Evolution of the COVID-19 Pandemic in El Salvador Applying SIR-Type Simulations

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ABSTRACT

This article studies the epidemiological dynamics of COVID-19 in El Salvador, using deterministic models such as SIR, which is based on the Susceptible-Infected-Recovered scheme, with constant transmission and recovery rates, and introducing the parameter of the global mortality rate. The simulations of the SIR model were modified in order to consider the intervention in the social dynamics of the population, through measures such as social distancing, appropriate hygiene, and mandatory quarantine at the country level. These measures have been managed in order to mitigate the evolution of the pandemic in the country. The 4,600 people held in Containment Centers had been assigned as the base population for simulations, because by April 5, 90% of the cases were confirmed among this group. The overall mortality rate has been assumed to be 3.5%, according to general international reports. The results were classified by scenarios: optimistic, semi-critical and critical with peaks of infection between 4% and 7.4% of the total population considered. It was established that 15% of the confirmed cases reach critical condition, while 3.5% of the total infected cases might die. The simulations are carried out since April 5, but assuming March 18 as the zero day, which corresponds to the first positive case identified in El Salvador.

Key words: COVID-19, SARS-COVID19, Pandemic, Epidemiology, Simulation models, SIR mathematical models

INTRODUCTIÓN

In a few months, the SARS-CoV-2 virus has gone from infecting wild animals to infecting more than 2.3 million people worldwide, with a balance of more than 160,000 deaths to date. This new virus, that generates the acute respiratory syndrome, COVID-19, is leading to a crisis of health systems of most countries in the world, and requires the scientific community to get down to work for analyzing the phenomenon, prevent contagion, study the evolution of the pandemic, and of course, to find medical treatments that can eliminate the virus from the body in order to save lives.

One of the methods to study the pandemic that the entire world is facing up, is the development and application of a deterministic or stochastic mathematical model, in order to simulate the epidemiological characteristics of the disease, which in turn allows decision-making and the establishment of operational measures aimed at the control and prevention of the contagion.

In the study of any epidemic, it is essential to answer questions about the possibilities of epidemiological control of the disease, as well as about the possibility of eradicating it. The answer to these two aspects depends on the transmission and recovery rates of the sick people, which in turn, depend on many other factors, among them, the social structure of the population and its connectivity, the sanitary conditions of the country, the power of infection of the agent, the vectors of the disease, and of course the installed capacity of health system and its effectiveness (*Hethcote, 2000*).

Currently, there is a great variety of models applied to epidemiological problems, including the use of stochastic differential equations, cellular automata, dynamic networks, and others. Network models are being used more and more, because they allow a more realistic simulation of the population structure and its evolution in relation to the transmission of diseases. These models are made up of interconnected nodes that can represent people and their social, economic or any other types of interrelationships (*Keeling & Eames, 2005*).

Since social interaction is highly changing, the evolution of the selected model should work in the same way, adapting to the variability that the social environment implies, which clearly can affect the speed and spread amplitude of an epidemic.

Of course, these characteristics make the analysis of epidemiological problems even more complex, since the social dynamics that determine contact between individuals must be taken into account. In cases such as the present pandemic, in which contagion occurs from person to person, it is expected that with the government regulations of promoting the decrease of social contact through distancing and other hygienic measures, it will have a positive effect on the evolution of the epidemic (*Gross & Blasius, 2008*).

In order to study the evolution of the COVID-19 pandemic in El Salvador, a deterministic SIR model was applied, modifying it with the introduction of the mortality parameter in order to analyze the possible evolution scenarios of COVID-19 infection. The spread of the disease among individuals under quarantine conditions in Containment Centers was analyzed. The SIR model provides a first approach to mathematical models of epidemiological prediction traditionally used to describe other epidemic outbreaks at an historical and global level.

METHODOLOGY

The SIR model has many variants and has been used to study the evolution of many diseases, including flu, dengue, and other respiratory viruses such as SARS. In this model the population is divided into three classes: Susceptibles S(t); Infected I(t) and Recovered individuals R(t), which are those who, having become ill, have relieved themselves and possibly acquired immunity to new infections. This model is described by a system of differential equations that include the parameters, δ, β and α, as follows:

$$\frac{dS(t)}{dt} = -\beta\, S(t)\frac{I(t)}{N(t)} + \delta\,\alpha\, I(t)$$

$$\frac{dI(t)}{dt} = \beta\, S(t)\frac{I(t)}{N(t)} - \alpha\, I(t)$$

$$\frac{dR(t)}{dt} = (1-\delta)\,\alpha\, I(t)$$

Where N(t) is the total population, β is the contagion rate, α is the recovery rate, and δ is the death rate due to the virus, ranging from 0 to 1 (*Arenas et al. 2009*).

