

Age Based Modelling of SARS-CoV-2 Contagion: the Italian case

Paolo Di Giamberardino
Sapienza University of Rome
Rome, Italy
paolo.digiamberardino@uniroma1.it

Fabio Albano
Sapienza University of Rome
Rome, Italy
albano.1773435@studenti.uniroma1.it

Daniela Iacoviello
Sapienza University of Rome
Rome, Italy
daniela.iacoviello@uniroma1.it

Federico Frasca
Sapienza University of Rome
Rome, Italy
frasca.1741836@studenti.uniroma1.it

Abstract—The paper deals with the modelling of the COVID-19 spread among people with different age. The model introduced is a simplified version of a full age based one where the division into age based groups of the population is performed only for distinguishing the initial contagion step. An identification procedure is performed on the basis of the data acquired for the Italian case showing that the model can describe and explain the actual differences between the different aged individuals with respect to the possibility to acquire the virus.

I. INTRODUCTION

Mathematical models are a powerful tool to analyse physical phenomena, to explain their behaviour and to be able to foresee future evolutions. An epidemic disease is one of such phenomena and several mathematical models have been proposed in literature. The specificity of some epidemics brings to the definition of particular models; one recent example is the case of HIV/AIDS [1], [2].

The same holds for the COVID-19, with several works in literature dealing with the definition or the use of a mathematical model to describe the ongoing infection spread, to imagine future scenarios and to validate possible actions to its containment, through the adaptation of classical models [3] or the design of new ones [4]–[8].

The present work focuses on the possibility to define a mathematical model able to describe the different behaviour of the infection propagation according to the age of the patients. In fact, it is evident, from the available information about the COVID-19 social effects, that older persons have a higher probability to get the virus, with dangerous consequences, while a relative low number of very young individuals is reported among the infected cases.

This description ability is here developed with the additional aim to maintain the mathematical model as simple as possible, which means a low number of parameters in its equations, to facilitate the identification processes.

The solution adopted follows the approach proposed in [9] for the tuberculosis, with the separation into age based classes

only for the people which can get the infection, regrouping all the age ranges together for describing the illness evolution.

Making use of such a model, the Italian case is considered for its numerical definition and characterization; the results show the effectiveness of such a choice since it is able to capture known behaviours and to give a numerical evaluation of the relationship between contagiousness of the SARS-CoV-2 and age of the patient.

The paper firstly introduces the mathematical model in II; an analysis, in terms of equilibrium and stability and their relationships with the basic reproduction number, is provided in Section III; the specific Italian case is addressed in Section IV with the discussion of the results. Some concluding remarks in Section V ends the paper.

II. THE MATHEMATICAL MODEL

In this section, a mathematical model for the COVID-19, which takes into account the classification of susceptible individuals according to the age, is adopted. The main goal is to describe the different effects, in terms of number of infected individuals, as evidenced by the statistic information on the number of diagnosed patients. This means that it is important, in the model adopted, to be able to distinguish the ability to get the infection according to the different individual age. The entire population is firstly classified into five main classes, according to their status with respect to the individual disease evolution: susceptible (S), latent (E), infectious (I), isolated (Q) and removed (R) persons. This classification includes classes usually present in virus spread dynamics; the susceptible individuals S are the ones that can be infected, latent individuals E are people infected by COVID-19, in the incubation period, not yet infective and with no evident symptoms, infected patients I are those which can transmit the virus to susceptible people, quarantined persons Q are the infected ones subject to social isolation, and removed individuals R are people who have been recovered from the disease.

