Time-window SIQR analysis of COVID-19 outbreak and containment measures in Italy

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***Abstract*—The COVID-19 disease caused by the coronavirus SARS-nCoV2 is currently a global public health threat and Italy is one of the countries mostly suffering from this epidemic. It is therefore important to analyze epidemic data, considering also that the government deployed laws limiting the societal activities. We model COVID-19 dynamics with a SIQR (susceptible – infectious – quarantined – recovered) model, where we take into account the temporal variability of its parameters. Particle Swarm Optimization is used to find out the best parameters in the case of Italy and of Italian regions where the epidemic has the greatest impact. The basic reproductive number is estimated by a novel approach that averages out different PSO fits computed considering different temporal time-windows and reducing possible noise in the data. The results on data collected from February 24 to April 24 show that our approach is able to fit the data with low errors and that the basic reproductive number is characterized by a descending trend in time from 3.5 to a value below 1.**

***Index Terms*—COVID-19, Coronavirus, Basic reproductive number, Particle Swarm Optimization, Italy**

I. Introduction

COVID-19 is the widespread respiratory disease caused by the novel SARS-nCov2 coronavirus, whose origin of is yet to be figured out by the World Health Organization (WHO), but it first influnced millions of citizens in Wuhan City of Hubei province in China since last December 2019. In only 3 months it reached such a global spread (more than 500000 cases) that it was declared a pandemic by WHO on March 11, 2020.

Italy is currently one of the most affected Western countries, accounting 192.994 cases so far. To contain the disease spread, the government introduced at first the quarantine for the infected people and then, as extreme measure, the complete lockdown of the country on March 10, 2020. The containment measures were increased on March 22 also interrupting any service and productive activity that wasn't a primary need for the citizens, following the steps covered by China and many other affected countries.

Despite all the efforts, the pandemic is still ongoing and researchers are directing increasing efforts towards the comprehension of this disease dynamics by modelling its spread [1], [2], [3], [4], [5], [6], [7], [8].

The basic model to describe epidemiological dynamics is the Susceptible-Infected-Recovered (SIR), that exploits the relationships between the three components listed in its name, i.e. the subpopulation that is prone to get the disease (susceptible S), the subpopulation of the infected individuals which spread the virus (infected I) and the set of individuals recovered, deceased, or immune (recovered R). This deterministic model has several alternatives that add components to represent other phenomena in the dynamic. In the case of COVID-19, the work in [1], [2], [3] exploits a variant of the SIR model which introduces also the variable Q to take into account the "quarantined" subpopulation, named SIQR model [9]. In particular the contribution in [1] presents as main case study the modelling of COVID-19 spread in Italy between February 20 and March 10. They investigate the effects of the initial mild restrictions imposed in the country at the beginning of the virus spread, finding out that these weren't effective. Indeed, according to their estimates the transmission coefficient (β) should be reduced at least of the 65% to appreciate a significant drop in the number of infectious individuals. However this model considers only the first phase of the epidemic and it doesn't take into account the lock down interventions imposed by the Italian government after March 10.

The work reported so far assume that the infection rate of the disease is constant in time. However, the speed of transmission can be changed through many measures, such as personal protective measures, community-level isolation, and lock down. On these grounds, we hereby present a study on the COVID-19 spread in Italy modelling the disease by a SIQR approach and searching for the optimal model parameters by the PSO algorithm, that fits data on both the number of fatalities/recovers and the quarantined populations. Furthermore, to account for temporal variation of the infection rate, model parameters estimation is performed by using a time-windowing approach, which helps us discovering how the spread of the disease evolves and and whether temporal modifications are related to the strict lock down measures taking effect since March 10.

II. Methods

The strategy used by several governments to reduce the diffusion of the disease has introduced the quarantine, so that sick people are forced to do not mix with others to do not infect susceptibles. Depending to the disease severity, quarantined people can stay at home or are hospitalised.

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This suggests us to model the dynamics of COVID-19 by a SIQR model. This is a model where the total population $N(t)$ is divided into four compartments $S(t)$, $I(t)$, $Q(t)$, and $R(t)$, with $N(t) = S(t) + I(t) + Q(t) + R(t)$. $S(t)$ denotes the susceptibles that can become infected and move to the infectious class $I(t)$. $Q(t)$ represents people in quarantine, and $R(t)$ is the number of persons that recover or die from the disease. Furthermore, individuals in R class get permanent immunity. The evidence that the SARS-nCov2 virus can be transmitted in the absence of symptoms [10] suggests us to exclude from the model the exposed status ($E(t)$), which accounts for individuals who experience a long incubation duration during which they are infected but not yet infectious.

