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Application of the Adam-Bashforth-Moulton Method to a Fractional-Order Mathematical Model of Dengue with Vector and Non-Vector Pathways

[*1]Ahman, Q.O., [1]Agbata, B.C., [1]Atabo, V.O., [1]Senewo, E.O., [1]Michael, B.D., & [2]Ezugorie, I.G.

[1]Department of Mathematics, Confluence University of Science and Technology, Osara. Nigeria.
[2]Department of Industrial Mathematics/Applied Statistics, Enugu State University of Science and Technology, Nigeria

***Corresponding author email:** ahmanqo@custech.edu.ng

Abstract
This study presents a novel fractional-order dengue virus transmission model that integrates vector and non-vector pathways. The model employs the Adam-Bashforth-Moulton (ABM) method to account for memory effects and long-term dependencies, offering a more accurate depiction of disease dynamics compared to traditional methods like the 4th-order Runge-Kutta method (RKM4). The fractional-order framework captures nonlinear interactions among human and mosquito populations, reflecting key epidemiological transitions, including susceptibility, exposure, infection, vaccination, and recovery. Simulation results demonstrate the superiority of ABM in predicting population dynamics, particularly in exposed and infectious compartments, while highlighting deviations in classical methods over time. Phase plots and absolute error analysis further underscore the accuracy and reliability of ABM in solving fractional-order systems. By comparing the results with recent literature, this study emphasizes the critical role of fractional-order methods in infectious disease modeling, addressing limitations in classical approaches and providing insights for public health interventions. These findings contribute to the growing body of knowledge advocating the use of fractional-order techniques for understanding complex epidemiological systems and informing effective disease control strategies.

Keywords: Fractional-order modeling; Dengue transmission dynamics; Adam-Bashforth-Moulton method; Memory effects in epidemiology; Infectious disease modeling.

Introduction

Dengue virus (DENV), caused by the dengue virus and primarily transmitted by *Aedes* mosquitoes, remains a major global health challenge, particularly in tropical and subtropical regions. The World Health Organization (WHO, 2024) estimates that there are 390 million dengue infections annually**,** with a significant number resulting in severe cases, such as dengue hemorrhagic fever and dengue shock syndrome (Alshehry et al., 2024; Nisar et al., 2024). Despite extensive public health efforts, including vector control measures and the development of vaccines, dengue continues to spread rapidly due to the complex interactions between human populations and mosquito vectors, exacerbated by factors such as urbanization, climate change, and global travel (Meena & Purohit, 2024; Olayiwola &Yunus, 2024).

Mathematical models have proven essential in understanding the dynamics of infectious diseases, especially in predicting the impact of various intervention strategies. Traditional **integer-order** models have provided foundational insights into the transmission dynamics of diseases like dengue (Pandey & Phaijoo, 2024), but they fail to capture the complex, memory-dependent dynamics that characterize real-world systems. These limitations have spurred the development of fractional-order models, which use derivatives of non-integer order to account for long-term memory effects and history-dependent processes (Usman et al., 2024; Meetei et al., 2024; Adel et al., 2024). Fractional-order models are particularly valuable in epidemiology as they allow for the incorporation of delayed and cumulative effects, which are essential for understanding the spread of diseases like dengue, where transmission dynamics are influenced by both vector and non-vector pathways (El-shenawy et al., 2024; Vijayalakshmi et al., 2024).

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The novelty of fractional-order models lies in their ability to capture non-local interactions **and** anomalous diffusion **processes**, which are critical in describing the diffusion of infectious agents and the response of host populations over time (Kumar et al., 2024; Vellappandi et al., 2024). The **fractional order** differential equations that govern these models introduce memory effects and feedback loops, offering a more accurate and flexible representation of the disease dynamics compared to traditional models (Islam et al., 2024; Naaly et al., 2024). In the case of dengue, these models have been further enhanced to account for both **vector** (mosquito) and **non-vector** (human-to-human) transmission pathways, providing a more comprehensive framework for investigating the DENV disease spread (Shanmugam & Byeon, 2024; Diethelm et al., 2004; Garrappa, 2010).

However, solving fractional-order differential equations presents unique computational challenges. Unlike integer-order systems, fractional derivatives are non-local, which complicates their numerical approximation using traditional methods (Podlubny,1999). To address this issue, specialized numerical techniques tailored to fractional calculus have been developed. Among these, the Adams-Bashforth-Moulton (ABM) method has proven to be a robust and efficient predictor-corrector scheme for solving fractional-order systems (Zhuang & Liu, 2006; Diethelm & Freed, 1999; Ford & Simpson, 2001). The ABM method has several advantages, including its ability to balance accuracy and computational efficiency**,** which is crucial for complex epidemiological models like those used in dengue transmission studies **(**Lubich, 1986; Baleanu et al., 2012; Chen & Holm, 2003). The ABM method offers an effective approach for approximating fractional derivatives by using a predictor-corrector scheme that iteratively improves the solution, thus allowing for precise simulations of disease dynamics while minimizing computational cost. It is particularly useful for systems with memory effects and delayed responses, both of which are integral features of dengue transmission models (Magin, 2006; Ezz-Eldien & Moaddy, 2015). This technique has been successfully applied to a range of fractional systems, demonstrating its versatility and reliability in accurately solving fractional-order differential equations (Ahmad et al., 2018; Diethelm, 2010; Hilfer, 2000).

In this study, we apply the ABM method to a fractional-order dengue model that integrates both vector and non-**vector** transmission pathways. The model incorporates the Caputo fractional derivative, which is widely used in epidemiological models due to its ability to represent systems with memory effects and delayed dynamics (Kumar & Singh, 2019). Through numerical simulations, we investigate the stability**,** accuracy**,** and computational performance of the ABM method in solving the model. Additionally, we compare the results obtained using the ABM method with those derived from other numerical approaches to demonstrate the advantages of ABM in handling the intricate dynamics of fractional-order systems. By presenting this novel application, we aim to contribute to the growing body of research on fractional-order modeling in epidemiology and provide a valuable tool for public health planning and **intervention strategies** against dengue fever.

Materials and Methods

DENV Fractional -Order Model Description

In this paper, we offer the following system of fractional order dengue virus disease model. The dengue fever epidemic model is divided into 8 classes with the Human population further divided into five (5) classes; Human Dengue fever susceptible class (H_S), Human Dengue fever imperfect vaccinated class(H_V), Human Dengue fever exposed class(H_E), Human Dengue virus infectious class (H_I)and Human Dengue fever recovered class (H_R).While the Mosquito population is further divided into three (3) classes; Mosquito Dengue fever susceptible mosquitoes' class (M_S), Mosquito Dengue fever exposed mosquitos' class (M_E)and Mosquito Dengue fever infectious mosquitos' class (M_E). The total population of humans is represented by T_h while the total population of the mosquitoes is represented by T_m and Total entire population is given as T_{hm} .

