

Article

A Modified SIRD Model to Study the Evolution of the COVID-19 Pandemic in Spain

Vicente Martínez 

Departament de Matemàtiques, Institut de Matemàtiques i Aplicacions de Castelló, Universitat Jaume I, E-12071 Castelló, Spain; martinez@uji.es

Abstract: In this paper, we use an SIRD model to analyze the evolution of the COVID-19 pandemic in Spain, caused by a new virus called SARS-CoV-2 from the coronavirus family. This model is governed by a nonlinear system of differential equations that allows us to detect trends in the pandemic and make reliable predictions of the evolution of the infection in the short term. This work shows this evolution of the infection in various changing stages throughout the period of maximum alert in Spain. It also shows a quick adaptation of the parameters that define the disease in several stages. In addition, the model confirms the effectiveness of quarantine to avoid the exponential expansion of the pandemic and reduce the number of deaths. The analysis shows good short-term predictions using the SIRD model, which are useful to influence the evolution of the epidemic and thus carry out actions that help reduce its harmful effects.

Keywords: pandemic; numerical simulation; SIRD model; mathematical modeling



Citation: Martínez, V. A Modified SIRD Model to Study the Evolution of the COVID-19 Pandemic in Spain. *Symmetry* **2021**, *13*, 723. <https://doi.org/10.3390/sym13040723>

Academic Editor: Stephen Anco

Received: 14 March 2021

Accepted: 14 April 2021

Published: 19 April 2021

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2021 by the author. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

1. Introduction

The detection of a new coronavirus (SARS-CoV-2) in December 2019 by the Municipal Health Commission in Wuhan (China) and its subsequent expansion throughout the world caused the World Health Organization (WHO) to declare a global pandemic of this infection on 11 March 2020. Its disease pattern has been named COVID-19. As of 2 May 2020, this disease has presented 3,272,202 confirmed cases and 230,104 deaths globally—with 25,264 in Spain [1].

In this work, we perform an analysis of the evolution of the epidemic in Spain using an SIRD model, which will be detailed below. The use of SIRD-type models to study epidemics has been very popular for decades [2–7]. They were proposed in 1927 [8] by two Scottish scientists: William O. Kermack, a biochemist, and Anderson G. McKendrick, a physicist and epidemiologist. For this reason, they are also known as Kermack–McKendrick models. These models show how an infection evolves when a certain number of sick people are detected within a healthy population. They are governed by systems of differential equations, which means that the solutions they provide are highly accurate from a mathematical point of view, but small variations in their parameters can cause significant changes in the solution.

Another drawback is that accurate knowledge of the evolution of the epidemic requires data that are only known at the end of it. Therefore, at the moment when the epidemic is taking place, it is difficult to predict its evolution in the long term. However, the simplicity of the model allows us to make quick parameter adjustments and carry out instant simulations and measure trends in the evolution of the epidemic in the short term.

In this paper, our aim is to analyze what has happened during the development of the epidemic and demonstrate how the SIRD model has great adaptability to predict the behavior of the COVID-19 pandemic in Spain during the course of the epidemic. Our analysis seeks to detect trends that allow short-term decisions to be made.

Fortunately, in today's society, the COVID-19 pandemic is not expected to be as devastating as the Spanish Flu Pandemic at the beginning of the last century, which took

place between 1918 and 1920 [9–11]. That terrible pandemic resulted in more than 40 million victims worldwide and Spain was one of the most badly-affected countries, with 8 million people infected and 300,000 deaths. The healthcare and technological resources, as well as the research potential that exists today, are far superior to those of the early twentieth century; it is therefore not likely to cause as many victims as in 1918 (in proportion to the population). At that time, the entire population was exposed to the risk of infection and there were not as many means of treatment as nowadays. Therefore, it is obvious that in this case, the isolation measures (quarantine) taken can alter the number of people exposed to the virus. This is one of the most effective actions to prevent contagion [12–15] and, consequently, deaths [16]. In Spain, several royal decrees have been published to ensure quarantine [17–19].

In addition to the works already considered about SIRD models, interested readers can find a wide variety of models for the study of the COVID-19 pandemic in the scientific literature published in the last months: using Bayesian and stochastic techniques [20–22], including mobility [23], confinement and quarantine [15,24], fractional models [25], and logistic models [26], among others.

2. Model Description

The simplest SIRD model considers three types of people:

- (S) Susceptible—the people who could become infected.
- (I) Infected—the people who are infected at that moment.
- (R) Recovered—the people who have had the disease and are now healthy.

In the case of the COVID-19 pandemic, many deaths have taken place [1,12,27], so we introduce a new variable. In this regard, we consider the variable that represents deaths:

- (D) Deceased—the people who have died of the disease.

If we assume that the population affected by the epidemic is N , satisfying $N = S + I + R + D$, the model, which we will call SIRD, it is governed by the following system of differential equations:

$$S'(t) = -\beta S(t)I(t), \quad (1)$$

$$I'(t) = \beta S(t)I(t) - \alpha I(t) - \gamma I(t), \quad (2)$$

$$R'(t) = \alpha I(t), \quad (3)$$

$$D'(t) = \gamma I(t). \quad (4)$$

This model depends on three parameters: α (recovery rate per unit of time), β (infected rate per unit of time), and γ (death rate per unit of time).

Figure 1 shows the usual way in which the variables S , I , R , and D evolve. No ranges appear, because they depend on each particular epidemic.

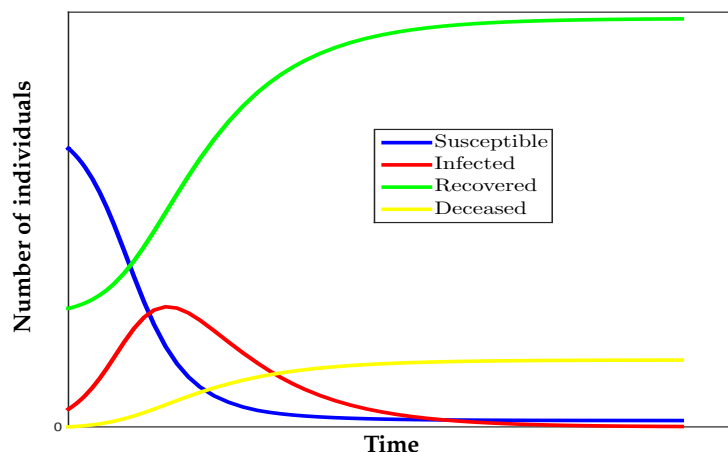


Figure 1. Typical behavior of an epidemic's evolution over time.

