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COVID-19 and other viruses: Holding back its spreading by massive testing

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Abstract

The experience of Singapore and South Korea makes it clear that under certain circumstances massive testing is an effective way for containing the advance of the COVID-19.

In this paper, we propose a modified SEIR model which takes into account tracing and massive testing, proving theoretically that more tracing and testing implies a reduction of the total number of infected people in the long run. We apply this model to the spreading of the first wave of the disease in Spain, obtaining numerical results.

After that, we introduce a heuristic approach in order to minimize the COVID-19 spreading by planning effective test distributions among the populations of a region over a period of time. As an application, the impact of distributing tests among the counties of New York according to this method is computed in terms of the number of saved infected individuals.

1. Introduction

The emergence of the coronavirus disease 2019 (COVID-19) and its mutations motivated actions on the inhabitants of several countries like isolation, social distance and others. The purpose of these restrictions is to slow down the spreading of the pandemic in order not to collapse health systems. Carrying out massive testing is a complementary way to control the pandemic. Throughout this article we will analyse the impact of testing on the number of infections and we will explain how we have developed an expert system to obtain test distributions which minimize the number of infections within a region and for a temporal horizon.

The classical SIR model and its variations are a powerful mathematical tool for predicting the evolution of epidemics around the world. The amount of literature studying the properties of solutions of such models is huge, see e.g. Brauer and Castillo-Chávez (2012), Ji and Jiang (2017), Jiao et al. (2020), Kuniya and Nakata (2012), Li and Muldowney (1995), Zhang and Teng (2007), Zhao et al. (2017) and the references therein among many others. In the present, much effort is taken in order to estimate the evolution of the COVID-19 pandemic, see e.g. Annas et al. (2020), Arcede et al. (2020), Britton et al. (2005), Chen, Lu et al. (2020), Chen, Rui et al. (2020), Gomes et al. (2020), Ndairou et al. (2020), Roda et al. (2020), Sauter and Pacheco (2020) and Xu et al. (2020).

The coefficients which are involved in the system of differential equations of a SIR model are constants in the simplest situation. However, it is more realistic in order to estimate the evolution of an epidemic to consider them as functions of time, as given in some of the above references. Moreover, when we need to take into account the impact of governmental actions like confinements, quarantines, restrictions on mobility and travelling and so on, the coefficients, especially the rate of transmission, can change abruptly. Thus, it is better to define them piecewise by choosing appropriate time intervals depending on the moments in which the governmental restrictions are more severe or, on the contrary, become more relaxed. This approach has been considered in several papers estimating the evolution of the COVID-19 pandemic in several countries, see Falco et al. (2020), Kwuimy et al. (2020), Lin et al. (2020), Mushayabasa et al. (2020), Niazi et al. (2020) and Tang, Bragazzi et al. (2020). Also, the parameters can depend on time due to seasonality (see He et al. (2020)).

Apart from tough measures leading to a lockdown, tracing, massive testing and isolation are very effective tools which help to contain the spread of the illness even without restrictive social distancing, as we can see in the examples of Singapore, South Korea and some Italian towns (see Romagnani et al. (2020)). The main drawback of massive testing is the economic burden. However, as pointed out in Eichenbaum et al. (2020) in the long run it pays off, as these policies can dramatically reduce the economic costs of the epidemic.

Thus, it is quite interesting to modify the SIR or SEIR model in order to measure their influence in the evolution of the pandemic and also to determine the best way to carry out massive testing. In Berger et al. (2020) the SEIR model is modified by taking into account testing and quarantine measures. It is shown that increasing testing the
governments could relax the quarantine conditions (implementing a targeted and more efficient quarantine), so that the economic and social costs would be smaller while maintaining constant the human costs. In Wang (2020) the author makes a qualitative analysis of a SIR model in which the infected individuals are divided into two groups: those undetected and those detected by means of some tests, which have a lower rate of transmission of the disease due to quarantine measures. It is shown that testing reduces the number of infections in the long term, avoiding in this way herd immunity. In Niazi et al. (2020) a model taking into account random massive tests is given. The impact of testing is analysed, obtaining the optimal values for the number of tests to be carried out each day in two possible testing policies to control the epidemic. In these papers, detection by tracing and random testing are put together. In Tang, Wang et al. (2020) a model in which contact tracing and quarantine are considered is used in order to estimate the evolution of the epidemic in Wuhan. In Ubaru et al. (2020) the problem of optimal testing for individuals under limited testing and tracing resources is studied by using a dynamic-graph based SEIR epidemiological model.

In this paper we modify the SEIR model in such a way that the impact of tracing and random testing can be measured separately. For this aim we assume that infected people who are detected are posed in quarantine and then they cannot infect other people any more; hence, only undetected infected individuals are able to spread the epidemic (of this, this is an ideal situation, being more realistic to consider that the rate of infection of those detected is lower, as given in Li et al. (2020))). In our model we differentiate two kind of detected infected individuals: people which are detected because either they are symptomatic or are direct contacts of infected individuals (and then detected by tracing) and people which are detected by means of massive random testing. These two methods of detection are complementary, as by tracing one detects people with symptoms and their contacts, whereas by testing one detects asymptomatic individuals that otherwise would remain undetected and would continue infecting other susceptible individuals.

In Section 3, we make a qualitative analysis of the model in the case where the coefficients are constants. We show first that, as in the standard SEIR model, all the solutions converge as times increases to a fixed point. The number of susceptible individuals in the long term determines the size of the epidemic. We prove that the limit number of susceptible individuals is an increasing function of the parameters of tracing and testing. That is, the more tracing and testing, the less number of infected people in the long term.

In Section 4, we estimate first the parameters of the model during the first wave of the COVID-19 epidemic in Spain if no massive testing is used. We consider the case where the parameters are functions of time and are defined piecewise by taking into account the moments where confinement restrictions were established or relaxed in Spain between March and June of 2020. After that we study the evolution of the epidemic when a constant number of tests is carried out each day, calculating the number of infected individuals which are saved in the long term for several values for the parameters which characterize tracing and testing.

However, a constant distribution of tests per day is far to be optimal. Moreover, it could be better to distribute the tests among different populations in a non-proportional way. Thus, the main purpose of this work is to develop an expert system that provides an effective distribution of tests among the populations of a region over a period of time. So, in Section 5 a heuristic method based on the proposed modified SEIR model is introduced in order to optimize the distribution of tests. In this section it is also explained how to estimate the parameters of the model by using the Differential Evolution technique. This technique was firstly introduced in Storn (1996) as an evolutionary method for optimizing nonlinear functions. Also, it has been employed for estimating parameters of infectious diseases models such as SIR, SIS, SEIR, SEIS and others Kotyrba et al. (2015). For example, it has been applied to estimate the SIR parameters of the COVID-19 pandemic in Italy (see Iorio and Li (2020)). Several improvements, versions and applications of this technique like the ones in Wang et al. (2015) and Yi et al. (2016) or the version employed in Iorio and Li (2006), which will be the one used in this paper, can be found in the literature.

Finally, in Section 6 we study the effectiveness of the proposed heuristic approach by an extensive computational analysis of the spreading of the COVID-19 pandemic in the New York counties during the months of April, May and June of 2020. The results of our distribution are also compared with a distribution which is homogeneous in time and proportional to the size of each population.

2. The model

The classical SEIR model is the following

\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\beta}{N} SI, \\
\frac{dE}{dt} &= \frac{\beta}{N} SI - \sigma E, \\
\frac{dI}{dt} &= \sigma E - \gamma I, \\
\frac{dR}{dt} &= \gamma I.
\end{align*}
\]

(1)

where \( N \) is the size of the population, \( S(t) \) is the number of the susceptible individuals to the disease, \( E(t) \) is the number of exposed people assuming that in the incubation period they do not infect anyone, \( I(t) \) is the number of currently infected individuals which are able to infect other people, \( R(t) \) is the number of individuals that have been infected and then removed from the possibility of being infected again or of spreading infection (which includes dead, recovered people and those in quarantine or with immunity to the disease). The constant \( \beta \) is the average number of contacts per person per time, \( \gamma \) is the rate of removal (1/\( \gamma \) is the average time after which an infected individual is removed), and 1/\( \sigma \) is the average time of incubation of the disease. All these parameters are non-negative.