The fractional differential equation (FDE) system of the dengue virus is presented as;

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$$\left.\begin{aligned}
&(1)\quad D^{\beta}H_S(t) = \Lambda_H + \phi_h H_R - \left(\mu_h + \sigma + \beta_h\right)H_S \\
&(2)\quad D^{\beta}H_V(t) = \sigma H_S - \left(\mu_h + \varepsilon\right)H_V \\
&(3)\quad D^{\beta}H_E(t) = \beta_h H_S - \left(\mu_h + \theta_h\right)H_E \\
&(4)\quad D^{\beta}H_I(t) = \theta_h H_E - \left(\mu_h + \delta_h + \tau_h\right)H_I \\
&(5)\quad D^{\beta}H_R(t) = \tau_h H_I - \left(\mu_h + \phi_h\right)H_R \\
&(6)\quad D^{\beta}M_S(t) = \Lambda_M - \left(\mu_m + \beta_m\right)M_S \\
&(7)\quad D^{\beta}M_E(t) = \beta_m M_S - \left(\mu_m + \theta_m\right)M_E \\
&(8)\quad D^{\beta}M_I(t) = \theta_m M_E - \left(\mu_m + \delta_m\right)M_I
\end{aligned}\right\} \qquad (1)$$

Subject to the initial conditions;

$$\left.\begin{aligned}
&H_S = H_{S0} > 0, H_V = H_{V0} \geq 0, H_E = H_{E0} \geq 0, H_I = H_{I0} \geq 0, \\
&H_R = H_{R0} \geq 0,\ M_S = M_{S0} > 0, M_E = M_{E0} \geq 0 \text{ and } M_I = M_{I0} \geq 0
\end{aligned}\right\} \qquad (2)$$

Where D^{β} denotes the Caputo fractional derivative of order β ($\beta \in (0,1]$) with the DENV human and mosquito infectivity rate β_h and β_m respectively defined as follows;

$$\beta_h = \rho_1 H_I + \rho_2 \omega M_I \text{ and } \beta_m = \eta_1 \omega H_I + \eta_2 M_I \qquad (3)$$

And other DENV fractional model variables and parameters descriptions are presented in **Table 1** and **Table 2** respectively.

Table 1: DEN Fractional Model Variables Description

Variables	Description	Values	Source
H_S	DENV Susceptible Human	406,250	Mohammed et al. 2024
H_V	Revaccinated Human	20000	Mohammed et al. 2024
H_E	DENV Exposed Human	369,150	Mohammed et al. 2024
H_I	DENV Infectious Human	156,170	Mohammed et al. 2024
H_R	DENV Recovered Human	20,000	Mohammed et al. 2024
M_S	DENV Susceptible Mosquitoes	40,200	Mohammed et al. 2024
M_E	DENV Exposed Mosquitoes	32,000	Mohammed et al. 2024
M_I	DENV Infectious Mosquitoes	21,200	Mohammed et al. 2024

Table 2: DEN Fractional Model Parameters Description

Parameters	Description	Value	Source
Λ_H	recruitment rate for human	0.0000406	Mohammed et al. 2024
Λ_M	recruitment rate for mosquito	0.0005789	Naaly et al. 2024
σ	Imperfect vaccination rate for human	0.8	Mohammed et al. 2024
ε	Vaccine waning rate for human	0.25	Mohammed et al. 2024
θ_h	Exposed to Infectious progression rate for human	0.1667	Naaly et al. 2024
θ_m	Exposed to Infectious progression rate for mosquito	0.1428	Naaly et al. 2024
τ_h	Infectious to Recovered progression rate for human	0.14286	Naaly et al. 2024
ϕ_h	Human Recovered to Susceptible progression rate	0.011	Naaly et al. 2024
μ_h	natural death rate for human	0.0000457	Naaly et al. 2024

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μ_m	natural death rate for mosquito	0.03	Naaly et al. 2024
δ_h	DENV disease death rate for human	0.33	Mohammed et al. 2024
δ_m	DENV disease death rate for mosquito	0.05	WHO,2024
ω	Biting rate for mosquitoes	0.5	Naaly et al. 2024
ρ_1	transmission probability rate from Human -to-human	0.001	Rahman et al. 2024
ρ_2	transmission probability rate from Mosquito-to-human	0.375	Naaly et al. 2024
η_1	transmission probability rate from Human -to-mosquito	0.375	Naaly et al. 2024
η_2	transmission probability rate from Mosquito -to-mosquito	0.02	Chitnis et al. 2024

The Algorithm of the Adams-Bashforth-Moulton (ABM) Method

The Adam-Bashforth-Moulton method is a predictor-corrector method used for solving fractional order differential equations. It combines two components: the **Adams-Bashforth method** (a predictor) and the **Adams-Moulton method** (a corrector). The Adams-Bashforth method uses previous values of the solution to predict the next value. After predicting the value using the Adams-Bashforth method, the Adams-Moulton method is applied to correct it. The process is repeated iteratively by using the corrected value for the next step. Thus, the algorithm of the method alternates between the Adams-Bashforth method (for prediction) and the Adams-Moulton method (for correction). It leverages past values to predict the future solution, then refines that prediction using a weighted combination of current and past values. Importance of using the fractional Adam-Bashforth Moulton method in obtaining the numerical solutions of the DENV model are;

• The ABM method per step uses only one additional function evaluation yet achieves high-order and better accuracy.

• The ABM method provides error control that is automatic and commonly used in many packaged ODE solvers.

• ABM method is a useful tool for numerical solutions of partial and fractional order differential equations, various fields such as Medicine, Chemistry and Engineering are using it, and thus the method has potential applications (Atokolo et al., 2024).

The Implementation of Adams-Bashforth-Moulton (ABM) Method

We hereby obtain an approximate solution of the fractional DENV model presented in (1) using the Adam–Bashforth–Moulton method as implemented by Atokolo et al. (2024).

We present the fractional DENV model (1) as follows;

$$\left.\begin{aligned} D^{\beta}A(\mathrm{t}) &= P\left(t, A(\mathrm{t}), 0 < \mathrm{t} < \xi\right) \\ A^{(n)}\left(0\right) &= A_0^{(n)}, n = 0,1,...,A, A = [\beta] \end{aligned}\right\} \quad (4)$$

Where $A = \left(H_S, H_V, H_E, H_I, H_R, M_S, M_E, M_I\right) \in R_+^8$ and

$Z\left(t, A(t)\right)$ Is a real valued function that is continuous?

Equation () above can thus be presented in the concept of fractional integral as follows;

$$A(t) = \sum_{n=0}^{A-1} A_0^{(n)} \frac{t^n}{n!} + \frac{1}{\Gamma(\beta+2)} \int_0^t (t-x)^{\beta-1} Z\left(x, A(x)\right) dx \quad (5)$$

As earlier stated, using the method used in [31], we let the step size $f = \frac{\xi}{T}, T \in$ with a grid that is uniform on $[0, \xi]$.

