



EPIDEMIC COVID MATHEMATICAL MODEL

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Abstract: This paper presents a mathematical model via non-linear systems of equations to describe the spread of the COVID-19 virus in the Italy and Brazil. The method used is that of competition between two species of Loka -Volterra. The result shows that there is a time limit to contain the spread of the virus and thus avoid an exponential increase of infected people. This time cannot exceed 60 days, because the numbers of removed (deaths) change little.

Keywords- Nonlinear Equation, Covid 19, Epidemic Propagation, Computational modeling

I. INTRODUCTION

Corona virus is a family of viruses that cause respiratory infections. The new corona virus agent was discovered on 31/12/19 after cases registered in China. It causes the disease called corona virus (COVID-19). The first human corona viruses were isolated for the first time in 1937. However, it was in 1965 that the virus was described as corona virus, due to the profile in microscopy, looking like a crown.

Most people are infected with the common corona virus throughout their lives, and young children are more likely to become infected with the most common type of virus. The most common corona viruses that infect humans are alpha corona virus 229E and NL63 and beta corona virus OC43, HKU1 [1].

The proposal of this article is to admit that COVID-19 disease spreads in a closed community through contact between infected and healthy people, thus defining an epidemic. The idea of a closed community is to consider a population that decreases because of death to the disease in question, and can only increase because of the birth rate. Therefore, emigration and immigration are not admitted.

The methodology used is based on the mathematical modeling of a system of nonlinear equations that correlate two competing species. In this model we will focus on the interaction between two species, where one of them has food in abundance (prey) and the second species feeds on the first (predator). The proposed model is predator prey that was studied by Loka and Volterra, around 1925 [2]. An example of using this method is mathematical modeling of a system of non-linear equations that correlate the amount of bacteria that produce biogas to the amount of biogas produced inside the bio digester, examining the conditions favorable to anaerobic digestion in the production of biomass and associating these factors with the energy conversion [3].

Thus, a qualitative study of non-linear equations is necessary, so that it is possible, through some considerations,

to describe a particular model of competition between two species of populations. In this case we consider the production of people infected and the quantity of healthy people as two populations that are directly affected by the amount of environmental resources available and we study general models of competition between two population species proposed in the literature.

A mathematical model proposed by the Italian mathematician V. Volterra (1960-1940) and the American A.J. Lotka (1880-1949) is given by:

$$\begin{cases} \frac{dx_1}{dt} = k_1x_1 - b_1(a_1x_1 + a_2x_2)x_1 \\ \frac{dx_2}{dt} = k_2x_2 - b_2(a_1x_1 + a_2x_2)x_2 \end{cases} \quad (1)$$

with $x_1(0) = x_1^0$, $x_2(0) = x_2^0$ e a_1, a_2, b_1, b_2 real positive.

It is noticeable that the system (1) is non-linear, which prevents us from solving it by existing systematic methods. But, in this case, we are more interested in knowing the behavior of populations, and not their values at every t instant. Thus, we raise some questions to determine if one of the species will overtake the other leading to extinction, or if both will live in the same habitat forever, having an asymptotic graphic behavior. We still want to know if there are values in $x_1(t) = x_1^*$ and $x_2(t) = x_2^*$ which satisfying the system, which remains unchanged over time (balance points).

Another question arises, when the two species are coexisting in balance, is what will happen to future populations if we add (or remove) some elements of the same species (stability). These issues can be clarified if we solve the system (1).

It is observed that every solution $x_1 = x_1(t)$, $x_2 = x_2(t)$ of (1) defines a curve in three-dimensional space- tx_1x_2 , given by the points $(t, x_1(t), x_2(t))$. On the

other hand, the set of points $(x_1(t), x_2(t)), t_0 \leq t \leq t_1$, also defines a curve in the plan- x_1x_2 , given by the path or orbit of the solution $x_1 = x_1(t), x_2 = x_2(t)$, and the plan- x_1x_2 is called the phase plan of the System solutions (1). Thus, we can think of the path $(x_1(t), x_2(t))$ as the solution's path in plan- x_1x_2 .

II. MATHEMATICAL MODEL

For each species of contagious disease we can estimate its rate of spread, as long as we have related the supposedly essential variables in an epidemic. Thus, we define healthy people $H = H(t)$, but sensitive to the epidemic (COVID-19), who can be infected when in contact with people who have contracted the disease; people infected with $I = I(t)$ who can transmit COVID-19; persons who conduct $C = C(t)$ of COVID-19, but do not transmit; persons removed $R = R(t)$ who are the isolated, or dead, or cured; and the total number of the population $P = H + I + C + R$.

