Modified SIQR model for the COVID-19 outbreak in several countries

Carla M. A. Pinto¹,² | J. A. Tenreiro Machado¹ | Clara Burgos-Simón³

¹School of Engineering, Polytechnic of Porto, Rua Dr António Bernardino de Almeida, 431, Porto, 4249-015, Portugal
²Centre for Mathematics, University of Porto, Portugal
³Institute of Multidisciplinary Mathematics, Valencia, Spain

Correspondence
Carla M. A. Pinto, School of Engineering, Polytechnic of Porto, Rua Dr António Bernardino de Almeida, 431, Porto 4249-015, Portugal.
Email: cap@isep.ipp.pt

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In this paper, we propose a modified Susceptible-Infected-Quarantine-Recovered (mSIQR) model, for the COVID-19 pandemic. We start by proving the well-posedness of the model and then compute its reproduction number and the corresponding sensitivity indices. We discuss the values of these indices for epidemiological relevant parameters, namely, the contact rate, the proportion of unknown infectious, and the recovering rate. The mSIQR model is simulated, and the outputs are fit to COVID-19 pandemic data from several countries, including France, US, UK, and Portugal. We discuss the epidemiological relevance of the results and provide insights on future patterns, subjected to health policies.

KEYWORDS
epidemiology, mSIQR model, real data fitting, SARS-CoV-2

1 INTRODUCTION

In December 2019, the world has awoken to a new challenge, or according to some, to a new type of “war”: not a conventional war, conducted by using ordinary weapons and battlefield tactics, between two or more states in open confrontation. In such war, the forces on each side are well defined, and the weapons are used to primarily target the opponent’s military resources. The current war is one in which the countries’ health systems are at stake, with major consequences in terms of human lives. A major burden is put primarily in the national health systems, and in some countries, they are already giving sights of exhaustion, burnout, and rupture.¹,² Nevertheless, the future sequels of this war are foreseen dramatic, not only in terms of lives, but also in what concerns the economic and social impact. Worldwide are confirmed 213,050,725 cases individuals infected with the Corona Virus Disease 19 (COVID-19), and 4,448,352 deaths, as of August 26, 2021. In Europe (EU/EEA), the figures are 35,848,469 and 748,358 for the number of infected people and deaths, respectively.³,⁴ We can find in the web useful sites providing accurate information on the evolution of the pandemic worldwide.⁵,⁶ Evermore, the world needs to revise the global strategy in terms of biological threats and to prepare for future viruses propagation. In fact, due to the global warming and to the invasion of the habitats of many natural species, it is expected the emergence of other pandemic. This can happen due to a variety of factors, such as the thawing the glaciers and the revival of frozen uncharted viruses or the stochastic mutations of known ones. Moreover, the rise of human fast travels, either for business or touristic purposes, introduces a propagation rate not faced previously in history.⁷,⁸

The World Health Organization (WHO) is currently developing an R&D blueprint, highlighting the Middle East Respiratory Syndrome (MERS-CoV) as a case study, for rapid medical-product development and deployment. This urgency
emerged from the 2014 Ebola epidemic in West Africa, which revealed deficiencies within existing mechanisms. The global health communities became cognizant of the requirement of a multifaceted plan to respond quickly and efficiently to the next epidemic. And this has arrived on January 2020, with the COVID-19.9

This COVID-19 pandemic is attributed to a new virus strain, the 2019-nCoV, or SARS-CoV-2, described as severe acute respiratory syndrome coronavirus 2, by the International Committee on Taxonomy of Viruses, and never identified in humans before.3 Coronaviruses are a large family of viruses, which can be transmitted between animals and humans. They can cause symptoms of a common cold, including respiratory symptoms, fever, cough, shortness of breath, and breathing difficulties. In severe cases, infection can cause pneumonia, severe acute respiratory syndrome, kidney failure, and even death, as it is seen in the 2012 MERS-CoV and the 2002 Severe Acute Respiratory Syndrome (SARS-CoV).

The emergence of the 2019-nCoV infection occurred in Wuhan, a Chinese city of 11 million people, in December 2019. It caused an outbreak of atypical pneumonia. Disease death figures had grown thousands per day, late January and early February 2020, which was described as the peak of the epidemic in China. The Chinese government started an unprecedented containment plan and managed to reduce the number of newly infected people to almost 0 (locals) and around 30 (imported), by the middle of March 2020.10

From the current available data, it is estimated that the COVID-19 attributed death rate is lower than those of SARS, MERS, or Ebola.11 Nevertheless, one has to be careful when computing such rates, for scientific and technical purposes. These values are usually obtained as the quotient of the number of deaths relative to the number of confirmed cases of infection. This calculation is not correct in what concerns time, since it should be the quotient of the number of patients who die by the total number of patients infected at the same time.12 This former calculation may lead to misleading interpretations. As an example, we highlight the case of the 2003 SARS epidemic, for which WHO reported a fatality rate of 4% (or as low as 3%) while the epidemic was evolving, and corrected later this value to 9.6% when it ended.13

The transmission of the 2019-nCoV is commonly done through droplets, from sneezing or coughing of a symptomatic carrier. Though, like other virus, 2019-nCoV may also be transferred from an infected person to a variety of surfaces, where it remains viable to infect a susceptible individual, for hours to days. Van Doremalen et al14 found that the 2019-nCoV could last a day on cardboard and between 2 and 3 days on plastic or stainless steel. These results brought considerable attention to daily ordinary items, such as packages left on doorsteps, plastic delivery bags, and grocery goods in stores, being host of live virus for several hours or days. In the air, this virus can last up to 3 h. Thus, walking into a room where someone previously coughed could pose a risk of infection. These findings support the assumption of the transmission rate of 2019-nCoV being higher than that of other diseases. The basic reproduction number, defined as the number of secondary cases, due to a single infected individual in a susceptible population, is suggested to be in the interval [2, 2.5]. The incubation period is believed to be in the 95% confidence interval of (4.5, 5.8) days. It is accepted a 14 day period of active monitoring or quarantine, after which 97.5% of those infected will develop symptoms of the disease.15,16