In addition, the initial conditions must be established:

$$S(0) = S_0 \geq 0;\ \ I(0) = I_0 \geq 0;\ \ R(0) = R_0 \geq 0$$

$$S(t) + I(t) + R(t) = S_0 + I_0 + R_0 = N$$

Besides, the basic number of reproduction is defined as

$$R_0 = \frac{\beta}{\alpha}$$

The contagion rate R_0, represents the average number of infections generated by an infected person, among healthy individuals. Its importance lies in the fact that it indicates if the outbreak of the disease is an epidemic, when $R_0 > 1$, otherwise the disease is controllable and leads to its disappearance. Moreover, it is necessary to know other values such as the incubation time and the time that one individual remains infectious (*Hethcote, 2000*).

According to the latest publications about the Coronavirus pandemic, the contagion can occur from one day before the onset of symptoms, up to 5 to 7 days from the onset of the disease. Furthermore, children can spread the virus for more than 7 days. Symptoms begin 1 to 4 days after the virus enters the body. That is, you can spread it to another person before you know you are sick. Finally, some people can become infected with the virus without developing symptoms, and may spread the virus to another person (Centers for Disease Control and Prevention, CDC). These observations allow us to adopt a valid criteria to define the parameters that intervene in the mathematical modeling of the pandemic.

The implementation of the model was executed by using Python programming language, solving numerically the equations of the SIR model. The following data were used as initial conditions:

Transmission Dynamics			Clinical Dynamics	
Population	**Parameters**	**Times**	**Morbidity**	**Recovering Times**
Quarantine: ~4,600 per.	R_0 = 1.3, 1.4, 1.5	Incubation time: ~5 days	Disease duration: <21 days	Hospital stay: ~10 days
Total: ~6,500,000	$a = R_0/Tin$	Infection time: 7 – 12 days		Hospitalization rate: 14%
Initial infected: 69	$\beta = a*R_0$		δ = 3.5 %	Recovery time in mild cases: ~11 days
Recovered: 5				
Deceased: 4				

RESULTS

The solutions obtained are shown in Figure 1, which indicates the possible evolution of the contagion by the virus, in case of not implementing any type of containment measures, in this way the populations of susceptible, infected, and recovered would behave as follows:
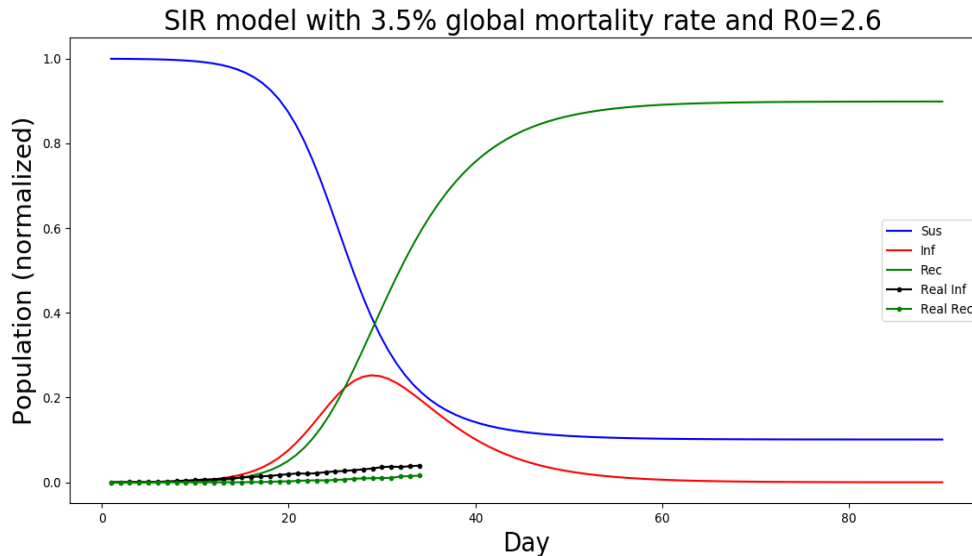
SIR model with 3.5% global mortality rate and R0=2.6

Figure 1: *SIR model without containment measures, with global mortality rate. Note that the maximum value of infected of the population considered is around 1161 people, which for N = 4600 is basically 25% of the population, the maximum peak of infected would be in about 32 days after confirming the first case on March 18, 2020.*

On the other hand, it is usual to classify the evolution of the disease by optimistic, semi-critical and critical scenarios. In the criterion of the research group we have chosen different values of the contagion rate in which they coincide in a timely manner with the numbers of infected, a critical scenario would be when the values tend to have a higher number of infected.