On the other hand, the recovery rate α may change during the course of the epidemic, influenced by new medical treatments, which are becoming increasingly effective as research progresses. In addition, the value of α can also change when the healthcare system is on the verge of collapse and the mildly ill are discharged to complete their recovery at home. Actually, such patients are not fully recovered, but the official data do not count them as infected. Considering the presented reasons, during the evolution of the epidemic, the predictions that can be made will only be reliable in the short term. However, this does not mean that they are not useful, since knowledge of these predictions can help to make decisions to minimize harmful effects during the course of the epidemic.

2.1. Equations Governing the Model

The SIRD epidemiological model that we are going to use to describe the evolution of the COVID-19 pandemic in Spain is a nonlinear ordinary differential equation system, presented in the previous section. It is governed by Equations (1)–(4), the formulation of which is described below.

Usually, the parameter β , infected rate per unit of time, is considered the product of two quantities: $\beta = p \cdot m$, where p is the probability that contact with an infected person results in an infection and m is the number of contacts made by an infected person. So, pmS is the number of people who have been infected by an infected person. Therefore, $pmSI$ is the number of susceptible people who have been infected by all the infected people. Now, substituting the value of pm for β , we obtain Equation (1):

$$S' = \left\{ \begin{array}{l} \text{Variation of susceptible people per unit of time} \\ \text{caused by all infected people} \end{array} \right\} = -\beta SI.$$

On the other hand, Equations (3) and (4) are deduced from the definitions of α and γ :

$$\begin{aligned} R' &= \text{Variation of recovered people per unit of time} = \alpha I, \\ D' &= \text{Variation of deaths per unit of time} = \gamma I. \end{aligned}$$

Finally, from the two previous expressions, Equation (2) is deduced:

$$I' = \text{Variation of infected people per unit of time} = \beta SI - \alpha I - \gamma I.$$

Obviously, when we face an unknown epidemic, the constants to be determined to ensure adequate action are the parameters α , β , and γ . For this reason, estimating them is a fundamental task that we will address in the following sections.

As discussed in the previous section, social isolation measures have been the most effective measures to control the spread of the epidemic and reduce the number of deaths [16]. In this way, the value of another important parameter has also been reduced. We refer to the number ρ_0 of infected people who have been infected by an infected person (we will call this the reproduction number). In mathematical terms:

$$\rho_0(t) = \frac{\beta}{\alpha + \gamma} S(t).$$

If this parameter is greater than 1, then the expansion of the epidemic is exponential and therefore uncontrollable. However, when it is less than 1, the number of new infections decreases over time and the epidemic tends to subside. The reader can find more details of this parameter in [28,29]. For this reason, social isolation is effective, since, for a given epidemic with a given parameter β , the only way to decrease ρ_0 is to decrease the number of people at risk of being infected, that is, $S(0)$.

2.2. Estimation of Parameters α and γ

Suppose that the infection has become stable. Therefore, the class of infected people will no longer increase, so the differential equation that governs this class is

$$\begin{cases} I'(t) &= -\alpha I(t) - \gamma I(t), t \geq 0 \\ I(0) &= I_0. \end{cases}$$

This equation has the following solution:

$$I(t) = I_0 e^{-(\alpha+\gamma)t}.$$

In this way, the proportion of individuals who remain infected at time $t \geq 0$, or in other words, the probability that an individual remains infected at time $t \geq 0$, is given by the quotient

$$\frac{I(t)}{I_0} = e^{-(\alpha+\gamma)t}.$$

Thus, the fraction of individuals who have left the infected class at time $t \geq 0$ will be

$$F(t) = 1 - e^{-(\alpha+\gamma)t}, t \geq 0,$$

where $F(t)$ takes the form of the distribution function of a random variable X , which is defined as the time it takes an individual to leave the infected class. In our case, this happens when an infected person has overcome the disease or has died.

Calculating the density function of the variable X , we obtain

$$f(t) = F'(t) = \begin{cases} (\alpha + \gamma) e^{-(\alpha+\gamma)t}, & t \geq 0, \\ 0, & t < 0. \end{cases}$$

Under these conditions, we can calculate the average time it takes for a sick person to leave the infected class.

$$E[X] = \int_{-\infty}^{+\infty} t f(t) dt = \int_0^{+\infty} t (\alpha + \gamma) e^{-(\alpha+\gamma)t} dt = \frac{1}{(\alpha + \gamma)}. \tag{5}$$

According to the available data [30,31], it takes an average of 14 days for an ill person to recover, while deaths occur on average 42 days after onset of the illness. If the fraction of deaths in relation to discharges of the sick in Spain as of 14 April 2020 [1] is $\frac{18579}{70853} \approx 0.26$, then $E[X] \approx 0.74 \times 14 + 0.26 \times 42 = 21.28$. From Equation (5), we have $\alpha \approx 0.0373$ and $\gamma \approx 0.0095$ in the case of the COVID-19 pandemic in Spain.