Fig.1 shows the compartmental model used that is described by the following ordinary differential equations (ODEs):

$$\begin{aligned}
\frac{dS}{dt} &= \frac{-\beta SI}{N} + \delta N + \rho S \\
\frac{dI}{dt} &= \frac{\beta SI}{N} - (\alpha + \eta)I \\
\frac{dQ}{dt} &= \eta I - \gamma Q \\
\frac{dR}{dt} &= \gamma Q + \omega I
\end{aligned}$$

where β denotes the infection rate (i.e. the rate of effective contacts leading to a secondary case of infection), δ is the birth rate, ρ stands for the natural death rate, α quantifies the recovering rate of asymptomatic individuals, η is the rate of detection of new cases, γ stands for the recovering of quarantined individuals, and ω is the recovery rate of infectious. Note that all these quantities are strictly positive. As reported in section I, to the best of our knowledge, the work that describe the CODIV-19 dynamic by SIQR model assume that the infectious rate β and the other coefficients are constant over time. While this is reasonable in the early days of the epidemic, the government interventions have changed people life style and this, in turns, has changed the speed of transmission. To deal with this observation, in the ODEs we can replace β by $\beta(t)$, δ by $\delta(t)$, and so on for all the other coefficients introduced above. Nevertheless, in order not to burden the notation, hereinafter we omit to explicitly write the time dependency.

Let us now discuss some further considerations on the model. First, the birth rate is set equal to the death rate, which is assumed not to be related to the infectious disease. This is reasonable due the time horizon of the data and the disease characteristics. Second, this ODEs model also assumes that the hypothesis of well-mixed population holds, i.e. any infected individual has a probability of contacting any susceptible individual that is reasonably well approximated by the average. Third, while in theory people can move from the I and Q classes to the R class, there are no data available yet on the number of recovered or deceased non-identified COVID-19 patients. For this reason we do explicitly not model this link between I and R (i.e. $\omega = 0$), whilst we introduce the rate α

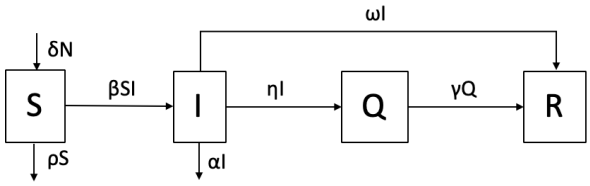


Fig. 1: SIQR compartmental model. The meaning of the symbols is described in section II.

with which patients from I become non-infectious, as also [1], [2], [3] do.

We also introduce in the model previous findings on the average incubation time, which was estimated to be 5 days [11], [12], and on the duration of the milder cases of disease, ranging from 5 up to 10 days [10]. Assuming an average time of duration from infection to recovery or fatality of non-isolated cases of 10 days, that corresponds to a rate of $r_d = 0.1/day$, and denoting as ϵ the fraction of infectious individuals tested positive and put in quarantine (Q), we obtain $\alpha = r_d(1-\epsilon)$. Furthermore, η related to the time until patients are tested positive and isolated, but also to the fraction of all infectious individuals that are tested positive [1]. These are mostly symptomatic patients, which we assume are isolated soon after the incubation time is over and first symptoms appear, i.e. after ~ 5 days, so that we have a rate $r_i = 0.2/day$. This results in $\eta = r_i\epsilon$.

According to all the considerations reported so far, the ODE model can be re-written as:

$$\begin{aligned}
\frac{dS}{dt} &= \frac{-\beta SI}{N} \\
\frac{dI}{dt} &= \frac{\beta SI}{N} - [r_d + \epsilon(r_i - r_d)]I \\
\frac{dQ}{dt} &= r_i\epsilon I - \gamma Q \\
\frac{dR}{dt} &= \gamma Q
\end{aligned}$$

From this disease model we can derive the basic reproduction number R_0, defined as the expected number of secondary cases produced by a single (typical) infection in a completely susceptible population. It is a dimensionless number playing an important role in helping to quantify possible disease control strategies because it reflects the transmissibility of a virus spreading under no control: indeed, a disease is likely to decline and eventually disappear when $R_0 \leq 1$. This quantity can be computed from an ODE compartmental model using the next generation matrix G, as proposed in [13], [14]. G is a square matrix where its ijth element is the expected number of secondary infections of type i caused by a single infected individual of type j, again assuming that the population of type i is entirely susceptible. G has also some desirable properties from a mathematical point of view and, in particular, it is a non-negative matrix: this guarantees there will be a unique real positive eigenvalue being strictly greater than all the others.

