MULTI-WAVE MODELLING AND SHORT-TERM PREDICTION
OF ICU BED OCCUPANCY BY PATIENTS WITH COVID-19
IN REGIONS OF ITALY

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Abstract. This study offers perspectives into COVID-19 dynamics by employing a phenomenological model representing multiple epidemiological waves. It aims to support decision-making for health authorities and hospital administrators, particularly in optimizing intensive care unit (ICU) bed management and implementing effective containment measures. Given the intricate complexity of ICU environments, utilizing a mathematical model to anticipate occupancy is highly beneficial and might mitigate mortality rates associated with COVID-19. The study focuses on the evolution of intensive care patient numbers across multiple epidemiological waves in Italian regions. Our methodology involves the application of a low-complexity phenomenological model with an efficient optimization procedure. ICU occupancy data from five populous Italian regions are utilized to demonstrate the model’s efficacy on describing historical data and providing forecasts for two-week intervals. Based on the analyzed ICU occupancy data, the study confirms the efficacy of the proposed model. It successfully fits historical data and offers accurate forecasts, achieving an average relative RMSE of 0.51% for the whole fit and 0.93% for the predictions, across all regions. Beyond the immediate context, the model low complexity and efficient optimization make it suitable to diverse regions and diseases, supporting the tracking and containment of future epidemics.

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1. Introduction

In December 2019, the admittance of patients with pneumonia symptoms with an unknown etiology was observed in Wuhan, China. Wuhan is a city with a population of 11 million and an important regional center with a great flux of people [1]. In common, most of these patients had visited a local market that sells fish and wild animal meat in precarious health conditions. Subsequent analysis demonstrated that the responsible was a new coronavirus disease named coronavirus disease 2019 (COVID-19) by the World Health Organization (WHO) in February 2020. The number of infected in China rose from 5 in late December 2019 to 51,174 on

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February 16, 2020, with 1666 deaths [2]. On March 11, 2020, with more than 118,000 cases and over 4200 deaths worldwide, WHO declared the COVID-19 outbreak a global pandemic [3].

The COVID-19 is originated from the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The coronaviruses are a group of enveloped and single-stranded ribonucleic acid (RNA) viruses that cause respiratory, enteric, hepatic, and neurological diseases in a variety of animal species, subdivided into alpha, beta, gamma, and delta genera [4]. The beta genera include respiratory diseases such as the Middle East Respiratory Syndrome (MERS) and SARS (SARS-CoV and SARS-CoV-2) [5]. Human coronaviruses have an animal origin, crossing species barriers, which were demonstrated by masked palm civets and camels (SARS-CoV and MERS, respectively) [6]. Bats were also a major natural host of the coronavirus, especially concerning the alpha and beta variants [7].

SARS originated as an epidemic in 2002, beginning in China and spreading to 29 countries, with more than 8000 cases and 700 deaths. The most common symptoms include fever, rigors, chills, myalgia, and dry cough, with 20–30% of patients developing atypical pneumonia, requiring mechanical ventilation or treatment in intensive care units (ICUs) [5]. Part of its potential to cause an epidemic is due to its rapid transmission mainly via droplets, aerosol, and fomites on surfaces in addition to dissemination predominantly nosocomially and between family members [8]. MERS was discovered in 2012, presenting symptoms similar to SARS-CoV, such as fever, cough, and shortness of breath, but with a higher mortality rate of roughly 30% [9]. Unlike SARS-CoV, animal-to-human contact plays a significant role in transmission by camels and especially camel calves. Presenting symptoms related to SARS-CoV, 50% of symptomatic patients require ICU treatment and up to 70% of them have need of mechanical ventilation. Until 2017, there were reported more than 2000 cases and 700 deaths, globally, although the Kingdom of Saudi Arabia (KSA) represents the majority of cases and deaths, with nosocomial transmission principally [10].

COVID-19 manifests symptoms resembling SAR-CoV, typically fever, dry cough, fatigue, and shortness of breath, with hospitalized patients presenting complications such as pneumonia, acute liver injury, and neurologic dysfunction [11–13]. As far as 20% of patients were hospitalized, nearly 5% necessitating ICU care, with up to 90% of them using mechanical ventilation [5]. Globally, the estimated case fatality rate varies from 0.6% on a cruise, to 3.5% in China [14]. As of the writing of this manuscript, 700 million COVID-19 cases and 6.9 million deaths by the disease were reported in the world [15].

