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# MODELLING THE COVID-19 PANDEMIC: VARIANTS AND VACCINES

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**Abstract.** In December 2019, a new coronavirus, the SARS-CoV-2, was detected in the Chinese city of Wuhan. Since then, many mathematical models have been developed to study the possible evolution of the COVID-19 disease and shed some light on the different biological processes of concern. On 14 December 2020, the United Kingdom reported a potentially more contagious and lethal variant of the virus, at the same time that different vaccines were being tested in order to prevent severe forms of the disease. In the following lines, we revisit a model proposed by our team, which took into account these two determining facts, showing its performance with real Italian data.

## 1 INTRODUCTION

In December 2019, a new coronavirus, SARS-CoV-2, was detected in the Chinese city of Wuhan ([1]). This new virus induced the coronavirus disease 2019 (COVID-19), which would spread all over the world in few months. On 30 January 2020, the World Health Organization declared this disease to be a Public Health Emergency of International Concern ([2]).

On 21 February 2020, the COVID-19 started to spread around Italy ([3]), becoming this country the epicenter of the epidemic in Europe, and 114 countries were affected by this disease as of 11 March 2020. This led the World Health Organization to declare it the first pandemic caused by a coronavirus ([4]).

In April 2020, some authors of this current writing published an open-access version of a first paper devoted to this disease (see [5]). In this paper, the authors proposed a $\theta$-SEIHRD model, based in the Be-CoDiS model ([6]). This publication was one of the precursors in the mathematical study of this disease, taking into account the effect of undetected infectious people (modelled by the parameter $\theta$), different infectiousness levels for hospitalized people and the

need of estimating the necessary beds in hospitals to face hospital saturation due to the lack of preparedness. This model was calibrated with real data from the epidemic in China.

With the continuous development of the disease and its start in Europe, we proposed a second model, a $\theta$-SEIHQRD model, considering the new features of the pandemic (see [7]). The main features were (1) the use of quarantine as a regular measure for infectious detected people with mild or no symptoms (compartment $Q$) and (2) the addition of two compartments associated to the deceases associated to undetected infected people (compartments $I_{D_u}$, for infectious undetected people who will die, and $D_u$, for the corresponding deaths). This model was validated with real data of the case of Italy.

The model revisited in this publication corresponds to [8], where we reference in detail the determining circumstances starting in December 2020 taken into account. Briefly, these circumstances were:

- The identification on 14 December 2020 of a new variant in the United Kingdom, currently known as Alpha variant. This variant was found out to be both more transmissible and lethal than the reference variant (see [9, 10]).
- The authorization of the European Medicines Agency (EMA) on 21 December 2020 to start vaccinating with the Comirnaty COVID-19 vaccine (Pfizer/BioNTech). From January to March 2021, the EMA approved three more vaccines: Spikevax (Moderna), Vaxzevria (Oxford, formerly known as AstraZeneca) and Jcovden (Johnson and Johnson, formerly known as Janssen).

Many models had been proposed at that time to simulate the evolution of the COVID-19 (e.g., [11], [7] and the references therein), but, to the best of our knowledge, the work here revisited was one of the precursors when studying the effects of new SARS-CoV-2 variants, along with vaccination against COVID-19 (see also [12]). Nowadays, there exist several models offering different points of view to study the effect of both circumstances (see, e.g., [13]). The model here revisited is a $\theta$-$ij$-SVEIHQRD model, where $\theta$ models the proportion of detected infectious people, as stated before, and we consider the following compartments: $S$ (susceptible), $E$ (exposed), $I$ (infectious before being able to be detected), $I_{\mathrm{u}}$ (undetected infectious), $H_R$ (hospitalized individuals who will recover), $H_D$ (hospitalized individuals who will die from COVID-19), $Q$ (quarantine), $R_{\mathrm{d}}$ (detected recoveries), $R_{\mathrm{u}}$ (undetected recoveries), $D$ (detected deaths) and $D_u$ (deaths of undetected infectious). Moreover, each infectious compartment (except for $Q$, for which we assume they are not able to infect due to their isolation) is split into $M \in \mathbb{N}$ subcompartments, where $M$ is the number of different variants; thus, we consider $E^{(i)}$, $I^{(i)}$, $I_{\mathrm{u}}^{(i)}$, $H_R^{(i)}$ and $H_D^{(i)}$, for $i \in \{1, \dots, M\}$. Concretely, for Italy we let $M = 2$, since we only take into account the reference variant and the Alpha variant. On the other hand, we consider compartments $V_j$, $j \in \{1, \dots, J\}$, $J \in \mathbb{N}$, for people effectively vaccinated from the $j$-th vaccine who we suppose that are immune to the disease[1]; in our case, $J = 4$, referring to the four vaccines previously mentioned. At this point, we did not consider resusceptibility in any of the three mentioned models, since not enough information was available at those moments.

