

# A Real-Time Identification Algorithm and Epidemic Model Associated with Social Distancing Index for Control Applications: COVID-19 Analysis and Simulations in the United States

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## ABSTRACT

The COVID-19 pandemic, caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is already the most worrying health problem worldwide. The virus spread rapidly across the countries, making many researchers looking for answers to mitigate the disease's effects. While vaccines are not available on a large scale, mathematical modeling has allowed the scientific community to perform forecasts for decision-making and social distancing policies to decrease the velocity of the COVID-19 transmission. However, dynamic models must represent the pandemic's reality considering validation criteria and an appropriate procedure that ensures realistic simulations. These principles are the only way to make an epidemiological model useful for studying and analyzing practical effects. From a control theory point of view, representative models ensure optimal solutions and allow a more reliable and robust control strategy. Therefore, this paper proposes a parameter identification algorithm for a dynamic pandemic disease model spread, including a new time-varying parameter for control applications. The developed framework uses an epidemiological model, denoted here as , capable of associating the real pandemic dynamics to its biological parameters and the population social mobility in real-time, which can be led by an appropriate optimal control strategy. Simulations and forecasts are performed comparing with official data of the epidemic in the United States.

## Introduction

The COVID-19 pandemic is indeed the most severe problem in terms of public health of the last hundred years in the world. The first disease case caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was reported in Wuhan (Hubei province), China, in December 2019 [1]. The virus spread rapidly across the countries, making Europe the epicenter of the epidemic in March 2020 and reaching North and South America, especially the United States and Brazil, killing millions of people. Since the World Health Organization (WHO) declared an international emergency on January 31, 2020, many researchers have been mobilized to find answers to mitigate the effects of the COVID-19. Although professionals well know this type of subject from the health area [2,3], other different scientific communities from

mathematics, physics, and engineering have proposed strategies of forecasts, decision-making, and social distancing to decrease the velocity of the disease transmission [4-6]. In this context, the art of mathematical modeling [7] appears as an efficient technique to analyze and develop practical solutions for dynamic systems like an epidemic. The first mathematical model on theoretical epidemiology was proposed by Kermack and McKendrick [8] whose differential equations can represent the dynamics of susceptible (not yet infected with the disease) individuals, the number of active infected, and the individuals that are recovered and became immune to the virus. Known as the SIR model, researchers have used its properties and structure to describe the COVID-19 epidemic. In the work of Wu et al. [9], the SIR model was used to analyze the

real transmission and death dynamics of the coronavirus in Wuhan, China. Furthermore, official data were employed in the model to estimate clinical severity and risks, which could support public health decision-making. Postnikov [10] demonstrated that the SIR model could be simplified to a logistic function in which simulation results presented good accuracy with real data. This model is applied in different forecast scenarios for India's current epidemic and four of its cities, as presented by Malavika et al. [11].

Nevertheless, equivalent models and expansions of the SIR model are used in epidemiological studies for COVID-19. Annas et al. [12] analyzed the stability and simulated outlines in Indonesia using a SEIR model and considering the epidemic effects due to isolation and vaccine. Rajagopal et al. [13] proposed a SEIRD model with fractional derivatives to represent the disease in Italy and predict the outbreak's peaks, in which the authors base the results on real data. Thus, as classes of individuals, dynamic parameters, and intervention measures are included, these extended models became more complex [14-16]. Besides, other types of model which use signals and time series, deterministic and stochastic approaches can be found in the literature [17-19]. It is clear that these models are indispensable to understand the epidemic dynamics in order to avoid new infection and death cases, and promote governmental policies which enhance recovered individuals and decrease the negative effects of the COVID-19. However, validation procedures are required to use the models in practice. Generally, the recent literature has presented COVID-19 epidemiological models with incomplete validation criteria or numerical algorithms which deteriorate the real parameters. On the other hand, the epidemiological models that represent realistic scenarios guarantee practical and feasible solutions. Hence, in particular, engineering applications such as simulation [20], design [21], education [22], optimization and control [23] bring us an important perspective to face this terrible disease.

Since few vaccines are previewed to be available to the people, especially in developing nations, social distancing is a fundamental method adopted by the governors to opposite the pandemic spread. The intention is to lower the probability of the virus transmission and slow the number of infected people. Flattening the curve of active infected prevents the collapse of the health systems caused by numerous patients with COVID-19 being treated and contributes to preventing the disease spread. The critical matter is when applying the social distancing and for how long. In this sense, the control engineering aided by epidemiological models can determine strategies of social distancing that balance health and economic aspects [24-27]. For this, a social distancing variable has to be incorporated into the epidemiological models. Based on the preceding, an identification algorithm for epidemic control is proposed in this work. The procedure is composed of two layers: the first one uses a discrete analytical equation to calculate the exact parameters which represent the system dynamics, and the second one, employing an optimization formulation used as a

slight adjustment, approximates as closely as possible the epidemic curves to the real data, aiming to fit the dynamic model. Moreover, a social distancing variable is incorporated into the algorithm to relate its real effects on the epidemic, allowing proper predictions and investigation for control strategies.

The paper is organized as follows: in Section 2, the proposed parametric identification algorithm is explained in detail using the adapted  $SIRD + \Psi$  model structure. In Section 3, the model identification is performed, validated, and applied to simulate scenarios in the United States at different periods of the COVID-19 pandemic. In Section 4, a perspective and design of optimal control techniques that could be employed using the epidemiological model to mitigate the pandemic are approached; and the conclusions are stated in Section 5.

## The Structure Model and Algorithm Description

The Susceptible-Infected-Recovered-Deceased (SIRD) model is used in this work since its equations are able to adequately describe the dynamic behavior of the SARS-CoV-2 [28,29]. As shown in the following, a dynamic variable representing the social distancing responses due to isolation policies is included in the model, denoted as  $SIRD + \psi$ .

### Epidemiological Model

The SIRD model examined in this paper describes the dynamics of a population divided into compartments of susceptible (S) and symptomatic (reported) infections (I). The reported infections may present moderate to severe symptoms and, after the infection period, individuals may recover (R) from the disease or, in severe cases, result in death (D).