In the context of the COVID-19 pandemic, where effective medicines were not yet available, understanding and diligently implementing effective prevention methods were crucial to curbing the spread of COVID-19. The disease, primarily transmitted through respiratory droplets and aerosols, demanded a multi-faceted approach to its prevention. From individual behaviors to population-wide interventions, a range of methods were used, mainly focusing on personal protective measures such as masks, hand hygiene, social distancing, as well as quarantine and isolation measures [16]. Preventive measures, especially social distancing and isolation, can lead to several socioeconomic and psychosocial challenges. Economic consequences, such as increased unemployment, particularly affecting positions with low technical expertise, and disarray in service, production, and transportation sectors have been observed [17, 18]. These factors, coupled with a rise in cases of depression and anxiety, contribute to a deterioration in mental health [19, 20].

The COVID-19 pandemic development, similarly to other pandemics such as MERS and SARS, benefited from mathematical models to study the spreading dynamics, planning a better use of the resources and when and how to lift the preventive measures [21–25]. The mathematical modelling approach can be stochastic, being statistical and very data-oriented, or deterministic, using differential equations to describe dynamic interrelations among the rates of change and population sizes, or a combination of both approaches [23].

The initial approaches in mathematical modeling of COVID-19 primarily revolved around explaining the dynamics of infection propagation and associated mortality. A pioneering work, by Hernandez-Vargas and Velasco-Hernandez, studied the SARS-CoV-2 dynamics in infected patients, elucidating critical aspects of viral dynamics and their implications for control strategies [26]. The spectrum of modelling efforts included an extensive exploration of infection transmission dynamics, surveillance mechanisms, and, notably, the evaluation of intervention strategies. Well-established compartmental models, like the Susceptible-exposed-infected-recovered
(SEIR), and the Susceptible-infected-recovered (SIR), were widely adopted to perform these analyses. [27–29]. Others considered quarantine and control measures, using models such as the Susceptible, un-quarantined infected, quarantined infected, confirmed infected (SUQC), and the Susceptible-infectious-quarantined-recovered (SIQR) models [30, 31]. Moreover, modified models were used in view of variables like vaccination and the economic impact of COVID-19 interventions [32], confinement strategy [33–35], asymptomatic patients [36], hospitalized patients [37], and a number of studies applying hybrid methods as reviewed by Perone [24].

A work from Khoshnaw et al. [38] uses a compartmental model with eight states, along with data from WHO status reports, to perform sensitivity analysis with different normalization techniques. These analyses show what are the critical parameters of the model, which are the ones that most affects the state variables. Similarly, Paiva et al. [37] also adopted an eight-state compartmental model to predict hospital bed occupancy by COVID-19 inpatients in São Paulo, Brazil. To achieve this goal, they solved a multi-objective optimization problem with four cost functions. Approaches like these bring a more detailed and qualitative view of epidemiological parameters and can provide insights about intervention strategies.

A particularly important area to forecast in the COVID-19 pandemic is the bed occupancy in wards and Intensive Care Units (ICU). Estimating the localization and number of hospitalized COVID-19 patients could improve resource allocation and decrease infection and possible deaths. To model bed occupancy, data as patient flux, Length of Stay (LoS), and the type of bed (ward or ICU) were taken into account [39]. Other studies, as the work of Leclerc et al., use patient bed pathways (sequence of transfers of individual patients between bed types during a hospital stay) as a variable [40].

A recent work in the field, by Gitto et al., used the Harvey growth model to describe and predict ICU bed demand for COVID-19 patients in the first epidemiological wave in Italy [41], a country that was severely impacted by the pandemic since its start [42]. Gitto et al.’s research shows that the Harvey model performs well to represent and predict the ICU bed demand indicator, when compared to the logistic and Gompertz models, both widely used for describing epidemics. An interesting method applied in their work is the hierarchical forecasting, using a top-down approach. This means that predictions are made in both national and regional level, enforcing the predictions for each of the regions to follow a proportion of the national level forecasts [41]. The goal of this technique is to guarantee the cohesion of the forecasts at all levels.

A known limitation of phenomenological models is the lack of an accessible epidemiological interpretability of model parameters. On the other hand, these models bring a more data-driven and quantitative approach that focus on obtaining predictions with as little error as possible, which is also a critically important information to decision makers. Another positive aspect of the phenomenological approach is the efficiency of the parameter estimation procedure and easiness of modelling, especially when using a closed form of a growth model, like the current work.