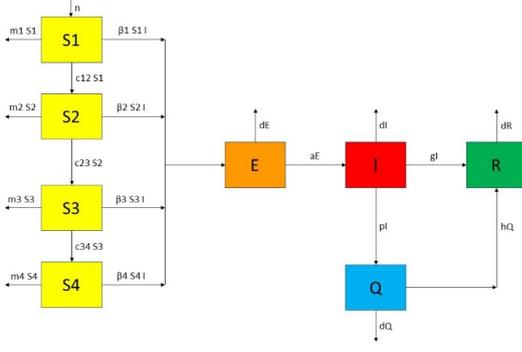


Fig. 1. Scheme of the epidemic evolution

A general model which introduces the dynamical characteristics of the different age ranges should consider, for each of the previous classes, a partition according to the population age; this means that the entire susceptible class S should be divided into n subclasses S_i , $i = 1, \dots, n$, class E into E_i , and so on. If the infection propagation is supposed to be given by contacts between susceptible and infected individuals, in the model would appear $n \times n$ transmission terms of the form $\beta_{i,j} S_i I_j$, $i, j = 1, \dots, n$, with $\beta_{i,j}$ the transmission factor between S_i and I_j groups. Along with the difficulty to handle a high dimensional model, the large number of parameters involved makes the identification procedures very difficult and with the necessity of a large amount of analytical data to be acquired.

Since the present work focuses on the characteristics of the infection propagation among people with different ages, a simplification is performed, introducing a model which maintains the differences among age ranges only for the part strictly devoted to the virus transmission.

This point of view is motivated by the fact that this model is intended to be used to study and identify the different rates at which the virus seems to have infected people with different ages. Since the interest is mainly in the analysis of the differences of the contagion only, after the infection the distinction among ages is not considered, so having only single compartments for the latent, the infectious, the isolated and the removed individuals, no matter how they are old.

The model obtained has a form already proposed in literature [9]; the age based classification is maintained for the susceptible individuals, to separate the effects of the virus transmission on each class, while all the remaining classes, E , I , Q and R , do not present the same classification. Then, the susceptible individuals are divided into four classes S_i according to their age: S_1 refers to young individuals which are less than 18, S_2 from 19 to 50, S_3 from 51 to 70 and S_4 older than 71. The choice of the ages for the classification follows the same choice adopted by the Italian Statistic Agency (ISTAT) for aggregated data about the virus evolution, which will be used for the numerical characterization of the model parameters.

A scheme of the classes and the interaction considered in the

mathematical model is reported in Figure 1 and it is described by the nonlinear continuous time dynamics

$$\begin{aligned}
 \dot{S}_1 &= N - \beta_1 S_1 I - c_{1,2} S_1 - m_1 S_1 \\
 \dot{S}_2 &= -\beta_2 S_2 I + c_{1,2} S_1 - c_{2,3} S_2 - m_2 S_2 \\
 \dot{S}_3 &= -\beta_3 S_3 I + c_{2,3} S_2 - c_{3,4} S_3 - m_3 S_3 \\
 \dot{S}_4 &= -\beta_4 S_4 I + c_{3,4} S_3 - m_4 S_4 \\
 \dot{E} &= \beta_1 S_1 I + \beta_2 S_2 I + \beta_3 S_3 I + \beta_4 S_4 I - aE - dE \\
 \dot{I} &= aE - pI - gI - d_I I \\
 \dot{Q} &= pI - hQ - dQ \\
 \dot{R} &= gI + hQ - dR
 \end{aligned} \tag{1}$$

where all parameters are positive. N is the average daily birth rate of the population; $c_{1,2}$, $c_{2,3}$ and $c_{3,4}$ are the growth rates from S_1 to S_2 , from S_2 to S_3 and from S_3 to S_4 respectively; β_1 , β_2 , β_3 and β_4 are the transmission rates for each class; m_1 , m_2 , m_3 and m_4 are the death rates of the four susceptible groups respectively; d is the average daily natural death rate in Italy; d_I is the specific death rate for the infected individuals, including the mortality rate of the disease; a is the activation rate of the latent COVID-19 patients; h is the quarantine rate; p is the prevention rate and g is the recovery rate. Part of the parameters values, the ones not directly involved in the epidemic propagation, are obtained from standard statistics on the population; the remaining ones will be computed on the basis of the data on the infected population. If no separation would be performed on the susceptible individuals, introducing $S = S_1 + S_2 + S_3 + S_4$ only, its dynamics is described by the equation

