Coronavirus, A Challenge for Sciences, Mathematical Modeling

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Abstract: *In the present article a study is made of the characteristics of the coronavirus, its transformation into a pandemic and its aggressiveness towards the life of the man; reference is made to a set of certain diseases that have historically turned into epidemics due to the speed with which they were transmitted among the population; in addition, in most cases, this occurs due to the delay in reacting to control the disease. We applied the generalized logistic model to model this process and conclusions are drawn regarding the development of the coronavirus until it becomes a pandemic.*
Keywords: *Model, epidemic, disease, transmission.*

I. Introduction

There are many diseases that are transmitted from person to person directly, and different forms of contagion are used for this purpose, often through speech or breathing or in some other way; but in many other cases this transmission can be carried out by means of a vector, the mosquito being the most common. It is said that the cases of maximum risk are adults of the third age and especially those who suffer from some chronic disease; but practice has shown that in the face of this disease, there is no one safe, and it can have a slow evolution that acts in a fulminating way.

Today the most worrying situation is given by coronavirus, a respiratory disease that so many lives have claimed, there are many ideas on how to fight this disease; but the method that most researchers agree on, is given by the method of isolating the infected to prevent possible transmission to other people [14].

One of the treatments that has already given results is interferon alfa b2, in addition to others already tested in the treatment of other diseases such as AIDS, hepatitis, among others. Alpha b2 interferon, was developed by the Cuban Genetic Engineering and Biotechnology Center and has already been used in different parts of the world with highly reliable results [3], [11].

In [1] different real-life problems are treated using equations and systems of differential equations, all of them only in the autonomous case; where examples are developed, and other problems and exercises are presented for them to be developed by the reader. The authors of [2] indicate a set of articles forming a collection of several problems that are modeled in varied processes, but in general the qualitative and analytical theory of differential equations is used in both autonomous and non-autonomous cases, in both books the authors address the problem of epidemic development.

In the work [15], the logistic model is used to simulate population growths that are applied to the development of epidemics, but in the first one, different forms of the logistic model are presented.

There are multiple works dedicated to the study of the causes and the conditions under which an epidemic can develop, among these we can indicate [10].

Ronald Ross in the appendix to his book "The Prevention of Malaria" in the 1911 edition, formulated a simple mathematical model in support of his argument that to eradicate malaria it was enough to decrease the mosquito population to a low level, yes it necessarily extinguishes -there. Later, in 1927 Kermack and McKendrick formulated a very general and complex mathematical model to describe the bubonic plague epidemic that had suffered India in 1906.

The first navigators who arrived in the Americas were impressed with the robustness and the healthy aspect of the Indians, who, in fact, fed abundantly on natural products, moved constantly, therefore had no

problems of sedentary lifestyle and did not cultivate habits harmful to health. Tobacco, for example, was used only sporadically and in rituals; the problems later created by the industrialization, commercialization and advertising of cigarettes did not exist.

This picture soon began to change; the Europeans brought with them, in addition to economic interest and firearms, microbes that caused diseases to which the Indians had no immunity. That way they could get seriously ill, and even die, from a simple flu. Other diseases were even worse, such as smallpox, a disease that no longer exists today; it disappeared after a successful worldwide vaccination campaign, conducted by the World Health Organization more than 40 years ago. But at that time the vaccine did not exist and, even if it did, it would not be applied to the Indians.

Over time, a real "biological war" was created: both in South America and in North America, the colonizers who wanted to take possession of indigenous lands spread, on their trails, the clothes of people who had smallpox. The Indians naively dressed them, contracted the disease and died like flies. In Brazil, the first smallpox epidemic occurred as early as 1563.

Other diseases from the Old World were being introduced: malaria, yellow fever, tuberculosis, bubonic plague. Soon the entire population of the colony was subject to them; black slaves, because of the poor conditions of life and nutrition; whites, because they lacked effective vaccines or treatments. To this was added another factor: the emergence of cities, which had precarious conditions of hygiene and sanitation.

On the other hand, health care was very deficient. Physicists, as doctors were called, were generally trained in Europe. The first medical school, in Salvador, only appeared with the arrival of the Royal Family in 1808. The number of physicists was small; most of the population consulted healers; hospital assistance oversaw Santa's Casas, charitable establishments that provided shelter and religious protection for the dying, but that did not have effective therapeutic resources.

