Indian Institute of Technology, Gandhinagar

Numerical simulations and stability analysis of a COVID-19 model using fractional derivatives

MA 202 Project Report
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Authors

Ashwani Rai 19110043
Juhi Parikh 19110152
Rushik Desai 19110146
Saagar Parikh 19110199

Under the guidance of:
Prof. Chetan Pahlajani
Prof. Dilip Sundaram
Prof. Satyajit Pramanik

Contents

1 Problem Statement

The COVID-19 pandemic hit globally in December 2019 when a certain virus strain from Wuhan, China started proliferating throughout the world. By the end of March 2020, lockdowns and curfews were imposed all over the world halting trade, commerce, education, and various other essential activities. It has been nearly a year since the WHO declared a pandemic but there is still a consistent rise of the cases even with the administration of various types of vaccines and preventive measure.

One of the main struggles that the healthcare workers face is to find out the how the virus is spreading amongst a community. The knowledge of this can be used to stop the spread of virus. This is a very important step towards getting things back into momentum to restore activities globally. Many attempts have been made under epidemiology to study the spread of COVID and many mathematical models have emerged as a result that can help with this. We would be exploring a fractional-order model in this report.

The coronavirus spread can be mathematically modelled using factors such as the number of susceptible people, exposed people, infected people, asymptotic people and the number of recovered people. The Khan-Atangana system is an integer-order coronavirus model that uses the above-mentioned factors. Since the coronavirus model depends on the initial conditions, the Khan-Atangana model uses the Atangana-Baleanu operater as it has a non variant and non local kernel. Instead, we replace the equations with fractional-order derivatives using the Grünwald-Letnikov derivative. The fractional order derivatives need to be fed with initial conditions and are useful to determine the spread due to their non-local nature. This project proposes to solve these fractional-order derivatives using numerical methods and analyse the stability of this epidemiological model.

2 The physical model and variables used to calculate the spread

The goal of the model is to understand how the trend of the active COVID cases is going to change. For this, first, a set of affected cases for a given period of time are taken to parameterize the mathematical model. Then the relationship between the different parameters is established by using integral differential equations. As we will see in the following equations, the model is parameterized using a fixed location which makes the model local in nature. To counter this, fractional-order derivatives are used. By changing the integral time-derivative with the fractional-order derivatives the equation becomes non-local in nature. The fractional-order derivatives have to be provided with a set of initial conditions to be solved. The equations are then solved by iteration using computational methods.

The physical model of the system is derived from the Khan-Atangana model for COVID-19 spread by using the same parameters. The relationship between these parameters is then developed as mentioned above and instead of using the Atangana-Baleanu derivative for solving the equations (used in the Khan-Atangana model), the Grünwald-Letnikov derivative is used to convert the integral derivative to fractional-order derivative and solve them. Considering the fact that COVID-19 can be imported quickly from the seafood market (reservoir or source) and without the loss of generality, the bat-host relationship was not considered.[2]

2.1 Parameters

- μ_1: Natural birth rate
- a_1: Natural death rate
- a_2: Host visiting reservoir
- b_1: Disease spread coefficient
- b_2: Disease spread coefficient relating sub groups A and F
- σ: Transmissibility multiple
- d: Proportion of the asymptomatic infection
- f_1: Spread rate after incubation period
- e_1: Spread rate joining sub groups C and D
- g_1: Recovery rate
- g_2: Removal rate
- e_2: Disease spread coefficient relating sub groups C and F
- f_2: Disease spread coefficient relating sub groups D and F
- μ_2: Removing rate of virus from the reservoir (F)
- N_h : Unknown hosts
- I_h : Infected hosts

The susceptible people A and the infected people C are related using the factor b_1AC. The susceptible people A and the people showing no symptoms of the infection D are related by σb_1AD, where $\sigma \in [0, 1]$ is the transmissibility multiple of D to C. The above parameters are consistent throughout the text.