The present work uses a phenomenological model, based on the Richards growth model, to describe the evolution of the number of ICU patients with COVID-19 across the pandemic and forecast the indicator for two weeks periods, with data from Italian regions. Differently from Gitto et al.’s work, that addresses only the first wave, the current work models the indicator evolution across multiple epidemiological waves. Another difference is that the modelling and forecasting done in the present work are strictly regional. Although studies that apply hierarchical forecasting bring a higher multi-level consistency for the predictions, modelling and forecasting an indicator like the ICU bed demand specifically for a given region is still useful to support local governments and hospitals in their strategical planning and fast reaction.

Thus, the objective of this study is to fit a model to describe the number of ICU patients across several epidemiological waves in Italian regions, being able to generate predictions that extrapolate the indicator behavior for two-week intervals. This is done by using a low complexity model, comprising a sum of Richards sigmoids, that requires optimizing only four parameters per epidemiological wave. In our previous research, the model performed well to describe and predict the daily number of deaths in Argentine cities [43]. A variation of the model, from a preceding implementation, also captured well the behavior of the accumulated and daily number of confirmed cases of the disease in different regions of the world [44, 45]. The application of such a model, to the best of the authors’ knowledge, has not yet been done to model the ICU bed occupancy indicator across multiple waves of the COVID-19 pandemic, hence the contribution of the present study.
2. MATERIALS AND METHODS

2.1. Mathematical model

To model the evolution of the number of ICU admissions of COVID-19 patients over time, the present work uses a phenomenological model. The total number of admitted COVID-19 patients in intensive care units in the first $t$ days of the pandemic is represented by the function

$$H_T(t) = \sum_{i=1}^{N} H_i(t),$$

(2.1)

in which $N$ is the number of epidemiological waves and $H_i(t)$ is an asymmetric sigmoid with its own set of parameters $\theta_i$. While the indicator is a discrete time series and assumes only integer values, the model uses continuous time functions to approximate its trend.

To appropriately model the dynamics of an epidemiological wave, each function $H_i(t)$ presents an acceleration phase and a deceleration phase. In fact, the formulation of each sigmoid is based on the Richards growth model, which is characterized by the following [46, 47] ordinary differential equation (ODE):

$$\frac{dH}{dt}(t) = \frac{1}{\delta \nu} H(t) \left( 1 - \left( \frac{H(t)}{K} \right)^\nu \right).$$

(2.2)

From (2.2), it can be noticed that the model presents, multiplied to $H(t)$, a rate $(\delta \nu)^{-1}$, called the growth rate, responsible for expressing the initial exponential growth of the indicator. Additionally, there is a term $\left( 1 - \left( \frac{H(t)}{K} \right)^\nu \right)$ that introduces a saturation to the model, describing a logistic growth. This term goes to zero when the number of occupied ICU beds $H(t)$ approaches $K$. Therefore, as an integer value, $K$ can be understood as the final number of occupied intensive care beds. The parameter $\nu$ defines the balance of the number of occupied hospital beds in each phase, controlling the asymmetry of the $H(t)$ curve.

Although the ODE (2.2) can provide a good intuition to understand the model’s characteristics, its use require solving the differential equation at every iteration of the algorithm. Thus, the analytical solution of this ODE is a far more efficient alternative, since it only requires the data to pass through the closed-form function. The solution is given [46–48] by:

$$H(t) = \frac{K}{\left( 1 + \nu e^{-\frac{(t-t_p)}{\delta}} \right)^\frac{1}{\nu}}.$$  

(2.3)

The function $H(t)$, in (2.3), has the four positive valued parameters $\nu$, $\delta$, $t_p$ and $K$, describing an asymmetric sigmoid function with a turning point in $t = t_p$.

