Evolution of Contagion by COVID-19 in El Salvador Applying SIR-Dynamic Simulations with the Monte Carlo Method

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The COVID-19 pandemic is at the present in full swing in El Salvador and experience in other countries forces us to make drastic public and health policy decisions to contain the disease. This report presents some estimates of the evolution of the disease under the conditions of social distancing and home quarantine ordered by the authorities. Estimates and projections provide evidence based on SIR-type mathematical models, applying the Monte Carlo method, to establish and evaluate the critical phases of the pandemic and its effects, so that more efficient measures and strategies can be re-evaluated to continue containing the entry into greater critical phases. The time-dependent SIR was used to calculate differents paramenters of pandemic in the country, using official data from March 18 up May 4. We found the recovery rate has a value of $\hat{\alpha} = (0.0658 \pm 0.0267)1/t$ with t measured in days, while the transmision rate is $\hat{\beta} = (0.108 \pm 0.001)1/t$, therefore, the basic reproduction number was calculated with the value of $\hat{R_0} = (3.18 \pm 0.21)$. The time-dependent SIR also was used to calculate the projections for infected cases and recovered cases, however, we analyzed the implementation of the Monte Carlo method in the numerical solution of infected cases. The maximum peak of the contagion is calculated using the solutions for infected cases, with and without applying Monte Carlo method, and it predicts between 1,320 and 1,488 individuals in infected state, and projecting that the time window for the critical period of the epidemic will be between the first and second week of June, while it would be attenuating only in mid-August. The error analysis include the error by the parameters and the prediction error.

Keywords: Covid-19, El Salvador, SIR Model, Monte Carlo method, basic reproduction number, transmission rate, recovery rate, fatality rate.

I. INTRODUCTION

According to the World Health Organization (WHO), the epidemiology is the study of the distribution and determinants of states or events (particularly diseases) related to public health, and the application of these studies to the control of diseases and other health problems. Epidemiological events caused by the outbreak of a pathogen that eventually will become an epidemic or even pandemic, can lead to serious threats to public health, including the loss of many human lives, as well as large economic and material losses.

The WHO has also defined the COVID-19 pandemic in 4 phases: i. Import cases phase; ii. Containment phase; iii. Community contagion phase, and; iv. Sustained transmission phase. El Salvador is already in the community contagion phase, even when the containment was dealt with, almost timely, through policies such as closings of ports, universities and schools, quarantine for migrants and social isolation. This measures were designed in order to reduce contact rates in the population and therefore reduce virus transmission, however the cases have increased significantly in recent weeks.

Consequently, it seems important to carry out studies on the evolution of a pathogen such as this novel Coronavirus, which has quickly become a pandemic, and is putting health systems worldwide in crisis. One of the most useful methods to study the evolution of the pandemic that we are facing, is the development and application of deterministic or stochastic mathematical models, which allows to estimate the evolution of the disease, in order to correctly guide decision-making to contain and minimize their effects.

For the study of epidemiological phenomena, mathematical models are used, most of which are a variant of the SIR model (Susceptible, Infected and Recovered) developed in 1927 by Kermack and McKendrick [1]. In this model, the population is divided into different groups, according to their status during an epidemic outbreak. This type of model can be simulated using a system of differential equations or by other methods [2–4].

A variant of the SIR epidemiological model considers the variables and parameters of the time-dependent equations, describing the course of the infectious disease, from a susceptible population ($S(t)$), which comes into contact with an infected population ($I(t)$); and once the infection period is over, the individual enters in a recovered state ($R(t)$), which may be retained for a period of immunity to the pathogen. The speed of contagion and the way in which the population is able to self-recover from the disease or not, determines whether it evolves into an epidemic or pandemic, as well as the possibility of further outbreaks or reinfections, and either the disease remains endemic or it becomes stationary between the population [3, 5].

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The SIR model is a basic method used to simulate differents scenarios. The transmision rate is heterogeneous across countries and far exceeds the recovery rate, which enables a fast spread [6]. In Italy, a Time-Dependent SIR was proved, and it concludes the usefulness of the Monte Carlo Methods in order to get better approximations because the susceptible populations is non-easy to determinate [7]. In [8] it is defined a simple discrete time stochastic SIR-type epidemic model to understand the spread of the COVID-19.

In order to study the evolution of the COVID-19 pandemic in El Salvador, we proposed a modified version of the time-dependent SIR model developed in [9], using a fatality parameter to analyze the possible evolution scenarios of the disease. Then, we use Monte Carlo method to introduce random variables in our simulation, as an extension of our research. The SIR model provides a first approach to mathematical models of epidemiological prediction, traditionally used to describe other epidemic outbreaks at a historical and global level [5].

The rest of the article is structured as follows: In Section II, we introduce basic concepts of the SIR Model and the set of differential equations that predict the behavior of the disease. A review of the time-dependent SIR Model is presented, considering the analysis of the fatality parameter in the time-dependent SIR model, and including random variables on it. In section III, we analized the transmision rate, recovered rate, basic reproduction number, fatality rate and the simulation for the number of infected people. In section IV we conclude about the numerical results and we add some suggestions.

