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Determination in Galicia of the required beds at Intensive Care Units

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Abstract By using a recent mathematical compartmental model that includes the super-spreader class and developed by Ndaïrou, Area, Nieto, and Torres, a procedure to estimate in advance the number of required beds at intensive care units is presented. Numerical simulations are performed to show the accuracy of the predictions as compared with the real data in Galicia.

Content

In the context of the present coronavirus pandemic, the COVID-19 epidemic has dramatically challenge the critical care capacity in every region or country in the world and therefore increasing the required intensive care units (ICUs). One of the main questions authorities have to address is: Are the resources to treat infected cases enough? In this respect, hospital beds, intensive care units (ICUs), and ventilators are crucial for the treatment of patients with severe illness. We have employed a compartmental mathematical model for COVID-19 to estimate in advance the number of required beds at intensive care units. The predictions have been performed in real time in Galicia (Spain) during the previous two months (March-April 2020) by using real data of the Epidemiological Service of our region. In this work we have estimated the number of required beds at ICUs and compared the predictions with the real data. The numerical predictions show a great agreement with the real data and the model could be used in other regions or countries and with this or other epidemics. The delay from new infected individuals and requited beds at UCIs can be used even in the case of not having appropriate mathematical model to predict the number of infected individuals in advance.

1. Introduction

The so-called coronavirus disease 2019 (COVID-19) can be defined as an infectious disease caused by severe acute

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respiratory syndrome coronavirus 2 (SARS-CoV-2). At this time, the origin of the pandemic is yet unknown, but the first reported cases were identified by December 2019 in Wuhan, the capital city of Hubei province in the People's Republic of China. Since 21st January, 2020 the Word Health Organization has published daily reports with the reported data from the affected countries. By March 11th, 2020, the Word Health Organization characterized this outbreak as a pandemic. At the time of submission of the first version the number of total confirmed cases was about 3 million and the number of deaths, approximately two thousand hundred people. Nowadays, globally, as 20th September 2020, there have been 30.675.675 confirmed cases of COVID-19, including 954.417 deaths, reported to WHO.

As indicated in [1] how to determine the needed intensive care units (ICUs) is not easy and fully understood. The ICU selection process is complex and much more during a epidemic like this and under bed pressure, prioritization, justice, expected outcome and extreme circumstances [2]. In the context of covid-19 epidemic, this coronavirus disease pandemic has dramatically challenge the critical care capacity in Galicia, Spain, Europe and in most countries in the world. Galicia is an autonomous community of Spain and located in the northwest Iberian peninsula and having a population of about 2,700,000 a total area of 29,574 km2. One of the main questions authorities have to address is: Are the resources to treat infected cases enough? In this respect, hospital beds, ICUs, and ventilators are crucial for the treatment of patients with severe illness [3,4].

From the mathematical point of view, it is possible to analyze the evolution of an infectious disease by using different techniques [5,6]. One option is to consider compartmental models, dividing the population into different classes and determining the rate of change among the different classes. The simplest model is usually referred as SIR, denoting Susceptible, Infected and Recovered individuals, and it can be extended to more complex models [7]. Following previous works [8–10], in [11] a model including the super-spreader class [14,15] has been presented, and applied to give an estimation of the infected and death individuals in Wuhan.

Many mathematical models and dynamical systems have been already developed. We stand out a mathematical model introduced taking into account the possibility of transmission of COVID-19 from dead bodies to humans and the effect of lock-down [16], the dynamical model of [17] considering the inter-action among the bats and unknown hosts (wild animals) and among humans and the infections reservoir (seafood market) or the eight-stages of infection compartmental model [18] where the authors implement an effective control strategy. For a detailed statistical analysis in some countries (Turkey and South Africa) we refer the reader to [19]. For the role of quarantine and isolation, see [20,21].

In this context it is crucial to know beforehand the needs of beds at ICUs, due to the huge resources needed for each of them. This problem cannot be lead to improvisation, since the technical needs are extremely specific, as well as the human resources. When there is no other option, improvisation; if possible, planning.