This eigenvalue is R_0, since R_0 is the spectral radius of G. According to [15], the next generation matrix can be computed as $\mathrm{G} = \mathrm{FV}^{-1}$, where F and V are square matrices defined as follows. Formally, let $\overline{x} = (x_1, x_1, \ldots, x_n)^T$ be the number of individuals in each of the n compartments, where the first $m < n$ contain infected individuals. Each one of the ODEs can be therefore re-written as

$$\frac{dx_i}{dt} = F_i(x) - V_i(x), \text{ for } i = 1, 2, \ldots, m \tag{1}$$

where $F_i(x)$ is the rate of appearance of new infections in compartment i, and $V_i(x)$ is the rate of other transitions between compartment i and other infected compartments. It is assumed that F_i and $V_i \in C^2$, and $F_i = 0$ if $i \in [m+1, n]$.

In our SIQR model the infected individuals are in the I and Q compartments and, hence, we can derive F and V as follows

$$F_I = \frac{\beta SI}{N} \quad F_Q = r_i \epsilon I$$
$$V_I = [r_d + \epsilon(r_i - r_d)]I \quad V_Q = \gamma Q$$
$$\mathrm{F} = \begin{bmatrix} \frac{\partial F_I}{\partial I}(x) & \frac{\partial F_I}{\partial Q}(x) \\ \frac{\partial F_Q}{\partial I}(x) & \frac{\partial F_Q}{\partial Q}(x) \end{bmatrix} = \begin{bmatrix} \frac{\beta S}{N} & 0 \\ r_i \epsilon & 0 \end{bmatrix}$$
$$\mathrm{V} = \begin{bmatrix} \frac{\partial V_I}{\partial I}(x) & \frac{\partial V_I}{\partial Q}(x) \\ \frac{\partial V_Q}{\partial I}(x) & \frac{\partial V_Q}{\partial Q}(x) \end{bmatrix} = \begin{bmatrix} r_d + \epsilon(r_i - r_d) & 0 \\ 0 & \gamma \end{bmatrix}$$

where the subscripts I and Q refer the infectious and quarantine classes. Note that F is entry-wise non-negative and V is a non-singular M-matrix. It is straightforward that

$$\mathrm{V}^{-1} = \begin{bmatrix} \frac{1}{r_d + \epsilon(r_i - r_d)} & 0 \\ 0 & \frac{1}{\gamma} \end{bmatrix}$$

and

$$\mathrm{G} = \mathrm{FV}^{-1} = \begin{bmatrix} \frac{\beta S}{N[r_d + \epsilon(r_i - r_d)]} & 0 \\ \frac{\eta}{r_d + \epsilon(r_i - r_d)} & 0 \end{bmatrix}$$

The eigenvalues of G are therefore 0 and $\frac{\beta S}{N[r_d + \epsilon(r_i - r_d)]}$, with the latter being R_0. Because a relatively small fraction of the population has been found positive for COVID-19, we are in the early phase of the epidemic and we can assume that $S \sim N$, obtaining $R_0 = \frac{\beta}{r_d + \epsilon(r_i - r_d)}$.

In order to optimise the model parameters we use the Particle Swarm Optimisation algorithm [16], a metaheuristic algorithm based on the concept of swarm intelligence appropriate to optimize nonlinear continuous functions well appropriated in this settings. The available data, described in section III, refer to quarantine (Q), to fatalities and recoveries (R), while no information is available for the true number of infectious I. This suggests a model optimization based on Q and R and, hence, the PSO algorithm searches for β, γ and ϵ by minimising the normalised residual sum of squares error (NRSS, defined as in [17]), thus reducing also the risk to overfit the data. To account for temporal variations in speed of transmission we use a time window approach for PSO fitting: to this end, the PSO works with consecutive time-series data of length w and the time data blocks are overlapped by a designated quantity o. Given data granularity, both w and o are positive integers and they are measured in days, with $o < w$. Furthermore, the initial conditions of each time window are the $(w - o)$th variable values estimated by the previous window, resulting in smooth transitions between consecutive time windows. Straightforwardly, the first initial conditions are the real data.