The usual health policies to prevent both being infected and spreading the infection by coronavirus are regular hand washing, covering mouth and nose when coughing and sneezing, and cooking very well meat and eggs. Are also included actions affecting the everyday life cycle, namely, staying at home, and similar actions.3 The countries plagued by this pandemic reacted at different velocities and applying distinct control measures. Some had previous experience from the 2002 SARS-CoV and the 2012 MERS-COV, and others had to quickly develop administrative approaches towards the outbreak.17

We observe an incredible interest of researchers throughout the world in the patterns of this pandemic. The latest research on COVID-19 can be searched on a database compiled by the World Health Organization (WHO).18 The database is updated daily from a variety of tools, namely, bibliographic databases, relevant journals’ hand searches of table of contents, and other relevant scientific papers. Hellwell et al19 proposed a mathematical model to measure the efficacy of contact tracing and isolation, to control COVID-19 outbreaks. The authors used specificities of this virus transmission and simulated the model for different numbers of cases. They found that neither contact tracing nor isolation were sufficient to contain outbreaks, unless very high levels of contact tracing were considered. Furthermore, the authors observed that if there is subclinical transmission or a substantial transmission before the onset of symptoms, the control fails within 3 months. With the available information concerning the virus and the outcomes of the proposed model, the authors concluded that around 80% of symptomatic contacts had to be traced and isolated to achieve control over 80% of the outbreaks. Tang et al20 revised a previously published model21 to include time-dependent contact and diagnose rates. They recalculated the daily reproduction ratio and suggested that when this rate is below 1, the epidemics has its peak and then will start to fall. These results emphasized the need for persistent and strict self-isolation, as a crucial public health intervention measure. Wu et al22 developed a susceptible-exposed-infectious-recovered (SEIR) model to simulate the Wuhan
epidemic since it was established in December 2019. They have also estimated the outbreak size in other Chinese cities. Important findings of the model suggested the development of stringent measures to stop the mobility of population in affected areas and to reduce within-population contact rates by canceling events of mass gatherings, schools closing, homeworking, among others. Ndaïrou et al.23 proposed a compartmental model for COVID-19 transmission and compared the results of their model to data from Wuhan. They considered the influence of super-spreaders in the transmission, and of the number of hospitalized people to estimate the need of intensive care units’ places. Odagaki24,25 modified a SIQR model to include infected and quarantined compartments, adapted to SARS-CoV-2 infection dynamics. The author provided the exact properties of the model and showed that the maximum number of infected individuals was a function of the quarantine rate. He showed that controlling the number of quarantined people was effective to slow down the pandemic. Furthermore, the author developed an optimal strategy for minimizing the maximum number of infected, and for controlling the outbreak, at early stages. Odagaki26 demonstrated that the oscillation of the infection curve could be self-organized in the SIQR model, in which the net rate of change was a function of the number of infected individuals. Other approaches to the SARS-CoV-2 infection can be found in Tenreiro et al.27 (and references therein).

With the aforementioned ideas in mind and taking the specificity of the COVID-19 infection, we propose a mathematical model for the early patterns of this pandemic. In Section 2, we describe the assumptions to assemble the model and write the corresponding system of delay ordinary differential equations (DDE). This is followed in Section 3, by the calculation of the reproduction number of the model, $R_0$. In Section 4, we give the sensitivity indices of $R_0$ for relevant parameters. We discuss the results of the numerical simulations of the model, for given initial conditions and parameter values in Section 5. Furthermore, we show the fitting of the patterns of the model to data available for the COVID-19 pandemic, in four countries (Portugal, France, UK, and USA), from February 2020 till December 2020. We complete the paper in Section 6 with the conclusions and remarks, opening a debate for future research.

## 2 | THE PROPOSED MATHEMATICAL MODEL

In this section, we propose a modified version of the Susceptible-Infected-Quarantined-Recovered (mSIQR) model,28,29 to describe the dynamics of the COVID-19 outbreak in several countries.

Let $t$ be time (days), We have divided the total population in seven classes (or compartments), namely, $S(t)$, $I_s(t)$, $I_d(t)$, $Q_h(t)$, $H(t)$, $R(t)$, $R_m(t)$, which denote the number of susceptible, infectious showing symptoms, infectious asymptomatic, quarantined (hospitalized), quarantined at home, recovered, and recovered from asymptomatic class individuals, respectively. Thus, the total population is given by $N(t) = S(t) + I_s(t) + I_d(t) + Q_h(t) + H(t) + R(t) + R_m(t)$. We assume the population has a homogeneous spatial distribution and the mixing of hosts follow the law of “mass action.” Thus, the local density of the total population is constant though the total $N(t)$ may vary with time.

In Figure 1, it is presented a schematic diagram of the dynamics of the COVID-19 infection. The distinct disease stages are reproduced by the compartments (rectangles), and the arrows imply the direction of progress of individuals in the disease. The two types of arrows signal two different knowledge states with respect to real data. The solid arrows indicate that there are available data, whereas the dashed arrows are used in the absence of it. All variables and parameters of the mSIQR model are defined in Table 1.