The manuscript is organized as follows. In Section 2, we recall the compartmental model for COVID-19 [11]. The usefulness of our model is then illustrated in Section 3 of numerical simulations, where by using the real data from Galicia we estimate the number of required beds at ICUs and compare the predictions with the real data. We end with Section 4 of conclusions, discussion, and future research.

2. The COVID-19 compartment model

The mathematical model described in [11] considers a constant total population of size N, which is subdivided into eight epidemiological classes:

1. susceptible class (S),
2. exposed class (E),
3. symptomatic and infectious class (I),
4. super-spreaders class (P),
5. infectious but asymptomatic class (A),
6. hospitalized (H),
7. recovery class (R), and
8. fatality class (F).

It is then described by the system of eight nonlinear ordinary differential equations:

$$\begin{cases} \frac{dS}{dt} = -\beta \frac{I}{N} S - l\beta \frac{H}{N} S - \beta' \frac{P}{N} S, \\ \frac{dE}{dt} = \beta \frac{I}{N} S + l\beta \frac{H}{N} S + \beta' \frac{P}{N} S - \kappa E, \\ \frac{dI}{dt} = \kappa \rho_1 E - (\gamma_a + \gamma_i) I - \delta_i I, \\ \frac{dP}{dt} = \kappa \rho_2 E - (\gamma_a + \gamma_i) P - \delta_p P, \\ \frac{dA}{dt} = \kappa (1 - \rho_1 - \rho_2) E, \\ \frac{dH}{dt} = \gamma_a (I + P) - \gamma_r H - \delta_h H, \\ \frac{dR}{dt} = \gamma_i (I + P) + \gamma_r H, \\ \frac{dF}{dt} = \delta_i I(t) + \delta_p P(t) + \delta_h H(t). \end{cases} \tag{1}$$

As for the parameters, next we provide a description of each of them as well as the numerical values used to model the spread of the disease in Wuhan:

1. $\beta = 2.55$ day^{-1} stands for transmission coefficient from infected individuals;
2. $\beta' = 7.65$ day^{-1} stands for transmission coefficient due to super-spreaders;
3. $l = 1.56$ is dimensionless and denotes the relative transmissibility of hospitalized patients;
4. $\kappa = 0.25$ day^{-1} stands for the rate at which exposed individuals become infectious;
5. $\rho_1 = 0.580$ is dimensionless and stands for the rate at which exposed individuals become infected;
6. $\rho_2 = 0.001$ is dimensionless and stands for the rate at which exposed individuals become sper-spreaders;
7. $1 - \rho_1 - \rho_2$ is dimensionless and denotes the progression from exposed to asymptomatic class;
8. $\gamma_a = 0.94$ day^{-1} denotes the rate of being hospitalized;
9. $\gamma_i = 0.27$ day^{-1} is the recovery date without being hospitalized;
10. $\gamma_r = 0.5$ day^{-1} is the recovery rate of hospitalized patients;
11. $\delta_i = \frac{1}{23}$ day^{-1} is the disease induced death rates due to infected individuals;
12. $\delta_p = \frac{1}{23}$ day^{-1} is the disease induced death rates due to super-spreaders individuals;
13. $\delta_h = \frac{1}{23}$ day^{-1} is the disease induced death rates due to hospitalized individuals.

A flowchart of model (1) is presented in [11] and included as Fig. 1.

The initial mathematical guess of considering the class of super spreaders has been confirmed in places such as Bhilwara (India), Brighton (UK), or Daegu (South Korea), just to mention some cases.

