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A Fractional Variable Order Model of COVID-19 Pandemic

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Abstract: 2020 has witnessed a rapidly spread pandemic COVID-19 which is one of the worst in the history of mankind. Scientists believe that COVID-19 spreads mainly from a person to another. Recent researches consider bats as a vector for COVID-19. This paper suggests a variable fractional order model for COVID-19 to figure out how bats and hosts interact, and how the seafood market affect people. The proposed model assumes that infection cannot be recovered. The basic reproduction number R_0 for real data on reported cases in Wuhan China was computed. Disease-free equilibrium points and proposed model stability are studied.

Keywords: Coronavirus, COVID-19 mathematical models, fractional calculus, fractional variable order models.

1 Introduction

The wide-spread coronavirus COVID-19 pandemic is the most crucial catastrophic worldwide emergency since WW II [1,2,3]. Since its rise in China, it has stricken all continents but Antarctica. The impact of COVID-19 outbreak has had a serious impact on all global sectors like economy, industry and education [3,4,5]. Recently, several scientists have suggested that bats are the vector for COVID-19 [6,7]. In other words, bats are the mammals in which Covid-19 originated. Using different mathematical models, coronavirus transmission dynamics through population networks in human societies have been described [6,8,9,10,11,12]. Few of them outline interaction dynamics between bats and an unknown host [9] (may be wild mammals) and the correlation between human and infection source. On the other hand, few models consider the memory of both the vector and the host. Since memory has an effect [13,14,15,16,17,18,19] on dynamics and COVID-19 spread, this paper highlights novel coronavirus mathematical modeling and dynamics (2019-nCoV) through a variable fractional order model [13,20,21]. The main infection reservoir here is seafood markets where bats and hosts leave their infection. Stuff purchased from this market are infectious as well. Based on the assumption that there are effective sources of infection in seafood markets, model (1) has been reduced as presented in (2).

Fractional order models are more effective to describe the spread of infectious diseases as the fractional order derivatives take memory and learning of the vector and the host into consideration [13,14,15,16,17,18]. In other words, fractional order derivatives do not only depend on the current state, but also on the historical state. It is noticed that real data gathered in epidemiological phenomena are closer to fractional order results than the corresponding integer order models [22].

Diseases vectors behaviour can be affected by memory, learning and experience [19]. Vectors distribution in food resources, host choice, and the ability to remember food location and host have significant effects on diseases transmission. Memory impact on vector behaviour can be investigated by fractional order derivatives [13,14,15,16,17,18]. The research presents a COVID-19 variable fractional order model based on the constant fractional order model as shown in [9]. The numerical solutions are obtained by predictor corrector method. The paper is divided into sections. Section two presents an introduction to fractional variable order derivatives. Section three discusses constant/variable fractional order models of COVID-19. Section four investigates Disease-Free Equilibrium points. Section five, however, focuses on the model Basic Reproduction Number. Finally, section six discusses the presented model numerical solutions.

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2 Preliminaries

The section provides definitions of variable-order fractional derivative – the constant-order fractional derivative extension. There are different approaches for defining fractional derivatives.
Definition 1. (Riemann–Liouville fractional order derivatives)
Let $\alpha(t)$ be a continuous and bounded function, then Riemann–Liouville variable fractional order derivative of $f(t):[a,b]\to\mathbb{R}$ is defined as [13]:
i) Left Riemann–Liouville derivative of order $\alpha(t)$ is defined by

$$ {}_{a}^{RL}D_{t}^{\alpha(t)}f(t)=\frac{1}{\Gamma(1-\alpha(t))}\frac{d}{dt}\int_{a}^{t}(t-\tau)^{-\alpha(t)}f(\tau)d\tau,\qquad 0<\alpha(t)\leq 1 $$

ii) Right Riemann–Liouville derivative of order $\alpha(t)$ is defined by

$$ {}_{t}^{RL}D_{b}^{\alpha(t)}f(t)=\frac{-1}{\Gamma(1-\alpha(t))}\frac{d}{dt}\int_{t}^{b}(t-\tau)^{-\alpha(t)}f(\tau)d\tau,\qquad 0<\alpha(t)\leq 1 $$

Definition 2. (Caputo fractional order derivatives $\alpha(t)$)
Let $\alpha(t)$ be a continuous and bounded function, then the Caputo variable fractional order derivative of $f(t):[a,b]\to\mathbb{R}$ is defined as [13]:
i) Left Caputo order derivative $\alpha(t)$ is defined by

$$ {}_{a}^{c}D_{t}^{\alpha(t)}f(t)=\frac{1}{\Gamma(1-\alpha(t))}\int_{a}^{t}(t-\tau)^{-\alpha(t)}f'(\tau)d\tau,\qquad 0<\alpha(t)\leq 1 $$

ii) Right Caputo fractional order derivative $\alpha(t)$ is defined by

$$ {}_{t}^{c}D_{b}^{\alpha(t)}f(t)=\frac{-1}{\Gamma(1-\alpha(t))}\int_{t}^{b}(t-\tau)^{-\alpha(t)}f'(\tau)d\tau,\qquad 0<\alpha(t)\leq 1 $$

