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Modeling the dynamics of novel coronavirus (2019-nCov) with fractional derivative

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Abstract The present paper describes the mathematical modeling and dynamics of a novel corona virus (2019-nCoV). We describe the brief details of interaction among the bats and unknown hosts, then among the peoples and the infections reservoir (seafood market). The seafood market are considered the main source of infection when the bats and the unknown hosts (may be wild animals) leaves the infection there. The purchasing of items from the seafood market by peoples have the ability to infect either asymptotically or symptomatically. We reduced the model with the assumptions that the seafood market has enough source of infection that can be effective to infect people. We present the mathematical results of the model and then formulate a fractional model. We consider the available infection cases for January 21, 2020, till January 28, 2020 and parameterized the model. We compute the basic reproduction number for the data is $\mathcal{R}_0 \approx 2.4829$. The fractional model is then solved numerically by presenting many graphical results, which can be helpful for the infection minimization.

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1. Introduction

One of the greatest assignments given to humankind is to control the environment within which they live. However some instructions have been given and boundaries have been placed such that some law of nature should not be violated. In the process of controlling nature, they have constructed very powerful instruments that allow them to have control of some important places like the sea, air and ground. The secure survival of their kind, and also eliminate each living being that can be a threat for their survival,

they have developed powerful weapons including guns, bombs, medications, technical instrument that can help them identify sickness, their origin, and how to eliminate them. Although they have succeeded so far to be on top of the game, violation of fundamental laws of nature has led to many natural disasters. For example failure to observe the law of cohabitation has led mankind to use heavy weapons to killing each other, some of the biggest that have been recorded in the history of mankind are World War 1 and 2, of course that there are many other genocides that have ended with mass loss of human live. Failure to observe the natural law of co-habitation has also led to xenophobia, a new man-made-disease that has spread around Africa and many other part of the world. While concepts like nationality have been introduced to divide mankind, while diplomatic, securities and many other measures have put in place to support the idea of

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nationality, mankind fails to understand that the world belong to nature and each leaving being therein are passengers. More precisely such concept has created many inequalities around the world. One can be in charge today but tomorrow he is no longer in charge the nature has recalled some of his parts. The misuse of sexual activity has led to many sexually transmitted diseases that have killed more than millions of souls in the last decades. One could list many other problems that occurred due to mankind violating the law of nature.

Mankind being in control of their environment does not grant them the right to have physical; interaction with all living being therein, even this does not give them right to eating whatever found in nature. Do we really have to eat everything? Do we really have to physically interact with every living being? The answer to these questions is of course no because, nature has offered mankind some fruits, vegetables, sea-foods and some meats that humans can use for their survival, however, there exist in nature other fruits, vegetables and sea-living being cannot be used for their survival. It is also true that there exist in nature some living being that do not have to be in any form of contact with humans. It is for instance widely believed that, the world deathly disease called HIV has its genesis from crossed species from chimpanzees to humans. This transmitted disease was pre-1980 unknown and transmission was not accompanied by visible signs or symptoms. It is also documented that, by 1980, HIV may have spread to five continents, also within this period around 300000 persons were infected. Ebola, a deathly infectious disease that has killed many humans around the world in the past last years is believed by scientists to have come from an infected animal such as a fruit bat or non-human primate. Lassa fever is believed to have come from rates. One can list many other deathly diseases that come from the interaction between humans and other living-beings. So far humans have developed several medical techniques and put in place many measure to prevent, even cure some the above listed diseases. While they thought to have master nature, the corona-virus occurs and has already killed many people in China, and has been discovered to other parts of the world including Europe and Africa. The 2019 corona-virus also called the Wuhan corona-virus, is a transmitted virus causing respiratory infection and highly transmitted from human to human. In this paper, we aim to suggest and present mathematical analysis underpinning the spread of such deathly disease and present some prediction with real world data.

The novel coronavirus (2019-nCoV) first case was detected in the city of Wuhan China which is the capital of Hubei province on December 31, 2019. After developing the pneumonia without a clear cause and for which the available vaccine or treatments were found not effective [2]. Further, it is shown the transmission of the virus from human to human [3]. The cases not only spread in the Wuhan city but also to the other cities of China. Besides this, the virus spread to other region of the world such as Europe, North America and the Asia specific. It is documented that appearance of the symptoms taking 2 to 10 days. The symptoms include coughing, the breathing difficulties, and the fever. As per January 28, 4593 cases were found infective with the virus and 132 deaths and due to the virus further information about the new cases and deaths are yet to come.

In the present paper, we consider the model formulation initially in integer order derivative and then apply the Atangana-Baleanu derivative. The purpose of using the

Atangana-Baleanu derivative to the model is that it has many properties such as their kernel is nonlocal and nonsingular, and the crossover behavior in the model can only be best described using this operator. The others operators such as Caputo, Caputo-Fabrizio which does not posses these properties may or may not well describe the dynamics of corona virus. Although in future, we study the this corona virus model in other operators such as Caputo and Caputo-Fabrizio and their comparison with Atangana-Baleanu derivative and will conclude which operator is more appropriate for this model. Research related Atangana-Baleanu derivative and their applications to various models arising in science and engineering can be seen in [4–8]. Some other related papers to the applications of Atangana-Baleanu derivative can be seen in [9–14]

We consider the reported cases since January 21, 2020 till January 28, 2020, which are higher than the initial days and formulate a mathematical model to parameterize the model. We give brief details about the mathematical modeling of the novel corona virus in Section 2. Some fundamental properties of the model and their stability will be explored in Section 3. We then, formulate the model in fractional derivatives and presented a numerical scheme for their solution in Section 4. The data versus model fitting for the given period will be shown in Section 5 and also, we briefly discuss the numerical results with many values of the fractional order ρ . Concluding remarks will be provided in Section 6.

2. Model formulation

2.1. Formulations of bats and hosts population

Assuming the transmission within the bats population take place and then the transmission occur to the hosts (it may be the wild animals). The hunting of the hosts and their travel to the seafood market which is consider to be the reservoir or virus. Peoples get risk of infection by exposing to the market. We start the model formulation by denoting the total size of the bats population by $N_b(t)$ which is classified further into four classes, the susceptible bats, $S_b(t)$, the exposed bats, $E_b(t)$, the infected bats, $I_b(t)$ and the recovered or removed bats $R_b(t)$ at any time t , so, $N_b = S_b + E_b + I_b + R_b$. The unknown host are denoted by $N_h(t)$ which is classified further into four subgroups, that is $S_h(t)$, $E_h(t)$, $I_h(t)$ and $R_h(t)$ respectively, show the susceptible, exposed, infected and the recovered or removed hosts. So that, $N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$. The interaction among bats and host population can represented through the following evolutionary differential equations:

$$\begin{aligned}
 \frac{dS_b}{dt} &= \Pi_b - \mu_b S_b - \frac{\eta_b S_b I_b}{N_b}, \\
 \frac{dE_b}{dt} &= \frac{\eta_b S_b I_b}{N_b} - (\mu_b + \theta_b) E_b, \\
 \frac{dI_b}{dt} &= \theta_b E_b - (\tau_b + \mu_b) I_b, \\
 \frac{dR_b}{dt} &= \tau_b I_b - \mu_b R_b, \\
 \frac{dS_h}{dt} &= \Pi_h - \mu_h S_h - \frac{\eta_{bh} S_h I_b}{N_h} - \frac{\eta_h S_h I_h}{N_h}, \\
 \frac{dE_h}{dt} &= \frac{\eta_{bh} S_h I_b}{N_h} + \frac{\eta_h S_h I_h}{N_h} - (\mu_h + \theta_h) E_h, \\
 \frac{dI_h}{dt} &= \theta_h E_h - (\mu_h + \tau_h) I_h, \\
 \frac{dR_h}{dt} &= \tau_h I_h - \mu_h R_h,
 \end{aligned} \tag{1}$$

subject to non-negative initial conditions. The population of susceptible bats is recruited through the birth rate Π_b where death rate in each class of bats is given by μ_b . The exposed bats after completing their incubation period become infected at the rate θ_b and join the infection class I_b . The recover or removal rate of the infected bats to class R_b is shown by τ_b . The infection that caused by the interaction of susceptible and infected bats at the rate η_b with the route $\eta_b S_b I_b / N_b$. The birth rate of the host is given by Π_h while the natural death rate in each class is given μ_h . The exposed host becomes infected at the rate θ_h and join the infection class I_h and τ_h is the removal or recovery rate of the infected host. The contact among the susceptible hosts and the infected bats take place through the route $\eta_{bh} S_h I_b / N_h$, where η_{bh} is the coefficient of disease transmission from infected bats to the healthy hosts. After getting the infection from the infected bats, the virus has the ability to spread within the host and shown by the route $\eta_h S_h I_h / N_h$, where η_h is the disease transmission coefficient among the host population classes S_h and I_h . The complete flow transfer among bats and hosts population are shown in Fig. 1.

2.2. Formulation of corona virus (seafood market) versus people

The total population of people is denoted by N_p which is classified further into five subgroups such as S_p, E_p, I_p, A_p and R_p which represent respectively, the susceptible, exposed, infected (symptomatic), asymptotically infected, and the recovered or the removed people. The evolutionary dynamics of the bats, host, people and the seafood market (reservoir), simply (bats-hosts-reservoir-people) is described through the nonlinear differential equations given by:

$$\begin{aligned} \frac{dS_p}{dt} &= \Pi_p - \mu_p S_p - \frac{\eta_p S_p (I_p + \psi A_p)}{N_p} - \eta_w S_p M, \\ \frac{dE_p}{dt} &= \frac{\eta_p S_p (I_p + \psi A_p)}{N_p} + \eta_w S_p M - (1 - \theta_p) \omega_p E_p - \theta_p \rho_p E_p - \mu_p E_p, \\ \frac{dI_p}{dt} &= (1 - \theta_p) \omega_p E_p - (\tau_p + \mu_p) I_p, \\ \frac{dA_p}{dt} &= \theta_p \rho_p E_p - (\tau_{ap} + \mu_p) A_p, \\ \frac{dR_p}{dt} &= \tau_p I_p + \tau_{ap} A_p - \mu_p R_p, \\ \frac{dM}{dt} &= b \frac{M I_h}{N_h} + \varrho_p I_p + \varpi_p A_p - \pi M. \end{aligned} \tag{2}$$

The birth and natural death rate of the people is given by the parameters Π_p and μ_p respectively. The susceptible people S_p will be infected through sufficient contacts with the infected people I_p through the term given by $\eta_p S_p I_p$ where the η_p is the disease transmission coefficient. The transmission among the asymptotically infected people with health people could take place at form $\psi \eta_p S_p A_p$, where ψ the transmissibility multiple of A_p to that I_p and $\psi \in [0, 1]$, when $\psi = 0$, no transmissibility multiple will exists and hence vanish, and if $\psi = 1$, then the same will take place like I_p infection. The parameter θ_p is the proportion of asymptomatic infection. The parameters ω_p and ρ_p respectively represent the transmission rate after completing the incubation period and becomes infected, joining the class I_p and A_p . The people in the symptomatic class I_p and asymptomatic class A_p joining these class R_p with the removal or recovery rate respectively by τ_p and τ_{ap} . The class M which is denoted be the reservoir or the seafood place or market. The susceptible people infected after the interaction with M , given by $\eta_w M S_p$, where η_w is the disease transmission coefficient from M to S_p . The host visiting the seafood market by purchasing the items (retail purchase) shown by b with $b M I_h / N_h$. The parameters ϱ_p and ϖ_p of the infected symptomatic and asymptotically infected respectively contributing the virus into the seafood market M . The removing rate of the virus from the seafood market M is given by the rate π . The complete transfer among people and seafood reservoir is depicted in Fig. 2.

Considering that the 2019-nCoV can be imported in short time to the seafood market with enough source of virus and thus, without loss of generality, ignoring of the interaction among bats and hosts, the model (2) can be reduced to the system below, which can be regarded base study model:

$$\begin{aligned} \frac{dS_p}{dt} &= \Pi_p - \mu_p S_p - \frac{\eta_p S_p (I_p + \psi A_p)}{N_p} - \eta_w S_p M, \\ \frac{dE_p}{dt} &= \frac{\eta_p S_p (I_p + \psi A_p)}{N_p} + \eta_w S_p M - (1 - \theta_p) \omega_p E_p - \theta_p \rho_p E_p - \mu_p E_p, \\ \frac{dI_p}{dt} &= (1 - \theta_p) \omega_p E_p - (\tau_p + \mu_p) I_p, \\ \frac{dA_p}{dt} &= \theta_p \rho_p E_p - (\tau_{ap} + \mu_p) A_p, \\ \frac{dR_p}{dt} &= \tau_p I_p + \tau_{ap} A_p - \mu_p R_p, \\ \frac{dM}{dt} &= \varrho_p I_p + \varpi_p A_p - \pi M. \end{aligned} \tag{3}$$

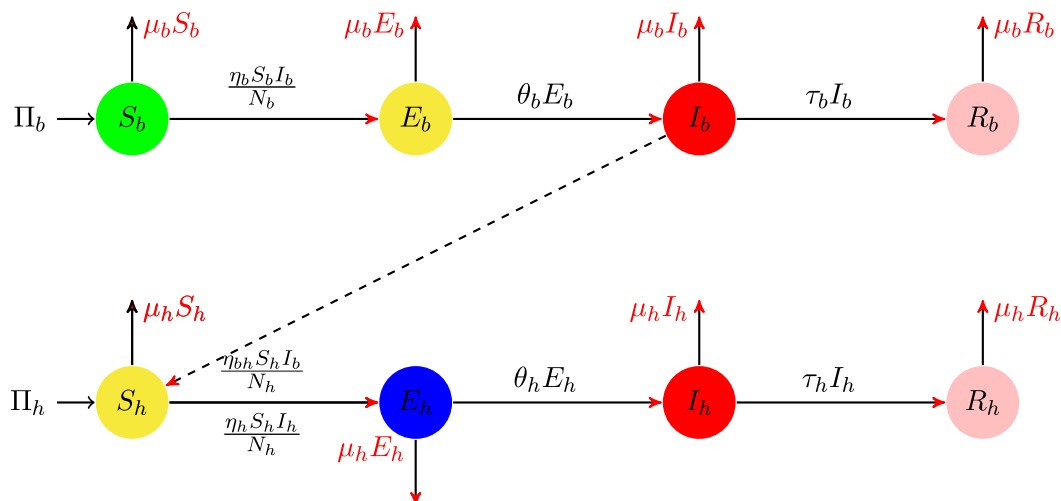


Fig. 1 Interaction among bats and host.

