Parabola Volume 59, Issue 1 (2023)

An epidemiological application of the Lotka-Volterra model to predict population dynamics of COVID-19

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1 Introduction

The use of mathematical modelling is increasingly prevalent in a number of branches of study, including physics and chemistry, and also in biology and economics. The world is currently combating outbreaks of a lethal disease, namely the coronavirus disease 2019 (COVID-19) caused by the coronavirus SARS-CoV-2. Evidence from the World Health Organization (WHO) suggests that COVID-19 spreads principally through people in close proximity. The virus spreads from an infected individual's mouth or nose in small liquid particles, commonly when they cough, sneeze, speak, sing, or breathe. The susceptible individual can contract the virus through short-range airborne transmission or droplet transmission. COVID-19 can also spread in poorly ventilated indoor locations, through long-range airborne transmission [16].

Over the last two years, scientists have presented papers on mathematical models as a tool to analyze the spread of such infectious diseases. This study aims to review the epidemiological applications of these mathematical models as well as employ a specific model to simulate active COVID-19 cases.

The Lotka-Volterra model, also known as the predator-prey model, was initially proposed by a US mathematician Alfred J. Lotka in 1910 [8]. In 1920, Lotka extended the model and went on to publish a book on biomathematics, where he analysed predator-prey interactions, in 1925 [9]. Vito Volterra, an Italian mathematician and physicist, published the same set of equations in 1926 as he had taken an interest in mathematical biology [15]. The Lotka-Volterra model has also been used in economic theory and its initial application is commonly credited to Richard Goodwin in 1965 [5].

As a pair of first-order non-linear ordinary differential equations, the Lotka-Volterra model is generally utilized to describe the dynamics of a biological system in which a prey and predator interact with each other. It is a simplified version of the Kolmogorov Model, where competition, disease, and mutualism are deemed negligible. Solutions to the pair of differential equations are deterministic, i.e., the initial conditions will provide a certain outcome and there is no randomness (geometric Brownian motion) [2].

In this work, the Lotka-Volterra model is investigated and the pair of differential equations are solved to show the stability conditions of the model's equilibrium. Previously, researchers have used the Lotka-Volterra model to study the interaction between humans and infectious diseases, which will be reviewed in this study. Using a susceptible-infected (SI) model, the Lotka-Volterra model's utility to predict the

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changes in population over a period of time will be presented using a simulation in the Matrix Laboratory (MATLAB) programming language. This allows readers to derive additional insights as this study takes existent literature a step forward by applying the Lotka-Volterra model to the pandemic that presently challenges our world. As with most mathematical models, several assumptions allow for the pair of differential equations to describe real-world problems, thus the merits and limitations of the model will be discussed to evaluate the extent to which the Lotka-Volterra model can be effectively used to predict the dynamic behavior of COVID-19.

2 Methodology

2.1 Theory

The conventional pair of first-order ordinary differential equations associated with the Lotka-Volterra model were considered [11]:

$$\frac{dx}{dt} = x - \alpha xy \tag{1}$$

$$\frac{dy}{dt} = \beta xy - y\,. \tag{2}$$

Here, x denotes the number of prey; y denotes the number of predators; $\frac{dx}{dt}$ and $\frac{dy}{dt}$ denote the instantaneous growth rates of the prey and predator populations, respectively; t denotes time; and α and β denote positive real parameters that describe the interaction of the two species.

The mathematical model discussed in this paper, inspired by the classic Lotka-Volterra model, assumes that COVID-19 infected individuals act as a predator that preys on susceptible individuals. As a result, the infection spread by the population of disease carriers has a similar role to the typical feeding process of the predator population in the Lotka-Volterra model.

It is important to note that a number of underlying assumptions exist for the Lotka-Volterra model [2]: The habitat and diet of the prey are unlimited, thus in the absence of predators, the prey population increases exponentially ($\frac{dx}{dt} \propto x$). The predator survives solely on the prey, thus in the absence of prey, the predator population decreases exponentially ($\frac{dy}{dt} \propto -y$). The predator has a limitless appetite, i.e., the predator will not stop eating the prey. Interactions between the predator and prey result in a loss for the prey population and a gain for the predator population. Therefore, the rate of change of population is proportional to the size of the population. The environment is constant and does not favour one species and genetic adaptation is inconsequential.

The same assumptions were employed for the epidemiological use of the mathematical model in this paper, with the inclusion of three additional assumptions: if a COVID-19 infected individual (predator) recovers, then they return to the susceptible individuals (prey) population. If an infected individual (predator) dies, then they are removed from the system. The human birth rate is equal to the human mortality rate, so infected individuals dying are replaced by new susceptible individuals being born.