With the available data, different scenarios were projected according to the current contagion rates, estimating 3 possible values of R01, R02, R03 = 1.3, 1.4, 1.5, which correspond to the optimistic, semi-critical, and critical scenarios, respectively, obtaining the result shown in Figure 2.

For convenience, N = 4,600 people were selected, according to the official data reported by the government of the containment centers, this was done because 90% of the known cases have been reported from there, therefore, it is not yet possible to make reasonable predictions of pandemic behavior at the national level.

Regarding the maximum numbers of infected for each scenario, the estimations of the model shows the result of 185, 259 and 339 infected, for the optimistic, semi-critical and critical case, respectively, which indicates that a projection of maximum infected is expected at 6th to 10th of May.
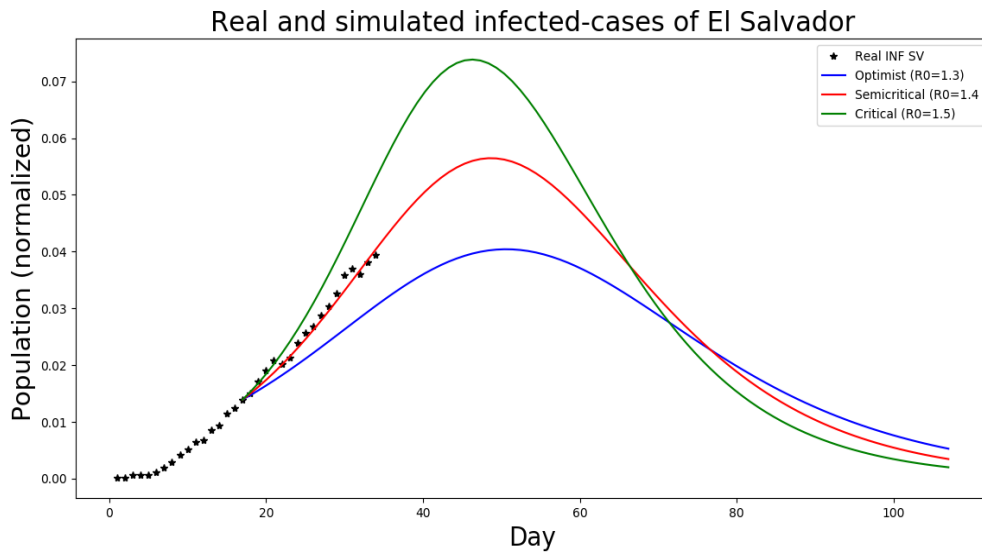
Figure 2: *SIR with global mortality rate of 3.5% for three different scenarios, note that since April 5th the values of active infected are in accordance with the semi-critical scenario, however, the last few days could indicate that the evolution of the Infected is moving to the critical stage.*

In addition, projections were made taking into account the initial conditions of April 5th for a maximum range of 90 days. For example, on April 6th were reported 69 active confirmed cases, and the solution curves predict 68, 69 and 70 cases for optimistic, semi-critical and critical respectively, which indicates that the data confirmed by the government fits to the semi-critical curve.
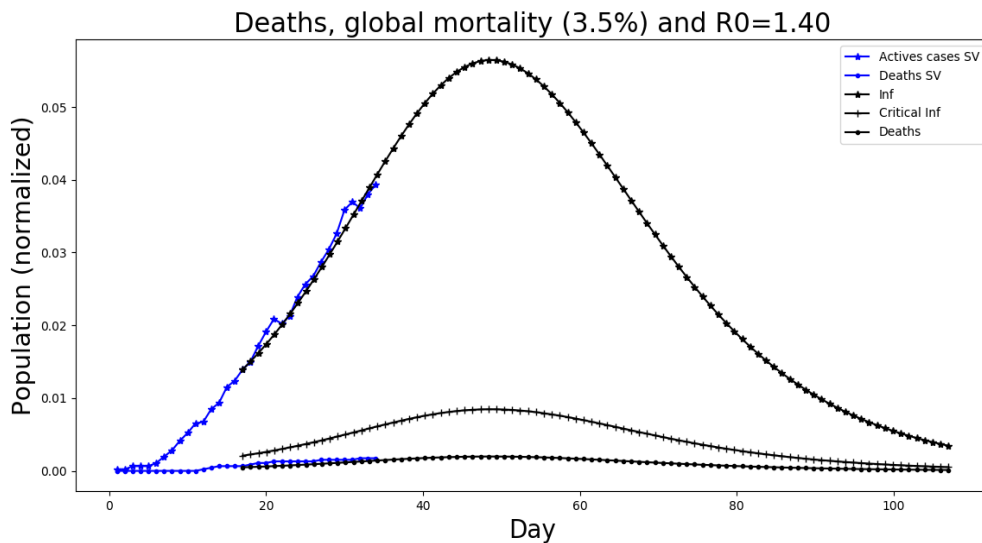