2.3. Estimation of Parameter β

In order to estimate the value of β , we consider that α and γ are known. Thus, system (1)–(4) is reduced to

$$\begin{cases} S'(t) &= -\beta S(t)I(t), \\ I'(t) &= \beta S(t)I(t) - \alpha I(t) - \gamma I(t). \end{cases}$$

Operating, we obtain

$$\frac{I'}{S'} = \frac{\beta S I - (\alpha + \gamma) I}{-\beta S I} = -1 + \frac{(\alpha + \gamma)}{\beta S} \Rightarrow I' = \left(-1 + \frac{(\alpha + \gamma)}{\beta S}\right) S'.$$

Therefore,

$$I = -S + \frac{(\alpha + \gamma)}{\beta} \ln S + C,$$

where C is the integration constant. Thus, the solutions of the system are given implicitly by

$$I + S - \frac{(\alpha + \gamma)}{\beta} \ln S = C. \tag{6}$$

To continue with our estimate of β , we need to make some assumptions: $S_0 = S(0)$, $I_0 = I(0)$, $S_\infty = \lim_{t \rightarrow +\infty} S(t)$, and $I_\infty = \lim_{t \rightarrow +\infty} I(t) = 0$. Now, substituting in (6) to remove C , we obtain

$$I_0 + S_0 - \frac{(\alpha + \gamma)}{\beta} \ln S_0 = S_\infty - \frac{(\alpha + \gamma)}{\beta} \ln S_\infty \Rightarrow \frac{\beta}{(\alpha + \gamma)} = \frac{\ln(S_0/S_\infty)}{I_0 + S_0 - S_\infty}.$$

Finally,

$$\beta = (\alpha + \gamma) \cdot \frac{\ln(S_0/S_\infty)}{I_0 + S_0 - S_\infty}. \quad (7)$$

Obviously, when the epidemic is evolving and has not yet ended, S_∞ is unknown and it will be necessary to estimate it with the data available at each moment.

3. Analysis of the COVID-19 Pandemic in Spain During the Course of the Disease

In order to have enough data for the estimates to have a significant value, we consider official data [1,27] provided by the Spanish Government from 11 March 2020, when the disease had been in the country for several weeks (or months, this is still unknown). We differentiate several stages in the evolution of the epidemic as the data have changed, either due to changes in case reporting criteria or due to changes in the trend of the disease.

3.1. First Stage: 11–21 March 2020

We consider data supplied by the Ministry of Health of the Spanish Government up to 21 March 2020. Table 1 shows the status of the epidemic up to that date. During the first days, official data were completed with data from the GitHub Enterprise group [32]. To fit an SIRD model that approximates the known values, the following data have been taken: $S_0 = 1,550,000$, $I_0 = 2039$, and $S_\infty = 5000$. The rest of the parameters have been estimated as follows:

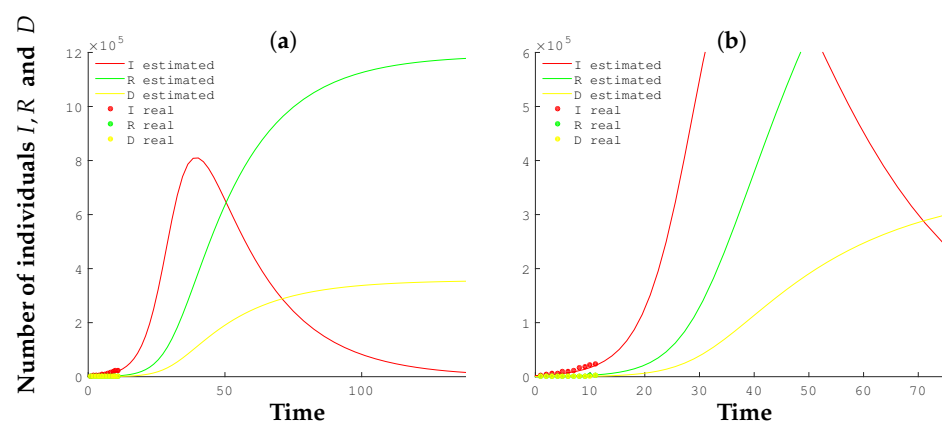
- The discussion of the above section allows us to consider the Recovered/Deceased fraction as $\frac{55}{183} \approx 0.3$, in accordance with the figures from 11 March 2020 (see Table 1). Taking 0.3 as the Recovered/Deceased fraction, we can estimate that $E[X] \approx 0.7 \times 14 + 0.3 \times 42 = 22.4$ days.
- From Equation (5) and considering $\gamma \approx 0.3\alpha$, we obtain $\alpha = 0.0343$ and $\gamma = 0.0103$.
- From Equation (7), we estimate β once α and γ are known. So, $\beta = 1.6554 \times 10^{-7}$.

In this work, we have chosen to use the MATLAB Ode Solver *ode45* [33] to solve the system (1)–(4). The results obtained are shown in Figure 2. In this first stage, when the epidemic is beginning to spread, the estimates show great uncertainty, although the forecasts are bleak: the number of infected people is around 800,000. It is surely this fact that led the Spanish authorities to take severe isolation measures [17]. It is true that there are more optimistic estimates, but also more pessimistic ones. The results obtained show a possible scenario. Figure 2 shows how the evolution of the epidemic may have progressed if no action had been taken and if the efficacy of the treatments had not improved. The figures about those recovered and deceased do not yet show a clear trend and we will not comment on them.

In Figure 2 and below, the evolution of the number of susceptible people is not shown because it is an unknown figure introduced by us to adjust the other variables that are of most interest in terms of allowing us to influence the subsequent development of the epidemic.

Table 1. Number of infected, recovered, and deceased people in Spain from 11–21 March 2020.

Date	Infected	Recovered	Deceased	Total Cases
11 March	2039	183	55	2277
12 March	4906	193	133	5232
13 March	5679	517	195	6391
14 March	6992	517	289	7798
15 March	9070	530	342	9942
16 March	10,187	1028	533	11,748
17 March	12,206	1081	623	13,910
18 March	16,026	1107	830	17,963
19 March	17,779	1588	1043	20,410
20 March	21,874	2125	1375	25,374
21 March	24,421	2575	1772	28,768

**Figure 2.** (a) Comparison of real data with the predictions of the SIRD model on 21 March 2020. (b) Zoomed-in graph of real data.

3.2. Second Stage: 22–31 March 2020

At this stage, we consider the data provided by the Ministry of Health of the Spanish Government up to 31 March 2020 (see Table 2). The values we have taken at this stage to adjust the aforementioned SIRD model have been as follows: $S_0 = 500,000$, $I_0 = 27,552$, and $S_\infty = 20,000$. The estimation of the other parameters has been carried out analogously to the previous section:

- We observed in the data that the Recovered/Deceased fraction follows the sequence tending towards 0.3 and $E[X] \approx 20$ days.
- From Equation (5) and $\gamma \approx 0.3\alpha$, we obtain $\alpha = 0.0385$ and $\gamma = 0.0155$. From Equation (7), we estimate the value of β once we know α and γ . So, $\beta = 3.171 \times 10^{-7}$.

