# Novel Approach for Monte Carlo Simulation of the new COVID-19 Spread Dynamics

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**Abstract**

*Abstract.* A Monte Carlo simulation in a novel approach is used for studying the problem of the outbreak and spread dynamics of the new virus COVID-19 pandemic in this work. In particular, our goal was to generate epidemic data based on the natural mechanism of the transmission of this disease assuming random interactions of a large-finite number of individuals in very short distance ranges. In the simulation we also take into account the stochastic character of the individuals in a finite population and given densities of people. On the other hand, we include in the simulation the appropriate statistical distributions for the parameters characterizing this disease. An important outcome of our work, besides the produced epidemic curves, is the methodology of determination of the effective reproductive number during the main part of the new daily cases of the epidemic. Because this quantity constitutes a fundamental parameter of the SIR-based epidemic models, we also studied how it is affected by small variations of the incubation time and the crucial distance distributions, and furthermore, by the degree of quarantine measures. Moreover, we compare our qualitative results with that of selected real epidemic data from some worldwide countries.

***Keywords***— COVID-19, Epidemic, Monte Carlo simulation, SIR model, Reproductive number

## 1 Introduction

Facing the problem of the spread of the new virus COVID-19, the standard procedure is to analyse or to fit the epidemic data with the appropriate mathematical models. This methodology is very useful, not only to determine the particular parameters of the disease, but also to forecast the evolution of its spread by using some typical figures of merit as the doubling time, the peaking time and the basic and affective reproductive numbers [1, 3, 2, 4]. Another approach is to work in the reverse problem, that is, to generate epidemic data consistent with the disease under study. By data we mean the fundamental ones, that is, the reported - confirmed "daily new cases" (DNC), expressing the daily rate of infected individuals [5]. The advantage of this methodology, materialized by a Monte Carlo (MC) simulation, is that allows the use of the stochastic character of the parameters used in the mathematics of the epidemics (the known classical SIR model and its extensions), and as well as, to include other extrinsic factors, like quarantine, physical distances and other specific social measures. In this methodology we are studying the set of people in a city or even in a country as a complicate system in which there is no sense to concentrate to the behaviour or habits of individuals or groups of them in detail. Besides, this is surely infeasible to be done. Two factors only must be taken to account, the first is the radius of movement or transport and the second the crucial physical distance for transmitting the disease. The choice of the appropriate range of values, because we are facing random variables with the associated distributions, is one of the main tool for manipulation the generated epidemic data. In order to be consistent with the new COVID-19 disease, we must use, initially, the medical data found in the literature. However, the spread of the disease differs widely among the countries and thus we are forced to focus on the particular ones with similar epidemic "picture". Another very important and useful outcome of this simulation is the so called "Effective reproductive number", $R_{\rm e}$, which is a function of time. From this we can determine also the fundamental parameter used in SIR-based models, the "Basic reproductive number", $R_o$. Both quantities present very large uncertainties when they are calculated from real epidemic raw data (the DNC), even in case of using parametrization mathematical models [6, 7, 8, 9]. The reason is, first, the large fluctuations of the data and secondly the mathematical procedure for determining $R_{\rm e}$ based on variations day-by-day, as we describe next. Finally, the project



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of our work and we suspect that the results can be useful for understanding and facing this serious worldwide pandemic.

## 2 Simulation methodology

The Monte Carlo (MC) simulation we developed is based on the idea to simulate the natural mechanism and process happened during the spread of the disease [10]. According to our claim that we must examine and study the community as a complicate system, we clarify the basic conditions as follows: a) the transmission of the virus is happened only if the physical distance becomes small by the sense of being in a crucial range where the transmission probability tends progressively to unity, b)assuming the condition (a) the daily step of movement every discrete time of one day which is free variable of the simulation because it depends on personal or social factors and c) the specific parameters of the particular disease of new COVID-19 which are mainly, the incubation time and the recovering time, being these two in some kind of convolution [11, 12, 13, 14, 15, 16]. The above three conditions constitute the core of the simulation and thus their mathematical description is essential. In particular, due to their stochastic character we might decide about their probability distribution and the appropriately chosen associated parameters, mainly the mean and standard deviation values. Beyond these, the population and the corresponding people density must be specified at the beginning of the simulation, both related to that is called "size" in the mathematical theory of epidemics. These conditions can be adapted to urban or country town cases in the implementation in real conditions. Below we describe these conditions in more details, where the first three constitute random processes and the fourth one just a set of given constant parameters [17, 18, 19].

