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Research Paper

Evolution of COVID-19 Disease Using a One Prey-Two Predator Model

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Abstract

Mathematical modeling is used to understand the dynamics of transmission of infectious diseases such as COVID-19, SARS, Ebola, and Dengue among populations. In this work, a one prey-two predator model has been developed to understand the underlying dynamics of COVID-19 disease transmission. We consider the infected, recovered, and death classes with the fact that an infected person can be transformed into the recovered or death group assuming that the infected ones are the prey, and the other two populations are the two predators in the one prey-two predator model. It was found that the proposed model has four equilibrium points; the vanishing equilibrium point (E_0), recovered and death-free equilibrium point (E_1), infected and recovered population-free equilibrium point (E_2), and the death-free equilibrium point (E_3). Stability analysis of the equilibrium points shows that all the other equilibrium points are locally stable. Global asymptotic stability of the recovered and death-free equilibrium point, infected and recovered free and death-free equilibrium point are also analyzed. Moreover, the existence and uniqueness of the solutions were proved. The parameters for the model are estimated from a data set that consists of the total number of infected, recovered, and death classes at a zone for the first 6 months of the year 2020 using the Nelder-Mead optimization method. During the first 6 months, the infected population increases at a higher rate, the recovered population, and the death class increase at a lower rate. However, some modifications to the system are needed. In future work, measures such as health precautions, vaccinations are needed to be considered to formulate the mathematical model and estimate parameters.

Keywords: Covid-19, local and global stability, mathematical modeling, parameter estimation

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Introduction

Mathematical modeling is used to understand the dynamics and behavior of the ecological interactions among the species such as prey and predator populations. Lotka and Volterra proposed the simplest model, which is known as the Lotka-Volterra model, of prey-predator interactions based on linear per capita growth rate [1]. Many fields like medicine [2], agriculture [3, 4] management, and social sciences [5] use mathematical modeling to model the dynamics of certain systems. Mathematical modeling can also be used to understand disease transmission among populations. Transmission of infectious diseases like COVID-19, SARS, Ebola, and Dengue can be easily understood using different mathematical models. In order to forecast disease outbreaks, avoid or cure these illnesses different mathematical models have been used in the literature [2, 6, 7, 8, 9]. Daniel Bernoulli in 1760 formulated and solved a model for the spread of smallpox in order to evaluate the effectiveness of variolation of healthy people with the smallpox virus [6]. In the 1920s, the emergence of compartmental diseases was taken place with the great work done by Kermack and McKendrick in 1927[7].

The world's deadly COVID-19 pandemic occurred in the ancient town of Wuhan Hubei Province, China, by the end of December 2019 spreading worldwide in 2020 and 2021. Initially, several unexplained cases of coughs, pneumonia, exhaustion, and fever were there among the people in Wuhan, China. The arrival of coronavirus resulted in the closure of businesses, schools, markets, traveling restrictions, curfew, lockdown, and reduction of gathering. With the arrival of SARS-CoV-2, the virus that causes COVID-19, researchers have been formulating mathematical models as a technique in getting an idea about the mode of transmission of the pandemic, impact of the pandemic, prevention, and control of the pandemic, the effect of the preventive measure on the pandemic [10,11–17]. Some recent developments of mathematical models and analysis are presented in [10], [16],[18]-[21],[23]-[37].

Traditionally, model validation is done by comparing the data with the model either qualitatively as stable or cyclic dynamic behavior, length of cycles, amplitudes, etc.… or quantitatively by estimating parameters in the field and calibrating the model to obtain a good fit for the data [38]. Fitting nonlinear models to time-series is a technique of increasing importance in population ecology [38], [39], [40]. In 2001, Jost and Arditi [38] applied this technique to assess the importance of predator dependence in the predation process by comparing two alternative models of equal complexity (one with and one without predator dependence) to predator–prey time series. Stochasticity in such data comes from both observation error and process error. They considered how these errors must be taken into account in the fitting process, and they developed eight different model selection criteria. Carpenter, Cottingham, and Stow in Ref.[39] fitted nonlinear difference equations to time series with observation errors, which were examined by stochastic simulation and analysis of plankton time series from two lakes. They showed that even modest observation errors cause errors in model identification and bias in parameter estimates and the latter problem can be corrected by estimation techniques that account for observation error, but model identification is difficult unless the state variables are manipulated. In Ref.[40], the authors applied model-fitting to test if typical ecological predator-prey time series data, which contain both observation error and process error, can give some information about the form of the functional response.

