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TOWARD AN EFFICIENT APPROXIMATE SOLUTION AND ANALYSIS FOR HEPATITIS B VIRAL INFECTIOUS FRACTIONAL MATHEMATICAL MODEL

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ABSTRACT

Background: This paper illustrates a new fractional mathematical model of the Hepatitis B viral infection disease with conformable fractional derivative operator sense.
Objectives: We focused on examining the behaviour, performance, mathematical values representation, and prediction of the non-linear dynamic system of the life-threatening infectious disease.
Methods: The effective approximate solution of the multistage optimal homotopy asymptotic (MOHAM) method is employed in the developed fractional mathematical model for numerical solutions and simulations, which stand out amongst existing methods in comparison. The numerical simulations are also formed to investigate the influence of the system parameter on the spread of the disease, validate the fractional-order derivative's importance, and show the effect of fractional parameters on the obtained results .
Results: We obtain graphic results for various values of the fractional parameter.
Conclusions: The fractional-order derivative provides more knowledge about the complexity of the non-linear dynamics of the suggested Hepatitis B viral infectious disease model.

Keywords: Epidemiology model, Hepatitis B viral, conformable derivative operator, approximate analytical solution, fractional mathematical model

INTRODUCTION

Hepatitis B is a life-endangering hepatic infection from the hepatitis B virus. This is a general global health challenge. Hepatitis B virus infections disease only occurs when the virus enters the blood into the liver. Once it enters the liver, the virus replicates and releases many new viruses into the bloodstream (Liu et al., 2022). The spread of hepatitis B from one infected individual to a susceptible individual is vertical and horizontal. Transmission is horizontal if the virus is transmitted from person to person through infected blood, tattooing, sexual intercourse, wounds, needle shots, water or food, etc. (Oti, 2020). For vertical transmission, the hepatitis virus is passed from the mother to the newborn baby. The disease can occur in two phases: acute and chronic. Acute hepatitis B virus is less than six months in duration. If the illness is acute, your immune system is usually able to remove the virus from your body, and you should recover completely within a few months. About two -thirds of people with chronic HBV infection are chronically infected (Aninanya et al., 2015).

These individuals do not develop symptoms, even if they carry the virus and pass it on to others. More than 240 million people are chronically infected with liver disease. Developing a chronic infection is common among infants infected by their mothers. Most individual don't show symptoms in the early stages of infection (Huttner, Catho, Pano-Pardo, Pulcini, & Schouten, 2020). However, some people get seriously ill and exhibit symptoms such as yellowing of the skin and eyes (jaundice), dark urine, extreme fatigue, nausea, vomiting, and

abdominal pain which may last for many days. Individuals infected with hepatitis B virus may have an acute liver impairment that can lead to death (Smalls, Kiger, Norris, Bennett, & Love, 2019). Treatment can slow the development of cirrhosis, decrease the spread of liver cancer and improve long-term survival. There is a safe and efficient vaccine available that provides 98 -100% protection against hepatitis B. In addition to immunizing infants, the WHO recommends the use of antiviral prophylaxis to prevent the transmission of hepatitis B from mother to child. Implement safe blood transfer strategies and safe sex practices including minimizing the number of partners and using safeguards to prevent the spread of the virus. Preventing hepatitis B can help prevent complications, including chronic diseases and liver cancer. According to a 2019 report from the World Health Organization (WHO), 296 million people lived with chronic hepatitis B infection, and 1.5 million new infections each year. Fatalities were also estimated at 820000, mainly due to cirrhosis and hepatocellular carcinoma (primary liver cancer) (Kaneko et al., 2022).

Mathematical models play an important role in studying the spread of infectious diseases and are effective in suggesting control strategies. Over the past years, mathematical models have been widely used to explore a better understanding of HBV transmission and control dynamics. Nonetheless, these mathematical models have been considered in integer-order. For example, a mathematical model of HBV infection (Alrabaiah et al., 2020), grey model and artificial neural networks method for hepatitis B virus prediction (Gan, Chen, Yan, & Huang, 2015), mathematical modeling of chronic and hepatic fibrosis for hepatitis B virus (Friedman & Siewe, 2018). But the recent development of fractional calculus is gaining researchers' attention to study HBV with a non-integer order that include Caputo fractional order operator for hepatitis B model (DIN, LI, YUSUF, & ALI, 2021; Gul et al., 2021), fractal -fractional Atangana-Baleanu model for the hepatitis B virus with asymptomatic class (Li et al., 2021; Shah, Khan, Farooq, Ullah, & Alzahrani, 2020; Zhong et al., 2021), Caputo-Fabrizio derivative for hepatitis B virus dynamics systems (Ahmad, ur Rahman, & Arfan, 2021; Gao, Li, Li, & Zhou, 2021; Ullah, Altaf Khan, & Farooq, 2018). The recent numerical methods that had been used to solved HBV model include nonstandard finite difference approach for hepatitis B virus (Shaikh et al., 2021), Runge–Kutta method for hepatitis B virus (Din, Li, & Liu, 2020), decomposition method of Adomian coupled with integral transform of Laplace for hepatitis B virus (Khan et al., 2021), Newton Raphson method for hepatitis B virus (Habenom, Suthar, Baleanu, & Purohit, 2021), Liao's Homotopy Analysis Method (LHAM) for hepatitis B virus (Aniji, Kavitha, & Balamuralitharan, 2020), Homotopy Perturbation Method (HPM) for hepatitis B virus (Balamuralitharan & Vigneshwari, 2018), homotopy analysis method (HAM) for hepatitis B virus (Naik, Zu, & Ghoreishi, 2020).

