Modeling, Analysis and Control of COVID-19 in Italy: Study of Scenarios

Paolo Di Giamberardino[a], Rita Caldarella and Daniela Iacoviello[b]

Dept. Computer, Control and Management Engineering Antonio Ruberti, Sapienza University of Rome,
via Ariosto 25, 00185 Rome, Italy

Keywords: COVID–19, Epidemic Model, Containment Measures Identification, Analysis of Scenarios.

Abstract: Since the beginning of 2020 in few weeks all the world has been interested by the pandemic due to SARS-CoV 2, causing more than 3 millions of dead people and more than 146 millions of infected patients. The virus moves with people and the most effective containment measure appears to be the severe lockdown; on the other hand, for obvious social and economic reasons, it can not be applied for long periods. Moreover, the increasing knwoledge on the virus and on its trasmission modes suggested various strategies, such as the use of masks, social distancing, disinfection and the fast identification of infected patients, up to the recent vaccination campaign. In this paper, the COVID-19 spread is studied referring to the Italian situation; the control actions introduced during 2020-2021 are identified in terms of their actual effects, allowing to study possible intervention scenarios.

1 INTRODUCTION

The COVID-19 emergency has been changing the entire world everyday life, resulting in more than 2.5 millions of dead people and more than 114 millions of infections, (World Health Organization, 2021). The most effective containment measures is the social distancing, applied by means of lockdown, masks wearing, general reduction of mobility and situations of encounter between people. Nevertheless, the lockdown, especially in the hard modality, can not be applied for long periods, both for economic and social reasons; therefore, a combination of different measures aiming at reducing the virus transmission is currently applied by most of the countries. A great effort has been devoted to understand the virus transmission modalities as well as to predict the virus diffusion depending on different control actions. Mathematical modeling of epidemics generally refers to a compartmental framework, in which the population is partitioned into classes, depending on their condition with respect to the infection: the class S of the susceptible subjects, including the healthy part of the population; the compartment E of the exposed individuals, i.e. the subjects in the incubation period; they are infected but not yet infective; the compartment I of the in-

fected patients that can infect the susceptible individuals; the class R of the removed subjects that includes individuals immunized because healed from the virus or vaccinated. This kind of basic model is usually referred as $SEIR$; for the peculiarities of COVID-19 in some cases it has been enriched with other classes; for example, in the $SIDARTHE$ model, (Giordano et al., 2020), the infected patients are discriminated also depending on the severity of their symptoms. In (Tang et al., 2020), a quite rich model is proposed, including groups of pre-asymptomatic infectious, hospitalized, quarantined susceptible, isolated exposed and isolated infected. Moreover, the pandemic characteristics of the disease motivate analysis where geographical displacements are considered, as in (Wu et al., 2020). Other models investigate an important characteristic of COVID-19 related to the greater sensitivity of the older age groups to the virus, (O'Driscoll et al., 2020; Di Giamberardino et al., 2020; Colombo et al., 2020). In (Radulescu et al., 2020) it is assessed the efficiency and effectiveness of the main control measures (closures, mobility restrictions, social distancing), in a sustainability context. This represents one of the main challenge of all the Governments that are trying to preserve the population health and the social/economic aspects of such containment measures. Since December 2020, vaccination campaign has started all over the world giving hope of a re-

[a] https://orcid.org/0000-0002-9113-8608
[b] https://orcid.org/0000-0003-3506-1455

677

turn to normal life. The technical and logistic diffi-
culties of applying massive vaccination campaign to
reach the herd immunity still require a coordination
with the other containment measures. The aim of this
paper is to consider the model of COVID-19 evolu-
tion proposed in ((Di Giamberardino and Iacoviello,
2021)) and (Di Giamberardino et al., 2020), to iden-
tify the main control actions applied during this first
year of pandemic in Italy and to study different sce-
narios. It will be stressed that all the available real
data regarding the number of infected patients are in-
fluenced by the application of the containment mea-
sures; moreover, it is important to identify mathemat-
ically the actions corresponding to the main contain-
ment measures as they are applied by the population.
The paper is organized as follows; in Section 2, the
considered mathematical model is recalled and anal-
ysed preserving the control actions presence and ef-
fects. In Section 3, the peculiarities of the available
data are discussed and the identification procedure is
proposed; numerical results are presented in Section
4, with the analysis of possible scenarios, while con-
clusions are in Section 5.