In this paper, a one prey-two predator model has been developed in such a way that the parameters of the model are found by using a set of COVID-19 data, which consists of the total number of infected people, recovered people, and dead population. The model is formulated to understand the dynamics of the spreading of COVID-19 data. The existence and uniqueness of the solutions were discussed and the conditions for the local and global asymptotic stability of the equilibrium points were established.

Materials and Methods

Model Formulation

We consider a system consisting of three classes: infected, recovered, and dead due to COVID-19. The infected population is developed based on the logistic law with carrying capacity $K \geq 0$ and with the infection rate a. This can be happened due to the reasons such as immigration between zones and reported new Corona cases. Moreover, the model is formulated assuming that infected ones get converted to both recovered and dead classes. Similar to the Lotka-Volterra model formulation, it is assumed that the infected and recovered classes, and infected and death classes have meetings proportional to the product between the corresponding two classes. The recovered population can be increased or decreased due to the immigration between zones. The mathematical model as a system of three ordinary differential equations can be written as

$$\frac{dx}{dt} = ax\left(1 - \frac{x}{K}\right) - dxy - cxz \qquad \text{Equation 1}$$

$$\frac{dy}{dt} = by + dxy \qquad \text{Equation 2}$$

$$\frac{dz}{dt} = cxz, \qquad \text{Equation 3}$$

where $x(0) \geq 0$, $y(0) \geq 0, z(0) \geq 0$. Here $x(t)$ is the infected population, $y(t)$ is the recovered population, and $z(t)$ is the dead class at the time t. However, for simplicity, these are represented as x, y, and z in the text of this paper. In the model, the parameters represent the following. a represents the growth rate of the infected population due to the factors such as traveling between zones and reported positive Corona cases, K represents the carrying capacity of the infected population, d is the cure rate, c is the rate of transmission from infected to dead class, b represents the rate of decrease or increase of recovered population due to the factors such as travelling between zones. The parameters a and b can take negative or positive values depending on the situation.

Parameter Estimation

This section illustrates the parameter estimation method used to estimate parameters for the model. Let $\boldsymbol{p}$ be the set of parameters of the systems of Ordinary Differential Equations. Then, the parameters can be obtained by minimizing the mean square error between the model output data $\boldsymbol{y}(t_j;\boldsymbol{p})$ and experimental or real data $(t_{j,}\boldsymbol{y_j})$. Thus, the objective function that needs to be minimized is

$$obj(\boldsymbol{p}) = \sum_{j=1}^{k} |\boldsymbol{y}(t_j;\boldsymbol{p}) - \boldsymbol{y_j}|^2.$$

In this work, the Nelder-Mead method is used to solve the above optimization problem [9]. The Nelder-Mead method, which was proposed by John Nelder and Roger Mead in 1965, is a numerical method that is used to find the minimum or maximum of an objective function in a higher-dimensional space. Algorithm 1 illustrates how the Nelder-Mead method works to find the optimal solution [10].

Algorithm 1: Nelder-Mead

```
1.Let $x_i$ denote the list of vertices in the current simplex, $i = 1, \dots, n+1$.
2.Order; Order and re-label the $n+1$ vertices from the lowest function value $f(x_1)$ to the highest function value $f(x_{n+1})$ so that $f(x_1) \leq f(x_2) \leq \cdots \leq f(x_{n+1})$.
3.Reflect; Compute the reflection point $x_r$ by
$x_r = \bar{x} + \rho(\bar{x} - x_{(n+1)})$,
where $\bar{x}$ is the centroid of the $n$ best points,
$\bar{x} = \sum \left(\frac{x_i}{n}\right), i = 1, \dots, n$.
If $f(x_1) \leq f(x_r) < f(x_n)$ then
    replace $x_{n+1}$ with the reflected point $x_r$.
    go to step 7.
end if
```