The use of this approach, further to consider the temporal variations due to life style changes eventually given by legislative initiatives, permits us also to attain a better estimate of the basic reproduction number. Indeed, on the one side, the use of single PSO fitting over the whole time-series may not be able to catch the temporal variations resulting in a poor estimate of the ODEs model and, hence, in a poor estimate of the value of R_0. On the other hand, if the PSO fits the data for different combinations of w and o, it returns a time-series of estimates for each ODE parameter with $\frac{d-o}{w-o}$ elements, where d is the number of days with available data. This, in turns, provide a time-series of R_0, one for each pair w and o.

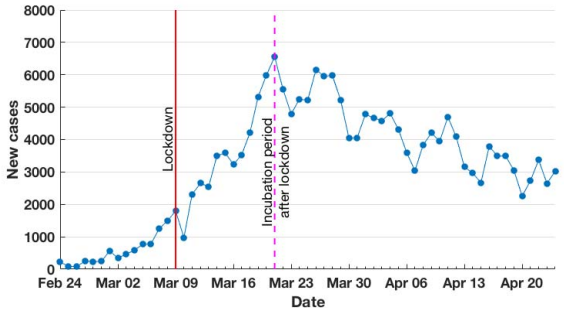
We can now compute R_0^*, that is the average value of these different R_0 attained for different (w, o), as described in algorithm 1: this approach acts as a filter reducing random noise due to acquisition data limitations given by the challenges the health system is coping with in this period, such as the daily data fluctuations due to delays from symptoms to swab execution, delays in laboratories for lack of reagents, etc. In algorithm 1 we consider only the maximum o per w, i.e. $o = w - 1$, so that we maximise the number of time windows extracted from the time-series data. Consequently, this results in a larger number of temporal windows inside the whole period, maximising the number of ODEs parameter time-series used, averaged out to estimate R_0^*, having also multiple parameters estimation per day.

III. Materials

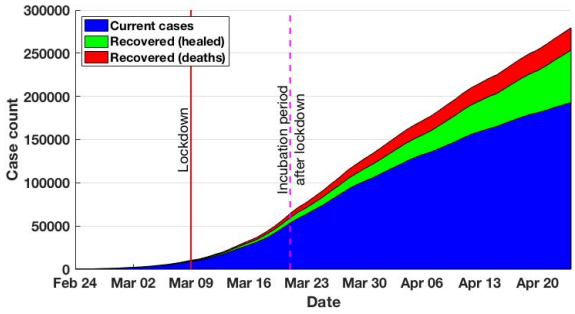
The dataset employed in this study collects the open source information provided by the Italian Civil Protection Department[1]. This data includes the daily updates on the number of patients hospitalised with symptoms, in intensive care or at home confinement, the total amount of current positive cases (hospitalised patients plus those at home confinement), news amount of current positive cases, the number of recovered, the number of deaths, the total number of people tested and the amount of tests performed. These details are available both for the entire country and for each region.

For the purpose of this work we included the acquisitions regarding the time frame from February 24 and April 24, which is the date we are submitting this contribution. In particular we considered the total amount of positive cases, which accounts for the hospitalised and the home confined, as the quarantined population Q, whereas the number of recovered plus the number of deaths represents the recovered population R of our model. Fig. 2 shows the variation in time of the new cases and the cumulative count of infected, dead, and recovered cases of our datasets, in the aforementioned

[1]The dataset is available at https://github.com/pcm-dpc/COVID-19.



(a) Daily new COVID-19 cases.



(b) Cumulative COVID-19 cases count.

Fig. 2: Variation in time of the number of new cases of COVID-19 in Italy as reported by the Civil Protection Department. Panel (a) represents the number of new infected individuals per day, whereas panel (b) reports the cumulative amount of cases highlighting also the recovered portion with the healed population in green and the deaths in red. The vertical continuous red line indicates when lockdown starts in the country, which is followed by a dotted purple line that represents the end of the incubation period of 14 days and the consequent appreciable effects of the containment measures.

