

Behavior of the epidemic due to the covid-19 virus in Mexico. Development of an algorithm

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Abstract

In the present paper, an algorithm was developed to represent the behavior of the current SARS-CoV-2 virus epidemic in Mexico, known as COVID-19, to obtain a likely scenario for the coming months and provoke a healthy discussion about the problem. The data reported by government entities is considered first by analyzing a simple model, via the construction of a polynomial, and then building an exponential type function, from the so-called logistic function. A numerical comparison is made with the officially provided data, and the graphs obtained from the solutions found are shown, including a brief explanation on how to interpret them appropriately. Finally, the possible scenario for the following months of the development of the epidemic in Mexico is discussed.

Keywords: Covid 19, epidemic, statistic applied, mathematical models, logistic function.

1. Introduction

Many diseases that affect organisms in the animal kingdom, particularly humans, are a result of a combination of environmental factors, including exposure to other organisms, such as viruses and bacteria. When this happens, an organism-to-organism transmission, known as contagion, can take place. Contagions that occur in one place, at a certain time, and on a massive scale are called epidemics.

Humans in general are very sensitive to changes in the environment that surrounds us. It is known that many of the components which we can consider part of living beings are viruses and bacteria. All of them are microscopic organisms and are often made up of small chains of nucleotides or proteins, particularly viruses that need a host to reproduce. The big problem for us is that when they achieve this reproduction, they cause a series of reactions in our body that range from temporary discomfort, while the reproduction cycle is carried out, to necroses in part of the various organs that serve as receptacles for such organisms, then a condition appears in the body known as infection [1-4].

For many of these infections, humans have developed the so-called antibodies, which are organisms part of our body that are responsible for "keeping at bay" and expelling foreign bodies that cause infections. But when these infections are very new, or hygiene conditions favor their reproduction and transmission, an epidemic is caused. Basically, according to the Dictionary a "disease that attacks a large number of people or animals in the same place and during the same period of time", e. g. the Spanish Language Dictionary [5].

Throughout the history of mankind, there have been many epidemics, in many places and of various kinds. In ancient times, very few epidemics were formally documented, and most of those that do have records were developed in what we can call Eurasia, the region of the world made up of Europe and Asia, considering the north region of the so-called Red Sea, such as those discussed below [6-11].

Thucydides rigorously recounts the desperation of doctors and patients in the face of the devastation of an epidemic for which neither knowledge nor remedies were known in Athens at the time of Pericles, during the Peloponnesian War against the Persians. And especially during the war against Sparta and her allies, in the year 430 before our era [12], [13].

The Antonine plague (165-180 BC) also known as the plague of Galen, because it was this famous doctor who adequately described it, was an epidemic possibly of smallpox or measles that affected the Roman Empire. It is believed that it was carried by troops returning from Lucius Verus's Parthian war in Mesopotamia [14-16].

In particular, in Mexico, the following epidemics have been documented.

There are records of three epidemics in the fifteenth century, in pre-Hispanic Mexico: the pestilential cold (1450), caused by low temperatures (year 7 Tochtli), one of the probable causes of the abandonment of Tula; diphtheria (possibly in 1456) in the Great Tenochtitlan; and exanthematic typhus (around 1496) in Xochtlán, Tequantépec and Amaxtlán [17-19].

In the 16th century, the following four epidemics were documented [20-23]: the Spanish invaders introduced smallpox (1520), which devastated the Great Tenochtitlan and allowed the Mexica people to be defeated, since many skillful and veteran warriors died [20,21]; measles (1531); salmonella (1545, called cocoliztli which means epidemic) that killed approximately 80% of the population (out of a population of approximately 15 million people); hemorrhagic fever (1576-1577) killing approximately 50% of the aboriginal population. In the eighteenth century, the epidemic called matlazahuatl (possibly typhus, from 1735 to 1736) killed approximately 40 thousand people in Mexico City [23].

In the 19th century, cholera (1833) killed some 324,000 inhabitants throughout the national territory; and there was yellow fever (1883) in Mazatlán, where 2,541 people died (16% of the population of this municipality) [23].

At the beginning of the 20th century, several epidemics appeared [23-26]. In Mazatlán, the first cases of the black plague of the bubonic variety (1902-1903), infected approximately 824 people and killed 582. Later, Spanish influenza (1918), left in Mexico about 500,000 deaths from a population close to 14 million people at that time [23], [24]. Poliomyelitis (1948-1955) affected 1,100 people and was eradicated by vaccination [26].