2.2 The Khan-Atangana Model

As per the Khan-Atangna model, the overall population is divided into 5 parts which are,

- A(t) = susceptible people
- B(t) = exposed people
- C(t) = infected people
- D(t) = asymptomatic people (people showing no symptoms of the infection)
- E(t) = recovered or removed people

Thus the total population N(t) can be written as N(t) = A(t) + B(t) + C(t) + D(t) + E(t). The class F denotes the reservoir (outbreak of infection) or the seafood market or place. The following non-linear differential equations show the relationship between these 5 groups:

$$\begin{aligned}
\frac{dA(t)}{dt} &= \mu_1 - a_1 A - \frac{b_1 A(C + \sigma D)}{N} - b_2 AF \\
\frac{dB(t)}{dt} &= \frac{b_1 A(C + \sigma D)}{N} + b_2 AF - (1-d) f_1 B - d e_1 B - a_1 B \\
\frac{dC(t)}{dt} &= (1-d) f_1 B - (g_1 + a_1) C \\
\frac{dD(t)}{dt} &= d e_1 B - (g_2 + a_1) D \\
\frac{dE(t)}{dt} &= g_1 C + g_2 D - a_1 E \\
\frac{dF(t)}{dt} &= a_2 \frac{F C_h}{N_h} + e_2 C + f_2 D - \mu_2 F
\end{aligned} \tag{1}$$

Now, neglecting the relationship between host and bat population, we get the equations as:

$$\begin{aligned}
\frac{dA(t)}{dt} &= \mu_1 - a_1 A - \frac{b_1 A(C + \sigma D)}{N} - b_2 AF \\
\frac{dB(t)}{dt} &= \frac{b_1 A(C + \sigma D)}{N} + b_2 AF - (1-d) f_1 B - d e_1 B - a_1 B \\
\frac{dC(t)}{dt} &= (1-d) f_1 B - (g_1 + a_1) C \\
\frac{dD(t)}{dt} &= d e_1 B - (g_2 + a_1) D \\
\frac{dE(t)}{dt} &= g_1 C + g_2 D - a_1 E \\
\frac{dF(t)}{dt} &= e_2 C + f_2 D - \mu_2 F
\end{aligned} \tag{2}$$

Following is the flow diagram that shows the relationship between the above-mentioned subgroups as developed by the given equations:

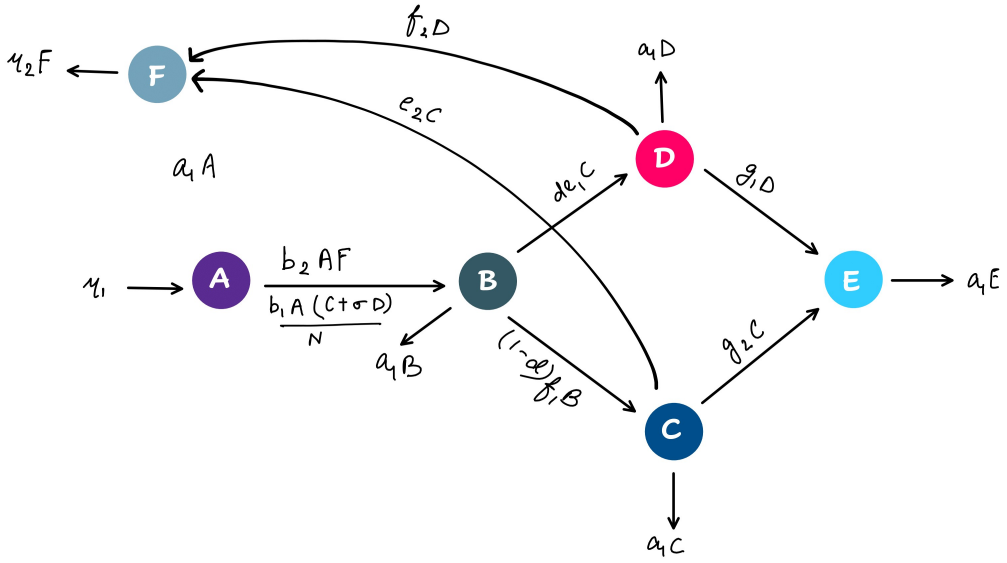

Figure 1: Relationship between the subgroups

As mentioned before, to non-localize, we convert the time derivative in the above integral order equation to that of fractional-order. The equations thus becomes as follows:

$$
\begin{aligned}
{}_aD_t^{p_1} A(t) &= \mu_1 - a_1 A - \frac{b_1 A(C+\sigma D)}{N} - b_2 AF \\
{}_aD_t^{p_2} B(t) &= \frac{b_1 A(C+\sigma D)}{N} + b_2 AF - (1-d) f_1 B - de_1 B - a_1 B \\
{}_aD_t^{p_3} C(t) &= (1-d) f_1 B - (g_1 + a_1) C \\
{}_aD_t^{p_4} D(t) &= de_1 B - (g_2 + a_1) D \\
{}_aD_t^{p_5} E(t) &= g_1 C + g_2 D - a_1 E \\
{}_aD_t^{p_6} F(t) &= e_2 C + f_2 D - \mu_2 F
\end{aligned}
\tag{3}
$$

The initial conditions are given as: $\mathrm{A}(0) = d_1$, $\mathrm{B}(0) = d_2$, $\mathrm{C}(0) = d_3$, $\mathrm{D}(0) = d_4$, $\mathrm{E}(0) = d_5$ and $\mathrm{F}(0) = d_6$. Moreover we use $0 < p_1, p_2, p_3, p_4, p_5, p_6 < 1$ to increase the degree of the freedom and obtain better results.

3 Solution Methodology

We will convert the integer-order equations obtained from the Khan-Atangana model to fractional-order equations. As mentioned in the physical model, due to the local nature of the integral differential equation, they are converted to fractional-order. By providing the initial conditions to the fractional order-derivatives, the system of the equation becomes non-local in nature. The additional parameters in the equations are used to provide an extra degree of freedom to obtain better solutions. We would be using the Grünwald-Leitnikov (GL) derivative to obtain the solution to the fractional-order derivatives. Grünwald-Leitnikov derivative is used to calculate the derivative of a function non-integer number of times.[3]

The Trapezoidal method is used to solve the integer-order integral. By calculating the parameters of the Grünwald-Letnikov derivative and integrating the fractional derivative we would get the equations for A(t), B(t), C(t), D(t), and E(t). The unknowns in the coronavirus model can be obtained by writing a MATLAB code to solve the equations obtained in section 4.5. To improve the accuracy of the model iterative methods with a small step size shall be used.

For the stability analysis, we analyse the eigenvalues corresponding to the Jacobian matrices at specific equilibrium points. First, we identify the equilibrium points and find the Jacobian matrices at these points. Then, we take the determinant of J - λI to obtain two 6 degree polynomials in λ. The solution of this polynomial equation will give the eigenvalues corresponding to the Jacobian matrix J. We will solve these 6 degree polynomial equations using the Newton-Raphson method and analyse the stability of the system at the equilibrium points.

4 Numerical Solution

As mentioned earlier, after obtaining the fractional-order derivatives, we would integrate them and using the Grünwald-Letnikov derivative, get a solution. Then calculating the unknowns in the original model using a computer program, we get an accurate trend of the spread of coronavirus cases.

4.1 System of Equations

Following are the final set of fractional order derivative equations that we would be using primarily to obtain the solution:

$$\begin{aligned}
{}_aD_t^{p_1} A(t) &= \mu_1 - a_1 A - \frac{b_1 A(C+\sigma D)}{N} - b_2 AF \\
{}_aD_t^{p_2} B(t) &= \frac{b_1 A(C+\sigma D)}{N} + b_2 AF - (1-d) f_1 B - d e_1 B - a_1 B \\
{}_aD_t^{p_3} C(t) &= (1-d) f_1 B - (g_1 + a_1) C \\
{}_aD_t^{p_4} D(t) &= d e_1 B - (g_2 + a_1) D \\
{}_aD_t^{p_5} E(t) &= g_1 C + g_2 D - a_1 E \\
{}_aD_t^{p_6} F(t) &= e_2 C + f_2 D - \mu_2 F
\end{aligned} \tag{4}$$