Definition 3. (Grünwald-Letnikov fractional order derivatives $\alpha(t)$)
Let $\alpha(t)$ be a continuous and bounded function, then the Grünwald-Letnikov variable fractional order derivative of $f(t):[a,b]\to\mathbb{R}$ is defined as [13]:

$$ {}_{0}^{GL}D_{t}^{\alpha(t)}f(t)=\lim_{h\to 0}h^{-\alpha}\sum_{j=0}^{[n]}(-1)^{j}\binom{\alpha(t)}{j}f(t-jh) $$

Where h is the step size, $n=\frac{t}{h}$, $[n]$ is the integer part of n and $0<\alpha(t)\leq 1$.
The above definitions indicate that by time, effect of memory on the considered system changes and the current state determines such. Thus, the effect of variable memory on the system can be characterized through variable fractional order derivative. Caputo derivative is attractive when physical models are presented due to physical interpretation clarity of the prescribed data [20,21]. Also Caputo derivative is essential because the initial conditions for the fractional-order models with the Caputo derivatives are the same as for the integer-order models [17,18]. The variable memory impact on epidemiology are discussed in several articles like [13,20,21].

3 Model derivation

The model assumes that transmission happens first within bats then move to hosts (wild animals), then such hosts are transmitted to seafood markets (reservoir/virus). When people buy from this market, they are at risk of getting infected. Bats and hosts interaction is illustrated in the following evolutionary differential equations:

$$ \begin{aligned} D^{\alpha(t)}(S_b)&=\Pi_b-\mu_b S_b-\frac{\eta_b S_b I_b}{N_b},\\ D^{\alpha(t)}(E_b)&=\frac{\eta_b S_b I_b}{N_b}-(\theta_b+\mu_b)E_b,\\ D^{\alpha(t)}(I_b)&=\theta_b E_b-(\tau_b+\mu_b)I_b, \qquad (1)\\ D^{\alpha(t)}(R_b)&=\tau_b I_b-\mu_b R_b, \end{aligned} $$

$$
\begin{gathered}
D^{\alpha(t)}(S_h) = \Pi_h - \mu_h S_h - \frac{\eta_{bh} S_h I_b}{N_h} - \frac{\eta_h S_h I_h}{N_h} \\
D^{\alpha(t)}(E_h) = \frac{\eta_{bh} S_h I_b}{N_h} + \frac{\eta_h S_h I_h}{N_h} - (\theta_h + \mu_h) E_h \\
D^{\alpha(t)}(I_h) = \theta_h E_h - (\tau_h + \mu_h) I_h \\
D^{\alpha(t)}(R_h) = \tau_h I_h - \mu_h R_h,
\end{gathered}
$$

where
$N_b = S_b + E_b + I_b + R_b$ represents the total bats population,
$N_h = S_h + E_h + I_h + R_h$ represents the total unknown host size,
The subgroups are defined as follows
S_b: Susceptible bats,
E_b: Exposed bats,
I_b: Infected bats,
R_b: Recovered/removed group of bats,
S_h: Susceptible host,
E_h: Exposed host,
I_h: Infected host,
R_h: Recovered/removed host.
Susceptible bats population is known through their birth rate represented in Π_b and each class death rate indicated by μ_b. After incubation period, exposed bats get infected at θ_b rate. They join the I_b infection class. Rate of recovering infected bats or moving them to class R_b is shown by τ_h. Susceptible and infected bats interaction causing the infection is presented at the rate η_h and through route $\frac{\eta_b S_b I_b}{N_h}$. Π_h indicates hosts birth rate while μ_h indicates each class death rate. Infection to exposed hosts happen at θ_h to join I_h infection class. τ_h presents the rate of recovering/removing infected host. Susceptible hosts and infected bats contact is through route $\frac{\eta_{bh} S_h I_b}{N_h}$; η_{bh} is infected bats to healthy hosts disease transmission coefficient. The virus spreads through hosts after receiving infection from bats as provided through route $\frac{\eta_h S_h I_h}{N_h}$, where transmission of disease among S_h and I_h classes is given by η_h coefficient.
N_p denotes people total population, further classified into five subgroups: S_p, E_p, I_p, A_p and R_p, respectively representing the susceptible, exposed, symptomatically infected, asymptomatically infected, and recovered/removed people. Bats, hosts, people and seafood markets evolutionary dynamics are described through nonlinear differential equations given by:

$$
\begin{gathered}
D^{\alpha(t)}(S_P) = \Pi_P - \mu_p S_P - \frac{\eta_P S_P (I_P + \psi A_P)}{N_P} - \eta_w S_P M, \\
D^{\alpha(t)}(E_P) = \frac{\eta_P S_P (I_P + \psi A_P)}{N_P} + \eta_w S_P M - (1-\theta_P)\omega_P E_P - \theta_P \rho_P E_P - \mu_p E_P, \\
D^{\alpha(t)}(I_P) = (1-\theta_P)\omega_P E_P - (\tau_P + \mu_P) I_P, \\
D^{\alpha(t)}(A_P) = \theta_P \rho_P E_P - (\tau_{aP} + \mu_P) A_P, \\
D^{\alpha(t)}(R_P) = \tau_P I_P + \tau_{aP} A_P - \mu_P R_P \\
D^{\alpha(t)}(M) = b\frac{M I_h}{N_h} + Q_P I_P + \varpi A_P - \pi M
\end{gathered}
\tag{2}
$$