Already in the current XXI century, influenza due to the A-H1N1 virus spread throughout the country without serious consequences [27]. And currently, two years have passed since the SARS-CoV-2 virus, commonly called Covid-19, was detected. It caused an epidemic in Wuhan (China) and spread rapidly throughout the world [28], consequently classified as a pandemic by the World Health Organization (WHO). Its rapid expansion has led to many errors in the policies of each nation, as it has resulted in a problem with many variants and many mutations. In the world, 383,509,779 accumulated confirmed cases and 5,693,824 deaths have been reported so far, and 10,040,768,270 doses of vaccine have been applied. In Mexico there are 5,068,985 total confirmed cases, 308,141 deaths and 167,682,458 doses of vaccine applied, as of February 4, 2022 [29].

Without a doubt, it has been a great achievement to have a vaccine available in such a short time to combat this epidemic, since it must be taken into account that when an epidemic caused by mutations or unknown viruses develops, no country and no system of health is ready. It has to be learned at the same time as it is fought, and it is necessary to develop ways to avoid new outbreaks by developing control measures, as in the case of poliomyelitis, measles, smallpox, and others. But once the behavior and symptoms of the epidemic have been learned more or less, actions are generated to protect society: prevention measures, where citizens must cooperate; generation of drugs to combat infection; a long-term solution (a vaccine), which unfortunately takes time and the cost is high in all respects; and lastly, monitoring that leads to trying to predict the development of the epidemic, although it will necessarily only be approximate. However, in record time, various palliative vaccines have been developed, considering that to achieve a vaccine that permanently immunizes against a virus or bacteria, or any other pathogen, around 10 years are needed on average [30, 31].

The first step is to learn the virus incubation period and its transmission velocity and method (speed, range, lethality, variants, active lifetime, etc.). So, it is important to find prediction methods, which constitute a great challenge. A basic tool to try to predict the behavior of an epidemic (of the pathogen that causes it) is statistics. But being an unknown pathogen in many aspects, traditional prediction methods may not be enough. In the long term and knowing the general behavior of the pathogen, it is possible to arrive at sufficiently satisfactory results, as long as the population likely to be affected becomes aware and consequently follows the suggestions of specialists: epidemiologists, infectious disease specialists, and others. It is a big responsibility and there is a risk of the political use of the problem if the measures are not entirely adequate. So, there must be an attitude of cooperation of the population, instead of just looking for and exaggerating possible government errors in combating the problem.

In this paper, we present a statistical study to generate an algorithm that allows projecting the epidemic situation due to the SARS-CoV-2 virus in Mexico, based on the data provided by government entities. To achieve this, a review will be made of the data reported daily from March 2020 on the number of confirmed cases of people infected with the virus. Initially, polynomials will be constructed to show the behavior from a given month with a five-month projection to observe two key moments: the point of the maximum number of confirmed infections per day and the corresponding decline in the number of confirmed cases, so that it will be possible to construct asymptotic curves showing the evolution of the epidemic. The data from the initial 28 weeks will be used first, to subsequently carry out the same algorithm with 52 weeks of data. The construction of the so-called logistic equation will be used, which will allow a more adequate modeling of the mentioned behavior. The resulting algorithm will be contrasted with data reported for several days over a year, so that we can observe how the values obtained by the algorithm approach the reported values as more recent data are considered, using data provided in the middle of 2021. [29]. It should be noted that this is only one possible model and is by no means intended to be the correct model, as many factors may not have been taken into account. As it has been observed, each country and each region presents a different way of evolving from the current epidemic. Therefore, we are currently interested in conducting this brief study only considering the case of Mexico.

2. Construction of an algorithm or procedure

To build mathematical models that are good enough to represent the behavior of any situation with scattered data (in our case, the behavior of an epidemic due to a virus), it is necessary to consider various statistical concepts. It is thus convenient to collect, organize, analyze, and interpret data to provide an acceptable explanation for the behavior of these data that are subject to uncertainty. The use of statistics is essential since it seeks to establish limits to the uncertainty of situations with scattered data and to give probable conclusions about different sets and/or relationships between such data sets.

2.1. About the data and its organization

So, for the construction of the mathematical model mentioned in the Introduction, the data provided by the Mexican government through official communications [29], starting February 28, 2020, are considered. The first 28 weeks of data, organized by week, are shown in Table 1. Since as of October 2020 a large part of the population stopped following sanitary measures, causing a rebound in the number of infections per day at the end of 2020, and because the government carried out a count readjustment for those dates, a new analysis of results will be carried out, considering a period of one year and with the newly updated data. It will then be necessary to reconsider the original model, extending the sample with which we will work and considering the adjustments made by a commission in charge of watching the mentioned epidemic in Mexico, dependent on the Ministry of Health. The 52-week results are shown in Table 2. It is not easy to obtain a behavioral model of something that is not known, so in the following lines, we venture a possibility.