For our purposes we need to modify system (1) in several ways.

First, in a real situation the coefficients of the model are not constants but functions of time. Moreover, these functions should not be continuous in general, because in an epidemic outbreak the governments impose restrictive measures to the population leading to a sudden change of the rate of transmission.

Second, as our intention is to analyze the efficiency of a testing method, the variable \( I(t) \) will consist of all currently infected individuals (not only of those able to infect) and a new variable \( D(t) \), the number of currently infected people which are detected, will be introduced. We will assume the ideal situation in which any detected individual is placed in quarantine, so this person is not able to infect anyone from that moment. Thus, the number of people with the capacity to infect others is \( I(t) - D(t) \). Also, we do not take into account that there could be people which are immune, so the variable \( R(t) \) will contain only dead and recovered individuals but neither those in quarantine nor immune ones.

Third, we aim to estimate dead and recovered people among the detected ones separately, so \( R(t) \) is split into three variables:

- \( F(t) \): number of dead individuals among the detected ones;
- \( R(t) \): number of recovered individuals among the detected ones;
- \( L(t) \): number of removed individuals among the undetected ones.

As a first step, we consider the situation where mainly people with symptoms and their direct contacts are detected, but there is no plan for massive testing. The rate of detection is given by the variable \( \rho(t) \) (0 < \( \rho(t) < 1 \)) and, therefore, \( D(t) = \rho(t) I(t) \).

With these new variables at hand system (1) becomes:

\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\beta(t)}{N} S(t)(1 - \rho(t)) I(t), \\
\end{align*}
\]
\[
\begin{align*}
\frac{dE}{dt} &= \frac{\beta(t)}{N} S(t) (1 - \rho(t)) I(t) - \sigma E(t), \\
\frac{dI}{dt} &= \sigma E(t) - \left( \rho(t) \left( \gamma_1(t) + \gamma_2(t) \right) + (1 - \rho(t)) \bar{\gamma}(t) \right) I(t), \\
\frac{dF_1}{dt} &= \gamma_1(t) \rho(t) I(t), \\
\frac{dR_1}{dt} &= \gamma_2(t) \rho(t) I(t), \\
\frac{dL}{dt} &= \bar{\gamma}(t)(1 - \rho(t)) I(t),
\end{align*}
\]
and the currently detected individuals are given by
\[
D(t) = \rho(t) I(t). 
\] (2)

Here, \( \gamma_1(t) \) is the rate of mortality of detected people at moment \( t \), \( \gamma_2(t) \) stands for the rate of recovery of detected people at moment \( t \), whereas \( \bar{\gamma}(t) \) is the rate of removal among those undetected.

In a second step, we describe the situation where a massive testing is planned in order to increase the number of detected people, which can be placed then in quarantine. For this aim we define the new variable \( T(t) \), which stand for the number of people for which have been detected at time \( t \) by the test programme among those currently infected \( I(t) \).

Hence, system (2) becomes:
\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\beta(t)}{N} S(t)(1 - \rho(t)) I(t) - T(t), \\
\frac{dE}{dt} &= \frac{\beta(t)}{N} S(t)(1 - \rho(t)) I(t) - T(t) - \sigma E(t), \\
\frac{dI}{dt} &= \sigma E(t) - \left( \rho(t) \left( \gamma_1(t) + \gamma_2(t) \right) + (1 - \rho(t)) \bar{\gamma}(t) \right) I(t), \\
\frac{dT}{dt} &= \Delta(t) - \left( \gamma_1(t) + \gamma_2(t) \right) T(t), \\
\frac{dF_1}{dt} &= \gamma_1(t) \rho(t) I(t) + \gamma_2(t) T(t), \\
\frac{dR_1}{dt} &= \gamma_2(t) \rho(t) I(t) + \gamma_2(t) T(t), \\
\frac{dL}{dt} &= \bar{\gamma}(t)(1 - \rho(t)) I(t) - \gamma(t) T(t),
\end{align*}
\]
where \( \Delta(t) \) is the number of detected people by testing at day \( t \) and \( \gamma(t) \) is the rate of death (recovery) among those detected by testing. The currently detected people are now calculated by
\[
D(t) = \rho(t) I(t) + T(t). 
\] (5)

Assuming that the individuals for the testing are chosen randomly, the variable \( \Delta(t) \) is approximated by
\[
\Delta(t) \approx a(t) \frac{(1 - \rho(t))I(t) - T(t)}{N - R_1(t) - F_1(t) - \rho(t)I(t) - T(t)},
\]
with \( a(t) \geq 0 \) being the number of tests performed at day \( t \). This formula can be simplified if we assume that \( N \gg R_1(t) + F_1(t) + \rho(t)I(t) + T(t) \), which is true in big populations. Hence,
\[
\Delta(t) \approx a(t) \frac{(1 - \rho(t))I(t) - T(t)}{N}. 
\] (6)

For simplicity we could assume that the rates of death and recovery are the same among the detected and the undetected people. In such a case, \( \gamma(t) = \gamma_1(t) + \gamma_2(t) \), and \( \gamma_1(t) = \gamma_1, \gamma_2(t) = \gamma_2 \). Thus, model (4) would be the following:
\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\beta(t)}{N} S(t)(1 - \rho(t)) I(t) - T(t), \\
\frac{dE}{dt} &= \frac{\beta(t)}{N} S(t)(1 - \rho(t)) I(t) - T(t) - \sigma E(t), \\
\frac{dI}{dt} &= \sigma E(t) - \left( \rho(t) \gamma(t) + (1 - \rho(t)) \bar{\gamma}(t) \right) I(t), \\
\frac{dT}{dt} &= \Delta(t) - \gamma(t) T(t), \\
\frac{dF_1}{dt} &= \gamma(t) \rho(t) I(t) + \gamma(t) T(t), \\
\frac{dR_1}{dt} &= \gamma(t) \rho(t) I(t) + \gamma(t) T(t), \\
\frac{dL}{dt} &= \bar{\gamma}(t)(1 - \rho(t)) I(t) - \gamma(t) T(t),
\end{align*}
\]
(7)

In this model we have not taken into account some important factors like the density of the population or mobility. It is shown in Li et al. (2018) that there is a weak relation between the density of the population and the rate of infection, being this rate greater if the population is more dense. Also, mobility plays a key role in the spreading of an epidemic as explained in Li, Wang et al. (2017) (see also Li, Dong et al. (2017) for its influence in other contexts). In this sense, we would like to do some comments. First, the inclusion of these factors would lead to an increment in the number of parameters to be estimated, which is problematic due to the limited amount of available data. Second, the impact of mobility is more important at the initial stage, when the virus has started its spreading. However, we estimate the model in a period when COVID-19 had already reached all the areas of the country or region and, moreover, the governmental restrictions reduced drastically people mobility. Finally, the influence of these factors can be absorbed by the other parameters of the model.

On the other hand, it is known that the latent period for COVID-19 is likely to be shorter that the exposed period (see Rai et al. (2021)), which means that infected people could transmit the virus before showing symptoms. Obviously, the SIR model can be modified in order to take into account this fact (see Brauer and Castillo-Chávez (2012)). However, this would lead to adding a new parameter without having any observed data about the exposed individuals. Also, as before, in our model this effect is absorbed by the parameter \( \beta \).

Thus, we prefer not to consider these factors explicitly and keep a simpler model which gives good enough estimations in order to study the impact of tracing and testing in the evolution of a pandemic.

3. Qualitative analysis in the case of constant coefficients

Our first aim is to prove theoretically that massive testing helps reducing the number of infected people in the long-term.