with the initial conditions

$$\begin{aligned} S_p(0) = S_p(0) \geq 0, E_p(0) = E_p(0) \geq 0, I_p(0) = I_p(0) \geq 0, \\ A_p(0) = A_p(0) \geq 0, \\ R_p(0) = R_p(0) \geq 0, M(0) = M(0) \geq 0. \end{aligned} \tag{4}$$

The total dynamics of the people can be obtained by adding the first five equations of the model (3), given by

$$\frac{dN_p}{dt} = \Pi_p - \mu_p N_p.$$

The feasible region for the model (3) is given by

$$\begin{aligned} \Omega = \left\{ (S_p(t), E_p(t), I_p(t), A_p(t), R_p(t)) \in \mathbb{R}_+^5 : N_p(t) \right. \\ \left. \leq \frac{\Pi_p}{\mu_p}, M \in \mathbb{R}_+ : \frac{\Pi_p}{\mu_p} \frac{\varrho_p + \varpi_p}{\pi} \right\}. \end{aligned} \tag{5}$$

3. Stability results

The present section explore the stability for the model (3) by considering first the disease free equilibrium and the basic reproduction number denoted by \mathcal{R}_0 . The disease free equilibrium for the model (3) is,

$$E_0 = (S_p^0, 0, 0, 0, 0) = \left(\frac{\Pi_p}{\mu_p}, 0, 0, 0, 0 \right). \tag{6}$$

Computing the basic reproduction number for the given model (3), we follows the work in [18], where the necessary computations of the matrices F and V are shown by

$$F = \begin{pmatrix} 0 & \eta_p & \psi\eta_p & \frac{\eta_w \Pi_p}{\mu_p} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \theta_p \rho_p + (1 - \theta_p) \omega_p + \mu_p & 0 & 0 & 0 \\ (\theta_p - 1) \omega_p & \mu_p + \tau_p & 0 & 0 \\ -\theta_p \rho_p & 0 & \tau_{ap} + \mu_p & 0 \\ 0 & -\varrho_p & -\varpi_p & \pi \end{pmatrix}.$$

The spectral radius $\gamma(FV^{-1})$ is the required basic reproduction number of the model (3), we is given by

$$\mathcal{R}_0 = \frac{\theta_p \rho_p (\mu_p + \tau_p) (\pi \psi \eta_p \mu_p + \Pi_p \varpi_p \eta_w) + (1 - \theta_p) \omega_p (\tau_{ap} + \mu_p) (\pi \eta_p \mu_p + \Pi_p \varrho_p \eta_w)}{\pi \mu_p (\mu_p + \tau_p) (\tau_{ap} + \mu_p) (\theta_p (\rho_p - \omega_p) + \mu_p + \omega_p)}.$$

Further, we can write \mathcal{R}_0 in the form

$$\begin{aligned} \mathcal{R}_0 &= \mathcal{R}_1 + \mathcal{R}_2, \\ \mathcal{R}_1 &= \frac{\theta_p \rho_p (\pi \psi \eta_p \mu_p + \Pi_p \varpi_p \eta_w)}{\pi \mu_p (\tau_{ap} + \mu_p) (\theta_p \rho_p + (1 - \theta_p) \omega_p + \mu_p)}, \\ \mathcal{R}_2 &= \frac{(1 - \theta_p) \omega_p (\pi \eta_p \mu_p + \Pi_p \varrho_p \eta_w)}{\pi \mu_p (\mu_p + \tau_p) (\theta_p (\rho_p - \omega_p) + \mu_p + \omega_p)}. \end{aligned}$$

Theorem 1. The DFE E_0 of the system (3) is locally asymptotically stable if $\mathcal{R}_0 < 1$.

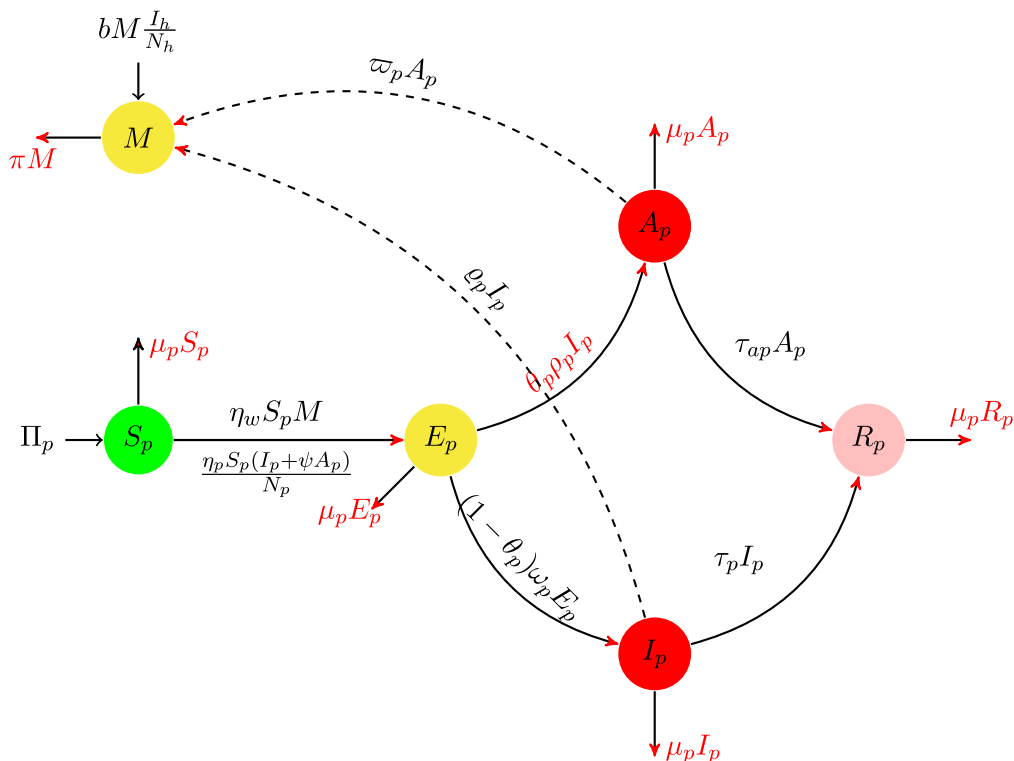


Fig. 2 Interaction among the people and the reservoir (seafood) market.

