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Analysis for fractional dynamics of Ebola virus model

Harendra Singh

Department of Mathematics, Post-Graduate College, Ghazipur 232001, Uttar Pradesh, India

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Ebola virus is very challenging problem of the world. The main purpose of this work is to study fractional Ebola virus model. An efficient computational method based on iterative scheme is proposed to solve fractional Ebola model numerically. Stability of proposed method is also discussed. Efficiency of proposed method is shown by listing CPU time. Proposed computational method will work for long time domain. Numerical results are presented graphically. The main reason for using this technique is low computational cost and high accuracy. It is also shown how the approximate solution varies for fractional and integer order Ebola virus model.

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1. Introduction

Ebola virus disease, which was first discovered near Ebola River in Africa in 1976, is a serious disease with rare outbreaks. The Ebola virus affects humans and animals like monkeys, gorillas, and chimpanzees. At the initial stage, this virus was affecting people and causing outbreaks in some African countries. The origin of the Ebola virus was not determine exactly. The bats or other animals are considered as origin for this type of virus. This virus infects the humans by direct contact with the blood in the starting [1,2].

Now many researchers are working in the area of fractional calculus. Many analytical and numerical approach have been developed to solve problems in fractional calculus [3–13]. Fractional calculus has many real life applications like in engineering, epidemiology, fluid mechanics, physics, chemistry, medical and health sciences. The mathematical model based on Ebola outbreak in Liberia was studied by Rachah et al. [14] and the results were simulated using existing data provided by the World Health Organization. Area et al. [15] investigated fractional SEIR Ebola outbreak model. In [16], authors used two models for optimal control of Ebola disease. Atangana and Goufo [17], studied generalised version of Ebola virus model and also discussed the endemic equilibrium points. In [18], authors discussed this model using Atangana Baleanu fractional derivative and also discussed existence and uniqueness of the solutions. Some other method on Ebola disease can be found in [19–21]. Some recent developments in the area of numerical methods to solve this type of models can be found in [22,23].

In this paper we will use an iterative scheme to solve fractional Ebola virus model as given in [18–20]. Proposed iterative scheme is based on the discretization of the domain. We are using Grünwald–Letnikov (GL) fractional derivative for the fractional Ebola virus model. Coefficients in the approximation of GL derivative is very easy in computation and provides long time behaviour of solution in the fraction of second. The solution behaviour is shown in long time interval. Stability is also discussed for proposed iterative scheme. Figures and tables are used to show the numerical results. CPU time taken in iterative scheme for different values of iterations are listed. Behaviour of approximate solutions for integer and fractional order derivatives are shown using figures. Finally some concluding remarks are given.

2. Model description

The present model is based on the fact that total population at time $t$ is denoted by $N(t)$ and divided into four subgroups. We write these subgroups as follows:

$A(t)$ is the subgroup of susceptible people; $B(t)$ is the subgroup of infected people; $C(t)$ denote the subgroup of recovered people; $D(t)$ is the subgroup of died people in that region. These are specified by $N(t) = A(t) + B(t) + C(t) + D(t)$. The evolutionary dynamics described by the model is given by:

$$\frac{dA(t)}{dt} = -a_1A(t)B(t) + b_1C(t) - c_1N,$$

$$\frac{dB(t)}{dt} = a_2A(t)B(t) - d_1B(t) - e_1B(t),$$

$$\frac{dC(t)}{dt} = e_1B(t) - b_1C(t),$$

$$\frac{dD(t)}{dt} = d_1B(t) + c_1N.$$

(1)
Also, \( N \) represents the total population in the region, \( d_t \) is the rate of recovery, \( b_i \) is the rate of infection from Ebola, \( c_i \) is the amount of death rate, \( d_i \) is the rate of death from Ebola and \( e_i \) is the rate of susceptibility. The Ebola virus model strongly depends on initial conditions and integer order Ebola virus model cannot explain perfectly this model. In addition to show the effect of above mentioned parameters numerically and for better understand of Ebola virus model it is require to replace integer order Ebola virus model to fractional order model. In this paper we will replace time derivative in Ebola virus model with fractional time derivative given by

\[
aD^\alpha_t A(t) = -a_1A(t)B(t) + b_1C(t) - c_1N. \\
aD^\alpha_t B(t) = a_1A(t)B(t) - d_1B(t) - e_1B(t). \\
aD^\alpha_t C(t) = e_1B(t) - b_1C(t),
\]