II. TIME-DEPENDENT SIR MODEL

A. SIR model with fatality rate

The equations for the typical SIR model including fatality rate are

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta \frac{S\left(t\right) I\left(t\right)}{N} + \Theta \alpha I\left(t\right), \tag{1}$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta \frac{S\left(t\right) I\left(t\right)}{N} - \alpha I\left(t\right), \tag{2}$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \left(1-\Theta\right) \alpha I\left(t\right), \tag{3}$$

where, α is the recovery rate, β is the transmission rate and Θ is the fatality rate, with a value of 0 for non-fatality and a value of 1 for 100% of fatality over all infected people. In [2] and [10], is presented the SIR Model considering natural deceased and the deceased caused by the spread of the COVID-19, nevertheless in our study, we assume there is not natural deceased in our population of interest. The typical SIR models recovered in the $\Theta \to 0$ limit. Therefore, we can orderly sum it to get:

$$\frac{\mathrm{d}(S+I+R)}{\mathrm{d}t} = 0, \tag{4}$$

This implies that $S(t) + I(t) + R(t) = N$, where N is the total population of interest. The model is known as Susceptible-Infected-Recovered (SIR) model, which defines three states: the susceptible state is a person without the disease at time t. The infected state is referred to a sick person or an asymptomatic person at time t who may infect another healthy person (susceptible). The recovered state is referred to a healed person of the disease at time t. The recovered state is due to an autoimmunity development or because of a cure. Some authors consider that in case $\Theta = 0$, the recovered state includes deceased. Therefore, $S(t)$, $I(t)$ and $R(t)$ represent susceptible, infected, and recovered people at a t time, respectively.

B. Time-Dependent SIR Model

In order to measure the transmission and recovery rates is necessary to perform a time-dependent SIR model. The typical SIR model has two constants: β as the transmission rate, which implies that each individual has an average of β contacts with random people, or in a simple way, the number of infected people per day. The α constant implies how many people are recovered per day. In general, they do not depend on time (SIR Model), but both of them are varying on time, so, we assume that $\alpha = \alpha(t) \geq 0$, $\beta = \beta(t) \geq 0$ and $\Theta = \Theta(t)$, with $0 \leq \Theta(t) < 1$, where Eqs. (1), (2) and (3) become:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\beta\left(t\right) \frac{S\left(t\right) I\left(t\right)}{N} + \Theta(t) \alpha\left(t\right) I\left(t\right), \tag{5}$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta\left(t\right) \frac{S\left(t\right) I\left(t\right)}{N} - \alpha\left(t\right) I\left(t\right), \tag{6}$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \left(1-\Theta(t)\right) \alpha\left(t\right) I\left(t\right). \tag{7}$$

Naturally, Θ is determined from data or fixed to global values. Its sum is still valid:

$$\frac{\mathrm{d}(S+I+R)}{\mathrm{d}t} = 0, \tag{8}$$

So, $S(t)$, $I(t)$ and $R(t)$ satisfy Eqs. (1), (2) and (3). The time discretization [1] implies to rewrite Eqs. (5), (6) and (7) as:

$$S_{i+1} = S_i - \beta_i \frac{S_i I_i}{N} + \Theta_i \alpha_i I_i,$$

$$I_{i+1} = I_i + \beta_i \frac{S_i I_i}{N} - \alpha_i I_i,$$

$$R_{i+1} = R_i + \left(1-\Theta_i\right) \alpha_i I_i,$$

clearly, for $T \geq t$ we can fix $S_{i-1} \approx N$ because at the beginning of the spread the infected cases appear in small

[1] Like $dS(t) \approx S(t+1) - S(t)$ and $S(t+1) = S_{i+1}$ for $i \geq 0$

quantities, for a population of 1000 people, and 10 first active cases $990/1000 = 0.99$, so, reordering:

$$S_{i+1} = S_i - \beta_i I_i + \Theta_i \alpha_i I_i, \tag{9}$$
$$I_{i+1} = I_i + \beta_i I_i - \alpha_i I_i, \tag{10}$$
$$R_{i+1} = R_i + (1 - \Theta_i)\, \alpha_i I_i, \tag{11}$$

Eqs. (9) and (10) give us some clue, because the numerical calculus for I_{i+1} and S_{i+1} do not preserve the population N although S_0 at $i = 0$ is $S_0 = N$, that implies an independence of the susceptible population in I_i. So, the main goal is to measure α_i and β_i, from Eq. 11, we got the equation for α_i:

$$\alpha_i = \frac{1}{1 - \Theta_i} \frac{R_{i+1} - R_i}{I_i}, \tag{12}$$

and using 10 and 12, we get β_i:

$$\beta_i = \frac{I_{i+1} - I_i + \frac{R_{i+1} - R_i}{1 - \Theta_i}}{I_i}, \tag{13}$$

Eqs. (12) and (13) generate a point-value of α and β for each t. If we know the historical data from 0 to t, we got α and β from 0 to $t - 1$, the values for transmission and recovery data, respectively. This methodology appears in the scientist literature for SIR model without fatality rate [9]. Here, we can define the fatality rate as:

$$\Theta_i = \frac{d_i}{I_i + R_i}, \tag{14}$$

where d_i, which was obtained from officially published information, represents the number of deaths, besides I_i is the number of infected people and R_i is the number of recovered people, at i time each. $\Theta_i \times 100$ is the porcentage of fatality. The R_0 is the basic reproduction number, defined in the introduction as the average number of secondary infections that occur when one infective is introduced into a completely susceptible host population [2]. Calculated as:

$$R_0 = \frac{\beta}{\alpha}, \tag{15}$$

this number is very important because it is used to check whether the disease will become an outbreak ($R_0 \geq 1$). In this research, R_0 also depends on t as:

$$R_{0i} = \frac{\beta_i}{\alpha_i}. \tag{16}$$

Using Eqs. (12) and (13) is possible to calculate R_0 from historical data, thus we got a numerical measure from 0 to $t - 1$. The algorithm is shown in Algorithm 1

Algorithm 1: determination of $\beta(t)$, $\alpha(t)$, $\Theta(t)$ and R_0 for Time-Dependent SIR Model