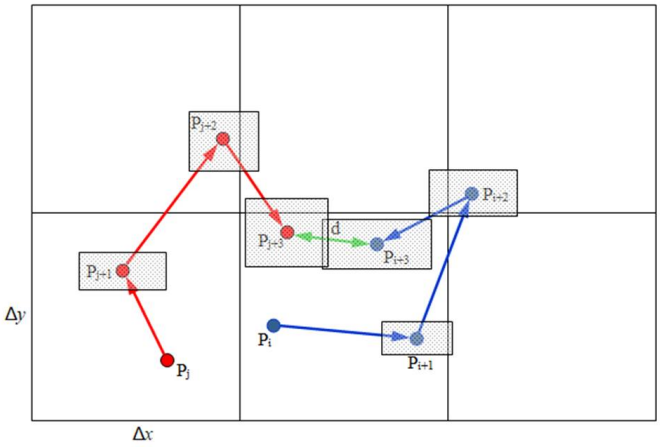


Figure 1: A random movement of two individuals $P_{\mathrm{i}}$ and $P_{\mathrm{j}}$ along a 2-D grid during three successive days. Their distance at the 3rd day is equal to $d$. The shade regions around any new location represent the uncertainty of the radial translations following Gaussian distribution in x and y coordinates.

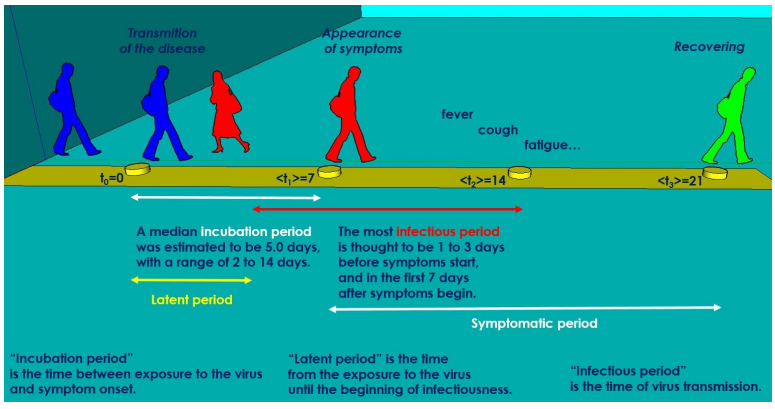


Figure 2: An abstract design showing the various time periods of the virus transmission mechanism from one infected individual to another. The time moments concern the mean values of the relevant random processes.

- Daily step of movement (DS random process): the movement of the dots, because they represent real individuals, must present realistic characteristics. The step must be that corresponding to walking distances in higher probability and transportations with lower probability. However, because the movements are performed relative to the previous location, the cumulative distance should be much greater than one step. This parameter has been chosen to be a fraction of the length corresponding to the dimension of a shell according to the selected people density and follows a Gaussian distribution. In a typical - baseline run we set a mean step equal to 1/4 of the grid dimensions with a std equal to 1/12 of the grid dimensions. In Fig. 1 an indicative sequence of random movement by using discrete steps of two individuals during three successive days is presented.

- Physical distance (PD random process): the physical distance is a delicate issue, in the sense of that it is the fundamental parameter causing infection among two individuals in short distance, if one of them already infected and passed the stage of incubation time of the virus. in order to introduce this condition in a realistic way, we must answer two fundamental questions, a) what is the appropriate relationship between the infection probability and the physical distance, and b) what is the statistical distribution and its parameters describing the variance of the probability related to this medical phenomenon. Even if an appropriate distribution is specified, the phenomenon in the real world is very complicate: we can imagine the pair of individuals, not only keeping a short or longer physical distance, but to wear a mask or not, to wear it incorrectly, the one of them having high or low virus load, straight orientation or not, and other circumstances playing their particular role in the probability of infection.

