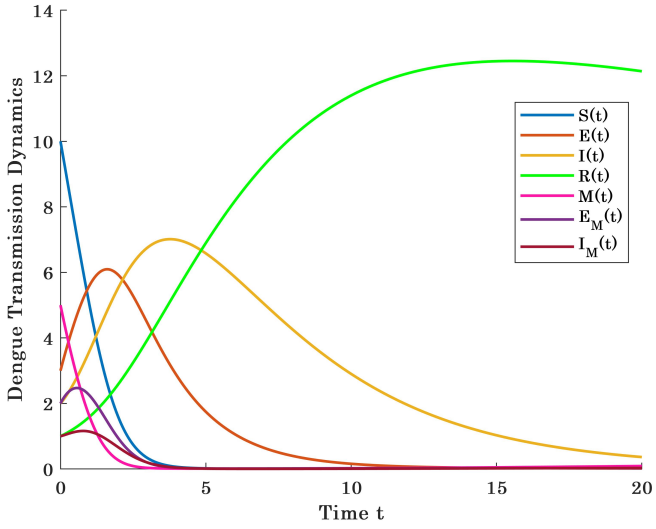

FIGURE 6. Dengue virus transmission dynamics (2.1) by CPEM (3.12)

7. CONCLUSION

This paper investigated an system of ordinary differential equation modeling the transmission of the dengue virus using an epidemiological framework. While traditional approaches such as Homotopy perturbation, Homotopy analysis, Adomian decomposition, variational iteration and Taylor series methods are commonly employed to solve epidemiological problems, we introduced a novel methods called the Chebyshev polynomial-exponential method (CPEM) and Tamimi-Ansari method (TAM) to derive semi-analytical solutions for the dengue transmission $SEIRMM_EM_I$ model. TAM efficiently decomposes the original equation into linear, nonlinear, and functional components, while CPEM solves the system of equations iteratively, facilitating convergence of the solutions. The numerical results are examined across various time intervals and a comparison of the semi-analytical solutions with numerical simulations (using the *ode*45 solver) showed that CPEM exhibited good agreement, whereas TAM was unable to accurately capture the disease dynamics over time. Numerical values were calculated using both methods to analyze the model's behavior and thus, innovative method like CPEM can make significant advantages in the field of epidemiology. Additionally, we observed that an increase in the transmission rate over time leads to a increase in the infected human population. In contrast, a higher treatment rate resulted in a decrease in the infected human population and an increase in the recovered human population. This paper offers valuable insights into dengue virus transmission dynamics, underscoring the need to lower infection rates by adopting preventive strategies. It stresses the significance of enhancing public awareness and employing proactive measures to curb the spread of the disease and promote early diagnosis. Managing dengue virus infections effectively focuses on providing supportive care to ease symptoms since no specific antiviral treatments exist.

Furthermore, implementing preventive strategies like mosquito born control and raising public awareness are vital for lowering transmission rates and reducing the occurrence of the disease. We conclude that effective measures to reduce contact rates can help control dengue virus transmission, while appropriate recovery strategies implemented by authorities can enhance recovery rates and mitigate the disease's impact.

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