Require: Inf, Rec, Fal Array ▷ The historical data array to perform.
Ensure: $\alpha, \beta, \Theta, R_0$ ▷ The array for our data of interest
1: **procedure** TDSIR(Inf, Rec, Fal) ▷ Definition of Function
2: Using 14 calculate $\Theta(t)$ as array.
3: From $\Theta(t)$ calculated, use 12 to calculate $\alpha(t)$ as array.
4: From $\Theta(t)$ calculated, use 13 to calculate $\beta(t)$ as array.
5: From $\beta(t)$ and $\alpha(t)$ calculated, use 16 to calculate $R_0(t)$ as array.
6: **return** a, b, t, r ▷ $\alpha, \beta, \Theta, R_0$
7: **end procedure**

C. Determination of $\beta(t)$, $\alpha(t)$, $\Theta(t)$ and R_0 for OLS Methods

Given a set $[x_1, x_2, x_3, ..., X_N]$ of independent variables and another set $[y_1, y_2, y_3, ..., y_N]$ of dependent variables, from 1 to N, we can construct a $f(x, m)$ model function, where m is an adjustable parameter through of residue

$$r_i = y_i - f(m, x_i) \tag{17}$$

and the sum of the residue's squares:

$$S = \Sigma(r_i)^2. \tag{18}$$

The idea of the optimization implies the need to minimize the sum of the residue's square in order to get m. For our case:

$$\hat{\beta}(t) = m_1 t + b_1, \tag{19}$$
$$\hat{\alpha}(t) = m_2 t + b_2, \tag{20}$$
$$\hat{\Theta}(t) = m_3 t + b_3, \tag{21}$$
$$\hat{R_0}(t) = m_4 t + b_4, \tag{22}$$

where m_j is calculate as

$$m_j = \frac{N\Sigma xy - \Sigma x \Sigma y}{N\Sigma x^2 - [\Sigma x]^2}, \tag{23}$$

and b_j as

$$b_j = \frac{\Sigma y \Sigma x^2 - \Sigma x \Sigma xy}{N\Sigma x^2 - [\Sigma x]^2}, \tag{24}$$

The algorithm for determination of lineal adjust for $\beta(t)$, $\alpha(t)$, $\Theta(t)$ and R_0 for OLS method is shown in Algorithm 2.

From Eqs. (9), (10), (11), (19), (20) and (21), we can predict infected and recovered people at the time $t + 1$ as:

Algorithm 2: determination of linear fit for $\beta(t)$, $\alpha(t)$, $\Theta(t)$ and R_0 for OLS method

Require: A, T Array ▷ The data array to perform.
Ensure: m, b ▷ the slope and intercept of mT+b
procedure OLS(a, t) ▷ Definition of Function for OLS
  Using 23 calculate m
  Using 24 calculate b
  return m, b ▷ the m is slope and b is the intercept
end procedure
procedure ORDER(m, b, TF) ▷ Definition of Function for new arrays
  $T = [0, TF]$ ▷ An array for T
  Using m_i and b_i get an array for $\beta(t)$, $\alpha(t)$ and $\Theta(t)$ through Eqs. 19, 20 and 21.
  return $\hat{\beta}(t)$, $\hat{\alpha}(t)$ and $\hat{\Theta}(t)$ ▷ As array
end procedure

$$S_{i+1} = S_i - \frac{\hat{\beta}(t) I_i S_i}{N} + \hat{\Theta}(t)\hat{\alpha}(t) I_i, \tag{25}$$

$$I_{i+1} = I_i + \frac{\hat{\beta}(t) I_i S_i}{N} - \hat{\alpha}(t) I_i, \tag{26}$$

$$R_{i+1} = R_i + \left(1 - \hat{\Theta}(t)\right) \hat{\alpha}(t) I_i, \tag{27}$$

using linear fit for transmission, recovery and fatality rate. We need R_0, I_0, and N to run the solution for Time-Dependent SIR Model.

Note that we do not apply the $S_i \approx N$ approximation in Eq. 25 and Eq. 26, because for $T \geq t$, being T a long period of simulation, we cannot hold that approximation, although the approximation is valid at the beginning of the spread.

The algorithm used in our simulations for $I(t)$, $S(t)$, $R(t)$ of Time-Dependent SIR Model is shown in Algorithm 3.

Algorithm 3: Simulation for $I(t)$, $S(t)$, $R(t)$ For Time-Dependent SIR Model

Require: $I0, R0, F0, D0$ ▷ Initial condition for infected, recovered, deceased people and the day of the initial conditions.
Require: $\hat{\alpha}(t), \hat{\beta}(t), \hat{\Theta}(t)$ ▷ Array of rates calculated in Algorithm 2.
Ensure: S, I, R ▷ The array of susceptible, infected and recovered people.
procedure TDSIRM$(I0, R0, S0, \hat{\alpha}(t), \hat{\beta}(t), \hat{\Theta}(t))$ ▷ Definition of Function for TDSIR arrays
  Using Eqs. $S0, I0, R0$ and $\beta_{D0}, \alpha_{D0}, \Theta_{D0}$ calculate for $i+1$ using 9, 10 and 11.
  return $S(t)$, $I(t)$ and $R(t)$ for $t \geq D0$ ▷ Array of simulated data for S,I and R.
end procedure

D. Time-Dependent SIR Model with Monte Carlo Method

The Monte Carlo method is an numerical approach for solving math problems using random variables [11]. Our proposal considered the addition of a random variable in $I(t)$, which is defined in Eq. 26. The intention was to improve our numerical solutions using those methods, since we can perform a solution for Eqs. 1, 2, 3 for each $\hat{\beta}(t)$, $\hat{\alpha}(t)$, $\hat{\Theta}(t)$, using linear fit or not; however, it needs more computational resources, time, etc.