  Moreover, the environmental conditions (relative humidity, air ventilation etc. contribute to the infection). For this reason, the crucial parameters in the mathematical approach must be considered as the effective ones incorporating all the cases described above in a good approximation. The success to this approximation can be verified only in comparison to real epidemic data analysis. The probability distribution that we assumed is the exponential one, whose the probability density function (PDF) is

$$f(x;\lambda) = \lambda e^{-\lambda x} \tag{1}$$

  where $x$ is a random variable (assumed $x > 0$) and $\lambda$ is the "rate parameter". The mean value is equal to $1/\lambda$ which is used in the runs of our simulation.

  As an alternative probability distribution we assumed a sigmoid function shape. In particular, we created a modified sigmoid function taking values from maximum 1 (for $d = 0$) to minimum 0 (for $d = \infty$). It is characterized by saturation of the distance (as a variable) at very low values close to zero. This probability distribution might approximate better to the real situation and is obtained by using an algorithm running inside the simulation code. This modified sigmoid function, assuming as variable the physical distance $d \geq 0$, is the following

$$f(d;d_r) = \frac{1}{1 + de^{d-d_r}} \tag{2}$$

  where $d_r$ is a reference parameter specifying in which distance we want to achieve a particular probability of infection. For instance, setting $d_r = 0.1931$ the probability of infection at a distance of 0.5 m is equal to 0.5. For the typical physical distance of 2 m the probability falls down to 0.0528 (or about only 5.3%). In the present study of the MC simulation we have used the exponential distribution with mean value 8 m.

- Incubation and recovering time (IR random process): these parameters are very crucial for a realistic simulation. We are forced basically to use mathematical principles because of their stochastic character, even both are related to medical processes inside a human body. It is known that the problems of waiting times are faced using the exponential distribution. Another more advance approach is to assume the Gamma distribution belonging to the same generic distribution family. It is di-parametric including the positive parameters, shape $\alpha$ and the rate $\beta$. The corresponding PDF is the following.

$$f(x;\alpha;\beta) = \frac{\beta^{\alpha}}{\Gamma(\alpha)} x^{\alpha-1} e^{-\beta x} \tag{3}$$

  where $x$ is a random variable, $x \in (0, \infty)$. The mean value is $\mu = \alpha/\beta$ and the variance $\sigma^2 = \alpha/\beta^2$.

  In our MC simulation, measuring the random variable of discrete time in days, we have chosen $a = 6$ (dimensionless) and $\beta = 2/3$ days$^{-1}$. Therefore, the mean value is 9 days incorporating also the "latent period" and the rms (square root of variance) is 4.9 days. These two parameters lead to a distribution which show characteristics consistent with most medical observations published in the literature. In Fig.

2 we present an abstract design of the transmission mechanism among two individuals as a function of time, where one of them is infected and the other is considered as susceptible. We have to face a random process and thus we investigated the most realistic assumption for the required distributions.

- Population, Area and Density (PAD given constants): in the simulation, we chose the total number of dots in a finite area. Therefore, the density is specified at the same time. The population density can be considered in large and very dense cities (e.g. like Paris) with around 20000 people per km$^2$ or for typical small size cities with a density around 2000-4000 people per km$^2$. In our runs we used the density of 2000-4000 people per km$^2$. As initial condition we have chosen 10 infected individuals, that is only 0.5% of the population.

# 3 Determination of the effective reproductive number

The effective reproductive number, $R_\mathrm{e}$ is a fundamental quantity expressing the degree of the transmission of the virus, that is, one infected individual to how many in average secondary individuals should transmit the virus during the average time period that he is sick. This quantity is a function of time can be determined in the frame of the SIR-based models as follows [20, 21, 22, 23, 24]:

$$R_\mathrm{e} = -\frac{\mathrm{d}S}{\mathrm{d}R} = \frac{\mathrm{d}(I+R)}{\mathrm{d}R} = 1 + \frac{\mathrm{d}I}{\mathrm{dt}}\frac{\mathrm{dt}}{\mathrm{dR}} = 1 + \left(\frac{a}{N}SI - \beta I\right)\frac{1}{\beta I} = R_0\frac{S}{N} \tag{4}$$