The susceptible individuals, $S$, acquire the SARS-CoV-2 infection when in contact with infectious individuals, $I_s$ and $I_d$, with rate $\beta$. The individuals showing symptoms of the disease, $I_s$, are more likely to spread the infection through droplets, when coughing or sneezing; thus, a modification parameter, $\xi > 1$, is multiplied by $I_s$ in the transmission term. The median incubation period of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is estimated around 5.1 days;15 thus, we consider for time delay, $\tau$, a value close to this one. We assume that the susceptible individuals at time $t$ can only contact the infected individuals at the same instant of time $t$, and not in the past time $t - \tau$. Moreover, the infected individuals at the past time $t - \tau$ only contact with the susceptible individuals at that time (i.e., $t - \tau$). We also consider that after being infected, the susceptible individuals leave their class immediately and move to the infection classes after a certain latent period, $\tau$.30 This is reflected in our model by adding the delayed form of the nonlinear incidence rate $\lambda(t) = \beta S(t - \tau)[S(t - \tau) + I_s(t - \tau)]$ on the equations of $\dot{I}_s(t)$ and $\dot{I}_d(t)$. Thus, after $\tau$ days, a proportion $(1 - p)$ of $S$ individuals move to class $I_s$ of symptomatic individuals, and a proportion $p$ to class $I_d$ of asymptomatic infectious individuals. Infectious symptomatic individuals, $I_s$, with severe symptoms, are admitted in the hospital, at rate $q$, and those with mild symptoms are advised to quarantine at home and move to class $H$. Individuals in class $Q_h$ either recover, at rate $\lambda$, and move to the recovered class $R$, or die from the disease, at rate $\mu$, and move to the compartment $D$. Individuals quarantining at home,
FIGURE 1 Flow chart of the mSIQR model, where $S$ denotes the susceptible population, $I_s$ the symptomatic infectious individuals, $I_u$ the asymptomatic infectious individuals, $Q_h$ the hospitalized infected individuals, $H$ the individuals quarantining at home, $R$ the recovered symptomatic individuals, and $R_m$ the recovered asymptomatic individuals.

| Variable/parameter | Description |
|--------------------|-------------|
| $S$                | Susceptible individuals |
| $I_s$              | Symptomatic infectious individuals |
| $I_u$              | Asymptomatic infectious individuals |
| $Q_h$              | Individuals in quarantine at the hospital |
| $H$                | Individuals in quarantine at home |
| $R$                | Recovered symptomatic individuals |
| $R_m$              | Recovered asymptomatic individuals |
| $b$                | recruitment rate |
| $d$                | natural death rate |
| $\beta$            | contact rate |
| $\xi$              | modification parameter |
| $p$                | rate of asymptomatic (unknown) infectious |
| $\epsilon$         | recovery rate of asymptomatic infectious |
| $\mu$              | disease mortality rate |
| $q$                | rate of quarantined individuals |
| $\lambda$          | recovery rate of hospitalized infected individuals |

$H$, have similar dynamics to those in class $Q_h$, either recovering and moving to the $R$ class, or dying from the disease. The asymptomatic individuals, $I_u$, fully recover and move to class $R_m$, at rate $\epsilon$, or die and move to the $D$ compartment at rate $\mu$.

The nonlinear system of delay differential equations (DDE) describing the dynamics of the mSIQR model is given by

\[
\begin{align*}
\dot{S}(t) &= b - \frac{\beta}{N} S(t) (\xi I_s(t) + I_u(t)) - dS(t), \\
\dot{I}_s(t) &= \frac{\beta(1-p)}{N} S(t - \tau) (\xi I_s(t - \tau) + I_u(t - \tau)) - I_s(t) - dI_s(t), \\
\dot{I}_u(t) &= \frac{\beta p}{N} S(t - \tau) (\xi I_s(t - \tau) + I_u(t - \tau)) - (\epsilon + \mu) I_u(t) - dI_u(t), \\
\dot{Q}_h(t) &= q I_s(t) - (\lambda + \mu) Q_h(t) - dQ_h(t), \\
\dot{H}(t) &= (1-q) I_s(t) - (\lambda + \mu) H(t) - dH(t), \\
\dot{R}(t) &= \lambda (Q_h(t) + H) - dR(t), \\
\dot{R}_m(t) &= \epsilon I_u(t) - dR_m(t).
\end{align*}
\]
2.1 | Positiveness of solutions

Let $X = C([-\tau, 0], \mathbb{R}^8)$ be the Banach space of continuous mapping from $[-\tau, 0]$ to $\mathbb{R}^8$ equipped with the initial conditions for system (1) given by

\[
S(\theta) \geq 0, I_s(\theta) \geq 0, I_u(\theta) \geq 0, Q_n(\theta) \geq 0, H(\theta) \geq 0, R(\theta) \geq 0, R_m(\theta) \geq 0, \forall \theta \in [-\tau, 0].
\]

**Lemma 1.** Given the initial conditions above, then all solutions $X(t) = (S(t), I_s(t), I_u(t), Q_n(t), H(t), R(t), R_m(t))$ of the model system (1) are positive and ultimately uniformly bounded on $[0, \infty)$.

**Proof.** It is assumed that all the dependent variables and parameters of the model are non-negative. Continuity of the right hand side of system (1) and its derivative imply that the model is well-posed for $N(t) > 0$.

Assume that the solution $X(t)$ of system (1) with a positive initial condition exists and is unique on $[0, b)$, where $0 < b < \infty$ (see\(^3\)). Since

\[
\dot{S}(t) = b - \frac{\beta}{N} S(t) (\xi I_s(t) + I_u(t)) - dS(t) \geq - \left( \frac{\beta}{N} S(t) (\xi I_s(t) + I_u(t)) + d \right) S(t),
\]

we have

\[
S(t) \geq S(0) \exp \left( - \int_0^t \frac{\beta}{N} S(t) (\xi I_s(\theta) + I_u(\theta)) + dd\theta \right) > 0, \forall t \in [0, b).
\]

Hence, one must have $I_s(t)$, $I_u(t) > 0$, $\forall t \in [0, b)$. Assume in contradiction that there exists $t_1, t_2 \in (0, b)$ such that $I_s(t_1) = 0$ and $I_s(t_2) > 0$, $(0, t_1)$, and $I_u(t_2) = 0$ and $I_u(t_2) > 0$, $(0, t_2)$. Choose $t_m = \min(t_1, t_2)$. Thus, for $t \in [0, t_m)$, one gets

\[
\begin{align*}
I_s(t) &= \frac{\beta(1 - p)}{N} S(t - \tau) (\xi I_s(t - \tau) + I_u(t - \tau)) - I_s(t) - dI_s(t) \geq -(1 + d)I_s(t) \\
I_u(t) &= \frac{\beta p}{N} S(t - \tau) (\xi I_s(t - \tau) + I_u(t - \tau)) - (\epsilon + \mu) I_u(t) - dI_u(t) \\
&\geq -(\epsilon + \mu + d) I_u(t).
\end{align*}
\]

Integrating the above inequalities from 0 to $t$ yields

\[
\begin{align*}
I_s(t) &\geq I_s(0) \exp \left( - \int_0^t (1 + d) d\theta \right) > 0, \\
I_u(t) &\geq I_u(0) \exp \left( - \int_0^t (\epsilon + \mu + d) d\theta \right) > 0
\end{align*}
\]

for all $t \in [0, t_m]$, which is in contradiction with $I_s(t) = 0$ and $I_u(t) = 0$. Thus, $I_s(t) > 0$ and $I_u(t) > 0$, for all $t \in [0, b)$. The other cases are treated analogously.