It is important to note that the data tables presented are only fully confirmed data. The problem generated by the virus commonly called COVID-19 is very unpredictable, by its very nature. For this reason, only the data provided by the entities responsible for one year are considered, this is done using only the data that is considered necessary, since during the development of the algorithm proposed here, more data emerged with a different dynamic develop.

Table 1: Confirmed Cases. First 28 Weeks

Data No.	days	Confirmed cases
1	7	5
2	14	12
3	21	164

4	28	585
5	35	1510
6	42	3441
7	49	6297
8	56	11633
9	63	19224
10	70	29616
11	77	42595
12	84	59567
13	91	81400
14	98	105680
15	105	133974
16	112	165455
17	119	202951
18	126	238511
19	133	282283
20	140	324041
21	147	370712
22	154	416179
23	161	462690
24	168	505751
25	175	543806
26	182	579914
27	189	616894
28	196	652364

Table 2: Confirmed Cases for 52 Weeks

Week	days	Confirmed cases
1	7	85
2	14	207
3	21	809
4	28	1869
5	35	3811
6	42	6796
7	49	11964
8	56	20286
9	63	31510
10	70	45157
11	77	63011
12	84	86295
13	91	112538
14	98	141994
15	105	175840
16	112	212678
17	119	251125
18	126	293931
19	133	338149
20	140	386989
21	147	437084
22	154	484292
23	161	526154
24	168	565911
25	175	603606
26	182	642743
27	189	681881
28	196	717684
29	203	747106
30	210	780989
31	217	813726
32	224	845974
33	231	883697
34	238	927239
35	245	970784
36	252	1010576
37	259	1058112
38	266	1101966
39	273	1156987
40	280	1219454
41	287	1290434
42	294	1367454
43	301	1441339
44	308	1512464
45	315	1601433
46	322	1711885
47	329	1816057
48	336	1909708
49	343	1973150
50	350	2028411
51	357	2071985
52	364	2113274

2.2. A first try. A polynomial model

Given how the pandemic generated by the Covid-19 virus has behaved, a 4th-degree polynomial was initially proposed, to find out the approximate number of confirmed infections on the selected day. But that also allows finding a rate of increase in accumulated cases per day, with data at the national level. The critical points corresponding to the mentioned polynomial were obtained, so that we define the function $y(t)$ = number of confirmed cases at time t (measured in days first and weeks later) and its corresponding derivative to t , namely $y'(t)$ = growth rate of confirmed cases at time t . Considering the condition $y'(t) = 0$, three roots were obtained, two of them imaginary, so only the positive real root was taken into account. Certain considerations were made to relate the values of the variable found with the number of days from the first case, thus considering the appearance of several infections per day, and its consequent decline in this data (infections per day). The polynomial obtained was the following,

$$y(t) = 0.0015988 t^4 + 0.15617 t^3 - 39.55 t^2 + 1002.3 t - 6986.9, \quad (1)$$

and its corresponding first derivative,

$$y'(t) = -0.0063952 t^3 + 1.7285 t^2 - 79.108 t + 1002.3, \quad (2)$$

which with the condition $y'(t) = 0$, provides the solutions

$$t_1 = 216.49, \quad t_2 = 26.898 + 0.69084 i, \quad t_3 = 26.898 - 0.69084 i, \quad (3)$$

being the real solution t_1 , the sought value since the other roots are imaginary. The extreme condition is obtained from the evaluation of the second derivative, obtaining a maximum as expected for the value t_1 shown in (3). That is, it would correspond to the existence of a maximum of infections on day 216 or 219, depending on whether it is convenient to take the nearest integer above or below the exact value for t_1 . The possibility of the beginning of the decline in the number of infections per day indicates that on day 219 (October 2, 2020) there should be a maximum in the registry of accumulated cases, and their corresponding growth should begin to be very slow if the epidemic behaved as it did during the first six months. The function (1) evaluated at the value obtained, namely $t_1 = 217$, should start to “flatten out”, that is, to have an asymptotic tendency. But due to its shape, it only shows the moment when the number of daily infections should decline. Hence, with the condition for the aforementioned derivative, it is found that approximately the number of confirmed infections as of October 2, 2020, should be 685,894. The official number recorded that day was 813,726, so the calculated amount represents a difference of 15.7% with respect to the official amount reported. For a preliminary test, it shows that it is possible to construct a polynomial in this way, one which represents approximately the time (day number) when the decline in the number of infections per day begins. Figure 1 and Figure 2, respectively, show the curves obtained for the function and for its derivative, where such points are observed.