[1]This is the characteristic of a *perfect* vaccine; although nowadays we know the current COVID-19 vaccines are not perfect, we did not have enough data at that time.

Hence, in the next section, we state the mathematical model particularized for Italy. Concretely, we comment the equations and the involved parameters in Section 2.1, we briefly expose our estimate for the effective reproduction number in Section 2.2, a quantity that was used in our conclusions, and finally present some results in Section 2.3.

## 2 MATHEMATICAL MODEL. APPLICATION TO THE CASE OF ITALY

In this section, we present a particularization of the model presented in [8], Section 2, for Italy, taking into consideration the Alpha variant and the four vaccines approved by the EMA between December 2020 and March 2021. Regarding the parameters, we consider dependence on the variant only for the transmission rates $\beta$ and the fatality rate $\omega$, based on the available information.

### 2.1 Mathematical model for Italy

Given all the characteristics stated in Section 1, next we present the equations associated to our $\theta$-$ij$-SVEIHQRD model, which is represented schematically in Figure 1.

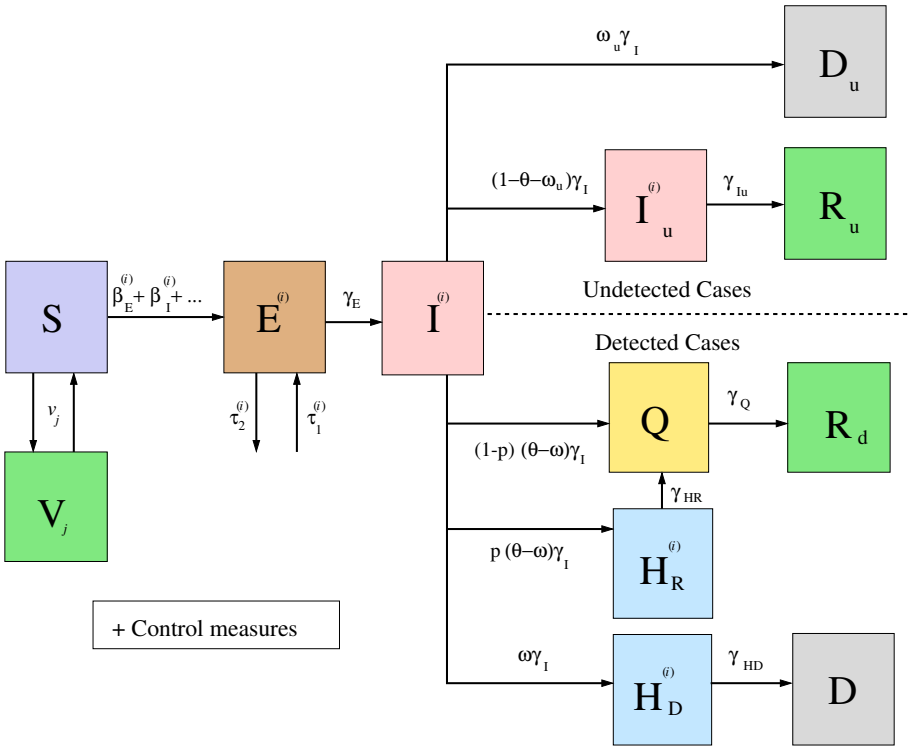


**Figure 1**: Diagram summarizing the model for COVID-19 in the case of Italy, given by system (1)–(2).

$$
\begin{aligned}
\dot{S} &= -\frac{S}{N}\sum_{i=1}^{2}\left(\beta_E^{(i)}E^{(i)}+\beta_I^{(i)}I^{(i)}+\beta_{I_\mathrm{u}}^{(i)}I_\mathrm{u}^{(i)}+\beta_{H_R}^{(i)}H_R^{(i)}+\beta_{H_D}^{(i)}H_D^{(i)}\right)-\sum_{j=1}^{2}v_j,\\
\dot{E}^{(i)} &= \frac{S}{N}\left(\beta_E^{(i)}E^{(i)}+\beta_I^{(i)}I^{(i)}+\beta_{I_\mathrm{u}}^{(i)}I_\mathrm{u}^{(i)}+\beta_{H_R}^{(i)}H_R^{(i)}+\beta_{H_D}^{(i)}H_D^{(i)}\right)-\gamma_E E^{(i)}+\tau_1^{(i)}-\tau_2^{(i)},\\
\dot{I}^{(i)} &= \gamma_E E^{(i)}-\gamma_I I^{(i)},\\
\dot{I}_\mathrm{u}^{(i)} &= (1-\theta-\omega_\mathrm{u})\gamma_I I^{(i)}-\gamma_{I_\mathrm{u}}I_\mathrm{u}^{(i)},\\
\dot{H}_R^{(i)} &= p(\theta-\omega^{(i)})\gamma_I I^{(i)}-\gamma_{H_R}H_R^{(i)},\\