The qualitative behaviour of the solutions of system (1) is simple and well known (see Brauer and Castillo-Chávez (2012)). There exists an interval of fixed points given by
\[
(S_m, E_m, I_m, R_m) = (S_m, 0, 0, N - S_m), S_m \in [0, N],
\]
and any solution with non-negative initial condition \((S_0, E_0, I_0, R_0)\) satisfying that \(N = S_0 + E_0 + I_0 + R_0\) converges to one of this fixed points as the time \( t \) tends to +\( \infty \). Supposing that \( R_0 = 0 \), the limit point is determined by the initial value of the susceptible \( S \) and is given by the equation
\[
\log \frac{S_0}{S_m} = \frac{\beta}{\gamma} \left( 1 - \frac{S_m}{N} \right). 
\] (8)

We consider system (7) in the following particular situation:

- The coefficients \( \beta, \rho, \sigma, \gamma_1, \gamma_2, \bar{\gamma}, \gamma \) are constant.
- The rates of death and recovery are the same among the detected and the undetected infected people, so \( \bar{\gamma} = \gamma = \gamma_1 + \gamma_2 \), \( \gamma_1 = \gamma_1, \gamma_2 = \gamma_2 \).
- The number of tests which are carried out per day \( \alpha \) is constant and positive and the approximation (6) is valid.

With such assumptions and putting together the variables \( F_1, R_1, L \), system (7) reads as
\[
\begin{align*}
\frac{dS}{dt} &= -\frac{\beta}{N} S((1 - \rho)I - T), \\
\frac{dE}{dt} &= \frac{\beta}{N} S((1 - \rho)I - T) - \sigma E, \\
\frac{dI}{dt} &= \sigma E - \gamma I, \\
\frac{dT}{dt} &= \alpha \frac{(1 - \rho)I - T}{N} - \gamma T, \\
\frac{dR}{dt} &= \gamma I.
\end{align*}
\] (9)
What we want to show is that the solutions of system (9) behave in the same way as those of system (1) and that the limit value $S_{\infty}$ is increasing with respect to the parameters $\alpha$ and $\rho$, showing in this way theoretically that more detection implies a lower number of infected people in the long-term.

The initial condition has to satisfy that $S_0 + E_0 + I_0 + R_0 = N$ and the variable $W = S + E + I + R$ remains equal to $N$ for every time $t \geq 0$.

It is straightforward to see that the unique fixed points of this system are:

$$\left( S_{\infty}, E_{\infty}, I_{\infty}, T_{\infty}, R_{\infty} \right) = \left( S_0, 0, 0, 0, N - S_0 \right) , \quad S_0 \in [0, N].$$

We observe also that the initial condition has to be non-negative. This implies that the solution is non-negative for every forward moment of time if, moreover, $(1 - \rho) I_0 - T_0 \geq 0$.

**Lemma 1.** If $S_0$, $E_0$, $I_0$, $T_0$, $R_0 \geq 0$ and $(1 - \rho) I_0 - T_0 \geq 0$, then $S(t)$, $E(t)$, $I(t)$, $T(t)$, $R(t)$, $y(t) = (1 - \rho) I(t) - T(t) \geq 0$ for all $t \geq 0$.

Also, $S(t) > 0$, for $t \geq 0$, if $S_0 > 0$, whereas $S(t) \equiv 0$ if $S_0 = 0$.

Moreover, if the solution is not a fixed point, then $I(t)$, $T(t)$, $R(t) > 0$ for all $t > 0$, and the following statements hold true:

1. If either $E_0 > 0$ or $E_0 = 0$, $S_0 > 0$ and $y_0 := (1 - \rho) I_0 - T_0 > 0$, then $E(t)$, $y(t) > 0$ for all $t > 0$.
2. If $E_0 = 0$, $S_0 = 0$ and $y_0 > 0$, then $E(t) = 0$, $y(t) > 0$ for all $t > 0$.
3. If $E_0 = 0$ and $y_0 = 0$, then $E(t) \equiv y(t) \equiv 0$.

**Proof.** It is easy to see from the first equation that $S(t) \geq 0$ for all $t \geq 0$. Moreover, $S(t) > 0$, for all $t \geq 0$, when $S_0 > 0$ and $S(t) \equiv 0$ if $S_0 = 0$.

If $E_0 = I_0 = 0$, we have a fixed point. Thus, either $I_0 > 0$ or $E_0 > 0$.

Let $E_0 > 0$. If $E_0 > 0$ for all $t \geq 0$, then it follows from the third and fourth equations in (9) that

$$I(t) = I_0 e^{\alpha t} + \int_0^t e^{(\alpha - \sigma) (t - r)} E(r) dr > 0,$$

(10)

$$T(t) = T_0 e^{-(\sigma + \gamma) t} + \frac{(1 - \rho) I_0 - T_0}{N} \int_0^t e^{-(\sigma + \gamma) (t - r)} I(r) dr > 0,$$

(11)

for all $t \geq 0$, and the function $y(t) = (1 - \rho) I(t) - T(t)$ satisfies

$$\frac{dy}{dt} + \frac{(\sigma + \gamma)}{N} y = (1 - \rho) \sigma E,$$

(12)

so that

$$y(t) = y(0) e^{-(\sigma + \gamma) t} + \int_0^t e^{-(\sigma + \gamma) (t - r)} (1 - \rho) \sigma E(r) dr > 0,$$

(13)

$\forall t > 0$.

From the last equation in (9) we infer that $R(t) > 0$ for every $t > 0$, as well.

Next, we prove that the function $E(t)$ cannot vanish at any point if $E_0 > 0$. Assume on the contrary the existence of a first moment of time $t_0 > 0$ such that $E(t_0) = 0$, so that $E(t) > 0$ for all $t \in [0, t_0)$. By the equality in (13) we conclude that $y(t) > 0$ for $t \in [0, t_0)$. Hence, from the second equation in (9) we get

$$E(t_0) = E_0 e^{-\alpha t_0} + \frac{\beta}{N} \int_0^{t_0} e^{-\alpha (t_0 - r)} S(r) ((1 - \rho) I(r) - T(r)) dr > 0,$$

(14)

which is a contradiction.

Let now $I_0 > 0$ and $E_0 = 0$. We have to study three cases: (1) $y_0 > 0$, $S_0 > 0$; (2) $y_0 > 0$, $S_0 = 0$ (3) $y_0 = 0$.

Let $y_0 > 0$, $S_0 > 0$. By continuity there is $t_0 > 0$ such that $I(t)$, $y(t) > 0$ for $t \in [0, t_0)$. Making use of (11) we obtain that $T(t) > 0$ for all $t \in (0, t_0]$. As the second equation in (9) we have

$$E(t) = E_0 e^{-\alpha t} + \frac{\beta}{N} \int_0^t e^{-\alpha (t - r)} S(r) y(r) dr > 0,$$

(15)

for all $t \in (0, t_0]$. As $S(t) > 0$ for every $t \geq 0$. Thus, taking any $0 < \epsilon \leq t_0$, we infer arguing as before in the interval $[\epsilon, t_0]$ that $E(t) > 0$, for all $t \geq \epsilon$, and that

$$I(t), y(t), T(t), R(t) > 0, \text{ for all } t \geq \epsilon,$$

as $S(t) > 0$ for every $t \geq 0$. Thus, taking any $0 < \epsilon \leq t_0$, we infer arguing as before in the interval $[\epsilon, t_0]$ that $E(t) > 0$, for all $t \geq \epsilon$, and that

$$I(t), y(t), T(t), R(t) > 0, \text{ for all } t \geq \epsilon,$$

as $S(t) > 0$ for every $t \geq 0$. Thus, taking any $0 < \epsilon \leq t_0$, we infer arguing as before in the interval $[\epsilon, t_0]$ that $E(t) > 0$, for all $t \geq \epsilon$, and that

$$I(t), y(t), T(t), R(t) > 0, \forall t \geq \epsilon.$$
From the second equation in (9) and $T (t) \geq 0$, $I (t) \to 0$ we infer the existence of $t_1 \geq t_0$ for which
\[
\frac{dE}{dt} \leq -\frac{\sigma - \frac{S_0}{N}}{4} \quad \text{for} \quad t \geq t_1.
\]
Thus,
\[
E (t) \leq E (t_1) - \frac{\sigma - \frac{S_0}{N}}{4} (t - t_1) \to -\infty,
\]
which is not possible because $E (t) \geq 0$.