The Monte Carlo method provides a better approach for introducing random variables in deterministic models in order to include noise or random behavior in the simulation of our specific problem [12].

In Eq. 26, we get:

$$\begin{aligned} I_0 &= I_0 \\ I_1 &= I_0 + \frac{B_0 I_0 S_0}{N} - \alpha_0 I_0 \\ I_2 &= I_1 + \frac{B_1 I_1 S_1}{N} - \alpha_1 I_1 \\ &= I_0 + \frac{B_0 I_0 S_0}{N} - \alpha_0 I_0 + \frac{B_1 I_1 S_1}{N} - \alpha_1 I_1 \end{aligned}$$

And so on...

New daily infected cases are calculated as:

$$new_{i+1} = (I_{i+1} - I_i) + (R_{i+1} - R_i) \tag{28}$$

if there are not deaths.

However, the new daily infected cases in the real world are not easy to predict, for instance, we propose to modify Eq. 26 as

$$I'_i = I_i + a(\delta_1 - \delta_2), \tag{29}$$

where the first term of the right side is calculated with Eq. 26. The second terms are calculated using the standard deviation of average new cases from historical data, a represents the deviation standard of new cases, therefore, $\delta_{1,2}$ represents the random variable from 0 to 1, which means that $a\delta_{1,2}$ lies in the $[-a, a]$ interval. Also, the derivative is:

$$\frac{\mathrm{d}I'}{\mathrm{d}t} = \frac{\mathrm{d}I}{\mathrm{d}t} \tag{30}$$

and still satisfies Eq. 2, because the random variable does not depend on time. The terms $a(\delta_1 - \delta_2)$ are only an initial condition for infected cases of the problem. The new sets of Time-Dependent SIR with Monte Carlo method are:

$$S_{i+1} = S_i - \frac{\hat{\beta}(t) I_i S_i}{N} + \hat{\Theta}(t)\hat{\alpha}(t) I_i, \tag{31}$$

$$I_{i+1} = I_i + \frac{\hat{\beta}(t) I_i S_i}{N} - \hat{\alpha}(t) I_i + a(\delta_1 - \delta_2), \tag{32}$$

$$R_{i+1} = R_i + \left(1 - \hat{\Theta}(t)\right) \hat{\alpha}(t) I_i, \tag{33}$$

This proposal is basically a stochastic-deterministic model, because the numerical solutions for SIR Model are perturbed due to a random variable based on the standard deviation for new daily cases of contagion.

The algorithm used in our simulations for $I(t)$, $S(t)$, $R(t)$ of Time-Dependent SIR Model with Monte Carlo method is shown in Algorithm 3.

Algorithm 4: Simulation for $I(t)$, $S(t)$, $R(t)$ For Time-Dependent SIR Model with Monte Carlo method

Require: $I0, R0, F0, D0$ ▷ Initial condition for infected, recovered, deceased people and the day of the initial conditions.

Require: $\hat{\alpha}(t), \hat{\beta}(t), \hat{\Theta}(t)$ ▷ Array of rates calculated in Algorithm 2.

Ensure: S, I, R ▷ The array of susceptible, infected and recovered people.

1: **procedure** TDSIRM($I0, R0, S0, \hat{\alpha}(t), \hat{\beta}(t), \hat{\Theta}(t)$, a) ▷ Definition of function for TDSIR arrays

2: Using $S0, I0, R0$, $\beta_{D0}, \alpha_{D0}, \Theta_{D0}$ and a calculate for $i+1$ using 31, 32 and 33.

3: **return** $S(t)$, $I(t)$ and $R(t)$ for $t \geq D0$ ▷ Array of simulated data for S, I and R.

4: **end procedure**

E. Error Analysis

The error analysis was calculated in two ways:

- Mean and standard deviation for $\hat{\beta}, \hat{\alpha}, \hat{\theta}$ and $\hat{R_0}$ in the numerical data and linear fit.
- Predictive error for $I(t)$ in the time-dependent SIR model and time-dependent SIR model with Monte Carlo method vs the real infected cases. Using:

$$Error = \frac{|real - simulated|}{real} \times 100 \tag{34}$$

For each I_i obtained from Eqs. 10 and 32.

The standard deviation that measures the dispersion of the data, relative to its mean value and determines the variation in each data point, is useful to examine the accuracy of calculated β and α parameters and its linear fit. In general, the best fit will be for standard deviation nearest to zero.

III. NUMERICAL RESULTS

A. Data

The actual data used in this work corresponds to those officially communicated by the government of El Salvador, from the identification of the first contagion, on March 18, registering daily infected, recovered and deceased cases until May 7, 2020, when the latest updates for the simulation were released (see Fig. 1).

B. Transmission and recovery rates

The transmission and recovery rates have been calculated with Eqs. 19 and 20, as we show in Table I we choose data from April 4 to May 7 in order to make a linear fit because it need a R_0 finite.

Parameter	m $(1/t^2)$	b $(1/t)$
$\hat{\alpha}$	0.00061293	0.0199291
$\hat{\beta}$	4.85504262e-05	1.06489232e-01

TABLE I. slope and intercept from April 4 to May 7

The α inverse is related to the recuperation time of the disease.

α and β was plotted by using real historical data, published by the Government of El Salvador, in Fig. 2. We can see that β decreases rapidly while α retains its shape but using the linear fit of α.

C. Fatality rate

The fatality rate and its linear fit, as described in Eq. 21 is shown in Fig. 3 and its numerical result is presented in Table II. We note a decreasing behavior for $\hat{\Theta}$ and Θ.

Parameter	m $(1/t)$	b
$\hat{\Theta}$	-0.00117411	0.07271722

TABLE II. Slope-point for $\Theta(t)$ from April 4 to May 7.