With regard to organized public health, little was done, there was a chief physicist, who, through assistants, supervised medical practice, and the sale of medicines was made at apothecaries, which still used leeches, which served to extract the "excess" blood or "poisoned" blood.

Two diseases took the sleep of the authorities and the life of the population: yellow fever and smallpox. Transmitted by the bite of the Aedes aegypti mosquito, it arrived in Brazil in the 17th century on ships that came from Africa, the first cases date from 1685, in Recife, and 1692, in the city of Salvador.

This epidemic outbreak forced the Empire to take measures that could be considered public health. The government, by means of a decree, tried to clean the cities by purifying the air, but even so, yellow fever continued to attack. The cause of the disease was not thought to be a mosquito.

It was in Cuba that scientist Carlos J Finlay discovered that yellow fever was transmitted by the Aedes aegypti mosquito. At first it was misunderstood, but then its merits were recognized for such a discovery; he had to go through the humiliation of being accused of a friar and wanting to attribute himself a right he did not have, but time proved his genius and dedication to science.

Zika, Dengue and Chikungunya are current diseases that many lives have claimed, and more than one occasion has turned into epidemics, transmitted by the Aedes aegypti mosquito. Hepatitis is a serious public health problem in many countries in the world, it is an inflammation of the liver; it can be caused by viruses, use of some medicines, alcohol and other drugs, as well as autoimmune, metabolic and genetic diseases. They are silent diseases that do not always present symptoms, but when they appear they can manifest through tiredness, fever, malaise, dizziness, nausea, vomiting, abdominal pain, yellowish skin and eyes, dark urine and light stools.

The problem of epidemic modeling has always been of great interest to researchers, such as the cases of [5], [4], [6], [7], [8], [9], [12] and [13] . In this work we will apply the generalized logistic model, where the case of the growth and decrease of the infected are applied in the same equation; to model the development of epidemics, a model that allows forecasts of future behavior.

II. Model Formulation

The process of infection by means of the coronavirus until effective measures are not taken has an exponential growth rapidly appearing many infected individuals, leading to many of them death if urgent measures are not taken. It is known that in order to study a model that simulates the process, it is necessary to see how the infected will vary with time; here the situation will be analyzed when they are in the process of growing or decreasing as a result of the treatment.

We will use the following notation, x(t) will represent the number of people infected at time t, it is also necessary to take into account that from the moment the disease appears, the number of patients will vary between a minimum value m that represents the remaining cases when the disease is fully controlled, and a maximum value M that represents the number of people subjective the disease, but initially the possibility that the contagion disappears, because they will always have companions, and other people with maximum risk so will have the following fraiche, region where they will be contagious in any tee.

$R = \{(t, x) \in R^2 / t > 0, m \le x \le M\}$

When the number of people infected is close to the maximum value, that is, they are infected with almost all the subjectable population, the process is considered of maximum risk, as it has become an epidemic.

$R_1 = \{(t, x) \in R^2 / t > 0, M - \beta_1 \le x \le M\}$

The R_1 region is called the maximum risk region.

When the number of infected people is close to the minimum value, that is, only those closest to the patient are contaminated, the process is considered to be of minimal risk, as in this case it will be possible to control the disease.

$R_2 = \{(t, x) \in R^2 / t > 0, m \le x \le m + \beta_2\}$

The R_2 region is called a comfortable region.

There is an intermediate number of infected people, from which it can be transformed into an epidemic that in a controlled process in correspondence with external factors or the attention that the patient is receiving, or the concern of himself regarding his disease.

$R_3 = \{(t, x) \in R^2 / t > 0, m + \beta_2 \le x \le M - \beta_1\}$

The R_3 region is called the doubt or traffic region, subject to constant changes.

In order to simulate the process, it is perceived that the variation of the infected population is due to the increase in that population, or that due to the influence of the treatment it can decrease, aspects that must be present in the model.