2.2 Literature Review

The approach taken to answer the research question is a combination of a literature review and a theory paper. The literature review component of this research paper utilized Google Scholar, Journal Storage (JSTOR), PubMed, ResearchGate, and Science Direct research databases, consisting of peer-reviewed articles. A search string was employed combining keywords including "Lotka-Volterra model", "predator-prey equations", "differential equations" paired with "epidemiological application", "diseases", and "COVID-19", using Boolean operators to broaden the search. Since the epidemiological application of the Lotka-Volterra model is novel, the published works are limited, resulting in the usage of the majority of the yielded search results.

2.3 Simulation

Simultaneously, the theory component of this research paper utilized the MATLAB programming language. Developed by MathWorks, MATLAB is a multi-paradigm programming language for numerical computation and visualization. A simulation was executed to compute the solutions to the Lotka-Volterra model and to present the model graphically.

In the simulation, the variables of initial time (t0), final time (tfinal), and initial predator and prey populations were primarily initialized. The domain of the time variable was set as $0 \leq t \leq 15$ with an arbitrary unit. The initial predator and prey populations were set as 50 units each to create an initial state of equilibrium. Next, a function was defined and named "LotkaODE", which was used to contain the pair of differential equations and simulate the system. For this simulation, the parameter values of $\alpha = 0.01$ and $\beta = 0.02$ were used. Then, the system was simulated using the MATLAB command `ode45` which performs a direct numerical integration of a set of ordinary differential equations using the Runge-Kutta method. The `ode45` command was appointed as it uses a 4th and 5th order pair that achieves a greater degree of accuracy [11]. Finally, the resulting populations were plotted against time.

3 Results

3.1 Theory

To acquire the equilibrium solutions to the pair of differential equations, the concept of an equilibrium must be understood. An equilibrium is defined as a "state of balance", therefore the infected individual and susceptible individual populations are not changing with respect to time, allowing for the pair of differential equations to be rewritten as:

$$x - \alpha xy = 0 \tag{3}$$

$$\beta xy - y = 0 \tag{4}$$

Solving for susceptible individuals (x) and infected individuals (y) yields the following two solutions:

$$x = 0 \text{ and } y = 0 \tag{5}$$

and

$$x = \frac{1}{\beta} \text{ and } y = \frac{1}{\alpha} \tag{6}$$

The first solution, Equation 5, shows that if there are no susceptible individuals and no infected individuals, i.e., the human species is extinct, then they will remain extinct until acted upon by an external factor. The second solution, Equation 6, shows another equilibrium where the number of susceptible individuals is equal to the ratio of 1 to the constant β and the number of infected individuals is equal to the ratio of 1 to the constant α. Both constants denote biological parameters that describe the interaction between the species, therefore populations at which the equilibrium occurs depend on the interaction coefficients.

The Jacobian matrix is used to determine the stability of the two fixed points, as it collects the partial derivatives of the multivariate function to find the local linearisation of the two equilibrium points. The eigenvalues are used to determine the linear stability properties of the equilibrium, hence the nature of the non-linear system of equations can be established.

The Jacobian matrix, J, for the epidemiological model of the Lotka-Volterra system is

$$J(x, y) = \begin{bmatrix} 1 - \alpha y & -\alpha x \\ \beta y & \beta x - 1 \end{bmatrix} \tag{7}$$

The Jacobian at the first fixed equilibrium point $(0, 0)$ is equal to

$$J(0, 0) = \begin{bmatrix} 1 & 0 \\ 0 & -1 \end{bmatrix} \tag{8}$$

The eigenvalues at the first fixed equilibrium point are

$$\lambda_1 = 1 \text{ and } \lambda_2 = -1 \,. \tag{9}$$

Since the first stationary point has one positive and one negative eigenvalue, it is classified as a saddle point which is unstable. The Jacobian at the second fixed equilibrium point $(\frac{1}{\beta}, \frac{1}{\alpha})$ is equal to

$$J(\frac{1}{\beta}, \frac{1}{\alpha}) = \begin{bmatrix} 0 & -\frac{\alpha}{\beta} \\ \frac{\beta}{\alpha} & 0 \end{bmatrix} \tag{10}$$

The eigenvalues at the second fixed equilibrium point are

$$\lambda_1 = i \text{ and } \lambda_2 = -i \,. \tag{11}$$

Since the secondary stationary point has eigenvalues that are both purely imaginary and conjugate to each other, it is classified as a center for closed orbits which is stable but not asymptotically stable.

Therefore, the solutions obtained are periodically oscillate on a closed ellipse about the fixed point with a frequency $\omega = \sqrt{\lambda_1 \lambda_2} = 1$ and a period $T = \frac{2\pi}{\omega} = 2\pi$.