4.2 Grünwald-Letnikov derivative

To understand how the solution is obtained, it is necessary to understand the Grünwald-Letnikov derivative. GL derivative proposes a numerical way to get the derivative of a function non-integer number of times. Following is the GL derivative of a function about a point:

$${}_aD_t^p g(t) = \lim_{h \to 0} \frac{1}{h^p} \sum_{j=0}^{[n]} (-1)^j \binom{p}{j} g(t - jh) \tag{5}$$

where $n = \frac{t-a}{h}$ and a is a real constant. The general fractional-order linear system can be considered as follows:

$${}_aD_{t_k}^p g(t) = Ax(t) + Bu(t)$$

Using the definition of fractional GL derivative as given in Eq. (5), at the points k_h(k = 1, 2,...) the p^{th} order Grünwald–Letnikov derivative has the following form:

$$\left(k - \frac{L}{h}\right) {}_aD_t^p g(t) = h^{-p} \sum_{j=0}^{k} (-1)^j \binom{p}{j} g(t_{k-j})$$

where the "memory length" is L, $t_k = k_h$, h is the step size taken for the calculation and the coefficients of the derivative $c_j^{(p)}$ (j = 0, 1,...) and can be obtained by taking the following expressions:

$$c_0^{(p)} = 0 \text{ and } c_j^{(p)} = (1 - \tfrac{1+p}{j})c_{j-1}^{(p)}$$

Further, using this the general from solution of the equation:

$$aD_t^p g(t) = g(y(t), t)$$

can be written as,

$$y(t_k) = g(y(t_k), t)h^p - \sum_{j=v}^{k} c_j^{(p)} y(t_{k-j}) \tag{6}$$

We will use the short memory principle to determine the lower index in the sum. By the use of the short memory principle, the lower index is considered as:

$$v = \begin{cases} 1 & \text{if } k < (L/h) \\ k - (L/h) & \text{if } k > (L/h) \end{cases}$$

4.3 Trapezoidal Method

Trapezoidal rule is used to calculate the integral of the function by taking the area under the curve as a trapezoid. Here we would be first integrating the integral order derivatives using the trapezoidal rule. The value of this would be used in the above equation of the Grünwald-Letnikov derivative of a function about a point. We will get the value of the function g (analogously A, B, D, E, F in our case) for Eq. (5) by solving the following set of equations using the Trapezoidal Method:[4]

$$A(t) = \int_0^t [\mu_1 - a_1 A - \frac{b_1 A(C + \sigma D)}{N} - b_2 AF]\, dt$$

$$B(t) = \int_0^t [\frac{b_1 A(C + \sigma D)}{N} + b_2 AF - (1 - d) f_1 B - de_1 B - a_1 B]\, dt$$

$$C(t) = \int_0^t [(1 - d) f_1 B - (g_1 + a_1) C]\, dt$$

$$D(t) = \int_0^t [de_1 B - (g_2 + a_1) D]\, dt$$

$$E(t) = \int_0^t [g_1 C + g_2 D - a_1 E]\, dt$$

$$F(t) = \int_0^t [e_2 C + f_2 D - \mu_2 F]\, dt$$

4.4 Newton-Raphson method

For the stability analysis of the epidemiological model, we would be using the Jacobian Matrix for the endemic equilibrium condition and disease-free equilibrium system denoted by J_1 and J_2. To determine the stability we would be calculating the eigenvalues of both of these matrices.

By doing so and examining the nature of the eigenvalues we would come to know whether the model at disease-free and endemic equilibrium points is stable or not.