The results obtained using the MATLAB Ode Solver considered in the first stage are shown in Figure 3. It is observed that the influence of the quarantine imposed by the Spanish Government begins to be noticed and the figures, although still worrying, are no longer so alarming.

Obviously, the approximations show trends that the model variables follow according to the aforementioned conditions. It is important to note that we are estimating the values of the variables that will later be officially counted according to the conditions described. In the event that these conditions change, the values of the variables would undergo changes. However, the information provided will continue to be useful for making medical and political decisions, since the observed trends are representative of the situation. In addition, the cases that are officially detected are those of people who have a serious evolution or an uncertain prognosis, for whom hospitalization is therefore required or at least require that a follow-up be carried out by Family Medicine Units. In summary, these are the cases that must be attended to urgently and followed up on. In the evolution of an epidemic caused by the action of a little-known virus, it is important to anticipate the ICU beds that may be

needed, and more so in this case, where the evolution of those infected with severe cases of COVID-19 require ICU care.

Table 2. Official data provided by the Spanish Government from 22–31 March 2020.

Date	Infected	Recovered	Deceased	Total Cases
22 March	27,552	3355	2182	33,089
23 March	33,183	3794	2696	39,673
24 March	38,809	5367	3434	47,610
25 March	45,084	7015	4089	56,188
26 March	49,844	9357	4858	64,059
27 March	54,273	12,285	5690	72,248
28 March	57,560	14,709	6528	78,797
29 March	61,075	16,780	7340	85,195
30 March	66,969	19,259	8189	94,417
31 March	70,436	22,647	9053	102,136

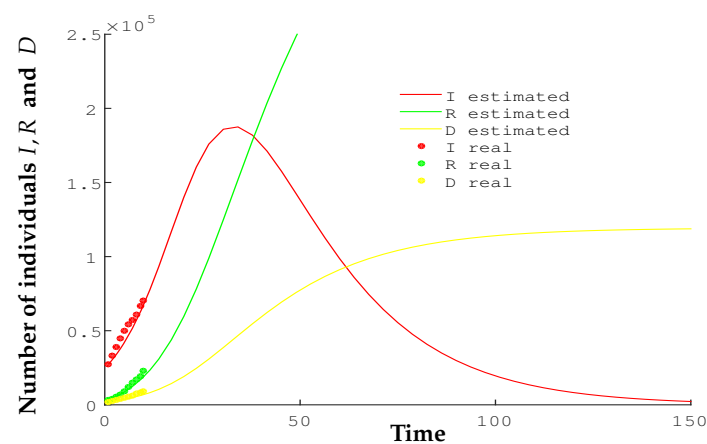


Figure 3. Comparison of the real data with the estimations of the SIRD model during the second stage.

3.3. Third Stage: 1–13 April 2020

At this stage, we will consider the data in Table 3.

Table 3. Official data provided by the Spanish Government from 1–13 April 2020.

Date	Infected	Recovered	Deceased	Total Cases
1 April	73,492	26,743	10,003	110,238
2 April	76,262	30,513	10,935	117,710
3 April	78,773	34,219	11,744	124,736
4 April	80,261	38,080	12,418	130,759
5 April	81,540	40,437	13,055	135,032
6 April	83,504	43,208	13,798	140,510
7 April	84,114	48,021	14,555	146,690
8 April	85,043	52,165	15,238	152,446
9 April	85,511	55,668	15,843	157,022
10 April	86,390	59,109	16,353	161,852
11 April	86,656	62,391	16,972	166,019
12 April	87,280	64,727	17,489	169,496
13 April	86,981	67,504	18,056	172,541

The values that we have taken in this stage to adjust the SIRD model, described in previous paragraphs, have been $S_0 = 170,000$, $I_0 = 73,492$, and $S_\infty = 20,000$. The other parameters have been estimated as follows:

- The Recovered/Deceased fraction has been observed to follow the sequence:

$$0.65, \dots, 0.58, \dots, 0.31, \dots, 0.27, \dots$$

Consequently, we have estimated the value 0.22, which produces good approximations for the data that are already known. Taking 0.22 as the Recovered/Deceased fraction, we can estimate that $E[X] \approx 20$ days.

- From Equation (5) and $\gamma \approx 0.22\alpha$, we obtain $\alpha = 0.041$ and $\gamma = 0.009$. From Equation (7) and the values of α and γ , we estimate β . So, $\beta = 4.7878 \times 10^{-7}$.

The results obtained using the MATLAB Ode Solver considered in previous stages are shown in Figure 4. These results are conditioned by the number of tests carried out, which provide us with the number of infected people, the number of patients discharged (in many cases the patients continue their convalescence at home, due to the saturation of hospitals), and the effectiveness of treatments.

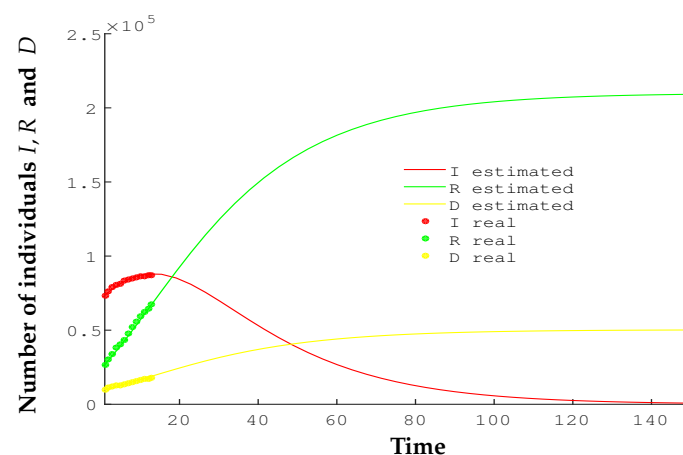


Figure 4. Comparison of the real data with the estimates of the SIRD model during the third stage.