$$\dot{S} = \dot{S}_1 + \dot{S}_2 + \dot{S}_3 + \dot{S}_4 = N - \tilde{\beta} S I - \tilde{m} S \tag{2}$$

where the weighted average transmission rate

$$\tilde{\beta} = \frac{\beta_1 S_1 + \beta_2 S_2 + \beta_3 S_3 + \beta_4 S_4}{S} \tag{3}$$

as well as the average weighted death rate

$$\tilde{m} = \frac{m_1 S_1 + m_2 S_2 + m_3 S_3 + m_4 S_4}{S} \tag{4}$$

are defined. They are time variant even if each m_i and β_i are assumed constant, differently from a classical approach, showing an actual improvement of the proposed model in the epidemic spread description. Expressions (3) and (4) can be useful also when dealing with the model (1) for sake of compactness.

III. MODEL ANALYSIS

Equilibrium and stability conditions, along with their relationships with the basic reproduction number R_0 are here shortly given.

A. Equilibrium conditions

The characteristics of the equilibrium points as well as of their stability are expected to follow the classical structure, with one epidemic free condition, with no infected individuals at steady state, used for the computation of the basic reproduction number R_0 , and one endemic condition.

Equilibrium points are computed solving the nonlinear system

$$\begin{aligned}
N - \beta_1 S_1^e I^e - c_{1,2} S_1^e - m_1 S_1^e &= 0 \\
-\beta_2 S_2^e I^e + c_{1,2} S_1^e - c_{2,3} S_2^e - m_2 S_2^e &= 0 \\
-\beta_3 S_3^e I^e + c_{2,3} S_2^e - c_{3,4} S_3^e - m_3 S_3^e &= 0 \\
-\beta_4 S_4^e I^e + c_{3,4} S_3^e - m_4 S_4^e &= 0 \\
\beta_1 S_1^e I^e + \beta_2 S_2^e I^e + \beta_3 S_3^e I^e + \beta_4 S_4^e I^e - aE^e - dE^e &= 0 \\
aE^e - pI^e - gI^e - d_I I^e &= 0 \\
pI^e - hQ^e - dQ^e &= 0 \\
gI^e + hQ^e - dR^e &= 0
\end{aligned}$$

From the last three equations, the relations

$$\begin{aligned}
E^e &= \frac{(p+g+d_I)}{a} I^e = \alpha_1 I^e \\
Q^e &= \frac{p}{(h+d)} I^e = \alpha_2 I^e \\
R^e &= \frac{g(h+d)+hp}{d(h+d)} I^e = \alpha_3 I^e
\end{aligned}$$

are obtained as function of I . The fifth equation can then be put in the form

$$(\beta_1 S_1^e + \beta_2 S_2^e + \beta_3 S_3^e + \beta_4 S_4^e - (a+d)\alpha_1) I^e = 0 \quad (5)$$

from which the two solutions

$$I^e = 0 \quad (6)$$

and

$$\beta_1 S_1^e + \beta_2 S_2^e + \beta_3 S_3^e + \beta_4 S_4^e - (a+d)\alpha_1 = 0 \quad (7)$$

are obtained.

From the first four equations the expressions of S_1^e , S_2^e , S_3^e and S_4^e as function of I^e can be obtained.

Then, the computation of the epidemic free equilibrium, the one corresponding to the solution (6), gives directly the equilibrium point $P^{e,1}$

$$\begin{aligned}
S_1^{e,1} &= \frac{1}{(c_{1,2} + m_1)} N \\
S_2^{e,1} &= \frac{c_{1,2}}{(c_{2,3} + m_2)} S_1^{e,1} \\
&= \frac{c_{1,2}}{(c_{2,3} + m_2)(c_{1,2} + m_1)} N \\
S_3^{e,1} &= \frac{c_{2,3}}{(c_{3,4} + m_3)} S_2^{e,1} \\
&= \frac{c_{1,2} c_{2,3}}{(c_{3,4} + m_3)(c_{2,3} + m_2)(c_{1,2} + m_1)} N \\
S_4^{e,1} &= \frac{c_{3,4}}{m_4} S_3^{e,1} \\
&= \frac{c_{1,2} c_{2,3} c_{3,4}}{m_4 (c_{3,4} + m_3)(c_{2,3} + m_2)(c_{1,2} + m_1)} N \\
I^{e,1} &= 0 \\
E^{e,1} &= 0 \\
Q^{e,1} &= 0 \\
R^{e,1} &= 0
\end{aligned}$$