\dot{H}_D^{(i)} &= \omega^{(i)}\gamma_I I^{(i)}-\gamma_{H_D}H_D^{(i)},
\end{aligned}
\tag{1}
$$

for $i\in\{1,2\}$, together with

$$
\begin{aligned}
Q(t) &= \mathrm{e}^{-\gamma_Q(t-t_0)}\left(Q(t_0)+\int_{t_0}^{t}q(s)\mathrm{e}^{\gamma_Q(s-t_0)}\mathrm{d}s\right),\\
&\quad \text{with } q=\sum_{i=1}^{2}\left[(1-p)\,(\theta-\omega^{(i)})\gamma_I I^{(i)}+\gamma_{H_R}H_R^{(i)}\right]\\
R_\mathrm{d}(t) &= R_\mathrm{d}(t_0)+\int_{t_0}^{t}\gamma_Q Q(s)\mathrm{d}s,\\
R_\mathrm{u}(t) &= R_\mathrm{u}(t_0)+\sum_{i=1}^{2}\int_{t_0}^{t}\gamma_{I_\mathrm{u}}I_\mathrm{u}^{(i)}(s)\mathrm{d}s,\\
D_\mathrm{u}(t) &= D_\mathrm{u}(t_0)+\sum_{i=1}^{2}\int_{t_0}^{t}\omega_\mathrm{u}(s)\gamma_I I^{(i)}(s)\mathrm{d}s,\\
D(t) &= D(t_0)+\sum_{i=1}^{2}\int_{t_0}^{t}\gamma_{H_D}(s)H_D^{(i)}(s)\mathrm{d}s,\\
V_j(t) &= V_j(t_0)+\int_{t_0}^{t}v_j(s)\mathrm{d}s.
\end{aligned}
\tag{2}
$$

for $j\in\{1,2\}$, where $v_j(t)$ is the number of people that get or lose immunity after being vaccinated from the $j$-th vaccine per unit time, at time $t$. Notice this depends on the efficacy of the vaccine through time, and thus an immune vaccinated individual is susceptible to lose this immunity after some time. We define this quantity as

$$
v_j(t)=\int_{0}^{t-\bar{t}_j}\dot{e}_j(s)u_j(t-s)\frac{A_S(t-s)}{F(t-s)}\mathrm{d}s,
\tag{3}
$$

being $u_j(\tau)$ the number of individuals that got a first dose of the $j$-th vaccine per unit time, at time $\tau$, $e_j(s)$ the efficacy of the $j$-th vaccine (the ratio of immune people by vaccination after $s$ days since their first dose)[2], $\bar{t}_j$ the time vaccination of the $j$-th vaccine started, $F(\tau)$ an

[2]This formulation also admits derivatives of $e_j$, $\dot{e}_j$, in a distributional sense.

estimation of the number of potentially vaccinable people at time $\tau$ and $A_S(\tau)$ an estimation of the vaccinable people in $S$ at time $\tau$, considering $\frac{A_S(\tau)}{F(\tau)} = 0$ when $F(\tau) = 0$ (or $\leq 0$ in the numerical approximations). We used real data for $u_j$ and $e_j$ functions, as detailed in [8], Section 3.1 and Annex.