In the current part of the process in which we find ourselves, that is, fully immersed in the course of the epidemic, there are many doubts about it; if we take into account the number of hidden carriers of the disease, the data obtained would change shape very significantly [16]. However, the estimates that have been obtained are very useful for managing actions in the short term. There may be 7 million people infected in Spain, as indicated in the previous reference, but at the moment what is of interest is managing cases with severe symptoms. These patients who require a follow-up are those detected among the people who are cared for in health centers and hospitals, and their tests indicate that they are infected and are included in the official figures of those infected. SIRD models can also estimate the magnitude of the death toll. Figure 4 indicates that the number of deceased people may be between 40,000 and 50,000 people with the data available on 13 April 2020.

The number of deaths will be known more accurately once the epidemic has been overcome and comparative analyses of the data on deaths are carried out for the months during which the epidemic has remained active and the same months in previous years. However, the data provided by the models can help make decisions that modify the final figure.

3.4. Fourth Stage: 14–23 April 2020

We consider the data in Table 3, adding the values in Table 4. We carry out estimations with the parameters of the third stage. At this stage, the Spanish Government has reported an increase in the number of tests carried out [1,27], which largely disarrange the parameters of the model considered in previous stages.

Figure 5 shows the evolution of the pandemic during this stage. A more detailed analysis indicates that on 14 April, there was a slight mismatch; which was accentuated on 15 April, with an upward trend in real data with respect to those expected by the SIRD measure. On 16 April, the change in trend was already evident in the data; during the days after 16 April, the change in the trend of the data was confirmed.

Table 4. Official data provided by the Spanish Government from 14–23 April 2020.

Date	Infected	Recovered	Deceased	Total Cases
14 April	70,853	88,201	18,579	177,633
15 April	74,797	88,889	19,130	182,816
16 April	72,963	95,627	19,478	188,068
17 April	74,662	97,021	20,043	191,726
18 April	77,357	98,134	20,453	195,944
19 April	80,587	98,771	20,852	200,210
20 April	82,514	100,382	21,282	204,178
21 April	85,915	100,757	21,717	208,389
22 April	89,250	101,617	22,157	213,024
23 April	92,355	88,111	22,524	202,990

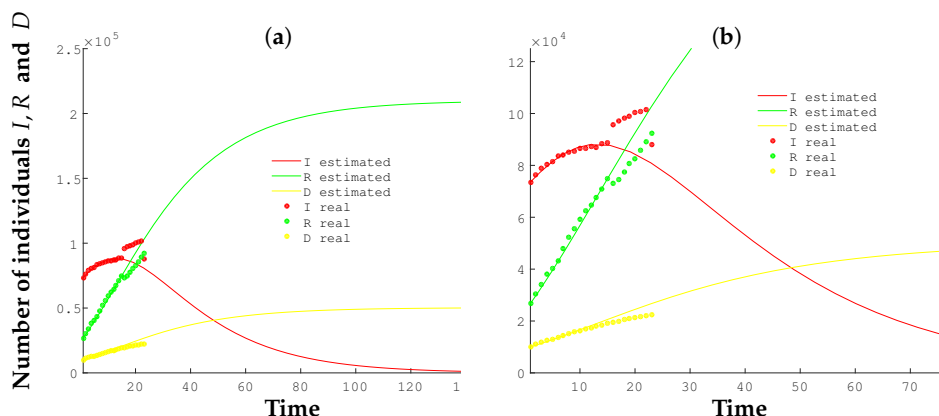


Figure 5. (a) Comparison of the state of the real data with the predictions of the SIRD model on 23 April 2020. (b) Zoomed-in graph of real data.

Given the circumstances, the model needs to be revised. The Spanish authorities have clarified [1,27] the way of accounting for the data and the types of tests being carried out. Figure 6 shows the official data regarding the increase in the number of people infected and the types of tests performed.

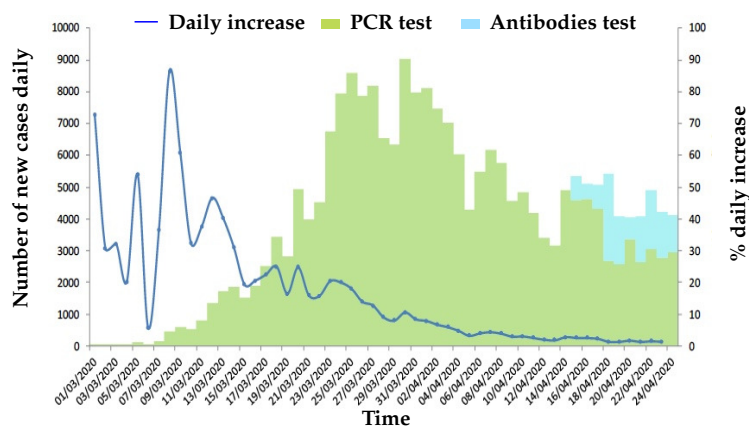


Figure 6. Types of tests carried out and the % increase in the number of infected people on 23 April 2020. Source: Spanish Government [1] on 24 April 2020.

3.5. Types of COVID-19 Screening Tests

- The Polymerase Chain Reaction technique (PCR test) amplifies the genetic material of the virus (RNA and DNA) to detect it. So far, it is the most reliable method, but it requires analysis in a laboratory.
- The test for coronavirus antibodies (antibody test) does not detect the virus, but it detects the antibodies that kill it. It is done with a blood test, which can be performed quickly and on a massive scale.

In the days prior to 23 April, PCR tests were performed in conjunction with other, less-reliable types of tests not reported by the health authorities. A small number of antibody tests were also carried out, indicating whether a person has had the disease but not whether they are currently suffering from it. As of 14 April, the antibody tests were increased to carry out analyses of the prevalence of the disease and find out how many people in the total population have already had the infection. In the opinion of the Spanish authorities, this way of accounting for those affected makes it difficult to compare the data with previous data, since patients who currently have the disease and those who have already had it without being detected are counted, which undermines the trends observed. The Government has stated that from 14 April, only those infected confirmed by PCR test will be counted.

At this point of the investigation we have two alternatives: to model the total data with all the tests or to model only the official data that offer a positive result with the PCR test. In this work, we adopt the second option, which focuses on modeling the epidemiological data that are useful for making short-term decisions and being able to influence the evolution of the epidemic.