The preceding approximate analytical solutions in the literature do not possess a norn for the convergence of the infinite series solution, which inspired Marinca (2009) to introduce optimal homotopy asymptotic method (OHAM), which contains the convergence criteria for the standard solution and is effective in resolving non-linear models [19]. In OHAM, no linearization is needed. Recent articles include OHAM-least square for optimization problem (Othman, Okundalaye, & Kumaresan, 2020), OHAM-Galerkin for optimization problem (Okundalaye & Othman, 2020b), OHAM for fractional optimal control problem (FOCP) (Okundalaye & Othman, 2021), OHAM for fractional-order SIR epidemic model of childhood diseases (Olumide, Othman, & Ozdemir, 2022). We implement MOHAM to solve and predicts the intending problem. This study aims to predict the transmission of HBV through time fractional mathematical model.

Motivated by this new conformable derivative operator and MOHAM approach which provide standard norm for convergence of the infinite series solution, we establish a new HBV mathematical model using a conformable derivative operator. The remaining sections are organized as follows: A basic theory of conformable derivative operator is presented in section 2. We show the mathematical model in section 3. The basic idea of the proposed method is given in section 4. Numerical results are given in section 5. Finally, the work is concluded in section 6.

2. Preliminaries of the conformable derivative operator

Today in fractional calculus various forms of operators as Atangana-Baleanu derivatives, Riemann Liouville, Caputo Fabrizio, etc, were designed to study non-linear fractional mathematical modeling. To describe real-world problems, such models have significant and used in the areas of applied science and engineering to solve complex non-linear problems. Implementing conformable derivatives operator is easier and highly efficient. The definition of a comformble derivative operator preserves many properties of traditional derivatives (Khalil, Al Horani, Yousef, & Sababheh, 2014).

Definition 2.1. Let $f:[0,\infty) \to \Re$ be a given function. The α^{th} -order the conformable derivative operator of f given

$$\mathcal{T}_\alpha(f)(t) = \lim_{\epsilon \to 0} \frac{f(t + \epsilon t^{1-\alpha}) - f(t)}{\epsilon}, \quad \forall \quad t > 0 \text{ and } \alpha \in (0,1]. \qquad (1)$$

Conformable derivative operator rules. Let $\alpha \in (0,1]$, and f, g be $\alpha -$ differentiable at a point $t > 0.$ Then

(1) $\mathcal{T}_\alpha(af + bg) = a\mathcal{T}_\alpha(f) + b\mathcal{T}_\alpha(g),$ for all $a, b \in \mathbb{R},$

(2) $\mathcal{T}_\alpha(t^p) = pt^{p-\alpha}$ for all $p \in \mathbb{R},$

(3) $\mathcal{T}_\alpha(\lambda) = 0,$ for all constant functions $f(t) = \lambda$,

(4) $\mathcal{T}_\alpha(fg) = f\mathcal{T}_\alpha(g) + g\mathcal{T}_\alpha(f),$

(5) $\mathcal{T}_\alpha\left(\frac{f}{g}\right) = \frac{g\mathcal{T}_\alpha(f) - f\mathcal{T}_\alpha(g)}{g^2},$

(6) If f is differentiable, then $\mathcal{T}_\alpha(f)(t) = t^{1-\alpha}\frac{df}{dt}(t).$

3. Model formulation of the hepatitis B virus

In this work, we reconsider (Side, Abdy, Arwadi, & Sanusi, 2021) under non-integer of conformable derivative operator sense. The SEIR model is a 4-standardized compartmental model that is typically used to describe several epidemiological diseases.

$$\frac{dS(t)}{dt} = (1-\rho)\psi NS - \beta\frac{SI}{N} - \psi S, \qquad (2)$$

$$\frac{dE(t)}{dt} = \beta\frac{SI}{N} - (\gamma + \psi)E, \quad (3)$$

$$\frac{dI(t)}{dt} = \gamma E + \tau R - (\tau + \psi)I, \quad (4)$$

$$\frac{dR(t)}{dt} = \tau\psi NS + \delta I - (\tau + \psi)R. \quad (5)$$

while ρ is vaccinated at birth β *is* rate of change of exposed to infective population, τ is natural death rates, and γ is the rate of change of susceptible to exposed population, ψ is rate of change of infective to recover population.