The rest of the parameters are explained in previous publications ([5, 7]), recalling that the superscript $^{(i)}$ stands for the variant we are referring to. Hence, here we only present the main changes we performed to adapt the new model:

- $\omega^{(i)}(t) \in [0, 1]$ is the instantaneous infection detected fatality ratio (iIdFR) at time $t$, for variant $i$; i.e., the proportion of new detected infections that will die of COVID-19, per unit time, compared to the total number of new infections (both detected and undetected), per unit time, for variant $i$. In [7], for the reference variant, we considered a constant value of $\omega^{(1)} = 1.4555\%$. However, we modified this quantity accordingly to the effect of vaccination. One of the priority groups when vaccination campaigns started was the elder people; this group indeed had higher death rates than younger people, and thus this led to a decrease of this iIdFR. We illustrated this change in a function $c_\omega(t)$ such that $\omega^{(1)}(t) = 1.4555 c_\omega(t)$. The details about this function can be found in the Annex of [8]. On the other hand, they reported in [10] a 58% higher mortality for variant Alpha, compared to the reference variant. Hence, we let $\omega^{(2)}(t) = (1 + k_\omega)\omega^{(1)}(t)$, being $k_\omega = 0.58$.

- $\theta(t) \in [\omega^{(2)}(t), 1 - \omega_u] \subset [0, 1]$ is the proportion of new infections that are detected and documented by the authorities, per unit time, compared to the total number of new infections (both detected and undetected), per unit time, at time $t$. Based on previous definitions of $\theta(t)$ ([5, 7]), for this case with two variants, we redefined it in the following way:

$$\theta(t) = \begin{cases} \theta_0, & \text{, if } t \leq t_{\theta_0}, \\ \dfrac{\omega(t)}{\omega_{\text{CFR}}(t)} \left( p_{\text{v}}^{(1)}(t) + (1 + k_\omega) p_{\text{v}}^{(2)} \right) & \text{, if } t > t_{\theta_0}, \end{cases} \tag{4}$$

  where $p_{\text{v}}^{(i)}(t)$ is an estimation of the ratio of infections produced by variant $i$ over the total number of infections and $\omega_{\text{CFR}}$ is a filtered version of an estimate for the Case Fatality Rate computed in terms of real data, as explained in [8], Section 2. To estimate $p_{\text{v}}^{(2)}(t)$, we considered the data reported by the Istituto Superiore di Sanità, as referenced in [8]: the cases due to variant Alpha represented a 17.8% of the total detected cases in Italy on 5 February 2021, a 54% on 18 February, a 86.7% on 18 March and a 91.6% on 15 April. Assuming there was no prevalence of this variant before 8 October 2020 (see the explanation of $\tau_1$ and $\tau_2$) and a prevalence of a 99% on 31 August 2021, defined $p_{\text{v}}^{(2)}(t)$ through a piecewise cubic Hermite interpolating polynomial.

- $\beta_E^{(i)}$, $\beta_I^{(i)}$, $\beta_{I_u}^{(i)}$, $\beta_{H_R}^{(i)}$, $\beta_{H_D}^{(i)} \in [0, \infty)$ (day$^{-1}$) are the respective contact rates for each compartment, for variant $i$. We redefine $\beta_{H_R}^{(i)}$ and $\beta_{H_D}^{(i)}$ as

$$\beta_{H_R}^{(i)} = c_{\beta_H}(t)\beta_{H_R,0}^{(i)}, \quad \beta_{H_D}^{(i)} = c_{\beta_H}(t)\beta_{H_D,0}^{(i)}, \tag{5}$$

  where $c_{\beta_H}(t) \in [0, 1]$ represents the effect of vaccinating the healthcare workers, one of the priority groups in Italy at the beginning of the vaccination campaign ([14]). We assume