We also plot a fatality global rate of 6.9%, in order to compare to the historical data of deceased in El Salvador.

D. Basic reproduction number

The basic reproduction number is calculated using Eq. 27, which value is calculated by counting at least 15 days after the first confirmed case (April 4), because R_0 depends on β and α, and α is zero for unrecovered people from Covid-19, however, the first recovered person occurrs at April 4. The linear fit of R_0 defined as $\hat{R_0}$ is shown in Table III.

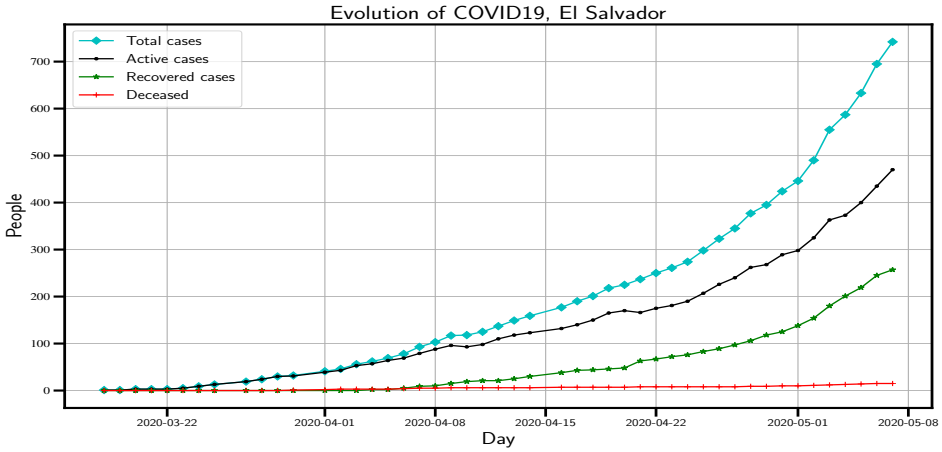

FIG. 1. Official data from the Goberment of El Salvador. From March 18 up May 4, El Salvador has 742 confirmated of cases. The 63.34% of the confirmated cases are in the active cases class, 34.63% are recovered people and 2.02% are deceased. The mean of new positives cases is 15.42 daily confirmated cases, however, the standard deviation is 15.32, that implies a range of $[0 - 30.74]$ new daily infected cases.

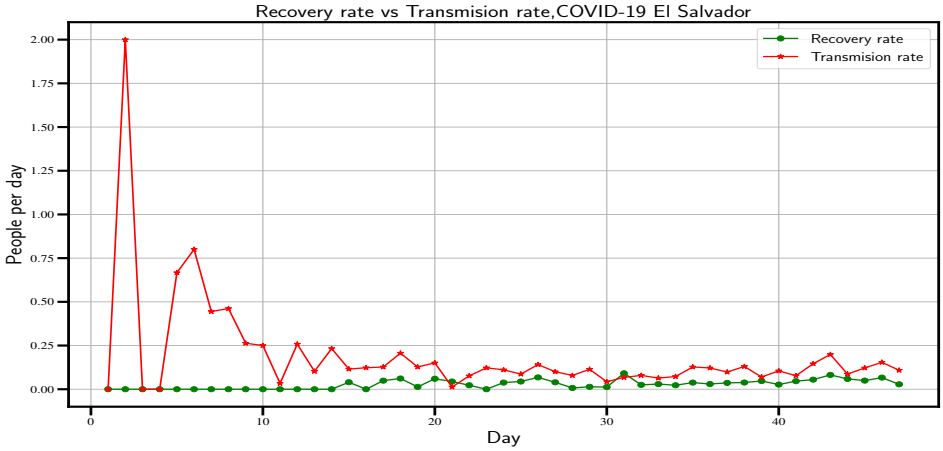

FIG. 2. Time-Evolution for transmission and recovery rates since March 18. For the linear fit, we choose the first recovered person until April 4, because R_0 is infinite if $\alpha = 0$

Parameter	m $(1/t)$	b
$\hat{R_0}$	-0.01549431	3.56146089

TABLE III. Slope-point for $\hat{R_0}$ from April 4 to May 7, the first recovered person is determinant for the initial value of R_0. At $t = 0$, the linear fit predicts a maximum value of $R_0 = 3.56$.

The Fig. 4 shows the R_0 and $\hat{R_0}$ data, there are two maximum values for R_0, but the linear fit predicts a reduction of $\hat{R_0}$ according to the last data of R_0. There are four values of R_0 in the range $R_0 \leq 1$, that provide a decreasing in the spread of the COVID-19 disease.

The error analysis for R_0 and $\hat{R_0}$ is discussed in III F.

E. Time-Evolution for TDSIR and TDSIR MC

The time evolution in the spread of the disease is calculated by two differents ways. For Time-Dependent SIR model (TDSIR) using Eqs. 10 and 11, and applying a Time-Dependent SIR model with Monte Carlo (TDSIR MC) using random variables with Eqs. 32 and 33.