The remaining variables, $Q_n(t)$, $H(t)$, $R(t)$, $R_m(t)$, are easily shown to be positive for $t \in [0, b)$. Furthermore, we are assuming that the total number of the population $N(t)$ is a constant, due to the small study period. Then,

\[
0 < \lim_{t \to \infty} N(t) < N(0).
\]

Since $N(t) > 0$ for $[-\tau, 0]$, and its value is bounded above, then the model (1) is dissipative (solutions are bounded). Consequently, the solution exists globally for all $t \geq 0$ in the invariant and compact set $\mathbb{R}_{0}^8$, and $b = \infty$. \qed
This section is devoted to the calculation of the basic reproduction number, \( R_0 \). It is defined as the number of secondary infections due to one single infected individual in a completely susceptible population.

The disease-free equilibrium of the mSIQR model is \( P_0 = (S_0, 0, 0, 0, 0, 0) \). We apply the next generation method\(^3\) to calculate \( R_0 \), for \( \tau = 0 \), and the local stabilities of its disease-free and the endemic equilibria. Let \( s_0 = S_0/N_0 \). The matrices for the new infection terms, \( F \), and the other terms, \( V \), are computed to be

\[
F = \begin{pmatrix}
\beta(1 - p)s_0 \xi & \beta(1 - p)s_0 \\
\beta p s_0 \xi & \beta p s_0
\end{pmatrix},
\]

\[
V = \begin{pmatrix}
1 & 0 \\
0 & \epsilon + \mu
\end{pmatrix}.
\]

The associative basic reproduction number, \( R_0 \), is thus

\[
R_0 = \rho(FV^{-1}) = \frac{[(\epsilon + \mu + d)(1 - p)s_0 + p(1 + d)] \beta s_0}{(1 + d)(\epsilon + \mu + d)},
\]

where \( \rho \) indicates the spectral radius of \( FV^{-1} \).

The nontrivial solutions of model (1) require that the eigenvalues \( \Lambda \) of the linearized system around \( P_0 \) satisfy \( \text{det}[\Lambda I - A_0(\theta) - A_1(\theta)e^{-\tau \Lambda}] = 0 \). Therefore, \( \Lambda \) is a root of the characteristic equation, where \( I \) is the identity matrix with dimension 7 \times 7. The Greek letter \( \theta \) is the vector of the parameters of the system, and

\[
A_0 = \begin{pmatrix}
-d & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & -(1 + d) & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & -(\epsilon + \mu + d) & 0 & 0 & 0 & 0 \\
0 & q & 0 & -\lambda & \lambda & 0 & 0 \\
0 & 1 - q & 0 & 0 & -\lambda & \lambda & 0 \\
0 & 0 & \epsilon & 0 & 0 & -d & 0
\end{pmatrix}
\]

and

\[
A_1 = \begin{pmatrix}
0 & -\beta \xi s_0 e^{-\tau \Lambda} & -\beta s_0 e^{-\tau \Lambda} & 0 & 0 & 0 & 0 \\
0 & \beta(1 - p)s_0 \xi e^{-\tau \Lambda} & \beta(1 - p)s_0 e^{-\tau \Lambda} & 0 & 0 & 0 & 0 \\
0 & \beta p s_0 \xi e^{-\tau \Lambda} & \beta p s_0 e^{-\tau \Lambda} & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0
\end{pmatrix}.
\]

The matrices \( A_0 \) and \( A_1 \) are sparse, and the following eigenvalues are easily obtained: \(-\lambda + \mu + d\) and \(-d\) with multiplicities 2 and 3, respectively. The remaining eigenvalues are computed by the determinant of the following matrix:

\[
M = \begin{pmatrix}
\Lambda + (1 + d) & F_1(\Lambda) \xi & F_1(\Lambda) \\
F_2(\Lambda) \xi & \Lambda + (1 + d) + F_2(\Lambda) \xi \\
F_2(\Lambda) & F_1(\Lambda) & \Lambda + (1 + d) + F_2(\Lambda)
\end{pmatrix},
\]

which is equivalent to

\[
[\Lambda + (1 + d)] [\Lambda + (\epsilon + \mu + d)] - [2F_1(\Lambda)F_2(\Lambda) \xi - (\Lambda + (1 + d))F_2(\Lambda) - (\Lambda + (\epsilon + \mu + d)) \xi F_1(\Lambda)] = 0.
\]

After some algebra manipulation, we obtain

\[
\Lambda^2 + G_1 \Lambda + G_2 = G_2 R_0 F_1(\Lambda)F_2(\Lambda),
\]

where

\[
G_1 = (1 + d) + (\epsilon + \mu + d); \quad G_2 = (1 + d)(\epsilon + \mu + d).
\]
Equation 4 is a continuous function of the delay \( \tau \). For \( \tau = 0 \), one obtains \( F_1(\Lambda) = C > 0, F_2 = C > 0, C \in \mathbb{R} \), and by the Descarte’s rule of signs, the two remaining eigenvalues have negative real parts for \( R_0 < 1 \). Thus, from this fact and Equation 3, we know that all eigenvalues have negative real parts. Consider now the case \( \tau > 0 \). We need to prove that the eigenvalues also have negative real parts in this case. We will show that Equation 3 does not have purely imaginary eigenvalues. By the way of contradiction, we assume that there is \( \omega > 0 \), such that \( \Lambda = i\omega \) is an eigenvalue of (3), i.e.,

\[
-\omega^2 + G_1i\omega + G_2 = G_2R_0F_1(i\omega)F_2(i\omega).
\]

Thus,

\[
\omega^4 + G_1^2\omega^2 + G_2^2 = G_2^2R_0^2|F_1(i\omega)F_2(i\omega)|^2 \leq G_2^2R_0^2
\]

and, therefore, if \( R_0 < 1 \), then the characteristic equation has no purely imaginary eigenvalues. We conclude that \( P_0 \) is locally stable for \( R_0 < 1 \).