Because the condition for creating an epidemic is $R_\mathrm{e} > 1$, the corresponding condition should be $S/N > 1/R_0$. Also, at $t = 0$ should be $R_\mathrm{e}(0) \equiv R_0$, at the peaking time $t = t_\mathrm{p}$ should be $R_\mathrm{e}(t_\mathrm{p}) = 1$ and at $t = \infty$ takes the value $R_t = R_0\frac{S}{N}(\infty) < R_0$. By using the expressions of Eq. 4 and using the third equation of SIR model, $\frac{\mathrm{d}R}{\mathrm{d}t} = \beta I$, we can determine $R_\mathrm{e}$ at any time $t$ based only the function $I$, as below

$$R_\mathrm{e} = 1 + \frac{1}{\beta I}\frac{\mathrm{d}I}{\mathrm{d}t} \tag{5}$$

The generated data from the MC simulation are not only the DNC corresponding to the theoretical function of $t$, $I$, but also that correspond to the theoretical functions $S$ and $R$. The determination of $R_\mathrm{e}$ requires only the knowledge of $I$ and as well as the parameter $\beta$. This parameter can be considered as a constant because constitutes an intrinsic characteristic of the disease under study and can be found in the literature. Nevertheless, having the raw epidemiological data of the epidemic spread in a country, the value of $\beta$ could be fitted (or adjusted) in order to be consistent with the corresponding raw epidemiological data referring to the daily recovered individuals, let us call DRC. Usually,these data are not reliable and as well as contain the relevant delay with respect to DNC ones. For this reason we prefer to "stay tied up" to the theory described by SIR-based models, as we have done in the above equations.

Below, we present the methodology to estimate the uncertainty of $R_\mathrm{e}$. According to Eq.5 the sources of the uncertainty are two, a) the uncertainty of $I$ due to its statistical fluctuations and b) the deviation of constant parameter, $\beta$, from a standard bibliographic value. However, the latter, is of secondary importance because, first a hypothetical deviation is expected to be relatively small and secondly because of an appropriate "fine tuning" can be performed. Therefore, in our calculations below we assume a fixed value for $\beta$.

In order to calculate the error's transmission from $I$ to $R_\mathrm{e}$ we can assume a short time period around $t = 0$, $\Delta t$, where $R_\mathrm{e}$ can be considered constant. This assumption is realistic, and we can also say necessary, because the recovering rate in this disease is finite and the variations can be only be calculated at least within this time period. Being $R_\mathrm{e}$ constant, we can write

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta\left(R_\mathrm{e} - 1\right)I \tag{6}$$

We integrate from an arbitrary time $t_{i-1}$ to $t_i$.

$$\int_{I_{t_{i-1}}}^{I_{t_i}} \frac{\mathrm{dI}'}{I'} = \beta\left(R_\mathrm{e} - 1\right)\Delta t \tag{7}$$

Leading to the expression

$$I_{t_i} = I_{t_{i-1}} e^{\beta(R_\mathrm{e}-1)\tau_R} \tag{8}$$

In the general case we can set $\beta\tau_R \equiv c$, even that $c$ differs slightly from unity in practice. As we can observe, according to this assumption of constant $R_e$ in finite time slots, its value depends on the logarithm of the ratio pf the two successive values of $I$ at the beginning and the the end of this time slot. This expression can also be very useful when a surveillance of the epidemic must be implemented for doing a reliable forecast to it during, mainly, during its mitigation stage. At this point, based on this equation, Eq. 8, we proceed to solve the algebraic equation for $R_e$ obtaining

$$R_e = 1 + \ln\left(\frac{I_{t_i}}{I_{t_{i-1}}}\right)^{1/c} \tag{9}$$

The values of $I$ follow the Poisson distribution, appearing the associated uncertainty as the corresponding rms, are considered $\delta I_{t_i} = k\sqrt{I_{t_i}}$ and $\delta I_{t_{i-1}} = k\sqrt{I_{t_{i-1}}}$ respectively, where $k$ is a positive constant factor greater than unity which used for the cases of observing larger fluctuations in the raw data of $I$. Therefore, the uncertainty of $R_e$ should be

$$\delta R_e = \sqrt{\frac{1}{I_{t_i}^2}(\delta I_{t_i})^2 + \frac{1}{I_{t_{i-1}}^2}\left(\delta I_{t_{i-1}}\right)^2} = \frac{k}{c}\sqrt{\frac{1}{I_{t_i}} + \frac{1}{I_{t_{i-1}}}} \tag{10}$$