an immediate effect of the vaccination in the decrease of new infections due to hospital contacts. This function is given by

$$c_{\beta_H}(t) = \frac{N_{\mathrm{H}} - N_{\mathrm{v,H}}(t - t_{\mathrm{vd}})}{N_{\mathrm{H}}}, \text{ if } t > t_{\mathrm{vac}}, \text{ and 1 elsewhere,} \tag{6}$$

where $N_{\mathrm{H}} = 1,974,324$ is the total number of healthcare workers in Italy ([14]) and $N_{\mathrm{v,H}}$ is an estimation of the total number of vaccinated healthcare workers, based on the official data reported in [15]. On the other hand, regarding the conclusions in [9] on the transmissibility of variant Alpha, we considered an increase of a 93% of the disease contact rates with respect to the reference variant, since the effective reproduction number $\mathrm{R_e}$ is proportional to these rates (see Section 2.2), i.e., $\beta_X^{(2)} = (1+k)\beta_X^{(1)}$, $k = 0.93$, for all $X \in \{E, I, I_{\mathrm{u}}, H_R, H_D\}$.

- $\gamma_{H_D}(t) \in (0, +\infty)$ ($\mathrm{day}^{-1}$) is the transition rate from compartment $H_D^{(i)}$ to compartment $D$, at time $t$. We consider in this case a non-constant function of $t$, basing ourselves in an official Italian *situation report* published on 1 March 2021 ([16]) on the average time between hospitalization and death, compared to a previous one published on 16 December 2020 ([17]). One can check Remark 3 in [8] to read the construction of this function $\gamma_{H_D}(t)$.

- $\tau_1^{(i)}(t)$ and $\tau_2^{(i)}(t) \in (0, +\infty)$ are the people infected with variant $i$ that arrive/leave from/to other territories, per day. According to [18] y [19], the first 13 reported cases of people infected with variant Alpha arriving at Italy came from the UK around 7 December 2020. Moreover, there existed suspicions that there were more cases previous to that date (see, e.g., [20]). Hence, we considered two imported cases of variant Alpha in Italy on 8 October 2020 (i.e., $\tau_1^{(2)}(8 \text{ October } 2020) = 2$) after calibration, taking into account this information and the incidence of this variant officially reported by the Istituto Superiore di Sanità, as aforementioned.

### 2.2 Computation of the effective reproduction number

For a model regarding different variants, we considered important computing an effective reproduction number for each of them. This quantity is defined as the expected number of cases generated by one individual infected with variant $i$ in a partially susceptible population.

On one hand, consider the infectious compartments $E^{(i)}$, $I^{(i)}$, $I_u^{(i)}$ and $H_R^{(i)}$ where the transition rates are constant. Let us choose a compartment $X^{(i)}$ among these four. The duration $s_X$ (day) of an individual in $X^{(i)}$ follows an exponential distribution with probability density function $f_X(s_X) = \gamma_X \mathrm{e}^{-\gamma_X s_X}$ and mean $1/\gamma_X$. Moreover, letting $\beta_X^{(i)}$ be the disease contact rate of compartment $X^{(i)}$, then

$$r_X^{(i)}(z, s_X) = \int_z^{z+s_X} \beta_X^{(i)}(\tau)\frac{S(\tau)}{N}\mathrm{d}\tau \tag{7}$$

is the number of infections generated by an individual entering compartment $X^{(i)}$ at time $z$ and leaving at time $z + s_X$. Finally, since $1/\gamma_X$ is the mean duration in compartment $X^{(i)}$, we

approximate the expected number of cases generated by an individual that enters compartment $X^{(i)}$ at time $z$ over its stay in this compartment as

$$\mathrm{R}_X^{(i)}(z) = \int_0^\infty f_X(s_X) r_X^{(i)}\left(z, \frac{1}{\gamma_X}\right) \mathrm{d}s_X = r_X^{(i)}\left(z, \frac{1}{\gamma_X}\right) = \int_z^{z+\frac{1}{\gamma_X}} \beta_X^{(i)}(\tau)\frac{S(\tau)}{N}\mathrm{d}\tau. \tag{8}$$