2 THE MATHEMATICAL MODEL

The mathematical model used in this paper is the one
proposed in (Di Giamberardino and Iacoviello, 2021;
Di Giamberardino et al., 2020), with the introduc-
tion of all the possible (and now) available contain-
ment measures, from the social distancing to the vac-
cination campaign. The classical *SEIR* model is en-
riched with the class Q of subjects isolated because
waiting the results of the swab test, and to split the
class of infected people into the category of undiag-
nosed patients I_u (infected and infectious, unaware
of their condition) and the category of infected di-
agnosed ones I_d (hospitalized or anyway isolated, re-
quiring assistance). The six dimensional system pro-
posed is

$$\dot{S} = B - \beta(1-u_2)SI_u + bnQ + cnu_5Q$$
$$- au_1S - d_SS - vu_6S \quad (1)$$
$$\dot{E} = \beta(1-u_2)SI_u - au_1E - kE - d_EE \quad (2)$$
$$\dot{I}_u = kE - au_1I_u - h_1I_u - h_2I_u - d_{I_u}I_u \quad (3)$$
$$\dot{I}_d = h_1I_u + h_1(1-n)Q + c(1-n)u_5Q$$
$$- (\gamma + \eta u_3)I_d - d_{I_d}(1-u_4)I_d \quad (4)$$
$$\dot{Q} = au_1(S+E+I_u) - bnQ - h_1(1-n)Q$$
$$- cu_5Q - d_QQ \quad (5)$$
$$\dot{R} = h_2I_u + (\gamma + \eta u_3)I_d - d_RR + vu_6S \quad (6)$$

The parameters introduced in (1)–(6) have the follow-
ing meanings, (see also (Di Giamberardino and Ia-

coviello, 2021) for more details). The death rates in
each class, possibly different each other, are denoted
by the d_* terms. B represents the constant rate of new
incoming individuals; parameter β is the contact rate,
including information of various factors, the aggres-
siveness of the virus, the frequency of the contacts be-
tween individuals and their duration. The natural tran-
sition between classes are weighted by the quantities
k, h_1, h_2 and γ. Parameter n is related to the fraction
of subjects that have a negative response from the test
campaign; it can be estimated as $\frac{S(t)}{S(t)+E(t)+I_u(t)}$ and it
is connected with b. The parameter b is the rate of
return from the quarantine to the health susceptible
people; from the Q class, after the results of the test,
negative with probability n or positive for the remain-
ing $1-n$, the transition to the corresponding class oc-
curs at rate c. Also the control actions are considered.
u_1 aims to stimulate, or force, a test campaign on the
population, with an efficacy coefficient a. u_2 models
the isolation indications to reduce possible contagious
sources; this isolation, that does not involve medical
structures, acts on the factor β for the part responsi-
ble of the frequency of individual contacts. The con-
trol u_3 represents the therapy action devoted directly
to counteract the virus by means of antiviral drugs
with coefficient of effectiveness η. u_4 is the therapy
actions aiming at reducing the side–effects of the in-
duced cardio–respiratory diseases; it is introduced as
a direct contribution to reduce the mortality rate and
it is bounded between zero (no therapy) and 1 (all in-
dividuals kept alive during the infection course). u_5
takes into account various kind of constraints influ-
encing the tests policy. u_6 regards the vaccination
strategy, with coefficient v denoting its efficiency.

2.1 Model Analysis

Since the very beginning of the epidemic alarm, in-
creasing containments measures have been applied
by all the governments; therefore, the available real
data concerning the epidemic spread are affected by
time–varying control actions aiming at reducing its
effects. This consideration suggested to include all
the controls u_i, $i = 1, ..., 6$, in the model analysis,
thus determining how the equilibrium points are influ-
enced by the interventions, both in their number and
in their stability properties. The following notations
are adopted, for sake of simplicity in the formulation,
with obvious meaning of the symbols

- $\bar{\beta}(t) = \beta(1-u_2(t))$
- $\bar{\gamma}(t) = \gamma + \eta u_3(t)$
- $\bar{d}_{I_d}(t) = d_{I_d}(1-u_4(t))$
- $m_1(t) = au_1(t) + d_S + vu_6(t) = \bar{a}(t) + d_S + \bar{v}(t) > 0$

- $m_2(t) = au_1(t) + k + d_E = \bar{a}(t) + k + d_E > 0$
- $m_3(t) = au_1(t) + h_1 + h_2 + d_{I_u}$
  $= \bar{a}(t) + h_1 + h_2 + d_{I_u} > 0$
- $m_4(t) = bn + cu_5(t)n = bn + \bar{c}(t)n > 0$
- $m_5(t) = bn + h_1(1-n) + cu_5(t) + d_Q$
  $= bn + h_1(1-n) + \bar{c}(t) + d_Q > 0$
- $m_6(t) = d_S + vu_6(t) = d_S + \bar{v}(t) > 0$