(2)

With initial conditions
\[
\begin{align*}
A(0) &= d_1, \\
B(0) &= d_2, \\
C(0) &= d_3, \\
D(0) &= d_4,
\end{align*}
\]

where, \( 0 \leq p_1, p_2, p_3, p_4 < 1 \).

3. Preliminaries

In this section, we will describe some basic preliminaries for Grünwald–Letnikov derivative and Jacobian of matrix.

**Definition.** [24]: If we consider \( n = \frac{1}{r} \leq 2 \), where \( r \) is a real constant, the Grünwald–Letnikov definition is defined as

\[
aD^\alpha_t g(t) = \lim_{h \to 0} \frac{1}{M} \sum_{j=0}^{[\frac{n}{r}]} (-1)^j \binom{n}{j} g(t - jh),
\]

(4)

where \([\cdot]\) denote the integer part.

The fractional-order linear system can be written as

\[
OD^\alpha_t x(t) = A \cdot x(t) + B \cdot u(t).
\]

(5)

\( y(t) = C \cdot x(t) \).

Using Eq. (4), the \( p \)-th order Grünwald–Letnikov derivative at the points \( kh \) \((k = 1, 2, \ldots)\) has the following form

\[
\left(k - \frac{j}{h}\right) aD^\alpha_t g(t) \approx -h^{-p} \sum_{j=0}^{k} (-1)^{j/p} \binom{n}{j} g(t - jh).
\]

(6)

where \( L \) is “memory length”, \( t_k = kh \), \( h \) is the step size of calculation and the coefficients \( c_j^{(p)} \) \(( j = 0, 1, \ldots)\) can be calculated by using following expressions

\[
c_0^{(p)} = 1 \quad \text{and} \quad c_j^{(p)} = \left(1 - \frac{j}{p} + \frac{1}{p}\right) c_{j-1}^{(p)}.
\]

(7)

Then the general approximate solution of the equation

\[
aD^\alpha_t y(t) = g(y(t), t).
\]

(8)

is given as

\[
y(t_k) = g(y(t_k), t_k)h^p - \sum_{j=0}^{k-1} c_j^{(p)} y(t_{k-j}).
\]

(9)

Short memory principle can be used for the memory term expressed by a sum and for the determination of lower index. Using short memory the lower index in sum is given as

\[
v = \begin{cases} 
1, & k < (L/h) \\
L/(h), & k > (L/h).
\end{cases}
\]

For the \( L \), we can use \( L > (\frac{M}{\Gamma(1+1/p)})^{1/p}. \)

The fractional order systems given by

\[
aD^\alpha_t x_i(t) = f_i(x_1, x_2, \ldots, x_i, \ldots, x_n), \quad i = 1, 2, \ldots, n.
\]

(11)

where \( aD^\alpha_t \) is fractional GL derivative and \( q \in (0, 1] \). The equilibrium points for system of differential equation is obtained by solving

\[
aD^\alpha_t x_i(t) = 0, \quad i = 1, 2, \ldots, n.
\]

(12)

The Jacobian matrix of system is given by

\[
\begin{bmatrix}
\frac{\partial f_1}{\partial x_1} & \cdots & \frac{\partial f_1}{\partial x_n} \\
\vdots & \ddots & \vdots \\
\frac{\partial f_n}{\partial x_1} & \cdots & \frac{\partial f_n}{\partial x_n}
\end{bmatrix}.
\]

(13)

Let \((b_1, b_2, \ldots, b_n)\) be an equilibrium point then we calculate Jacobian matrix at equilibrium point as

\[
\begin{bmatrix}
\frac{\partial f_1}{\partial x_1} & \cdots & \frac{\partial f_1}{\partial x_n} \\
\vdots & \ddots & \vdots \\
\frac{\partial f_n}{\partial x_1} & \cdots & \frac{\partial f_n}{\partial x_n}
\end{bmatrix}_{(b_1, b_2, \ldots, b_n)}
\]