On the other hand, letting $X^{(i)} = H_D^{(i)}$, in this case, the transition rate is a time dependent function $\gamma_X : (0, +\infty) \to \mathbb{R}$. Assume there exists some $\underline{\gamma} > 0$ such that $\gamma_X(t) \geq \underline{\gamma} > 0$, for all $t \in (t_0, +\infty)$. Then, the probability density function associated to the days $s_X$ that an individual spends in compartment $X^{(i)}$ when entering at time $z$ is

$$f_{X,z}(s_X) = \gamma_X(z + s_X)\mathrm{e}^{-\int_0^{s_X}\gamma_X(z+u)}\mathrm{d}u, \tag{9}$$

and has mean

$$s_X(z) = \int_0^\infty \mathrm{e}^{-\int_0^s \gamma_X(z+u)\mathrm{d}u}\mathrm{d}s \leq \frac{1}{\underline{\gamma}}. \tag{10}$$

Notice that $s_X(t) = 1/\underline{\gamma}$ when $\gamma_X$ is constant. Then, considering the mean $s_X$, we approximate the expected number of cases generated by one individual entering compartment $X^{(i)}$ at time $t$ as

$$\mathrm{R}_X^{(i)}(z) = \int_0^\infty f_{X,z}(s) r_X^{(i)}\left(z, s_X(z)\right) \mathrm{d}s = r_X^{(i)}\left(z, s_X(z)\right) = \int_z^{z+s_X(z)} \beta_X^{(i)}(\tau)\frac{S(\tau)}{N}\mathrm{d}\tau. \tag{11}$$

Given these two approximations, we estimate the effective reproduction number associated to variant $i$ as

$$\begin{aligned}\mathrm{R}_\mathrm{e}^{(i)}(t) \;=\; & \int_t^{t_E} \beta_E^{(i)}(\tau)\frac{S(\tau)}{N}\mathrm{d}\tau + \int_{t_E}^{t_I} \beta_I^{(i)}(\tau)\frac{S(\tau)}{N}\mathrm{d}\tau + (1-\theta(t_I)-\omega_u(t_I))\int_{t_I}^{t_{I_\mathrm{u}}} \beta_{I_\mathrm{u}}^{(i)}(\tau)\frac{S(\tau)}{N}\mathrm{d}\tau \\ & + p(t_I)\left(\theta(t_I) - \omega^{(i)}(t_I)\right)\int_{t_I}^{t_{H_R}} \beta_{H_R}^{(i)}(\tau)\frac{S(\tau)}{N}\mathrm{d}\tau + \omega^{(i)}(t_I)\int_{t_I}^{t_{H_D}} \beta_{H_D}^{(i)}(\tau)\frac{S(\tau)}{N}\mathrm{d}\tau,\end{aligned} \tag{12}$$

where

$$\begin{aligned} t_E &= t + \frac{1}{\gamma_E}, \quad t_I = t + \frac{1}{\gamma_E} + \frac{1}{\gamma_I}, \quad t_{I_\mathrm{u}} = t + \frac{1}{\gamma_E} + \frac{1}{\gamma_I} + \frac{1}{\gamma_{I_\mathrm{u}}}, \\ t_{H_R} &= t + \frac{1}{\gamma_E} + \frac{1}{\gamma_I} + \frac{1}{\gamma_{H_R}}, \quad t_{H_D} = t + \frac{1}{\gamma_E} + \frac{1}{\gamma_I} + s_{H_D}(t). \end{aligned} \tag{13}$$

Given this for one concrete variant, the total expected number of secondary cases produced by one individual infected of SARS-CoV-2, independently of the variant, can be estimated by

$$\mathrm{R}_\mathrm{e}(t) = \frac{\mathcal{E}^{(1)}(t)\mathrm{R}_\mathrm{e}^{(1)}(t) + \mathcal{E}^{(2)}(t)\mathrm{R}_\mathrm{e}^{(2)}(t)}{\mathcal{E}^{(1)}(t) + \mathcal{E}^{(2)}(t)}, \tag{14}$$

where

$$\mathcal{E}^{(i)} = \frac{S}{N}\left(\beta_E^{(i)}E^{(i)} + \beta_I^{(i)}I^{(i)} + \beta_{I_\mathrm{u}}^{(i)}I_\mathrm{u}^{(i)} + \beta_{I_{D_\mathrm{u}}}^{(i)}I_{D_\mathrm{u}}^{(i)} + \beta_{H_R}^{(i)}H_R^{(i)} + \beta_{H_D}^{(i)}H_D^{(i)}\right) + \tau_1^{(i)} - \tau_2^{(i)}, \tag{15}$$

$i \in \{1, 2\}$, is an estimate of the number of susceptible individuals entering compartment $E^{(i)}$, per unit time, at time $t$.