Figure 3: *Comparison between the evolutions of infected, critically infected, and deceased, assuming that the percentage of critically ill infected is about 15% of the total infected, while the deceased is determined by 3.5% of the total infected.*

In the case of Figure 3, it is possible to have up to 259 people in infected state, 15% (39 people) in a critical state, and between 10 and 12 deaths on 49 days after the first infection. The foregoing suggests that with the current measures the disease is being contained, however, it should be noted that the mortality rate was assumed to be 3.5%, being actually a global average rate and not the national one.

CONCLUSIONS

Despite the fact that enough data has already been collected in different countries, the models that are built with them are not entirely reliable to be extrapolated, due to the different way in which the virus and the derived disease can behave, the differences in the measures of containment in each country, and also, by the differences between health systems and their ability to react. This situation complicates the implementation of mathematical simulation and analysis of models in countries where the pandemic has not yet fully developed.

The simulations shows how social dynamics, and government containment decision-making, influenced the evolution of the epidemic. In particular, it is observed that the higher the transmission rate of the β disease, the shorter the time necessary to reach the state of maximum infection. On the other hand, having a low transmission rate β, the probability of contagion between individuals tends to decrease and slows down, the curve flattens and the time to reach the maximum peak is prolonged. This is the way governments are struggling to decrease the intensity of the epidemic outbreak.

From the presented data, it seems that the pandemic in El Salvador has been relatively contained until now, indicating to the population the use of hygienic and protective measures, social distancing and mandatory quarantine, as well as isolating suspicious and positive cases. The parameters α, β, and δ have been evaluated in different ways, based on data from last literature about the topic, and recent statistical information on the progression of the disease in different countries. However, it is clear that these parameters assume particular behaviors, depending on local conditions and they are varying from country to country. Consequently, the results obtained must be taken with reserve regarding its predictive potential.

According to the results obtained, even though the containment measures tend to flatten the curve, a maximum peak is expected between 46 and 52 days after day 0, which according to official reports corresponds to March 18th, 2020, with a percentage of infected cases of up to 7.2% of the population confined in the Containment Centers. This means that the entire process of development and control of the disease could last around 3 or 4 months, as long as the containment conditions are maintained. Relaxing these measures could dramatically change the scenario, rapidly moving it to a situation of greater infection of people and higher morbidity.

The research group has also advanced in the most accurate simulation of the epidemiological phenomenon, using different approaches as time-dependent SIR models, which include new variables and parameters, and require greater computational capacity to run programmatic codes. The results of these calculations are in progress and will be presented in a second article.

REFERENCES

1. Arenas, A. J., González-Parra, G., Moraño, J. A. (2009). Stochastic modeling of the transmission of respiratory syncytial virus (RSV) in the region of Valencia, Spain. Biosys. 96 (3): pp. 206-212

2. Green, D. M., Kiss, I. Z., Kao, R. R. (2006). Parameterization of individual-based models: Comparisons with deterministic mean-field models, J. Theor. Biol., 239(3): pp. 289-297.

3. Gross, T., Blasius, B. (2008). Adaptive coevolutionary networks: a review, J. R. Soc. Interface March 6, 2008 5: pp. 259-27.

4. Hethcote, H. W. (2000). The Mathematics of Infectious Diseases. SIAM REVIEW 42: pp. 599-653.

5. Keeling, M. J., Eames, K. T. D. (2005). Networks and epidemic models, J. R. Soc. Interface 2(4): pp. 295-307

6. Marceau, V., Noel, P. A., Hebert-Dufresne, L., Allard, A., Dube, L. J. (2010). Adaptive networks: Coevolution of disease and topology, Phys. Rev. E 82(3): pp. 036116