The fact that every solution converges to a fixed point has been established.

Finally, let us prove (15). From (16) and the above convergences we have
\[
\int_0^\infty \left( \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} \right) dt = -\gamma \int_0^\infty I (t) dt = \alpha (1 - \rho) \left( \frac{S_0}{N} + E_0 + I_0 \right) = S_0 - (S_0 + E_0 + I_0) = S_0 = N + R_0.
\]

Integrating the fourth and first equations in (9) and putting all together we obtain
\[
\int_0^\infty \frac{dT}{dt} dt = -T_0 = \alpha (1 - \rho) \frac{S_0}{N} \int_0^\infty I (t) dt - \frac{\alpha + \gamma}{N} \int_0^\infty T (t) dt,
\]
\[
\log S_0 - \log S_0 = -\delta (1 - \rho) \frac{S_0}{N} \int_0^\infty I (t) dt + \frac{\beta}{N} \int_0^\infty T (t) dt = -\delta (1 - \rho) \frac{S_0}{N} \int_0^\infty I (t) dt + \frac{\beta a (1 - \rho)}{N (a + \gamma N)} \int_0^\infty I (t) dt + T_0 \frac{\beta}{\alpha + \gamma N} = -\delta (1 - \rho) \frac{S_0 - N + R_0}{N + R_0} + T_0 \frac{\beta}{\alpha + \gamma N},
\]
giving rise to relation (15). \ \qed

We aim now to analyse expression (15) in order to show that $S_0$ is an increasing function of $\alpha$ and $\rho$. We denote $S_0 (\alpha)$ the value of $S_0$ for $a$ assuming the rest of the parameters being constant. In the way we define the function $S_0 (\alpha)$.

**Theorem 4.** We assume the conditions of Theorem 2 and that $S_0 > 0$ and either $E_0 > 0$ or $y_0 > 0$. Then $S_0 (a_1) > S_0 (a_2)$, if $a_1 > a_2$, and $S_0 (\rho_1) > S_0 (\rho_2)$, if $\rho_1 > \rho_2$.

**Proof.** We write (15) in the form
\[
(a + \gamma N) \log \frac{S_0}{S_0} = \frac{\beta}{\alpha + \gamma N} \left( N - R_0 - S_0 \right) - T_0 \beta = 0.
\]

We observe that Lemma 1 implies that $y (t) > 0$, for $t > 0$, so from the first equation in (9) we obtain that $S (t)$ is strictly decreasing and then $S_0 < S_0$. Analysing the function
\[
f (x) = (a + \gamma N) \log \frac{x}{S_0} + \frac{\beta}{\alpha + \gamma N} \left( N - R_0 - x \right) - T_0 \beta
\]
we deduce that:
- $f (S_0) = \beta (1 - \rho) \left( N - R_0 - S_0 \right) - T_0 \beta = \beta (1 - \rho) \left( I_0 + E_0 - T_0 \right) \geq 0$.
- $f$ has a maximum at $x_0 = \frac{a + \gamma N}{\beta (1 - \rho)}$, $f (x_0) \geq 0$.
- $f$ is increasing if $0 < x < x_0$ and $f (x) \to -\infty$ as $x \to 0^+$.
- $f$ is decreasing if $x > x_0$ and $f (x) \to -\infty$ as $x \to +\infty$.

We state that $f (x_0) > 0$. Indeed, if $f (x_0) = 0$, then $x_0 = S_0$, and this is moreover the only point where the function vanishes. Then $S_0 = S_\infty$, which is impossible because $S (t)$ is a strictly decreasing function.

Therefore, the above properties imply that the equation $f (x) = 0$ has exactly two solutions $0 < x_1 < x_0$, $x_2 > x_0$. It follows from $S_0 < S_0$ and $S_0 \in (x_1, x_2]$ that $S_0 = x_1$.

Denote by $g^a (x)$ the function $f (x)$ for the value $a$. It is easy to see that
\[
g^{a_1} (x) < g^{a_2} (x) \text{ for any } x < S_0 \text{ if } a_1 > a_2,
\]
assuming that the other parameters are constant. From here we conclude that $S_0 (a_1) > S_0 (a_2)$ if $a_1 > a_2$.

In the same way, considering the functions $h^\rho (x)$ we obtain that
\[
h^\rho_1 (x) < h^\rho_2 (x) \text{ for any } x \in (0, N - R_0] \text{ if } \rho_1 > \rho_2,
\]
while the other parameters remain constant. Hence, $S_0 (\rho_1) > S_0 (\rho_2)$ if $\rho_1 > \rho_2$.

In the epidemic models a crucial parameter is the basic reproduction number, which is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual over the course of its infection period.

The variables $S$ and $R$ are disease free, whereas $E, I$ and $T$ are the infective variables. We consider the equilibrium $(N, 0, 0, 0, 0)$ and the linearization around it of the subsystem of (9) corresponding to the infective variables, which is given by
\[
\frac{dx}{dt} = \begin{pmatrix} -\sigma & 0 & \beta (1 - \rho) & -\beta & 0 \\ 0 & \sigma & -\gamma & 0 & 0 \\ a - \rho \gamma & a - \rho N & \frac{\beta}{\alpha + \gamma N} & -\gamma & 0 \end{pmatrix} x = J x.
\]

Following van den Driessche and Watmough (2002) we calculate the reproduction number $R_0$ by splitting the matrix $J$ into the rest of the Jacobian matrix associated to the rate of new infections $F$ and the one associated to the net rate out of the compartments $V$:
\[
F = \begin{pmatrix} 0 & 0 & 0 \\ \sigma & 0 & 0 \\ 0 & 0 & \gamma \end{pmatrix},
\]

The basic reproduction number is equal to the spectral radius of the matrix $F V^{-1}$ when this matrix is non-negative. As the eigenvalues of the matrix
\[
F V^{-1} = \begin{pmatrix} \frac{\beta (1 - \rho)}{\gamma} & \frac{\beta (1 - \rho)}{\gamma} & -\frac{\beta}{\gamma} \\ 0 & 0 & 0 \\ \frac{a - \rho \gamma}{\gamma} & \frac{a - \rho N}{\gamma} & -\frac{\alpha}{\gamma} \end{pmatrix}
\]
are $\lambda_1 = 0$ and $\lambda_2 = \lambda_3 = \frac{1}{\gamma} \left( \beta (1 - \rho) - \frac{a}{N} \right)$, we obtain that
\[
R_0 = \frac{1}{\gamma} \left( \beta (1 - \rho) - \frac{a}{N} \right)
\]
provided that this quantity is non-negative, which is the usual situation as $a / N$ is small in great populations.

We can easily see that the zero solution of system (17) is asymptotically stable if and only if $R_0 < 1$. Indeed, the characteristic equation for the eigenvalues of the matrix $J$ is the following:
\[
\lambda^3 + a_2 \lambda^2 + a_1 \lambda + a_0 = 0,
\]
where
\[
a_2 = \sigma + 2 \gamma + \frac{a}{N},
\]
\[
a_1 = \sigma (\gamma + \frac{a}{N} + \gamma) + \gamma,
\]
\[
a_0 = \sigma \gamma \left( \frac{a}{N} + \frac{\sigma (\gamma + \gamma) + \frac{a}{N}}{N} \right).
\]
According to the Routh–Hurwitz stability criterion, all the eigenvalues have negative real part if and only if $a_2, a_0 > 0$ and $a_1 a_2 - a_0 > 0$. It is clear that
\[
a_2 > 0,
\]
\[
a_1 a_2 - a_0 = \sigma \gamma (\gamma + \sigma) + \left( \sigma + 2 \gamma + \frac{a}{N} \right) (\sigma + \gamma) \left( \frac{a}{N} + \gamma \right) + \sigma \gamma (1 - \rho) > 0,
\]
\[
a_0 = \sigma \gamma^2 (1 - R_0).
\]
Thus, the result follows.