With (2.3), a closed form for the derivative of $H(t)$ with respect to $t$ can be extracted:

$$\frac{dH}{dt}(t) = \frac{K}{\delta} \frac{e^{-\frac{(t-t_p)}{\delta}}}{\left( 1 + \nu e^{-\frac{(t-t_p)}{\delta}} \right)^\frac{\nu+1}{\nu}}.$$  

(2.4)

Thus, using (2.3) and (2.4), it is possible to describe the behavior of both the accumulated and daily number of occupied ICU hospital beds for a single epidemiological wave, finding the optimal value for the four parameters. In this process, $K$ represents the maximum number of occupied ICU beds at the end of the wave, while $\delta$ influences the growth rate. The parameter $\nu$ controls the asymmetry of the curve, balancing the number of occupied beds before and after $t = t_p$, which is the day when the daily number of ICU patients stops to increase and starts to decrease.
The dynamics of multiple epidemiological waves is captured through combining several of these sigmoids in a sum, as expressed in (2.1). This is done in the fitting procedure, where, for each sigmoid, their four parameters are calibrated, fixed and then incorporated into the sum, which will be used in fitting of the next sigmoid.

2.2. Transition points

An important aspect of modelling the multi-wave dynamics of an epidemic is identifying the transition points between the waves. This will determine when each new sigmoid will be added to the model. Ideally, the number of sigmoids should be equal to the number of epidemiological waves, in order to minimize the model complexity while still being able to describe the trend observed in the real data.

For this purpose, this work uses an algorithm \[44, 45, 48\] to extract the transition points from the accumulated indicator. The algorithm starts by normalizing the cumulative indicator and applying the Euler’s method to extract the first order derivative with respect to \(t\).

To reduce the impact of the noise generated by the numerical derivation, a filtering process is applied to the output. This process involves using three types of filters: a moving average filter, a median filter and a Butterworth low-pass filter.

The moving average filter \(\bar{x}[i]\) can be expressed as (2.5), while the median filter \(\tilde{x}[i]\) can be described by (2.6).

The low-pass filter, on the other hand, uses an implementation from the signal processing module of the SciPy library. The digital filter can be characterized by the following transfer function:

\[
H(z) = \frac{b_0 + b_1 z^{-1} + \cdots + b_m z^{-m}}{a_0 + a_1 z^{-1} + \cdots + a_n z^{-n}},
\]

where \(m\) is the order of the numerator, which represent the number of zeros, and \(n\) is the order of the denominator, expressing the number of poles. The vector of parameters \(a = [a_0, a_1, a_2, \cdots, a_m]\) and \(b = [b_0, b_1, b_2, \cdots, b_n]\) are returned by the butter function from SciPy, which designs the Butterworth filter. The function takes into account the filter order \(N\), a normalized cutoff frequency \(\omega_c\), a sampling rate, defined as the number of data points in the input data, and the specified filter type, in this case, being low-pass. The normalized cutoff frequency is calculated as the ratio between a cutoff frequency in days and the Nyquist frequency, which was defined as half of the sampling rate. Having the vector of parameters \(a\) and \(b\), the algorithm uses the lfilter function from SciPy to efficiently apply the designed filter to the input data.

The actual filtering process starts by applying a moving average filter, with a 14-day window, then a second order Butterworth low-pass filter with a 21-day cutoff frequency and a median filter with a 14-day window. Additionally, to correct the delays introduced by the filters, a shift operation that advances the signal by 25 days is performed.

After this, the second derivative of the indicator is also extracted, by applying the same numerical method. The algorithm then identifies the points in which the second derivative changes from a negative value to a positive one. In these points, the cumulative indicator is transitioning from a deceleration behavior to an acceleration behavior, evidencing that a new epidemiological wave is starting [45].

Instead of checking when the curve changes from lower to greater than zero, a small real valued threshold \(\epsilon\) is considered. Thus, it is possible to adjust the algorithm sensitivity to the fluctuations in the second order derivative. Hence, if a region presents really subtle waves, using a small threshold will make the model more sensitive. This will generate more transition points, suggesting a model with greater complexity.
Figure 1. Identification of the transition points between epidemiological waves of COVID-19 in Lombardia, using the ICU bed occupancy indicator.

The described process is illustrated in Figure 1, where the top sub-figure shows the normalized cumulative indicator, the middle sub-figure shows the filtered first derivative and the bottom figure shows the second derivative. The transition points, which are the output of this algorithm, are identified by the red circles and the vertical dash-dotted lines. The threshold is represented by the horizontal dotted lines in the bottom figure, and was established as $\varepsilon = 1 \times 10^{-6}$ for Lombardia and Lazio, $\varepsilon = 2 \times 10^{-6}$ for Veneto, $\varepsilon = 3 \times 10^{-6}$ for Campania and $\varepsilon = 5 \times 10^{-6}$ for Sicilia. Despite the normalization, slightly larger thresholds were applied to certain regions to detect more subtle changes and correctly determine the transition points between the waves.