The proposed model for COVID-19 is that the individual must be isolated and can be cured and become immune to the disease, or die. Considering here the relatively short incubation period $C \cong 0$, and the constant population (counting the dead). Then

$$P = H + I + R, t \geq 0 \text{ t is the time.} \quad (2)$$

The system of differential equations describing this dynamic was proposed by Hoppessteadt [4-5]:

$$\begin{cases} \frac{dH}{dt} = -\alpha HI \\ \frac{dI}{dt} = \alpha HI - \beta I \\ \frac{dR}{dt} = \beta I \end{cases} \quad (3)$$

where α is the infection rate, β is the removal rate. We also have that the initial conditions are $I(0) = I_0, R(0) = 0$ and $H(0) = H_0 = P - I_0$.

The system (3) consists of non-linear equations that are coupled, but since the first two equations depend only on H and I , we can reduce them to an equation

$$\frac{dI}{dH} = \frac{\alpha HI - \beta I}{-\alpha HI} = -1 + \frac{\beta}{\alpha H} \quad (4)$$

Whose solution is given by separation of variables

$$dI = dH + \frac{\beta}{\alpha H} dH$$

Integrating both sides of equality

$$\int dI = \int dH + \frac{\beta}{\alpha} \int \frac{dH}{H}$$

which results in

$$I = \frac{\beta}{\alpha} \ln H - H + \gamma$$

Using the initial conditions, we obtain the value of the constant γ

$$\gamma = -\frac{\beta}{\alpha} \ln H_0 + P$$

Thus

$$I = P + \frac{\beta}{\alpha} \ln \left[\frac{H}{H_0} \right] \quad (5)$$

From equation (4), it follows that $\frac{dI}{dH} > 0$ if $\frac{\beta}{\alpha H} > 1$, that is, if $H < \frac{\beta}{\alpha}$. Therefore, I is an increasing function if $H < \frac{\beta}{\alpha}$.

Similarly, I is decreasing if $H > \frac{\beta}{\alpha}$.

Supposing now that the disease has no cure and that a contaminated person dies, then it is important to know the value of R at every moment.

From the system (3), taking the first and third equations, we can write them down in a reduced way as a single equation

$$\frac{dH}{dR} = -\frac{\alpha}{\beta} H$$

Resolving for H by separating variables

$$\int \frac{dH}{H} = -\frac{\alpha}{\beta} \int dR$$

Results

$$H = H_0 e^{-\frac{\alpha}{\beta} R} \quad (6)$$

Now, using equation (2) in the third equation of the system (3), comes

$$\frac{dR}{dt} = \beta(P - H - R)$$

or, with the help of equation (6), we have

$$\frac{dR}{dt} = \beta \left(P - R - H_0 e^{-\frac{\alpha}{\beta} R} \right) \quad (7)$$

We can solve this equation supposing that the people taken R are small enough, we can write

$$e^{-\frac{\alpha}{\beta} R} \cong 1 - \frac{\alpha}{\beta} R + \frac{1}{2} \left(\frac{\alpha}{\beta} R \right)^2 + \dots \quad (8)$$

where we used the property $e^x \cong 1 + x + \frac{1}{2}x^2 + \dots$

So that equation (7) is approximately equal to

$$\frac{dR}{dt} = \beta \left[P - H_0 + \left(\frac{\alpha}{\beta} H_0 - 1 \right) R - \frac{\alpha^2 H_0}{2\beta^2} R^2 \right]$$

Solving the equation by separating variables and by integration by partial fractions,

$$\int_0^R \frac{dR}{R^2 + 2pR + q} = -\beta \int_0^t dt$$

where

$$\begin{cases} p = \frac{\beta^2}{H_0 \alpha^2} \left(\frac{\alpha}{\beta} H_0 - 1 \right) \\ q = \frac{-2\beta^2}{H_0 \alpha^2} (P - H_0) \end{cases}$$

This type of integral can be calculated using the "completing the square" procedure, that is

$$R^2 + 2pR + q = (R + p)^2 + q - p^2$$

Now considering the following variable change

$$R + p = u$$

and $k^2 = p^2 - q$. So we have for the integral

$$\int_0^R \frac{dR}{R^2 + 2pR + q} = \int \frac{du}{u^2 - k^2}$$

Changing variables $u = k \cosh \theta$, we obtain:

$$\int_0^R \frac{du}{u^2 - k^2} = \frac{1}{k^2} \int \frac{k \sinh \theta d\theta}{\cosh^2 \theta - 1}$$

or

$$\int_0^R \frac{dR}{R^2 + 2pR + q} = \frac{1}{k} \int \frac{d\theta}{\sinh^2 \theta}$$

which results in

$$R(t) = -p + \delta \tanh(\delta \beta t) \tag{9}$$

where

$$\delta = \sqrt{2 \frac{\beta^2}{\alpha^2 H_0} \left\{ \frac{\beta^2}{2\alpha^2 H_0} \left(1 - \frac{\alpha}{\beta} H_0 \right)^2 + (P - H_0) \right\}}$$