2.1. Equilibrium points

2.1.1. Basic reproduction number

One of the key tools in any compartmental model is to determine the basic reproduction number, which can be read as a measure of the spread of the disease in the population. Using the next generation matrix approach [12], this quantity has been determined for the model (1) by considering the generation matrices F and V given by [11]

$$J_{\mathscr{F}} = \begin{bmatrix} 0 & \beta & \beta' & \beta l \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}.$$

and

$$J_{\mathscr{V}} = \begin{bmatrix} \kappa & 0 & 0 & 0 \\ -\kappa\rho_1 & \gamma_a+\gamma_i+\delta_i & 0 & 0 \\ -\kappa\rho_2 & 0 & \gamma_a+\gamma_i+\delta_p & 0 \\ 0 & -\gamma_a & -\gamma_a & \gamma_r+\delta_h \end{bmatrix}.$$

By computing the spectral radius of $F \cdot V^{-1}$, the basic reproduction number R_0 is therefore obtained and given by

$$R_0 = \frac{\beta\rho_1(\gamma_a l+\gamma_r+\delta_h)}{(\gamma_a+\gamma_i+\delta_i)(\gamma_r+\delta_h)} + \frac{(\beta\gamma_a l+\beta'(\gamma_r+\delta_h))\rho_2}{(\gamma_a+\gamma_i+\delta_p)(\gamma_r+\delta_h)} = 4.375, \tag{2}$$

by considering the values of the parameters given before.

2.2. Local stability

The following result has been obtained in [11].

Theorem 1. *The disease free equilibrium of system (1), that is,* $(N,0,0,0,0,0,0)$*, is locally asymptotically stable if* $R_0 < 1$ *and unstable if* $R_0 > 1$.

Proof (*Sketch of the proof*). First of all, it is remarkable in system (1), equations number 5, 7 and 8 are uncoupled. The Jacobian matrix associated to the remaining variables is given by

$$J_M = \begin{bmatrix} -\kappa & \beta & \beta' & l\beta \\ \kappa\rho_1 & -\varpi_i & 0 & 0 \\ \kappa\rho_2 & 0 & -\varpi_p & 0 \\ 0 & \gamma_a & \gamma_a & -\varpi_h \end{bmatrix}. \tag{3}$$

The characteristic polynomial of the latter matrix is given by

$$\lambda^4 + b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_4,$$

with

$$\begin{aligned}
a_1 &= \kappa + (\gamma_r+\delta_h) + (\gamma_a+\gamma_i+\delta_i) + (\gamma_a+\gamma_i+\delta_p),\\
a_2 &= -\beta\kappa\rho_1 - \beta'\kappa\rho_2 + \kappa(\gamma_r+\delta_h) + \kappa(\gamma_a+\gamma_i+\delta_i) + (\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_i)\\
&\quad + \kappa(\gamma_a+\gamma_i+\delta_p) + (\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_p) + (\gamma_a+\gamma_i+\delta_i)(\gamma_a+\gamma_i+\delta_p),\\
a_3 &= -\beta\gamma_a\kappa l\rho_1 - \beta\gamma_a\kappa l\rho_2 - \beta\kappa\rho_1(\gamma_r+\delta_h) - \beta'\kappa\rho_2(\gamma_r+\delta_h)\\
&\quad - \beta\kappa\rho_1(\gamma_a+\gamma_i+\delta_p) - \beta'\kappa\rho_2(\gamma_a+\gamma_i+\delta_i)\\
&\quad + \kappa(\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_i) + \kappa(\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_p)\\
&\quad + \kappa(\gamma_a+\gamma_i+\delta_i)(\gamma_a+\gamma_i+\delta_p) + (\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_i)(\gamma_a+\gamma_i+\delta_p),\\
a_4 &= -\beta\gamma_a\kappa l\rho_2(\gamma_a+\gamma_i+\delta_i) - \beta\gamma_a\kappa l\rho_1(\gamma_a+\gamma_i+\delta_p)\\
&\quad - \beta'\kappa\rho_2(\gamma_a+\gamma_i+\delta_i)(\gamma_r+\delta_h) - \beta\kappa\rho_1(\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_p)\\
&\quad + \kappa(\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_i)(\gamma_a+\gamma_i+\delta_p).
\end{aligned}$$