Based on [9], Π_P and μ_p indicates natural birth/death rates respectively. S_P contact with I_P cause the infection given by $\eta_p S_P I_P$ where η_p is the coefficient indicating disease transmission. Virus transmission from asymptomatically infected people to healthy people is given by $\eta_P S_P \psi A_P$; where ψ is A_P transmissibility multiple to I_P and $\psi \in [0,1]$. When $\psi = 0$, there will be no transmissibility multiple; and if $\psi = 1$, the same will take place like I_P infection. θ_b denotes asymptomatic infection. After the incubation period and being infected-class I_P and A_P respectively - ω_P represents transmission rate. Symptomatic class is I_P and asymptomatic class is A_P, joining class R_P, with τ_P and τ_{aP} removal/recovery rate respectively. The class M is the reservoir or seafood market. $\eta_w M S_P$ indicates susceptible people who got infected after interacting with M, the coefficient of disease transmission from M to η_w is given by η_w. b with $\frac{bMI_h}{N_h}$ signifies hosts who purchase items from seafood market (retail purchase). Q_p and ϖ_P - symptomatically and asymptomatically infected respectively - transmit the virus into M. π is the rate of virus removal from M. Figure 2 illustrates virus transfer among people and reservoir. Considering that the COVID-19 can be rapidly transmitted to seafood markets. Thus, without loss of generality nor ignoring bats and hosts interaction, model (2) can be summarized as shown below. It can be considered a model for base study as follows:

$$
\begin{aligned}
D^{\alpha(t)}(S_P) &= \Pi_P - \mu_p S_P - \frac{\eta_P S_P(I_P+\psi A_P)}{N_P} - \eta_w S_P M,\\
D^{\alpha(t)}(E_P) &= \frac{\eta_P S_P(I_P+\psi A_P)}{N_P} + \eta_w S_P M - (1-\theta_P)\omega_P E_P - \theta_P \rho_P E_P - \mu_p E_P,\\
D^{\alpha(t)}(I_P) &= (1-\theta_P)\omega_P E_P - (\tau_P+\mu_p) I_P,\\
D^{\alpha(t)}(A_P) &= \theta_P\rho_P E_P - (\tau_{aP}+\mu_p) A_P,\\
D^{\alpha(t)}(R_P) &= \tau_P I_P + \tau_{aP} A_P - \mu_p R_P\\
D^{\alpha(t)}(M) &= Q_P I_P + \overline{\omega}_P A_P - \pi M
\end{aligned}
\tag{3}
$$

4 Disease-free equilibrium points

Equilibrium point in a dynamical system is a solution that does not change by time To reach this point in model (3), let

$$D^{\alpha(t)}(S_P) = D^{\alpha(t)}(E_P) = D^{\alpha(t)}(I_P) = D^{\alpha(t)}(A_P) = D^{\alpha(t)}(R_P) = D^{\alpha(t)}(M) = 0$$

Consequently, disease-free equilibrium point E_0 is

$$E_0(S_p^0, 0, 0, 0, 0, 0) = \left(\frac{\Pi_P}{\mu_p}, 0, 0, 0, 0, 0\right)$$

5 The basic reproduction number

Following the work in [9] to evaluate the basic reproduction number R_0 by the matrices F and V which given by

$$F = \begin{pmatrix} 0 & \eta_P & \psi\eta_P & \frac{\eta_P \Pi_P}{\mu_P} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

$$F = \begin{pmatrix} \theta_P\rho_P + (1-\theta_P)\omega_P + \mu_P & 0 & 0 & 0 \\ (1-\theta_P)\omega_P & \mu_P + \tau_P & 0 & 0 \\ -\theta_P\rho_P & 0 & \tau_{aP}+\mu_P & 0 \\ 0 & -Q_P & -\overline{\omega}_P & \pi \end{pmatrix}$$

The spectral radius $\gamma(FV^{-1})$ is the required basic reproduction number given by $R_0 = R_1 + R_2$ where

$$R_1 = \frac{\theta_P\rho_P(\pi\psi\eta_P\mu_P + \Pi_P\overline{\omega}_P\eta_w)}{\pi\mu_P(\tau_{aP}+\mu_P)(\theta_P\rho_P + (1-\theta_P)\omega_P + \mu_P)},$$

$$R_2 = \frac{(1-\theta_P)\omega_P(\pi\eta_P\mu_P + \Pi_P Q_P \eta_P)}{\pi\mu_P(\tau_P+\mu_P)(\theta_P(\rho_P-\omega_P)+\mu_P+\omega_P)}.$$