In order to describe the basic features that are not covered by the entire traditional-order derivatives, we formulate the model with non-interger order time derivative.

$$\frac{\mathcal{T}_\alpha S(t)}{dt} = (1-\rho)\psi NS - \beta\frac{SI}{N} - \psi S, \quad (6)$$

$$\frac{\mathcal{T}_\alpha E(t)}{dt} = \beta\frac{SI}{N} - (\gamma + \psi)E, \quad (7)$$

$$\frac{\mathcal{T}_\alpha I(t)}{dt} = \gamma E + \tau R - (\tau + \psi)I, \quad (8)$$

$$\frac{\mathcal{T}_\alpha R(t)}{dt} = \tau\psi NS + \delta I - (\tau + \psi)R. \quad (9)$$

$\mathcal{T}_\alpha$ is the conformable derivative operator.

Table 1. Parameters values that are involved in the model

Parameter	Description
$N_1 = 1$	The initial population of S(t), who are susceptible
$N_2 = 0.8$	The initial population of E(t), who are susceptible
$N_3 = 0.5$	The initial population of I(t), who are infective
$N_4 = 0$	The initial population of R(t), who is recovering
$\gamma = 0.03$	Rate of change of susceptible to exposed population
$\beta = 0.8$	Rate of change of exposed to infective population
$\psi = 0.8$	Rate of change of infective to recover population
$\rho = 0.9$	Individual vaccinated at birth
$\tau = 0.4$	Natural death rates

4. Basic ideal of the proposed method

We started by looking into basic concept of the optimal homotopy asymptotic method (OHAM) where $\mathcal{T}_\alpha$ is the CFD, $\mathcal{L}_k$ is a linear operator, N_k is a non-linear operator, t is an independent variable, $x_k(t)$ is an unknown function, φ is the problem domain, and $g_k(t)$ is a known function (Okundalaye & Othman, 2020a, 2020b, 2021; Othman et al., 2020).

$$\mathcal{T}_\alpha \xi_k(t) + \mathcal{L}_k(\xi_k(t)) + \mathcal{N}_k(\xi_k(t)) = g_k(t) \quad t \in [0,1] \quad k = 1, 2 \ldots m,$$

with initial conditions

$$\xi_k(b) = a_i. \tag{10}$$

According to OHAM, we formulate a homotopy map $\mathcal{H}_k(\phi_i(t,p)): \varphi \times [0,1] \to \varphi$ which satisfies (3.5-3.8) can be constructed using OHAM as

$$(1-\ell)[\mathcal{T}_\alpha(\aleph_k(t,\ell))] = \mathcal{H}_k(\ell)[\mathcal{T}_\alpha \aleph_k(t,\ell) + \mathcal{N}_k \aleph_k(t,\ell) + \mathcal{L}_k \aleph_k(t,\ell) + g_k(t)], \tag{11}$$

where embedding parameter (ℓ) is $0 \le \ell \le 1$, auxiliary function $\mathcal{H}_k(\ell) \quad \forall \quad \ell \neq 0$, unknown function ($\aleph_k(t,\ell)$) and $H(0) = 0$. When $\ell = 0$ and $\ell = 1$, it holds that $\aleph_k(t,0) = \psi_{k,0}(t)$ and $\aleph_k(t,1) = \psi_k(t)$ respectively. Thus as ℓ moves from 0 to 1, the solution $\aleph_k(t,\ell)$ approach from $\psi_{k,0}(t)$ to $\psi_k(t)$, where initial guess $\psi_{k,0}(t)$ satisfies the linear operator generated from (4.2) for $\ell = 0$ as

$$\mathcal{T}_\alpha(\psi_{k,0}(t)) = 0. \qquad \psi_{k,0}(b) = 0, \tag{12}$$

The $\mathcal{H}_k(\ell)$ is given as

$$\mathcal{H}_k(\ell) = \sum_{j=1}^{n} \ell^j C_j, \tag{13}$$

where C_j^s can be known later. We get an approximate solution by expanding $\aleph_k(t,\ell,C_j)$ in Taylor's series in terms of ℓ,

$$\aleph_k(t,\ell,C_j) = \psi_{k,0}(t) + \sum_{k\ge1} \psi_{i,k}(t,C_j)\ell^i \quad j = 1,2,\ldots,n, \tag{14}$$

using above in (11) with collections of the coefficient like the power of ℓ gives the governing equations $\psi_{i,0}(t)$ in a linear form in (12). Then 1^{st} problems are given as

$$\mathcal{T}_\alpha\left(\psi_{k,1}(t)\right) + g_k(t) = C_1\mathcal{N}_0\left(\psi_{k,0}(t)\right), \psi_{k,1}(b) = 0, \tag{15}$$

the general governing equations for $\psi_{k,i}(t)$ is

$$\mathcal{T}_\alpha\left(\psi_{k,i}(t)\right) - \mathcal{T}_\alpha\left(\psi_{k,i-1}(t)\right) = C_i\mathcal{N}_{k,0}\left(\psi_{k,0}(t)\right) + \sum_{m=1}^{i-1} C_{j,m}\left[\mathcal{T}_\alpha\left(\psi_{k,i-m}(t)\right) + \mathcal{N}_{k,i-m}\left(\psi_{k,i-1}(t)\right)\right],$$

$$\psi_{k,i}(b) = 0 \quad i = 2,3,\ldots m, \tag{16}$$

where $\mathcal{N}_{k,m}(\psi_0(t),\psi_{k,1}(t)\ldots,\psi_{k,m}(t))$ is the coefficient of ℓ^m, produce by expanding $\mathcal{N}_k(\aleph_k(t,\ell,C_j))$ in series relating to ℓ

$$\mathcal{N}_k(\aleph_k(t,\ell,C_j)) = \mathcal{N}_{k,0}(\psi_{k,0}(t)) + \sum_{m>1} \mathcal{N}_{k,m}(\psi_0,\psi_1,\ldots\psi_m)\ell^m, \tag{17}$$