3.2 Literature Review

Scientists have presented applications of the Lotka-Volterra model in a plethora of fields, particularly in biology. Research from el Arabi et al. [1] has shown combinations and comparisons between the Lotka-Volterra model and other models such as the Susceptible, Infected, Recovered (SIR) model and the Monod model, proving that these non-linear coupled systems of equations do not yield analytical solutions. As a result, there is a need for the Runge-Kutta method, which proved to be an efficient method in solving the non-linear coupled systems [1].

In addition, scientists have explored an extension of the Lotka-Volterra model in which some infectious disease is introduced in the system. In research by Das [4], a modification of the standard predator-prey model is inspected; a parasitic disease infects the predator population and creates a new variable. It is important to note that an additional assumption is naturally added: the parasite is horizontally transmitted. In this work, it is observed that “the introduction of disease in the predator population stabilizes predator-prey oscillations”, potentially offering an explanation as to why natural populations tend to be relatively stable in the real world [4].

Alternately, research by Ghasemabadi and Doust [6] employs a different approach of introducing disease to the predator population. By introducing the disease to the prey population, the predator population is assumed to contract the disease only by eating the prey. The mathematical model proposed in this paper shows that, despite the infectious disease persisting in the predator population, the system remains “well-defined” as none of the species would be extinct, i.e., the system was persistent. Three epidemiological threshold quantities were identified for the model [6].

The outbreak of the COVID-19 pandemic has unwrapped a few direct applications of the Lotka-Volterra model. New research from Mohammed et al. [12] utilized fractional derivatives to “provide more adequacies in estimating the natural behaviors of the model” [12]. This is because the non-integer derivatives provide smaller incremental changes which improve the accuracy of the results as a whole: “The existence and boundedness of the non-negative solution of the fractional model [is] proved” and “the local stability [of the solutions are] also discussed based on Matignon’s stability conditions” [12].

Meanwhile, a similar application of the Lotka-Volterra model is presented in research by Okuonghae & Omame [14], where they first seek predicative tools to obtain the constants. Then, by numerical simulations, they show the effect of control measures to reveal the mathematics behind “decreasing the incidence (and prevalence) of COVID-19”, with Lagos, Nigeria as a sample. The researchers used the common control measures of social distancing, the usage of face masks, and case detection via contact tracing and subsequent testings. Their results show that “if at least 55% of the population comply with the social distancing regulation with about 55% of the population effectively making use of face masks while in public, the disease will eventually die out in the population” [14].

3.3 Simulation

Using the solutions found by the MATLAB command `ode45`, the model was presented graphically.

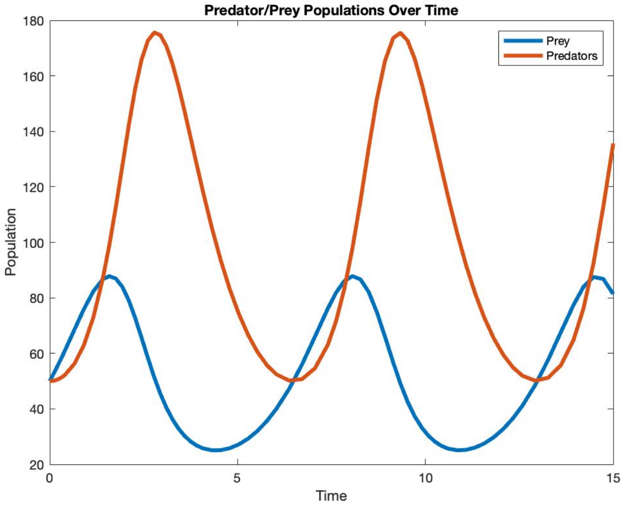

Figure 1: Variations in predator/prey populations over time

Figure 1 illustrates changes in the predator and prey populations against time and two sinusoidal curves out of phase are observed.

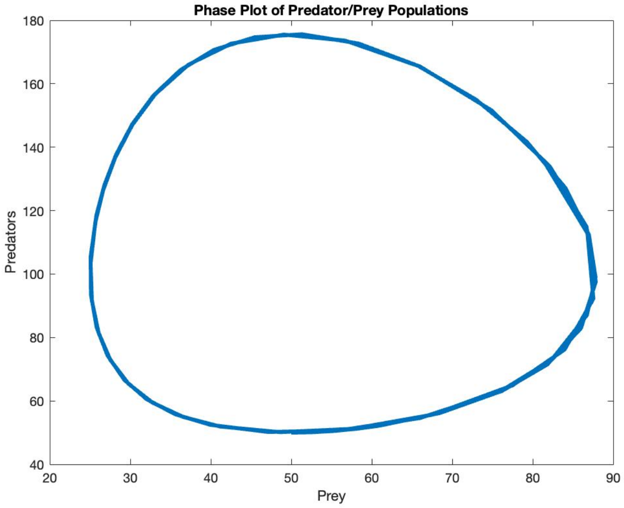

Figure 2: Phase plot of predator/prey populations

Figure 2 is a phase plot of predator populations against prey populations to compare how their numbers change relative to each other. It is observed that the populations oscillate on a closed ellipse around the fixed point.