Theorem 1. The DFE E_0 of the system (3) is locally asymptotically stable if $R_0 < 1$. We obtain the Jacobian matrix at DFE as follows.

$$J = \begin{pmatrix} -\mu_p & 0 & -\eta_p & -\psi\eta_p & 0 & -\frac{\eta_w\Lambda_p}{\mu_p} \\ 0 & -\mu_p - \theta_p\rho_p - (1-\theta_p)\omega_p & \eta_p & \psi\eta_p & 0 & -\frac{\eta_w\Lambda_p}{\mu_p} \\ 0 & (1-\theta_p)\omega_p & -\mu_p - \tau_p & 0 & 0 & 0 \\ 0 & \theta_p\rho_p & 0 & -\mu_p - \tau_{ap} & 0 & 0 \\ 0 & 0 & \tau_p & \tau_{ap} & -\mu_p & 0 \\ 0 & 0 & Q_p & \overline{\omega}_p & 0 & -\pi \end{pmatrix}$$

The characteristics equation is

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0,$$

Where

$$\begin{aligned}
a_1 &= \tau_{ap} + \delta + \theta_p\rho_p + (1-\theta_p)\omega_p + 3\mu_p + \tau_p,\\
a_2 &= (\mu_p+\tau_p)(\theta_p\rho_p + (1-\theta_p)\omega_p + \mu_p) - \eta_p(1-\theta_p)\omega_p\\
&\quad + (\tau_{ap}+\mu_p)(\theta_p(\rho_p-\omega_p)+\mu_p+\omega_p) - \psi\eta_P\theta_p\rho_p + \pi(\tau_{ap}+\mu_p)\\
&\quad + (\mu_p+\tau_p)(\tau_{ap}\nu+\mu_p) + \pi(\theta_p(\rho_p-\omega_p)+\mu_p+\omega_p) + \pi(\mu_p+\tau_p),\\
a_3 &= \pi(\theta_p\rho_p + (1-\theta_p)\omega_p + \mu_p)[(\tau_{ap}+\mu_p)(1-R_1) + (\mu_p+\tau_p)(1-R_2)]\\
&\quad + (\mu_p+\tau_p)(\delta(\tau_{ap}+\mu_p) - \psi\eta_p\theta_p\rho_p) + \eta_p\theta_p\omega_p(\tau_{ap}+\mu_p)\\
&\quad + (\tau_{ap}+\mu_p)[(\mu_p+\tau_p)(\theta_p(\rho_p-\omega_p)+\mu_p+\omega_p) - \eta_p\omega_p],\\
a_4 &= \pi(\mu_p+\tau_p)(\tau_{ap}+\mu_p)(\theta_p\rho_p + (1-\theta_p)\omega_p + \mu_p)(1-R_0).
\end{aligned}$$

All the coefficients are positive when $R_0 < 1$ so the disease-free equilibrium point is locally asymptotically stable if $R_0 < 1$.

6 Numerical results and discussions

The paper applies the predictor-corrector method to solve model (3) with initial conditions: $S_P(0) = 8065518$, $E_P(0) = 200000$, $I_P(0) = 282$, $A_P(0) = 200$, $R_P(0) = 0$, $M(0) = 50000$. The basic reproduction for the given data is $R_0 = 2.4829$. The research studies system behaviour in two cases (see from figure 1 to figure 6). In the first case, we consider the variable fractional-order $\alpha(t) = 0.8 - 0.005t$ while in the second case, $\alpha(t) = 0.8 - 0.01\sin(\pi t)$ is a periodic function. We compare the results of the fractional variable order with the results of the classical constant fractional order when $\alpha(t) = 0.8$. Using the variable fractional-order $\alpha(t) = 0.8 - 0.005t$ indicates that the model memory has a decreasing function. Thus, behavior of the model gets slower by time. However, using the variable fractional-order $\alpha(t) = 0.8 - 0.01\sin(\pi t)$ indicates that model memory has a periodic function, making its behavior periodic as well.
The parameters values are considered follows [9]:
$\Pi_p = \mu_p N_p = 107644.22451$ per year, $\mu_p = \frac{1}{76.79\times 365}, \eta_p = 0.05, \psi = 0.02, \eta_w = 0.000001231, \theta_P = 0.1243, \omega_P = 0.00047876, \rho_P = 0.005, \tau_P = 0.09871, \tau_{aP} = 0.854302, Q_p = 0.000398, \overline{\omega}_P = 0.001$ and $\pi = 0.01$