To calculate the eigenvalues we will make use of the characteristic equation of the Jacobian using $det(A - \lambda I) = 0$. We will obtain a six-degree polynomial equation which we will solve using the Newton-Raphson Method. Newton-Raphson method is used to calculate the roots of a real-valued function using better approximations by an iterative method. An approximation of the root is taken first then if it satisfies some prescribed condition, then a better approximation is used. Geometrically a tangent is drawn at the initial guess and the point where the vertical line from the intersection of tangent and X-axis cuts the curve is taken as the next approximation. For the characteristic equation obtained by us, the first approximation was taken after observing the graph of the equation that we plotted using an online graphing software.[5]

4.5 Final Solution

Using the solution of the Grünwald-Letnikov derivative and the value of the function obtained using the trapezoidal method we get the final solution from the following:

$$A(t) = (\mu_1 - a_1 A(t_{k-j}) - \frac{b_1 A(t_{k-j})(C(t_{k-j}) + \sigma D(t_{k-j}))}{N} - b_2 A(t_{k-j}) F(t_{k-j}))^{p_1} - \sum_{j=v}^{k} c_j^{(p)} A(t_{k-j})$$

$$B(t) = (\frac{b_1 A(t_{k-j})(C(t_{k-j}) + \sigma D(t_{k-j}))}{N} + b_2 A(t_{k-j}) F(t_{k-j}) - (1-d) f_1 B(t_{k-j}) - d e_1 B(t_{k-j}) - a_1 B(t_{k-j}))^{p_1} - \sum_{j=v}^{k} c_j^{(p)} B(t_{k-j})$$

$$C(t) = ((1-d) f_1 B(t_{k-j}) - (g_1 + a_1) C(t_{k-j}))^{p_1} - \sum_{j=v}^{k} c_j^{(p)} C(t_{k-j})$$

$$D(t) = (d e_1 B(t_{k-j}) - (g_2 + a_1) D(t_{k-j}))^{p_1} - \sum_{j=v}^{k} c_j^{(p)} D(t_{k-j})$$

$$E(t) = (g_1 C(t_{k-j}) + g_2 D(t_{k-j}) - a_1 E(t_{k-j}))^{p_1} - \sum_{j=v}^{k} c_j^{(p)} E(t_{k-j})$$

$$F(t) = (e_2 C(t_{k-j}) + f_2 D(t_{k-j}) - \mu_2 F(t_{k-j}))^{p_1} - \sum_{j=v}^{k} c_j^{(p)} F(t_{k-j})$$

5 Stability of the Model

For the stability analysis of the epidemiological model, first the Jacobian matrices for the system of equations are to be determined at the disease-free equilibrium point and endemic equilibrium point denoted by J_1 and J_2 respectively. To analyse the stability, the eigenvalues corresponding to both of these matrices are calculated using the aforementioned Newton-Raphson method. Then, by examining the nature of those eigenvalues we would conclude whether the model at the disease-free and endemic equilibrium points is stable or not.
We analyze the following system of equations:

$$\begin{aligned}
aD_t^{p_1}A(t) &= \mu_1 - a_1 A - \frac{b_1 A(C+\sigma D)}{N} - b_2 AF = 0 \\
aD_t^{p_2}B(t) &= \frac{b_1 A(C+\sigma D)}{N} + b_2 AF - (1-d)f_1 B - de_1 B - a_1 B = 0 \\
aD_t^{p_3}C(t) &= (1-d)f_1 B - (g_1 + a_1)C = 0 \\
aD_t^{p_4}D(t) &= de_1 B - (g_2 + a_1)D = 0 \\
aD_t^{p_5}E(t) &= g_1 C + g_2 D - a_1 E = 0 \\
aD_t^{p_6}F(t) &= e_2 C + f_2 D - \mu_2 F = 0
\end{aligned} \tag{7}$$

We will be finding the stability of this model at two equilibrium points:

- **Disease-free equilibrium point -** characterized by the non-existence of infected nodes ($\frac{\mu_1}{a_1}$, 0, 0, 0, 0, 0)
- **Endemic-equilibrium point -** characterized by the existence of the infected nodes $(4.76 \times 10^7, -3.65 \times 10^7, -1.37 \times 10^5, -2.61 \times 10^4, -2.75 \times 10^6, -8.07 \times 10^3)$

The general fractional-order system can be considered as

$$aD_t^q x_i(t) = f_i(x_1, x_2, ...x_i, ..., x_n),\ i = 1, 2, ...n$$

For this system, the Jacobian matrix is defined as:

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \vdots & \ddots & \\ \frac{\partial f_n}{\partial x_1} & \cdots & \frac{\partial f_n}{\partial x_n} \end{bmatrix}$$

At an equilibrium point $(b_1, b_2, \ldots\ b_n)$, the Jacobian matrix is given by:

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \vdots & \ddots & \\ \frac{\partial f_n}{\partial x_1} & \cdots & \frac{\partial f_n}{\partial x_n} \end{bmatrix}_{(b_1, b_2, b_3 ..., b_n)}$$

Using Eq.(4) as our system of equations, we get the following Jacobian matrix:

$$J = \begin{bmatrix} a_1 - \frac{b_1 A(C+\sigma D)}{N} - b_2 F & 0 & -\frac{b_1 A}{N} & -\frac{b_1 \sigma A}{N} & 0 & -b_2 A \\ \frac{b_1 A(C+\sigma D)}{N} + b_2 F & (1-d)f_1 - de_1 - a_1 & \frac{b_1 A}{N} & \frac{b_1 \sigma A}{N} & 0 & b_2 A \\ 0 & (1-d)f_1 & -(g_1 + a_1) & 0 & 0 & 0 \\ 0 & de_1 & 0 & -(g_2 + a_1) & 0 & 0 \\ 0 & 0 & g_1 & g_2 & -a_1 & 0 \\ 0 & 0 & e_2 & f_2 & 0 & -\mu_2 \end{bmatrix}$$

We use the following values of parameters for calculations:

$$\begin{aligned} \mu_1 &= 107644.22451, \\ \mu_2 &= 0.01, \\ a_1 &= \frac{1}{76.79}, \\ b_1 &= 0.05, \\ b_2 &= 0.000001231, \\ \sigma &= 0.02, \\ d &= 0.1243, \\ f_1 &= 0.00047876, \\ f_2 &= 0.001, \\ e_1 &= 0.005, \\ e_2 &= 0.000398, \\ g_1 &= 0.09871, \\ g_2 &= 0.854302 \end{aligned}$$

5.1 Disease-free equilibrium point

The Disease-free equilibrium point is ($\frac{\mu_1}{a_1}$, 0, 0, 0, 0, 0) . The Jacobian matrix at this point is :

$$J_1 = \begin{bmatrix} -0.0130 & 0 & -0.0500 & -0.0010 & 0 & -10.1754 \\ 0 & -0.0141 & 0.0500 & 0.0010 & 0 & 10.1754 \\ 0 & 0.0004 & -0.1117 & 0 & 0 & 0 \\ 0 & 0.0006 & 0 & -0.8673 & 0 & 0 \\ 0 & 0 & 0.0987 & 0.8543 & -0.0130 & 0 \\ 0 & 0 & 0.003 & 0.0010 & 0 & -0.100 \end{bmatrix}$$

We find the eigenvalues corresponding to matrix J1 using the Newton-Raphson method discussed above.

λ_1 = - 0.0130,
λ_2 = - 0.0130,
λ_3 = - 0.1118,
λ_4 = - 0.0067,
λ_5 = - 0.0173
λ_6 = - 0.8673.

For 0< p_i <1, i = 1, 2, 3, 4, 5, 6 we observe that all eigenvalues for J1 are negative. Thus the system is **stable at the disease-free equilibrium point.**

5.2 Endemic equilibrium point

The Endemic equilibrium point is $(4.76 \times 10^7, -3.65 \times 10^7, -1.37 \times 10^5, -2.61 \times 10^4, -2.75 \times 10^6, -8.07 \times 10^3)$. The Jacobian matrix at this point is :

$$J_2 = \begin{bmatrix} -0.0023 & 0 & -0.2885 & -0.0058 & 0 & -58.7180 \\ -0.0108 & -0.0141 & 0.2885 & 0.0058 & 0 & 58.7180 \\ 0 & 0.0004 & -0.1117 & 0 & 0 & 0 \\ 0 & 0.0006 & 0 & -0.8673 & 0 & 0 \\ 0 & 0 & 0.0987 & 0.8543 & -0.0130 & 0 \\ 0 & 0 & 0.003 & 0.0010 & 0 & -0.100 \end{bmatrix}$$

The eigenvalues corresponding to matrix J2 are

λ_1 = - 0.0130,
λ_2 = - 0.08673,
λ_3 = - 0.1120,
λ_4 = - 0.0195,
λ_5 = - 0.0127
λ_6 = + 0.0061.