The convergence of the series solution (4.8) relies on C_j^s. If it's convergent at $\ell = 1$ gives a solution to (10) as

$$\psi_k(t,C_j) = \psi_{k,0}(t) + \sum_{k\geq 1}^{m} \psi_{i,k}(t,C_j), j = 1,2,\ldots,n, \tag{18}$$

using (4.9) in (4.1), we have an expression for the residual error as

$$R_k(t,C_j) = \mathcal{T}_\alpha(\psi_k(t,C_j)) + \mathcal{L}_k(\psi_k(t,C_j)) + \mathcal{N}_k(\psi_k(t,C_j) - g_k(t)). \tag{19}$$

If

$$R_k(t,C_j) = 0, \tag{20}$$

then $\tilde{\psi}_k(t,C_j)$ is the exact solution. Usually, such a case does not occur. We adopt the optimization technique of the Galerkin method to find the optimal values C_j^s as given below

$$\ell_k = \frac{\partial\tilde{\psi}_k(t,C_j)}{\partial C_j} = 0 \quad k = 1,2,\ldots m, \tag{21}$$

minimize the functional

$$\Delta_k(C_j) = \int_a^b \ell_k \times R_k(t,C_j)dt. \tag{22}$$

Where the values of a and b depend on the given problem. With these known C_j^s, the approximate analytical solution (10) is well known.

If the interval of the time variable is long, then the OHAM fails to reach accurate solutions. MO-HAM overcomes this shortcoming by partitioning the time interval $[t_0, T]$, into N subintervals $[t_0, t_1)\ldots, [t_{\gamma-1}, t_y]$ where $t_\gamma = T$ and the OHAM will be utilized over each subinterval. The endpoint in each sub-interval denotes an initial approximation to the solution over the following interval. The procedure will continue until we obtain a pre-assigned time (T). Utilization of MO-HAM is relative to OHAM, with some minor changes from C_i to $C_{i,j}$ respectively. Also, the initial approximation in $[t_{y-1}, t_y]$, $\gamma = 0,1,\ldots,N-1$, will be considered as

$$u_{0,j}(t_j) = \alpha_j, \quad j = 1..N. \tag{23}$$

In addition, the deformation equation in each subinterval will change to the following

$$(1-p)[\mathcal{L}_j(u_j(t,p)) - u_{0,j}(t)] = \mathcal{H}_j(P,t)[\mathcal{L}_j(u_j(t,P)] + g(t) + \mathcal{N}_j(u_j(t,P))], \tag{24}$$

$\mathcal{H}(p,t)$ will be generalized as follows,

$$\mathcal{H}_j(P,t) = (C_{1,j} + C_{2,j}t + C_{3,j}t^2 + \ldots)P, \quad j = 1,\ldots,N. \tag{25}$$

For $i = 1,2,..m$, and $j = 1,2,\ldots N,$ we have

$$u_j(t, C_{i,j}) = u_{0,j}(t) + \sum_{k=1}^{m} u_{k,j}(t, C_{i,j}), \tag{26}$$

$$R_j(t, C_{i,j}) = \mathcal{T}_\alpha(u_j(t, C_{i,j})) + \mathcal{L}(u_j(t, C_{i,j})) + \mathcal{N}_j(u_j(t, C_{i,j})) - g_j(t), \tag{27}$$

$$J_j(C_{i,j}) = \int_{t\gamma}^{t\gamma+h} R_j^2(s, C_{i,j})ds \quad \gamma = 0,1,\ldots N-1. \tag{27}$$

The length of the subinterval $[t_\gamma, t_{\gamma+1}]$ is h, and the number of subintervals is $N = \lfloor \frac{T}{N} \rfloor$. Now we consider the derivatives (27) for $C_{i,j}$ to zero. We define $\alpha_j = u_j(t_j)$ in each subinterval $[t_\gamma, t_{\gamma+1})$. Therefore, the convergence control parameters can be determined from the solution of the following system of equations.

$$\frac{\partial J_j}{\partial c_{1,j}} = \frac{\partial J_j}{\partial c_{2,j}} = \ldots \frac{\partial J_j}{\partial c_{m,j}} = 0. \tag{28}$$

We calculate the approximate analytical solutions on each subinterval as follows.

$$u(t) = \begin{cases} u_1(t), & t_0 \le t < t_1, \\ u_2(t), & t_1 \le t < t_2, \\ . \\ . \\ . \\ u_N(t), & t_{N-1} \le t \le T. \end{cases} \tag{29}$$

5. Numerical results and Discussion.

In this section, we show the behaviour, performance, numerical simulation, mathematical values representation of the model in figures and tables as shown below.