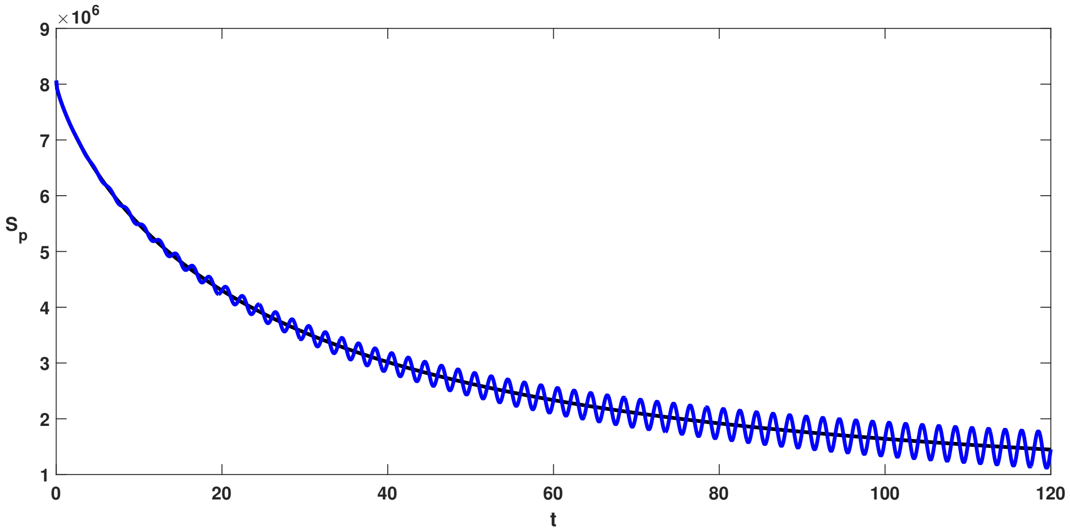

Fig.1a: The susceptible people at $\alpha = 0.8$ (Black line)and $\alpha = 0.8 - 0.01sin(\pi t)$ (Blue line)

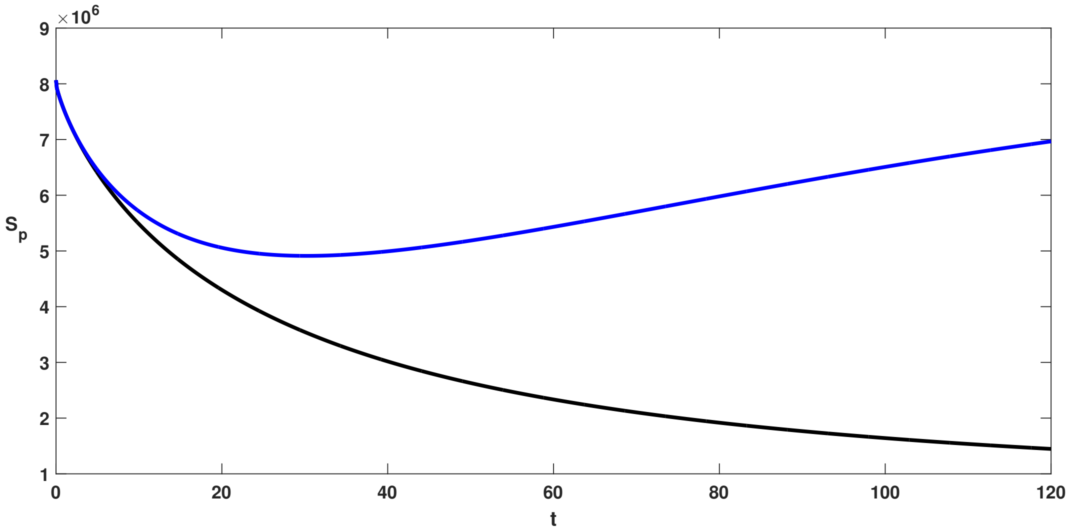

Fig. 1b: The susceptible people at $\alpha = 0.8$ (Black line) and $\alpha = 0.8 - 0.005t$ (Blue line)

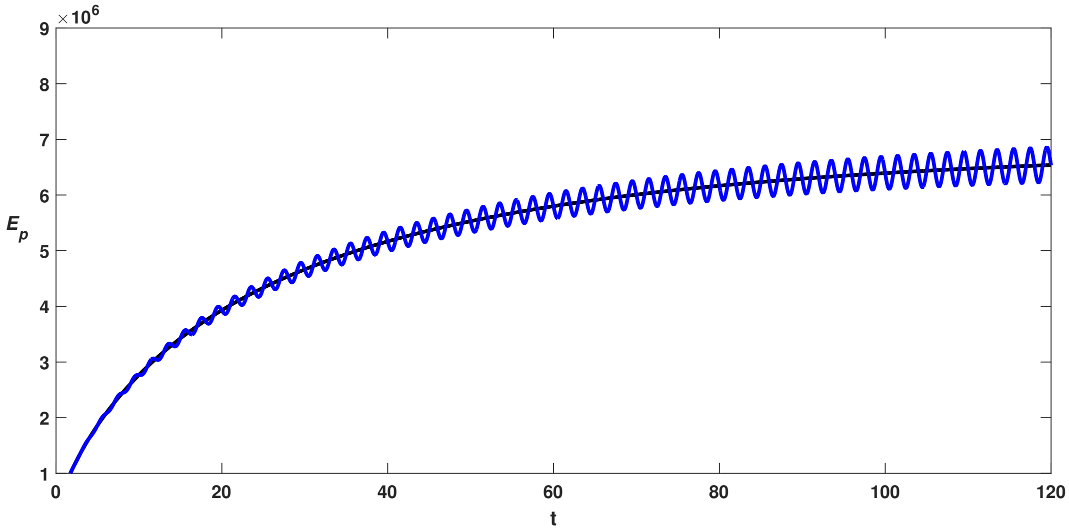

Fig.2a: The Exposed people at $\alpha = 0.8$ (Black line)and $\alpha = 0.8 - 0.01 sin(\pi t)$ (Blue line)

7 Conclusion

In this paper, the interaction between COVID-19 vectors (bats) and unknown hosts, then between people and coronavirus reservoir (seafood market) are presented through a variable fractional-order model. The basic reproductive number R_0, disease-free equilibrium points and stability are discussed. Numerical solutions of the proposed model are presented to study the effect of the variable memory as a function of time on the spread of COVID-19 pandemic.