To determine the equilibrium points, assuming constant control actions, the second members of the equations (1)-(6) are put equal to zero, thus determining the disease-free one (*DFE*), always present, given by:

$$P_1^e = \begin{pmatrix} S_1^e & E_1^e & I_{u1}^e & I_{d1}^e & Q_1^e & R_1^e \end{pmatrix}^T$$

with $E_1^e = I_{u1} = I_{d1} = 0$ and

$$S_1^e = \frac{Bm_5}{d_Q m_1 + m_4 m_6} \tag{7}$$

$$Q_1^e = \frac{B\bar{a}}{d_Q m_1 + m_4 m_6} \tag{8}$$

$$R_1^e = \frac{B\bar{v}m_5}{d_R(d_Q m_1 + m_4 m_6)} \tag{9}$$

Note that in the disease free case the probability n of having negative COVID-19 test (and so to be healthy) is equal to 1. A second equilibrium point, the endemic one, may exist, depending on model parameters and control actions:

$$P_2^e = \begin{pmatrix} S_2^e & E_2^e & I_{u2}^e & I_{d2}^e & Q_2^e & R_2^e \end{pmatrix}^T \tag{10}$$

with

$$S_2^e = \frac{m_2 m_3}{k\bar{\beta}} \qquad E_2^e = \frac{m_3}{k} I_{u2}^e$$

$$Q_2^e = \frac{\bar{a}m_2 m_3}{k\beta m_5} + \frac{\bar{a}}{m_5}\left(\frac{m_3}{k} + 1\right) I_{u2}^e$$

$$I_{d2}^e = \frac{1}{\bar{\gamma} + \bar{d}_{I_d}}\left(h_1 I_{u2}^e + (1-n)(h_1 + \bar{c})Q_2^e\right)$$

All these quantities, with the exception of S_2^e, depend on I_{u2}^e, and are well defined once I_{u2}^e is. Its expression is given by:

$$I_{u2}^e = \frac{\bar{a}m_2 m_3 m_4 + k\bar{\beta}m_5 B - m_1 m_2 m_3 m_5}{\bar{\beta}(\bar{\beta}m_2 m_3 m_5 k - \bar{a}m_3 m_4 - \bar{a}km_4)} \tag{11}$$

This solution can be accepted only if positive; by substituting the definitions of m_i, $i = 1,...,5$ it can be easily shown that the denominator is always positive,

whereas the sign of the numerator depends on the condition:

$$\frac{\bar{\beta}kBm_5}{m_2 m_3(m_4 m_6 + d_Q m_1)} - 1 > 0 \tag{12}$$

The existence condition of the endemic equilibrium point P_2^e is related to the concept of the *reproduction number*, that is the number of secondary cases produced by one infected subject in a completely susceptible population during its infectious period. This indicator, important to have information on the epidemic evolution, can be estimated starting from the real data; a different model based approach implies the evaluation of the next generation matrix in the disease free equilibrium, (7), that includes the functions related to vaccination, when possible, and the test campaign. The computation starts considering in the dynamics (1)–(6) the classes directly involved in the spread of the infection, i.e. E, I_u, I_d and Q, and therefore only the equations (2)–(5). By using the notations with the m_i, $i = 1,\ldots,6$, quantities, the reduced system (2)–(5) may be written enhancing the contributions due the infection, $\mathcal{F}$, and the ones due to changing the health condition, $\mathcal{V}$:

$$\begin{pmatrix} \dot{E} & \dot{I}_u & \dot{I}_d & \dot{Q} \end{pmatrix}^T = \mathcal{F} - \mathcal{V} \tag{13}$$

where

$$\mathcal{F} = \begin{pmatrix} \beta SI_u \\ 0 \\ 0 \\ 0 \end{pmatrix} \tag{14}$$

$$\mathcal{V} = \begin{pmatrix} m_2 E \\ -kE + m_3 I_u \\ -h_1 I_u - [(h_1 + \bar{c})(1-n)Q - (\bar{\gamma} + d_{I_d})I_d] \\ -\bar{a}(S + E + I_u) + m_5 Q \end{pmatrix} \tag{15}$$

The variations of $\mathcal{F}$ and $\mathcal{V}$ with respect to the variables E, I_u, I_d and Q yield the matrices F and V respectively:

$$F = \left.\frac{\partial \mathcal{F}}{\partial(E, I_u, I_d, Q)}\right|_{P_e^1} \quad V = \left.\frac{\partial \mathcal{V}}{\partial(E, I_u, I_d, Q)}\right|_{P_e^1} \tag{16}$$

Under these positions, the reproduction number $\mathcal{R}$ is given by the dominant eigenvalue of the matrix FV^{-1}, in the present case its $\{1,1\}$ element; the computation easily yields:

$$\mathcal{R} = \frac{\bar{\beta}kS_1^e}{m_2 m_3} \tag{17}$$

Note that $\mathcal{R}$ is the same quantity as in (12), related to the existence of the endemic equilibrium P_2^e depending on its value with respect to the threshold 1. From (17) it is evident that the introduction of the vaccination, present in the terms $m_1(t)$ and $m_6(t)$, reduces

the reproduction number; this is in agreement with the first data of the vaccination campaign in the United Kingdom. By studying the Jacobian matrix of the system (1)–(6), it is possible to establish a stability condition and to link it with the reproduction number $\mathcal{R}$. In particular, for the disease free equilibrium P_1^e two negative eigenvalues, $-d_R$ and $-(\bar{\gamma} + \bar{d}_{I_d})$, are easily identifiable; for the reduced Jacobian matrix:

$$\tilde{J} = \begin{pmatrix} -m_1 & 0 & -\bar{\beta}S_1^e & m_4 \\ 0 & -m_2 & \bar{\beta}S_1^e & 0 \\ 0 & k & -m_3 & 0 \\ \bar{v} & 0 & h_1 & 0 \end{pmatrix} \quad (18)$$

the characteristic equation evaluated in P_1^e yields four roots obtained from the following polynomial:

$$P(\lambda) = \lambda^4 + N_3\lambda^3 + N_2\lambda^2 + N_1\lambda + N_0 \quad (19)$$

where $N_3 = m_1 + m_2 + m_3 + m_5$ and the other coefficients depend on $\mathcal{R}$:

$$\begin{aligned} N_2 &= m_2m_3(1-\mathcal{R}) + (m_2+m_3)(m_1+m_5) \\ &+ m_1m_5 - \bar{a}m_4 \end{aligned} \quad (20)$$

$$\begin{aligned} N_1 &= m_2m_3(1-\mathcal{R})(m_1+m_5) \\ &+ (m_2+m_3)(m_1m_5 - \bar{a}m_4) \end{aligned} \quad (21)$$

$$N_0 = m_2m_3(1-\mathcal{R})(m_1m_5 - \bar{a}m_4) \quad (22)$$

By substituting the expressions of the quantities m_i, $i = 1,...,5$, it results the positiveness of $m_2 \cdot m_3$ and of $m_1 \cdot m_5 - \bar{a}m_4$. Therefore, by using Routh's arguments, the negativeness of the real parts of the roots of $P(\lambda)$ depends on the positiveness of the quantity $1 - \mathcal{R}$. It is possible to conclude that in this case only the disease free equilibrium P_1^e exists and it is stable. Also in the proposed approach, that includes the control actions as structural part of the modeling, it can be deduced that if the reproduction number is smaller than 1 there exists a unique equilibrium point, the disease free equilibrium one, and it is stable; otherwise, for $\mathcal{R} > 1$, the equilibrium points are two and the disease free one is not stable any more. It is useful to stress that, for the assumed choice of including the control actions in the analysis, both P_1^e and P_2^e are influenced by the containment measures. The disease free equilibrium one, P_1^e, could be interpreted as follows; when a population is in that condition by means of the control actions introduced and for the model parameters, if the quantity $\mathcal{R}$ is smaller than one then the population will remain near the P_1^e equilibrium point, without allowing the spread of the epidemic. Referring to COVID-19 (and therefore assuming fixed model parameters) and to the expression (17) of $\mathcal{R}$, a suitable application of social distancing (thus acting on $\bar{\beta}$), of swab tests and quarantine (thus acting on $\bar{a}$ and $\bar{c}$), medication (acting on $\bar{\gamma}$) and vaccination (control $\bar{v}$) would lead the population to the disease free equilibrium point.

3 CONTROL ACTIONS IDENTIFICATION

Since the very beginning of the pandemic, it appeared fundamental the collection of real consistent data, to be able to understand what was happening in a situation for which the entire world was unprepared. In this paper the real data regarding the Italian situation are considered; they have been downloaded from the Civil Protection website (Protezione Civile,): in particular, it is considered the number of positive patients I_{real}, corresponding to the I_d ones of this model, the number of subjects officially recovered R_{real} and the ones dead for the virus direct and indirect effects D_{real}. Due to the presence of asymptomatic subjects, the last two groups of data correspond to the output of the I_d compartments weighted by the recovery ($\bar{\gamma}$) and death ($\bar{d}_{I_d}$) coefficients respectively. One of the difficulties in using COVID-19 real data regards the consistency in their collections, especially in the first period of the epidemic spread; moreover, due to the increased awareness of the importance of some information (for example, the number of swab tests, or of hospitalized patients) it has been decided, only with some delay, to collect new kind of data, that, therefore, are not available since the very beginning of the epidemic emergency. Among the European Nations the modalities of how deaths are counted are different (depending on the dominant cause of death) or data are grouped in different ways. Moreover, some fluctuations in the number of swab tests processed during the week–ends alter the trend of the number of subjects positive to COVID-19, thus suggesting to use, as a possible indicator of the course of the pandemic, the normalized number with respect to the total number of tests. Some of the parameters introduced in the proposed model (1)–(6) can be assumed known from the medical literature, as the incubation time or the recovery rate; they will be discussed in the next section. As far as the identification of the control actions included in the model, note that the contribution of control u_6 exists only starting from January 2021. The actions, u_i $i = 1,...,6$, are included in the variables defined in Subsection 2.1, $\bar{a}(t)$, $\bar{\beta}(t)$, $\bar{\gamma}(t)$, $\bar{d}_{I_d}(t)$, $\bar{c}(t)$, $\bar{v}(t)$, respectively. Moreover, in order to improve the quality of the identification and simplify the numerical implementation, it can be stressed the relation among the two control actions u_3 and u_4, and therefore among the variables $\bar{\gamma}(t)$ and $\bar{d}_{I_d}(t)$. In the equation (4) the two contributions related to healing and to death are assumed separated since they correspond to different therapy actions. Nevertheless, their effects are strictly related, since a patients can leave the I_d compartment only healing or dying; moreover,