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4.Expand;
if $f(x_r) < f(x_1)$ then
    compute the expansion point $x_e$ by $x_e = \bar{x} + \chi(x_r - \bar{x})$.
end if
if $f(x_e) < f(x_r)$ then
    replace $x_{n+1}$ with $x_e$ and go to Step 7.
else
    replace $x_{n+1}$ with $x_r$ and go to Step 7.
end if
5.Constract;
if $f(x_r) \geq f(x_n)$ then
    perform a contraction between $\bar{x}$ and the better of $x_{n+1}$ and $x_r$.
end if
Outside contract;
If $f(x_n) \leq f(x_r) < f(x_{n+1})$ then
    Calculate $x_{oc} = \bar{x} + \gamma(x_r - \bar{x})$.
    if $f(x_{oc}) \leq f(x_r)$ then
        replace $x_{n+1}$ with $x_{oc}$
        go to Step 7.
    else
        go to Step 6.
    end if
end if
Inside contract;
If $f(x_r) \geq f(x_{n+1})$ then
    Calculate $x_{ic} = \bar{x} + \gamma(x_{n+1} - \bar{x})$
end if
if $f(x_{ic}) \geq f(x_{n+1})$ then
    replace $x_{n+1}$ with $x_{ic}$
    go to Step 7.
else
    go to Step 6.
end if
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6.Shrink; Evaluate the $n$ new vertices
$x' = x_r + \sigma(x_i - x_1), i = 2, \ldots, n + 1$.
Replace the vertices $x_2, \ldots, x_{+1}$ with the new vertices $x'_2, \ldots, x'_{n+1}$.
7.Stopping Condition; Order and re-label the vertices of the new simplex as $x_1, x_2, \ldots, x_{n+1}$ such that $f(x_1) \leq f(x_2) \ldots \leq f(x_{n+1})$.
if $f(x_{n+1}) - f(x_1) < \varepsilon$ then
    stop, where $\varepsilon > 0$ is a small predetermined tolerance.
else
go to Step 3.
end if
```

Results and Discussion

Population Dynamics

Existence and Uniqueness of Solutions of the System

The existence and uniqueness of the system are proved using the existence and uniqueness theorem. The system of differential equations can be written in the following form and is analyzed by considering the continuity of the functions f, g and h, which are the derivatives of x, y and z and the continuity of their partial derivatives with respect to x, y and z at the given initial conditions.

$$\frac{dx}{dt} = f(x, y, z)$$
$$\frac{dy}{dt} = g(x, y, z)$$
$$\frac{dz}{dt} = h(x, y, z)$$

Equilibrium Points and Their Existence

By setting right-hand sides of Equations 1, 2 and 3 to zero, four equilibrium points were found.

$$\frac{dx}{dt} = 0 \text{ gives } ax\left(1 - \frac{x}{K}\right) - dxy - cxz = 0 \qquad \text{Equation 4}$$

$\frac{dy}{dt} = 0$ gives $by + dxy = 0$ Equation 5

$\frac{dy}{dt} = 0$ gives $cxz = 0$ Equation 6

By Equation 5, we can obtain $y = 0$ or $x = -\frac{b}{d}$

By Equation 4, we can obtain $x = 0$ or $a\left(1 - \frac{x}{K}\right) - dy - cz = 0$

By Equation 6, we can obtain $x = 0$ or $z = 0$

By considering $y = 0$ and $z = 0$ with $x = 0$ one can obtain $(0, 0, 0)$ as a solution. Also, by considering $a\left(1 - \frac{x}{K}\right) - dy - cz = 0$ with $z = 0$ and $y = 0$ we can obtain $(K, 0, 0)$ as the next solution. Also, by taking $a\left(1 - \frac{x}{K}\right) - dy - cz = 0$, $y = 0$ and $x = 0$ into account, $(0, 0, \frac{a}{c})$ can be obtained as the solution. Finally, when $x = -\frac{b}{d}$ and $z = 0$, we can obtain $(-\frac{b}{d}, \frac{a}{d}\left(1 + \frac{b}{dK}\right), 0)$ as a solution.