Proof. For the proof, we obtain at DFE E_0 , the Jacobian matrix below,

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

In above Jacobian matrix, the two eigenvalues are negative, that is $-\mu_p$ (twice) and the rest can be obtained through the characteristics equation below:

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

where

$$\begin{aligned} a_1 &= \tau_{ap} + \delta + \theta_p\rho_p + (1-\theta_p)\omega_p + 3\mu_p + \tau_p, \\ a_2 &= \underbrace{(\mu_p + \tau_p)(\theta_p\rho_p + (1-\theta_p)\omega_p + \mu_p) - \eta_p(1-\theta_p)\omega_p}_{+ (\tau_{ap} + \mu_p)(\theta_p(\rho_p - \omega_p) + \mu_p + \omega_p) - \psi\eta_p\theta_p\rho_p} \\ &\quad + \pi(\tau_{ap} + \mu_p) + (\mu_p + \tau_p)(\tau_{ap} + \mu_p) + \pi(\theta_p(\rho_p - \omega_p) + \mu_p + \omega_p) + \pi(\mu_p + \tau_p), \\ a_3 &= \pi(\theta_p\rho_p + (1-\theta_p)\omega_p + \mu_p)[(\tau_{ap} + \mu_p)(1 - \mathcal{R}_0) + (\mu_p + \tau_p)(1 - \mathcal{R}_2)] \\ &\quad + (\mu_p + \tau_p)(\delta(\tau_{ap} + \mu_p) - \psi\eta_p\theta_p\rho_p) + \eta_p\theta_p\omega_p(\tau_{ap} + \mu_p) \\ &\quad + (\tau_{ap} + \mu_p)((\mu_p + \tau_p)(\theta_p(\rho_p - \omega_p) + \mu_p + \omega_p) - \eta_p\omega_p), \\ a_4 &= \pi(\mu_p + \tau_p)(\tau_{ap} + \mu_p)(\theta_p\rho_p + (1-\theta_p)\omega_p + \mu_p)(1 - \mathcal{R}_0). \end{aligned}$$

In above equation the term under braces are less than \mathcal{R}_0 and the coefficient a_4 is positive when $\mathcal{R}_0 < 1$, and thus all the coefficients are positive. Further, the criteria of Rough-Hurtwitz for the fourth order polynomial is $a_i > 0$ for $i = 1, 2, \dots, 4$ and $a_1a_2a_3 - a_1^2a_4 - a_3^2 > 0$ can be easily satisfied by using the above coefficients. So, the model (3) at the disease free equilibrium is locally asymptotically stable if $\mathcal{R}_0 < 1$.

3.1. Endemic equilibria

For the endemic equilibrium of the model (3), we denote it by E^* and $E^* = (S_p^*, E_p^*, I_p^*, A_p^*, R_p^*, M_p^*)$, given by

$$\begin{aligned} S_p^* &= \frac{\Pi_p}{\lambda + \mu_p}, \\ E_p^* &= \frac{\lambda S_p^*}{\theta_p\rho_p - \theta_p\omega_p + \mu_p + \omega_p}, \\ I_p^* &= \frac{E_p^*(1-\theta_p)\omega_p}{\mu_p + \tau_p}, \\ A_p^* &= \frac{E_p^*\theta_p\rho_p}{\tau_{ap} + \mu_p}, \\ R_p^* &= \frac{A_p^*\tau_{ap} + I_p^*\tau_p}{\mu_p}, \\ M_p^* &= \frac{A_p^*\varpi_p + I_p^*\varrho_p}{\pi}, \end{aligned} \tag{7}$$

where

$$\lambda^* = \frac{\eta_p(\psi A_p^* + I_p^*)}{A_p^* + E_p^* + I_p^* + R_p^* + S_p^*} + \eta_w M_p^* \tag{8}$$

which satisfies the equation below,

$$P(\lambda^*) = m_1(\lambda^*)^2 + m_2\lambda^* = 0, \tag{9}$$

where

$$\begin{aligned} m_1 &= \pi(\mu_p + \tau_p)(\tau_{ap} + \mu_p)(\theta_p(\rho_p - \omega_p) + \mu_p + \omega_p), \\ m_2 &= \pi\mu_p(\mu_p + \tau_p)(\tau_{ap} + \mu_p)(\theta_p(\rho_p - \omega_p) + \mu_p + \omega_p)(1 - \mathcal{R}_0). \end{aligned} \tag{10}$$

Obviously, $m_1 > 0$ and $m_2 \geq 0$ whenever $\mathcal{R}_0 < 1$, so that $\lambda^* = -m_2/m_1 \leq 0$. Thus, no endemic equilibrium exists whenever $\mathcal{R}_0 < 1$.

4. Fractional corona virus model

Before presenting the model in fractional derivative, we give the definition of fractional derivative and their integral below:

Definition 1. Let a function $g \in C^1(b_1, b_2)$, where $b_2 > b_1$, and $0 \leq \rho \leq 1$, then the representation of the Atangana-Baleanu derivative is given by:

$${}^{ABC}D_t^\rho g(t) = \frac{\mathcal{C}(\rho)}{1-\rho} \int_a^t g(\kappa) E_\rho \left[-\rho \frac{(t-\kappa)^\rho}{1-\rho} \right] d\kappa. \tag{11}$$

Definition 2. The fractional integral associated to the Atangana-Baleanu derivative is given by:

$${}^{ABC}I_t^\rho g(t) = \frac{1-\rho}{\mathcal{C}(\rho)} g(t) + \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \int_a^t g(\kappa)(t-\kappa)^{\rho-1} d\kappa, \tag{12}$$

where $\mathcal{C}(\rho)$ is the normalization function.

We generalize the model (3) by applying the Atangana-Baleanu derivative and obtain the model below:

$$\begin{aligned} {}^{ABC}D_t^\rho S_p &= \Pi_p - \mu_p S_p - \frac{\eta_p S_p (I_p + \psi A_p)}{N_p} - \eta_w S_p M, \\ {}^{ABC}D_t^\rho E_p &= \frac{\eta_p S_p (I_p + \psi A_p)}{N_p} + \eta_w S_p M - (1-\theta_p)\omega_p E_p - \theta_p\rho_p E_p - \mu_p E_p, \\ {}^{ABC}D_t^\rho I_p &= (1-\theta_p)\omega_p E_p - (\tau_p + \mu_p) I_p, \\ {}^{ABC}D_t^\rho A_p &= \theta_p\rho_p E_p - (\tau_{ap} + \mu_p) A_p, \\ {}^{ABC}D_t^\rho R_p &= \tau_p I_p + \tau_{ap} A_p - \mu_p R_p, \\ {}^{ABC}D_t^\rho M &= \varrho_p I_p + \varpi_p A_p - \pi M, \end{aligned} \tag{13}$$

where ρ represent the fractional order parameter and D_t^ρ is the fractional derivative, the model variables in (13) are non-negative and has appropriate initial conditions.

4.1. Numerical scheme

We give a numerical procedure for the solution of the fractional epidemic model (13) by adopting the procedure shown in [15]. The application of this scheme can be seen in many real world problems, see for example [16,17] and the references there in.