The variation of isolated people over time is given by

$$\frac{dR}{dt} = \frac{\beta^3 \delta^2}{2\alpha^2 H_0} \sinh^2 \left(\frac{\delta \beta}{2} t - \theta \right) \tag{10}$$

where $\theta = \tanh^{-1} \left[\frac{\frac{\alpha}{\beta} H_0 - 1}{\delta} \right]$.

The maximum function point (10) is given by the time derivative equal to zero, $\frac{dR}{dt} = 0$, which results in

$$t_{\max} = \frac{2\theta}{\delta \beta} \tag{11}$$

Equation (11) is the maximum point of the curve. Here, the COVID-19 reaches its maximum point of isolated people. In other words, one can predict when this might happen.

III.RESULTS

In this model we have the time of contamination t in a population that depends on the beginning of the contagion [6]. The constants α and β depend on the initial data $I(0) = I_0$, $R(0) = 0$, and $H(0) = H_0 = P - I_0$.

In the case of Italy we have the record of the first case was on January 30, 2020 and after 30 days there were 31 thousand infected, with 2.5 thousand dead. Thus, we can associate the variables of the third equation, the system (2), as $R(30) = 2.5 \times 10^3$ and $I(30) = 31 \times 10^3$ obtaining 2.68×10^{-3} .

From the second equation of the system (2), we can solve this by assuming that $S(t)$ is constant and that on average 10% of the P population are sensitive to contamination. Thus, we have for Italy with 60.48 million inhabitants, that is, $P = 60.48 \times 10^6$ which implies $H_0 = 6.048 \times 10^6$. With these data we solve the second equation of the system (2) by integration resulting in the value of the parameter $\alpha = 0.038 \times 10^{-6}$. Figure (1) shows the rate of change $\frac{dR}{dt}$ with time t , with the maximum time $t_{\max} = 17.62$ days for a removed value of $R = 4,932$. This indicates that in the case of Italy, 30 days after the contamination peaked at approximately 17 days. Today, 24/03/2020, in Italy there are already 6000 dead [7].

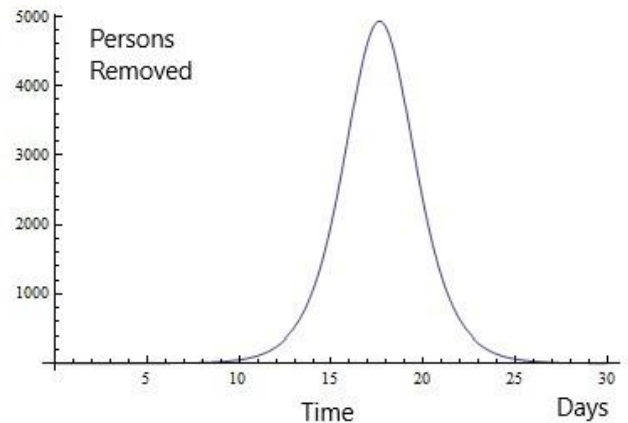


Fig 1 - Variation of persons removed over time in the case of Italy

In the case of Brazil using recent data [7] with a population of 200 million and following the same methodology for the case of Italy, we obtain table 1

TABLE 1
INPUT PARAMETERS: BRAZIL CASE.

Time Days	I Infected	H Sensitive	R Withdrawn	β	α
0	1	2×10^7	0	-	-
30	1.891	-	34	$5,9 \cdot 10^{-4}$	$0,12 \cdot 10^{-7}$

The data are inserted in equation (10), obtaining figure (2). In it are observed the results for three different containment moments (health barriers) 30, 60 and 90 days. These barriers are the measures used by governments to prevent the spread of the COVID – 19

In figure (2) we have to preserve table 1, but on different days of containment, it can reduce the numbers of removed. The curve for 30 days of containment shows a result of approximately 3750 removed. For the 60 curve, this value falls to 1790 and to 90 days 1245 removed.