The four equilibrium points are summarized following.

1. The vanishing equilibrium point, $E_0 = (0,0,0)$, always exist.
2. The recovered and death-free equilibrium point, $E_1 = (\tilde{x}, 0,0)$, where $\tilde{x}= K$, always exist.
3. The infected and recovered-free equilibrium point, $E_2 = (0,0, \hat{z})$,where and $\hat{z} = \frac{a}{c}$, exists provided that $a > c$.
4. The death free equilibrium point can be defined as $E_3 = (\breve{x}, \breve{y}, 0)$, where $\breve{x} = -\frac{b}{d}$ and $\breve{y} = \frac{a}{d}\left(1 + \frac{b}{dK}\right)$. Provided that $b < d$ and $\frac{a}{d}\left(1 + \frac{b}{dK}\right) > 0$.

Local Stability Analysis

The local asymptotic stability of the system of Equations 1, 2 and 3 at each equilibrium point is studied by computing the Jacobian matrix and finding the eigenvalues evaluated at each equilibrium point. For stability of the equilibrium points, the real parts of the eigenvalues of the Jacobian matrix evaluated at each equilibrium point must be negative. Thus, the conditions for which each equilibrium point to be locally asymptotically stable were found. Jacobian matrix for the system is:

$$J(x,y,x) = \begin{pmatrix} a - \frac{2ax}{k} - dy - ez & -dx & -ex \\ fy & -b + fx & 0 \\ gz & 0 & -c + gx \end{pmatrix}$$

Jacobian matrix at each equilibrium point is evaluated and the following results were obtained,

1. E_0 is locally asymptotically unstable since $a > 0$ always.

$$J(E_0) = \begin{pmatrix} a & 0 & 0 \\ 0 & -b & 0 \\ 0 & 0 & -c \end{pmatrix}$$

2. E_1 is locally asymptotically stable if $fk < b$ and $gk < c$

$$J(E_1) = \begin{pmatrix} -a & -dk & -ek \\ 0 & -b + fk & 0 \\ 0 & 0 & -c + gk \end{pmatrix}$$

   a. Eigenvalues are $-a, -b + kf$ and $-c + gk$

3. E_2 is locally asymptotically stable if $\frac{cf}{g} < b$ and $gk < c$ by applying Routh's Criterion.

$$J(E_2) = \begin{pmatrix} -\frac{ac}{gk} & -\frac{dc}{g} & -\frac{ec}{g} \\ 0 & -b + \frac{fc}{g} & 0 \\ \frac{ga}{e}(1 - \frac{c}{gk}) & 0 & 0 \end{pmatrix}$$

4. By applying the Routh's criterion [12], E_3 is locally asymptotically stable if $b < kf$ and $gb < cf$.

Global Stability Analysis

The global stability behavior of the system of equations at the coexistent equilibrium point is investigated using the Lyapunov stability theorem [41]. By showing that the time derivative of the selected Lyapunov function is negative definite, the global asymptotic stability of the equilibrium points E_1, E_2, and E_3 were analyzed. The time derivative of the selected Lyapunov function was negative definite under some conditions for both the above equilibrium points. The selected Lyapunov function is,

$$V(x, y, z) = P\left(x - x^* - x^* ln\ \frac{x}{x^*}\right) + \left(y - y^* - y^* ln\ \frac{y}{y^*}\right) + Q(z - z^* - z^* ln\ \frac{z}{z^*})$$

where P and Q are arbitrary constants. By finding the time derivative of V and substituting P= 1 and $Q = \frac{1}{c}$ following equation is obtained.

$$\frac{dv}{dt} = \frac{-a(x - x^*)^2}{K} + (z - z^*)(x(1 - c) + cx^*) \qquad \text{Equation 7}$$

For equilibrium point E_1, $y^* = 0$ and $z^* = 0$ therefore,