Where $t_g = gr, g = 0,1,...,T..$

Therefore, the fractional order model of the DENV presented in (1) using ABM method can be approximated as follows:

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$$\left.\begin{aligned} H_{S(k+1)}(\mathrm{t}) &= H_{S0} + \frac{f^{\beta}}{\Gamma(\beta+2)}\left\{\Lambda_H + \phi_h H_R^n - \left((\mu_h+\sigma) + \left(\rho_1 H_I^n + \rho_2 \omega M_I^n\right)\right) H_S^n\right\} \\ &+ \frac{f^{\beta}}{\Gamma(\beta+2)}\sum_{x=0}^{k} b_{x,k+1}\left\{\Lambda_H + \phi_h H_{Rx} - \left((\mu_h+\sigma) + \left(\rho_1 H_{Ix} + \rho_2 \omega M_{Ix}\right)\right) H_{Sx}\right\} \end{aligned}\right\} \quad (6)$$

$$\left.\begin{aligned} H_{V(k+1)}(\mathrm{t}) &= H_{V0} + \frac{f^{\beta}}{\Gamma(\beta+2)}\left\{\sigma H_S^n - (\mu_h+\varepsilon) H_V^n\right\} \\ &+ \frac{f^{\beta}}{\Gamma(\beta+2)}\sum_{x=0}^{k} b_{x,k+1}\left\{\sigma H_{Sx} - (\mu_h+\varepsilon) H_{Vx}\right\} \end{aligned}\right\} \quad (7)$$

$$\left.\begin{aligned} H_{E(k+1)}(\mathrm{t}) &= H_{E0} + \frac{f^{\beta}}{\Gamma(\beta+2)}\left\{\left(\rho_1 H_I^n + \rho_2 \omega M_I^n\right) H_S^n - (\mu_h+\theta_h) H_E^n\right\} \\ &+ \frac{f^{\beta}}{\Gamma(\beta+2)}\sum_{x=0}^{k} b_{x,k+1}\left\{\left(\rho_1 H_{Ix} + \rho_2 \omega M_{Ix}\right) H_{Sx} - (\mu_h+\theta_h) H_{Ex}\right\} \end{aligned}\right\} \quad (8)$$

$$\left.\begin{aligned} H_{I(k+1)}(\mathrm{t}) &= H_{I0} + \frac{f^{\beta}}{\Gamma(\beta+2)}\left\{\theta_h H_E^n - (\mu_h+\delta_h+\tau_h) H_I^n\right\} \\ &+ \frac{f^{\beta}}{\Gamma(\beta+2)}\sum_{x=0}^{k} b_{x,k+1}\left\{\theta_h H_{Ex} - (\mu_h+\delta_h+\tau_h) H_{Ix}\right\} \end{aligned}\right\} \quad (9)$$

$$\left.\begin{aligned} H_{R(k+1)}(\mathrm{t}) &= H_{R0} + \frac{f^{\beta}}{\Gamma(\beta+2)}\left\{\tau_h H_I^n - (\mu_h+\phi_h) H_R^n\right\} \\ &+ \frac{f^{\beta}}{\Gamma(\beta+2)}\sum_{x=0}^{k} b_{x,k+1}\left\{\tau_h H_{Ix} - (\mu_h+\phi_h) H_{Rx}\right\} \end{aligned}\right\} \quad (10)$$

$$\left.\begin{aligned} M_{S(k+1)}(\mathrm{t}) &= M_{S0} + \frac{f^{\beta}}{\Gamma(\beta+2)}\left\{\Lambda_M - \left(\mu_m + \left(\eta_1 \omega H_I^n + \eta_2 M_I^n\right)\right) M_S^n\right\} \\ &+ \frac{f^{\beta}}{\Gamma(\beta+2)}\sum_{x=0}^{k} b_{x,k+1}\left\{\Lambda_M - \left(\mu_m + \left(\eta_1 \omega H_{Ix} + \eta_2 M_{Ix}\right)\right) M_{Sx}\right\} \end{aligned}\right\} \quad (11)$$

$$\left.\begin{aligned} M_{E(k+1)}(\mathrm{t}) &= M_{E0} + \frac{f^{\beta}}{\Gamma(\beta+2)}\left\{\left(\eta_1 \omega H_I^n + \eta_2 M_I^n\right) M_S^n - (\mu_m+\theta_m) M_E^n\right\} \\ &+ \frac{f^{\beta}}{\Gamma(\beta+2)}\sum_{x=0}^{k} b_{x,k+1}\left\{\left(\eta_1 \omega H_{Ix} + \eta_2 M_{Ix}\right) M_{Sx} - (\mu_m+\theta_m) M_{Ex}\right\} \end{aligned}\right\} \quad (12)$$

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$$\left.\begin{aligned} M_{I(k+1)}(\mathrm{t}) &= M_{I0} + \frac{f^{\beta}}{\Gamma(\beta+2)}\left\{\theta_m M_E^n - (\mu_m+\delta_m) M_I^n\right\} \\ &+ \frac{f^{\beta}}{\Gamma(\beta+2)}\sum_{x=0}^{k} b_{x,k+1}\left\{\theta_m M_{Ex} - (\mu_m+\delta_m) M_{Ix}\right\} \end{aligned}\right\} \quad (13)$$

Where;

$$\left.\begin{aligned} H_{S(k+1)}^n(\mathrm{t}) &= H_{S0} + \frac{1}{\Gamma(\beta)}\sum_{x=0}^{k} z_{x,k+1}\left\{\Lambda_H + \phi_h H_{Rx} - \left((\mu_h+\sigma) + \left(\rho_1 H_{Ix} + \rho_2 \omega M_{Ix}\right)\right) H_{Sx}\right\} \\ H_{V(k+1)}^n(\mathrm{t}) &= H_{V0} + \frac{1}{\Gamma(\beta)}\sum_{x=0}^{k} z_{x,k+1}\left\{\sigma H_{Sx} - (\mu_h+\varepsilon) H_{Vx}\right\} \\ H_{E(k+1)}^n(\mathrm{t}) &= H_{E0} + \frac{1}{\Gamma(\beta)}\sum_{x=0}^{k} z_{x,k+1}\left\{\left(\rho_1 H_{Ix} + \rho_2 \omega M_{Ix}\right) H_{Sx} - (\mu_h+\theta_h) H_{Ex}\right\} \\ H_{I(k+1)}^n(\mathrm{t}) &= H_{I0} + \frac{1}{\Gamma(\beta)}\sum_{x=0}^{k} z_{x,k+1}\left\{\theta_h H_{Ex} - (\mu_h+\delta_h+\tau_h) H_{Ix}\right\} \\ H_{R(k+1)}^n(\mathrm{t}) &= H_{R0} + \frac{1}{\Gamma(\beta)}\sum_{x=0}^{k} z_{x,k+1}\left\{\tau_h H_{Ix} - (\mu_h+\phi_h) H_{Rx}\right\} \\ M_{S(k+1)}^n(\mathrm{t}) &= M_{S0} + \frac{1}{\Gamma(\beta)}\sum_{x=0}^{k} z_{x,k+1}\left\{\Lambda_M - \left(\mu_m + \left(\eta_1 \omega H_{Ix} + \eta_2 M_{Ix}\right)\right) M_{Sx}\right\} \\ M_{E(k+1)}^n(\mathrm{t}) &= M_{E0} + \frac{1}{\Gamma(\beta)}\sum_{x=0}^{k} z_{x,k+1}\left\{\left(\eta_1 \omega H_{Ix} + \eta_2 M_{Ix}\right) M_{Sx} - (\mu_m+\theta_m) M_{Ex}\right\} \\ M_{I(k+1)}^n(\mathrm{t}) &= M_{I0} + \frac{1}{\Gamma(\beta)}\sum_{x=0}^{k} z_{x,k+1}\left\{\theta_m M_{Ex} - (\mu_m+\delta_m) M_{Ix}\right\} \end{aligned}\right\} \quad (14)$$

From equations (9) to (14) we have that

$$\left.\begin{aligned} &b_{x,k+1} = k^{\beta+1} - (k-\beta)(k+1)^{\beta}, x = 0 \\ &(k-x+2)^{\beta+1} + (k+x)^{\beta+1} - 2(k-x+1)^{\beta+1}, 1 \le x \le k \\ &1, x = k+1 \end{aligned}\right\} \quad (15)$$