2.3. Model fitting procedure

In order to find the optimal parameters to model the studied indicator, an algorithm solves a series of optimization problems of the form

$$\min_{\delta_j, \nu_j, t_{p,j}, A_j} J \left( \sum_{j=1}^{N} H(t, \delta_j, \nu_j, t_{p,j}, K_j), y(t) \right)$$

subject to $\delta_j, \nu_j, t_{p,j}, K_j > 0$. 

\[ (2.8) \]
In this formulation, the objective function consists of a cost function denoted by \( J \), which quantifies the accumulated squared deviations between the output of the mathematical model and the accumulated indicator \( y(t) \). This function places an increased importance on the latest data points by incorporating a multiplication factor proportional to \( t \). The function is, therefore, similar to a discrete version of the integral of time squared error (ITSE) and can be described as

\[
J(f, g) = \sum_{t=1}^{N} (t \times (f(t) - g(t))^2).
\]  

Thus, to minimize the cost function for a given epidemiological wave, the algorithm will seek an optimal set of parameters \( \phi^* = [\nu, \delta, t_p, K] \), to minimize this weighted quadratic difference between the model output and the actual accumulated number of occupied ICU beds by COVID-19 patients up to the \( t \)th day of the pandemic. The problem also involves four inequality constraints, to assure that the parameters \( \delta_j, \nu_j, t_{p,j} \), and \( K \) are positive.

The value of \( N \) is constant and represents the index of the last epidemiological wave being modelled. Thus, the model fitting procedure consists of solving this problem for \( N = 1, 2, 3, \ldots, N_w \), where \( N_w \) is the number of epidemiological waves present in the real data. In fact, for each epidemiological wave, this problem is solved twice. First, the algorithm fits the model fixing the parameter \( \nu = 1 \), using a symmetric sigmoid. After this, a second optimization step is performed without fixing any parameter, using the optimal parameters from the first step as the initial point.

It is relevant to emphasize that, for each epidemiological wave \( N \), after the four optimal parameters are obtained, they are stored and used in the model for the fitting of the subsequent sigmoid. This means that when the \( k \)th wave is being modelled, the model consists of a sum of \( k - 1 \) sigmoids with known parameters and one sigmoid with unknown parameters. Therefore, every optimization routine involved in this fitting procedure involve only four parameters, for the last sigmoid. So, the whole process will require solving \( 2N_w \) constrained optimization problems with 4 controlled variables. The increased importance of most recent data points, leveraged by the multiplying factor \( t \) in the minimized cost function \( J(f, g) \), is especially useful in this case. This is because the parameters that are being calibrated influence mostly the final portion of the curve, since the previous sigmoids have their optimal parameters fixed. A visual representation of the fitting process described is shown in Figure 2.

To computationally solve these problems and obtain the optimal values for the parameters, this work applies the Sequential Least Squares Programming (SLSQP) method, first implemented by Dieter Kraft [49]. The choice of this specific algorithm was motivated by the fact that methods that sequentially solve quadratic subproblems
are well known to address constrained optimization problems efficiently [50]. As the current work uses the Python programming language, the method was imported from the SciPy library optimization toolbox [51].

2.4. Evaluating the model fit and predictions

The metric used to evaluate the quality of the model fit and its predictions is the relative root mean squared error (rRMSE), described by:

\[
rRMSE(f, g) = \frac{1}{\max(g(t))} \sqrt{\frac{\sum_{t=1}^{N} (f(t) - g(t))^2}{N}},
\]

An advantage of using the RMSE metric instead of the mean squared error (MSE) is that it presents the same unit as the real data. The division by the maximum value of the real data up to the analyzed point in time, given by \( \max(g(t)) \), provides the relative version of this indicator, preferably formatted as a percentage. This metric is included in every plot with the model fit, to quantify the error.

An overview of the whole process is shown in Figure 3. First, the transition point detection algorithm is run to obtain the times, in days, in which the real indicator data will be split. These points are used by the optimization algorithm to determine when each sigmoid will be added and fitted. Then, the optimal parameters are stored and the model fit is evaluated through the rRMSE metric and charts to improve interpretability. Another detail that is worth to be mentioned is that, before the optimization algorithm is run, both the cumulative and the daily indicator are normalized. This is done by dividing both by a scaling factor, defined by the maximum value of the accumulated indicator. The same scaling factor is multiplied at the end of the process to restore the original amplitude of the indicator in the plots and numerical results.