When the number of susceptible individuals is less than \( N_0 \), we replace \( R_0 \) by the effective reproduction number at time \( t_i \), given by

\[
R_i = \frac{1}{\gamma} \left( \frac{S(t)}{N} \beta (1 - \rho) - \alpha \right).
\]

Finally, we observe that \( R_0 < 1 \) is equivalent to the inequality

\[
\beta (1 - \rho) < 1.
\]

Thus, the coefficient \( \tilde{R}_0 = \frac{\beta (1 - \rho)}{\gamma + \frac{\alpha}{\gamma}} \) could be also used as a reproduction number, which corresponds to the one used in Niazi et al. (2020).

4. Validation of the model by applying it to the COVID-19 spreading in Spain

In this section, we estimate the parameters of model (2) during the first wave of the COVID-19 pandemic in Spain. After estimating the parameters, we introduce the massive test detection. Solving system (4) with a constant number of test per day we show numerically that the final number of susceptible \( S_w \) would have been greater had a program for testing been implemented. We show also the increasing dependence of \( S_w \) with respect to the parameter \( \rho \).

We will assume that the rates of death and recovery are the same among the detected and the undetected infected people. Therefore, \( \theta_1(t) = \gamma_1 (t) + \gamma_2 (t) \), and \( \tilde{\theta}_1 (t) = \gamma_1 (t) \), \( \tilde{\theta}_2 (t) = \gamma_2 (t) \).

Taking into account that during the pandemic the government implemented at certain moments of time restrictive measures of confinement leading to reduction of mobility, following Gutierrez and Varona (2020), Lin et al. (2020) and Tang, Bragazzi et al. (2020) the rate of transmission \( \beta (t) \) will be a piecewise continuous function with a finite number of discontinuities such that in each interval of continuity the form of the function reads as:

\[
\beta (t) = \beta_0 - \beta_1 \left( 1 - e^{-\sigma (t-t_0)} \right).
\]

We extend this approach to the functions \( \gamma_1 (t) \), \( \gamma_2 (t) \), so that they are also piecewise defined functions of the form:

\[
\gamma_i (t) = \gamma_{i0} - \gamma_{i1} \left( 1 - e^{-\sigma (t-t_0)} \right).
\]

As observed in Roda et al. (2020) the parameters \( \rho (t) \) and \( \beta (t) \) are somehow dependent, which means that for a given sample there exist several combinations of these parameters that fit well the data. This is the problem of nonidentifiability. To avoid this drawback we use the study of seroprevalence in Spain for the first wave of the epidemic and choose an average value for the parameter \( \rho \), so it is not estimated.

It has been estimated (see Lauer et al. (2019) and Rai et al. (2021)) that the mean value of the incubation period of the virus is about five days, so we take \( \sigma = 1/5 \). There are other studies which give a larger period of incubation. For example, in Wu et al. (2020) the estimated value is around six.

Also, we choose an average value for \( \rho \) given by the study of seroprevalence in Spain of Instituto de Salud Carlos III (2020). According to this work, at the end of May of 2020 5.2% of the population of Spain had been infected by the virus (which gives about 2,400,000 infected people as the population is 47 millions), whereas an approximate number of 230,000 people were detected by the COVID tests at that moment. Thus, the average rate of detection during the first wave of the pandemic in Spain was approximately equal to 0.1.

We estimate the parameters of the model in the period from February 20, 2020 to May 17, 2020. Taking into account the points of confinement, we split this interval into the following four subintervals: (1) 20/02-12/03; (2) 12/03-1/04; (3) 1/04-21/04; (4) 21/04-17/05.

We need to estimate the parameters of the functions \( \beta (t) \), \( \gamma_1 (t) \) and \( \gamma_2 (t) \) in each subinterval. For this aim we use the observed values of the variables \( D(t), F_1(t), R_1(t) \), that is, the number of currently infected, dead and recovered individuals which were detected. We have taken the sample given by the Spanish Health Ministry (see https://github.com/datadista/datasets/tree/master/COVID19, sections ccaa_covid19_confirmeds_pcr, ccaa_covid19_fallecidos, ccaa_covid19_actuales), using only the number of infected people detected by means of a PCR test. The value of the constant \( a \) is 0 and the variable \( T (t) \) is equal to 0 as well (that is, there is no massive testing). The observed value at time \( t_i \) will be denote by \( D_i \), \( F_i \), and \( R_i \), respectively. We consider in each interval the pondered average of the euclidean norm of each observed variable:

\[
\text{Error} = a_1 \sum_{i=1}^{n} \left( D_i - D(t_i) \right)^2 + a_2 \sum_{i=1}^{n} \left( F_i - F(t_i) \right)^2 + a_3 \sum_{i=1}^{n} \left( R_i - R(t_i) \right)^2,
\]

where \( a_1 + a_2 + a_3 = 1 \). We have chosen \( a_1 = 0.35, a_2 = 0.3 \).

On the 20th of February the number of detected active infected individuals was 3, so the estimate of the real number of infected subjects is \( 3/\rho = 30 \). At that moment there were detected neither dead nor recovered people. We assume that there were no removed subjects at all at the initial stage of the pandemic. Hence, the initial value of the problem is given by:

\[
I_0 = 30, F_0 = 0, R_0 = 0, S_0 = N - I_0 - E_0 - F_0 - R_0 - L_0.
\]

As we do not have a hint for the value of \( E_0 \), we estimate it.

The estimate of the parameters is carried out by means of the minimization of the target function (18) after solving system (2) when the values of the parameters go through a grid of points. The results in each interval of time are the following:

1. 20/02-12/03: \( \beta (t) = \beta_0 = 1.04, \gamma_1 (t) = \gamma_{10} = 0.0069, \gamma_2 (t) = \gamma_{20} = 0.014, E_0 = 160 \). In this interval, we have looked for constant functions \( \beta (t), \gamma_1 (t), \gamma_2 (t) \), so \( \beta_1 = \gamma_{11} = \gamma_{21} = 0 \).

2. 12/03-1/04: \( \beta (t) = 0.6 - 0.596(1 - e^{-0.095(t-23.1)}), \gamma_1 (t) = 0.012 - 0.001(1 - e^{-0.055(t-21)}), \gamma_2 (t) = 0.016 + 0.041(1 - e^{-0.025(t-21)}), E_0 = 160 \).

3. 1/04-21/04: \( \beta (t) = 0.04 - 0.033(1 - e^{-0.055(t-41)}), \gamma_1 (t) = 0.0095 - 0.008(1 - e^{-0.055(t-41)}), \gamma_2 (t) = 0.055 - 0.025(1 - e^{-0.44(t-41)}), E_0 = 94 \).

4. 21/04-17/05: \( \beta (t) = 0.02 - 0.0065(1 - e^{-0.095(t-61)}), \gamma_1 (t) = 0.0055 - 0.004(1 - e^{-0.075(t-61)}), \gamma_2 (t) = 0.025 + 0.01(1 - e^{-0.93(t-61)}) \).

In Figs. 1–3 we can see the estimate of the detected currently infected, dead and recovered individuals over the whole period.
In Fig. 4 we can see the prediction given by the estimate of the first two intervals, that is, using only the observed data until the first of April. The number of currently infected people detected at the peak of the pandemic is lower than the one given in the estimate. This reflects the fact that on 28th of March the Spanish Government established more severe measures of confinement by forbidding any non-essential activity and allows us to know what would have happened without these measures. After some period this restriction was withdrawn, so the slope of the curve of observed values increased again. Despite these changes, the predicted values give a fairly good picture of the future evolution of the epidemic in Spain from the first of April until the end of May. First, the model predicts pretty good the moment of time when the peak of the pandemic curve is reached. Second, it correctly predicts a monotone decayment of the number of active infected individuals during May leading to a low incidence rate at the end of the month.

In Fig. 5 we have the prediction of the currently infected individuals in the fourth interval when we use the observed data of the first three intervals, that is, until the 21th of April. In this case, the predicted values are close to the observed ones.

Further we intend to estimate the impact of a massive random testing on the final number of infected people during the first wave in Spain. For this aim we solve system (7) with three different values of the parameter $\alpha$; namely, when we carry out 50,000, 100,000 and 150,000 random tests per day.