The difference in retention from 30 days to 60 is 1960 and from 60 to 90 days are 545. Therefore, it is not recommended to keep this contention for more than 60 days. For there is no significant reduction in the number of people removed, apart from the economic losses that can accompany so many days of confinement.

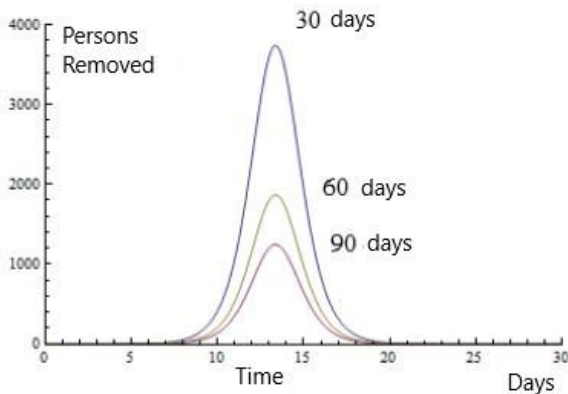


Fig. 2 - Variation of removed persons in three cases of containment

The mathematical model has a factor β in the second equation of the system (3), which we interpret as a barrier factor. See that the second equation, system (3), indicates the rate of infected, but has a term $-\beta I$ that decreases this rate. Therefore, this term serves as a containment factor for the progression of the epidemic.

The figure (3) shows two graphics. One graphic (A) showing the data of those infected until March 14, 2020 by the Ministry of Health. The other graphic (B) shows the data recorded along with the theoretical curve generated by the proposed system of nonlinear equations (3) for the infected. The result of the graphic (B) figure (3), shows that from the moment of using the barrier measures, the data are close to the theoretical curve. We would have a peak of 3400 infected in 28 days after the first recorded case. Therefore, the sanitary measures adopted are important for reducing the

contagion and cannot pass 60 days, because the effect of the drop in the numbers of removed is small.

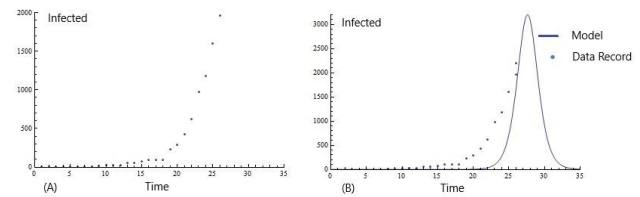


Fig. 3 - Recorded data and theoretical model

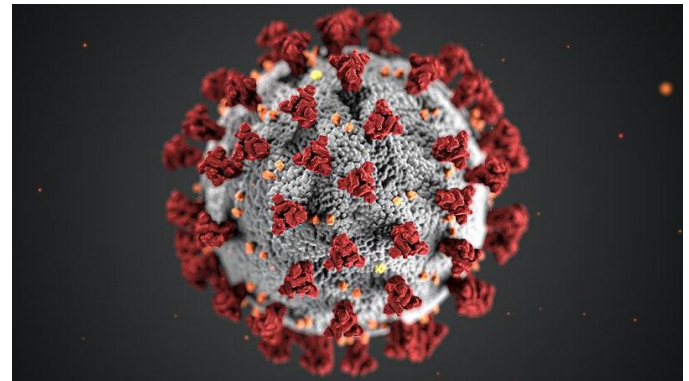


Fig. 4 - COVID -19.

IV. CONCLUSION

The model presented is an approximation of the reality of the spread of an epidemic, in the case of COVID -19 figure (4). The system of non-linear equations (3) applied for the COVID-19 contagion showed interesting results regarding the time limit for population containment, that is, avoid leaving their homes. Another measure, such as containment, to try to contain the disease advance was to suspend the interstate road transport for 15 days. This limit cannot exceed 60 days, after this limit it is not guaranteed that the method of containment works well.

With data collected from the Ministry of Health, figure (1), it was possible to compare the numbers of infected with the results of the model (3). The graph (B), figure (3), shows the importance of using health barriers (containment) to prevent the spread of the virus. When states began to impose restrictive measures on circulation; the observed data on the infected approach the model (3) which already counts in the second equation of the system (3) a containment factor $-\beta I$.

How can we use the proposed model in future perspectives? It will be to make a complete and detailed survey as accurate as possible of the numbers of infected and deaths in all Brazilian states. Then, add to the model (3) the economic impacts caused by the use of health barriers and social isolation.

We can also add equation (3) where the system of differential equations that describes this dynamic has been proposed can be put into a term that are the recovered individuals (who have recovered from the disease and acquired immunity). Thus, society gradually becomes immune and returns to its normal routine until then.

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