First of all, we have to define the initial susceptible population, although this value is unnecesary over the $S_i \approx N$ approximation, where N is the initial population, in order to calculate β, α, Θ and R_0. However, to simulate a complete period of the disease is necessary to make that approximation. The criterion selected are:

- According to Table V, $\hat{R_0}$ varies from 2.97 to 3.39, stimated for El Salvador case, cionsidering that the population in containment centers for infected people is nearest of 4,600 people. Also it is possible

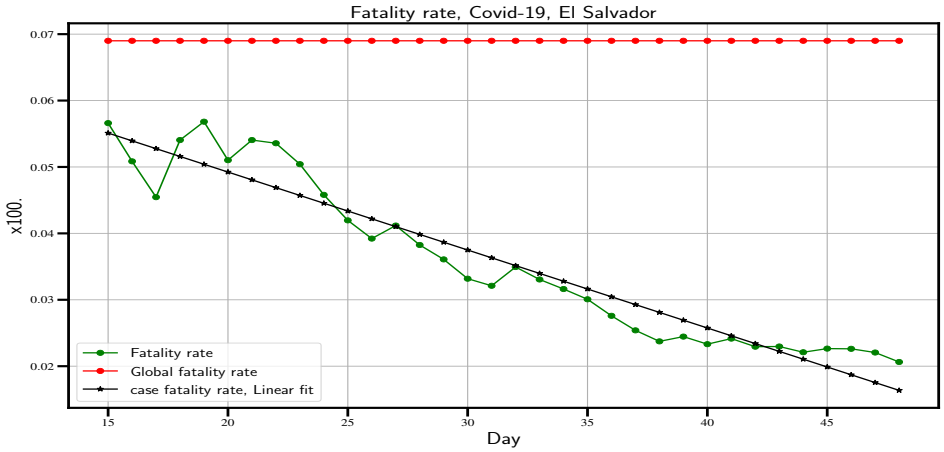

FIG. 3. Plot of the Eqs. 21, 14 and 0.069 (global value). The latest data shows a decreasing of the case fatality rate of El Salvador, keeping on 2% of deceased due to the Covid-19 spread.

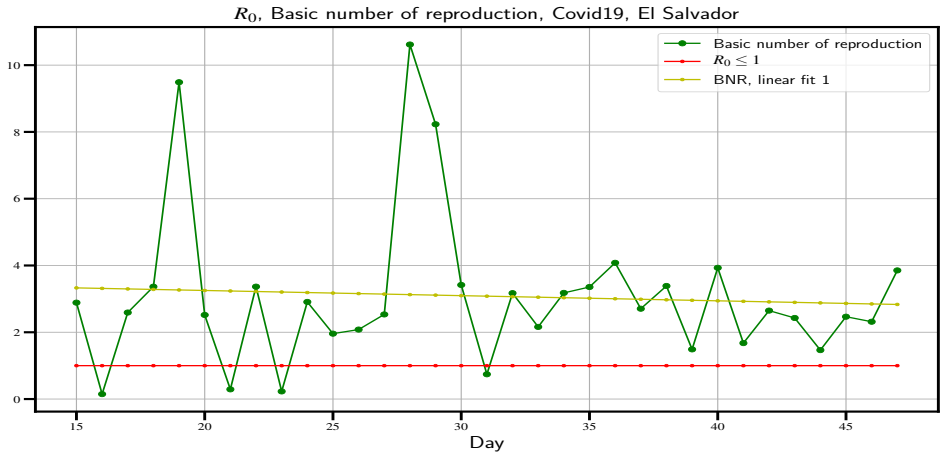

FIG. 4. The time-evolution for the basic reproduction number. In this figure are shown R_0 and $\hat{R}_0$, the linear fit predicts a decreasing on time, and the mean values is on Table V.

to fix about 12,000 susceptible people as an initial value for N.

- In the Table IV, we can see from Worldometer, the next values from some of the nearest countries to El Savador:

Country	Total cases	population (million)	percentage rate of total infected (%)
Guatemala	967	17.9	0.0005
Honduras	1823	9.9	0.018
Costa Rica	769	5.0	0.015
Panamá	8282	4.3	0.1926
El Salvador	889	6.4	0.013

TABLE IV. Local rates of infected population per country.

El Salvador has about 6.4 million population, according to Tab. IV, we have a range of susceptible population using the percentage of total infected cases per country. In the best and worst cases, we could have a minimun of 320 and a maximun of 12,326 infected cases at the peak of the curve. However, for simulation purposes, we estimate $N = 12,000$ as a susceptible population.

Now, with $N = 12,000$ and linear fits of α, β and Θ tabulated in Tables I and II, we simulated the number of active and recovered cases for $15 - 150$ days via TDSIR and TDSIR MC.

The Fig. 5 shows the maximum number of active cases for TDSIR and TDSIR MC obtaining about 11% and 12.4%, respectively, for the range of $83 - 87$ days after the first case of the defined population $(12,000)$. The prediction error is analized in section III F. Therefore, the predicted value for infected cases is according to the methodology selected.

The Fig. 6 shows the prediction for 10 days before the last recovered person for TDSIR and TDSIR MC. The

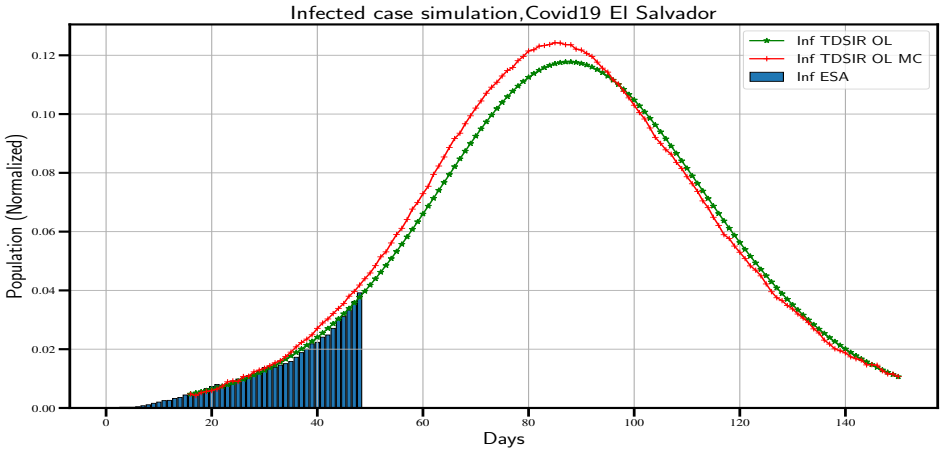

FIG. 5. Simulation of active cases of Covid-19 in El Salvador. We can see the range of maximum values of active cases through TDSIR and TDSIRMC method.

prediction error is briefly discussed in section III F.