Thus, the  $SIRD + \psi$  model is expressed by the following nonlinear differential equations:

$$\begin{cases} \frac{ds}{dt} = -(1 - \Psi(t)) \frac{\beta(t)I(t)S(t)}{N(t)} \\ \frac{dI}{dt} = (1 - \Psi(t)) \frac{\beta(t)I(t)S(t)}{N(t)} - (\gamma(t) + \alpha(t))I(t) \\ \frac{dR}{dt} = \gamma(t)I(t) \\ \frac{dD}{dt} = \alpha(t)I(t) \end{cases} \quad [SIRD + \Psi], \quad (1)$$

wherein the parameter  $\beta(t)$  is the transmission rate;  $\gamma(t)$  is the recovery rate, removing some individuals from the infected class, and the parameter  $\alpha(t)$  denotes the observed mortality rate of the virus. Social distancing index caused by mobility reduction measures is expressed by  $\psi(t)$ , denoting restrictions on the circulating of people, i.e.,  $\Psi(t)=1$  stands for a complete lockdown, whereas  $\psi(t)=0$  means no social distancing. Note that these parameters may not be constant and may vary according to the stage of the pandemic. It is reasonable to think that, in the case of the virus does not mutate, the identified disease parameters tend to stabilize at a natural point. However, new events, such as changes

in medical treatments or new government protocols, can affect the disease dynamic and consequently modify the SIRD parameters.

The size of the total population exposed is denoted by  $N(t)$  and, in this work, it is assumed that natural deaths balance the newborns; which holds that  $N(t) = N_0 - D(t) = S(t) + I(t) + R(t)$ , wherein  $N_0$  is the initial population size (before the contagion). Moreover, the term  $\beta(t)I(t)/N(t)$  represents the average number of contacts that is sufficient for viral transmission from one susceptible individual, per unit of time. Also,  $\beta(t)I(t)/N(t)S(t)$  counts as the total number of new cases from the number of susceptible individuals, per unit of time. Another essential information in epidemiology is the basic reproduction number, usually denoted by  $R_0$ . This factor can measure the average potential transmissibility of the disease. In a practical analysis, the  $R_0$  how many expected cases could be generated by a single primary case in a population where all individuals are susceptible. Theoretically, this property does not vary in a stabilized contagions situation due to the virus's supposed and predetermined nature. However, the virus's biological characteristics are not constant, and health policy measures change the number of susceptible people over time. The effective reproduction number  $R_t$  represents how the pandemic, indeed, is spreading. In a dynamic systems viewpoint,  $R_t$  calculates the epidemic velocity. If  $R_t > 1$ , the infection is spreading, and the number of infected people increases at the beginning of the epidemic. Otherwise, if  $R_t < 1$  it means more individuals leaving from the infected class than new infections occurring, either recovering or dying and, therefore, the epidemic ceases.

As will be seen later, the effective reproduction number is given according to the epidemiological parameters calculated and the registered social distancing index along time.

### Identification Algorithm

Recent numerical algorithms have been applied to calculate the parameters of the COVID-19 model [30-33]. Nonetheless, due to the degree of freedom given by Eq. 1, different parametric values can produce equivalent results in relation to the number of susceptible, infected, recovered, and deceased individuals. In other words, there is no one unique solution for the parameters which solver the numerical estimators. Although mathematical and graphical criteria have been used to validate these dynamic models when compared with real data, different values for the same parameters affect the epidemic characterization, for instance, the effective reproduction number ( $R_t$ ). Therefore, in order to be able to describe the pandemic behavior, especially for forecast and control, it is proposed a two-step identification method for the parameters  $\beta(t)$ ,  $\gamma(t)$  and  $\rho(t)$ . As the first step, this procedure includes a discrete analytical formulation derived from Eq. 1 and, subsequently, an optimization algorithm based on the Ordinary Least Square minimization method to adjust the found parameters in a small defined bound. Thus, the algorithm developed here ensures appropriate parameters that characterize the epidemic's

reality since analytical calculations are used from the  $SIRD + \Psi$  model concepts, and it can adjust the model responses according to the official data.

As the published data are available with a sampling time of  $T_1$  and the proposed algorithm organizes time series packs of  $T_2$  units of time used as calculus basis, the first layer calculates the exact values of the parameters from a discrete analytical mode as follows:

$$\bar{\gamma}(k) = \frac{R(k_f) - R(k_i)}{\sum_{i=k_i}^{i=k_f} I(i)} \quad (2)$$

$$\bar{\alpha}(k) = \frac{D(k_f) - D(k_i)}{\sum_{i=k_i}^{i=k_f} I(i)} \quad (3)$$

$$\bar{\beta}(k)(1 - \bar{\Psi}(k)) = \frac{I(k_f) - I(k_i) + (\bar{\alpha}(k) + \bar{\gamma}(k)) \sum_{i=k_i}^{i=k_f} I(i)}{\sum_{i=k_i}^{i=k_f} S(i)I(i)/N(i)} \quad (4)$$

wherein  $k = 1, 2, 3, \dots, j$  with  $j = T_p/T_2$  being the number of time series packs and  $T_p$  the pandemic duration.  $\bar{\Psi}(k)$  is the average social mobility index within the interval of the time series pack  $k$ , delimited by the first and last points which are  $k_i$  and  $k_f$  respectively. Furthermore, note that, for any generic parameter,  $\chi(t) = \chi(k)$ , in which  $t \in [(k-1)T_2, kT_2]$ . Nevertheless, assuming that the data might be corrupted by minor issues, for instance, cases that are not reported in the day and are accumulated for the next day, or misreported cases, the calculated parameters are strictly adjusted by the second layer (optimization stage). This method allows improving identification reliability since this situation has been seen in different countries [26]. Once again, the available real data from the same interval  $i \in [k_i, k_f]$  are used to minimize the OLS problem, providing the data vector  $S, I, R$  and  $D$ . On the optimization loop, a dynamic  $SIRD + \Psi$  model takes into account the decision variables  $\beta, \gamma, \alpha$  and the initial values  $S(k_i), I(k_i), R(k_i)$  and  $D(k_i)$  to estimate the values of  $I, R$  and  $D$  from  $k_i$  to  $k_f$ . At each interaction, the optimization layer minimizes the error between the real data and its estimated values from the  $SIRD + \Psi$  model choosing the decision variables accordingly,  $\beta, \gamma, \alpha$ . The error is then calculated as:

$$Er_I(i) = (I(i) - \hat{I}(i, \hat{\beta}(1 - \Psi(t)), \hat{\gamma}, \hat{\alpha}))^2,$$

$$Er_R(i) = (R(i) - \hat{R}(i, \hat{\beta}(1 - \Psi(t)), \hat{\gamma}, \hat{\alpha}))^2,$$

$$Er_D(i) = (D(i) - \hat{D}(i, \hat{\beta}(1 - \Psi(t)), \hat{\gamma}, \hat{\alpha}))^2,$$

for which the variables  $\hat{I}, \hat{R}, \hat{D}$  are estimated according to the  $SIRD + \Psi$  model equations. The complete optimization problem is formulated as follows:

$$\min_{\beta, \gamma, \alpha} j = \sum_{i=k_i}^{i=k_f} (w_1 Er_I(i) + w_2 Er_D(i)),$$

$$\text{s.t.:} \quad \delta \bar{\beta}(1 - \bar{\Psi}) \leq \beta(1 - \Psi(t)) \leq \bar{\delta} \bar{\beta}(1 - \bar{\Psi}), \quad (5)$$

$$\underline{\delta} \bar{\gamma} \leq \gamma \leq \bar{\delta} \bar{\gamma},$$

$$\underline{\delta} \bar{\alpha} \leq \alpha \leq \bar{\delta} \bar{\alpha}.$$

wherein  $\underline{\delta}$  and  $\bar{\delta}$  are the uncertainty interval to define the lower and upper bound of each decision variable on the optimization problem, and  $w_1, w_2$  are taken as positive weighting values tuning parameters, used to normalize the magnitude order of the total cost concerning variables  $Er_1$  and  $Er_r$ .

The optimization algorithm employs a window of  $k_f - k_i + 1$  units of time. The second layer finally provides as output the optimal values  $\beta_{opt}, \gamma_{opt}$  and  $\alpha_{opt}$  that can be used for forecasting and control and to calculate the effective reproduction number  $R_t$ . The algorithm also fit the  $SIRD + \psi$  model curve with real data using the optimal parameters. It is worth mentioning that this is an innovative and fundamental advantage of the method proposed in this work: to identify the relation between real social mobility, which may be used as a means of control strategy, and the parameters of the current pandemic. As depicted in the work of Fernandez-Villaverde and Jones [34], dealing the  $SIRD + \psi$  model with  $\beta$  associated with social distancing, the effects on the epidemic can be analyzed as a function of transmission rate inherent to the virus and health policies, which connects the model better and improves accuracy to fit data. As a result, the proposed methodology allows reliable forecasting, mainly regarding stringency formulations.

The parameters  $\beta, \gamma, \rho,$  and  $\psi$  are used to calculate the pandemic growth velocity since they are related to the rate of infected individuals. Thus, assuming that, at the beginning of the pandemic,  $S \approx N, R_t$  can be approximated as follows:

$$R_t(k) \approx \frac{(1 - \bar{\Psi}(k))\beta(k)}{\gamma(k) + \alpha(k)} \quad (6)$$

### Design of Parameterization and Implementation

Since government data sources disclose daily samples of the pandemic dynamics, counting the infections cases and deaths, the unit of time as calculus basis used in the algorithm is day. Therefore, it is intuitive to choose a sampling time of  $T_1 = 1$  day for the discrete-time dynamics samples in the interval  $i$ . Still, as the algorithm organizes the data in time series packs composed of each  $T_2$  days,  $T_2$  is tuned as the disease's average incubation period. Thus, each estimated epidemiological parameter  $x(k)$  refers to the pandemic's dynamics behavior for each  $T_2$  days along the time. Finally, the proposed identification algorithm is illustrated by the system shown in Figure 1. The procedure starts collecting the available real data from the first ( $k = 1$ ) time series pack of  $T_2$  days split into  $T_1$  sample periods within the interval points  $i \in [k_i, k_f]$ . Using the number of active infected  $I(i)$ , recovered  $R(i)$ , and fatal  $D(i)$  cases, the epidemiological parameters are calculated in the first layer of the system through the Eqs. 2, 3 and 4. Considering the data are reliable, the obtained parameters define the epidemiological characteristics properly since the set of equations provides a unique solution. Nonetheless, noises and small errors mislead the measurements. Thus, these parameters are sent to the second layer, where a fine-tuning using the optimization algorithm ensures the best values to improve the dynamics curves. In this sense, in each period of  $T_2$  days, we have the epidemiological parameters to calculate the current pandemic situation using the  $R_t$  and simulate scenarios and predictions. These stages run continuously in the loop until the epidemic ends.