And

$$z_{x,k+1} = \frac{f^{\beta}}{\beta}\left[(k-x+1)^{\beta} + (k-x)^{\beta}\right], 0 \le x \le k. \quad (16)$$

Results

In this section, we conduct some investigations numerically to demonstrate the effectiveness and applicability of the ABM method for the fractional DENV disease model presented in equation (1). The findings show that the ABM method is systematic and efficient in dealing with a variety of essential fractional calculus difficulties. All the numerical computations were performed using the MATLAB software package and numerical values in Tables 1 and 2 for the variables and parameters, respectively. The results obtained are as follows;

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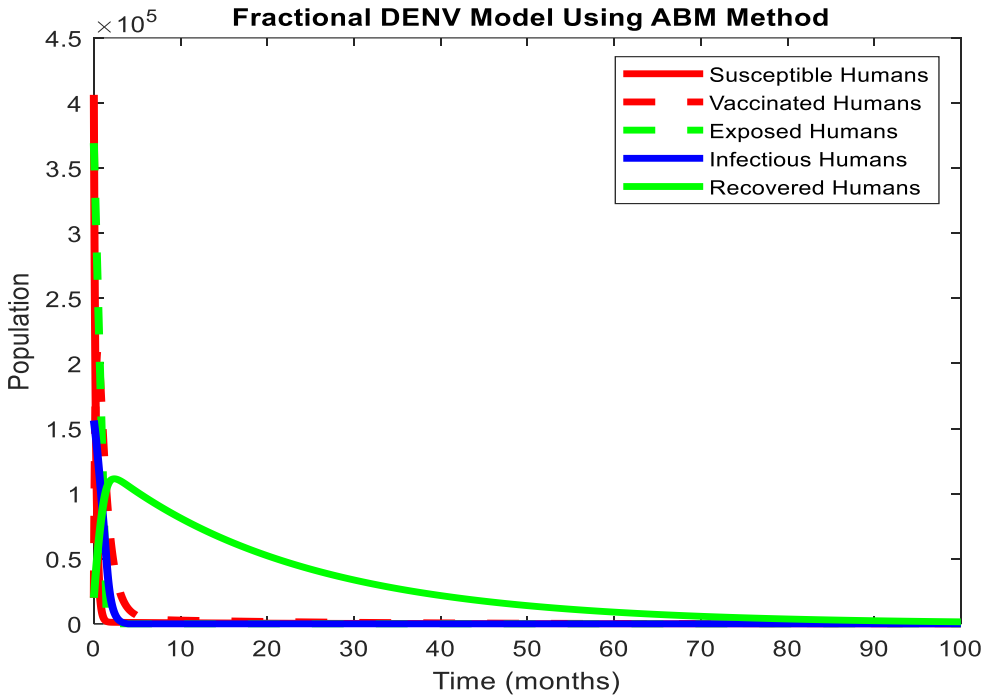

Figure 1: Human Population Fractional Order DENV Model Solution Using ABM Method

Figure 1 illustrates the transitions between human populations in different DENV epidemiological human compartments (Susceptible, Vaccinated, Exposed, Infected, and Recovered) under fractional-order dynamics. The fractional-order Adam-Bashforth-Moulton **(ABM)** method is used to model memory effects and long-term dependencies in population changes over time. The sharp decline in the susceptible population is due to vaccination and exposure, while the infected population decreases over time as individuals recover, highlighting the dynamics of disease progression and control.

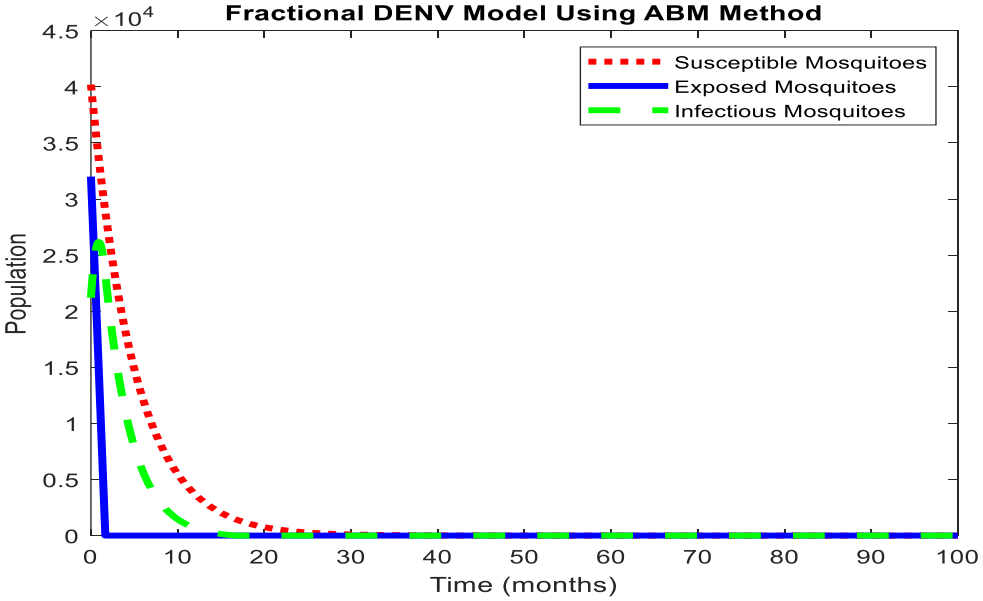

Figure 2: Mosquito Population Fractional Order DENV Model Solution Using ABM Method

Figure 2 shows the transitions between mosquito populations in different DENV epidemiological compartments (Susceptible, Exposed, and Infected) under fractional-order dynamics using the Adam-Bashforth-Moulton**(ABM)** method. The susceptible mosquito population rapidly declines due to mosquito exposure and

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infection reflecting the impact of the disease's spread in the vector population. The model highlights memory effects and long-term dependencies over time.