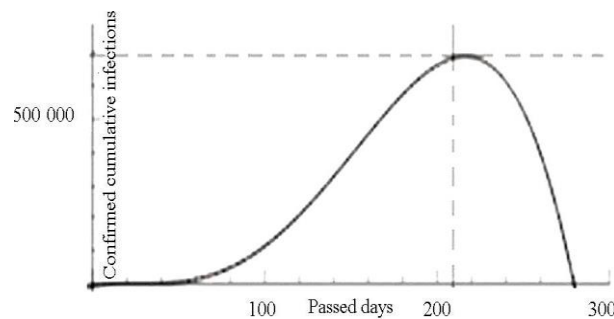


Fig. 1: Graph of the Function $Y(T)$, of the Behavior of the Pandemic, for an Interval of $-100 \leq t \leq 300$.

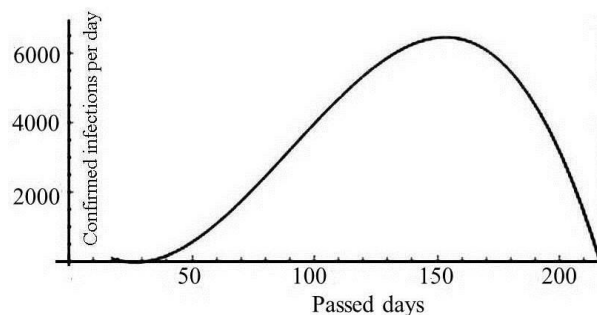


Fig. 2: Graph of the Function $Y'(T)$, for an Interval of $0 \leq t \leq 250$.

As previously mentioned, the function in (1) is not entirely correct, because apart from the very diverse variations of infections per day, due to multiple factors that are difficult to control, a more appropriate model would allow us to construct a function that at infinity of the variable behaves asymptotically, towards a value that indicates the trend of the number of infections to zero. Thus, we now consider the function used for population growth, also known as the logistic function, for which we will need to solve the logistic equation,

$$\frac{dP}{dt} = P(a - bP), \quad (4)$$

where:

P = population at any instant of time

a = constant to be determined, according to the conditions of the problem

b = constant to be determined according to the conditions of the problem

Equation (4) can be written in another way, by separating the factors, considering the need to have a single variable on each side of the equality, from which when integrating we obtain,

$$P(t) = \frac{(aP_0)}{bP_0 + (a - bP_0)e^{-at}}, \quad (6)$$

being:

a = constant to be determined

b = constant to be determined

P_0 = Initial population

The logistic function that allows a better approximation of the problem has been obtained. Considering the initial condition, namely the value of the function for the initial time ($t = 0$), which will be the initial population P_0 , in our case the number of confirmed infections, which can be taken arbitrarily, not necessarily on day zero of the epidemic.

2.3. A more realistic model

Taking into account equations (4) and (6), we now build an algorithm that allows us to model the development of the COVID-19 pandemic, closer to its occurrence, by considering the possibility of an asymptotic behavior that reflects the decline in infections in an unknown time. In the limit to infinity, for the population function (6) it is observed that the maximum population M of possible contagions is as,

$$M = \frac{a}{b} \quad (7)$$

That is the maximum population (maximum number of confirmed infections) is not related to the initial population, but to the two constants that we must determine. To do so, we use the data provided in Table 1, in (1) and (2) equations in order to solve (6).

From (2), which represents the growth rate of the number of infections per day, for two arbitrary time values, for which the number of confirmed infections is known (populations at those chosen moments), we define $t_0 = 98$ and $t_1 = 196$, for which we have,

$$P(t_0 = 98) = 105680 \text{ and } P(t_1 = 196) = 652324,$$

Which by substituting in (2) they give the growth rate of infections for those days, and from (4) for $P(t)$ as a function instead of $y(t)$, we have the system of linear equations,

$$\begin{cases} 3831 = 105680(a - 105680b) \\ 3746 = 652364(a - 652364b) \end{cases} \quad (8)$$

Whose solution gives $a \approx 42145(10^{-8})$ and $b \approx 5.58(10^{-8})$. Now substituting the values of time used in (2),

$$P'(98) = 3831 \text{ and } P'(196) = 3746,$$

And substituting in (7) one has $M = 755339$, which will be the maximum number of infections for $P_0 = 652363$ corresponding to the selected day $t_0 = 196$, so that (6) is reduced to,

$$P(t) = \frac{27495.7663}{0.0364 + 0.00575e^{(-4.21 \times 10^{-2})t}} \quad (9)$$

Expression (9) constitutes a more adequate approximation of the behavior of the epidemic in Mexico, as can be seen from the following considerations.