the two controls u_3 and u_4 generally refer to the medication aspect ascribable to the same kind of resources. Therefore a unique control parameter can be identified yielding both the actions; more precisely, it is assumed a relation between u_3 and u_4:

$$\bar{\gamma}(t) = \gamma + \eta u_3(t) = h_3 u_4(t) \tag{23}$$

where parameter h_3 is related to the rate of healing for infected patients. The following cost index is proposed, aiming at fitting the available real data:

$$J(\bar{a}, \bar{\beta}, \bar{\gamma}, \bar{c}, \bar{v}) = \int_{t_0}^{t_f} [w_1(I_{real}^N(t) - I_{model}^N(t))^2$$

$$+ w_2(I_{real}(t) - I_d(t))^2 + w_3(R_{real}(t) - R_{I_d}(t))^2$$

$$+ w_4(D_{real}(t) - D(t))^2 + w_5(V_{real}(t) - V(t))^2]dt \tag{24}$$

where $I_{model}^N(t)$ is the number of new diagnosed infections obtained by adding the variation of the number of infected patients, of the recovered and the dead individuals between two consecutive days; $I_{real}^N(t)$ is the same quantity calculated on real data; $R_{I_d}(t)$ are the subjects recovered from the I_d compartment $R_{I_d}(t) = (\gamma + \eta u_3(t))I_d(t)$ and $R_{real}(t)$ the official real value of healed subjects; $D(t)$ is the number of dead patients obtained from the model $D(t) = d_{I_d}(1 - u_4(t))I_d(t)$ and $D_{real}(t)$ the official corresponding quantity; V_{real} is the number of subjects vaccinated with the two doses corresponding to the quantity $\bar{v}S$ of the model. The parameters w_i, $i = 1,..,5$ are the weights indicating the relevance of each term in the optimization procedure. The period considered covers all the pandemic year, from the March 2020 to the end of February 2021, in which different and complementary containment measures have been adopted by the Italian Government. The main adopted containment measures may be summarized as follows:

- from February 23 to March 8, 2020: introduction in the north of Italy of increasing containment measures;

- from March 9 to May 3, 2020: severe lockdown in the entire nation, with the suspension of all *non–essential* activities; this period is called "Phase 1";

- from May 3 to June 10, 2020: almost all the activities started again; this period is the "Phase 2";

- from June 11 to October 12, 2020: it is the period with less restrictions; it is the "Phase 3";

- from October 13 to November 2, 2020: introduction of increasing containment measures with mandatory use of mask;

- from November 3 to December 21, 2020: it was introduced the curfew from 10 pm to 5 am; moreover it was adopted a classification mechanism of each region in three classes indicated by colours,

yellow, orange, red, with increasing level of restrictions depending on the diffusion of the virus and of the sanitary situation at territorial level. This phase could be recalled as the "Phase of colours";

- from December 22, 2020 to January 6, 2021: the strategy based on the colours was reinforced; all Italy was in the orange level but it became red in the holidays;

- from January 7 to February 28, 2021: the strategy with colours of the period November 3 - December 21 2020 was adopted with reinforced containment rules.