In order to apply the Liénard–Chipard test [13], it might be proved that $a_i > 0, i = 1,2,3,4$ as well as $a_1a_2 > a_3$. In doing so, the coefficients a_i can be rewritten in terms of the basic reproduction number as

$$\begin{aligned}
a_1 &= \kappa + (\gamma_r+\delta_h) + (\gamma_a+\gamma_i+\delta_i) + (\gamma_a+\gamma_i+\delta_p),\\
a_2 &= (1-R_0)(\kappa(\gamma_a+\gamma_i+\delta_i) + \kappa(\gamma_a+\gamma_i+\delta_p)) + \kappa(\gamma_a+\gamma_i+\delta_p)\tfrac{\beta\rho_1}{(\gamma_a+\gamma_i+\delta_i)}\\
&\quad + \kappa(\gamma_a+\gamma_i+\delta_i)\tfrac{\beta'\rho_2}{(\gamma_a+\gamma_i+\delta_p)} + \beta\gamma_a l\rho_1\kappa\Big(\tfrac{1}{(\gamma_r+\delta_h)} + \tfrac{(\gamma_a+\gamma_i+\delta_p)}{(\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_i)}\Big)\\
&\quad + \beta\gamma_a l\rho_2\kappa\Big(\tfrac{1}{(\gamma_r+\delta_h)} + \tfrac{(\gamma_a+\gamma_i+\delta_i)}{(\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_p)}\Big)\\
&\quad + (\kappa+\gamma_a+\gamma_i+\delta_i)(\gamma_r+\delta_h) + ((\gamma_r+\delta_h)+(\gamma_a+\gamma_i+\delta_i))(\gamma_a+\gamma_i+\delta_p),\\
a_3 &= \kappa(1-R_0)((\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_p) + (\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_i)\\
&\quad + (\gamma_a+\gamma_i+\delta_i)(\gamma_a+\gamma_i+\delta_p)) + \kappa(\gamma_a+\gamma_i+\delta_p)\tfrac{\beta\rho_1(\gamma_r+\delta_h)}{(\gamma_a+\gamma_i+\delta_i)}\\
&\quad + \kappa(\gamma_a+\gamma_i+\delta_i)\tfrac{\beta'\rho_2(\gamma_r+\delta_h)}{(\gamma_a+\gamma_i+\delta_p)}\\
&\quad + \kappa(\gamma_a+\gamma_i+\delta_p)\beta\gamma_a l\rho_1\Big(\tfrac{1}{(\gamma_r+\delta_h)} + \tfrac{1}{(\gamma_a+\gamma_i+\delta_i)}\Big)\\
&\quad + \kappa(\gamma_a+\gamma_i+\delta_i)\beta\gamma_a l\rho_2\Big(\tfrac{1}{(\gamma_r+\delta_h)} + \tfrac{1}{(\gamma_a+\gamma_i+\delta_p)}\Big)\\
&\quad + (\gamma_a+\gamma_i+\delta_i)(\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_p),\\
a_4 &= \kappa(\gamma_a+\gamma_i+\delta_i)(\gamma_r+\delta_h)(\gamma_a+\gamma_i+\delta_p)(1-R_0).
\end{aligned}$$

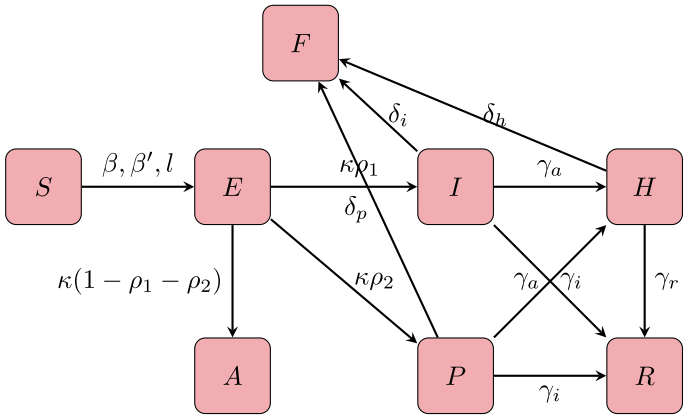

Fig. 1 Flowchart of model (1).