3.6. Fifth Stage: 23 April to 2 May 2020

At this stage, we will recover the data from 1 April, assuming that the data from 14–23 April are outside the model, but as we have already explained, they are not relevant in our study because our objective is to detect trends to modify the evolution of the epidemic in the short term. Therefore, we add the data from Table 3 to those of Table 5.

Figure 7 shows the model estimates compared to the actual data according to the following parameters: $S_0 = 170,000$, $I_0 = 73,492$, $S_\infty = 20,000$, $\alpha = 0.0362$, $\gamma = 0.0054$, and $\beta = 3.9898 \times 10^{-7}$. On this occasion, we have noted an improvement in medical treatments, patient care in less-saturated ICUs, and also a greater number of days that a patient remains in the hospital in order to provide longer care. So, $E[X] \approx 24$ days and the Recovered/Deceased fraction ≈ 0.15 .

The SIRD model shows good behavior with these parameters. The estimate of deaths in this new situation is now around 38,000 people, far from the catastrophic figures of the beginning of the epidemic.

Table 5. Official data provided by the Spanish Government of Spain from 23 April–2 May 2020.

Date	Infected	Recovered	Deceased	Total Cases
23 April	88,111	92,355	22,524	202,990
24 April	87,295	95,708	22,902	205,905
25 April	85,712	98,732	23,190	207,634
26 April	85,069	100,875	23,521	209,465
27 April	84,403	102,548	23,822	210,773
28 April	79,695	108,947	24,275	212,917
29 April	76,842	112,050	24,543	213,435
30 April	75,714	114,678	24,824	215,216
1 May	74,234	117,248	25,100	216,582
2 May	73,300	118,902	25,264	217,466

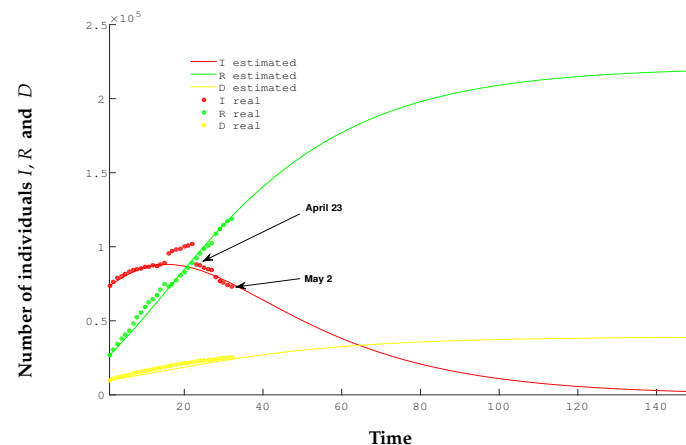


Figure 7. Comparison of the real data with the estimates of the SIRD model during the fifth stage.

4. Discussion

The SIRD model that we have presented, like other models, is strongly dependent on the initial data used to adjust the parameters. For this reason, political authorities should publish the data without any kind of censorship or manipulation. Considering different initial data, we are able to estimate how catastrophic it would have been if the Spanish Government had not taken measures of social isolation on 14 March 2020 [17]. The displayed data in Figure 2 indicate that the number of people infected with active disease would have been around 800,000, while once the isolation measures were taken, they slowed down at the end of March. The maximum number of people infected with active disease and positive PCR was 87,280 (see Table 3) and it was reached on 12 April 2020. Approximately only 11% of those were probably infected without isolation measures. The delay in noticing the effect of the measures is largely due to the incubation period of the virus, estimated between 10 and 14 days after infection [34].

The model also depends on the exposed people to the virus by means of the variable S of susceptible people. At each stage of the pandemic, depending on the strictness of the isolation measures, this variable may be greatly higher or lower. In this sense, an exposure rate could be included in the model. However, when we vary the initial data of variable S of people susceptible to being infected, the results do not differ from obtained data.

The precision of the estimated parameters is determined by the theoretical reasoning of Sections 2.2 and 2.3, and by the good behavior of the model against the observed data. In this sense, some studies [20,21] using Bayesian techniques, show a similar behavior in the estimates.

Figure 8 shows the evolution of the reproduction number ρ_0 during the latency period of the first wave of the COVID-19 pandemic. If we consider the stages in which we have focused our study, a strong decrease in this parameter can be observed during stages 2 and 3 (from 22 March–13 April) when the harsh quarantine measures imposed by the Spanish Government [17–19] had an effect. At this point, the incubation period must be taken into account, which means that the effects of the taken measures have several days of delay. From the fourth stage (13 April), the decrease is less due to relaxation of the isolation measures. Taking this parameter into account, we obtain useful information that allows us to take preventive measures in order to minimize the damage that the pandemic may cause.

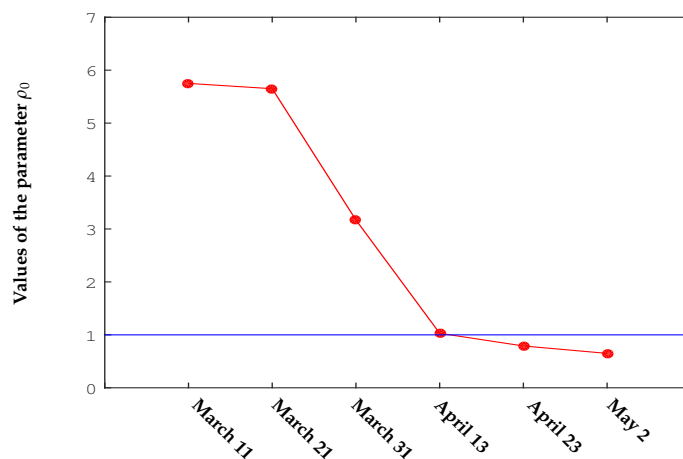


Figure 8. Values of the parameter ρ_0 (reproduction number) over time in Spain during the first wave of the COVID-19 Pandemic.

5. Conclusions

An analysis has been performed on the evolution of the epidemic caused by the SARS-CoV-2 virus in Spain during the months of March and April, when the epidemic was in its most active phase. We observed good short-term predictions using the SIRD model, which have been described in previous sections. It has been discussed that short-term predictions are useful to influence the evolution of the epidemic and thus carry out actions that help reduce its harmful effects. For example, we confirmed the estimates made [16] regarding the usefulness of the quarantine imposed by the Spanish Government to reduce the number of deaths.