$$\frac{dv}{dt} = \frac{-a(x - x^*)^2}{K} + z(x(1 - c) + cx^*) \qquad \text{Equation 8}$$

For equilibrium point E_2, $x^* = 0$ and $y^* = 0$ therefore,

$$\frac{dv}{dt} = \frac{-ax^2}{K} + (z - z^*)x(1 - c) \qquad \text{Equation 9}$$

For equilibrium point E_3, $z^* = 0$, therefore,

$$\frac{dv}{dt} = \frac{-ax(x - x^*)^2}{K} + z(x(1 - c) + cx^*) \qquad \text{Equation 10}$$

Time derivative given by Equation 8 is negative definite if $cx^* < x(c-1)$. Therefore, E_1 is globally asymptotically stable under the above condition. The time derivative given by Equation 9 is negative definite if one of the following conditions holds.

1. $z < z^*$ and $1 < c$ or
2. $z > z^*$ and $1 > c$

Therefore, E_2 is globally asymptotically stable under any one of the above two conditions. Time derivative given by Equation 10 is negative definite if $cx^* < x(c-1)$. Therefore, E_3 is globally asymptotically stable under above condition.

Parameter Estimation

In order to estimate the parameters, the Nelder-Mead method is used and data from https://datahub.io/core/covid-19#resource-time-series-19-covid-combined were used. Here we assumed that the individuals in the recovered population do not travel out of the zone. Then, the estimated parameters of the model are,

$$a = 1, K = 200000, b = 0, c = 0.0007, d = 0.001$$

Figures 1, 2, and 3 show the time series evaluation of the infected, recovered, and death classes. One can see from the model that if the COVID-19 disease exists in society then the infected population is growing due to the slow recovery process and the low number of deaths. The recovered population also blowing up at a lower rate. It can be observed that the death class also increases at a lower rate within the 6 months period. Note that health precautions and vaccinations were not considered in the selected dataset.

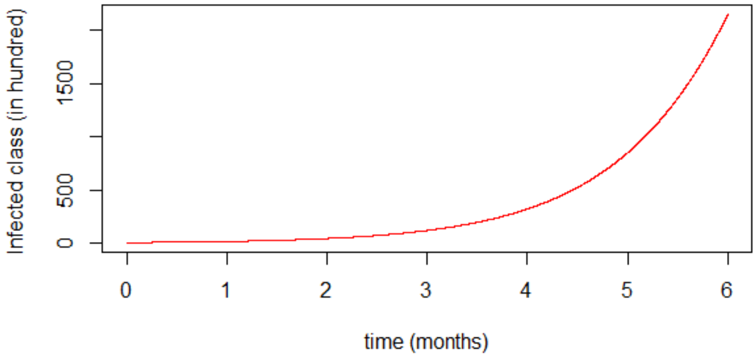

Figure 1. Variation of infected class with time.

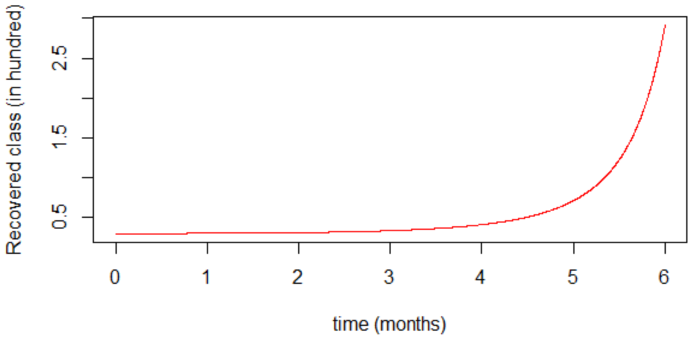

Figure 2. Variation of recovered class with time.

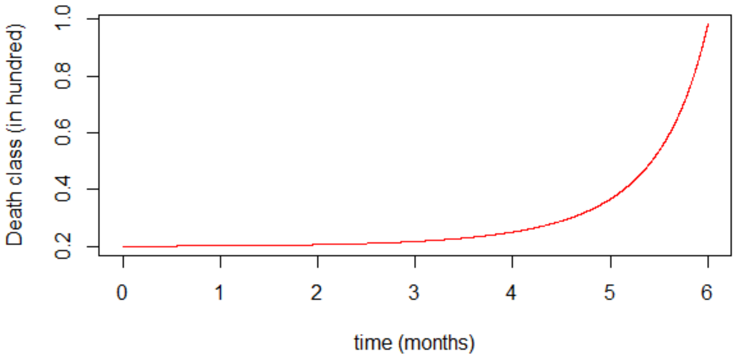

Figure 3. Variation of death class with time.

Conclusion

In this work, we have formulated a mathematical model that can be used to analyze the evolution of the Coronavirus. There exist unique solutions for the formulated system of ordinary differential equations. We have found four equilibrium points and all four equilibrium points are locally stable under some conditions. Global asymptotic stability of the recovered and death-free equilibrium point, infected and recovered free and death-free equilibrium point are also analyzed. The model parameters for the model were estimated using the Nelder-Mead optimization method. During the first 6 months, the infected population increases at a higher rate, the recovered population, and the death class increases at a lower rate. However, some modifications are needed. In the future, measures such as health precautions, vaccinations are needed to be considered for estimations of parameters in the model.

Conflict of Interest

The Authors declare no conflict of interest.

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