The increase in the number of people infected by the coronavirus is due to the encounter of an infected person $x(t)$ with a healthy person susceptible to contagion $M - x(t)$, where it is necessary to take into account a coefficient of contagion k, as not always the person it is contagious; this growth could be expressed through an equation of form,

$$\frac{dx}{dt} = k_1 x (M - x) \quad x(0) = x_0 \qquad (2)$$

In the equation of variation of the infected population given by the Cauchy problem (2) the growth of this population was considered because here $\frac{dx}{dt}$ where $x(t) < M$; and the solution of this equation has the form,

$$x(t) = \frac{CM e^{Mkk_1 t}}{1 + C e^{Mk_1 t}}$$

Making use of the initial condition $x(0) = x_0$, we must,

$$c = \frac{x_0}{M - x_0}$$

So, the solution to the Cauchy problem (2), has the form,

$$x(t) = \frac{M x_0}{e^{-Mk_1 t}(M - x_0) + x_0}$$

If the condition is met $x(1) = n_1$ if you must,

$$k_1 = \ln \left[\frac{n_1(M - x_0)}{x_0(M - n_1)} \right]^{\frac{1}{M}}$$

So, the solution will be,

$$x(t) = \frac{M x_0}{(M - x_0)\left[\frac{x_0(M - n_1)}{n_1(M - x_0)}\right]^t + x_0} \qquad (3)$$

From the expression (3) it is possible to obtain the solution for any t, this allows making predictions regarding the infected cases at any time; furthermore, under these conditions, it is possible to obtain the moment when the infected reach a given value, for the case in which the number of infected is increasing.

From here it can be seen that for t large enough $x(t) \to M$. This means that for a sufficiently long time, if the necessary prophylactic measures are not taken, the entire population will be infected; giving rise to an epidemic as previously indicated in different cases of disease.

And the graph corresponding to the function $x(t)$ that constitutes the solution to the Cauchy problem (2) given by expression (3), has the form
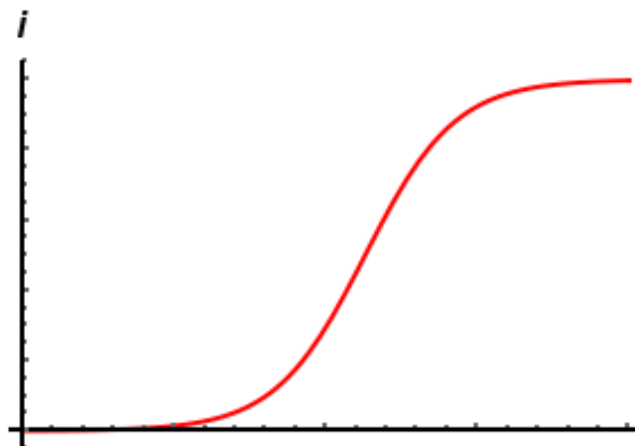
Figure1: Infection growth.

From this expression (3) it follows that, for a sufficiently large $t, x(t) \rightarrow M$ will be required, and therefore it will enter the region R_1 from a given t, and therefore it will enter the region of development of the epidemic, which should be avoided, by health agents and common sense government officials.

When the number of recovered people is greater than the number of the accumulated infected population, then the variation of the infected is negative, that is to say, it would be a decreasing function, and therefore it constitutes a point of inflection of the curve. In order to determine with certainty that moment when the total amount of infected is less than the recovered, it is necessary to make a simulation of this process of recovery, in which case it is necessary to denote by $R(t)$ an approximation by increasing the amount of the recovered in the moment t, this process is given has the following Cauchy problem,

$$R^{'} = kR, R(0) = R_0 \qquad (4)$$

Here, the following growth condition will be considered,

$$R(t_1) = R_1. \qquad (5)$$

The solution to the problem (4-5) has the form.

$$R(t) = \left(\frac{R_1}{R_0}\right)^{\frac{t}{t_1}} sg(t - t_r)$$

Because the function R (t) is such that $R(t) \neq 0$, only for $t > t_r$, since the recovered ones do not appear since the beginning of the process.