4 | SENSITIVITY ANALYSIS

In this section, analyze the sensitivity indices of the reproduction number, \( R_0 \), to relevant parameters of the mSIQR model. It is measured the relative change of \( R_0 \), subjected to the variation of a given parameter. Therefore, we compute the corresponding values for the parameters adopted in the follow-up in Section 5. The signs of the sensitivity indices may be found in Table 2. A positive sign implies that increases in the corresponding parameter values translate in an increase in the value of \( R_0 \). Inversely for a negative sign, a negative index means than an increase in the parameter values implies a decrease in the value of \( R_0 \).

We note that for increased values of the contact rate, \( \beta \), of the parameter accounting for more infectiousness of symptomatic individuals, \( \xi \), and of the proportion of asymptomatic (unknown) infected, \( p \), \( R_0 \) increases. These are all parameters related to higher severity of the disease. On the other hand, an increase in the recovery rate of asymptomatic individuals, \( \epsilon \), as well as on the disease mortality rate, \( \mu \), is associated with a decrease in \( R_0 \), since less infectious people infect a smaller number of susceptible individuals.

In Figures 2 and 3, we depict the variation of \( R_0 \) with some of these parameters. In Figure 2, we observe that \( p \), the proportion of unknown infected, has a significant role in the value of \( R_0 \). From a biological perspective, not knowing the real proportion of asymptomatic infected individuals, brings additional caution and disrupts the implemented measures to fight the disease, since you cannot fight something not observable. The values for the proportion of asymptomatic infectious vary between 17% and almost 50%.\(^{33}\) In general, asymptomatic infections may be missed, unless they are confirmed by reverse transcriptase polymerase chain reaction (RT-PCR) tests or other laboratory procedures. In most countries, these tests are in an early implementation phase, with the governments starting testing the elderly and people with co-morbidities. This means a substantial delay in inferring the real proportion of asymptomatic. Additionally, symptomatic infectious individuals may also be missed if they do not seek medical attention.\(^{34,35}\) Another challenge to control COVID-19 emerged, when recovered patients tested positive for 2019-nCOV. In fact, four patients who had positive RT-PCR test results, 5 to 13 days, were detected, after being discharged from the hospital. These patients met the criteria for hospital discharge or discontinuation of quarantine in China (absence of clinical symptoms and radiological abnormalities and 2 negative RT-PCR test results).\(^{36}\) Thus, some of the recovered patients are virus carriers. More research, in the form of longitudinal studies on larger cohorts, could improve disease prognosis.

In Figure 3, we vary, simultaneously, the contact rate, \( \beta \), and the modification parameter, \( \xi \), which accounts for the increased infectiousness of symptomatic individuals. It is clear from the plot that a more severe scenario, with higher values of the reproduction number (i.e., a higher number of secondary infectious), is associated with increased contact rates and values of the modification parameter. This puts the emphasis on the potential role of some public health measures, also known as, non-pharmaceutical interventions (NPIs), aiming at reducing contact rates in the population, thus halting the virus transmission. Two essential strategies are at hand in these cases: mitigation and suppression. Mitigation is focused on reducing the peak, while protecting those most at risk from severe infection. On the other hand, suppression points to the reversion of epidemic growth, by decreasing new cases’ numbers and sustaining the epidemics forever (at least until a new vaccine becomes available). Both interventions bring concerns/difficulties and their effectiveness may

| Parameter | \( \beta \) | \( \xi \) | \( p \) | \( \epsilon \) | \( \mu \) |
|-----------|-----------|-----------|--------|--------|--------|
| Sign of the sensitivity index | + | + | + | - | - |

TABLE 2 Parameters of model (1)
be limited. Suppression has been implemented in China, South Korea, and Europe with success, but at the costs of social and economic burdens. In the long-run, this may impact negatively health and well-being. As far as mitigation goes, it fails to protect those at higher risk from severe disease and mortality will be high. Bottom line, multiple measures have to be integrated if a substantial and meaningful impact on stopping transmission is to be achieved.37

5 | NUMERICAL SIMULATIONS AND DISCUSSION

In this section, we analyze the numerical simulations of the mSIQR model (1). The initial conditions are set for each country by using the official numbers of inhabitants, of infected in the first day of the pandemic, and deceased individuals. The values of the parameters are given for each country; according to official data, recruitment rate, death rate, and the other parameters are assumed.13,38,39 As mentioned before, the median incubation period of SARS-CoV-2 was estimated to be 4–5 days.15 Thus, we consider a delay of 5–7 days, to account for the appearance of the first symptoms. We remark that many parameters are still unknown, namely, the transmission route, the incubation period, and the survival rates, since their true values will be released only after the pandemic is over. Nevertheless, delivering a list of trustworthy numbers of probable, suspected, confirmed cases and close contacts, updated daily, is a pre-condition for the generation of accurate and precise epidemiological parameters as inputs into mathematical models for disease transmission. This would contribute to increase the awareness of the pandemic evolution and to optimize responses.40

We simulate the mSIQR model for epidemiological valid parameter values and fit the results to real data in four countries, namely, Portugal, France, UK, and USA.

5.1 | Portugal

We seek for the suitable parameters of the mSIQR model to fit the real data of infected population in the country. The data are retrieved from the European Centre for Disease Prevention and Control.41 The fitting has been carried out working with infected cases in 2020, concretely from February 25, 2020, when COVID-19 infections officially started, to December 2, 2020.
It is important to remark that to avoid the possible error in the daily data collection, we have only taken into account the information from each Wednesday. The reason underneath this choice is that Wednesday is a weekday and, as such, the feasible counting error made during the weekends has already been diluted.