4 NUMERICAL RESULTS

The data considered in this paper regards the period February 2020 (the very beginning of data collection) up to April 2021; the real data used are taken from the Civil Protection website ((Protezione Civile,)). First, the model is identified by minimizing the cost function (24) and determining the functions $\bar{a}$, $\bar{\beta}$, $\bar{\gamma}$ and $\bar{c}$ related to the controls, u_1, u_2, u_3, u_5 and u_6, considering the simplification in (23). Therefore, it is possible to establish a correlation between the official containment measures applied, and the identified functions. In fact, generally it is not easy to "convert" the complexity of any Government actions, thought as the combination of different containment measures, into a function, also considering the different reactions of the population. Finally, some interesting scenarios are studied. In (1)–(6), some of the parameters can be considered known, since related to the population characteristics, and obtained from the ISTAT website (Istituto Nazionale di Statistica,): $B = 1.69 \cdot 10^3$; $d_S = d_R = 2.81 \cdot 10^{-5}$. Other parameters are assumed known only as mean values, considering their medical meaning and the estimation given by the physicians, (Di Giamberardino and Iacoviello, 2021): $k = \frac{1}{4}$; $d_E = d_Q = d_{I_u} = d_S$; $d_{I_d} = \frac{1}{12}$; $b = \frac{1}{14}$; $h_1 = \frac{1}{5}$; $h_2 = \frac{1}{21}$; $h_3 = \frac{1}{40}$. As far as the choice of the weights in the cost index, with a *trial and error* procedure the following values are taken up to December 2020 (when the vaccination was not available): $w_1 = 0.4$, $w_2 = w_3 = w_4 = 0.2$, $w_5 = 0$; while, after January 2021 the choices $w_1 = 0.4$, $w_2 = 0.2$, $w_3 = w_4 = 0.15$, $w_5 = 0.1$ are adopted. The minimization of the cost index (24), $\min_{(\bar{a}, \bar{\beta}, \bar{\gamma}, \bar{c})} J(\bar{a}, \bar{\beta}, \bar{\gamma}, \bar{c})$, with respect to the functions $(\bar{a}, \bar{\beta}, \bar{\gamma}, \bar{c})$, is implemented by using the Matlab® function *fmincon*, thus obtaining the fitting of the real data considered, see Figs.1–3. In all the figures, the dotted lines indicate the starting
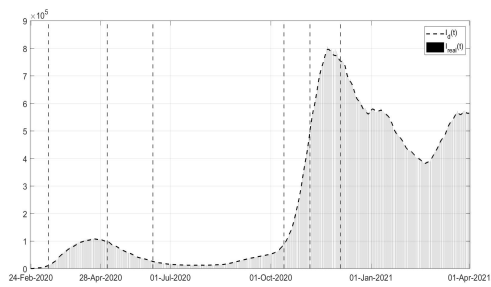
Figure 1: Infected patients $I_d(t)$ estimated from the model versus the corresponding real data.
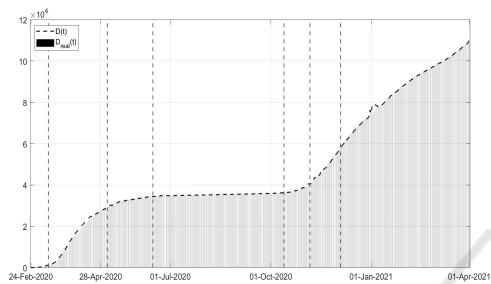

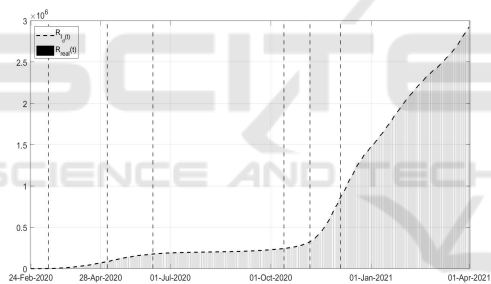Figure 2: Dead patients $D(t)$ estimated from the model versus the corresponding real data.

Figure 3: Recovered subjects $R_{I_d}(t)$ estimated from the model versus the corresponding real data.

Figure 4: Reconstructed evolution of $\bar{a}$ related to the control action $u_1(t)$.

Figure 5: Reconstructed evolution of $\bar{\beta}(t) = \beta(1 - u_2(t))$.

Figure 6: Reconstructed evolution of $\bar{\gamma}(t)$ corresponding the control action $u_3(t)$ and $u_4(t)$ according to the simplification in (23).

Figure 7: Reconstructed evolution of $\bar{c}$ corresponding to the control action $u_5(t)$.

days of the main containment measures listed in the previous Section.

It can be noted the general good fitting to the corresponding real data of the variables $I_d(t)$, $D(t)$ and $R_{I_d}(t)$, also in the sudden variations of the total number of infected patients, in the periods April-May and November-December 2020. The minimization of the cost index (24) yields the evolution of the functions $\bar{a}$, $\bar{\beta}$, $\bar{\gamma}$ and $\bar{c}$, filtered on a window of 14 days, Figs. 4 - 7.

Besides some fluctuations, due to variability of real data, it can be noted the general increasing trend of the strongly related functions $\bar{a}$ and $\bar{c}$, corresponding to the test campaign and the efficiency of the test policy, in particular from July 2020 to January 2021, Figs. 4 and 7. The therapy capability, both at reducing the side-effects of COVID-19, as well as to counteract
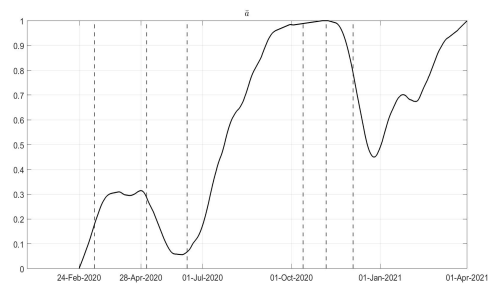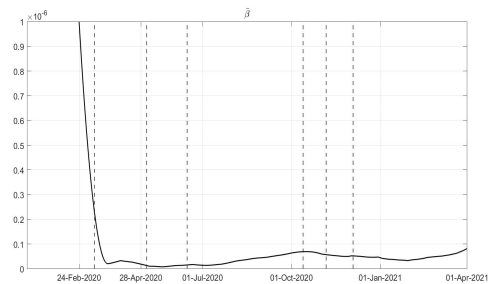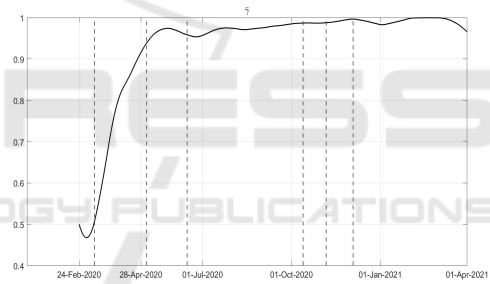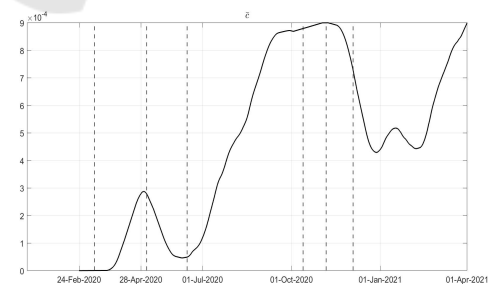
the virus, is shown in Fig.6 by means of the function $\bar{\gamma}$; note, as reasonable and desirable, the increased capability in contrasting the infection.