Applying the procedure in [15], our model (13) taking the shape below:

$$\begin{aligned} {}^{AB}D_t^\rho S_p &= \mathcal{H}_1(t, S_p, E_p, I_p, A_p, R_p, M), \\ {}^{AB}D_t^\rho E_p &= \mathcal{H}_2(t, S_p, E_p, I_p, A_p, R_p, M), \\ {}^{AB}D_t^\rho I_p &= \mathcal{H}_3(t, S_p, E_p, I_p, A_p, R_p, M), \\ {}^{AB}D_t^\rho A_p &= \mathcal{H}_4(t, S_p, E_p, I_p, A_p, R_p, M), \\ {}^{AB}D_t^\rho R_p &= \mathcal{H}_5(t, S_p, E_p, I_p, A_p, R_p, M), \\ {}^{AB}D_t^\rho M &= \mathcal{H}_6(t, S_p, E_p, I_p, A_p, R_p, M), \end{aligned} \tag{14}$$

The novel corona virus model further can be shown as:

$$\begin{aligned}
 S_p(t) - S_p(0) &= \frac{(1-\rho)}{\mathcal{C}(\rho)} \mathcal{H}_1(t, S_p) + \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \int_0^t \mathcal{H}_1(\kappa, S_p)(t-\kappa)^{\rho-1} d\kappa, \\
 E_p(t) - E_p(0) &= \frac{(1-\rho)}{\mathcal{C}(\rho)} \mathcal{H}_2(t, E_p) + \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \int_0^t \mathcal{H}_2(\kappa, E_p)(t-\kappa)^{\rho-1} d\kappa, \\
 I_p(t) - I_p(0) &= \frac{(1-\rho)}{\mathcal{C}(\rho)} \mathcal{H}_3(t, I_p) + \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \int_0^t \mathcal{H}_3(\kappa, I_p)(t-\kappa)^{\rho-1} d\kappa, \\
 A_p(t) - A_p(0) &= \frac{(1-\rho)}{\mathcal{C}(\rho)} \mathcal{H}_4(t, A_p) + \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \int_0^t \mathcal{H}_4(\kappa, A_p)(t-\kappa)^{\rho-1} d\kappa, \\
 R_p(t) - R_p(0) &= \frac{(1-\rho)}{\mathcal{C}(\rho)} \mathcal{H}_5(t, R_p) + \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \int_0^t \mathcal{H}_5(\kappa, R_p)(t-\kappa)^{\rho-1} d\kappa, \\
 M(t) - M(0) &= \frac{(1-\rho)}{\mathcal{C}(\rho)} \mathcal{H}_6(t, M) + \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \int_0^t \mathcal{H}_6(\kappa, M)(t-\kappa)^{\rho-1} d\kappa.
 \end{aligned} \tag{15}$$

Using $t = t_{n+1}, n = 0, 1, 2, \dots$, in above equation leads to the system below:

$$\begin{aligned}
 S_p(t_{n+1}) - S_p(t_0) &= \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_1(t_n, S_p) \\
 &+ \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \sum_{k=0}^n \int_{t_k}^{t_{k+1}} \mathcal{H}_1(\kappa, S_p)(t_{n+1}-\kappa)^{\rho-1} d\kappa, \\
 E_p(t_{n+1}) - E_p(t_0) &= \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_2(t_n, E_p) \\
 &+ \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \sum_{k=0}^n \int_{t_k}^{t_{k+1}} \mathcal{H}_2(\kappa, E_p)(t_{n+1}-\kappa)^{\rho-1} d\kappa, \\
 I_p(t_{n+1}) - I_p(t_0) &= \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_3(t_n, I_p) \\
 &+ \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \sum_{k=0}^n \int_{t_k}^{t_{k+1}} \mathcal{H}_3(\kappa, I_p)(t_{n+1}-\kappa)^{\rho-1} d\kappa, \\
 A_p(t_{n+1}) - A_p(t_0) &= \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_4(t_n, A_p) \\
 &+ \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \sum_{k=0}^n \int_{t_k}^{t_{k+1}} \mathcal{H}_4(\kappa, A_p)(t_{n+1}-\kappa)^{\rho-1} d\kappa, \\
 R_p(t_{n+1}) - R_p(t_0) &= \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_5(t_n, R_p) \\
 &+ \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \sum_{k=0}^n \int_{t_k}^{t_{k+1}} \mathcal{H}_5(\kappa, R_p)(t_{n+1}-\kappa)^{\rho-1} d\kappa, \\
 M(t_{n+1}) - M(t_0) &= \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_6(t_n, M) \\
 &+ \frac{\rho}{\mathcal{C}(\rho)\Gamma(\rho)} \sum_{k=0}^n \int_{t_k}^{t_{k+1}} \mathcal{H}_6(\kappa, M)(t_{n+1}-\kappa)^{\rho-1} d\kappa,
 \end{aligned} \tag{16}$$

Using the two points lagrange interpolation polynomial for the simplification of the integral in (16), we obtain in the following the numerical scheme for corona virus model (13) given by,

$$\begin{aligned}
 S_p(t_{n+1}) &= S_p(t_0) + \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_1(t_n, S_p) + \frac{\rho}{\mathcal{C}(\rho)} \\
 &\times \sum_{k=0}^n \left[\frac{h^\rho \mathcal{H}_1(t_k, S_p)}{\Gamma(\rho+2)} ((n+1-k)^\rho (n-k+2+\rho) \right. \\
 &- (n-k)^\rho (n-k+2+2\rho)) - \frac{h^\rho \mathcal{H}_1(t_{k-1}, S_p)}{\Gamma(\rho+2)} \\
 &\left. \times ((n+1-k)^{\rho+1} - (n-k)^\rho (n-k+1+\rho)) \right], \tag{17}
 \end{aligned}$$

$$\begin{aligned}
 E_p(t_{n+1}) &= E_p(t_0) + \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_2(t_n, E_p) + \frac{\rho}{\mathcal{C}(\rho)} \\
 &\times \sum_{k=0}^n \left[\frac{h^\rho \mathcal{H}_2(t_k, E_p)}{\Gamma(\rho+2)} ((n+1-k)^\rho (n-k+2+\rho) \right. \\
 &- (n-k)^\rho (n-k+2+2\rho)) - \frac{h^\rho \mathcal{H}_2(t_{k-1}, E_p)}{\Gamma(\rho+2)} \\
 &\left. \times ((n+1-k)^{\rho+1} - (n-k)^\rho (n-k+1+\rho)) \right], \tag{18}
 \end{aligned}$$

$$\begin{aligned}
 I_p(t_{n+1}) &= I_p(t_0) + \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_3(t_n, I_p) + \frac{\rho}{\mathcal{C}(\rho)} \\
 &\times \sum_{k=0}^n \left[\frac{h^\rho \mathcal{H}_3(t_k, I_p)}{\Gamma(\rho+2)} ((n+1-k)^\rho (n-k+2+\rho) \right. \\
 &- (n-k)^\rho (n-k+2+2\rho)) - \frac{h^\rho \mathcal{H}_3(t_{k-1}, I_p)}{\Gamma(\rho+2)} \\
 &\left. \times ((n+1-k)^{\rho+1} - (n-k)^\rho (n-k+1+\rho)) \right], \tag{19}
 \end{aligned}$$

$$\begin{aligned}
 A_p(t_{n+1}) &= A_p(t_0) + \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_4(t_n, A_p) + \frac{\rho}{\mathcal{C}(\rho)} \\
 &\times \sum_{k=0}^n \left[\frac{h^\rho \mathcal{H}_4(t_k, A_p)}{\Gamma(\rho+2)} ((n+1-k)^\rho (n-k+2+\rho) \right. \\
 &- (n-k)^\rho (n-k+2+2\rho)) - \frac{h^\rho \mathcal{H}_4(t_{k-1}, A_p)}{\Gamma(\rho+2)} \\
 &\left. \times ((n+1-k)^{\rho+1} - (n-k)^\rho (n-k+1+\rho)) \right], \tag{20}
 \end{aligned}$$