Furthermore,

$$
\begin{aligned}
&a_1a_2 - a_3 = (1-R_0)(\kappa+(\gamma_a+\gamma_i+\delta_i))\kappa(\gamma_a+\gamma_i+\delta_i)\\
&+(1-R_0)(\kappa+(\gamma_r+\delta_h)+(\gamma_a+\gamma_i+\delta_p))\kappa(\gamma_a+\gamma_i+\delta_p)\\
&+(\kappa+\gamma_a+\gamma_i+\delta_p+\gamma_a+\gamma_i+\delta_i)\left(\tfrac{\beta\rho_1}{(\gamma_a+\gamma_i+\delta_p)}+\tfrac{\beta\gamma_a I\rho_1}{(\gamma_a+\gamma_i+\delta_i)}\right)\kappa(\gamma_a+\gamma_i+\delta_p)\\
&+(\kappa+\gamma_a+\gamma_i+\delta_p+\gamma_a+\gamma_i+\delta_i)\left(\tfrac{\beta'\rho_2}{(\gamma_a+\gamma_i+\delta_p)}+\tfrac{\beta\gamma_a I\rho_2}{(\gamma_a+\gamma_i+\delta_p)}\right)\kappa(\gamma_a+\gamma_i+\delta_i)\\
&+(\kappa+\gamma_r+\delta_h+\gamma_a+\gamma_i+\delta_i)\tfrac{\beta\gamma_a I\rho_1\kappa}{(\gamma_r+\delta_h)}+(\kappa+\gamma_r+\delta_h+\gamma_a+\gamma_i+\delta_p)\tfrac{\beta\gamma_a I\rho_2\kappa}{(\gamma_r+\delta_h)}\\
&+(\kappa+(\gamma_a+\gamma_i+\delta_i))(\gamma_r+\delta_h)+(\gamma_r+\delta_h+\gamma_a+\gamma_i+\delta_i)(\gamma_a+\gamma_i+\delta_p),
\end{aligned}
$$

which implies the result. □

3. Numerical simulations: the case study of Galicia

During the pandemic, several reports have been produced to predict the number of required beds at the intensive care units. In doing so, we have used during March and April, 2020, the same values for the parameters in the differential system (1) as for the Wuhan predictions [11]. In Fig. 2 we have plotted both real data and the predictions of the mathematical model. In the simulations of Wuhan it was fixed $N = 11,000,000/250$, and in the Galician case $N = 2,700,000/(1.55 * 250)$. This extra factor of 1.55 is due to the spread of the Galician population. It has been determined in the first days of the pandemic and later has been proved to be an adequate value. Moreover, we have fixed as initial conditions: $S_0 = N - 2, E_0 = 0$, $I_0 = 1, P_0 = 2, A_0 = 0, H_0 = 0, R_0 = 0$, and $F_0 = 0$.

In order to numerically solve the system of differential Eqs. (1), the Matlab code `ode45` has been used, which is based on an explicit Runge–Kutta (4,5) formula. The initial conditions have been fixed taking into account the real data provided by the Galician government during the first days of the pandemic, which allowed us to do the prediction in Fig. 2. The real data are also showed in Fig. 2, which shows the accurate of the model and the predictions. This is the main tool to afterwards predict the number of beds that would be necessary, day by day, at the intensive care units.

By using the simulation, we have done a prediction of the requirements at the intensive care units, computing the 2.5% of the sum of the new infected individuals of the previous 20 days. In Table 1 we show the predicted values as well as the real number of beds that have been required.

4. Conclusions and discussion

The management of resources during the pandemic is essential and this work concludes a method for predicting the number of beds at ICUs.