The approximate limit values of susceptible individuals $S_\infty$ in the long run are the following:

| $\alpha$ | $S_\infty$       |
|---------|-----------------|
| 0       | 44,364,000      |
| 50,000  | 44,452,000      |
| 100,000 | 44,535,000      |
| 150,000 | 44,614,000      |

Therefore, the number of infections which are saved with massive testing is 88,000, 171,000 and 250,000, respectively. In Fig. 6 one can see the evolution of the number of susceptible without massive tests and carrying out 100,000 tests per day.

We can measure also the effect of increasing the value of the parameter $\rho$ while the other parameters remain unchanged, and varying the value of $\alpha$ at the same time as well:

| $\alpha$ | $\rho$ | $S_\infty$       | Number of saved infections |
|---------|--------|-----------------|----------------------------|
| 0       | 0.1    | 44,364,000      | 1,008,000                  |
| 0       | 0.15   | 45,372,000      | 1,062,000                  |
| 50,000  | 0.15   | 45,426,000      | 1,112,000                  |
| 100,000 | 0.15   | 45,476,000      | 1,162,000                  |
| 0       | 0.3    | 46,592,000      | 2,197,000                  |
| 100,000 | 0.3    | 46,587,000      | 2,223,000                  |
5. Distribution approach

In the previous section we have analysed the impact of massive testing when the number of tests which are carried out each day is constant. It is clear that such an homogeneous distribution is not optimal. Therefore, in this section we implement a heuristic method which allows us to increase the number of saved infections. Unlike the previous situation, where we needed to estimate the parameters of the model only once, now it will be necessary to make the estimation a lot of times. Due to this, the parameters have to be estimated using an automatic method. For this aim a genetic algorithm will be implemented.

5.1. Estimation of the parameters

The expert system that we have developed uses the Differential Evolution technique for estimating the parameters of model (7). The differences between this method and other evolutionary algorithms are mainly in the mutation and recombination phases in which weighted differences from the space vector, despite random quantities, are used to obtain perturbations. We have employed the Differential Evolution Algorithm described in Iorio and Li (2006). In this method, a given array of numbers (or genes) containing given particular values of the parameters to be estimated is called a chromosome. The initial population is a set of N chromosomes. It is randomly generated and Algorithm 1 describes the procedure which generates a new population from the current population \( P_G \) formed by N chromosomes, where we denote by \( P_G \), \( G = 0, 1, 2, \ldots \), the population at the iterate \( G \). We denote by \( x_{i,G} \), \( i = 1, \ldots, N \), the chromosome number \( i \) in the population \( P_G \). This sequence of chromosomes converges to the optimal values for the parameters.

Algorithm 1 generates one descendant for each chromosome \( i \) belonging to the current population \( P_G \). Basically three different chromosomes with index \( r_1 \neq r_2 \neq r_3 \neq i \) are randomly selected from \( P_G \). At Step 3, the descendant \( u_{i,G+1} \) is generated by \( u_{i,G+1} = x_{i,G} + K \cdot (x_{r_1,G} - x_{r_2,G}) + F \cdot (x_{r_1,G} - x_{r_2,G}) \). The differential \( K \) combines \( x_{r_1,G} \) and \( x_{r_2,G} \) whereas the differential \( F \) sets the step size. The coefficients \( K, F \in (0, 1) \) are constants.

The selected chromosome is replaced by its descendant if it is better in the sense that the value of a fitness function is lower. As in the previous section, we use as the fitness function the pondered average of the euclidean norm of each observed variable, given in (18). The algorithm is repeated until no replacement happens within a maximal number of successive generations.

5.2. Obtaining the planning distribution

The aim of the distribution method is to plan the distribution of tests among the locations of a region over the instants of time within a temporal horizon, that is, to decide how many tests is better to assign to each location at each instant of time. The objective of this planning is to minimize the total number of infected individuals in a given region and in a temporal interval or, what is the same, to maximize the number of saved infections. The main purpose of such distribution is to plan an effective massive testing combined with tracing.

The distribution method is based on forecasting the number of infected people which would be saved after the assignment of one testing team to one location at one instant of time within the temporal horizon. This procedure has to be repeated for each location and each moment of time. Let \( K \) be the number of people tested per instant (day, week or month) by a testing team, \( L = \{l_1, \ldots, l_M\} \) be the set of locations (counties, towns, etc.), and \( T = \{1, 2, \ldots, T\} \) be the set of instants of time, being \( t \) the current instant. Firstly, we calculate the gain matrix \( G = \{g_{l,t}\} \), that forecasts the number of saved infections due to the assignment of \( K \) tests at location \( l \) and instant \( t \). Secondly, the optimal test distribution is obtained from this matrix according to a heuristic method that provides the distribution matrix \( D = \{d_{l,t}\} \), which indicates the number of tests to be distributed in each location \( l \) at each instant \( t \). So, the procedures gain matrix (Algorithm 2) and test_distribution (Algorithm 3) are used to obtain \( G \) and \( D \), respectively.

Algorithm 2 returns the gain matrix \( G \). Initially, the parameters \( (\rho(t), \eta(t), \sigma, \ldots) \) and the initial state variables \((S_i(t), E_i(t), I_i(t), \ldots)\) are estimated by the Differential Evolution technique for each location \( l \) from the historical data of the coronavirus spreading until the current instant \( t \). Then, for each location we solve system (7) twice with initial conditions at the moment \( t \). Firstly, it is solved with no test assignment. Secondly, it is solved but assigning \( K \) tests only to the location \( i \) and the instant \( t + i \), \( 1 \leq i \leq 14 \). The difference of infected cases at \( t + i + 1 \) in both predictions provides the gain value \( g_{l,t+i} \), that is, the number of saved infections corresponding to testing \( K \) people in the location \( l \) and instant \( t \). However, if the effective reproduction number at time \( t + i \) and the location \( l \), \( R_{l,t+i} \), is lower than 1, it is considered that there is no gain since the pandemic is in a decline phase, so \( g_{l,t+i} = 0 \). Besides, we observe that given that the circumstances are variable and the expert system uses the procedure in a dynamic way, running it every day, a myopic approach that focuses on obtaining gain values for the next 14 days after the current instant \( t \) is used.

Once the gain matrix is obtained, Algorithm 3 is called in order to heuristically maximize the number of saved infections. So, first of all the location-instant pair \((l^*, t^*)\) with largest gain value is chosen. Then, as many tests as possible are allocated to the population \( l^* \) and instant \( t^* > t \). This quantity \( d_{l^*,t^*} \) depends on several constraints such as
the number of remaining tests, the maximum number of people which are able to be tested at this location per day, the number of available tests at Step 4, the quantity of tests assigned to the number of people which are able to be tested at this location per day, the number of available tests, the maximum number of people which are able to be tested at this location per day, the number of available tests, the maximum number of people which are able to be tested at this location per day, the number of available tests, the maximum number of people which are able to be tested at this location per day, the number of available tests.

Algorithm 3: test_distribution

1. **Algorithm 2: gain_matrix**

   1. **foreach** $i \in \mathcal{L}$ do
   2. estimation of parameters and state variables for $l$
   3. for $i = 1$ to $14$ do
   4. if $R_{1,;$ $i} \geq 1$ then
   5. $\beta =$ prediction of infected cases at $t + 1 + i$ without testing
   6. $p =$ prediction of infected cases at $t + i + 14$ assigning $K$ tests at $t + i$
   7. $G_{i} = \beta - p$
   8. else
   9. $G_{i} = 0$
   10. **return** $G$

   11. **Algorithm 3: test_distribution**

   1. **while** $\#test > 0$ do
   2. $G_{i} =$ element of $G$ with maximum value
   3. $d_{i} =$ maximum number of feasible tests distributable to location $l^*$ and instant $t^*$
   4. $\#test = \#test - d_{i}\cdot t$
   5. $G_{i} =$ $0$
   6. **return** $D$

We note that it is convenient to refresh the estimate of parameters and the state variables for each moment of time $t$, being necessary to compute again both the gain and distribution matrices each time new data about the coronavirus spreading are reported. Thus, the proposed approach is used in a dynamic way.