While the corresponding relative one is

$$\frac{\delta R_e}{R_e} = \frac{k/c}{1 + \ln\left(\frac{I_{t_i}}{I_{t_{i-1}}}\right)^{1/c}} \frac{\sqrt{I_{t_i} + I_{t_{i-1}}}}{\sqrt{I_{t_i} I_{t_{i-1}}}} \tag{11}$$

In the segment around the peak of the DNC curve, we theoretically expect $R_e = 1$. Indeed, from Eq.11 we obtain this value because of maximum of the curve (having an extremum), where $I_{t_i} \approx I_{t_{i-1}}$. At this region, the relative uncertainty takes its minimum value and becomes

$$\delta R_e = \frac{k}{c}\sqrt{\frac{2}{I_{t_i}}} \tag{12}$$

The basic reproductive number, $R_0$, can be calculated by the above equations by using the values at the first time slot (typical is of the order of 13 days), that is, $I_0$ and $I_{t_1}$. Definitely, $R_0$ is the maximum value of $R_e$, as it can be easily proved from Eq. 4 where at $t = 0$ the fraction $S/N$ takes its maximum value and then is decreasing due to monotonically decreasing of $S$.

Implementing the above methodology on the simulation program we use two processes for improving the accuracy of $R_e$ determination. The first concerns a digital filtering, reducing the statistical fluctuations, and the second is a moving average algorithm, both realized by functions of Matlab [25].

# 4 Implementation and results

## 4.1 Results generated by the simulation

During the run of the MC simulation the $N$ dots within the assumed area are categorized by using colors: a) the black for representing the susceptible individuals, b) the red for representing the infected individuals and c) the green for the recovered individuals. The dots change their location day-by-day representing the random movement of the individuals in the real world. In Fig. 3 we present a diagram with the daily new data (DNC) generated by the MC simulation. In Fig. 4 the corresponding effective reproductive number calculated by the MC simulation as a function of time (red circles and spline solid line) is shown. We used also a smoothed curve (green solid line) by moving average of 13 chosen as the optimum time interval. Focusing on the peaking time in both plots, we observe that the value $R_e = 1$ corresponds to the peaking time, as one might expect according to the SIR-based models. Moreover, apart of the general decreasing trend, we observe some slow variations, before and after the value corresponding to the peak, a phenomenon which is hard to be explained in a simple way. These variations are visible also in the obtained $R_e$ from real epidemiological data (see 4.2). The maximum value is around 1.80 and the minimum, relatively adequate accurate value, is at the level of 0.2 around the day 40.

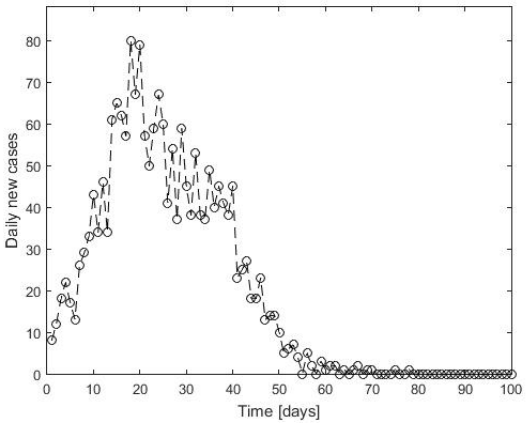


Figure 3: The generated epidemiological data (DNC) by the MC simulation, counted day-by-day during the run and cumulated along the whole area of movement.

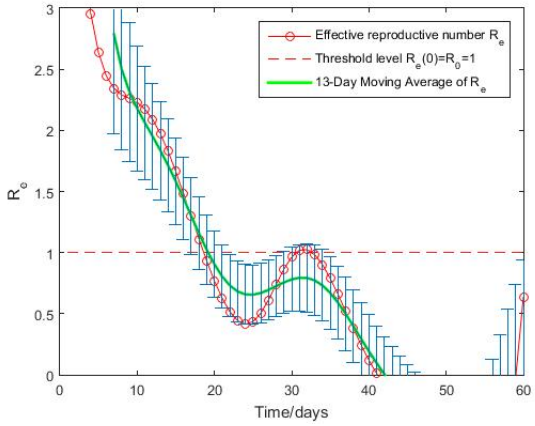


Figure 4: The effective reproductive number from the MC simulation as a function of time. The error bars correspond to the moving average values.