### 2.3 Results for the case of Italy

In the following lines, we summarize some results obtained in [8] for this particular case. The model is numerically solved through the Runge-Kutta 4 method, with a time step of 6 hours. The choice of initial values for our compartments is detailed in both [7] and [8], as well as the efficacy functions and the functions of first administered doses for the vaccination process. It is also explained the methodology for parameter identification; concretely, this methodology consists of a multiobjective optimization based on the Weighting Achievement Scalarizing Function Genetic Algorithm (WASF-GA, see [21] for more information). Finally, the reader can find all the time series used for the resolution in `https://github.com/momat-ucm/T-SIR-T`.

In Figure 2, we show some results depending on the choices of the control measures since 26 May 2021; in particular, we present four different scenarios: (red) the control measures are maintained, (yellow) we propose adaptive control measures depending on the 14-day cumulative incidence, (purple) the control measures are slightly relaxed, and (green) the control measures are more relaxed. The obtained results are compared to the actual real evolution of the disease in Italy during Summer 2021 (not included in [8] since that paper is prior to these data).

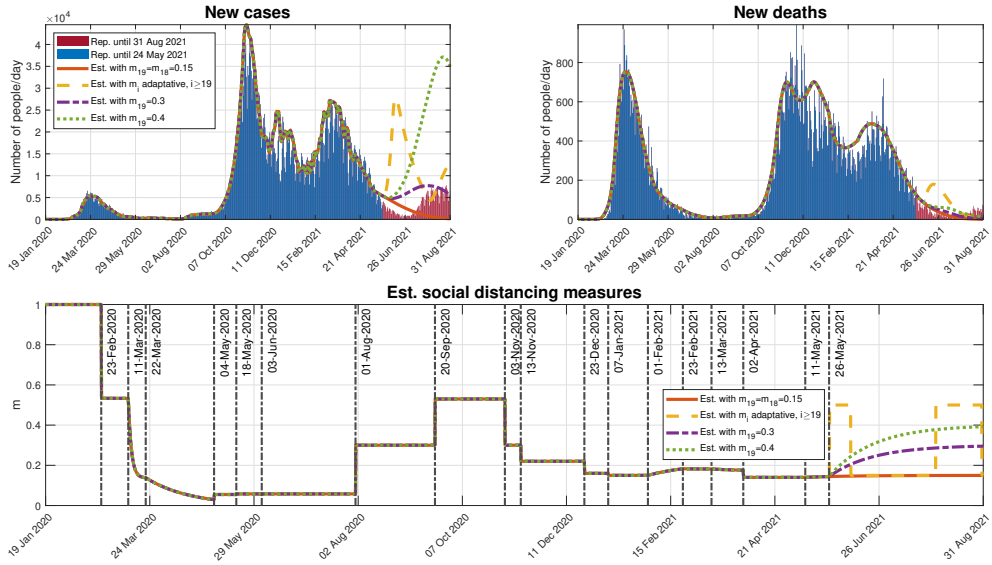


**Figure 2**: Results obtained from the calibration of our model up to 26 May 2021, presenting four different scenarios set in Section 2.3 and comparing them to official reported data from 26 May 2021 to 31 August 2021. **Top-left:** New detected cases per day. **Top-right:** New detected deaths per day. **Bottom:** Function modeling the social distancing measures.

In Figure 3, we focus on the yellow scenario, with adaptive control measures, showing the new detected cases and deaths for each variant, the 14-day cumulative incidence and the evolution of the effective reproduction number. For this last representation, we observed how the global effective reproduction number was lower than 1, proposing the disease was remitting, but the effective reproduction number associated to the second variant was over 1, which indicated that the second variant was starting to prevail, finally leading to a third wave.

