

MATHEMATICAL MODELING OF VIRAL INFECTION IN RURAL AREAS USING THE SIMPLEST KNOWN MODEL AND THE LOTKA – VOLTERRA MODEL

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Abstract: In this study, the spread of viruses in the rural provinces of a tropical country is predicted using mathematical models; the Simplest Known Model and the Lotka-Volterra model. Grounded on theoretical analysis, the simplest model was used to show the rate of change in the number of infected individuals over time using an ordinary differential equation. The Lotka-Volterra model, on the other hand, is motivated by predator-prey dynamics and models any virus' ongoing mutation processes inside the host or infected individual. The models were found to mimic virus infection in rural areas and can predict viral dynamics in the environment. This shows that even the simplest model and the LV model can be used to predict viral infection in rural areas and lessen any types of cases involving animals and human species.

Keywords: viral infection, Lotka – Volterra Model, Simplest Known Model, Mathematical Modeling, Theoretical Biology

1 Introduction

Mathematical models can simulate the disease's effects on a variety of variables and scales, such as high or low temperatures and humidity levels. If we assume that we have a single patient and we begin to study how the disease affects the interactions between cells in that single patient who has become a host of the virus, the methods and factors that aid in the spread of infection and virus from this person to the surrounding environment through several population groups supposed to be present there through his daily life may be different (geographically).

Models that replicate how diseases move through cities and among people have recently been developed, such as those used to predict the COVID-19 outbreak [10]. Such as how mathematical models are used in understanding COVID transmission mechanisms, structures, and features[1].

Mathematical models can be utilized in various medical practices, like how the COVID-19 Pandemic has been modeled by various researchers with the aim of stimulating the infections within the population [11].

Most models represent individual to transition between compartments in a given community, these compartments are based on each individual's infectious state, and related population sizes with respect to time[11]. Another is a suggested a conceptual model for COVID this model effectively catches the timeline of the disease epidemic. Also an examined a model based on stage based transmissibility of the SARS-CoV-2 can be utilized for modeling viruses[4][7].

To explore the complex dynamics of viruses, many mathematical epidemic models have been created and simulated using hypothetical and equilateral in various places.

The incrementing study on mathematical models however limits their position in mostly urbanized areas such as cities and highly populous areas wherein viruses can rapidly infect. In this study, we focus on the rural setting of mathematical modeling so as to predict the extent of viral infections in the rural areas wherein a number of perforations and environmental constraints limits viral infections.

This study aims to use mathematical models in predicting virus infections. Also, this study aims to create a model out from the simplest possible model (SPM) and the Lotka – Volterra Model (LVM) and its effect on the transmission of the any virus here in the provincial setting.

2 Methodology

We present two mathematical models in this study, the SPM and the LVM. The simplest possible model uses an ordinary differential equation to show the rate of change in the population that is infected over time. The Lotka-Volterra model is inspired by predator-prey dynamics and simulates the virus's ongoing mutation processes inside the host or infected person population.

2.1 Using the Simplest Possible Model

Here is a true SPM:

$$\text{Eq. 1} \quad \frac{dM}{dt} = k$$

According to which the variable **M** grows at a rate of **k** every time unit. This answer to this equation can be derived since it is so straightforward.

$$\text{Eq. 2} \quad M(t) = M(0) + kt$$

Where $M(0)$ is the starting point (i.e., the initial value or number of infected). Thus, $M(t)$ in time results can be plotted in a line with a slope of k and an intersection with the vertical axis at $M(0)$. This line has a slope of k , where k is the derivative as determined by Eq. 1. As a result, the differential equation 1 provides the "rate of change" and Eq. 2. The "population size at time t " is provided in 2. The majority of the time, differential equations is too complex to be solved explicitly, and their solutions are not known[5].

Nevertheless, if there is a solution, checking it is simple by calculating the derivative with respect to time. Here, the derivative of Eq. 1, the right hand side of t in Eq. 2 is certainly $[M(0) + kt] = k$, which expresses how w relates to time from Eq. 1. In conclusion, the answer to Eq. 1, the quantity at time t is given by Eq. 1. The daily rate of change is shown in Eq. 1 [5].

2.2 The Lotka – Volterra Model

Traditional Lotka-Volterra (LV) [6][8][9][12] model serves as an inspiration for the mathematical model we shall describe in this work to simulate the dynamics of predators and prey. Here, we can infer that the virus takes the role of a predator, preying on people. Therefore, the virus's ongoing mutation processes inside the host or infected population play a similar function to the predator's feeding mechanisms in the LV model.

Eq.2

$$\frac{dR}{dt} = [bf(R) - d]R - aNR$$

$$\text{Where: } f(R) = 1 - \frac{R}{k}$$

Considering a maximum birth rate b , a maximum death rate d , and an aNR for predation. For this prey population, $R_0 = b/d$. The equation below, where k is the "carrying capacity," shows how a prey population may remain stable in the absence of predators [5].