2.5. Data sources

The data used in this work was extracted from the repository [52], provided by the Civil Protection Department of Italy. This source provides several COVID-19 related indicators that can express the trend of the disease transmission. Although some indicators are offered at province level, the hospitalization and ICU occupation data is provided only at the regional level.

Thus, for the present study, the five most populous regions of Italy were selected and the daily and accumulated number of ICU admissions were extracted. The regions are Lombardia, Lazio, Campania, Veneto and Sicilia.

3. Results and discussion

The model was applied to describe the first six waves of the pandemic in each of the five most populous regions of Italy. The start date for all the regions is February 24, 2020. As the epidemic across the five regions presented different dynamics, the end date of the sixth wave varied from April to October 2022. Figure 4 shows the daily number of occupied ICU beds by COVID-19 patients and the transition points used by the model.

From the figure, it is possible to see that the incidence of each wave was synchronized for all regions, with different intensities. The calculated transition points are also properly placed between the waves, splitting the intervals for the inclusion of each sigmoid of the model.

The results for the regions of Lombardia, Lazio, Campania, Veneto and Sicilia are presented in Table 1. In the table, the regions are distributed in columns, with their relative root mean squared errors (RMSE) values underneath their names. Six rows present the error values for the fit up to each of the six analyzed waves. The last two rows, however, present their Mean and Median, respectively, in order to summarize the results. For each region, it is also presented a breakdown of the results for the whole fit, including the predictions’ interval, and the results for only the predictions for the last two weeks of unseen data. Each row also presents cells highlighted in green and red, indicating the lowest and highest error value in it, respectively.
Figure 3. Flowchart describing the general functionality of the algorithm.

Figure 4. Comparison between the daily number of ICU patients with COVID-19 for the studied regions, including the calculated transition points.
Table 1. Relative RMSE of the model fit for the first six epidemiological waves of COVID-19 in the regions of Lombardia, Lazio, Campania, Veneto and Sicilia.

<table>
<thead>
<tr>
<th>Region</th>
<th>Lombardia</th>
<th>Lazio</th>
<th>Campania</th>
<th>Veneto</th>
<th>Sicilia</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fit Interval</td>
<td>All fit</td>
<td>Predictions</td>
<td>All fit</td>
<td>Predictions</td>
<td>All fit</td>
</tr>
<tr>
<td>Relative RMSE - Up to wave 1</td>
<td>0.35%</td>
<td>0.47%</td>
<td>1.41%</td>
<td>1.42%</td>
<td>2.90%</td>
</tr>
<tr>
<td>Relative RMSE - Up to wave 2</td>
<td>0.58%</td>
<td>2.02%</td>
<td>0.47%</td>
<td>1.36%</td>
<td>0.91%</td>
</tr>
<tr>
<td>Relative RMSE - Up to wave 3</td>
<td>0.25%</td>
<td>0.99%</td>
<td>0.22%</td>
<td>0.26%</td>
<td>0.39%</td>
</tr>
<tr>
<td>Relative RMSE - Up to wave 4</td>
<td>0.22%</td>
<td>0.20%</td>
<td>0.22%</td>
<td>0.64%</td>
<td>0.37%</td>
</tr>
<tr>
<td>Relative RMSE - Up to wave 5</td>
<td>0.19%</td>
<td>0.35%</td>
<td>0.20%</td>
<td>0.51%</td>
<td>0.35%</td>
</tr>
<tr>
<td>Relative RMSE - Up to wave 6</td>
<td>0.17%</td>
<td>0.01%</td>
<td>0.17%</td>
<td>0.16%</td>
<td>0.30%</td>
</tr>
<tr>
<td>Mean</td>
<td>0.29%</td>
<td>0.52%</td>
<td>0.45%</td>
<td>0.72%</td>
<td>0.87%</td>
</tr>
<tr>
<td>Median</td>
<td>0.23%</td>
<td>0.27%</td>
<td>0.22%</td>
<td>0.57%</td>
<td>0.38%</td>
</tr>
</tbody>
</table>

From the Mean values of the relative RMSE, in Table 1, it is possible to calculate that the average for all regions is 0.51% for the whole fit and 0.93% for the predictions. This indicates that the overall fit was really good. It is also clear that the fit for the Lombardia region was the most outstanding, showing the lowest relative RMSE values for four of the six intervals and the lowest average of the five regions. The fit for the regions of Lazio and Veneto were also excellent, presenting low Mean values for the errors, and even lower Median values. Although Lazio hadn’t had any green rows for the six intervals, it stood up by presenting a Median error of 0.22%, the lowest of all studied localities.