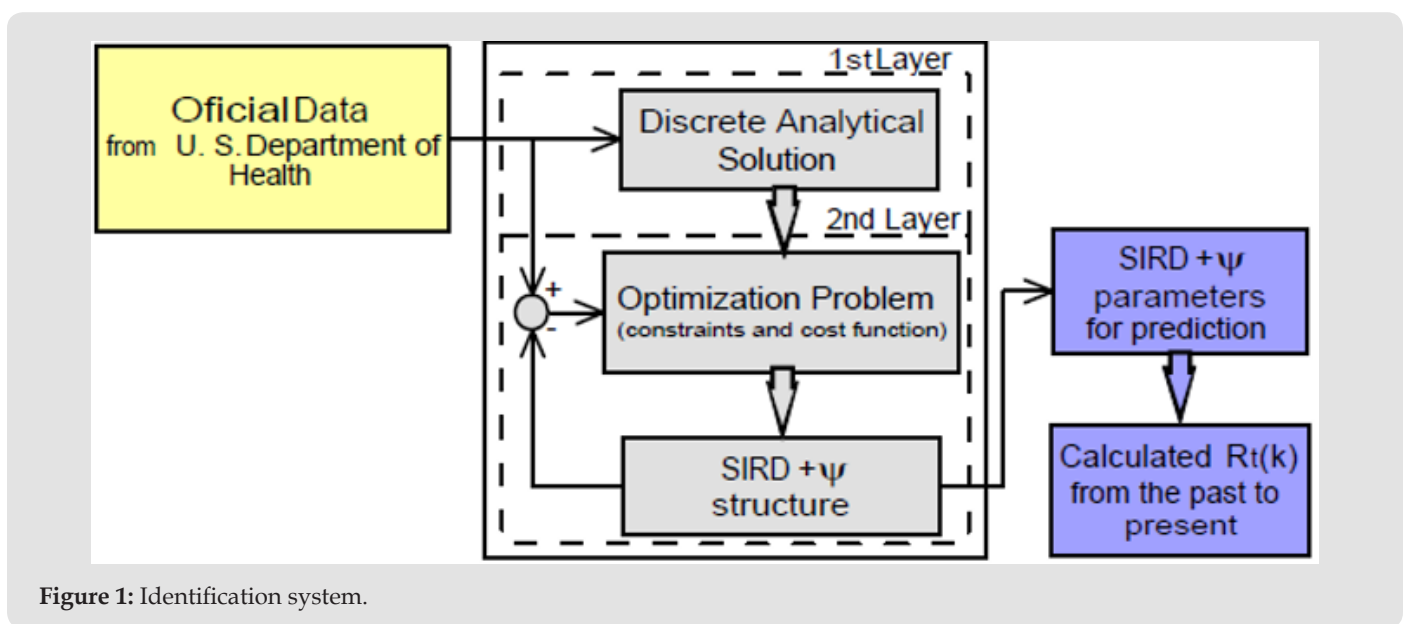


Figure 1: Identification system.

### Results and Discussion

The identification procedure considers the number of cumulative cases, cumulative deaths, and active infected cases, for

which we use the available dataset from official entities [35-37]. In this scenario, we propose the identification algorithm for  $T_1 = 1$  and  $T_2 = 14$  days, which means that the model is simulated every day

and the parameters would slightly change every two weeks. For the social distancing index, we consider the rates provided by OpenPath [35]. This metric considers people’s access patterns and entries in workplaces and several locations, including business facilities, gyms, healthcare stations, government locations, and educational centers. The methodology is to compare people’s access to these locations to their accesses before the COVID-19 pandemic, thus, being possible to illustrate the social mobility trend around the country. Figure 2 illustrates the social distancing index in the United States from March 8, 2020, until December 12, 2020 for each week. In this section, we present the results of the identification procedure. In order to improve the model fit, we propose the weighing gains of the cost function in Eq. 5 as  $w_1 = 1$  and  $w_2 = 25$ . Moreover, we define the uncertainty intervals as 10% to parameters  $\gamma$  and  $\alpha$ , and 20% to parameter beta, since the inclusion of the variable  $\Psi(t)$  can add noise in the model dynamic and compromise the identification robustness. We propose 3 scenarios to analyze the performance and reliability of the identification procedure, diving the data set in 3 periods: the first one is from February 1 to May 20, defined as the beginning of the pandemic using 120 days of data. The second

scenario goes beyond, until September 17, where it is related to the middle period of the pandemic, using 240 days of data. The last scenario is the current stage of the pandemic, wherein the data goes until December 13, totaling 327 days of data. For the model curves, we proposed a error margin of 10% as an extrapolation of the identified model dynamics. The pandemic curves for validating the first scenario with identification algorithm are depicted in Figures 3-5. In this stage, it was used 110 days to identify the parameters considering the sample time of  $T_2$ . The last 10 days are used as prediction of the model, in which the last identified values of  $\beta$ ,  $\gamma$  and  $\alpha$  are kept constants in this forecast period, as well as the last value of  $\Psi(t)$ . It can be noticed that the curves of cumulative infected cases and deaths present a very well fit. However, the new cases, new deaths recovered, and active infections curves still present an error between the real data and the curves. These results are expected since the algorithm considers the error minimization only for the cumulative cases and deaths, while the other curves are not considered in the identification procedure. Nevertheless, when it is inputted more information into the identification procedure, all curves’ fitting improves.

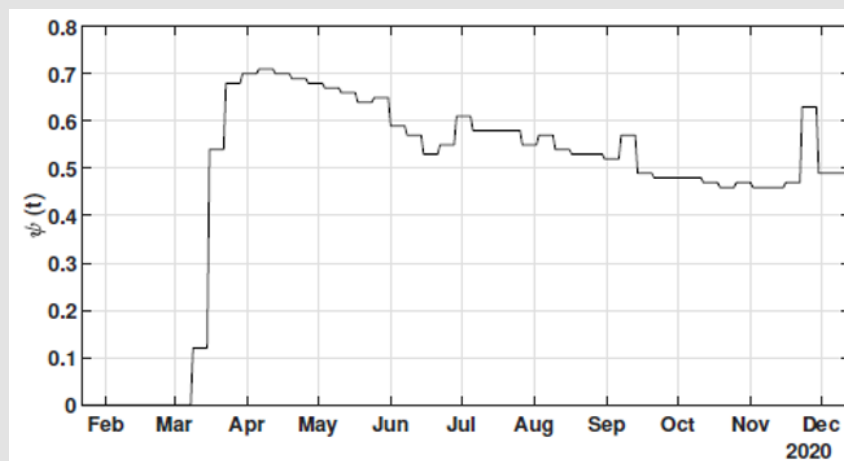


Figure 2: Social distancing index in the United States.