We graph the function of the behavior of the epidemic (9) in the range of values $(-196, 100)$, as shown in Figure 3, and which as can be seen is asymptotic, as the epidemic is expected to behave, having as limit a maximum value of confirmed infections, and so tending to zero value in the number of infections per day.

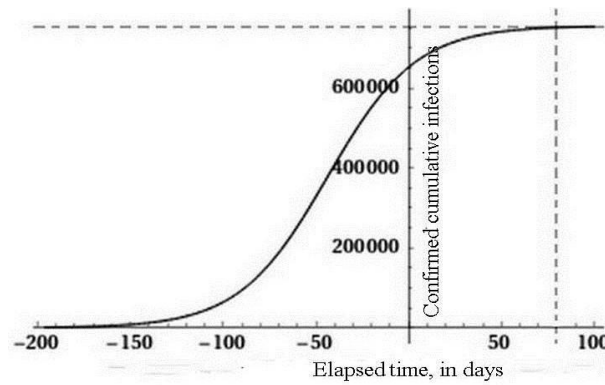


Fig. 3: Behavior of the Epidemic in an $(-196,100)$ Interval for the Logistic Function (9).

Figure 3 shows that from about $t = 80$, the function begins to have linear behavior since the number of infections per day would begin to reduce, and from that point, the curve apparently "flattens". That is, considering $t = t_m - t_0$, with $t_0 = 196$, the result is $t_m = 276$, it would be expected, according to our logistic function, that the number of infections per day would stabilize, and we would find ourselves in the stage of exit of the pandemic for day 276 (November 30, 2020) since the beginning of the pandemic in Mexico, reaching a number of infections no greater than $P(t \rightarrow \infty) \approx 755378$ of confirmed cases by COVID-19.

Up to this point in the data analysis, only the first 6 months of the epidemic were considered. In addition, in October 2020, a large part of the population stopped following the sanitary measures (despite the calls to continue following them), and also year-end parties began to be held, as well as clandestine events with 200 to 300 people in much of the country, causing a sudden increase in confirmed infections by the end of 2020. Due to the above, since the government carried out a readjustment of the count for this data (which was updated on the CONACYT page), a new analysis of results carried out for a longer period of time (one year) and with updated data, as well as the consideration of the sudden increase in confirmed cases at the end of the year, shows better the behavior to be observed.

Updating the data of confirmed cases and extending these for 52 weeks, we obtain a polynomial similar to the one obtained with the six-month data, with which we will represent the number of confirmed cumulative cases of infection. The polynomial obtained for these new data (Table 2) is,

$$y_2(t) = 0.00033884 t^4 - 0.23951 t^3 + 67.844 t^2 - 3273.6 t + 30124, \quad (10)$$

$$t_1 = 28.080, t_2 = 251.03 + 151.65i, t_3 = 251.03 - 151.65i, \quad (11)$$

And the corresponding first derivative, which with the condition $y'(t) = 0$ allows to obtain,

Where only the solution t_1 is useful as it can be seen, which is real and positive, as it should be. In addition, an extreme value for the function is obtained by evaluating the second derivative in the possible real root t_1 of the first derivative. The obtained value indicates the existence of a minimum of the function $y_2(t)$, which indicates that the polynomial obtained from the new data does not provide information on the possible day on which the epidemic will reach its peak, nor on what date the contagion curve will begin to "flatten". So, we will now use the so-called logistic equation but apply it to the data in Table 2.

Starting from the initial approach, with the first data considered, we now turn to the logistic equation in the following way,

$$P_2(t) = \frac{(aP_0)}{bP_0 + (a - bP_0)e^{-at}} \quad (12)$$

Furthermore (7) can also be used so that can be define,

$$M_2 = \frac{a}{b} \quad (13)$$

We now proceed to determine the maximum population, considering the new data (Table 2) and the growth rate expressed by evaluating the derivative of the function $y_2(t)$, to find the solution of (4). The growth ratio with the data in Table 2 is,

$$y'_2(t) = 0.0013554 t^3 - 0.71853 t^2 + 135.69 t - 3273.6, \quad (14)$$

And using two arbitrary values of t from Table 2, of which the populations are known (number of confirmed infections), namely $t_0 = 182$ and $t_1 = 364$, we have $P_2(t_0) = 642743$ and $P_2(t_1) = 211327$. Evaluating (14) in those same values of t , we have,

$$P'_2(182) \approx 5793 \text{ y } P'_2(364) \approx 16284 \quad (15)$$

With these values, a solution to equation (4) is sought, and the system of equations is obtained:

$$\begin{cases} 5793 = 642743(a - 642743b) \\ 16284 = 2113274(a - 2113274b) \end{cases} \quad (16)$$