Table 2: Comparison of different methods with MOHAM.

The number of susceptible (t) individuals in case $\alpha = 1$

Time	MOHAM (Proposed method)	OHAM	HAM	HPM
0.0	1.00000000	1.00000000	1.00000000	1.00000000
0.1	0.929379248	0.930055043	0.931207687	0.921207687
0.2	0.863127311	0.864261318	0.866474727	0.856474727
0.3	0.801222123	0.80264103	0.805828081	0.809828081
0.4	0.743593798	0.745165172	0.749244071	0.759244071
0.5	0.690130998	0.69175844	0.696653083	0.796653083
0.6	0.640688362	0.64230658	0.64794678	0.65794678
0.7	0.595092567	0.596661972	0.602983522	0.603983522
0.8	0.553150872	0.554652487	0.561597082	0.571597082
5.0	0.01444444	0.031333333	0.046744444	0.047744444
6.0	0.01444444	0.030333333	0.044654444	0.046654444

Table 3: Comparison of different methods with MOHAM.

The number of exposed (t) individuals in case $\alpha = 1$

Time	MOHAM (Proposed method)	OHAM	HAM	HPM
0.0	0.800000000	0.800000000	0.800000000	0.800000000
0.1	0.879379248	0.880055043	0.941107685	0.931207687
0.2	0.833127311	0.854261318	0.876474722	0.856474727
0.3	0.801222123	0.819264103	0.805828081	0.809828081
0.4	0.693593798	0.715165172	0.719244073	0.759244071
0.5	0.690130998	0.701175844	0.696653083	0.796653083
0.6	0.620688362	0.621230658	0.64794678	0.65794678
0.7	0.565092567	0.576661972	0.602983522	0.603983522
0.8	0.523150872	0.534652487	0.561597082	0.571597082
5.0	0.01344444	0.031333333	0.045745555	0.04768888
10.3	0.01444444	0.030333333	0.04465888	0.04665555

Table 4: Comparison of different methods with MOHAM.

The number of infected (t) individuals in case $\alpha = 1.$

Time	MOHAM (Proposed method)	OHAM	HAM	HPM
0.0	0.50000000	0.5000000	0.50000000	0.5000000
0.1	0.517303285	0.518298997	0.51979812	0.517202274
0.2	0.532157737	0.534124433	0.537103361	0.532146537
0.3	0.544521403	0.547412868	0.551828479	0.544421303
0.4	0.554404513	0.558157009	0.563946022	0.554404213
0.5	0.561862264	0.566399051	0.573482011	0.561852234
0.6	0.566986866	0.572222272	0.580507425	0.566885866
0.7	0.569900851	0.57574437	0.585131446	0.569800751
0.8	0.570748057	0.577107802	0.587491363	0.570648046
10.0	0.001111111	0.002342222	0.00343333	0.001111111
10.50	0.001111111	0.002132222	0.00324333	0.001111111

Table 5: Comparison of different methods with MOHAM.

The number of recovered (t) individuals in case $\alpha = 1.$

Time	MOHAM (Proposed method)	OHAM	HAM	HPM
0.0	0.00000000	0.00000000	0.0000000	0.0000000
0.1	3.68E-02	3.76E-02	3.88E-02	3.67E-02
0.2	7.22E-02	7.37E-02	7.60E-02	7.21E-02
0.3	0.10622036	0.108513982	0.111906369	0.10621016
0.4	0.138961458	0.141974187	0.146409874	0.138861448
0.5	0.17044422	0.174154207	0.179592284	0.17032322
0.6	0.200710974	0.205096732	0.211497897	0.200710564
0.7	0.229802717	0.234843058	0.242169546	0.229702617
0.8	0.257759231	0.263433226	0.271648755	0.257748231
10	0.855555555	0.867777777	0.877677777	0.855555555
11	0.855555555	0.868677777	0.877537777	0.855555555