The model fit for the data from Campania and Sicilia, on the other hand, showed the highest number of negative highlights, although it was also fairly good, with the Mean and Median of the relative RMSE values lower than 2%. For both of these regions, the automatic suggestion of transition points didn’t converge to a reasonable fit, when applying the optimization procedure. For Sicilia, the first transition point was manually changed from day 213 to day 150. For Campania, the first transition point was discarded, since it was too low and redundant.

The region of Lombardia has a population of almost 10 million, according to data from January 2023 [53]. This value is more than twice the population of Veneto and Sicilia, and more than 70% greater than the population of Lazio and Campania. This difference is a possible reason for the better fit, since a more densely populated region is susceptible to a faster spread of the virus, rising the number of patients in ICUs. The case of Veneto, which is the second least populous of the five regions, is somewhat different. Although it has around 17% less inhabitants than Lazio, the daily number of COVID-19 patients in ICUs in the regions was similar in magnitude, considering the six analyzed waves. For the first wave specifically, Veneto had a peak of about 350 occupied ICU beds per day, while Lazio had a peak of 200, approximately. These differences are clearly shown by Figure 4.

Many factors could explain this behavior, such as the safety measures took by the governments of each region, socioeconomic profile and also the availability of properly equipped hospitals and ICUs. Another factor that may have contributed to intensify the effects of the first wave of the pandemic in Lombardia and Veneto was that these regions had the first confirmed cases and deaths of the country, respectively, in late February 2020 [54].

In fact, the response of each region to the pandemic was different, influencing the intensity of the virus transmission across the analyzed months. For example, the containment strategies adopted for Lombardia and Veneto were notably different. While Veneto followed a more proactive testing strategy since the start, including symptomatic and asymptomatic patients, and presented robust containment measures early on, Lombardia took a more conservative approach and enforced these measures with a slight delay [55, 56]. In spite of these differences, the intervention of health authorities and governments, that started from 9 to 12th of March 2020 in the most affected regions, was effective to slow down the progression of the pandemic and the spread across the country [57].

The observed differences in the magnitude for the number of ICU beds are also reflected in the optimal parameters of the fitted model. The $K$ parameter of the first sigmoid, without normalization, was 68156 for Lombardia, 13239 for Veneto, 10939 for Lazio, 4455 for Campania, and 3054 for Sicilia. This parameter is
valuable to compare the amplitude of the indicator, since it describes, in this case, the expected final number of ICU admissions if the pandemic had stopped at the end of the wave.

For Lombardia, Figure 5 details the model fit and predictions, comparing them to the actual data. In this figure, there are six rows, representing the model fit up to the first six epidemiological waves, and two columns. Column (a) shows the cumulative indicator, comparing the actual data with the model, while Column (b)
Figure 6. Model fit and predictions for the (a) accumulated and (b) daily number of ICU admissions of COVID-19 patients for the first three epidemiological waves in Lazio.

exhibits the same comparison for the daily indicator. Additionally, there is a vertical dash-dotted line before the last 14 days of each wave, separating the portion of data used to fit the model from the two-week portion used to assess its predictions. The graphs in the first column also show a detail to help the visualization of the short-term predictions.

The region of Lombardia presented a first wave with a peak of almost 1400 admissions per day, around the 40th day of the pandemic. After this, a plateau of about 100 days took place, followed by two new waves slightly smaller than the first one, with similar magnitudes. In contrast, the three subsequent waves were characterized by subtle changes, with significantly smaller magnitudes compared to their predecessors. The model fit for Lombardia was really good across all six waves, achieving an average relative RMSE of 0.29%. The worst case occurred for the second wave, especially for the deceleration phase, where the model presented a steeper decline than the real data. Consequently, the predictions for the 14 days following the second transition point were the least accurate, showing a relative RMSE of 2.02%. Nevertheless, the model fit demonstrated a notable recovery in accuracy as the acceleration phase of the third wave started.