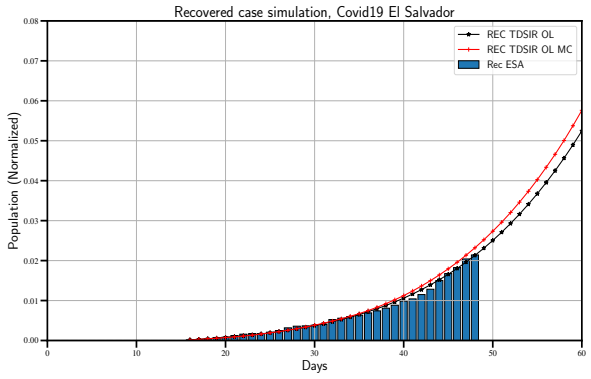

FIG. 6. Plot of the recovered people from historical data until May 4. The simulated cases are shown using the TDSIR and TDSIR MC method. We can see in the TDSIR case a better approximation, however, is necessary more future research.

F. Error Analysis

For each parameter, we measured the mean value and its standard deviation, those values are in Table V.

Parameter	Mean	STD
α	0.0389	0.0215
$\hat{\alpha}$	0.0346	0.009
Θ	0.036	0.012
$\hat{\Theta}$	0.0445	0.0166
β	0.1080	0.0394
$\hat{\beta}$	0.1077	0.0007
R_0	3.0811	2.2697
$\hat{R_0}$	3.1896	0.2191

TABLE V. Mean and STD for parameters

The α and $\hat{\alpha}$ are distinguishable because α is calculated via Eq.12 and its data is used to approach a linear fit defined as $\hat{\alpha}$, using Eq. 20. That condition produces a different value for its mean value and standar deviation. The mean and standar deviation of α implies a range of $[0.0171, 0.0604]$ as recovery rates, its inverse range is $[16.55, 58.48]$ days, the inverse is defined as the recovery time of a sick person. The 58.48 days, imply a big error, however, 16.55 is according to real data from recovered people of COVID-19. On the other hand, for $\hat{\alpha}$ we got a range of $[0.0256, 0.043]$ for $T = [15, 45]$ days, those values are out of real recovery time range, although, in case $T = [15 - 150]$ we have a mean of 0.0658 and STD of 0.0267, that implies a range of $[0.0391, 0.0925]$ and its inverse has a range of $[10.81, 25.57]$ days of recovery time for a sick person of COVID-19, with that value an infected person could become a recovered person in a range of $10 - 25$ days.

Now, in case of R_0 we got a range of $[0.81, 5.35]$ from historical data, its mean is 3.08 in El Salvador. In case of the linear fit, we got a range of $[2, 97, 3.41]$ and a mean of 3.20, both of them are according to international values of R_0 for COVID-19 [13].

Briefly, we discussed the case of β and $\hat{\beta}$, bassically, is defined as transmisión rate or $\alpha \times R_0$. Both of them have a mean of 0.10 people per day, that is 0.10 new infected for one infected person. We expect that the curve shown in Fig. 2 has an improvement in the next few days, because the $\alpha(t) < \beta(t)$ relation must change to $\alpha(t) > \beta(t)$ when we got about the maximum infected value.

In regards to the case of fatality rate, we got a value of 3.6% and 4.4% calculated as a mean for Θ and $\hat{\Theta}$, respectively. That value implies that the 3.6% or 4.4% of infected cases migth die. The lastest data of deceased due to COVID-19 in Fig. 3 shown a 2.2% of case fatality rate.

The error prediction for infected cases via TDSIR and TDSIR MC are shown in Fig. 7.

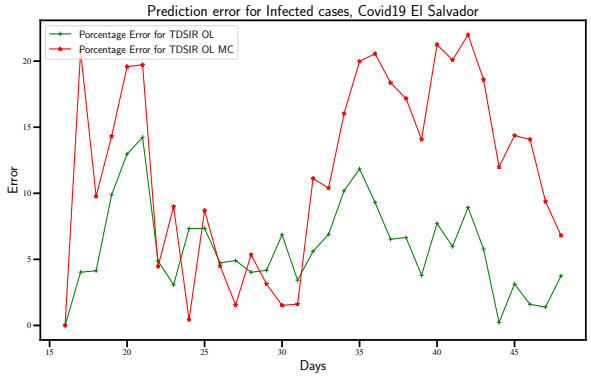

FIG. 7. Prediction error for infected cases using TDSIR and TDSIR MC from April 5 to May 4. The TDSIR MC and TDSIR present a mean value of 11.8% and 5.9%, respectively. Error prediction has been based in the historical data of infected cases in El Salvador.

The mean prediction error is an useful tool because it gives us a variation of cases in the selected range.

For TDSIR and TDSIR MC, the maximum infected cases are 11.0% and 12.4% of $12,000$ people that are equivalent to $1,320$ and $1,488$ cases, respectively. The error prediction for TDSIR has a mean value of 5.9%, that implies the maximum infected cases are in range $[1242, 1398]$ individuals, while the mean error for TDSIR MC is around 11.8%, which indicates the maximum infected cases are in range $[1312, 1664]$ individuals.

In the case of error prediction of recovered people, we plot the error prediction in Fig. 8. The prediction error does not present much variation between the TDSIR and TDSIR MC because the random variable was added in infected cases from methodology in Eq. 32.