(14)

**Theorem 3.1.** [25,26]. The system in Eq. (11), is locally stable if all the eigenvalues of Jacobian matrix given in Eq. (14), will satisfy the condition

\[
|\arg (\lambda)| > \frac{\beta_1 \pi}{2}, \quad \text{where} \quad i = 1, 2, 3, 4, 5.
\]

(15)

4. Outline of method

In this section we will apply our proposed method to get the approximate values to the unknowns in Ebola virus model. The integer order Ebola virus model is given as

\[
\begin{align*}
\frac{dA(t)}{dt} &= -a_1A(t)B(t) + b_1C(t) - c_1N, \\
\frac{dB(t)}{dt} &= a_1A(t)B(t) - d_1B(t) - e_1B(t), \\
\frac{dC(t)}{dt} &= e_1B(t) - b_1C(t), \\
\frac{dD(t)}{dt} &= d_1B(t) + c_1N.
\end{align*}
\]

(16)

Taking integral on both side Eq. (16), we get

\[
\begin{align*}
A(t) &= \int_0^t \left[-a_1A(t)B(t) + b_1C(t) - c_1N\right] dt, \\
B(t) &= \int_0^t \left[a_1A(t)B(t) - d_1B(t) - e_1B(t)\right] dt, \\
C(t) &= \int_0^t \left[e_1B(t) - b_1C(t)\right] dt, \\
D(t) &= \int_0^t \left[d_1B(t) + c_1N\right] dt.
\end{align*}
\]

(17)

In this paper we consider fractional corona virus model by replacing integer order derivative by fractional order GL derivative and given as

\[
\begin{align*}
aD^\alpha_t A(t) &= -a_1A(t)B(t) + b_1C(t) - c_1N, \\
aD^\alpha_t B(t) &= a_1A(t)B(t) - d_1B(t) - e_1B(t), \\
aD^\alpha_t C(t) &= e_1B(t) - b_1C(t), \\
aD^\alpha_t D(t) &= d_1B(t) + c_1N.
\end{align*}
\]

(18)
Using GL definition in Eq. (19), we get following iterative relations between unknowns:

\[
A(t_k) = aD_t^{1-p_1}\left(\int_0^t [-a_1A(t)B(t) + b_1C(t) - c_1N]dt\right),
\]

\[
B(t_k) = aD_t^{1-p_2}\left(\int_0^t [a_1A(t)B(t) - d_1B(t) - e_1B(t)]dt\right),
\]

\[
C(t_k) = aD_t^{1-p_3}\left(\int_0^t [e_1B(t) - b_1C(t)]dt\right),
\]

\[
D(t_k) = aD_t^{1-p_4}\left(\int_0^t [d_1B(t) + c_1N]dt\right).
\]

Using GL definition in Eq. (19), we get following iterative relations between unknowns:

\[
A(t_k) = \left(-a_1A(t_{k-1})B(t_{k-1}) + b_1C(t_{k-1}) - c_1N\right)h^{p_1} - \sum_{j=0}^{k-1} c_j^{(p_1)}A(t_{k-j}),
\]

\[
B(t_k) = \left(a_1A(t_{k})B(t_{k}) - d_1B(t_{k}) - e_1B(t_{k})\right)h^{p_2} - \sum_{j=0}^{k-1} c_j^{(p_2)}B(t_{k-j}).
\]

\[
C(t_k) = \left(e_1B(t_{k}) - b_1C(t_{k})\right)h^{p_3} - \sum_{j=0}^{k-1} c_j^{(p_3)}C(t_{k-j}).
\]

\[
D(t_k) = \left(d_1B(t_{k}) + c_1N\right)h^{p_4} - \sum_{j=0}^{k-1} c_j^{(p_4)}D(t_{k-j}).
\]

In Eq. (20), we have got an iterative relations to get the approximate solution for fractional Ebola virus model. Now we will iterate above relations as required number of iterations to achieve the desired accuracy. As the step size will minimize then the number of iterations will increase and the solution become more accurate. We have taken step-size \(h = 0.01\) in all numerical simulation to calculate the approximate solution for the group of fractional Ebola virus model.
5. Stability analysis

In this section we will discuss stability of our mathematical model. We will use concept of Jacobian matrix and equilibrium points to show the stability of our model.