The identification of $\bar{\beta}(t)$ is particularly interesting, Fig. 5; the decrement of the identified function
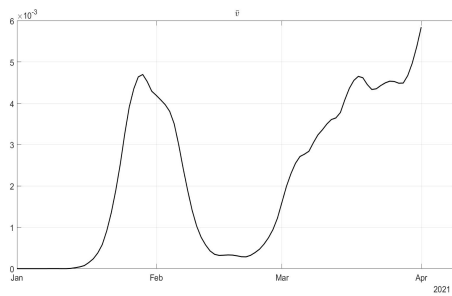
Figure 8: Reconstructed evolution of $\bar{v}$ corresponding to the control action $u_6(t)$.

$\bar{\beta}(t)$ corresponds to an increment of the control $u_2(t)$. It models the limitations of the possible contacts between susceptible subjects and infected patients. Note that, while up to June (i.e. during the severe lockdown and the start of Phase 3) the function $\bar{\beta}(t)$ had low values (and so the control was very effective), in the summertime the restrictions became less severe, with an increase of $\bar{\beta}(t)$ that reached its maximum in October 2020. The negative effects of the corresponding low values of control $u_2(t)$ were observed at the end of November with the peak of the second epidemic wave, see Fig. 1. Also the first three months of the vaccination campaign are considered, Fig. 8; it can be noted, after the middle of February 2021, the monotonic increase in the vaccination action. It is worth to be stressed that the identified controls correspond to the actions as they were really applied by the population. One of the difficulty in facing this pandemic is to balance the need of stopping the infection and the social/economic problems involved in the reduction of activities. Therefore, the choice of ad hoc containment measures, effective but not too restrictive, represents one of the challenge of any Government. Another difficulty relies in the fact, stressed in this paper, that the available data are influenced, since the very beginning of the pandemic, by the containment measures applied.The availability of a model that fits the controlled data and identify the main containment measures, as they were applied by the population, allows to partially overcome this problem and study some scenarios. In particular, assuming the same functions $\bar{a}$, $\bar{c}$ and $\bar{\gamma}$ as at the end of February 2021, the following cases are studied: Scenario 1: introduction, at the beginning of March 2021, of a severe lockdown, as in the period March 2020- April 2020; Scenario 2: introduction, at the beginning of March 2021, of mild measures, as in the period July 2020- October 2020; Scenario 3: study the effects of the application of severe lockdown starting in October 2020. The results obtained in the three cases are all intuitive from a qualitative point of view; here also