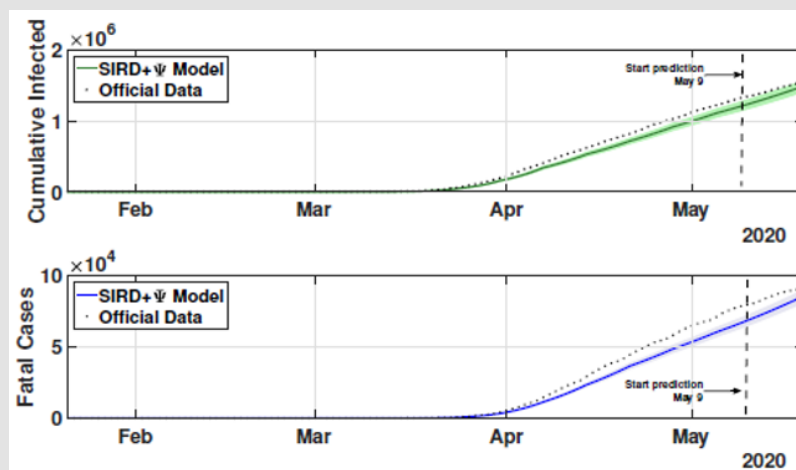


Figure 3: Cumulative and fatal cases for the first scenario from February 21 to May 20.

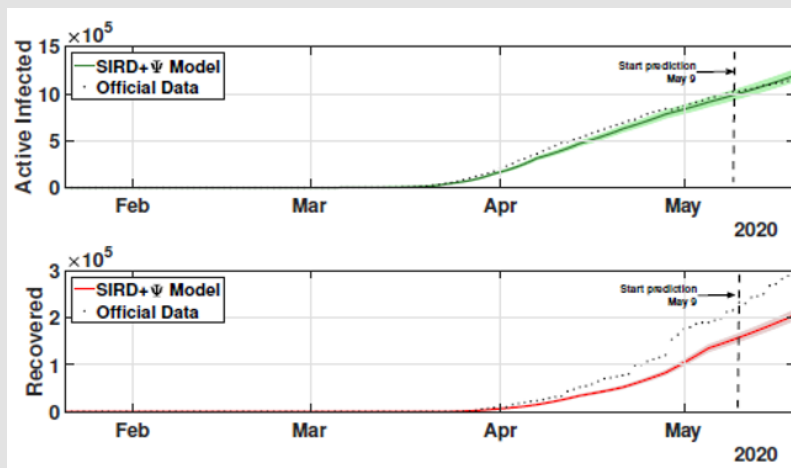


Figure 4: Active and recovered cases for the first scenario from February 21 to May 20.

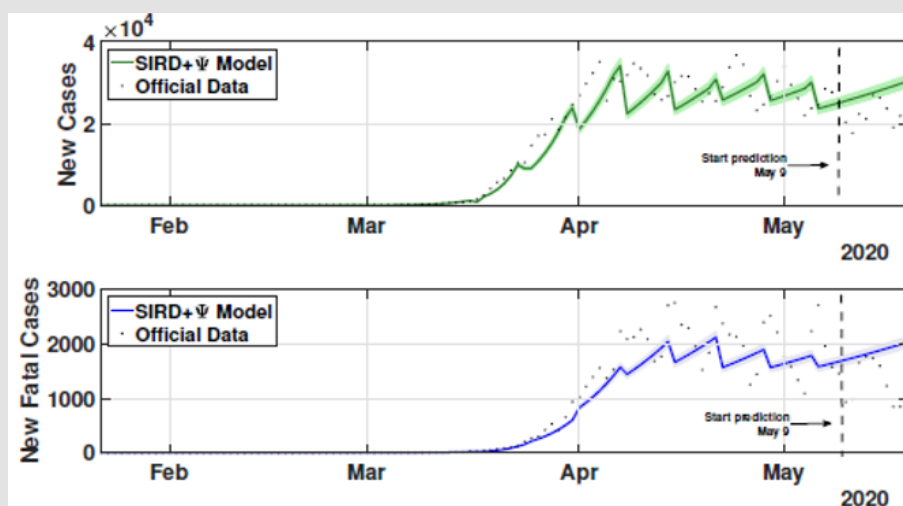


Figure 5: New infected and new fatal cases for the first scenario from February 21 to May 20.

These effects can be shown in Figures 6-8. In these cases, we used the first 224 day to identify the model parameters to the same time window  $T_2 = 14$  days, and we use the last 16 days to validate the estimated pandemic curves. As can be seen, the model curves and the data agreement improves, including for the curves of new cases, new deaths, active infected individuals, and recovered cases. Moreover, since the model fit improves with more available data, it allows the designer to perform longer forecasting periods, significantly influencing control strategies' design. Finally, we perform the identification procedure to the total available dataset, using the 327 days (also, with  $T_2 = 14$  days). In this last scenario, we still perform the validation stage using the last 20 days, keeping the last identified parameters constants in the forecast period. The parameters are identified to the first 307 days of data considering. Figure 9 shows the identified parameters for the last scenario and Figures 10-12 show the pandemic model curves and the real data. The effective reproduction number of all time including the three scenarios is shown in Figure 13. Although the  $R_t$  values found are

consistent, it is important to highlight that its estimations depend on the measured data and, thereby, unreported or delayed reported cases produce some errors in these calculations. Furthermore, to illustrate the model fit, we propose the coefficient of determination metrics, R-square, which analyzes how properly the dataset can be explained by the model curves given by the percentage variation between both variables. The more the R-square approaches 1, the more reliable the identified model is to represent the dataset. Table 1 depicts the R-square coefficients for the three proposed scenarios.

Table 1: R-square metrics for model curves in each identified scenario.