As all the eigenvalues for J2 are not negative, the system is **asymptotically unstable at the Endemic-equilibrium point**.

6 Results and Discussion

6.1 Graphs

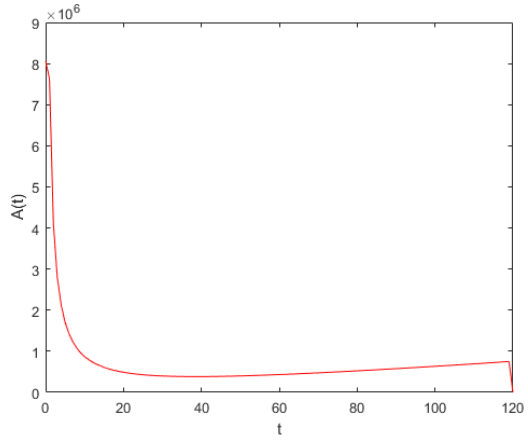

Figure 2: Performance of group (A) with time

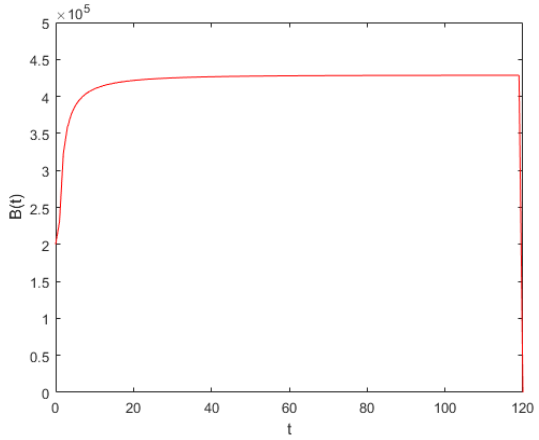

Figure 3: Performance of group (B) with time

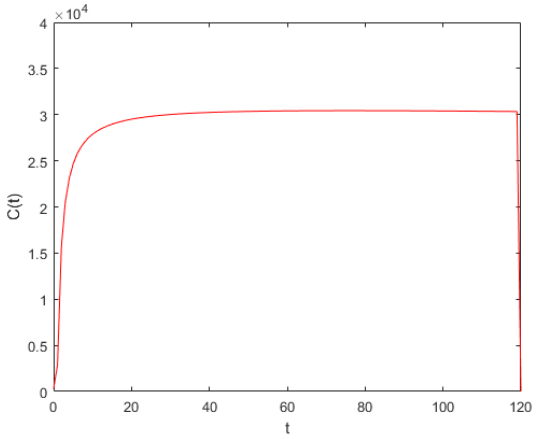

Figure 4: Performance of group (C) with time

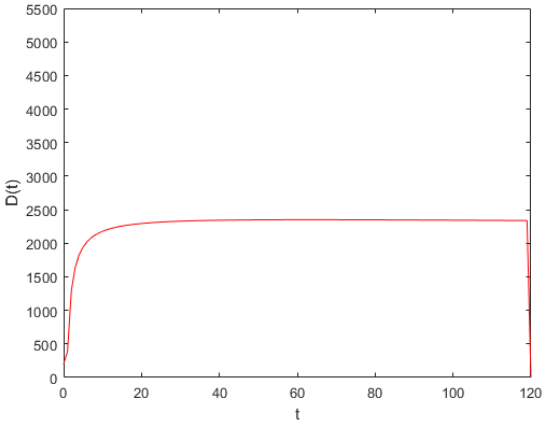

Figure 5: Performance of group (D) with time

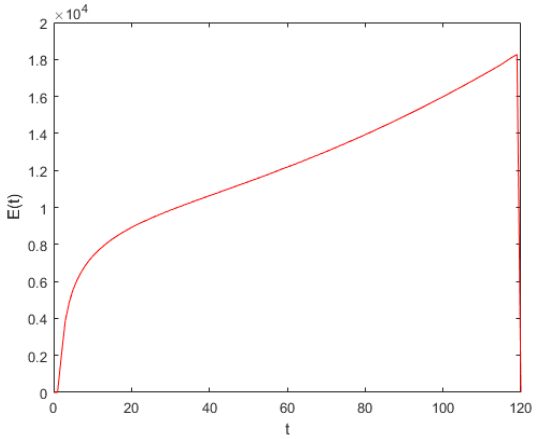

Figure 6: Performance of group (E) with time

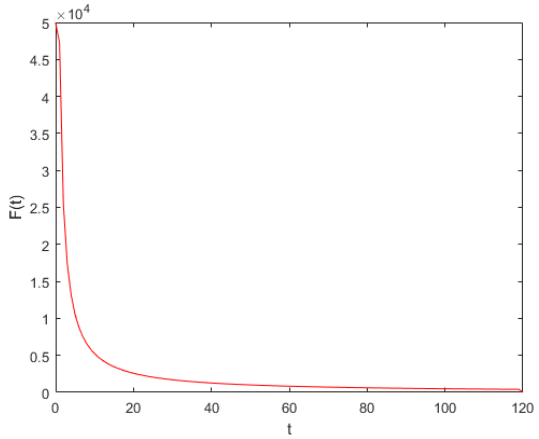

Figure 7: Performance of group (F) with time

6.2 Analysis of the graphs

- Fig. 2 shows the behaviour of the group of (A) with time and it can be seen that the susceptible people group decreases and tends to zero.
- Fig. 3 shows exposed group (B) with respect to time. The number of exposed people increases with time but plateaus after a certain point.
- Fig. 4 shows the group of infected or symptomatic people (C) with respect to time which initially increases, but after some time, starts to flatten similar to group (B). This means people recover after treatment.
- Fig. 5 shows asymptomatically infected group (D) with respect to time and it is evident that it increases with time.
- Fig. 6 shows the group of people who are recovered or removed (E) with respect to time. From Fig. 5, it can be seen that it increases with time, which shows that the proposed model is accurate and useful.
- Fig. 7 shows the performance of reservoir group (F) with time. From Fig. 6, it can be seen that it decreases, that is, reservoir after some time becomes negligible.