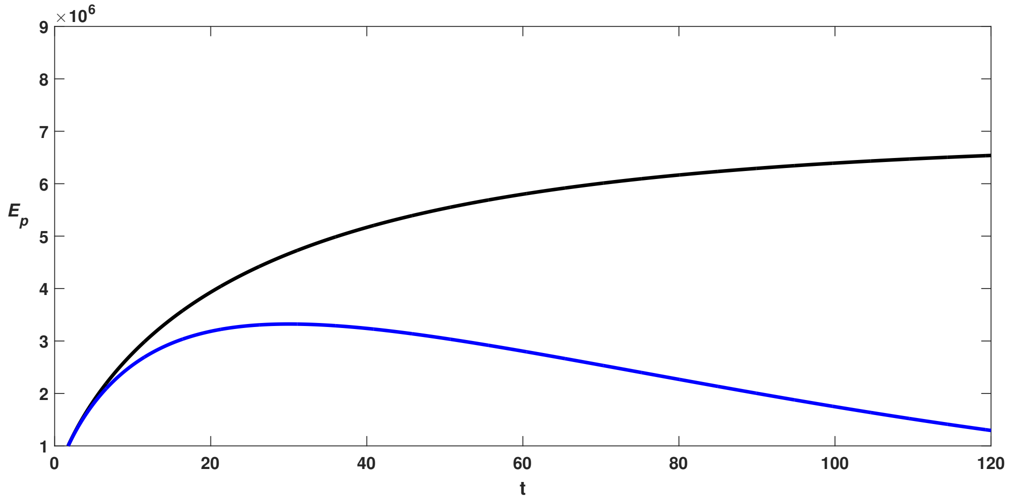

Fig. 2b: The Exposed people at $\alpha = 0.8$ (Black line) and $\alpha = 0.8 - 0.005t$ (Blue line)

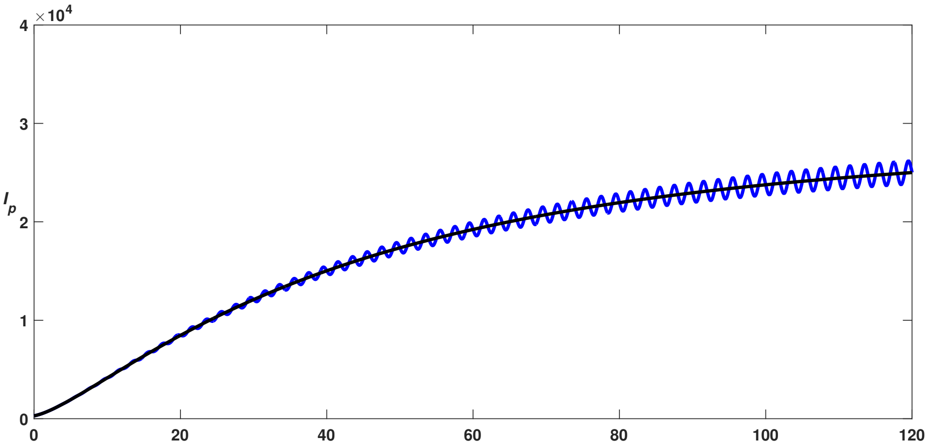

Fig.3a: The Infected people at $\alpha = 0.8$ (Black line)and $\alpha = 0.8 - 0.01 sin(\pi t)$ (Blue line)

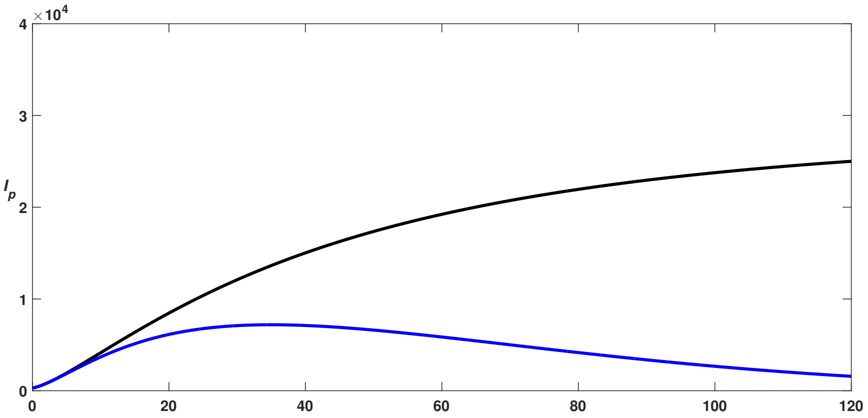

Fig. 3b: The Infected people at $\alpha = 0.8$ (Black line) and $\alpha = 0.8 - 0.005t$ (Blue line)