The fitting has been performed using an optimization algorithm named the Particle Swarm Optimization (PSO).\textsuperscript{42} It is an iterative meta-heuristic consisting of the evaluation of different sets of parameters, which selects the set with minimal quadratic error. In our setting, the error is given by the difference between the real data and the mSIQR model (1) infected compartment outputs. Table 3 collects the model parameters obtained using the PSO algorithm, with exception of the contact rate, $\beta$, which will be discussed below. Note that the parameter values obtained by this optimization algorithm are in agreement with the ones assumed in the previous studies.\textsuperscript{13,38,39}

Due to the variety of health policies implemented by the government, since the beginning of the pandemics, the contact rate, $\beta$, changed over time. To overcome this issue, we considered different contact rates at different time intervals. The time periods were set to closely match the official dates for the contingency measures for the pandemics, defined by the Portuguese Government, to take effect. It is important to remark that these measures may be reflected in the data after 1 or even 2 weeks; thus, it is possible that the considered periods slightly from the exact dates.

Table 4 collects the time periods together with the corresponding contact rates obtained by the PSO algorithm.

Figure 4 shows the fitting of the real data, namely, the infected population from Portugal, between February 25, 2020, and December 2, 2020, by the results of the simulations of the mSIRQ model, for the same period. Parameter values are depicted in Tables 3 and 4. As is observed, the contact rate, $\beta$, increases in the periods in which there are more reported cases of infection (red dots in Figure 4) and decreases otherwise.

### 5.2 France

We fit the outcomes of the mSIQR model to the number of French COVID-19 infected population. The data have been retrieved from European Centre for Disease Prevention and Control,\textsuperscript{41} and every Wednesday from February 25, 2020, to

| Parameter | $p$ | $\xi$ | $\mu_q$ | $\mu_h$ | $\lambda$ | $\epsilon$ | $q$ |
|-----------|-----|-------|---------|---------|-----------|----------|-----|
| Value     | 0.6000 | 1.0917 | $5.365 \times 10^{-4}$ | 0.0001 | 0.7776 | 0.9486 | 0.8000 |

**TABLE 3** Fitted values of the parameters of the mSIQR model using PSO algorithm according to COVID-19 data in Portugal

| Beginning of the period | End of the period | Contact rate ($\beta$) |
|-------------------------|-------------------|------------------------|
| 1st Period | February 26, 2020 | March 29, 2020 | 1.195 |
| 2nd Period | March 30, 2020 | May 12, 2020 | 0.880 |
| 3rd Period | May 13, 2020 | May 25, 2020 | 0.890 |
| 4th Period | May 26, 2020 | June 8, 2020 | 1.000 |
| 5th Period | June 9, 2020 | August 22, 2020 | 0.910 |
| 6th Period | August 23, 2020 | October 7, 2020 | 0.980 |
| 7th Period | October 8, 2020 | November 30, 2020 | 1.045 |
| 8th Period | December 1, 2020 | December 2, 2020 | 0.9000 |

Note: These contact rates have been obtained by the PSO algorithm.

**TABLE 4** Time periods and their corresponding contact rates in Portugal

![Figure 4](wileyonlinelibrary.com)
Fitting of the number of French infected population (red dots) by the outcomes of the mSIQR model (blue lines), from February 25, 2020, till December 2, 2020. Parameters are given in Tables 5 and 6. Real data collected from European Centre for Disease Prevention and Control [Colour figure can be viewed at wileyonlinelibrary.com]

![Graph showing data fitting](image)

**TABLE 5** Values of the fitted parameters of the mSIQR model according to COVID-19 data in France

| Parameter | Value |
|-----------|-------|
| $p$       | 0.5000 |
| $\xi$     | 1.1999 |
| $\mu_q$   | 0.0019 |
| $\mu_h$   | 0.0117 |
| $\lambda$ | 0.9235 |
| $\epsilon$| 0.9598 |
| $q$       | 0.8000 |

**TABLE 6** Time periods and their corresponding contact rates in France

| Beginning of the period | End of the period | Contact rate ($\beta$) |
|-------------------------|-------------------|------------------------|
| 1st Period              | February 26, 2020 | March 30, 2020         | 1.060 |
| 2nd Period              | April 1, 2020     | May 25, 2020           | 0.800 |
| 3rd Period              | May 26, 2020      | July 15, 2020          | 0.810 |
| 4th Period              | July 16, 2020     | September 2, 2020      | 1.030 |
| 5th Period              | September 3, 2020 | October 14, 2020       | 0.910 |
| 6th Period              | October 15, 2020  | October 28, 2020       | 0.975 |
| 7th Period              | October 29, 2020  | November 11, 2020      | 0.920 |
| 8th Period              | November 12, 2020 | November 18, 2020      | 0.900 |
| 9th Period              | November 19, 2020 | December 2, 2020       | 0.900 |

December 2, 2020 (Figure 5). Table 5 collects the fitted model parameters (except the contact rate) using the PSO algorithm. Table 6 lists the time periods together with the corresponding contact rates.

### 5.3 United Kingdom

UK’s data have been retrieved from the source, and at every Wednesday from February 25, 2020, to December 2, 2020. Table 7 collects the fitted model parameters (except the contact rate) using the PSO algorithm. Table 8 lists the time periods together with the corresponding contact rates.

Figure 6 plots the fitting of the real data from UK infected population (red dots) by the outcomes of the mSIQR model (blue lines), from February 25, 2020, till December 2, 2020. The model parameters are given in Tables 7 and 8. Real data of UK infected population are retrieved from the European Centre for Disease Prevention and Control.