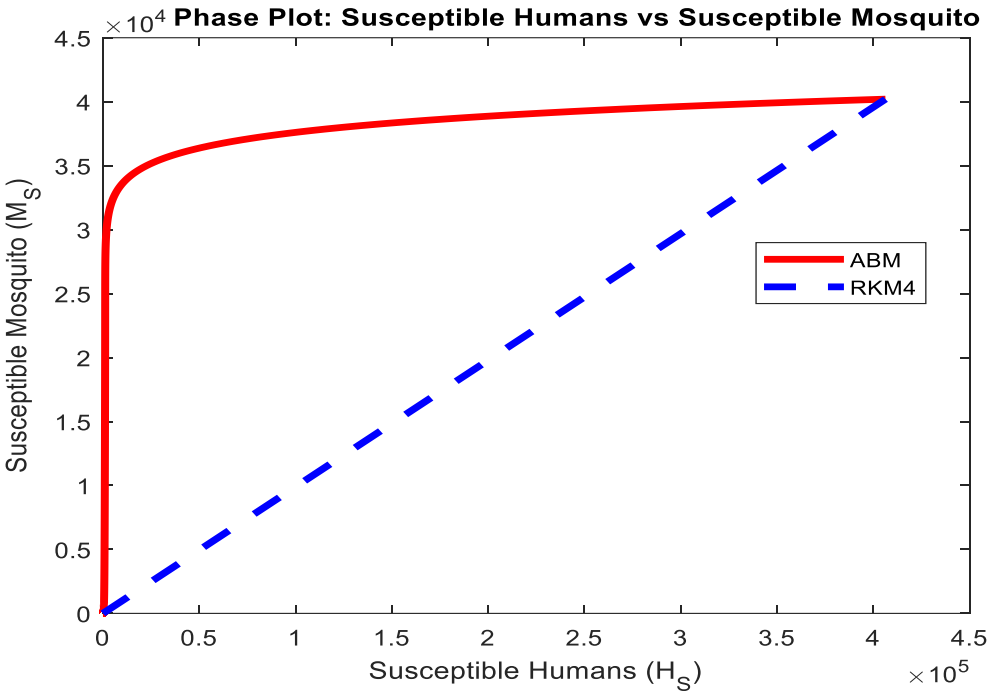

Figure 3: Phase Plot of Susceptible Humans vs Susceptible Mosquitoes

Figure 3 is a phase plot that shows the interaction between susceptible humans and susceptible mosquitoes over time. The Adam-Bashforth-Moulton (ABM) method (red solid line) captures the nonlinear dynamics of the interaction more accurately compared to the 4th-order Runge-Kutta method (RKM4, blue dashed line). The deviation between the two methods highlights the impact of fractional-order dynamics, especially over longer periods.

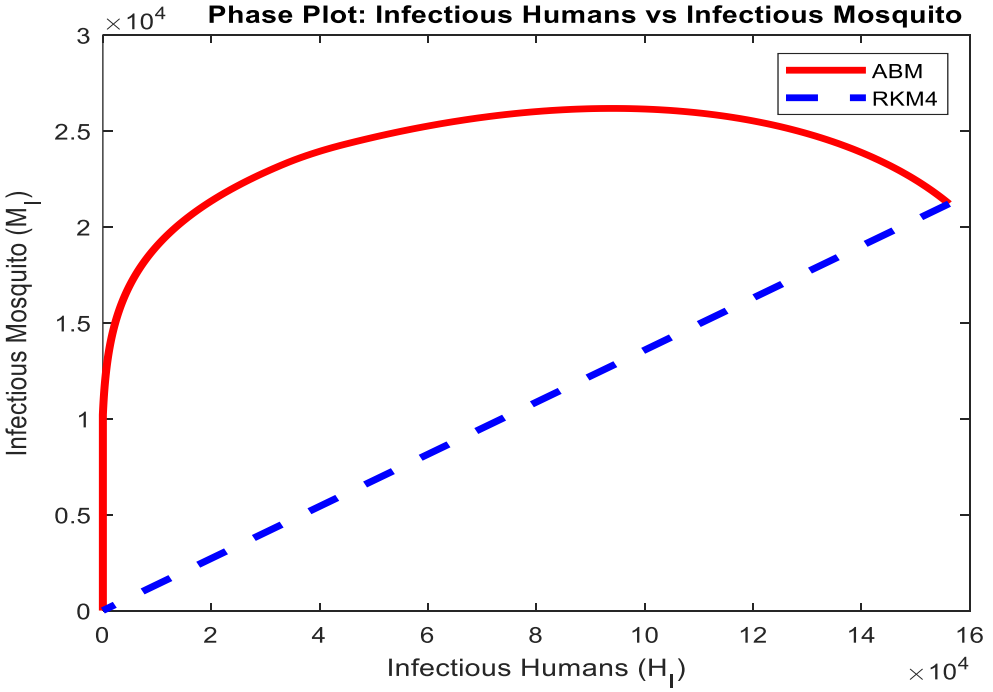

Figure 4: Phase Plot of Infectious Humans vs Infectious Mosquitoes

Figure 4 is a phase plot visualizes the relationship between infectious humans and infectious mosquitoes over time. The ABM method (red solid line) demonstrates more complex dynamics influenced by memory effects, whereas RKM4 (blue dashed line) produces a simpler trajectory. This highlights the advantage of ABM in

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capturing the intricate behavior of fractional-order systems.

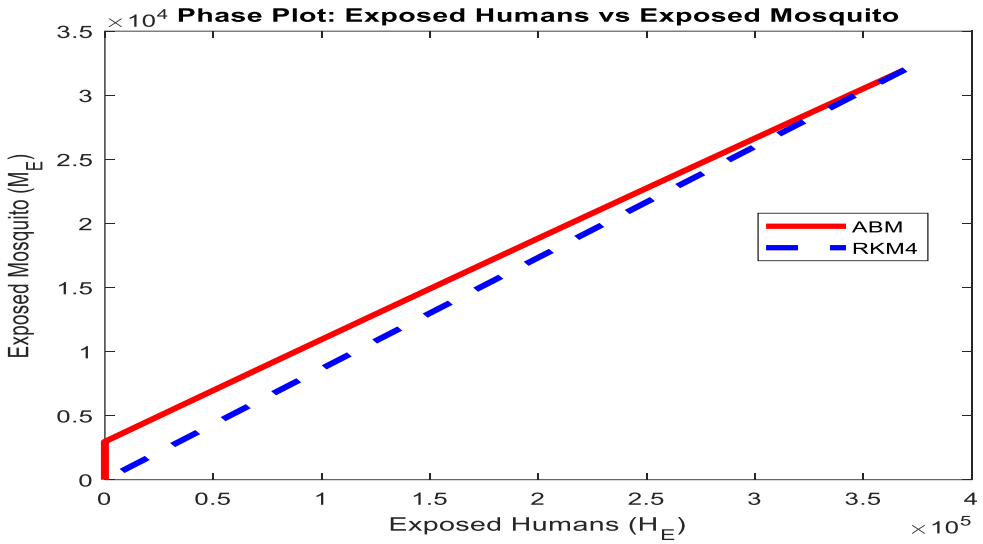

Figure 5: Phase Plot of Exposed Humans vs Exposed Mosquitoes

Figure 5 is a phase plot that compares the relationship between exposed humans and exposed mosquitoes using fractional-order dynamics. Results from the Adam-Bashforth-Moulton (ABM) method align closely with the Runge-Kutta Method of order 4 (RK4), indicating consistency in the modeled relationship between human and mosquito exposures over time.

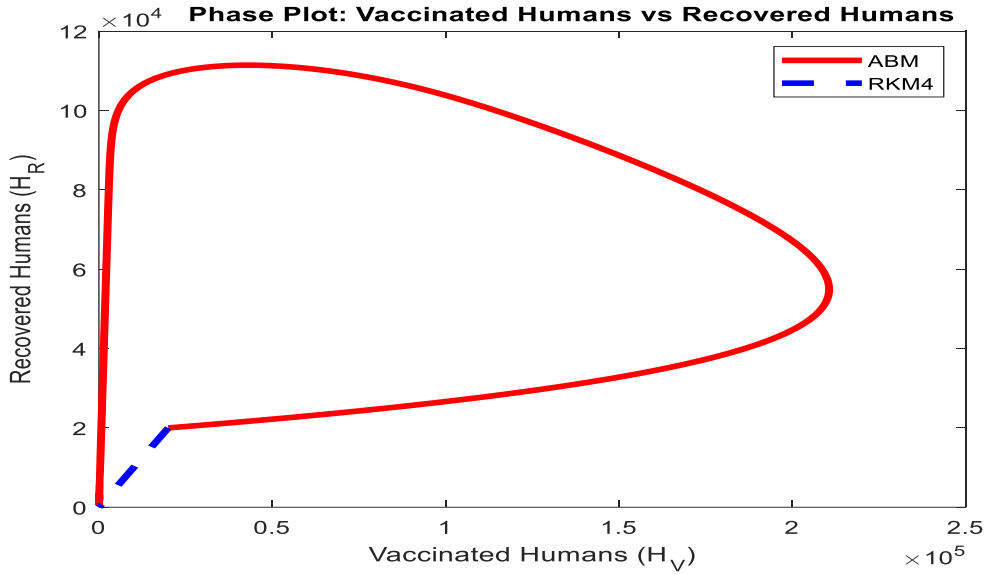

Figure 6: Phase Plot of Exposed Humans vs Exposed Mosquitoes

Figure 6 is a phase plot illustrating the relationship between vaccinated humans and recovered humans under fractional-order dynamics. The Adam-Bashforth-Moulton (ABM) method captures nonlinear interactions, with vaccinated individuals transitioning into recovery over time. The curved trajectory represents the long-term effects of vaccination and recovery dynamics.