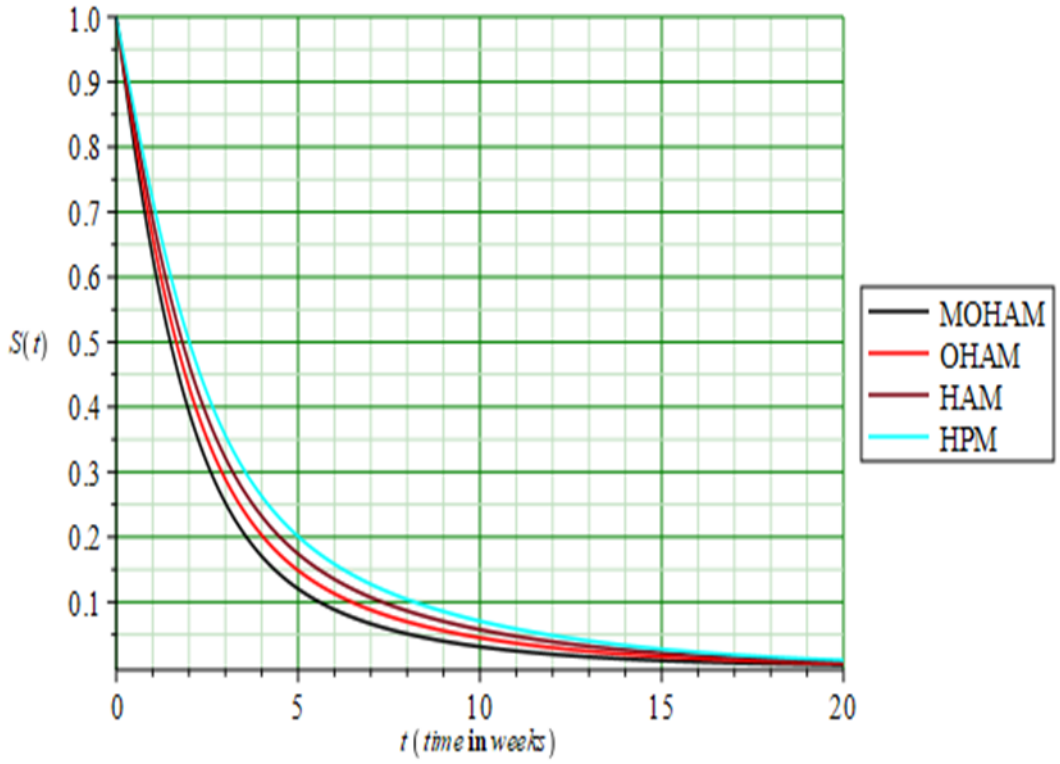

Figure 1: MOHAM = black, OHAM = red, HAM = burgundy, HPM = cyan. $\alpha = 1$

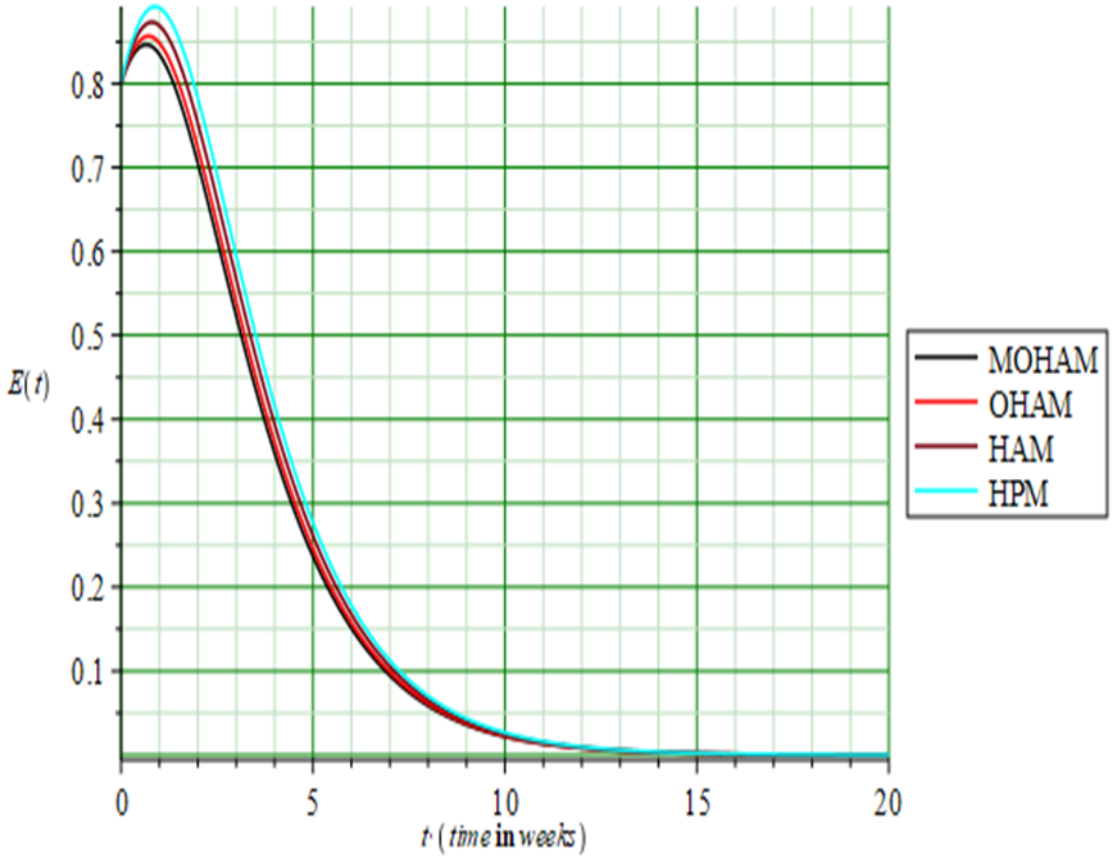

Figure 2: MOHAM = black, OHAM = red, HAM = burgundy, HPM = cyan. $\alpha = 1$.