For the case of $I^e \neq 0$, the same expressions of the S_i^e as functions of I^e , once substituted into (7), give an equation for I^e . Its expression is quite long: it is a polynomial equation of degree four with coefficients depending on the system parameters. Among the four roots of the polynomial equation, the actual number of admissible solutions depends on the parameters values, since only real positive quantities can be accepted as feasible solutions. Due to its dependence on the parameters, this aspect will be reconsidered in the numerical sections.

B. Computation of the basic reproduction number R_0

The basic reproduction number R_0 is a quantity associated to the infectivity of the virus: if it is greater than 1, the higher is its value the faster is the propagation; for values smaller than 1 the spread autonomously decreases and stops, with the number of infected individuals going to zero at steady state. It is related to the stability properties of the system, as evidenced in the sequel.

The computation of the basic reproduction number R_0 can be performed starting from the mathematical model of the epidemic spread and using the next generation matrix approach [10]. The part of the dynamics (1) directly involved in the epidemic spread must be considered

$$\begin{aligned}
\dot{E} &= \beta_1 S_1 I + \beta_2 S_2 I + \beta_3 S_3 I + \beta_4 S_4 I - aE - dE \\
\dot{I} &= aE - pI - gI - d_I I \\
\dot{Q} &= pI - hQ - dQ
\end{aligned} \quad (8)$$

According to the computation procedure [10], such a sub-dynamics has to be rewritten as

$$\begin{pmatrix} \dot{E} \\ \dot{I} \\ \dot{Q} \end{pmatrix} = \begin{pmatrix} \beta_1 S_1 I + \beta_2 S_2 I + \beta_3 S_3 I + \beta_4 S_4 I \\ 0 \\ 0 \end{pmatrix} - \begin{pmatrix} aE + dE \\ -aE + (p+g+d_I)I \\ -pI + (h+d)Q \end{pmatrix} \quad (9)$$

separating the terms which take into account the infection acquisition from the terms of epidemic evolution, i.e. transitions between classes. Once the matrices

$$\begin{aligned}
\mathcal{F} &= \frac{\partial}{\partial(E, I, Q)} \Big|_{P^{e,1}} \begin{pmatrix} \beta_1 S_1 I + \beta_2 S_2 I + \beta_3 S_3 I + \beta_4 S_4 I \\ 0 \\ 0 \end{pmatrix} \\
&= \begin{pmatrix} 0 & \beta_1 S_1^{e,1} + \beta_2 S_2^{e,1} + \beta_3 S_3^{e,1} + \beta_4 S_4^{e,1} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \\
\mathcal{V} &= \frac{\partial}{\partial(E, I, Q)} \Big|_{P^{e,1}} \begin{pmatrix} aE + dE \\ -aE + (p+g+d_I)I \\ -pI + (h+d)Q \end{pmatrix} = \\
&= \begin{pmatrix} (a+d) & 0 & 0 \\ -a & (p+g+d_I) & 0 \\ 0 & -p & (h+d) \end{pmatrix}
\end{aligned} \quad (10)$$

and

$$\mathcal{V}^{-1} = \begin{pmatrix} \frac{1}{(a+d)} & 0 & 0 \\ \frac{a}{(a+d)(p+g+d_I)} & \frac{1}{(p+g+d_I)} & 0 \\ \frac{ap}{(a+d)(p+g+d_I)(h+d)} & \frac{p}{(a+d)(h+d)} & \frac{1}{(h+d)} \end{pmatrix} \quad (11)$$

are computed, the basic reproduction number R_0 is given by the eigenvalue with the largest modulus of the matrix