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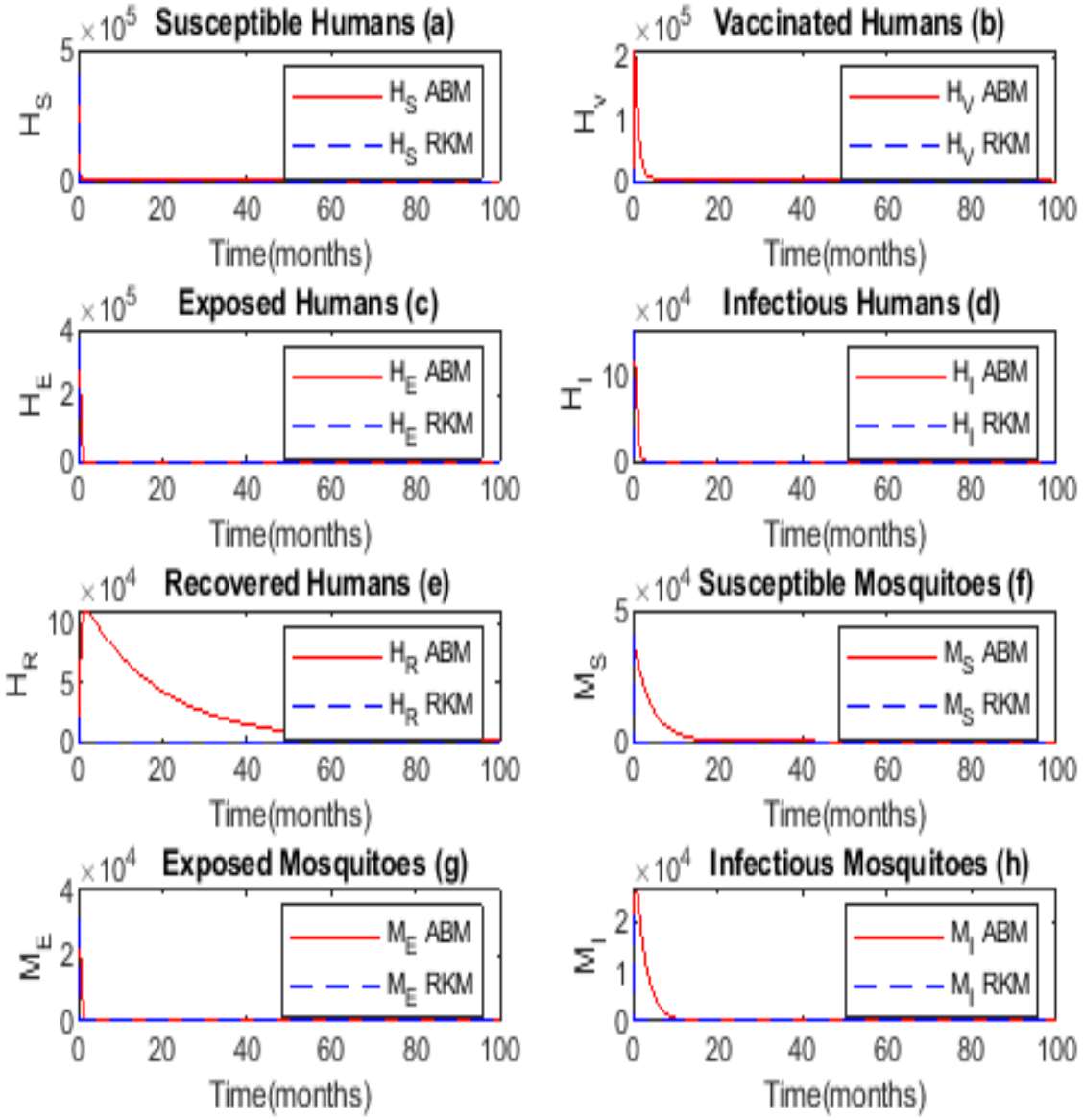

Figure 7: Humans and Mosquitoes population simulation for ABM vs RKM

Figure 7 is the time-series plots comparing population dynamics for humans and mosquitoes under the ABM and RKM4 methods. ABM (solid lines) provides a more accurate representation of fractional-order dynamics, while RKM4 (dashed lines) shows deviations, particularly in exposed and infectious compartments. This emphasizes the significance of fractional-order methods for capturing the memory effects in disease modeling.

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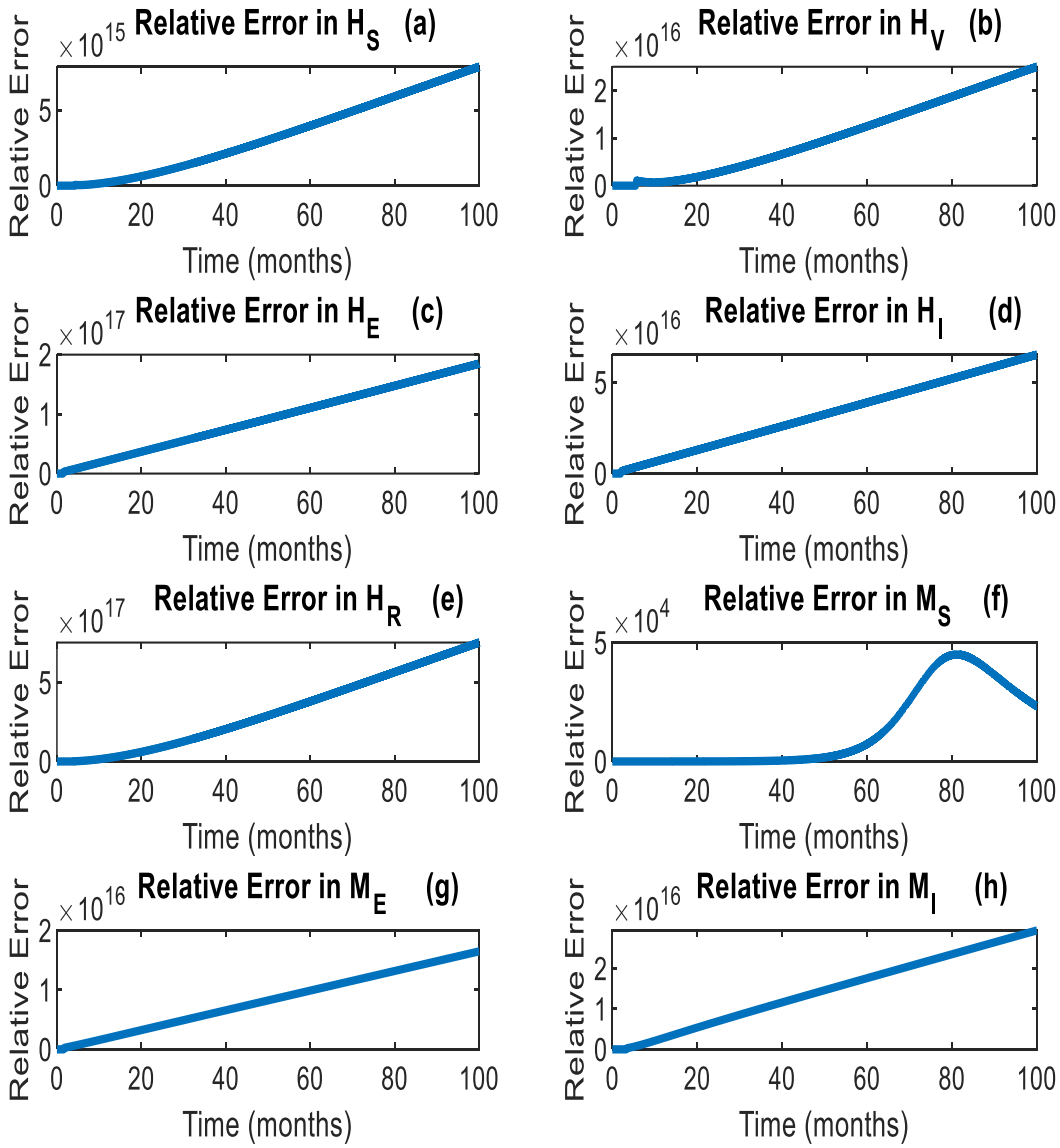