### 5.4 United States

We proceed by the fitting of the infected population in USA, from February 25, 2020, to December 2, 2020. The real data are gathered from the European Centre for Disease Prevention and Control every Wednesday. The model parameters have been fitted using the PSO algorithm, and they are collected in Tables 9 and 10. Figure 7 shows a comparison between the infected population outcomes from the mSIQR model and the data retrieved from the European Centre for Disease Prevention and Control in USA.
### TABLE 7
Values of the fitted parameters of the mSIQR model according to COVID-19 data in UK

| Parameter | $p$ | $\xi$ | $\mu_q$ | $\mu_h$ | $\lambda$ | $\epsilon$ | $q$ |
|-----------|-----|------|-------|--------|---------|---------|-----|
| Value     | 0.6000 | 1.0000 | 0.0010 | 0.0103 | 0.9042 | 0.9900 | 0.8000 |

### TABLE 8
Time periods and their corresponding contact rates in UK

| Period     | Beginning of the period | End of the period | Contact rate ($\beta$) |
|------------|-------------------------|-------------------|-----------------------|
| 1st Period | 26-February 26, 2020    | April 1, 2020     | 1.140                 |
| 2nd Period | 02-April 2, 2020        | April 22, 2020    | 0.955                 |
| 3rd Period | 23-April 23, 2020       | June 10, 2020     | 0.960                 |
| 4th Period | 11-June 11, 2020        | July 15, 2020     | 0.980                 |
| 5th Period | 16-July 16, 2020        | August 26, 2020   | 1.081                 |
| 6th Period | 27-August 27, 2020      | September 30, 2020| 1.031                 |
| 7th Period | 1-October 1, 2020       | October 21, 2020  | 1.035                 |
| 8th Period | 22-October 22, 2020     | November 10, 2020 | 1.100                 |
| 9th Period | 11-November 11, 2020    | November 18, 2020 | 1.085                 |
| 10th Period| 19-November 19, 2020    | December 5, 2020  | 1.220                 |

### FIGURE 6
Fitting of the number of UK infected population (red dots) by the outcomes of the mSIQR model (blue lines), from February 25, 2020, till December 2, 2020. Parameters can be found in Tables 7 and 8. Data taken from European Centre for Disease Prevention and Control41 [Colour figure can be viewed at wileyonlinelibrary.com]

### FIGURE 7
Fitting of the number of COVID-19 infected population in USA (red dots) by the outcomes of the mSIQR model (blue line), from February 25, 2020, to December 2, 2020. Parameters in Tables 9 and 10. Real data gathered from European Centre for Disease Prevention and Control41 [Colour figure can be viewed at wileyonlinelibrary.com]

### TABLE 9
Values of the fitted parameters of the mSIQR model according to COVID-19 data in USA

| Parameter | $p$ | $\xi$ | $\mu_q$ | $\mu_h$ | $\lambda$ | $\epsilon$ | $q$ |
|-----------|-----|------|-------|--------|---------|---------|-----|
| Value     | 0.5000 | 0.2419 | $1.3769 \times 10^{-6}$ | $4.2521 \times 10^{-5}$ | 0.6762 | 0.9429 | 0.8000 |
TABLE 10  Time periods and their corresponding contact rates in USA

| Period          | Beginning of the period | End of the period | Contact rate (\(\beta\)) |
|-----------------|-------------------------|-------------------|--------------------------|
| 1st Period      | February 26, 2020       | April 1, 2020     | 1.930                    |
| 2nd Period      | April 2, 2020           | April 22, 2020    | 1.500                    |
| 3rd Period      | April 23, 2020          | June 10, 2020     | 1.490                    |
| 4th Period      | June 11, 2020           | July 15, 2020     | 1.605                    |
| 5th Period      | July 16, 2020           | August 26, 2020   | 1.590                    |
| 6th Period      | August 27, 2020         | September 30, 2020| 1.770                    |
| 7th Period      | October 1, 2020         | October 21, 2020  | 1.925                    |
| 8th Period      | October 22, 2020        | November 10, 2020 | 2.230                    |
| 9th Period      | November 11, 2020       | November 18, 2020 | 2.750                    |
| 10th Period     | November 19, 2020       | December 2, 2020  | 3.150                    |

TABLE 11  Reported cases of 2019-nCOV infection for a set of countries, as of August 19, 2021\(^{13}\) (rounded to k or M)

| Country       | Total confirmed | Total deaths |
|---------------|-----------------|--------------|
| United States | 37.97 M         | 626 k        |
| Brazil        | 20.6 M          | 576 k        |
| France        | 6.5 M           | 112 k        |
| Spain         | 4.8 M           | 83 k         |
| Italy         | 4.5 M           | 129 k        |
| Iran          | 4.8 M           | 104 k        |
| Germany       | 3.9 M           | 92 k         |
| Japan         | 1.4 M           | 15 k         |
| Portugal      | 1.02 M          | 17 k         |
| South Korea   | 243 K           | 2k           |
| China         | 122 k           | 5.6 k        |
| Singapore     | 66.8 k          | 52           |
| New Zealand   | 3.227           | 26           |

5.5  Remarks

The figures of the pandemic as of August 19, 2021, are given in Table 11, for a set of countries.

The countries have been heterogeneous in the implementation of control measures. Even with only 1 week apart with respect to the application of social distance and closing schools and commerce, were observed differences in the magnitude of thousands of deaths and poor control, as can be seen from the active infection numbers.\(^{3,43}\) The worst countries in Europe are Russia, France, and UK. They are followed by Turkey, Spain, and Italy. In the EU/EEA, as of week 2021-32, 35,848,469 cases of infection have been reported. France takes the lead with 6,471,035, followed by Spain (4,719,266), Italy (4,440,669), and Germany (3,823,139). These four countries are also the ones with a heavier death burden, with Italy at the first place, with 128,432, followed by France (112,702), Germany (91,871), and Spain (82,595). The pandemic in USA has been characterized by an increasingly large number of deaths, and the load of hospitals to manage, in intensive care units (ICU), has been very distant from their capacity.\(^{44}\) US citizens went from being worried about confinement measures in the beginning, to be overwhelmed by the major deaths tolls due to the fast disease progression.\(^{45,46}\) Singapore, after being considered as an example to control the pandemic, faced other outbreaks, with thousands of new reported infection cases. This was due to the opening of the economy and the re-entrance of the 200,000 foreign workers in the country. The social proximity of these foreign workers in the social houses they live in, boosted the spread of the infection again. Strict control measures to slower the transmission has to be established again.\(^{47}\) New Zealand has been so far the country with low case rates, small number of deaths, and hospital admissions. New Zealand’s President Jacinda Kate started an inflexible public health intervention, with compulsory self-isolation for travelers, border closure, national lockdown, isolation of cases, and close contacts, which significantly impacted the figures of the pandemic. Together with the geographical isolation, this led to a first elimination of COVID-19 pandemic around June 2020. Though a few successive cases have burst, due to border incursions, the aggressive health policies provide positive outcomes with respect to disease control.\(^{48}\)