6.3 Time of computation

After implementing the proposed model and solving the problems using the specified numerical methods, we obtain the following time of execution of the attached MATLAB code (averaged over several iterations): **11.893 seconds**

6.4 Conclusion

The figures in this paper show that the solution varies continuously depending on fractional derivatives and on the values of parameters. From the numerical methods and stability analysis discussion, it can be seen that, at a time t, the proposed model depends on its parameters. Thus, the values of these parameters play a key role in determining the number of recovered people and infected people. The proposed technique is effective to show the behaviour of the solution in a very long time period which is helpful to predict the coronavirus model accurately. This method can be used in investigating many similar biological models showing wide applicability of the proposed method.

7 References

[1] Singh, Harendra, et al. "Numerical Simulation and Stability Analysis for the Fractional-Order Dynamics of COVID-19." Results in Physics, vol. 20, 2021, p. 103722. Crossref, doi:10.1016/j.rinp.2020.103722.

[2] Khan MA, Atangana A. Modeling the dynamics of novel coronavirus (2019-nCov) with fractional derivative. Alexandria Eng J 2020;59(4):2379–89. https://doi.org/10.1016/j.aej.2020.02.033.

[3] Wikipedia contributors. "Grünwald–Letnikov Derivative." Wikipedia, 26 Dec. 2019, en.wikipedia.org/wiki/Gr%C3%BCnwald%E2%80%93Letnikov_derivative.

[4]"Trapezoidal Rule." Wikipedia, 12 Jan. 2021, en.wikipedia.org/wiki/Trapezoidal_rule.

[5]"Newton's Method." Wikipedia, 4 May 2021, en.wikipedia.org/wiki/Newton