	Scenario 1	Scenario 2	Scenario 3
Cumulative cases	0.9858	0.9992	0.9991
Fatal cases	0.9684	0.9835	0.9917
Active infected	0.9928	0.9786	0.9665
Recovered	0.8643	0.951	0.9526

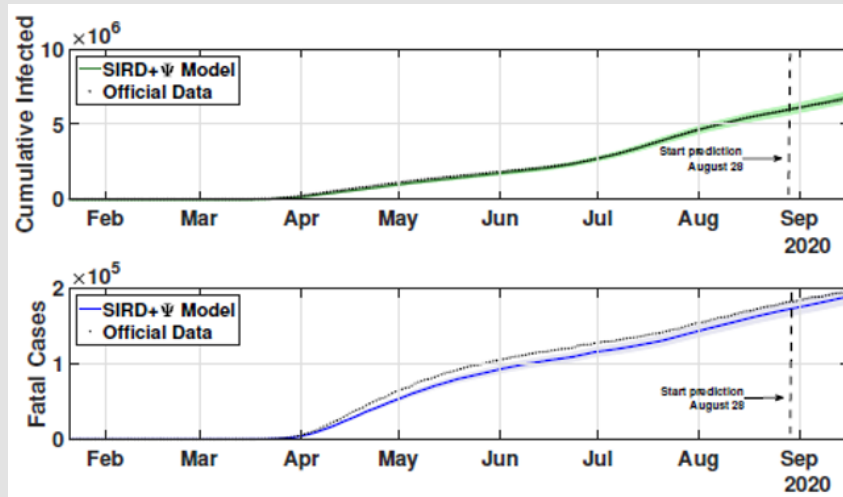


Figure 6: Cumulative and fatal cases for the second scenario from February 21 to September 17.

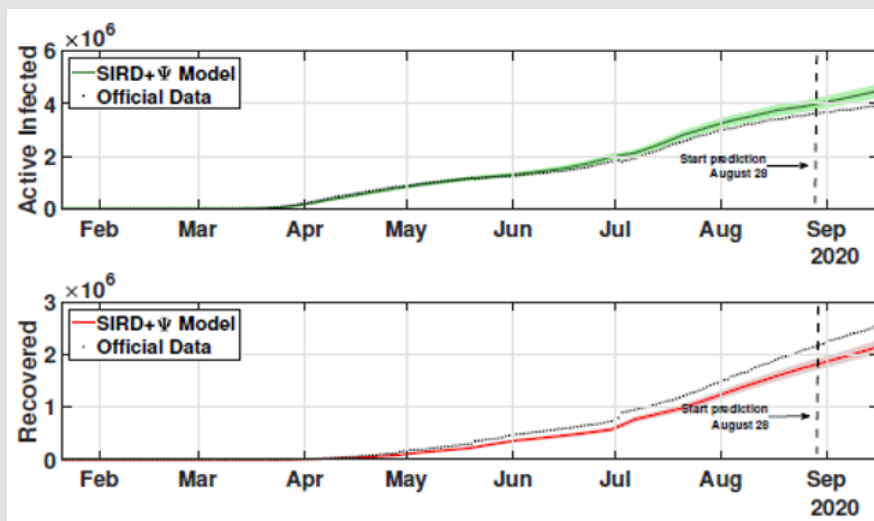


Figure 7: Active and recovered cases for the second scenario from February 21 to September 17.

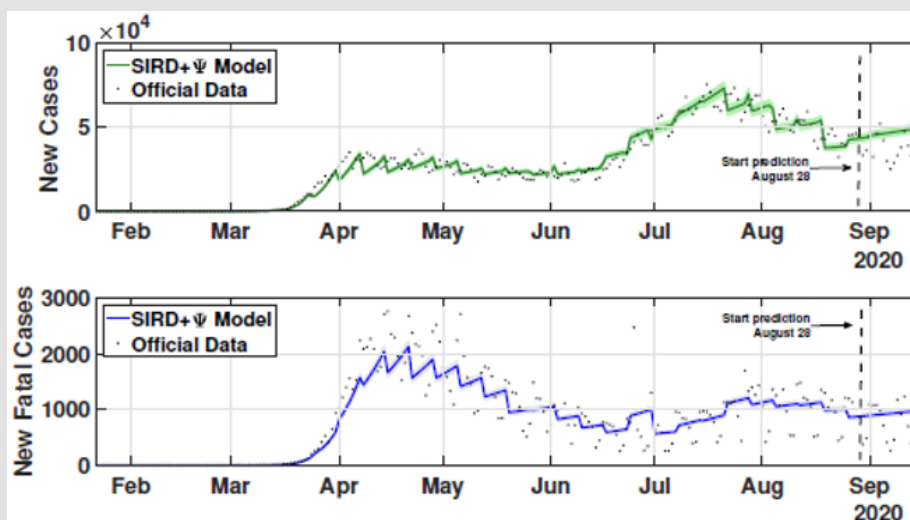


Figure 8: New infected and new fatal cases for the second scenario from February 21 to September 17.

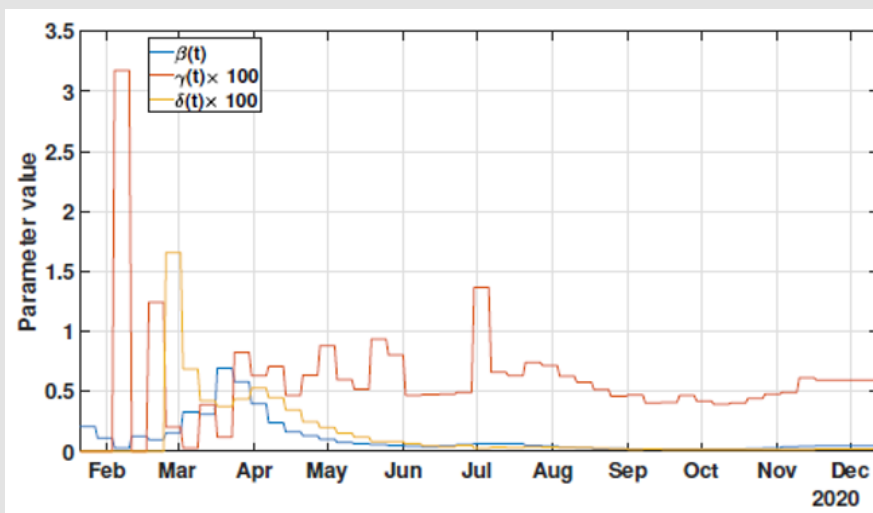


Figure 9: Identified parameters  $\beta, \gamma$  and  $\alpha$  for the third scenario from February 21 to December 13.