In summary, from what is written since WHO declared COVID-19 as a Public Health Emergency of International Concern, on January 30, 2020, the countries are deciding on the basis of what they learn from the neighbor next door. Nobody knows, including official entities, the exact number of COVID-19 illnesses, hospitalizations, and deaths for a variety of reasons. It can be mentioned the heterogeneity of symptoms, which range from mild illness to severe, the delay in the onset of symptoms, the reporting, and testing, is being done with relevant interludes; some people may get the disease and...
never be tested or seek medical attention. Moreover, there may be differences in the way the official data from COVID-19 in each country is being released, namely, the number of active cases, of reported deaths, and recovered people.45

6 | CONCLUSIONS

Ever since the 2009 H1N1 influenza outbreak, mathematical models and computational methods have been used to predict the patterns of disease transmission. The outcomes of the models provide insights on how to proceed to flatten the curve of active infections and stop the spread of the disease. Though it is known that every model is imperfect, if used in the right way, it is better than flying blind.

In this study, we propose the mSIQR model, for the dynamics of the COVID-19 pandemic in the world. Our model is a simple model but reflects the patterns seen in the COVID-19 pandemic throughout the world, before the beginning of the vaccination process. The model is fitted with COVID-19 data from several countries, and the fitting is adequate. Having said this, there are still major aspects of the pandemic that remain unanswered, such as the source of the infection, though it is known is a zoonotic disease, the transmission rate, the survival and death rates, the immunity period, incubation period, and others. Nevertheless, from an extensive survey of papers on COVID-19 published in the literature, we were able to provide epidemiological reasonable estimates for the parameters. Future work will focus in a more realistic model for the dynamics of the pandemic, subjected to the influence of policy measures, treatment, and vaccines,49,50 though we can only obtain an accurate mSIQR model, after the outbreak ends.

The evolution of the pandemic is still uncertain. Accurate and precise parameter values are needed as inputs into epidemiological models, to predict and advise on policy measures. Clinical spectrum and 2019-nCOV infections severity profile are required, in particular those from patients with mild or sub-clinical presentations. Asymptomatic carriers are a threat for the halting of the pandemic. Moreover, pre-symptomatic transmission also causes concerns and undermines tracing. The emphasis is also in more testing, which could mean a spike in the active case counts, but would provide trustworthy figures of the real pandemic.

The governments are put under considerable pressure, with consequences of the outbreak spreading from public trust to economy. Any mismanagement implies political costs, and governments are asked to be transparent; otherwise, public opinion will enter a mistrust cycle.51

Meanwhile, throughout the world, researchers from several health organizations continue to conduct studies, running against time, to find the most effective treatment and the most powerful vaccine. An effective treatment may lower the severity of the disease in some cases and decrease the demand for critical care beds. WHO announced, on March 20, 2020, a large global trial, named SOLIDARITY, to identify new treatments for 2019-nCOV. The four most promising therapies, according to WHO, are remdesivir, experimental antiviral compound; chloroquine and hydroxychloroquine, malaria medications; lopinavir and ritonavir, HIV drugs; and that same combination plus interferon-beta, an immune system messenger that can help cripple viruses. The French biomedical research agency, INSERM, informed that will conduct an add-on trial in Europe, Discovery, following WHO’s example, testing the same drugs, except for chloroquine.52 In what concerns vaccines, there are pharmaceutical giants and laboratories working in their development since almost the beginning of the pandemics.53,54 Testing in humans continues, and currently, some of these pharmaceutics are already producing third shot doses of their vaccines, to boost immunity in specific groups of people.55,56 Israel is taking the lead with the approval of a third dose to elderly late July 2021.50

The future encompasses a major global effort, gathering learning and experience from across the world and scientific areas, to be able to progress in the understanding of this disease, and other future probable ones. Significant investments have to be made to provide effective treatment and vaccines to everyone. The UN Secretary-General António Guterres, in his message of April 24, 2020, pleads for the global collaboration to a faster development, production, and non-discriminatory access to new COVID-19 tools.57 Moreover, the director-general, Tedros Adhanom Ghebreyesus, publicly asked drug-makers to prioritize the supply of COVID-19 vaccines to the poorer countries, since only 1% of their inhabitants received a COVID-19 vaccine shot and the majority only had one shot. The disparities between countries may delay the control of the pandemic worldwide, with the appearance of more aggressive variants.58 The infectious disease specialist, Jesse Goodman, refers that “Even if we don’t have a critical situation right at the moment … there’s a realistic possibility that variants will continue to evolve that have potential to avoid vaccine immunity.” Anthony Fauci, the director of the National Institute of Allergy and Infectious Diseases Fauci, adds that “you still have a fixed immunogen and a virus that’s changing. Sooner or later, you’re going to get a mutant that evades that.”58 Thus, uncertainty still rules our daily lives and advises to continue to mask up and to maintain social distance in public places, even when fully vaccinated.
We end this study with a sentence that resumes the importance of models, *All models are wrong, but some are useful*—George E. P. Box.

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CONFLICT OF INTEREST

This work does not have any conflict of interest.

ORCID

Carla M. A. Pinto
https://orcid.org/0000-0002-0729-1133

J. A. Tenreiro Machado
https://orcid.org/0000-0003-4274-4879

Clara Burgos-Simón
https://orcid.org/0000-0001-6385-4263

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