$$\mathcal{F}\mathcal{V}^{-1} = \begin{pmatrix} \frac{a\beta_1 S_1^{e,1} + \beta_2 S_2^{e,1} + \beta_3 S_3^{e,1} + \beta_4 S_4^{e,1}}{(a+d)(p+g+d_I)} & * & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad (12)$$

which is easily given by

$$R_0 = \frac{a(\beta_1 S_1^{e,1} + \beta_2 S_2^{e,1} + \beta_3 S_3^{e,1} + \beta_4 S_4^{e,1})}{(a+d)(p+g+d_I)} \quad (13)$$

Comparing the expression of R_0 in (13) with the equation (5) it is possible to enrich the considerations given for the equilibria and their stability conditions. In fact, if $R_0 < 1$, expression (13) is equivalent to

$$\beta_1 S_1 + \beta_2 S_2 + \beta_3 S_3 + \beta_4 S_4 - \frac{(a+d)(p+g+d_I)}{a} < 0 \quad (14)$$

This condition, for equation (5), corresponds to the admissibility of the solution $I^e = 0$ only, since (7) does not satisfy the sign constraint. This means that under the condition $R_0 < 1$ only the epidemic free equilibrium does exist. On the other hand, $R_0 > 1$ means that solution (7) is admissible and endemic equilibrium points can exist. The validation of the correspondence between R_0 and stability characteristics are discussed in next subsection, after some computations.

C. Stability analysis

The relationship between the reproduction number R_0 and the equilibrium stability of the system can be confirmed studying local stability properties of the equilibrium points; to this aim, the dynamic matrix of the local linearised dynamics in the neighbourhood of an equilibrium point is given by the Jacobian matrix evaluated in such a point. When dealing with the epidemic free equilibrium P^{e1} , the matrix assumes the form

$$J(P^{e1}) = \begin{pmatrix} J_{1,1} & J_{1,2} & 0 \\ 0 & J_{2,2} & 0 \\ 0 & J_{3,2} & J_{3,3} \end{pmatrix} \quad (15)$$

where the important matrices are

$$J_{1,1} = \begin{pmatrix} -c_{1,2} - m_1 & 0 & 0 & 0 \\ c_{1,2} & -c_{2,3} - m_2 & 0 & 0 \\ 0 & c_{2,3} & -c_{3,4} - m_3 & 0 \\ 0 & 0 & c_{3,4} & -m_4 \end{pmatrix} \quad (16)$$

$$J_{2,2} = \begin{pmatrix} -(a+d) & \beta_1 S_1^e + \beta_2 S_2^e + \beta_3 S_3^e + \beta_4 S_4^e \\ a & -(p+g+d_I) \end{pmatrix} \quad (17)$$

$$J_{3,3} = \begin{pmatrix} -(h+d) & 0 \\ h & -d \end{pmatrix} \quad (18)$$

Thanks to its block structure, stability of the matrix (15) is assured once the roots of the polynomial

$$\lambda^2 + (a+d+p+g+d_I)\lambda + (a+d)(p+g+d_I) - a(\beta_1 S_1^e + \beta_2 S_2^e + \beta_3 S_3^e + \beta_4 S_4^e) \quad (19)$$

have negative real part. For the Routh–Hurwitz criterion, the two roots satisfy such a condition if and only if the coefficients

of the polynomial are all positive. This corresponds to require that the inequality

$$(a+d)(p+g+d_I) - a(\beta_1 S_1^e + \beta_2 S_2^e + \beta_3 S_3^e + \beta_4 S_4^e) > 0 \quad (20)$$

is satisfied. It is easy to verify that it corresponds to the condition $R_0 < 1$. This result confirms that when $R_0 < 1$ the epidemic free equilibrium is the only equilibrium point of the system and it is (locally) asymptotically stable.