So that,

$$b \approx 8.89 \times 10^{-10} \text{ and } a \approx 958 \times 10^{-10} \Rightarrow M_2 \approx 10781026$$

With $P_0 = 2113274$, corresponding to day $t_0 = 364$, the last data considered, and we have the logistic function,

$$P_2(t) = \frac{20254.32}{0.0019 + 0.0077e^{-9.58 \times 10^{-3}t}}, \quad (17)$$

where:

$$t = t_m - t_0$$

t_m = sample time to predict

t_0 = initial time,

Expression (17) can be considered a more realistic representation of the behavior of the epidemic in Mexico. Figure 4 shows the function found on an interval $-364 \leq t \leq 600$.

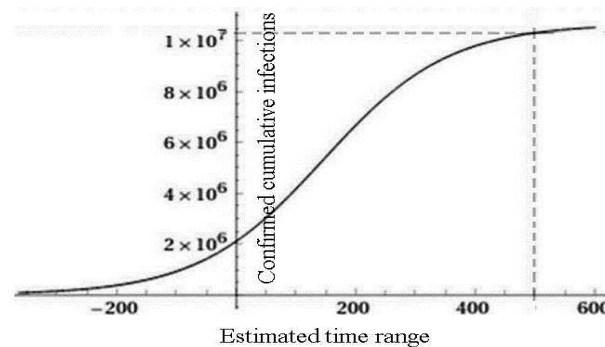


Fig. 4: Logistic Function for the Behavior of the Pandemic, in An $-364 \leq t \leq 600$ Interval.

Figure 4 shows that from $t = 500$ the function begins to have linear behavior since the number of infections per day would begin to decrease, and from that point, the new curve tends to "flatten out". That is, considering $t = t_m - t_0$ and with the values of time $t_0 = 364$, $t = 500$, we have $t_m = 864$. According to this new logistic function and with the updated data, a stabilization in the number of infections per day would be expected and we could consider being in the exit stage of the epidemic by day 864. (July 11, 2022), counting from day zero of having started in Mexico, reaching a number of confirmed COVID-19 infections of $P_2 \approx 10\,660\,169$.

With the procedure shown, based on the records provided by the country's authorities, it is found that the epidemic due to the SARS-CoV-2 virus manifests signs of lasting more than 2 years at the national level, with the possibility of around ten million confirmed infections. It is a scenario that no one wants, but it is a likely one; unless the public's attitude of disbelief and distrust towards the actions of government agencies and the preventive measures proposed by health officials is corrected.

3. Results and discussion

It is necessary to make a comparison between the obtained expression from the possible behavior of the epidemic and the monitoring results released by the health authorities. We will take a couple of sample values for t_m and figure out the amount of infected population predicted by the logistic function (17), to compare with the official data and determine the percentage of difference.

With the sample values $t_{m1} = 91$, $t_{m2} = 182$, $t_{m3} = 196$, $t_{m4} = 364$, and taking into account the adjustment in the official figures, considering $t = t_m - t_0$, for $t_0 = 364$ we have $t_1 = -273$, $t_2 = -182$, $t_3 = -168$, $t_4 = 0$. So, $P_2(-273) = 188987$, $P_2(-182) = 441021$, $P_2(-168) = 501344$, $P_2(0) = 2109830$. Retrieving the values of Table 2, and comparing, the percentage differences obtained are, $\varepsilon_1 = 67.93\%$, $\varepsilon_2 = 31.38\%$, $\varepsilon_3 = 30.14\%$, $\varepsilon_4 = 0.16\%$, respectively, seeing that as the epidemic evolves, the margin of error shrinks, which allows us to consider the procedure shown here adequate to represent the behavior of the epidemic in Mexico.

On the other hand, reviewing the data on confirmed infections, it is observed that once the first stage of infections is over (approximately six months), the number of such confirmed infections doubles approximately every three weeks in the second half of 2020. Later, in periods of three months; and already in the second half of 2021, periods of four to five months are observed. Considering that the official number of total infections as of February 2, 2022, was 5,068,985, and given the indicated doubling period, it is possible that in effect there will be around 10,000,000 by July of this year (2022), as calculated with the algorithm presented. Furthermore, observing how the epidemic has evolved, with increases in infections every almost half a year, as shown in Figure 5, that possibility cannot be ruled out.