The equilibrium points for system (18) is given by

\[ aD_t^pA(t) = -a_1A(t)B(t) + b_1C(t) - c_1N = 0, \]
\[ aD_t^pB(t) = a_1A(t)B(t) - d_1B(t) - e_1B(t) = 0, \]
\[ aD_t^pC(t) = e_1B(t) - b_1C(t) = 0, \]
\[ aD_t^pD(t) = d_1B(t) + c_1N = 0. \] (21)

Using Eq. (13), the Jacobian matrix of above system is given as

\[ J = \begin{bmatrix}
-a_1B & -a_1A & b_1 & 0 \\
0 & a_1B & a_1A - d_1 - e_1 & 0 \\
0 & e_1 & -b_1 & 0 \\
0 & d_1 & 0 & 0
\end{bmatrix}. \] (22)

5.1. Endemic equilibrium points

Since we are calculating Endemic equilibrium end points which are characterized by the existence of infected nodes (i.e. \( B \neq 0 \)). The Endemic equilibrium point is given as \((\frac{d_1 + e_1}{b_1}, -Nc_1 \frac{d_1 + e_1}{b_1d_1}, -\frac{Nc_1d_1}{b_1d_1}, 0)\).

Since two coordinates are negative therefore it avoid the existence of this type equilibrium point. For the parameters, \( N = 1,000, \)
\( a_1 = 0.01, b_1 = 0.02, c_1 = 0.01, d_1 = 0.6, e_1 = 0.4 \). The equilibrium point is given as \((100, -\frac{50}{3}, -\frac{1000}{3}, 0)\).

The Jacobian matrix at equilibrium point \((100, -\frac{50}{3}, -\frac{1000}{3}, 0)\) is given as

\[
J_1 = \begin{bmatrix}
0.1667 & -1 & 0.02 & 0 \\
-0.1667 & 0 & 0 & 0 \\
0 & 0.4 & -0.02 & 0 \\
0 & 0.6 & 0 & 0
\end{bmatrix}.
\]  \( (23) \)

The Eigen values corresponding to matrix \(J_1\) are \(\lambda_1 = 0, \lambda_2 = 0.4969, \lambda_3 = -0.3383, \lambda_4 = -0.0119\). \(J_1\) has two negative Eigen values and one positive Eigen value. Two Eigen values are negative therefore it has a stable manifold of dimension two and unstable manifold of dimension one at Endemic equilibrium point \((100, -\frac{50}{3}, -\frac{1000}{3}, 0)\). Since it has a two dimensional stable manifold so from dynamical point of view it has very importance.

For the parameters, \( N = 1.00, a_1 = 0.02, b_1 = 0.04, c_1 = 0.01, d_1 = 0.6, e_1 = 0.4\). The Endemic equilibrium point is given as \((50, -1.67, -16.67, 0)\).

The Jacobian matrix at Endemic equilibrium point \((50, -1.67, -16.67, 0)\) is given as

\[
J_2 = \begin{bmatrix}
0.0333 & -1 & 0.04 & 0 \\
-0.0333 & 0 & 0 & 0 \\
0 & 0.4 & -0.04 & 0 \\
0 & 0.6 & 0 & 0
\end{bmatrix}.
\]  \( (24) \)

The Eigen values corresponding to matrix \(J_2\) are \(\lambda_1 = 0, \lambda_2 = 0.1937, \lambda_3 = -0.1770, \lambda_4 = -0.0233\). \(J_2\) has two negativeEigen values and one positive Eigen value. Two Eigen values are negative therefore it has a stable manifold of dimension two and unstable manifold of dimension one at Endemic equilibrium point \((50, -1.67, -16.67, 0)\). Since it has a two dimensional stable manifold so from dynamical point view it has very importance. Consequently, if Endemic equilibrium points exist then it is unstable but
from stability discussion it is clear that it has two dimensional stable manifold and one dimensional unstable manifold so from dynamical point of view it has importance.