IV. APPLICATION TO A REAL EXAMPLE: THE ITALIAN CASE

The characterisation of the COVID-19 in terms of the different effects on people according to their age in here studied making use of the mathematical model (1). The parameters present in the model can be divided into two groups: one which is independent on the disease, and whose values can be obtained from statistical data on the population; the second which is strongly dependent on the epidemic impact on the population evolution, whose values can be obtained analysing the dynamic evolution of the population under the epidemic spread. The first set is reported in Table I, with their numerical values collected from the Italian statistical institute (ISTAT) [11]. The second set is represented by $\beta_1, \beta_2, \beta_3, \beta_4$ and d_I ; their numerical values are the object of the identification procedure described in the sequel.

TABLE I
VALUES OF VIRUS-INDEPENDENT PARAMETERS USED IN THE NUMERICAL SIMULATIONS

$c_{1,2}$	$1.3699 \cdot 10^{-04}$	m_1	$6.3 \cdot 10^{-7}$
$c_{2,3}$	$9.1324 \cdot 10^{-05}$	m_2	$2 \cdot 10^{-6}$
$c_{3,4}$	$1.3699 \cdot 10^{-04}$	m_3	$1.4 \cdot 10^{-5}$
		m_4	$1.4 \cdot 10^{-4}$
a	1/10	d	$2.8 \cdot 10^{-5}$
p	1/3	g	1/20
h	1/20		

The case of Italy is considered, since it has been one of the most affected Country for which reliable official data are available.

Information that can be retrieved on the official documents of national agencies [11], [12] are referred to the total number of infected and dead individuals collected daily. This data structure corresponds to the quantities defined in the model, where only the total number of infected I is introduced. However, this information is not sufficient to distinguish the actual contribution of each age class to the number of infected. The problem could be overcome once the information on the daily evolution of infected and dead individuals would be available for each age class but with the complication of the necessity to adopt a full age-based model as discussed in the Introduction. In such a case, the problem can be made more complicated by the conspicuous increment of the number of parameters involved.

The approach here adopted aims at keeping the problem simple enough to be handled with the data available from the official sources. According to the model adopted, the missing

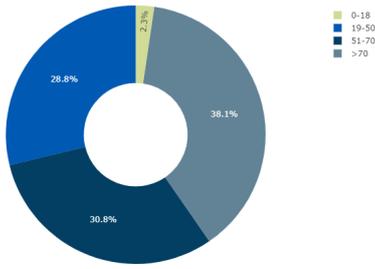


Fig. 2. Average distribution of infected people among age groups ([12])

information on the age-based evolution of the epidemic is recovered making use of the averaged informations like the one reported in Fig. 2, where the mean distribution of the number of infected cases among four age groups is provided.

Then, all the identification procedure is based on the knowledge of the daily reports of the total number of infected and dead individuals along with the global time invariant distribution given in Fig. 2. The approach here followed to determine the transmission rates β_i is based on the assumption that the differences of the epidemic effects on different aged people are time invariant; then, they can be seen as constant ratios between the β_i terms, so that they model scale factors of disease incidence according to the age. So, the ratios can be assumed to measure the different impact of the virus diffusion depending to the age of the subjects. The number of infected individuals as reported by [12] is depicted in Fig. 3 by the bar graph, their daily variation is given in Fig. 4, while Fig. 5 shows, with the bar graph, the number of people dead for COVID-19. Collected data start from February 24 and they have been considered up to June 25. In the figures the two

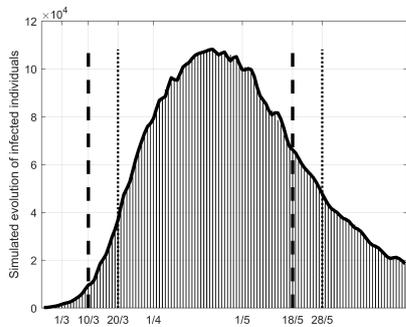


Fig. 3. Time history of the simulated number of infected individuals (solid curve), compared with the given real data (bar graph)

dates March 10 and May 18 are evidenced: they correspond to the beginning and the end of the total lock-down imposed by the Government. In Fig. 4 also ten days after the start and the end of the lock down are marked, corresponding to the average time for the activation rate of the virus: this time represents a delay in the effects of the containment measures. It is interesting to note that a direct inspection of Fig. 4 is