For Lazio, Campania, Veneto and Sicilia, a comparison between the model output and the real indicator for the first three waves is presented in Figures 6, 7, 8 and 9, respectively. In these figures, the row labeled with (a) shows the comparison for the accumulated indicator, while the row labeled with (b) presents it for the daily indicator.

Overall, the model fit and predictions were satisfactory for all the regions, with a few exceptions. In the case of Campania, for example, the peak of the first wave was identified with a slight delay by the model, who suggested a sigmoid curve who was less right skewed than the actual data of the indicator. A similar behavior occurred in the results of Sicilia, where the acceleration phase of the first wave was less steep than in the actual data. In both cases, the model suggested higher values for the daily number of occupied hospital beds right before the turning point, but a lower value for the peak of the epidemiological wave. On the other hand, the trend of the deceleration phase, that usually lasts longer, for the first wave was successfully captured by the model for all regions.

For the final portion of the second wave in both Campania and Sicilia, the model indicated a more abrupt decline in the daily number of ICU admissions than the real data, leading to less precise predictions for the
forthcoming two weeks. Thus, the relative RMSE of the predictions for the fit up to this wave in Sicilia and Campania were 5.14% and 3.55%, respectively, scoring the highest error values across all studied regions for this interval.

In a general sense, from the results in Table 1 and Figures 5, 6, 7, 8 and 9, one may see that all the regions presented a relatively high error value for the predictions at the end of the second wave. This may have happened
because of the proximity between the second and the third wave, whose acceleration and deceleration phases present a considerable overlap. In Figure 4, this becomes clearer once the transition points of each region between the second and third wave are considerably spread, although the wave peaks were approximately synchronized. This may indicate that the algorithm struggled to suggest a good transition point for this section.

Despite the challenges discussed above, the satisfactory overall performance of the model enforces the importance of the results. The two-week predictions provided by the model could support hospital administrators to manage the availability of ICU beds for patients in the upcoming days. The results showed that the model is able to forecast the behavior with a low error for different stages of the pandemic. This information could also be useful for local governments to assess the overall severity of the pandemic at a given time. The most accurate way to track this would be to always feed the model with the latest available data and get the predictions for the 14 days ahead.

### 4. Conclusion

This work has applied a phenomenological model based on a sum of asymmetric sigmoids to describe the evolution of the number of occupied ICU beds by COVID-19 patients. The main novelty here is the ability to model and forecast the indicator across multiple epidemiological waves with such a model. Therefore, the outputs of the present study are valuable to monitor the pandemic status across all its different stages.

The algorithm is able to analyze the input data and to automatically suggest a set of transition points. This minimizes the effort to adapt it to be applied to data from other regions. The obtained results were really good for all studied regions, with an average relative RMSE of 0.51% for the whole fit and 0.93% for the predictions. The behavior in the historical data was successfully captured by the model, and the short-term predictions presented a low error value for most cases. The proposed model presents a low complexity, with four controlled variables, resulting in an efficient fitting procedure. A known limitation, from its phenomenological nature, is the lack of direct correspondence between the model parameters and biological or epidemiological factors. Nevertheless, valuable insights and hypotheses can still be derived from the model parameters and outputs, aiding in quantifying observed pandemic behaviors within specific locations.
The number of ICU patients in a specific region is a crucial indicator to be tracked during an epidemic. Predicting it for upcoming dates is even more important, as it helps the hospitals to manage their resources in order to guarantee the availability of sufficiently equipped beds to accommodate the infected individuals.

Future works might experiment with applying the model to other regions, other pandemic indicators and also other diseases, due to its non-specific nature. Different phenomenological models and error formulations could also be tested and compared in a posterior research. Moreover, the transition points detection algorithm has the potential to be automated and integrated to the fitting step, since their suggestions led to an optimal fit to the real data in most cases. This integration could be done in the form of an application or toolbox to help the modelling and tracking of future epidemics, reducing the lead time to take containment actions. This would also help to make the information widely available, allowing people with no expertise to run the model scripts to benefit from its results and insights.

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References


[53] Italian National Institute of Statistics (ISTAT), Popolazione residente al 1° gennaio 2023 per età, sesso e stato civile (2024).


[56] H. Secon, 2 regions of Italy took different approaches to fighting the coronavirus. Their results show that widespread testing and early social distancing really work (2020).


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