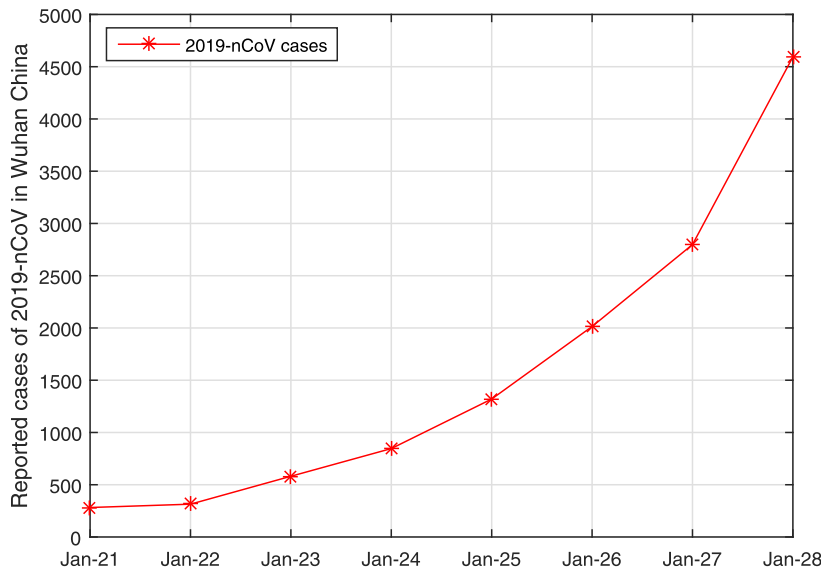


Fig. 3 Reported cases of 2019-nCoV in Wuhan China.

Table 1 Fitted and estimated parameters values for Corona virus model (13), when $\rho = 1$.

Parameter	Description	Value	Source
Π_p	Birth rate	$\mu_p \times N_p(0)$	Estimated
μ_p	Natural mortality rate	$\frac{1}{76.79 \times 365}$	[1]
η_p	Contact rate	0.05	Fitted
ψ	Transmissibility multiple	0.02	Fitted
η_w	Disease transmission coefficient	0.000001231	Fitted
θ_p	The proportion of asymptomatic infection	0.1243	Fitted
ω_p	Incubation period	0.00047876	Fitted
ρ_p	Incubation period	0.005	Fitted
τ_p	Removal or recovery rate of I_p	0.09871	Fitted
τ_{ap}	Removal or recovery rate of A_p	0.854302	Fitted
ϱ_p	Contribution of the virus to M by I_p	0.000398	Fitted
ϖ_p	Contribution of the virus to M by A_p	0.001	Fitted
π	Removing rate of virus from M	0.01	Fitted

$$\begin{aligned}
 R_p(t_{n+1}) = & R_p(t_0) + \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_5(t_n, R_p) + \frac{\rho}{\mathcal{C}(\rho)} \\
 & \times \sum_{k=0}^n \left[\frac{h^\rho \mathcal{H}_5(t_k, R_p)}{\Gamma(\rho+2)} ((n+1-k)^\rho (n-k+2+\rho) \right. \\
 & \left. - (n-k)^\rho (n-k+2+2\rho) \right) - \frac{h^\rho \mathcal{H}_5(t_{k-1}, R_p)}{\Gamma(\rho+2)} \\
 & \times \left((n+1-k)^{\rho+1} - (n-k)^\rho (n-k+1+\rho) \right) \Big], \quad (21)
 \end{aligned}$$

and

$$\begin{aligned}
 M(t_{n+1}) = & M(t_0) + \frac{1-\rho}{\mathcal{C}(\rho)} \mathcal{H}_6(t_n, M) + \frac{\rho}{\mathcal{C}(\rho)} \\
 & \times \sum_{k=0}^n \left[\frac{h^\rho \mathcal{H}_6(t_k, M)}{\Gamma(\rho+2)} ((n+1-k)^\rho (n-k+2+\rho) \right. \\
 & \left. - (n-k)^\rho (n-k+2+2\rho) \right) - \frac{h^\rho \mathcal{H}_6(t_{k-1}, M)}{\Gamma(\rho+2)} \\
 & \times \left((n+1-k)^{\rho+1} - (n-k)^\rho (n-k+1+\rho) \right) \Big]. \quad (22)
 \end{aligned}$$

In the next section, we consider the scheme shown above for the solution of the model (13).

5. Data fitting and numerical results

5.1. Data fitting

For the parameterizations of the model (13), we consider some of the parameters values from the literature and the rest are fitted or estimated from the Wuhan city of China, using the least curve fitting technique. The real data available sense January 21 to January 28, 2020 are shown in Fig. 3. The total population of the Wuhan city for the year 2019 is 8,266,000 [1]. The life expectancy in China for the year 2019 is 76.79, so we estimate $\mu_p = 1/76.79$ per year. The parameter Π_p is estimated from $\Pi_p/\mu_p = 8,266,000$, and assumed that this is to be the limiting population in the disease absence, so $\Pi_p = 107644.22451$ per year. For the initial values of the model variables, we use the total initial population

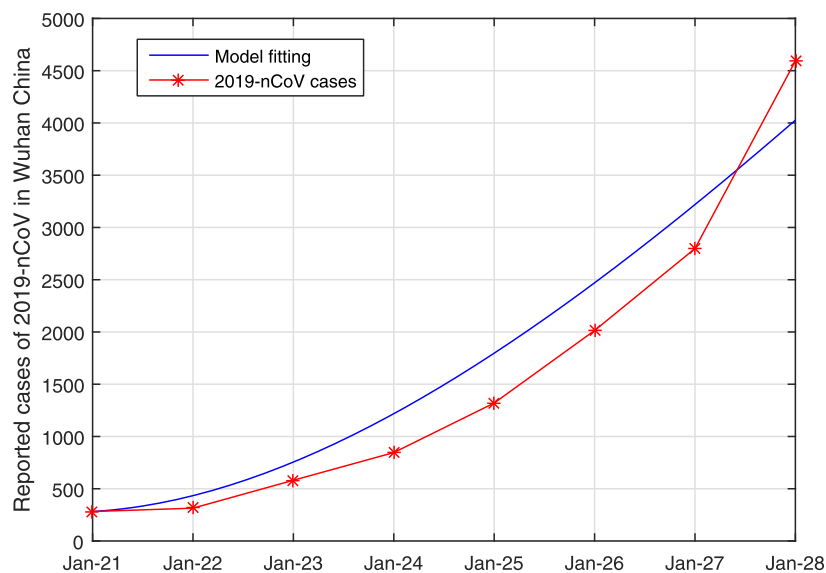


Fig. 4 Reported cases of 2019-nCoV in Wuhan China versus model fitting.