a quantification is possible, providing a support in the containments measures decision process. In the first two scenarios, regarding the spring 2021, also a first small percentage of vaccination effect is included. In both cases, it is assumed an immunization after an average period of 60 days (it depends on the kind of vaccine) and a percentage of population immunized by vaccination of about 0.05% (it depends on the rate of administration of the vaccine, on the availability of doses and on the logistic capability for a mass vaccination campaign). By considering Fig. 9, in which two opposite strategies are adopted starting in March 2021, it can be seen that with a severe lockdown the total number of infected patients rapidly decreases in less than one month, reaching almost the same value of October 2020. By applying mild containment measures as in summer 2020, a rapid increase is shown; the bar plot shows the real trend of infected patients depending, of course on the containment measures adopted, as a balance between the two extreme possible choices. These results confirm the importance of applying containment measures, despite the vaccination campaign, until the herd immunity is achieved. In Fig. 10 it is proposed an ex-post analysis of what could have happened if in November 2020 a severe lockdown was applied. The attention is focused to that period since, as seen in Fig.1, it represents the onset of the second wave, consequence of different issues: the summertime mild restrictions with travels, the weather conditions, the re-opening of many activities that implied a reduction of the social distancing. In Fig. 10 it can be seen that the peak of infections could have been significantly lower with a value of infected patients at the end of January reduced of about 60%. Obviously, the lockdown lowers the curve; nevertheless the modeling approach allows to establish for how long it is advisable to extend specific control actions. In this paper, the containment measures are identified as applied by the population; nevertheless, among the possible future developments, optimal scheduling could be proposed, as well as resources allocation, taking into account the limitations under material and logistic points of view. Moreover, the effects of the vaccination campaign will be included, as well as its relations with the other containment measures; other scenarios regarding past and future possible choices for the control actions will be investigated: in the globalized world pandemic is not an exception and the severe lockdown could not be the unique solution but should be integrated with strategies able to consider contemporary different requirements, in a complex framework.
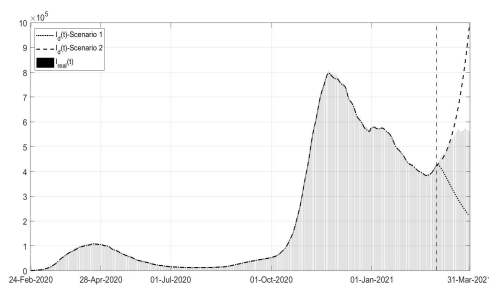
Figure 9: Scenario 1 and 2: Comparison of the possible evolution of the number of diagnosed infected patients $I_d(t)$ with respect to different strategies and real data.
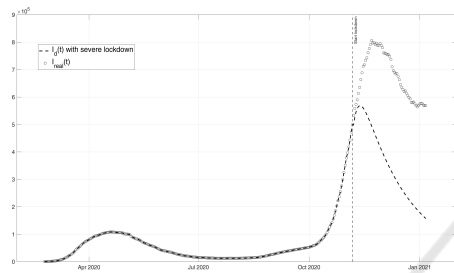

Figure 10: Scenario 3: Comparison of the real evolution of the number of diagnosed infected patients $I_d(t)$ with the one obtained in the hypothetical scenario 3.

5 CONCLUSIONS

The diffusion of the COVID-19 is modeled in this paper introducing an enriched *SEIR* model. The proposed representation is analysed with respect to the existence of the equilibrium points, their stability and the reproduction number, including also the containment measures applied since the very beginning of the pandemic. Italian data are used to fit the model and to identify the containment measures as they were actually applied by the population. This allows to predict the virus diffusion, depending on the controls applied, and also to study what would have occurred with a different strategy in a specific period of this pandemic year. These results, while being predictable from a qualitatively point of view, appear interesting in order to analyse whether a severe lockdown could be the unique solution to stop the virus diffusion or if different control scheme could be effective as well. Until the ongoing application of an intensive vaccination campaign will start to produce sensible effects, the combination of different containment measures seems to be fundamental in reducing the virus diffusion, although the severe lockdown has appeared to be the most effective one, but realistically possible only if adopted for limited time periods.

REFERENCES

Colombo, R., M.Garavello, F.Marcellini, and E.Rossi (2020). An age and space structured sir model describing the COVID-19 pandemic. *Journal of Mathematics in Industry*, 10:1–20.

Di Giamberardino, P. and Iacoviello, D. (2021). Evaluation of the effect of different policies in the containment of epidemic spreads for the COVID-19 case. *Biomedical signal processing and control*, 65(102325):1–15.

Di Giamberardino, P., Iacoviello, D., Albano, F., and Frasca, F. (2020). Age based modelling of SARS-CoV-2 contagion: The Italian case. *24th Int. Conference on System Theory, Control and Computing*.

Di Giamberardino, P., Iacoviello, D., Papa, F., and Sinisgalli, C. (2020). Dynamical evolution of covid-19 in italy with an evaluation of the size of the asymptomatic infective population. *IEEE Journal of Biomedical and Health Informatics*, pages 1–1.

Giordano, G., Blanchini, F., Bruno, R., Colaneri, P., Filippo, A. D., and Colaneri, M. (2020). Modeling the COVID-19 epidemic an implementation of population wide interventions in Italy. *Nature Medicine*, 26.

Istituto Nazionale di Statistica. *https://www.istat.it/en/*.

O'Driscoll, M., Santos, G. R. D., Wang, L., D. A. T. Cummings, A. S. A., Paireau, J., Fontanet, A., Cauchmez, S., and Salje, H. (2020). Age-specific mortality and immunity patterns of SARS-CoV-2. *Nature*, 590:140–145.

Protezione Civile. *http://www.protezionecivile. gov.it/*.

Radulescu, A., Williams, C., and Cavanagh, K. (2020). Management strategies in a SEIR-type model of COVID-19 community spread. *Nature. Scientific Reports*, 21256.

Tang, B., Bragazzi, N. L., Li, Q., Tang, S., Xiao, Y., and Wu, J. (2020). An updated estimation of the risk of transmission of the novel coronavirus (2019-nCov). *Infectious diease modeling*, 5.

World Health Organization (2021). *https://www.who.int/*.

Wu, J., K.Leung, and G.M.Leung (2020). Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *Lancet*, pages 1–9.