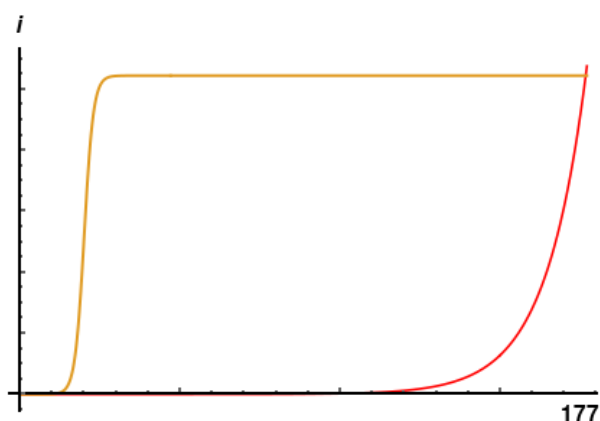Here it is necessary to determine the point t_p, such that,

$$x(t_p) < R(t_p)$$

Figura2: Ponto de cambio de concavidade da curva.

When the treatment of patients is such that the total infected population does not exceed those recovered, then the variation in those infected would be negative; this indicates that the infection curve would change its concavity, in which case this variation could be expressed through the following Cauchy problem,

$$\frac{dx}{dt} = k_1 x(m-x), x(0) = x_0 \quad (6)$$

The equation of variation of the infected population given by the Cauchy problem (6) shows the decrease of the patients, in correspondence with the indicated before, because here $\frac{dx}{dt} < 0$, since $x(t) > m$, and the solution of this equation has the shape,

$$x(t) = \frac{Cme^{mk_2 t}}{-1 + Ce^{mk_2 t}}$$

Due to the initial condition,

$$c = \frac{x_0}{x_0 - m}$$

So, the solution to the Cauchy problem (4), has the form,

$$x(t) = \frac{mx_0}{e^{-mk_1 t}(x_{0-m}) + x_0}$$

If the condition is met $x(1) = n_2$ if you have to,

$$k_2 = \ln \left[\frac{n_2(m - x_0)}{x_0(m - n_2)} \right]^{\frac{1}{m}}$$

So, the solution will be,

$$x(t) = \frac{mx_0}{(x_0-m)\left[\frac{x_0(m-n_2)}{n_2(m-x_0)}\right]^t + x_0} \quad (7)$$

From the expression (7) it is possible to obtain the solution for any t, this makes it possible to make predictions regarding the infected at any time; furthermore, under these conditions, it is possible to obtain the moment when the infected reach a given value when the number of infected is decreasing.

From here it can be seen that for t large enough $x(t) \rightarrow m$. This means that for a sufficiently long time the disease will go into full control due to the decrease in the infected population as a result of the measures taken by the health system.

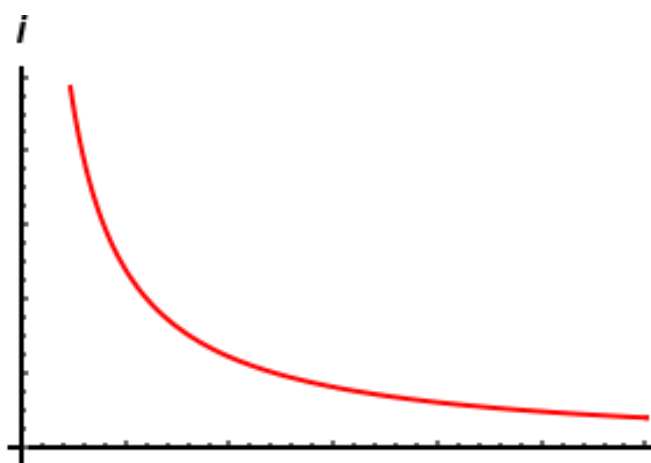The graph corresponding to this function given by expression (7), is given below,

Figure3: Decrease of the infected.

This graph corresponds to the statistical results given in the data presented, corresponding to a region, when the process is facing the elimination of the disease. For a sufficiently large $t, x(t)$ it will approach the m and, therefore, it will enter the comfort region, thus the population will start to enjoy health in general, as long as there is no change in the existing conditions that can lead to a new infection olla.

In this way, our model proposal in general can be represented by the following equation,

$$\frac{dx}{dt} = \delta_1 k_1 x(M - x) + \delta_2 k_2 x(m - x) \quad (8)$$

Here you have to $\delta_i (i = 1,2)$, take values in the binary set, that is, $\delta_i \in \{0,1\}$, Besides that, $\delta_1 + \delta_2 = 1$, because in the process, the contaminated population is increasing or decreasing, being mutually exclusive for that reason.