Figure 8: Humans and Mosquitoes population simulation for Relative Error

Figure 8 is the plot of relative error between the ABM and RKM4 methods for all compartments. The error grows over time, especially in compartments with high interaction rates, indicating the limitations of RKM4 in accurately solving fractional-order systems. Fluctuations in mosquito compartments suggest higher sensitivity to parameter changes.

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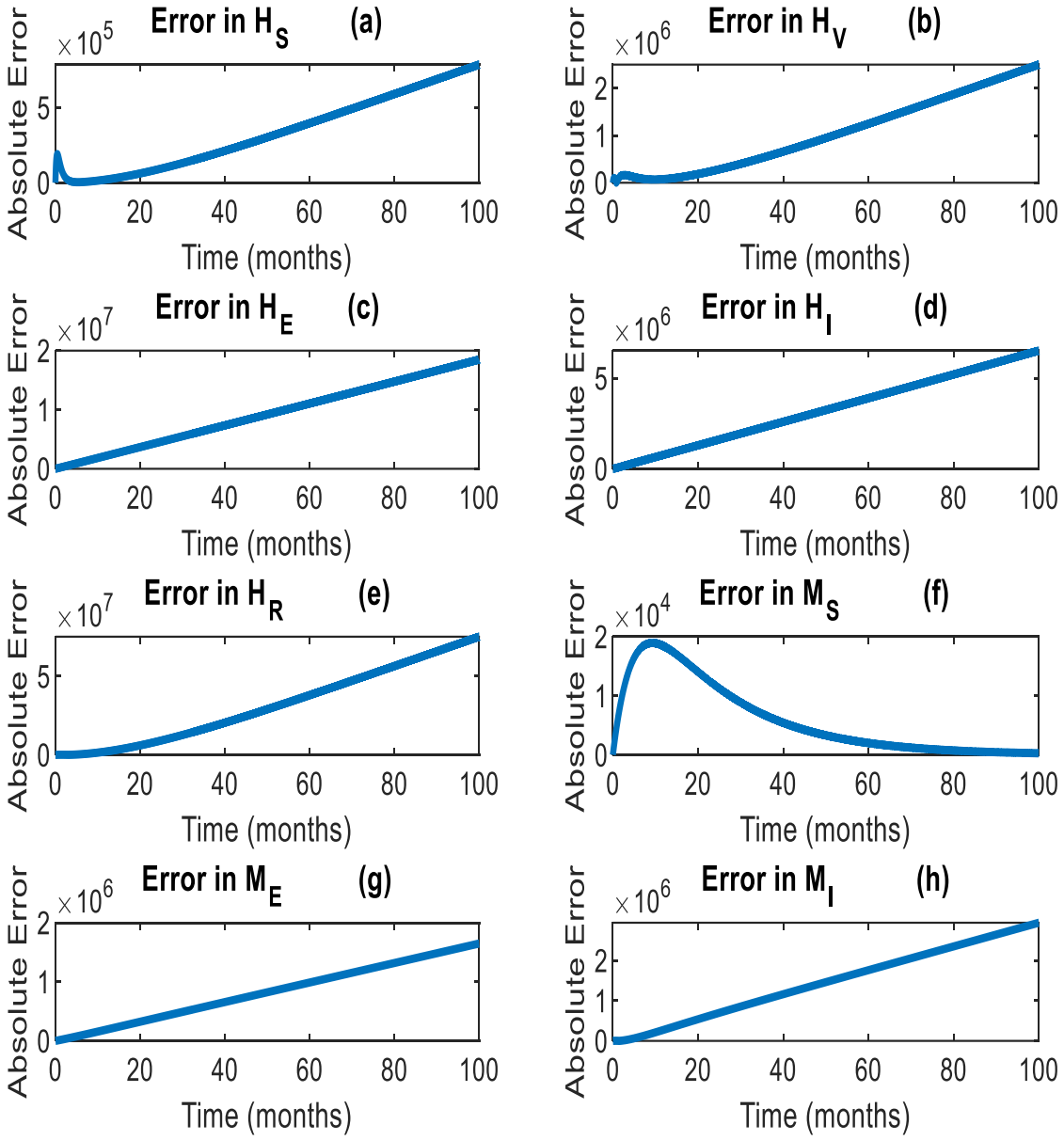

Figure 9: Humans and Mosquitoes population simulation for Absolute Error

Figure 9 illustrates the absolute error between the Adam-Bashforth-Moulton (ABM) method and RKM4 for human and mosquito populations across all compartments. The minimal absolute error underscores the accuracy and reliability of the ABM method in solving the fractional-order dengue model, similar to the results observed in Figure 8.