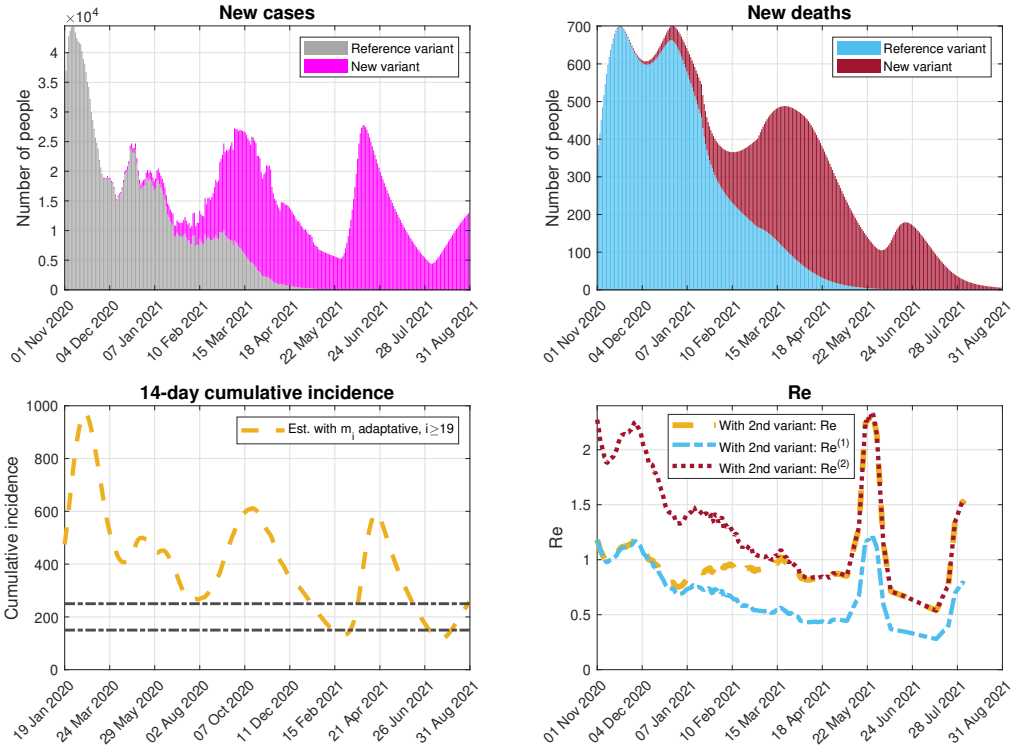


**Figure 3**: Results obtained from the calibration of our model up to 26 May 2021, focusing on the yellow scenario (adaptive control measures). **Top-left:** Daily detected cases caused by each variant. **Top-right:** Daily detected deaths caused by each variant. **Bottom-left:** 14-day cumulative incidence. **Bottom-right:** Effective reproduction numbers.

## 3 CONCLUSIONS

This publication pretended to simulate the impact of new SARS-CoV-2 variants and COVID-19 vaccines, to estimate a qualitative behaviour of the disease as soon as possible due to the emergency of the situation, validating it with the particular case of Italy. Here we summarize some conclusions obtained from this study:

- At that point, the vaccination rates were not enough to avoid a new wave if the control measures were relaxed too fast; concretely, there was a third wave due to the rapid spread of variant Alpha (see Figure 2).
- We observed that obtaining an effective reproduction number $R_e < 1$ is not enough for having the disease under control if a more contagious variant (in this case, variant Alpha) has an associated effective reproduction number greater than 1 (see Figure 3).

In this revision of the model, we compare in Figure 2 the proposed future scenarios to the actual real data reported in Italy from 26 May 2021 to 31 August 2021. We observe how, until the beginning of July, the red scenario fits accurately the new data; however, then both new

cases and deaths increase. Although the purple scenario captures well the behaviour for the new cases, we did not capture in any scenario the possibility of the deaths increasing again. This could be due to the emergence of variant Delta and its spreading through Italy starting around July 2021; this variant indeed was estimated to be more lethal than both the reference and the Alpha variant (see [22]).

## ACKNOWLEDGMENTS

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