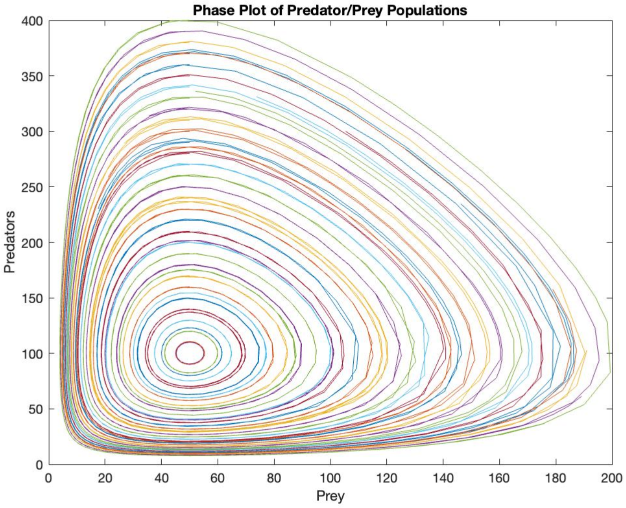

Figure 3: Phase plot of predator/prey populations with varying initial population sizes

Figure 3 is a more general phase plot that demonstrates the effects of varying initial population sizes of both species.

4 Discussion

While appointing the Lotka-Volterra model to predict population dynamics of COVID-19 may have its merits, there are a few limitations of the model to consider. The first assumption in this investigation, $\frac{dx}{dt} \propto x$, is not realistic in this application simply because there are other causes of death for COVID-19 susceptible individuals, which includes but is not limited to, natural causes, other infectious viruses or diseases, and accidents.

Furthermore, the second assumption in this investigation, $\frac{dy}{dt} \propto -y$, may also seem impractical. New research suggests that Omicron, a variant of COVID-19, may have human-to-animal transmissions, demonstrating that the infected individuals (predator) do not survive solely on the susceptible individuals (prey) [7]. However, research from the Centers for Disease Control and Prevention (CDC) shows that "based on the available information to date, the risk of animals spreading COVID-19 to people is considered to be low."; therefore, the system will not be influenced by outside factors and will remain unaffected [3].

The third assumption in this investigation is only permitted by the sixth assumption, proposing that there is no immunity against COVID-19, which may be supplemented by viral mutations of SARS-CoV-2. While unrealistic in the short term, studies from Maragakis and Kelen [10] show that "natural immunity to the coronavirus weakens (wanes) over time", suggesting that these assumptions may prove to be practical [10].

The seventh assumption in this investigation is not realistic because it is rarely accurate; it is made to simplify the model.

In terms of the results presented here, there are also several limitations to take into consideration. The first solution, Equation 5, indicates a state of equilibrium where both populations, predator and prey, are extinct. This circumstance, albeit possible, is highly improbable. Another limitation that arises from the first solution is the ability of the prey population to "bounce back even when subjected to extremely low population numbers" [2]. Known as the "atto-fox problem", this is a common problem that appears in other simplified biological models [13].

Moreover, the second solution, Equation 6, indicates a second state equilibrium where both populations are equal to the reciprocal of the interaction coefficients. These values are far more likely to transpire than Equation 5; however, scientists may currently find difficulties in calculating the parameters that describe the interaction of the two species due to a lack of available information.

5 Conclusion

In this paper, the Lotka-Volterra model is introduced in an epidemiological application. Two solutions and their eigenvalues are solved to understand that one solution is an unstable saddle point and the other solution is a stable center for closed orbits. Existing literature surrounding the topic is reviewed and the limitations of the model in terms of predicting the population dynamics of COVID-19 are evaluated. A future outlook for this research project may explore different models to find the most appropriate epidemiological representation. Furthermore, the implications of individuals gaining immunity from COVID-19 through newfound vaccinations on the model may be investigated.

Overall, despite some of its relatively unrealistic characteristics, the Lotka-Volterra model can be used to predict the basic dynamic behaviour of COVID-19.

6 Acknowledgements

I would like to extend my gratitude to my mentor, Nyasha Maforo at the University of California, Los Angeles, for guiding me, as well as to my parents and sister for their continuous support.

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