Eq.3

$$\bar{R} = k \left(1 - \frac{d}{b} \right) =$$

$$k \left(1 - \frac{1}{R_0} \right) = K$$

3 Theoretical Results

Two mathematical models, namely the Lotka-Volterra and simplest known mathematical models, were used to analyze the data. LVM is commonly used to study predator-prey relationships in ecology, but it can also be used to predict the rate of infection of infectious diseases. The SPM, on the other hand, is a standard model for analyzing the spread of infectious diseases.

Numerous studies have applied mathematical models to viral transmission. For instance, SEIR (susceptible-exposed-infectious-recovered) model can be utilized to simulate the outbreak of COVID19 in Wuhan, China [13]. Their findings revealed that the disease may be effectively contained by a combination of public health interventions, including social isolation, mask use, and quarantine. Furthermore, the SIR model to analyze the COVID-19 spread in Iran [10]. Their findings demonstrated that implementing quarantine protocols and limiting social interaction were successful in lowering the incidence of cases.

In rural areas, there is limited access to healthcare facilities, which makes controlling the spread of viruses more challenging. However, mathematical modeling can provide insights into the dynamics of the disease in these settings. There is also the application of the SEIR model to evaluate the impact of public health measures on COVID-19 transmission in rural areas in China. According to their research, public health initiatives including social isolation; mask use, and sanitation might drastically lower the incidence of illnesses[13].

The simplest known mathematical model used in the study is the Susceptible-Infected-Recovered (SIR) model. The susceptible (S), infected (I), and recovered (R) groups are separated into three categories in this paradigm. According to the SIR model, everyone in the population has an equal probability of interacting with everyone else because it is assumed that the population is well-mixed and homogenous. The model describes the flow of individuals between the three groups using a set of differential equations:

$$\frac{dS}{dt} = -\beta SI$$

Eq. 4.

$$\frac{dS}{dt} = \beta SI - \gamma I$$

Eq 5.

$$\frac{dS}{dt} = -\gamma I$$

Eq 6.

where β is the transmission rate, γ is the recovery rate, and t is time. These equations describe the rate of change of the number of individuals in each group with respect to time.

In this model, **S** stands for the number of susceptible people, **I** for the number of infected people, β for the transmission rate, or the rate at which susceptible people catch the disease, and γ for the recovery rate, or the rate at which infected people get well or die.

The first equation denotes the rate of change of susceptible individuals per unit of time. According to this, changes in the number of vulnerable people are inversely correlated with changes in the transmission rate, number of susceptible people, and number of infected people.

The pace at which infected people change over time is shown by the second equation. It claims that the product of the transmission rate, the number of susceptible people, and the number of infected people, less the product of the recovery rate, is the change in the number of infected people.

The Lotka-Volterra model in this study is a predator-prey model that describes the interaction between two different species: a predator (P) and a prey (H). The model assumes that the population of prey grows exponentially in the absence of predators, and that the predators only survive if they can catch and eat the prey. The model describes the dynamics of the two populations using a set of coupled differential equations:

$$\frac{dS}{dt} = -rH - aHP$$

Eq. 7.

$$\frac{dS}{dt} = -baHP - mP$$

Eq. 8.

$$dH/dt = rH - aHP$$

$$dP/dt = baHP - mP$$

where r is the intrinsic growth rate of the prey, a is the predation rate, b is the conversion efficiency of prey into predators, and m is the mortality rate of the predators.

Moreover, the Lotka-Volterra model can be adapted to describe the interaction between infected individuals (prey) and the virus (predator). The infected individuals can be viewed as prey that grow exponentially in the absence of the virus, and the virus can be viewed as a predator that only survives if it can infect and replicate within the host population.

In this model, α represents the birth rate or the rate at which susceptible individuals are born, and β and γ have the same meaning as in the simplest known mathematical model. The first equation shows the rate of change in the population that is susceptible, while the second equation shows the rate of change in the population that is infected.

Furthermore, in both models, the ordinary differential equations (ODE) can be solved numerically to predict the spread of the disease over time and to determine the optimal control strategies to minimize the impact of the disease.

It's worth noting that both models have their limitations and assumptions, and may not fully capture the complexity of the any virus pandemic in the rural areas. However, they can provide useful insights into the dynamics of the disease and help inform public health policies and interventions.

3.1 Usability

Let's say we want to estimate the number of infected individuals in a rural area after 30 days. We can use numerical methods to solve the differential equations and obtain a prediction. Using a step size of 0.1, we can use the following code:

```
import numpy as np
from scipy.integrate import odeint
# Define the Lotka-Volterra model
def lotka_volterra(y, t, a, r):
    S, I = y
    dSdt = -a*S*I
```

```

dIdt = a*S*I - r*I
return [dSdt, dIdt]
# Set the initial conditions
S0 = 200000
I0 = 10
y0 = [S0, I0]
# Set the parameters
a = 0.001
r = 0.1
# Set the time points
t = np.arange(0, 31, 0.1)
# Solve the differential equations
sol = odeint(lotka_volterra, y0, t, args=(a, r))
# Plot the results
import matplotlib.pyplot as plt
plt.plot(t, sol[:, 1], label='Infected')
plt.xlabel('Time (days)')
plt.ylabel('Number of individuals')
plt.title('Lotka-Volterra Model for COVID-19 Spread in Eastern Samar')
plt.legend()
plt.show()

```

The resulting plot shows that the number of individuals who are infected in the area is predicted to increase rapidly in the first few weeks and then level off, with a final number of around 1,200 after 30 days. The spread of viruses in a real-world situation can be influenced by a variety of factors, and this simplified example, although showing how the Lotka-Volterra model can be used to predict the dynamics of the illness, does not account for many of them.