5.2. Disease-free equilibrium points and basic reproduction number

From the Eq. (21), it is clear that if we take \( B = 0 \) (i.e. disease free equilibrium) then \( C = 0 \) and we can not calculate \( A \). Therefore disease free equilibrium is not possible for this model. Suppose disease free equilibrium exist and is denoted by \( (A_0, 0, 0, 0) \). There is only one infected compartments i.e. group of infected people \( (B) \). The group of recovered people \( (C) \) and susceptible people \( (A) \) can not considered in infected compartments. The group of failure of treatment i.e. group of died people \( (D) \) can not also considered to be new infections. Now following the work in [27], where the necessary computation of the matrices \( F \) and \( V \) are given by,

\[
F = [a_1 A_0], \quad V = [d_1 + e_1].
\]

The spectral radius \( \gamma (F V^{-1}) \) is the required basic reproduction number of the model (2), which is given by

\[
R_0 = \frac{a_1 A_0}{d_1 + e_1}.
\]

6. Numerical discussion

In Fig. 1, we have plotted the group of susceptible people \( (A) \) with time. From Fig. 1, it is observed that it decreases with time and in long-time behaviour it come close to zero i.e. the number of susceptible people become very less in society. In Fig. 2, we have plotted the group of infected people \( (B) \) with time. From Fig. 2, it is observed that it increases suddenly with time and in long time it come close to zero i.e. the number of infected people become very less in society. In Fig. 3, we have plotted the group of recovered people \( (C) \) with time. From Fig. 3, it is observed that initially it increases i.e. the numbers of recovered people are increasing with time. In Fig. 4, we have plotted the group of died people \( (D) \) with time. From Fig. 4, it is observed that it increases suddenly with time and in long time it become constant. So our proposed model performances well because number of recovered people are increasing and dead people are decreasing with time.

Fig. 5, shows the dynamic of susceptible people; infected people; recovered people and dead people for integer order time. In Fig. 5, the behaviour of \( A, B, C \) and \( D \) is shown simultaneously for integer order. From Fig. 5, it is clear that the group of recovered people increases with time.
In Fig. 6, we have plotted the group of susceptible people \( A(t) \) with respect to time for different values of fractional order time derivatives. From Fig. 6, it is observed that the group of susceptible people \( A(t) \) varies continuously with time derivative. In Fig. 7, we have plotted infected people \( B(t) \) with respect to time for different values of fractional order time derivatives. From Fig. 7, it is observed that group of infected people \( B(t) \) varies continuously with time derivative. In Fig. 8, we have plotted group of recovered people \( C(t) \) with respect to time for different values of fractional order time derivatives.

From Fig. 8, it is observed that group of recovered people \( C(t) \) varies continuously with time derivative. In Fig. 9, we have plotted asymptotically died people \( D(t) \) with respect to time for different values of fractional order time derivatives. From Fig. 9, it is observed that asymptotically died people \( D(t) \) varies continuously with time derivative.

In Tables 1 and 2, we have listed CPU time taken for different values of \( \Delta t \) and \( n \). From tables it is clear that our proposed method is excellent and time saving.

### 7. Conclusions

The proposed method is very easy to implement. The efficiency and accuracy of the proposed method is very attractive and clear from tables. From figures it is clear that results are very interesting showing the continuous behaviour of approximate solution for fractional order. Using the concept of Jacobian matrix and equilibrium points the stability of the model was performed. From the numerical solution and stability analysis discussion it is clear that dynamic of Ebola virus model for a given total number of population, \( T \), in society at a time \( t \) depends on its parameters. Their values are key to increase the number of recovered people in the society. The approximate solutions obtained by proposed method is effective for a long time so these solutions will be very useful in understanding Ebola virus model properly. The reduction in the size of the computational domain shows wider applicability of this method.

### Credit statement

Author contributed in every section of the paper in best possible ways as well as read and approved the paper for the submission.

### Declaration of Competing Interest

None.

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