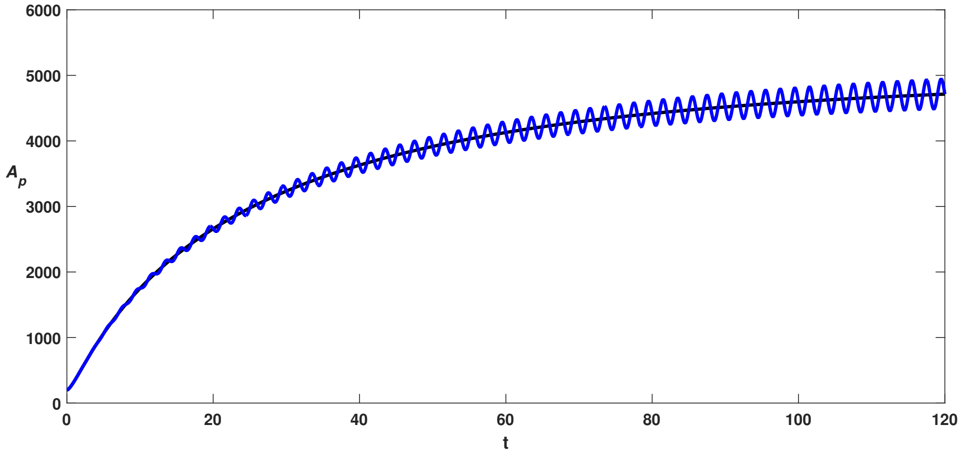

Fig.4a: The asymptotically infected people at $\alpha = 0.8$ (Black line) and $\alpha = 0.8 - 0.01 sin(\pi t)$ (Blue line)

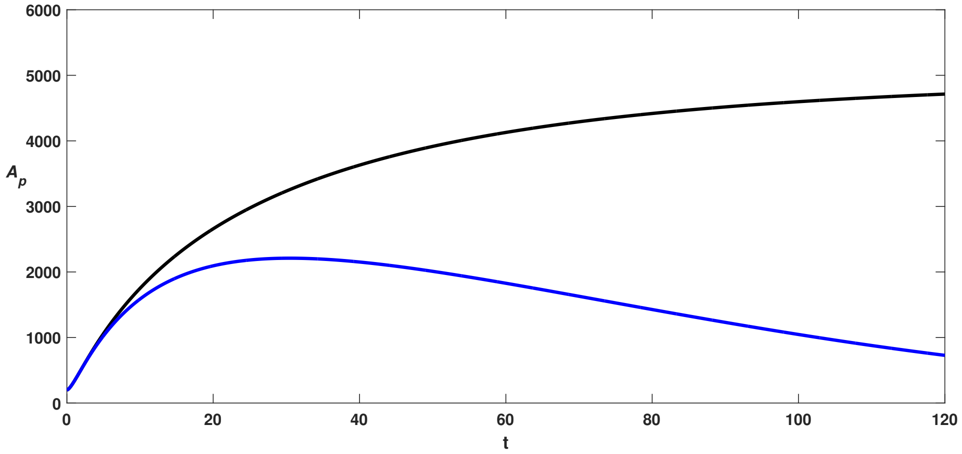

Fig.4b: The asymptotically infected people at $\alpha = 0.8$ (Black line)and $\alpha = 0.8 - 0.005t$ (Blue line)

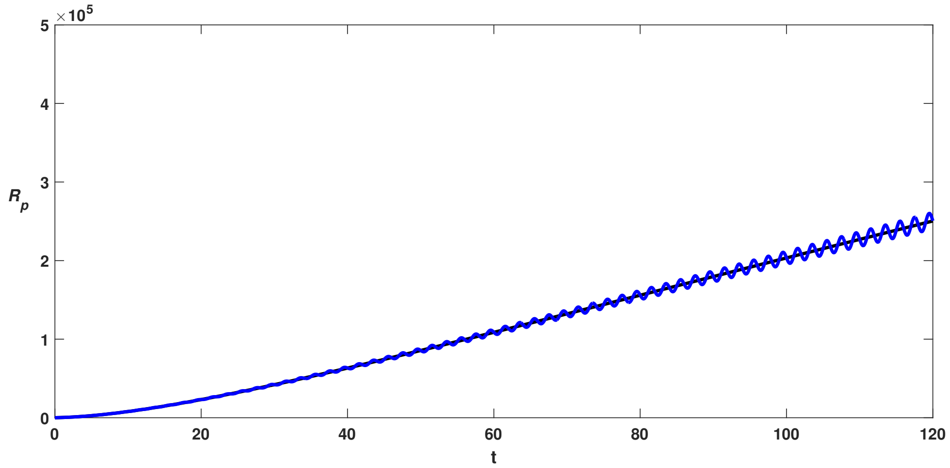

Fig.5a: The recovered/removed people at $\alpha = 0.8$ (Black line)and $\alpha = 0.8 - 0.01 sin(\pi t)$ (Blue line)