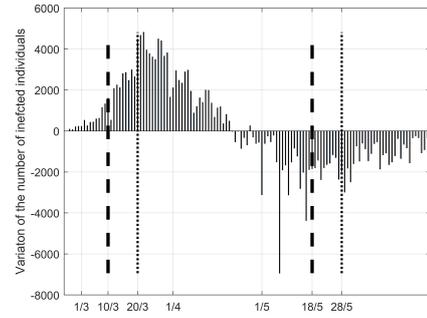


Fig. 4. Variation of the number of infected individuals according to the official data [12]

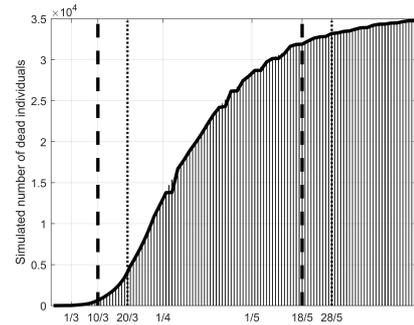


Fig. 5. Time history of the simulated number of dead individuals (solid curve), compared with the given real data (bar graph)

sufficient to see the initial increment of the daily infected individuals, the constant continuous reduction during the lock down, with an initial and final delay of about 10 days, and then, with the containment measures relaxed, a new increment.

The identification procedure has been performed assuming the values for the transmission rates β_i and for the death rate of infected individuals d_I constant over two days, to have time varying evolutions homogeneous with the data and, at the same time, to smooth their behaviour. The solution has been computed minimising both the error between the simulated and the real values of the infected individuals, and the error of the corresponding values of the dead persons, using a cost function where the error on the dead individuals is weighted four times the one on the infected subjects; such a scale factor has been introduced to make the order of magnitude of the two errors comparable. During the minimization procedure, the best values for the ratios between the infection factors β_i are found making use of a gradient-like approach.

The quality of the result of the identification procedure is evidenced in Figs. 3 and 5 by the solid line fitting the bar graphs. Since the main goal of this work is to reconstruct and analyse the differences between the transmission rates of the different ages, it is important to show what the identification procedure has given for the β_i . According to the assumption adopted, the time histories of the four coefficient β_i have the

same shape, being different each other only for a constant factor. Then, in Fig. 6 the values of β_1 , obtained from the system identification, are reported. The evolution of the values

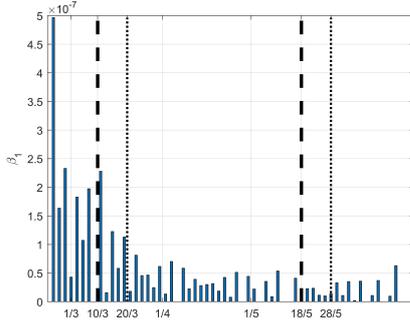


Fig. 6. Time history of the estimated transmission factor β_1

for the other three transmission rates have the same shape of Fig. 6, with the difference in the amplitude, defined according to the ratios

$$\frac{\beta_2(t)}{\beta_1(t)} = 5.5, \quad \frac{\beta_3(t)}{\beta_1(t)} = 8.6, \quad \frac{\beta_4(t)}{\beta_1(t)} = 18.4, \quad (21)$$

A check of the correctness of the choice of assuming a constant factor between the transmission factors can be represented by Fig. 7, where the time histories of the percentage of infected individuals for the four classes are reported, compared with the constant values assumed from data in Fig. 2. Actually, their evolution along almost four months confirms that the percentages given in Fig. 2 are almost time invariant, and the hypothesis of a constant ratio between the coefficients β_i is strongly supported. The results obtained show two important