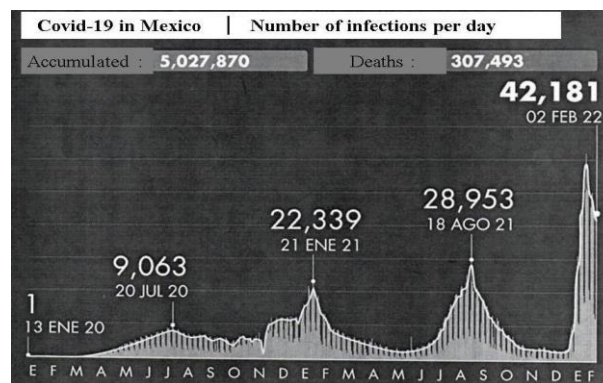


Fig. 5: Distribution of Infections Per Day (Source: Ministry of Health, Mexico) [29].

4. Conclusions

As it has been shown, based on the data obtained from official sources, it was possible to develop an algorithm whose starting point is the proposition of a quartic polynomial, which in the positive part of the values of the variable resembles an exponential type function. The results of this first test later helped to develop an algorithm that allows obtaining an equation based on the population growth theory. Of course, this is only a test of what can be done, considering the enormous number of variables that intervene, including the attitude of the population, to obtain effective control and eradicate or at least greatly mitigate an epidemic. There must be an attitude of cooperation of the population, instead of just looking for and exaggerating possible government errors in combating the problem.

Based on the results obtained with the last elaborated function, and the most recent data update by the authorities, we managed to obtain a logistic function to try to represent the future behavior of the pandemic in our country (Mexico). These results make us see that, regardless of the information given by the news or unofficial media, the current situation in the country still has a long time and a long way to go. Therefore, it is not advisable to rush into non-essential activities or events, since they could alter the rhythm of the pandemic, and even causes the situation to last for an even longer time than that already suggested in this work and others like it.

We must also highlight that the function formulated with this work presents us with a very considerable possible number of infected people compared to the population of the country (126,014,024 registered by the INEGI in its 2020 Population Census) [32]. Therefore the need for vaccination against the SARS-CoV-2 virus is reiterated, as this action can largely counteract the number of deaths and allow that of the ten million possible infections by July 2022, deaths will be very few or even nonexistent.

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References

- [1] D.R. Wessner, The origins of viruses, *Nature Education* 3 (2010) 37.
- [2] National Institute of Health, *Microorganisms in built environments: Impacts on human health, microbiomes of the built environment*, <https://www.ncbi.nlm.nih.gov/books/NBK458822/>. February 2020. Accessed: January 27, 2022.
- [3] Ma.A. Sánchez, T. González, T.R. Ayora, Z.E. Martínez, N.A. Pacheco, ¿Qué son los microbios?, *Ciencia* (2017) 10-17.
- [4] J.M. Uriarte, *Virus y bacterias*, Caracteristicas.co., <https://www.caracteristicas.co/virus-y-bacterias/>. Revised 2019. Accessed: January 27, 2022
- [5] Real Academia Española. *Diccionario de la Lengua Española* (21th ed.), Espasa, Madrid, 2000; 859
- [6] Ch.A. Smith, *Plague in the ancient world: A study from Thucydides to Justinian*, *The Student Historical Journal* 28 (1996). <http://people.loyno.edu/~history/journal/1996-7/Smith.html> Accessed January 27, 2022.
- [7] W. Lederman, *El hombre y sus epidemias a través de la historia*, *Rev. Chil. Infect. Edición de Aniversario* (2003) 13-17 <https://doi.org/10.4067/S0716-10182003020200003>.
- [8] M.E. Habichi, F.D. Pate, E. Varoto, F.M. Galassi, *Epidemics and pandemics in the history of humankind and how governments dealt with them. A review from the Bronze Age to the Early Modern Age*, *Rivista Trimestrale di Scienza dell'Amministrazione* 2 (2020) 1-32. Available online: <http://www.rtsa.eu> – ISSN 0391-190X ISSNe 1972-4942
- [9] R. Leal, *Breve historia de las pandemias*, *Psiquiatria.com*. <https://psiquiatria.com/bibliopsiquis/breve-historia-de-las-pandemias/>. 23/04/2020. Accessed: January 27, 2022.
- [10] P. Galeana, *Las epidemias a lo largo de la historia*, *Antropología Americana* 5 (2020) 13-45.
- [11] C. Iglesias, *Historia de las pandemias*, *Letras Libres*, junio 2021; <https://letraslibres.com/revista/historia-de-las-pandemias/>. Accessed January 27, 2022.
- [12] Tucídides, *Historia de la guerra del Peloponeso*, *Historiadores griegos*, Ed. Aguilar, Madrid (1969) Libro II, Caps. 48-54.
- [13] J. Dagnino, ¿Qué fue la plaga de Atenas?, *Rev. Chil. Infect.* 28 (2011) 374-380. <https://doi.org/10.4067/S0716-10182011000500013>.
- [14] J.R. Fears, *The plague under Marcus Aurelius and the decline and fall of Roman Empire*, *Infect Dis N Am* 18 (2004) 65-77. [https://doi.org/10.1016/S0891-5520\(03\)00089-8](https://doi.org/10.1016/S0891-5520(03)00089-8).
- [15] E. González, I. García, *La primera peste de los antoninos (165-170). Una epidemia en la Roma Imperial*, *Asclepio* LIX (2007) 7-22. <https://doi.org/10.3989/asclepio.2007.v59.i1.215>.
- [16] M. Calvo, *La peste antonina: la pandemia que diezmó el Imperio Romano*, *Historia Digital* 37 (2021) 1-3.
- [17] J.R. Collado, *Historia antigua de México como fuente de aproximación a la enfermería transcultural*, *Desarrollo Cientif Enferm.* 18 (2010) 38-43.
- [18] A. Mandujano, L. Camarillo, M.A. Mandujano, *Historia de las epidemias en el México Antiguo. Algunos aspectos biológicos y sociales*. *Casa del Tiempo* 4 (2003) 9-21. Available on line: <http://www.uam.mx/difusion/revista/abr2003/mandujano.pdf>.
- [19] I.N. Gutiérrez, *Las epidemias del México prehispánico*, *Rev. Med. Cine.* 16e (2020), 237-245. Available on line: https://gredos.usal.es/bitstream/handle/10366/145920/epidemias_del_Mexico_prehispanico_un_bre.pdf?sequence=1 <https://doi.org/10.14201/rmc202016e237245>.
- [20] G. García, *La conquista de México, Carácter de la conquista española en América y en México*, Cd. Máximo, Ed. Fuente Cultural, 1901; 235-236.