Table 2 Partial rank correlation coefficient (PRCC) values of \mathcal{R}_0 with corresponding p-values.

Parameter	Description	PRCC values	p values
Π_p	Birth rate	0.3603	0.0000
μ_p	Natural mortality rate	-0.8589	0.0000
η_p	Contact rate	0.4111	0.0000
ψ	Transmissibility multiple	0.2435	0.0000
η_w	Disease transmission coefficient	0.5799	0.0000
θ_p	The proportion of asymptomatic infection	-0.1991	0.2744
ω_p	Incubation period	0.4359	0.0000
ρ_p	Incubation period	0.3195	0.0000
τ_p	Removal or recovery rate of I_p	-0.3323	0.0000
τ_{ap}	Removal or recovery rate of A_p	-0.2766	0.0000
ϱ_p	Contribution of the virus to M by I_p	0.3340	0.0000
ϖ_p	Contribution of the virus to M by A_p	0.3023	0.0000
π	Removing rate of virus from M	-0.4738	0.0000

$N_p(0) = 8,266,000$, so that $N_p(0) = S_p(0) + E_p(0) + I_p(0) + A_p(0) + R_p(0)$. The initial value for the infected people to be considered from the data is $I_p(0) = 282$, we assume that there is no recovery from the infection yet, so $R_p(0) = 0, E_p(0) = 200000, A_p(0) = 200, S_p(0) = 8065518$ and $M(0) = 50000$. Using these initial values and simulated the model (13), we obtain the values of the parameters shown in Table 1, where as the basic reproduction number is estimated $\mathcal{R}_0 \approx 2.4829$. The data fitting versus model (13) is shown in Fig. 4 when $\rho = 1$.

5.2. Global sensitivity analysis

The main purpose of the sensitivity analysis for an epidemic model is to investigate the dominant factors associated with a certain interventions that affects the disease dynamics greatly. We do the sensitivity analysis by using the techniques as a combination of Latin hypercube sampling (LHS) and PRCC to find out the associated factors that are considered to influential. This PRCC technique is considered to be reliable and the efficient method in order to measure monotonic and nonlinear association among inputs and output results in the model. The sensitivity analysis gives the PRCC and the associated p-values, by which one can determine uncertainty level in an epidemic model. The most dominant parameters associated to an epidemic model are to be those who has small p-value while having high PRCC.

We present the PRCC analysis in order to determine the parameters that play essential role in contribution to variations in the outcome of the basic reproduction number \mathcal{R}_0 . The parameters used in the present analysis are given in Table 2 including their PRCC and p-values and the PRCC results as bar-graph is shown in Fig. 5. It can be observed from Table 2, that the most sensitive parameter is μ_p with the high PRCC value followed by $\eta_w, \pi, \omega_p, \eta_p, \Pi_p, \varrho_p, \tau_p, \rho_p, \varpi_p, \tau_{ap}, \psi, \theta_p$.

5.3. Numerical results

In the present section, we consider the model (13) and using the parameters values shown in Table 1 to obtain the graphical results. The time unit is taken in days. Fig. 6 describes the individuals behavior for different values of the fractional order ρ . Fig. 7 is obtained by varying the initial values, which shows the asymptotical stability of the endemic equilibrium.

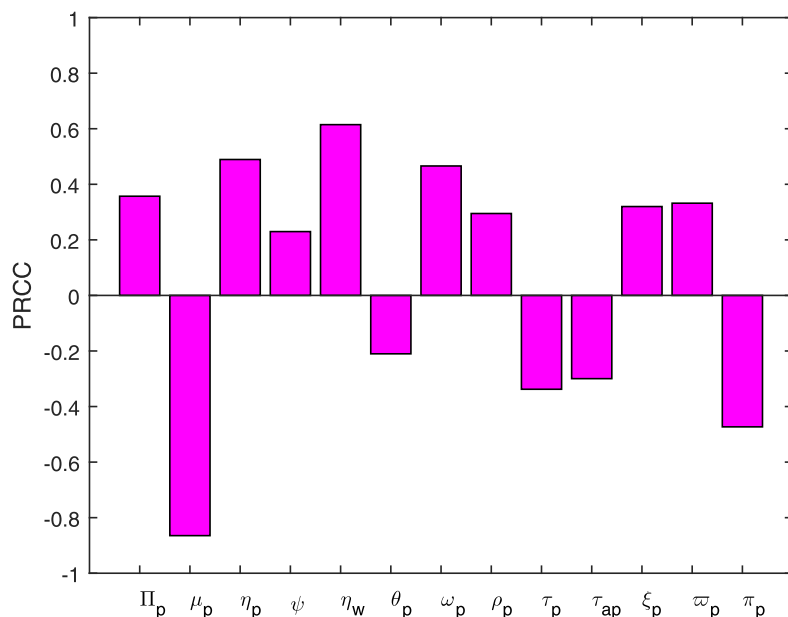


Fig. 5 Partial rank correlation coefficient (PRCC) results for significance of parameters involved in \mathcal{R}_0 .