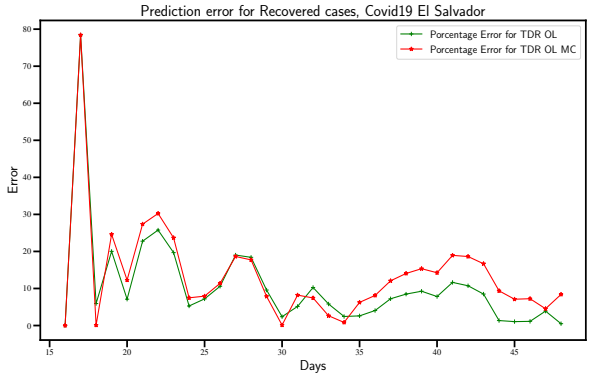

FIG. 8. Prediction error for recovered cases using TDSIR and TDSIR MC from April 5 to May 4. The TDSIR MC and TDSIR presents a maximum value of 30% and 25%, respectively, ignorating the point data of 80% for the second point. Error prediction was calculated using the historical data for recovered cases in El Salvador.

IV. CONCLUSIONS

In this work, ana innovative methodology has been presented, that is capable of taking advantage of the official data of infected, recovered and deceased, to make an estimate of the actual progression of those infected, and consequently a forecast of the time when the peak of the epidemic will be reached, and how many people it will affect at the end. The model used is an original variant of the well-known SIR model.

The time-dependent SIR model is used in order to stimate: transmission, recovered and fatality rates, as also, a simulations of the infected cases using Monte Carlo methods as a random variable. Using the results of transmision and recovered rates is possible to measure the basic reproduction number. By this point, we preffer the linear fit in order to estimate the rates defined. For recovered rate, we have the numerical results of $\hat{\alpha} = (0.0658 \pm 0.0267)1/t$, with t means days. It implies that the sick person would be in the recovered state in 10-25 days in El Salvador.

The basic reproduction number R_0 calculated applying TDSIR, and using data from the last 4 weeks is $\hat{R_0} = (3.18 \pm 0.21)$, it means that one infected person migth spread another 3 person as average. therefore the current measures, quarantine and social distancing, taken in the country will be the key to improve this scenario, or at least prevent it from worsening.

According to the implemented model and the adjustment of parameters based on the official information provided by the government of El Salvador, the time window of the critical period of the epidemic will be between the first and second week of June, while it would be attenuating in mid-August, reaching an estimated of $(1,320 \pm 78)$ people caculated through of TDSIR simulation or $(1,488 \pm 176)$ people calculated using the TDSIR MC simulation, who will posible fall in an infected state, and 15 per cent of these (198-223 people), falling in a critical condition, at the peak of the curve, about 83-87 days later than the zero day, which corresponds to the day of the first contagion detected. The foregoing suggests that with the current measures the disease is being contained so far.

Briefly, we conclude that the fatality rate calculated as $\hat{\Theta} = (4.4 \pm 1)\%$, indicates that the pandemic of the COVID-19 in El Salvador would cause between $45 - 71$ deceased after the TDSIR simulation, while after the TDSIR MC simulation would cause between $51 - 80$ deceased at the maximum peak of infected cases. Therefore, the last data of the fatality rate is 2.2% as it shown in Fig. 3, while the fatality global rate is 6.9%. El Salvador presents a low fatality rate respect to the global one.

The codes were implemented by Phyton for this report, and it is expected to serve as the basis for periodic monitoring of the local evolution of the epidemic and its parameters and of course other kind of deceases. As more information becomes available, estimates may become more accurate. The lack of some information, such

as the problems due to under-registry, the decisions made on the number of daily tests carried out by the Ministry of Health, and the criteria of those to whom they are being applied, affect the criteria taken in modeling, and tends to increase the error by the here estimated parameters.

[1] W. O. Kermack, A. G. McKendrick, and G. T. Walker, Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character **115**, 700 (1927).

[2] H. H. W, SIAM REVIEW **42**, 599 (2000).

[3] A. A. J, González-Parra, G, and M. J. A, Biosystems **96**, 206 (2009).

[4] G. D. M, K. I. Z, and K. R. R, Journal of Theoretical Biology **293**, 289 (2006).

[5] K. M. J and E. K. T. D, J. R. Soc. Interface **2**, 295 (2005).

[6] A. A. Toda, "Susceptible-infected-recovered (sir) dynamics of covid-19 and economic impact," (2020), arXiv:2003.11221 [q-bio.PE].

[7] G. C. Calafiore, C. Novara, and C. Possieri, "A modified sir model for the covid-19 contagion in italy," (2020), arXiv:2003.14391 [physics.soc-ph].

[8] X. Bardina, M. Ferrante, and C. Rovira, "A stochastic epidemic model of covid-19 disease," (2020), arXiv:2005.02859 [q-bio.PE].

[9] Y.-C. Chen, P.-E. Lu, C.-S. Chang, and T.-H. Liu, "A time-dependent sir model for covid-19 with undetectable infected persons," (2020), arXiv:2003.00122 [q-bio.PE].

[10] D. de Pereda Sebastián, *Modelización matemática de la difusión de una epidemia de peste porcina entre granjas*, Master's thesis, Universidad Complutense de Madrid (2010).

[11] Y. M. Sobol, *A primer for the Monte Carlo method* (CRC Press, Washington DC, 1994).

[12] H. P. Langtangen, *A Primer on Scientific Programming with Python*, 5th ed. (Springer-Verlag Berlin Heidelberg, Germany, 2016).

[13] L. Q, G. X, W. P, and et al, N Engl Journal Med **382**, 1199 (2020).