- [21] S. Guevara, Primera pandemia del Nuevo Mundo: La viruela de 1520 en México. Noticonquista, <http://www.noticonquista.unam.mx/amoxlti/1951/1947>. Accessed August 13, 2020.
- [22] S. E. Guevara, La construcción sociocultural del cocoliztli en la epidemia de 1545 a 1548 en la Nueva España. Tesis Doctoral, 2017 Cap I, Universitat Autònoma de Barcelona.
- [23] F. Navarrete, Epidemias y colonialismo, 500 años de historia. Noticonquista, <http://www.noticonquista.unam.mx/amoxlti/1950/1947>. Accessed August 13, 2020.
- [24] S. Pulido, La Gripe Española: La pandemia de 1918 que no comenzó en España. Gaceta Médica (2018). <https://gacetamedica.com/investigacion/la-gripe-espanola-la-pandemia-de-1918-que-no-comenzo-en-espana-fy1357456/>. Accessed August 13, 2020.
- [25] S.B. Fernández, A cien años de la Constitución de 1917, las grandes epidemias ocurridas en México, Revista CONAMED 22 Extra (2017) 16-20.
- [26] González-Rubio, La poliomielitis y su erradicación en México y las Américas. Reto histórico de salud hecho realidad, RevSalJal Año 5-1 (2018) 49-51.
- [27] M. Betancourt-Cravioto, P. Kuri-Morales, Situación actual de la influenza A(H1N1) en el mundo, Gaceta Médica de México 146 (2010) 437-440.
- [28] J. Vallejo, La pandemia en México y su impacto psicológico, EXLEGE Año 4, 6 (2020) 239-250. Available online: https://bajo.delasalle.edu.mx/revistas/exlege/pdf_6/exlege_06_art_017-vallejo_montiel.pdf
- [29] Informe Técnico Diario COVID-19., Subsecretaría de Prevención y promoción de la Salud. https://www.gob.mx/cms/uploads/attachment/file/663098/Comunicado_Tecnico_Diario_COVID-19_2021.08.20.pdf. Accessed August 20, 2021, last accessed February 4, 2022.
- [30] N.Y. Department of Health, The science behind vaccine research and testing. How vaccine are made and tested, Last medically Review on December 6, 2018, https://www.health.ny.gov/prevention/immunization/vaccine_safety/science.htm. Accessed January 27, 2022.
- [31] A. Boulanger, Everything You Need to Know About vaccinations, <https://www.healthline.com/health/vaccinations>, November 27, 2019. Accessed January 27, 2022.
- [32] INEGI, Censo de Población y Vivienda 2020, <http://cuentame.inegi.org.mx/poblacion/habitantes.aspx?tema=P>. Accessed January 27, 2022.