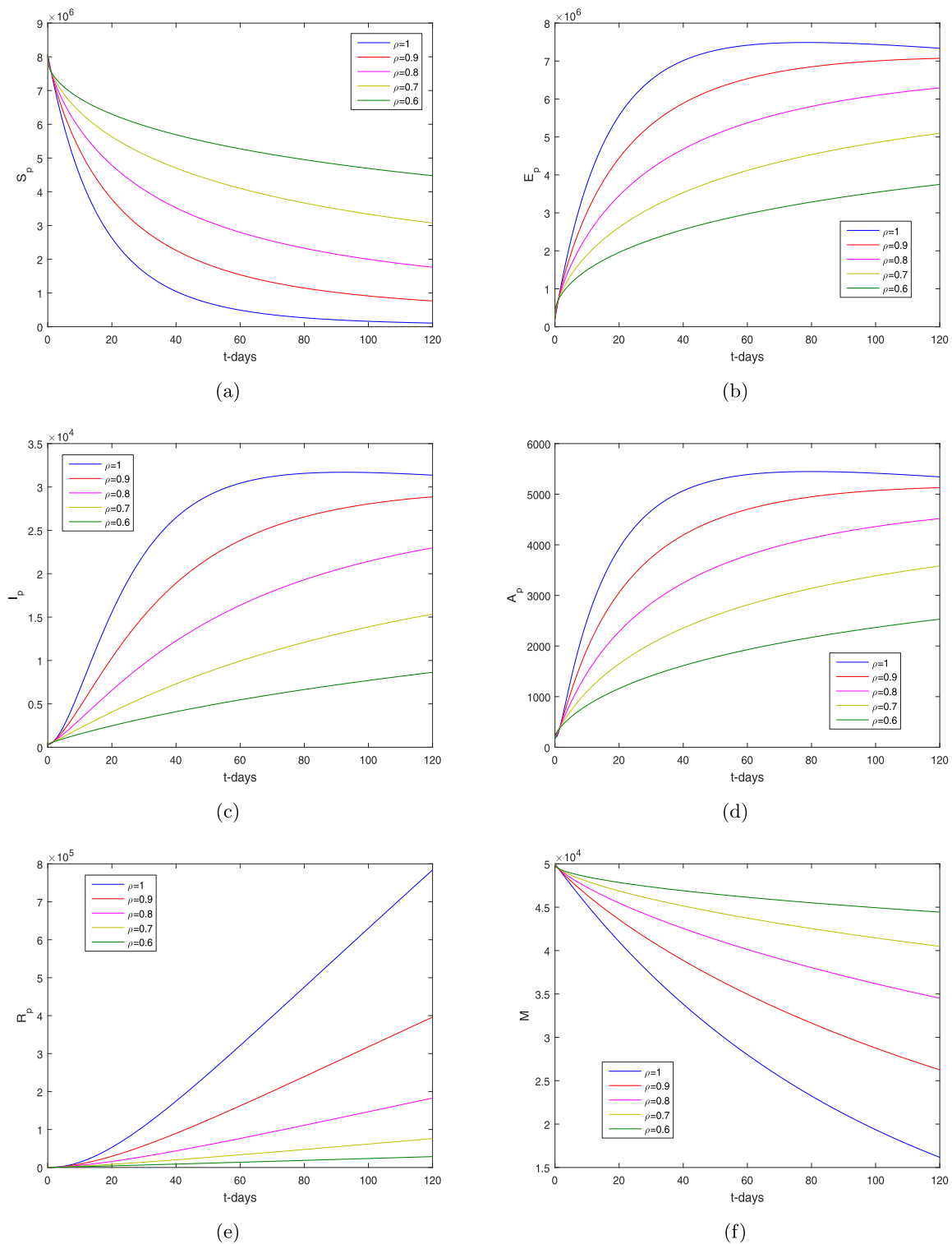


Fig. 6 The dynamics of corona virus model for different ρ .

6. Conclusion

We presented the mathematical modeling and the dynamics of novel corona virus (2019-nCoV) which is emerged recently in Wuhan China. We presented a brief details on the available

resources that take place in the generation of infection and formulated the mathematical model. The mathematical results for the model are obtained. We found that the corona virus model is locally asymptotically stable when $\mathcal{R}_0 < 1$. Further, we formulated a fractional model in Atangana-Baleanu derivative.

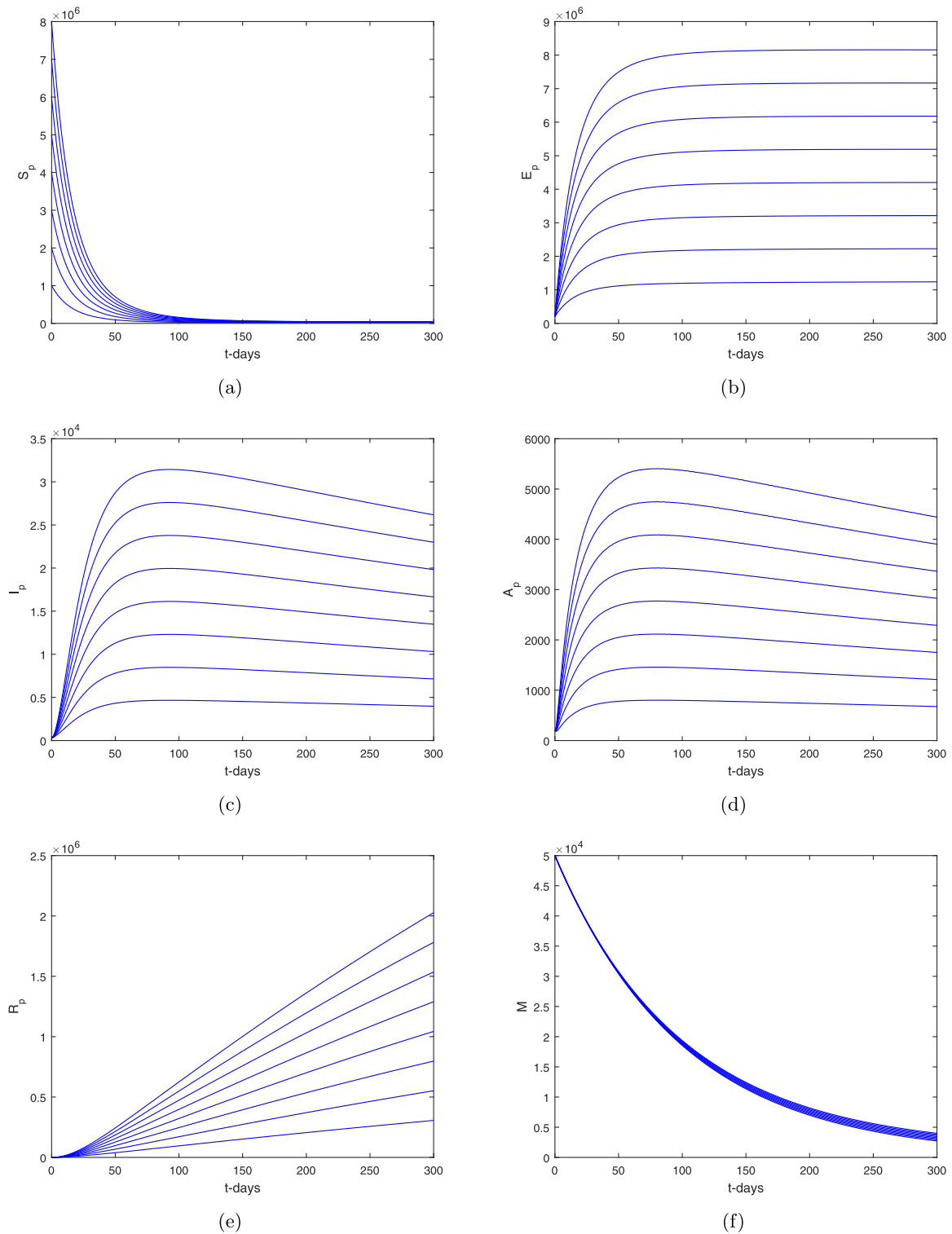


Fig. 7 The dynamics of corona virus model with various initial conditions.

The real sadistical data were fitted to the model for the integer case $\rho = 1$. We found the basic reproduction for the given data is $\mathcal{R}_0 \approx 2.4829$. For the solution of the fractional epidemic model, we presented a numerical scheme and obtained various

graphical results. The decreasing of the fractional order parameters leads to decrease the infection in the infected compartments. We believe that this model is the beginning of the disease dynamics with not enough data in hands and also the

infection is not yet control, so, we will study in future a clear picture of the Wuhan virus through mathematical model with complete record of outbreaks.

Declaration of Competing Interest

No conflict of interests exists regarding the publication of this paper.

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