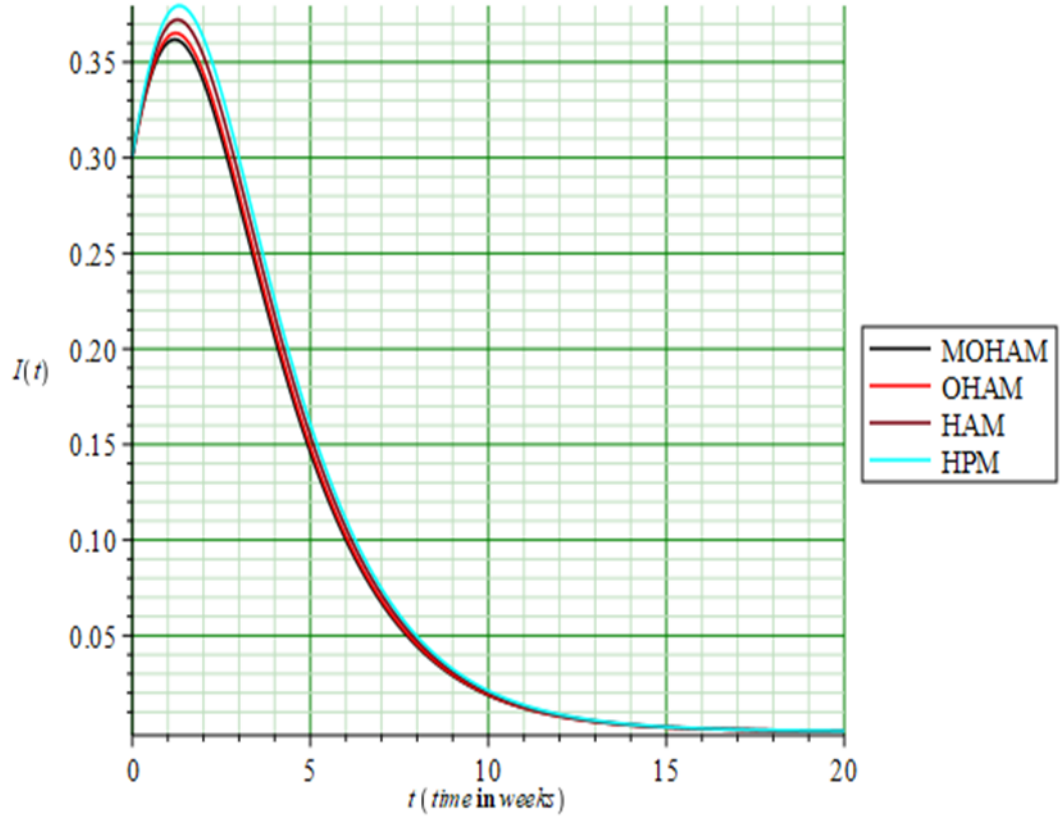

Figure 3: MOHAM = black, OHAM = red, HAM = burgundy, HPM = cyan. $\alpha = 1$.

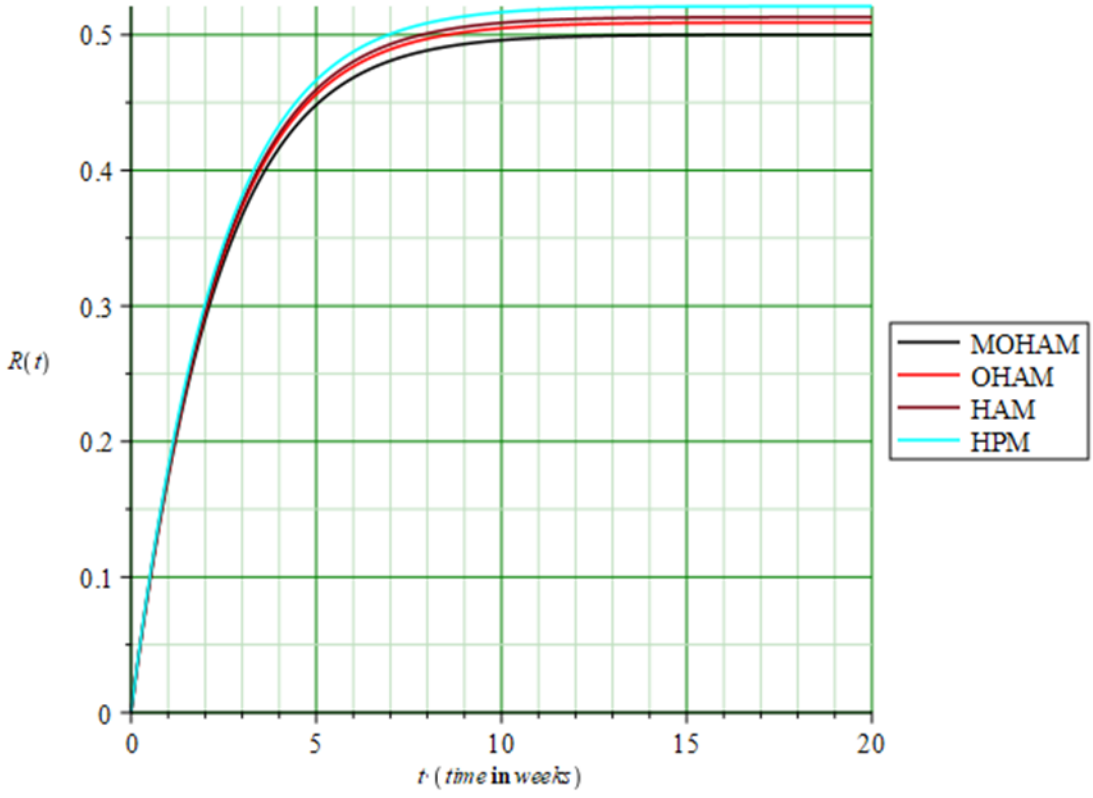

Figure 4: MOHAM = black, OHAM = red, HAM = burgundy, HPM = cyan. $\alpha = 1$.