From the first days of April a decreasing number of actively infected patients was observed. In the days following the end of this study, it is expected that the epidemic will diminish if adequate isolation measures are maintained. A change in conditions could have a rebound effect on the number of people infected and the evolution could take, as of today, an uncertain path.

A more reliable representation of the behavior of the epidemic is to present its evolution in pieces, that is, to change the parameters as conditions have changed in relation to isolation measures, improvement of medical treatments, etc. If we take the parameters that best fit the constraints imposed in each case, a more appropriate global behavior can be observed. Figure 9 shows the fit of a piecewise SIRD model at each stage that has been described considering changes in conditions during the evolution of the epidemic.

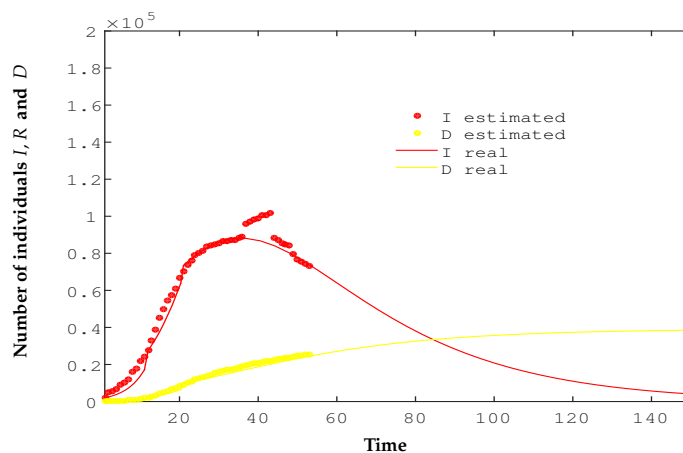


Figure 9. Comparison of real data with the estimates of the piecewise SIRD model during the evolution of the epidemic.

Models are generated according to the data collected under certain conditions, which, as we have seen throughout the development of the epidemic, are changing. The number of diagnostic tests performed is not the same every day and treatments gradually become more effective, which affects the number of discharges. In addition, we remember with pain those hard weeks when ICUs were overflowing and many patients waited at home for the test to be performed, which also alters the exact date of positive diagnoses. On the other hand, it should be remembered that the data arrive a few days late, they are communicated the day after they are collected, and the virus also has an incubation period of 10 to 15 days. If these constraints are taken into account, the estimates made largely describe the evolution of the epidemic.

We present a model that allows us to adjust the parameters in real time when the disease is latent. Given the simplicity of the calculation of its parameters, one quickly obtains estimates on the number of infected people. In this way, adequate institutional actions could apply to minimize infections and to prevent overloading the health system. Another advantage of our model is its simplicity that permits an easy adaptation for similar infections.

Funding: This research was supported by the Institut de Matemàtiques i Aplicacions de Castelló, Departament de Matemàtiques, Universitat Jaume I, Spain.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The datasets used in this paper are publicly available in the references.

Acknowledgments: The author is grateful for several useful comments from unknown reviewers.

Conflicts of Interest: The author declares no conflict of interest.

References

- Spanish-Government. Web of Instituto de Salud Carlos III. Available online: <https://covid19.isciii.es> (accessed in 20 April 2020).
- Brauer, F.; Castillo-Chavez, C. *Mathematical Models in Population Biology and Epidemiology*, 2nd ed.; Springer: New York, NY, USA, 2001.
- Brauer, F.; Feng, Z.; Castillo-Chávez, C. Discrete epidemic models. *Math. Biosci. Eng.* **2010**, *7*, 1–15. [[CrossRef](#)] [[PubMed](#)]
- Haefner, J.W. *Modeling Biological Systems*; Springer: New York, NY, USA, 2005.
- Martcheva, M. *An Introduction to Mathematical Epidemiology*; Springer: New York, NY, USA, 2015.
- Sameni, R. Mathematical Modeling of Epidemic Diseases; A Case Study of the COVID-19 Coronavirus. *arXiv* **2020**, arXiv:2003.11371.
- Fernández-Villaverde, J.; Jones, C.I. *Estimating and Simulating a SIRD Model of COVID-19 for Many Countries, States, and Cities*; Working Paper 27128; National Bureau of Economic Research: Cambridge, MA, USA, 2020.
- Kermack, A.O.; McKendrick, A.G. A Contribution to the Mathematical Theory of Epidemics. *Proc. R. Soc. Lond.* **1927**, *115*, 700–721; reprinted in *Bull. Math. Biol.* **1991**, *53*, 33–55.
- Belser, J.A.; Tumpney, T.M. The 1918 flu, 100 years later. *Science* **2018**, *359*, 255. Available online: <https://science.sciencemag.org/content/359/6373/255> (accessed on 23 April 2020). [[CrossRef](#)] [[PubMed](#)]
- Morens, D.M.; Fauci, A.S. The 1918 Influenza Pandemic: Insights for the 21st Century. *J. Infect. Dis.* **2007**, *195*, 1018–1028. [[CrossRef](#)] [[PubMed](#)]
- Pulido, S. The Spanish Flu: The 1918 Pandemic that Did not Start in Spain. Available online: <https://gacetamedica.com/investigacion/la-gripe-espanola-la-pandemia-de-1918-que-no-comenzo-en-espana-fy1357456/> (accessed on 20 April 2020). (In Spanish)
- Remuzzi, A.; Remuzzi, G. COVID-19 and Italy: What next? *Lancet* **2020**, *395*, 1225–1228. [[CrossRef](#)]
- Nokkaew, A.; Modchang, C.; Amornsamankul, S.; Lenbury, Y.; Pimpunchat, B.; Triampo, W. Mathematical modeling of infectious disease transmission in macroalgae. *Adv. Differ. Equ.* **2017**, *2017*, 1–8. [[CrossRef](#)]
- Prem, K.; Liu, Y.; Russell, W.; Kucharski, A.J.; Eggo, R.M.; Davies, N. The effect of control strategies to reduce social mixing on outcomes of the COVID-19 epidemic in Wuhan, China: A modelling study. *Lancet Public Health* **2020**. [[CrossRef](#)]
- Tang, B.; Xia, F.; Tang, S.; Bragazzi, N.L.; Li, Q.; Sun, X.; Liang, J.; Xiao, Y.; Wu, J. The effectiveness of quarantine and isolation determine the trend of the COVID-19 epidemics in the final phase of the current outbreak in China *Int. J. Infect. Dis.* **2020**. [[CrossRef](#)]
- Flaxman, S.; Mishra, S.; Gandy, A.; Unwin, H.J.T.; Coupland, H.; Mellan, T.A.; Zhu, H.; Berah, T.; Eaton, J.W.; Guzman, P.N.P.; et al. Report 13: Estimating the number of infections and the impact of non-pharmaceutical interventions on COVID-19 in 11 European countries. *arXiv* **2020**, arXiv:2004.11342.