## 4.2 Qualitative discussions and comparisons

By the MC simulation we have studied the effect of the degree of quarantine, by means of the positive effect to the spread dynamic of an epidemic. We have set three degrees of quarantine by reducing the movement range of the individuals and the rms deviation in steps of 0.25, from zero (no quarantine) to 0.75. Because of the fluctuations caused by the stochastic process of the MC simulation we were running the MC simulation 10 times and calculating the mean and rms value for each particular quantity. In Fig. 5, 6, 7 and 8 these results are plotted with the associated fitted curves. In Table 1 the obtained numerical results are summarized.

| Quarantine degree[%] | Percentage of size % | DNC peak value [cases] | DNC peaking time [days] | $R_0$ |
|---|---|---|---|---|
| 0 | 99.3 | 69 | 26 | 1.80 |
| 25 | 99.2 | 53 | 32 | 1.73 |
| 50 | 98.7 | 46 | 43 | 1.80 |
| 75 | 92.7 | 33 | 42 | 1.63 |

Table 1: Summary of the MC simulation results related to the effect of the quarantine degree, with the same density and the mean daily step and the STD of daily step being the baseline one., that is, 7.90 m and 2.64 m respectively. The density was set 2000 p/km$^2$.

Observing these results we find some interesting consequences of the quarantine as follows: The percentage of size shows a very small decrease of 6% within the 100 days of time scale under study. Also, the greater the degree of quarantine the decrease the DNC peak value, while the peaking time extending accordingly. Concerning the basic reproductive number $R_0$, we observe that it shows negligible variation compared with the statistical errors and thus we can consider it as constant. As we know from the SIR-based epidemic models, $R_0$ is a fundamental quantity related to the two basic parameters, the transmission rate and the recovering rate and therefore can not be affected seriously by the quarantine alone. The overall variations, from 0 to 75%, due to the quarantine are: the DNC peak value is coming down by 53%, while the DNC peaking time extends by 61%.

## 4.3 Results analysing real epidemiological data

For comparing the results of the MC simulation with real epidemiological data we have chosen a country where the raw data and any parametrization of them present a "picture" very close to the theoretical as well as with relatively small fluctuations. This country is Switzerland where, beside the above characteristics, the compliance with the measures is largely secured. Therefore, can be considered as a reference for comparison. In Fig. 9 and Fig. 10 the NDC data parametrized by the LPE-SG model and the $R_e$ are shown respectively [26]. The results of the MC simulation we developed show a generic consistency with the real ones, by means of the DNC shape, peaking time, overal time scale of the epidemic and the $R_e$ drop-off shape.

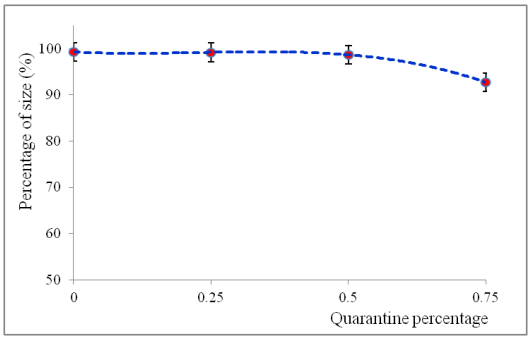


Figure 5: The size percentage as a function of quarantine degree. The dotted line represents a 2nd degree polynomial fit.

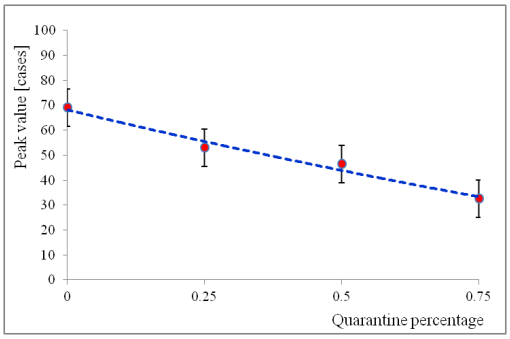


Figure 6: The peak value of DNC as a function of quarantine degree.The dotted line represents a 2nd degree polynomial fit.