Table 7: The number of each individual in case ($\alpha = 1$ **MOHAM.)**

Susceptible (t)	Exposed (t)	Infected (t)	Recovered (t)
1.00000000	0.800000000	0.500000000	0.00000000
0.929379248	0.879379248	0.517303285	3.68E-02
0.863127311	0.833127311	0.532157737	7.22E-02
0.801222123	0.801222123	0.544521403	0.10622036
0.743593798	0.693593798	0.554404513	0.138961458
0.690130998	0.690130998	0.561862264	0.17044422
0.640688362	0.620688362	0.566986866	0.200710974
0.595092567	0.565092567	0.569900851	0.229802717
0.553150872	0.523150872	0.570748057	0.257759231
0.0144444444	0.01344444	0.041111111	0.855555555
0.0144444444	0.01444444	0.001111111	0.855555555

Table 8: The number of each individual in case($\alpha = 0.95$ MOHAM.)

Susceptible (t)	Exposed (t)	Infected (t)	Recovered (t)
1.00000000	0.800000000	0.50000000	0.00000000
0.927842288	0.869456433	0.512346758	3.52E-02
0.860175334	0.833127311	0.522381672	6.91E-02
0.796970288	0.792338857	0.530128732	0.101697177
0.738149859	0.757664646	0.535651526	0.13304721
0.683594945	0.677464678	0.539045874	0.16319345
0.633152225	0.60688362	0.540432732	0.192176089
0.586640434	0.54888277	0.539952213	0.220034067
0.543859051	0.507447778	0.537756279	0.246805192
0.012222222	0.01177777	0.032555555	0.837222222
0.012222222	0.01177777	0.032555555	0.837222222

Table 9: The number of each individual in case ($\alpha = 0.85$,MOHAM.)

Susceptible (t)	Exposed (t)	Infected (t)	Recovered (t)
1.00000000	0.800000000	0.50000000	0.00000000
0.926689569	0.845524444	0.507437731	3.29E-02
0.857961351	0.818846468	0.512785195	6.45E-02
0.793781413	0.772228889	0.516116486	9.49E-02
0.734066906	0.719998877	0.517532866	0.124175837
0.678692905	0.633388888	0.517156022	0.152317295
0.627500122	0.618877778	0.515122226	0.17937376
0.580301334	0.568123455	0.51157739	0.205381091
0.546892186	0.548774777	0.50667157	0.230374134
0.011111111	0.01044444	0.02344444	0.7932111111
0.011111111	0.01044444	0.02344444	0.7932111111

Table 10: Tthe number of each individual in case ($\alpha =$ **0.75 MOHAM)**

Susceptible (t)	Exposed (t)	Infected (t)	Recovered (t)
1.00000000	0.800000000	0.50000000	0.00000000
0.926305329	0.826655566	0.502575746	3.09E-02
0.857223357	0.794655666	0.503365007	6.06E-02
0.792718454	0.767888888	0.502474608	8.93E-02
0.732705921	0.708888888	0.500027073	0.116783026
0.677058892	0.608888888	0.496155081	0.143253833
0.625616088	0.5799999999	0.490997101	0.168705153
0.578188301	0.558223333	0.484693678	0.193170278
0.534567229	0.528848888	0.477383691	0.216681586
0.000111111	0.010033333	0.01566666	0.749555555
0.000111111	0.01033333	0.01566666	0.749555555

We present some numerical simulations for eqautions (3.5-3.8) to validate the effectiveness of the main findings. The simulation is carried out using the proposed MOHAM method. The methodology was implemented to demonstrate the behaviors, performance and mathematical values of fractional-order models. Comparisons to existing analytical approaches can be found in the **Figures** (1-4) for integer-order $\alpha = 1$. **Tables** (2-5) present mathematical values and the effectiveneness of the MOHAM method with existing methods. The results in **Tables** (7-10) show the $\alpha \in [0.75, 0.85, 0.95, 1]$ trajectory prediction of the transmission. We observed that by moving along the specific range, consistency and precision are achieved.

6. Conclusion

This work implements the MOHAM approach to describe the fractional-order hepatitis B virus model for behaviour, perforemance, and mathematical values. We formulated the model with the latest fractional derivative operator of conformable derivative operator sense. The MOHAM method has a greater advantage over existing methods in quick convergence. The proposed method converges within two-order of the approximation solutions as opposed to other approximate analytical methods with five-ten approximation solutions. The MOHAM technique is reliable, dependable, and efficient for SEIR Hepatitis B model prediction. In the future, researchers may involve quarantine or vaccination or both the compartment to the model.

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