To control the infection process it will be necessary to determine a set of points $\{t_1, t_2, \ldots, t_n, \ldots\}$ such that when $x(t)$ represents an arc of the curve corresponding to function (3) such that $x(t_i)$ is sufficiently close to the maximum risk region R_1; this value will be taken as an initial condition $x(t_i)$ and the solution to the Cauchy problem corresponding to equation (6) with this initial condition is determined, so the next arc will enter the comfort region, this process will be repeated continuously, each time that adverse conditions appear, that is to say, whenever a new infection occurs, this will allow the control of the disease; because in practice it would mean that when the infected increase, measures will be taken by all those involved in the process to reverse the situation.

In this general case, the graph corresponding to the process with the participation of health agents, the government and society in general, has the form,
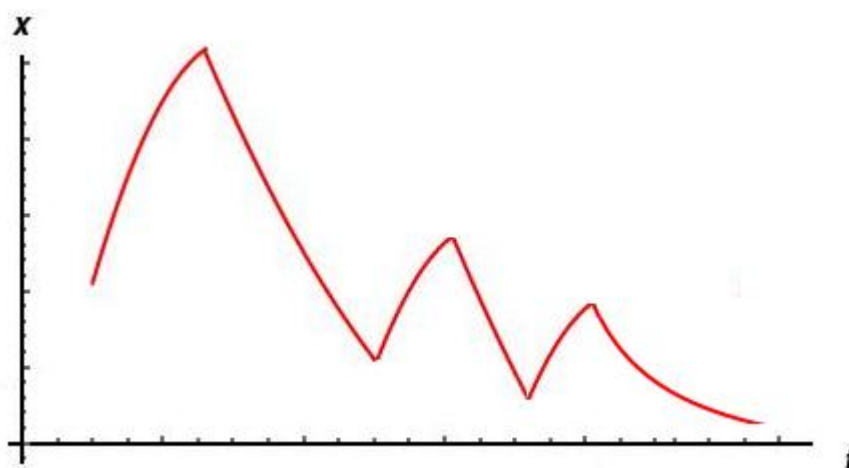

Figure 4: General case of disease control.

This graph shows that an epidemic does not follow a uniform Gausian curve, since the disease can, once controlled, have a new reappearance from these remaining cases, this constitutes a more realistic view of the situation; and all that the factors involved can do to definitively control the disease and thus prevent the epidemic from appearing again.

Observation: From what is shown in this work, it is good to persevere that in order to reduce the contagion, and therefore prevent new cases from appearing, the values of the parameters, M, m, and k_1 must be kept to a minimum, these parameters are associated with the contacts. , the remnants, is to say those who remain after controlling the disease are asymptomatic cases, and the contagion coefficient respectively, so it is necessary to avoid contact of the contagious with these susceptible people.

III. Conclusion

1. Due to the danger to the life of the home, it is of paramount importance to study the characteristics of the coronavirus, the ways of transition and the methods of combating the disease, which would allow a more effective treatment to patients.

2. Historically there have been diseases that, due to their spread, have become epidemics, but never with the danger of the coronavirus.

3. At the stage of the development of the epidemic, the number of people infected has grown exponentially, but this is not natural, so as it progresses it adjusts to a logistic model.

4. It is evident that those infected at any time will be in the range,
$R = \{(t,x) \in R^2 / t > 0, m \leq x \leq M\}$

5. Equation (8) simulates the process of variation of the infected population, which contains, as particular cases, equations (2) and (6) in the case of growth or decrease of the infected population.

6. The graphs of functions (3) and (7) correspond to the behaviors in the two main stages corresponding to the growth and decrease of the infected population in a region, a country or in the world.

7. The decrease in the infected population is in line with the prophylactic measures taken by health authorities, such as isolation of the contaminated and effectiveness of the treatment applied.

8. The practice shows that the decrease in infected cases is associated with the decrease in contacts, the number of remnants and the contagion coefficient, respectively. The maximum value of the infected is reached approximately at the moment $t = t_p$.

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