17. Spanish-Government. Royal Decree 463/2020, of March 14, Declaring the State of Alarm for the Management of the Health Crisis Situation Caused by COVID-19. Available online: <https://www.boe.es/eli/es/rd/2020/03/14/463> (accessed on 20 March 2020). (In Spanish)
18. Spanish-Government. Royal Decree 476/2020, of March 27, Extending the State of Alarm Declared by Royal Decree 463/2020, of March 14, Declaring the State of Alarm for the Management of the Situation of Health Crisis Caused by COVID-19. Available online: <https://www.boe.es/eli/es/rd/2020/03/27/476/con> (accessed on 20 April 2020). (In Spanish)
19. Spanish-Government. Royal Decree 487/2020, of April 10, Which Extends the State of Alarm Declared by Royal Decree 463/2020, of March 14, Which Declares the State of Alarm for the Management of the Situation of Health Crisis Caused by COVID-19. Available online: <https://www.boe.es/eli/es/rd/2020/04/10/487> (accessed on 20 April 2020). (In Spanish)
20. Berihuete, A.; Sánchez-Sánchez, M.; Suárez-Llorens, A. A Bayesian Model of COVID-19 Cases Based on the Gompertz Curve. *Mathematics* **2021**, *9*, 228. [[CrossRef](#)]
21. Taghizadeh, L.; Karimi, A.; Heitzinger, C. Uncertainty quantification in epidemiological models for the COVID-19 pandemic. *Comput. Biol. Med.* **2020**, *125*, 104011. [[CrossRef](#)] [[PubMed](#)]
22. Umar, M.; Sabir, Z.; Zahoor Raja, M.A.; Shoaib, M.; Gupta, M.; Sánchez, Y.G. A Stochastic Intelligent Computing with Neuro-Evolution Heuristics for Nonlinear SITS System of Novel COVID-19 Dynamics. *Symmetry* **2020**, *12*, 1628. [[CrossRef](#)]
23. Aràndiga, F.; Baeza, A.; Cordero-Carrión, I.; Donat, R.; Martí, M.C.; Mulet, P.; Yáñez, D.F. A Spatial-Temporal Model for the Evolution of the COVID-19 Pandemic in Spain Including Mobility. *Mathematics* **2020**, *8*, 1677. [[CrossRef](#)]
24. De la Sen, M.; Ibeas, A.; Agarwal, R.P. On Confinement and Quarantine Concerns on an SEIAR Epidemic Model with Simulated Parameterizations for the COVID-19 Pandemic. *Symmetry* **2020**, *12*, 1646. [[CrossRef](#)]
25. Ndairou, F.; Area, I.; Nieto, J.J.; Silva, C.J.; Torres, D.F.M. Fractional model of COVID-19 applied to Galicia, Spain and Portugal. *Chaos Solitons Fractals* **2021**, *144*, 110652. [[CrossRef](#)] [[PubMed](#)]
26. Cherniha, R.; Davydovych, V. A Mathematical Model for the COVID-19 Outbreak and Its Applications. *Symmetry* **2020**, *12*, 990. [[CrossRef](#)]
27. Spanish-Government. Web of Ministerio de Sanidad, Consumo y Bienestar Social. Available online: <https://www.mscbs.gob.es> (accessed in 20 April 2020). (In Spanish)
28. Diekmann, O.; Heesterbeek, J.A.P. *Mathematical Epidemiology of Infectious Diseases: Model Building, Analysis and Interpretation*; Wiley: New York, NY, USA, 2000.
29. Heesterbeek, J.A.P. A Brief History of R_0 and a Recipe for its Calculation. *Acta Biotheor.* **2002**, *50*, 189–204. [[CrossRef](#)]
30. Thevarajan, I.; Nguyen, T.H.O.; Koutsakos, M.; Druce, J.; Caly, L.; van de Sandt, C.E.; Jia, X.; Nicholson, S.; Catton, M.; Cowie, B.; et al. Breadth of concomitant immune responses prior to patient recovery: A case report of non-severe COVID-19. *Nat. Med.* **2020**, *26*, 453–455. [[CrossRef](#)]
31. Spanish-Government. *Coronavirus Disease, COVID-19*; Alerts Coordination Center and Health Emergencies. Available online: https://www.mscbs.gob.es/profesionales/saludPublica/ccayes/alertasActual/nCov-China/documentos/20200326_ITCoronavirus.pdf (accessed on 20 April 2020). (In Spanish)
32. GitHub Enterprise. GitHub CSSEGISandData. Available online: https://github.com/CSSEGISandData/COVID-19/tree/master/csse_covid_19_data/csse_covid_19_time_series (accessed on 20 April 2020).
33. Shampine, L.F.; Reichelt, M.W. The MATLAB ODE Suite. *SIAM J. Sci. Comput.* **1997**, *18*, 1–22. [[CrossRef](#)]
34. McAloon, C.; Collins, A.; Hunt, K.; Barber, A.; Byrne, A.W.; Butler, F.; Casey, M.; Griffin, J.; Lane, E.; McEvoy, D.; et al. Incubation period of COVID-19: A rapid systematic review and meta-analysis of observational research. *BMJ Open* **2020**, *10*, e039652. [[CrossRef](#)] [[PubMed](#)]