6. Computational experience: distributing tests among the New York counties

In this section we will analyse the computational results of the proposed distribution approach by measuring the number of saved infections and also by comparing it with a distribution of tests which is homogeneous in time and proportional to the size of each population. As an application, we will apply this method to the New York state, which pandemic data are disaggregated by counties and available in Data (2020). The period of time chosen for our study is from the first of April to the first of July of 2020. The reason for choosing it is that it was during this period when the pandemic spreading was most virulent. Although the first case was detected on the first of March, in the majority of the counties there were no registered cases until the 15th of March. The historical data in this period are used in order to simulate the pandemic spreading and also to measure the effectiveness of the possible distributions of tests. In this regard, the distribution obtained by our approach is compared with the distribution of tests which is homogeneous in time and proportional to the number of inhabitants of every county. It is important to observe that as the data about the recovered individuals are not reported, we have estimated them by supposing an average recovery time of 14 days. Then, the historical recovery data have been built by using the cumulative detected cases in the last 14 days for every moment of time.

Algorithm 4 shows the procedure that has been used in order to compute the number of saved infections after applying our distribution method. Initially, we estimate the parameters of model (7) for the whole period of study. However, as the conditions and parameters are different according to different circumstances as the lockdown phases, the use of masks, etc. the parameters are defined and estimated piecewise for each week. This is similar to what is done in Section 4 but now the intervals are fixed in periods of seven days because the purpose of this study is to develop a fully automatic decision system, avoiding thus the necessity to define the intervals with dependence on the government restrictions as lockdown or curfew. We will refer to these parameters as the simulation parameters.

Regarding the settings of the Differential Evolution technique which have been used in this application, a population of $N = 5$ chromosomes has been fixed. Usually, the population size of genetic algorithms is higher but due to the large number of parameters to be estimated this size has been adjusted to the available RAM computer memory. The coefficients $K, F \in (0, 1)$ were randomly generated at each iteration. Finally, the estimation is stopped when a maximum number of 1000 iterations are carried out without any replacement. Our numerical experiments were performed on a PC with a 2.33 GHz Intel Xeon dual core processor, 8.5 GB of RAM, and with the operating system LINUX Ubuntu 18.04.5.

Secondly, for each day $t$, algorithms 2 and 3 are used for planning the test distribution but computing the gain matrix using only the historical data until $t$, given that we need to suppose the data of later instants to be unknown. We need to define a matrix $D'$ containing the distribution of tests on each location at each moment of time over the whole period. At any instant $t$ we only apply the obtained test distribution for the next day, so the column $t + 1$ in $D'$ is replaced by the column $t + 1$ in the matrix $D_t$ that is $D_{t+1} = D_{t+1}$. We repeat this procedure for each moment of time. We note that when we advance from $t$ to $t + 1$ in order to obtain a new matrix distribution $D$ we need to estimate again all the parameters, as the report data is now available for one day more. After computing the matrix $D'$ we calculate the difference between the estimated infected cases at time $M$ without testing $I_{\hat{}_{\hat{}}} (M)$ and the estimated infected cases after applying our test distribution $I_{\hat{}} (M)$, which provides the total number of saved infections.

Algorithm 4: saving

1. **Algorithm 3: test_distribution**

   1. **Algorithm 2: gain_matrix**

   1. **while** $\#test > 0$ do
   2. $G_{i} =$ element of $G$ with maximum value
   3. $d_{i} =$ maximum number of feasible tests distributable to location $l^*$ and instant $t^*$
   4. $\#test = \#test - d_{i}\cdot t$
   5. $G_{i} =$ $0$
   6. **return** $D$

   1. **while** $t < M$ do
   2. estimation of parameters = estimated parameters until $t$
   3. obtain $G$ and $D$ using the estimation parameters
   4. for each $l / do$
   5. compute $I_{\hat{}} (M)$ without testing and using the simulation parameters
   6. compute $I_{\hat{}} (M)$ applying the distribution $D'$ and using the simulation parameters
   7. compute $I_{\hat{}} (M)$ without testing and using the simulation parameters
   8. compute $I_{\hat{}} (M)$ applying the distribution $D'$ and using the simulation parameters
   9. **return** $I_{\hat{}} (M) - I_{\hat{}} (M)$

We note that in order to obtain the test distribution we employ the estimation of parameters at each iteration, whereas the simulation parameters are used for predicting the model and measuring the effectiveness of testing. Both estimations do not need to have the same values since the first ones are calculated with the information which is available until the current moment of time and the simulation parameters are estimated using the data until the last instant of time.

Regarding the cases which are detected from the application of random tests, they are estimated by using expression (6), where, for each location and instant $t$, $a(t)$ is the number of tests to be applied. Besides, in our computational experiments, the detected cases by testing have been multiplied by a factor with the following values:
Table 1
Number of infected cases and saved infections with 10,000 tests per day limitation.

| # Tests | Factor | Hom. Inf. | Approach Inf. | Hom. saving | Approach saving | Advantage |
|---------|--------|-----------|---------------|-------------|-----------------|-----------|
| 10,000  | 1      | 3,365,384 | 3,365,783     | 34          | 433             | 399       |
| 10,000  | 3      | 3,364,519 | 3,365,716     | 101         | 1,298           | 1197      |
| 10,000  | 9      | 3,363,923 | 3,364,514     | 303         | 3,894           | 3591      |
| 50,000  | 1      | 3,364,824 | 3,365,666     | 151         | 993             | 842       |
| 50,000  | 3      | 3,362,819 | 3,365,365     | 452         | 2,998           | 2546      |
| 50,000  | 9      | 3,357,442 | 3,364,462     | 1,355       | 8,375           | 7020      |
| 100,000 | 1      | 3,364,744 | 3,365,519     | 298         | 1,073           | 775       |
| 100,000 | 3      | 3,362,612 | 3,364,924     | 893         | 3,205           | 2312      |
| 100,000 | 9      | 3,357,124 | 3,363,144     | 2,673       | 8,693           | 6020      |
| 500,000 | 1      | 3,363,334 | 3,364,346     | 1,471       | 1,483           | 12        |
| 500,000 | 3      | 3,361,467 | 3,361,416     | 4,401       | 4,350           | −51       |
| 500,000 | 9      | 3,354,169 | 3,352,700     | 13,117      | 11,648          | −1469     |

It is important to take into account that the product of this factor and the number of daily tests \(a(t)\) cannot be greater than the total population of the location.

We have carried out two types of computational experiments for different quantities of available tests. In the first of them, the daily testing capacity is restricted to 10,000 tests per day. In the second, the daily testing capacity is restricted to 10% of the total tests to apply in the whole period.

Table 1 shows the results obtained by our experiments. Column #Tests indicates the number of tests to be assigned. These have been: 10, 50, 100 and 500,000. So, 12 simulations, corresponding to the four possible numbers of tests and the three factor values indicated in Column Factor, have been carried out. Hom. Inf. and Approach Inf. columns show the estimated infected cases by using the homogeneous distribution and our approach, respectively. On the other hand, Hom. Saving and Approach Saving columns show the number of saved infections with both methods. The number of infected cases from the first of April to the first of June of 2020, including both those detected and not detected, have been estimated in 3,365,817. For this aim, #Tests indicates the number of tests to be assigned. These have been: 10,000, 50,000, 100,000 and 500,000.