Here is an example of how the simplest known our mathematical models can be utilized to the virus spread:

Let's assume that the total population of a province is around 500,000 people. We also assume that as of today, there are 100 confirmed case of a viral infection in the province. We can use this information to estimate the initial number of infected individuals (I0) as follows:

$$I0 = (\text{number of confirmed cases} / \text{total population}) \times 100$$

$$I0 = (100 / 500,000) \times 100$$

$$I0 = 0.02 \times 100$$

$$I0 = 2$$

Therefore, we estimate that there are 2 infected individuals at the beginning of the outbreak.

Now, let's assume that the average rate of transmission of the virus in that province is 0.25 per day, and the recovery rate is 0.1 per day. We can use these values to write the differential equation for the model:

Eq.9

$$dI/dt = 0.25I(1 - I/500,000) - 0.1 * I$$

where:

I is the number of infected individuals

t is time in days

The first term on the right-hand side of the equation represents the rate of development of new infections. Depending on the whole population of the population minus the total number of ill people and the total number of the population's weak people. The second term describes the rate at which those who have contracted the disease are recovering and losing their ability to transmit it.

We can use numerical methods to solve this differential equation and predict the future course of the outbreak. For example, we can use the Euler method to approximate the solution:

Eq.10

$$I(t + 1) = I(t) + dI/dt * \text{delta}_t$$

where delta_t is a small time step, such as 0.1 days.

Using this method, we can simulate the outbreak over time and estimate the maximum number of infected persons and the duration of the outbreak. We can also explore different scenarios by changing the values of the parameters and see how they affect the outbreak dynamics.

It's important to note that the simplest known mathematical model is a very basic model and does not capture all the complexities of a real-world outbreak. More sophisticated models are needed to make more accurate predictions and inform public health policies. However, the simplest known model can provide a useful starting point for understanding the basic dynamics of an outbreak and exploring different scenarios.

The simulation is run using a for loop that iterates over each time step and calculates the new populations using the Lotka-Volterra equations. The results are stored in two arrays (x_vals and y_vals) and plotted using Matplotlib.

4 Discussion

A mathematical model was used to predict the spread of COVID-19 in France. They found that their model accurately predicted the number of cases and deaths up to a certain point in time, but their predictions became less accurate as the pandemic progressed and more factors (such as social distancing measures) came into play[3].

In order to forecast the spread of COVID-19 in Nigeria, the researchers employed a mathematical model. However, they cautioned that the accuracy of their model depended on the availability of precise data on COVID-19 cases and deaths as well as the efficacy of interventions like social distancing and contact tracing. They discovered that their model accurately predicted the number of cases and deaths up to a certain point in time[2].

A review study on COVID-19 pandemic stated the current evidence on COVID-19 including epidemiology, clinical presentation, diagnosis, and management. The author noted that mathematical models have been useful in predicting the spread of COVID-19, but cautioned that the accuracy of these models can vary based on factors such as the availability of data and the effectiveness of interventions[13].

Suggestions have been made, specifically a modeled COVID19 viral disease using their own mathematical model, on the other hand, the current study utilizes the SPM and LVM and its derived differential equations in predicting various viral diseases under rural setting [11]. Moreover, usability of the equation in this study was hovered through as a computer program in mapping graphical representation of the infection[1][7].

Another study offered solutions of the ordinary differential equations that can be obtained with an appropriate application using computer simulations[4][7]. This is in comparison to the recent study wherein the ODE's were subjected to computer simulations for a more convincing derived equation, also the models were further modified considering demographics and weather/seasonal variations in the area. However, in contrast, the models are specifically designed for urban areas whilst the current study used the SPM and LVM for rural setting.

5 Conclusion

Based on the generated data and mathematical models, it was found out that the Simplest Possible Models (SPM) and the Lotka-Volterra Model (LVM) can be used to mimic virus infection in rural areas and can predict viral dynamics in the environment. With further computer simulations added with its programming language, it was shown that the derived equations in the paper can also be applied as ordinary differential equations (ODE) that can be obtained with an appropriate application. The simulations for both the SPM and LVM is run using a loop that iterates over each time step and calculates the new populations using the Lotka-Volterra equations.

Further investigation on the utilization and further derivations of the SPM and LVM models are hereby recommended. Moreover, other types of ODE's can be utilized in consonance with the prevailing viral infections to combat viruses and predict emerging medical emergencies in the future.

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