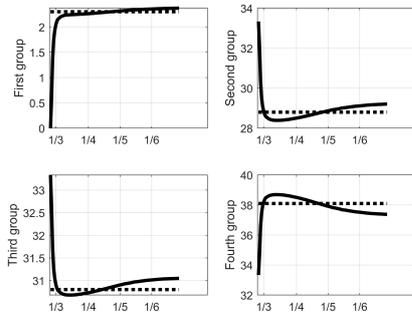


Fig. 7. Time history of the percentage of infected people in the four classes modelled

facts regarding the epidemic spread and the effects on the different ages. The first is contained in Fig. 6: there, they are evident the high values for the transmission factors when no control actions were performed yet, that is before the beginning of the lock down, the decreasing values during the social containment and the new, small but evident, increment after the end of the isolation. It is also evident the presence of

the delay of about 10 days from the actions (lock-unlock) and the effects (decrement-increment). The second is represented by the factors which relates the transmission coefficient for the different age classes. Such coefficients can be assumed to measure the different spread of the contagion among the population, according to the age. They show an increment depending on the higher age, high and comparable for 19–50 years old people (5.5 times the younger) and for 51–70 years old (8.6 times) but with a very high increment for the older class (18.4 times). These values reflect the actual situation, where the highest number of infections involved individuals over 70 years old, with a corresponding higher number of victims.

V. CONCLUSIONS

In the paper the usefulness of a mathematical model able to describe the contagion behaviour of the COVID-19 with respect to different ages of the patients has been shown. The example of Italian case has been taken for the model parameters identification; numerical simulations show interesting results on the whole behaviour of the epidemic spread in terms of global infection coefficients as well as on the possibility to retrieve a numerical evaluation of the relationship between the infectivity and the age.

REFERENCES

- [1] T. Vasanthi and V. Vijayalakshmi, "Mathematical models for the study of HIV/AIDS epidemics," *proc. IEEE International Conference on advances in Engineering, Science and Management*, pp. 108–112, 2012.
- [2] P. Di Giamberardino, L. Compagnucci, C. D. Giorgi, and D. Iacoviello, "Modeling the effects of prevention and early diagnosis on HIV/AIDS infection diffusion," *IEEE Transactions on Systems, Man and Cybernetics: Systems*, pp. 2119–2130, 2019.
- [3] I. Cooper, A. Mondal, and C. G. Antonopoulos, "A sir model assumption for the spread of covid-19 in different communities," *to appear in Chaos, Solitons and Fractals*, 2020.
- [4] B. Tang, X. Wang, Q. Li, N. L. Bragazzi, S. Tang, Y. Xiao, and J. Wu, "Estimation of the transmission risk of the 2019-nCoV and its implication for public health interventions," *Journal of Clinical Medicine*, vol. 9, no. 2, 2020.
- [5] J. T. Wu, K. Leung, and G. M. Leung, "Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study," *The Lancet*, 2020.
- [6] B. Ivorra, M.R.Ferrández, M.Vela-Pérez, and A.M.Ramos, "Mathematical modeling of the spread of the coronavirus disease 2019 (covid-19) taking into account the undetected infections. the case of china," *Commun Nonlinear Sci Numer Simulat*, vol. 88, 2020.
- [7] B. Wang, S. Xu, and M. Mansouri, "Modeling the emergence of covid-19: a systems approach," *IEEE 15th International Conference of System of Systems Engineering (SoSE)*, 2020.
- [8] P. Di Giamberardino, D. Iacoviello, F.Papa, and C.Sinisgalli, "Dynamical evolution of covid-19 in italy with an evaluation of the size of the asymptomatic infective population," *in press, IEEE Journal of Biomedical and Health Informatics*, 2020.
- [9] Y. Zhao, M. Li, and S. Yuan, "Analysis of transmission and control of tuberculosis in mainland china, 2005-2016, based on the age-structure mathematical model," *Int J Environ Res Public Health*, vol. 14, 2017.
- [10] M. Martcheva, "An introduction to mathematical epidemiology," *Text in Applied Mathematics 61*, Springer, 2015.
- [11] "ISTAT, italian istituto nazionale di statistica," <https://www.istat.it/en/>, 2020.
- [12] "ISS, italian istituto superiore di sanità," <https://www.iss.it/en/coronavirus>, 2020.