Table 2
Ratios saving/tests with 10,000 tests per day limitation.

| # Tests | % Homogeneous | % Approach |
|---------|---------------|------------|
| 10,000  | 3.03          | 38.94      |
| 50,000  | 2.71          | 16.75      |
| 100,000 | 2.67          | 8.69       |
| 500,000 | 2.62          | 2.33       |

Table 3
Planning for 100,000 tests.

| Day     | County       | # Tests |
|---------|--------------|---------|
| 12/04   | New York City| 10,000  |
| 16/04   | Rensselaer   | 10,000  |
| 20/04   | Delaware     | 10,000  |
| 23/04   | Ulster       | 10,000  |
| 24/04   | Franklin     | 10,000  |
| 25/04   | Cortland     | 10,000  |
| 26/04   | Onondaga     | 10,000  |
| 27/04   | Fulton       | 10,000  |
| 28/04   | Oswego       | 10,000  |
| 29/04   | New York City| 10,000  |

The saving/test ratios of the distribution with the daily limitation of 10% of the total number of tests are reported in Table 5 for \(factor = 9\). The cases with 10,000 and 50,000 tests show again how higher restrictions of the daily capacity reduce effectiveness given that its daily capacity is more restricted and as a consequence its ratio decreases. The cases with 500,000 and 1,000,000 tests illustrate how a higher daily capacity allows us to overcome the homogeneous distribution although the ratio decreases. On the contrary, the ratio of the homogeneous distribution is less variable.

Test increments, whereas the effectiveness of the homogeneous distribution is practically independent of the total tests. On the other hand, the effectiveness of the proposed distribution is notoriously higher but finally, due to the loss of its effectiveness when increasing the number of tests, both are similar for 500,000 tests. At last, Table 3 specifies the corresponding distribution for 100,000 tests with \(factor = 1\). Given that imposing a constant capacity of testing per day, which is independent of the total number of tests, is a very strict limitation, we have also carried out experiments in which the capacity per day was limited to 10% of the total number of tests. This computational experience is reported in Table 4. In this case the advantage of the proposed approach is always higher than the homogeneous approach even in a new case with 1,000,000 tests, which illustrates how high quantities of tests are also effective if they are not highly restricted by the daily capacity of testing.

The saving/test ratios of the distribution with the daily limitation of 10% of the total number of tests are reported in Table 5 for \(factor = 9\). The cases with 10,000 and 50,000 tests show again how higher restrictions of the daily capacity reduce effectiveness given that its daily capacity is more restricted and as a consequence its ratio decreases. The cases with 500,000 and 1,000,000 tests illustrate how a higher daily capacity allows us to overcome the homogeneous distribution although the ratio decreases. On the contrary, the ratio of the homogeneous distribution is less variable.

Table 6 specifies the corresponding distribution planning for 1,000,000 tests and \(factor = 1\). The counties of Chenango, Chemung, Delaware, Franklin, Washington and Orleans are fully tested (the inhabitants for each county have been obtained from Department of Health of N.Y.S. (2010)). Note that for 100,000 tests the distribution planning is the same as the one reported in Table 3.
vaccines. The line is to adapt a similar distribution approach to the distribution of the proposed distribution method. Also, an interesting future research by an extensive computational experience showing the advantages of applied to the spreading of COVID pandemic in the New York counties. Besides, we have theoretically proved how massive testing helps reducing the number of infected people in the long-term.

In this work a SEIR model for analysing the efficiency of test distributions has been introduced. It contemplates both detected and non-detected infected individuals in order to measure the impact of testing. Since the values of the parameters of the model can change abruptly due to severe governments measures like lockdown, curfew, etc., the coefficients of the model are defined piecewise in given intervals of time and are functions of time. This model has been applied for simulating the phase-based transmissibility of a novel coronavirus. In Infectious Diseases of Poverty 9, 2020/12/04.

| Day       | County     | Tests  |
|-----------|------------|--------|
| 12/04     | Nassau     | 100,000|
| 17/04     | Oswego     | 100,000|
| 19/04     | Oneida     | 100,000|
| 21/04     | Ontario    | 100,000|
| 22/04     | Chemung    | 88,830 |
| 23/04     | Nassau     | 100,000|
| 24/04     | Washington | 63,216 |
| 25/04     | Franklin   | 51,599 |
| 26/04     | Delaware   | 47,980 |
| 26/04     | Orleans    | 42,883 |
| 27/04     | Chenango   | 50,477 |
| 28/04     | Westchester| 100,000|
| 29/04     | Rensselaer | 55,015 |

7. Conclusions

In this work a SEIR model for analysing the efficiency of test distributions has been introduced. It contemplates both detected and non-detected infected individuals in order to measure the impact of testing. Since the values of the parameters of the model can change abruptly due to severe governments measures like lockdown, curfew, etc., the coefficients of the model are defined piecewise in given intervals of time and are functions of time. This model has been applied to the spreading of the COVID pandemic in Spain. Besides, we have theoretically proved how massive testing helps reducing the number of infected people in the long-term.

Secondly, we describe the Differential Evolution technique, which is a genetic algorithm for the estimation of parameters, and develop a heuristic approach for distributing tests. This approach have been applied to the spreading of COVID pandemic in the New York counties by an extensive computational experience showing the advantages of the proposed distribution method. Also, an interesting future research line is to adapt a similar distribution approach to the distribution of vaccines.

| Table 4 | Number of infected cases and saved infections with 10% tests per day limitation. |
|---------|---------------------------------------------------------------------------------
| # Tests | Hom. Inf. | Approach Inf. | Hom. saving | Approach saving | Advantage |
| 10,000  | 1         | 3,365,783     | 3,365,709   | 34            | 108        | 74         |
| 10,000  | 3         | 3,365,716     | 3,364,944   | 101           | 323        | 222        |
| 10,000  | 9         | 3,365,514     | 3,364,851   | 303           | 966        | 663        |
| 50,000  | 1         | 3,365,666     | 3,365,280   | 151           | 537        | 386        |
| 50,000  | 3         | 3,365,365     | 3,364,209   | 452           | 1,608      | 1,156      |
| 50,000  | 9         | 3,364,462     | 3,361,026   | 1,355         | 4,791      | 3,436      |
| 100,000 | 1         | 3,365,519     | 3,364,744   | 298           | 1,073      | 775        |
| 100,000 | 3         | 3,364,924     | 3,362,612   | 893           | 3,205      | 2,312      |
| 100,000 | 9         | 3,363,144     | 3,357,124   | 2,673         | 8,693      | 6,020      |
| 500,000 | 1         | 3,364,346     | 3,360,256   | 1,471         | 5,561      | 4,090      |
| 500,000 | 3         | 3,361,416     | 3,354,512   | 4,401         | 11,305     | 6,904      |
| 500,000 | 9         | 3,352,780     | 3,341,480   | 13,117        | 24,337     | 11,220     |
| 1,000,000| 1         | 3,362,884     | 3,355,417   | 2,933         | 10,400     | 7,467      |
| 1,000,000| 3         | 3,357,058     | 3,344,645   | 8,759         | 21,172     | 12,413     |
| 1,000,000| 9         | 3,339,880     | 3,316,234   | 25,937        | 49,583     | 23,646     |

| Table 5 | Ratio saving/tests with 10% tests per day limitation. |
|---------|------------------------------------------------------|
| # Tests | % Homogeneous | % Approach |
| 10,000  | 3.03         | 9.66       |
| 50,000  | 2.71         | 9.59       |
| 100,000 | 2.67         | 8.69       |
| 500,000 | 2.62         | 4.87       |
| 1,000,000 | 2.60    | 4.96       |

| Table 6 | Planning for 1,000,000 tests. |
|---------|--------------------------------|
| Day     | County | Tests  |
| 12/04   | Nassau | 100,000|
| 17/04   | Oswego | 100,000|
| 19/04   | Oneida | 100,000|
| 21/04   | Ontario| 100,000|
| 22/04   | Chemung| 88,830 |
| 23/04   | Nassau | 100,000|
| 24/04   | Washington| 63,216 |
| 25/04   | Franklin| 51,599 |
| 26/04   | Delaware| 47,980 |
| 26/04   | Orleans | 42,883 |
| 27/04   | Chenango| 50,477 |
| 28/04   | Westchester| 100,000|
| 29/04   | Rensselaer| 55,015 |

CRedit authorship contribution statement

José L. Sainz-Pardo: Conceptualization, Methodology, Software, Data curation, Writing – original draft, Writing – review & editing, Visualization, Supervision. José Valero: Conceptualization, Methodology, Software, Data curation, Writing – original draft, Writing – review & editing, Visualization, Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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