Discussion

The DENV fractional-order model, analyzed using the Adam-Bashforth-Moulton (ABM) method, provides valuable insights into the transmission dynamics of dengue virus within human and mosquito populations. The fractional-order approach incorporates memory effects and long-term dependencies, enabling a more realistic representation of disease progression and control strategies over time. **The human dynamics in Figure 1**highlights the transitions among human compartments under fractional-order dynamics. The sharp decline in the susceptible human population is attributed to effective vaccination and exposure, while the gradual decrease

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in the infected population over time reflects recovery dynamics. These results emphasize the importance of vaccination programs and recovery rates in mitigating dengue spread. Additionally, the memory effects inherent in fractional-order modeling provide a more comprehensive understanding of population interactions over extended periods, which is critical for developing long-term control strategies. The mosquito dynamics in **Figure 2** illustrate the dynamics within the mosquito population, where the susceptible mosquitoes decline rapidly due to exposure and infection. The ABM method captures the nonlinear relationships and long-term dependencies in the vector population, reflecting the importance of controlling vector exposure to curb the DENV disease. The decline in the mosquito population highlights the effectiveness of targeted interventions, such as insecticides or environmental management. The phase plots in Figures 3–6 offer a detailed view of the interactions between human and mosquito populations. Figure 3 demonstrates the interplay between susceptible humans and susceptible mosquitoes. The ABM method captures the nonlinear and fractional-order dynamics better than the RKM4 method, especially over longer periods. Figure 4 shows the relationship between infectious humans and infectious mosquitoes. The ABM method reveals more complex dynamics, including memory effects, whereas RKM4 simplifies these interactions, potentially leading to inaccuracies. Figure 5 compares exposed humans and exposed mosquitoes, showing alignment between ABM and RKM4 results, indicating consistency in capturing exposure dynamics. Figure 6 highlights the relationship between vaccinated and recovered humans, where the ABM method effectively captures nonlinear recovery trends influenced by vaccination. The curved trajectories underscore the long-term impact of vaccination in disease control. Figures 7 and 8 emphasize the differences between the ABM and RKM4 methods. The time-series plots (Figure 7) reveal that ABM more accurately captures the memory effects in population dynamics, while RKM4 shows deviations, particularly in the exposed and infectious compartments. The absolute error plots (Figure 8) further validate the superiority of ABM, as the error grows over time in RKM4, particularly in high-interaction compartments. This suggests that fractional-order dynamics are better suited to modeling complex DENV disease systems. Figure 9 demonstrates the overall accuracy of the ABM method across all compartments. The minimal absolute error across human and mosquito populations confirms the reliability of ABM in solving fractional-order systems. This underscores its potential as a robust method for modeling infectious diseases with memory effects, making it a valuable tool for policymakers and researchers.

Comparison with Existing Literature

The results of our fractional-order dengue model exhibit significant alignment with findings from prior studies while also providing unique insights. For instance, Alshehry et al. (2024) demonstrated the effectiveness of the Caputo–Fabrizio fractional derivative in capturing long-term memory effects in dengue transmission dynamics. Similarly, our study, employing the Caputo fractional derivative, highlights how fractional-order dynamics accurately model the nonlinear interaction between human and vector populations over time. Meena and Purohit (2024) explored the dynamics of dengue fever using fractional operators, emphasizing the importance of incorporating memory effects. Consistent with their results, our findings reveal that fractional-order methods like the Adam-Bashforth-Moulton (ABM) method provide more precise population dynamics compared to classical methods like the 4th-order Runge-Kutta method. Additionally, Usman et al. (2024) incorporated vaccination strategies into their fractional-order dengue model, showcasing their impact on reducing susceptible and infected populations. Our model extends these findings by visualizing the dynamic transitions between vaccinated and recovered populations, further emphasizing the long-term benefits of vaccination under fractional-order dynamics. Pandey and Phaijoo (2024) investigated dengue dynamics in Nepal, incorporating optimal control strategies. While their study highlighted the role of control measures in minimizing disease spread, our results contribute to this understanding by demonstrating the superior accuracy of fractional-order methods in simulating the dynamics of DENV disease progression and control. Furthermore, the analysis by Nisar et al. (2024) reviewed the role of fractional-order models in life sciences, emphasizing their ability to capture real-world phenomena more accurately than integer-order models. Our findings align with this perspective, as the ABM method captures intricate relationships between exposed and infected compartments, which are otherwise oversimplified in traditional methods. In terms of numerical techniques, studies such as Diethelm et al. (2004) and Garrappa (2010) underscored the reliability and efficiency of fractional Adams methods. Our results corroborate these observations by demonstrating the robustness of the ABM method in reducing absolute error, as shown in Figures 8 and 9, especially when compared to the classical RKM4 method. Finally, Vijayalakshmi et al. (2024) employed advanced optimal control approaches with fractional-order analysis, emphasizing the importance of clinical treatment in enhancing dengue viremia models. Our study complements this by highlighting the nonlinear interactions between vaccinated and recovered populations, showcasing the potential of fractional-order models in improving public health interventions.

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Implications for Public Health

The results presented in this study have critical implications for public health decision-making and the design of effective intervention strategies:

1. **Vaccination Programs:** The decline in the susceptible human population (**Figure 1**) underscores the importance of vaccination campaigns as a primary control measure. The recovery trends further suggest that sustained vaccination efforts could significantly reduce the infected population over time.
2. **Vector Control:** The rapid decline in susceptible mosquito populations (**Figure 2**) highlights the need for targeted vector control strategies, such as insecticide spraying, habitat destruction, and the use of biological agents. These measures can disrupt mosquito exposure and infection cycles, as reflected in the model dynamics.
3. **Memory Effects in Population Behavior:** The incorporation of memory effects in the ABM method reveals that population responses to interventions, such as vaccination or vector control, are influenced by historical exposure. This finding suggests that public health strategies should consider long-term dependencies, such as the impact of sustained campaigns or delays in interventions.
4. **Improved Predictive Modeling:** The demonstrated accuracy of the ABM method compared to RKM4 (**Figures 7–9**) highlights the need for public health models to adopt fractional-order approaches. These models can provide more reliable projections, enabling policymakers to allocate resources more effectively and plan for future outbreaks.

Broader Applications, Limitations and Future Research

This study emphasizes the need for further exploration of fractional-order dynamics in public health modeling. The findings suggest potential applications in other vector-borne diseases, such as malaria and chikungunya, where memory effects may play a critical role in disease progression. Additionally, integrating fractional-order models with spatial or stochastic frameworks could enhance their applicability in real-world scenarios, such as urban dengue outbreaks or interventions in resource-limited settings. The computational complexity of fractional-order methods, such as the Adam-Bashforth-Moulton (ABM) approach, may limit scalability for larger or more intricate systems without further optimization. From a public health perspective, the ability of fractional-order models to capture the nonlinear dynamics of disease transmission offers a powerful tool for assessing the impact of various interventions. Future research should focus on validating these models with empirical data and exploring their potential to guide real-time decision-making in outbreak management.

Conclusion

This study demonstrates that the fractional-order Adam-Bashforth-Moulton (ABM) method provides a robust and comprehensive framework for modeling dengue virus transmission dynamics, outperforming traditional methods such as the 4th-order Runge-Kutta method (RKM4). By incorporating memory effects and long-term dependencies, fractional-order methods offer a more realistic representation of epidemiological processes. This approach not only aligns with findings in recent literature but also addresses key limitations inherent in classical modeling techniques. Consequently, the results of this study contribute to the growing body of evidence advocating for the integration of fractional-order methods in infectious disease modeling, with potential implications for research advancements and public health practices.

Recommendations

Based on the findings of this study, we recommend that:

1. Further research should be conducted to validate the results using larger datasets, diverse geographical regions, and advanced modeling techniques.
2. Policymakers and health agencies are encouraged to integrate these insights into strategic planning for disease control and prevention.
3. Researchers should also explore technological advancements and novel mathematical models to improve accuracy and predictive capabilities.
4. Interdisciplinary collaboration among epidemiologists, data scientists, and public health professionals is essential for developing comprehensive solutions.
5. Translating these findings into real-world applications, such as improved vaccination programs and vector control measures, will enhance disease management efforts.

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