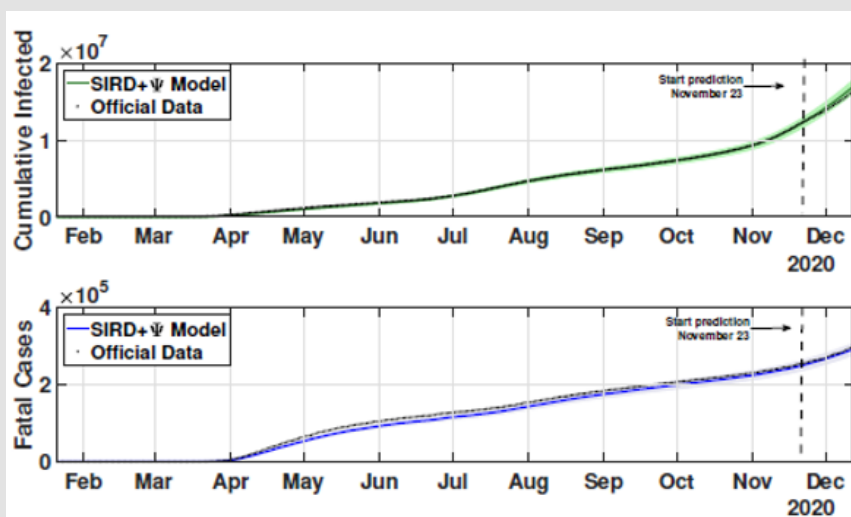


Figure 10: Cumulative and fatal cases for the third scenario from February 21 to December 13.

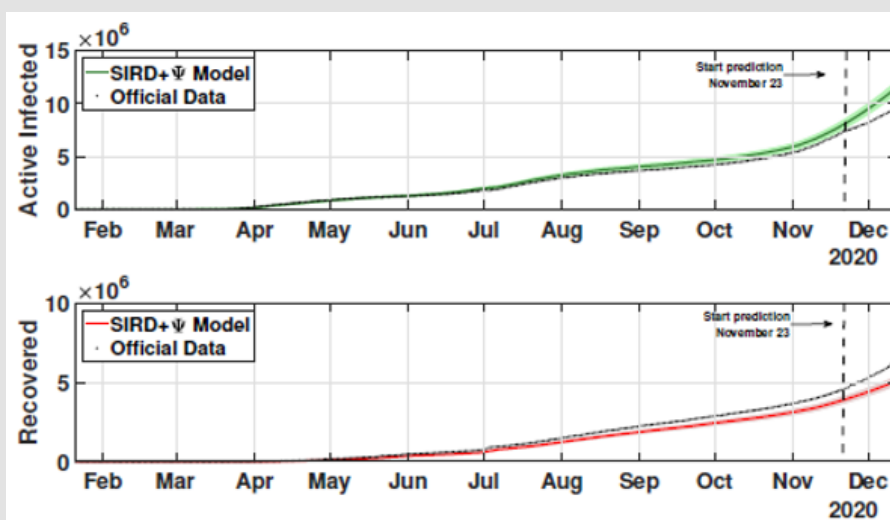


Figure 11: Active and recovered cases for the third scenario from February 21 to December 13.



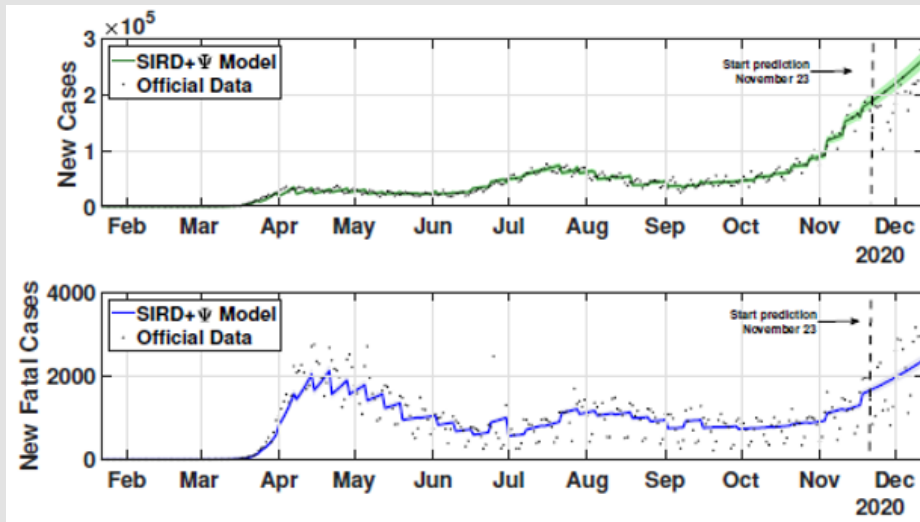


Figure 12: New infected and new fatal cases for the third scenario from February 21 to December 13.

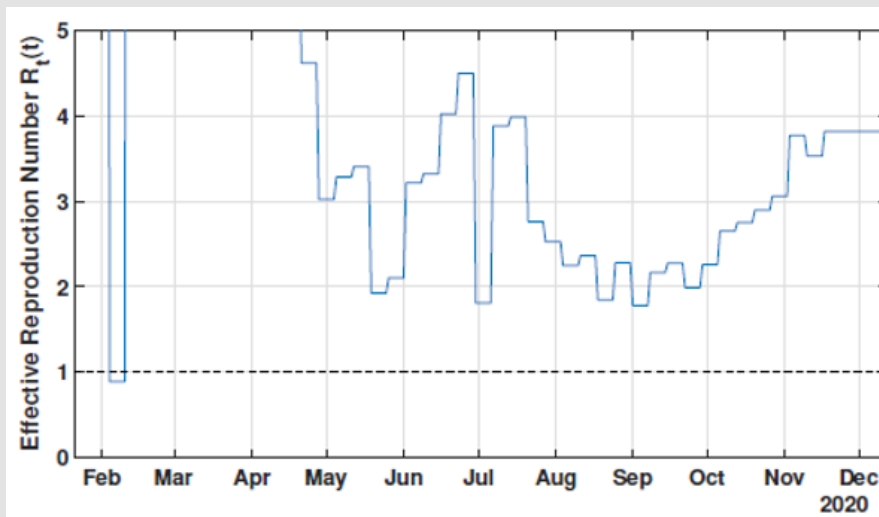


Figure 13: Effective reproduction number  $R_t$ .