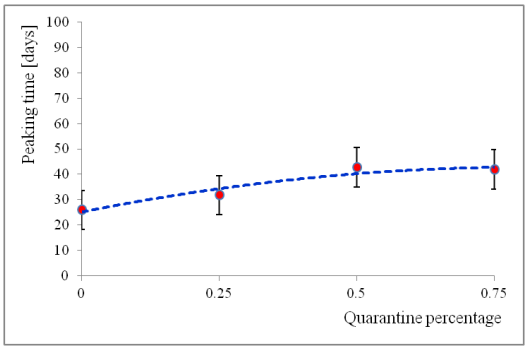


Figure 7: The peaking time of DNC as a function of quarantine degree. The dotted line represents a 2nd degree polynomial fit.

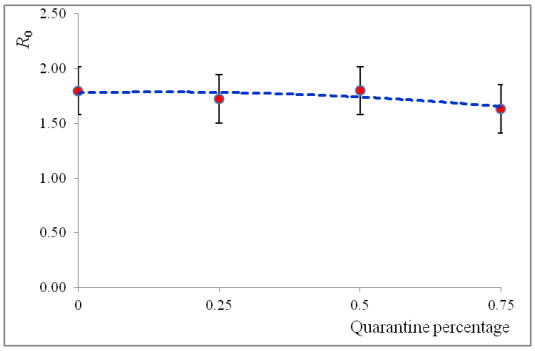


Figure 8: The basic reproductive number as a function of quarantine degree. The dotted line represents a 2nd degree polynomial fit.

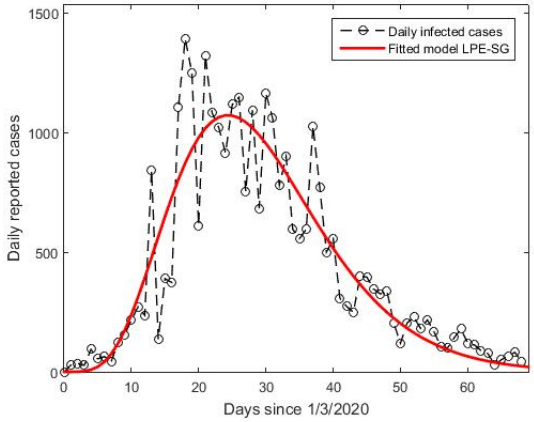


Figure 9: The epidemiological data (DNC) for the first phase of epidemic outbreak in Switzerland since 1/3/2020, obtained from [5].

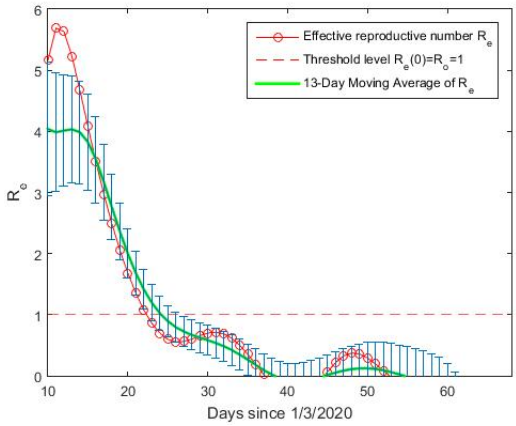


Figure 10: The effective reproductive number as a function of time for the first phase of epidemic outbreak in Switzerland, reproduced as given in [20].

## Conclusions

A Monte Carlo simulation has been developed aiming to study the spread dynamics of the new COVID-19 virus. The novel approach we followed in methodology is based on fundamental mechanisms during the spread of the epidemic. One issue of key importance was the realistic selection of statistical distributions so that the results of the simulation correspond to those recorded to date in various countries during the first and second "waves" of the epidemic. This task was faced by studying the proper statistical distributions and their associated parameters. Moreover, we described the mathematical process for determining the effective reproductive number as it changes during the MC simulation. This quantity as a very important playing a role of "figure of merit" helping to survey and understand the dynamics of the epidemic spread. We also studied the effect of quarantine

at various levels of its implementation on the shape of the epidemic curve and its parameters. In addition, we present some indicative real epidemic results analysed using specific parametrization model.

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