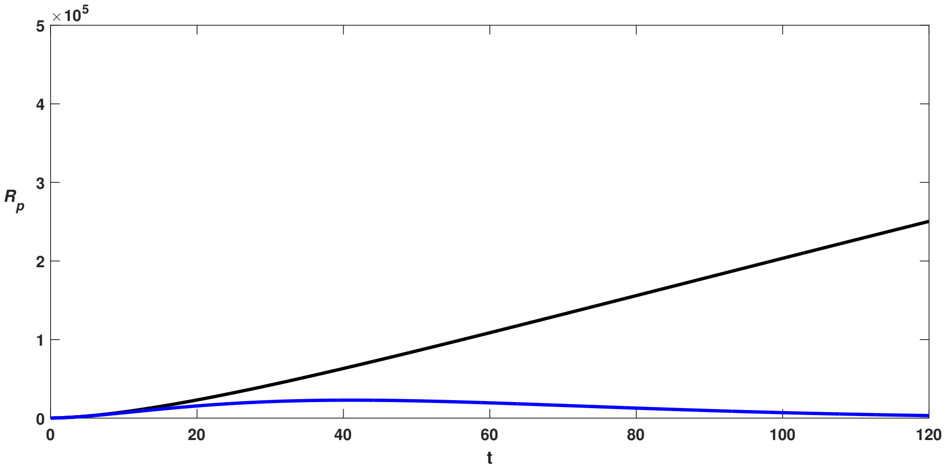

Fig.5b: The recovered/removed people at $\alpha = 0.8$ (Black line)and $\alpha = 0.8-0.005t$ (Blue line)

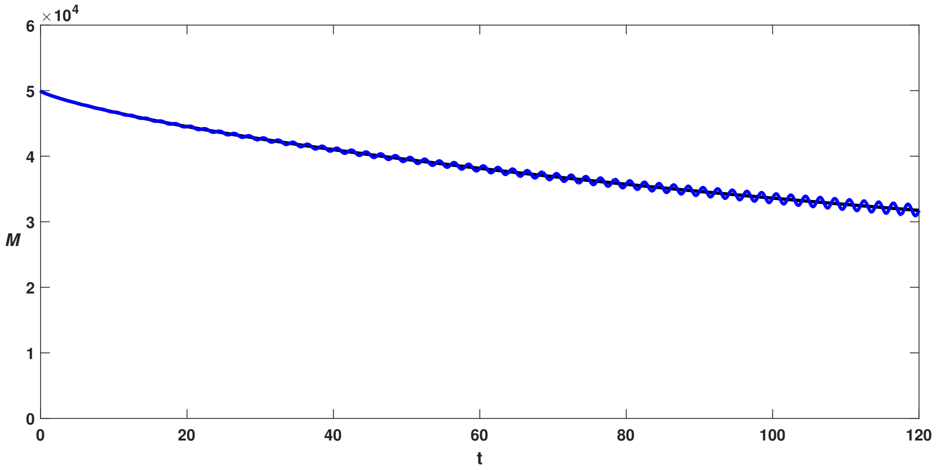

Fig.6a: The reservoir density at $\alpha = 0.8$ (Black line)and $\alpha = 0.8-0.01sin(\pi t)$ (Blue line)

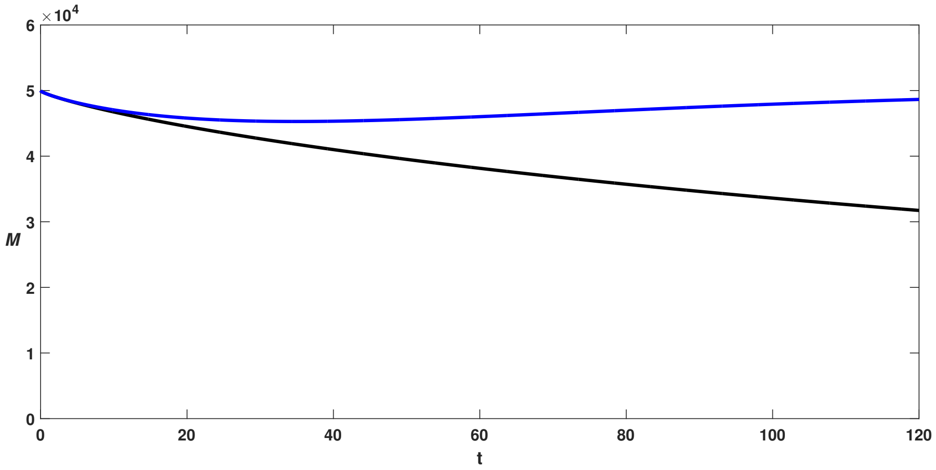

Fig.6b: The reservoir density at $\alpha = 0.8$ (Black line)and $\alpha = 0.8-0.005t$ (Blue line)

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