The predictions of beds at the ICU's has been and is one of the keystones of this pandemic. The data about severity of the confirmed cases has changed several times since the beginning of the pandemic. This is normal in emerging diseases, in which initially the worst cases are detected and, as the disease progresses it is possible to identify milder cases. Following the data from Wuhan, the 31% of the first 99 cases required intensive care, but in 1,099 cases of 532 hospitals in China, only 5% were admitted to intensive care units. From the data of European Union and United Kingdom, 30% of the confirmed cases has been hospitalized, and 4% has been considered as critical. In a similar way, in Spain, from the first 18,609 cases with complete information, 43% has been hosptalized and 3.9% has been at ICU's.

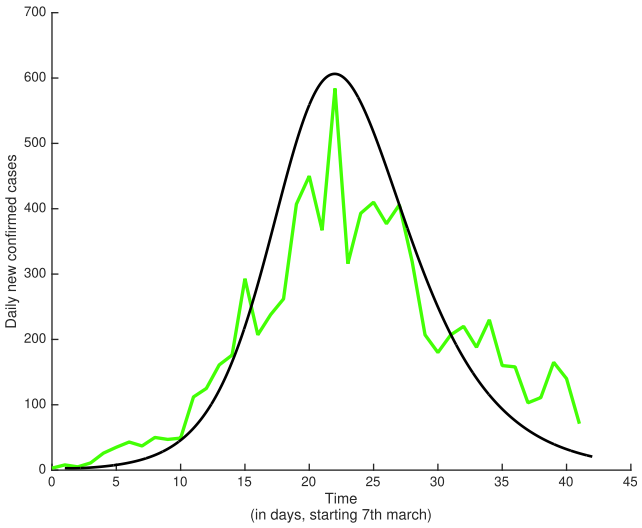

Fig. 2 Number of confirmed cases per day. The green line corresponds to the real data while the black line ($I + P + H$) has been obtained by solving numerically the system of ordinary differential Eq. (1), by using the Matlab code `ode45`. Moreover, we have shifted one day the results of the numerical system.

Table 1 Estimated number of beds and real value during the pandemic in Galicia.

Date	Estimation	Real value
March 17	8	12
March 18	11	15
March 19	15	19
March 20	20	29
March 21	27	35
March 22	36	47
March 23	47	55
March 24	60	69
March 25	74	86
March 26	88	98
March 27	103	112
March 28	118	123
March 29	132	134
March 30	145	149
March 31	156	158
April 01	166	165
April 02	174	178
April 03	181	178
April 04	186	170
April 05	189	170
April 06	192	162
April 07	191	158
April 08	191	155
April 09	188	151
April 10	182	144
April 11	175	140
April 12	165	136
April 13	154	133
April 14	141	128
April 15	126	123

In the case study of Galicia, as mentioned, there was not an important sustained community transmission, which allowed to have a better scenario, as compared with other regions of Spain and Europe.

The approach we have followed is to predict in advance the number of new infected individuals. In doing so, we have considered the mathematical model (1), for which we have computed the basic reproduction number and analyzed the local stability. As a second step, with this prediction in advance, we have predicted the number of beds at ICUs as shown in the manuscript, which has been showed to be accurate.

It seems extremely important to have a tool which allows to predict the number of beds at ICU which would cover real needs, assuming confinement of the population for at least one month. This would help for new outbreaks of the disease. If confinement is not applied to the population, then they might be considered different values of the parameters in the differential system (1), but the prediction based on the curve produced by the model would remain extremely useful for the management of resources.

Ethics approval and consent to participate

Not applicable.

Availability of data and material

All the data used in this work has been obtained from official sources. Moreover, the system of nonlinear differential Eqs. (1) can be numerically solved to obtain the same results as showed.

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Author's contributions

The authors contributed equally to this work. All authors read and approved the final manuscript.

Declaration of Competing Interest

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

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