### Perspectives of Control Engineering Applications

As commented before, the field of control engineering may offer interesting solutions for the COVID-19 pandemic. In this area, mathematical theorems, computational algorithms, and engineering projects are developed to interfere in dynamic systems aiming at specific objectives. In particular, dynamic optimization techniques are particularly appropriate in pandemic situations because they can deal with nonlinear, unstable, multivariable, and complex systems [38]. We can cite the algorithms of Dynamic Real-time Optimization (D-RTO) and Model Predictive Control (MPC) that differentiate themselves very solely in few concepts and elements. In general, the conventional MPC is a type of D-RTO, since it applies an optimization problem for tracking. On the other hand, the D-RTO operates processes in an economic viewpoint [38,39]. The fact is that for any of these strategies, a valid model is crucial to assure reliable predictions and optimal conditions. Also, at least

one manipulated variable is required to control other variables in any system. Thus, the proposed identification algorithm presented in this work ensures the applicability of control systems on the COVID19 pandemic, associating the social mobility index as manipulated variable, updating epidemiological parameters, and validating the model in real-time from collected data.

The approach is to propose optimal levels of social mobility considering economic and health aspects. As can be seen in Figure 14, the control system calculates optimal stringency values ( $u(k)$ ) to guide public administration guidelines. Based on a pattern that describes health policies as a function of stringency values, governmental measures are elaborated, and public decrees are applied to the population. Thus, a new social mobility and responses from the human behavior are obtained, producing new social distancing dynamics ( $\psi(t)$ ) and, hence, changing the epidemic velocity. Finally, for every  $T_2$  days, updated data feed the

control system to determinate new stringency measures during the epidemic. The control system uses internally the proposed identification algorithm to calculate the optimal solutions. Also, with the historical data, the population responses must be modeled

according to policy measures. A simple first-order equation with nonlinear gains is proposed by Morato et al. [30] and demonstrated by Pataro et al. [27] with relevant results. Therefore, the system presented here has a real possibility to be implemented in practice.

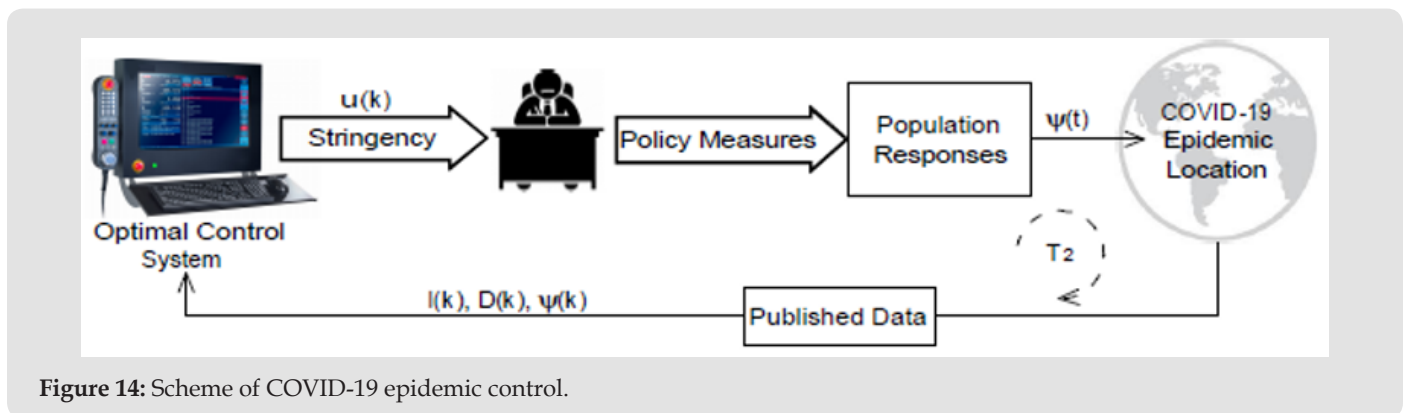


Figure 14: Scheme of COVID-19 epidemic control.

## Conclusion

The paper proposed an identification algorithm able to calculate epidemiological parameters considering the social distance effects. The procedure uses a SIRD+  $\Psi$  structure and discrete analytical solutions to ensure correct parameters according to measured data and the epidemiological concepts. The pandemic's velocity can be estimated using the effective reproduction number, and simulations and forecasts are performed to support decision-making. The proposed scenarios have shown that the estimated model dynamics become more precise with more data. These results are achieved by performing the procedure for identifying parameters using a moving window associated with the real data. When it is provided more numerous and reliable data to the algorithm, the better is the model fitting results. Moreover, this can benefit algorithm forecasting, providing longer predictions with small errors. Furthermore, the parameter identification algorithm is adjustable and can be tuned in various manners to accomplish finely adjusted curves. The cost function can be customized to include other compartments to minimize the error or be chosen different weight constants to prioritize the optimized variable. According to the data fidelity used to estimate the model curves, the uncertainty bounds can also be changed. The sample time of the parameters change can be chosen to adjust the local data situation correctly. Finally, it is demonstrated that control engineering can be an alternative to deal with the pandemic if no enough vaccines are still available. The proposed algorithm can be incorporated into a control system to offer an adaptive model and predictions that allow optimal social distancing guidance. Thus, future works including dynamic optimization and applications will be done to investigate the impact in the U.S.

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