Algorithm 1 Window-based R_0^* estimation algorithm

allDays is a vector of dates from 2020/02/24 to 2020/04/24
allWindowWidths is a set of equally spaced integer values in [2,14]
NRSS($\mathbf{W}$) is the residual sum of squares computed for the predicted values of a set of days contained in a time-window $\mathbf{W}$

for i in *allWindowWidths* **do**
    $\mathbf{W^i}$ is an array of collection containing all the time-windows that can be extracted from the data (*allDays*) for $w = i$ and $o = i - 1$

    for j = 1 to *length*($\mathbf{W^i}$) **do**
        ${\mathbf{W^i}}_j$ is the jth collection extracted from $\mathbf{W^i}$
        $\beta^*[j] = \underset{\beta}{arg\,min}(\text{NRSS}({\mathbf{W^i}}_j))$
        $\epsilon^*[j] = \underset{\epsilon}{arg\,min}(\text{NRSS}({\mathbf{W^i}}_j))$
    end for

    for d in *allDays* **do**
        $\mathbf{J}$ = all the indeces s.t. $d \in {\mathbf{W^i}}_j$

        for j in $\mathbf{J}$ **do**
            $R_0^i[d]$ += $\beta^*[j]/(r_d + \epsilon^*[j](r_i - r_d))$
        end for

        $R_0^i[d] = R_0^i[d]/length(\mathbf{J})$
    end for

    R_0^* += R_0^i
end for

$R_0^* = R_0^*/length(allWindowWidths)$

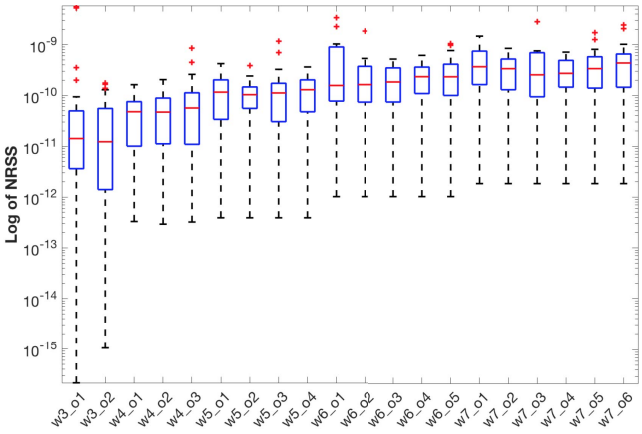


Fig. 3: Box plot showing the sum of the NRSS values computed on the estimates of R and Q provided by our model when different combinations of window size w and overlap o are used. For instance, the x-axis label $w3\_o2$ indicates that three days are in the window with two days of overlap with the previous one.

timeframe. In particular in Fig. 2a and 2b a red line shows when the lockdown starts in the country. Despite the desired effect of this emergency measure, after March 10 there is still an increase in the infected population. This does not imply that the lockdown was unsuccessful, but its efficacy is just delayed due to the incubation period of the virus. Indeed, the majority of people starts showing symptoms at most after 14 days that they've been infected [12]. These 14 days latency is marked with a dotted purple line, which happens to corresponds to the start of the decrease of the new cases number (Fig. 2a).

IV. Experimental setup and Results

As mentioned in section II, in order to take into account in our model the variations in the infection rate, we fitted the PSO

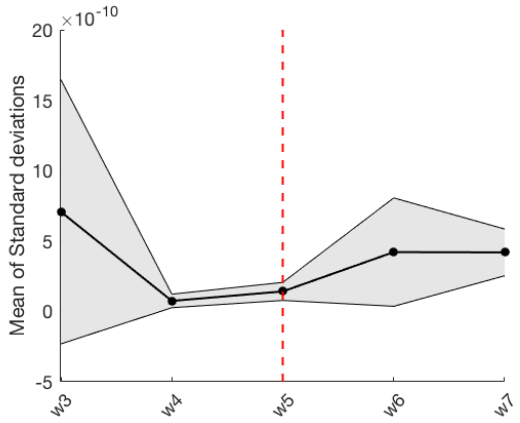


Fig. 4: Average value of the standard deviations of the NRSS values for each window length w_i. The gray shadow shows the standard deviation of each value and the dotted red line highlights the chosen value for w.

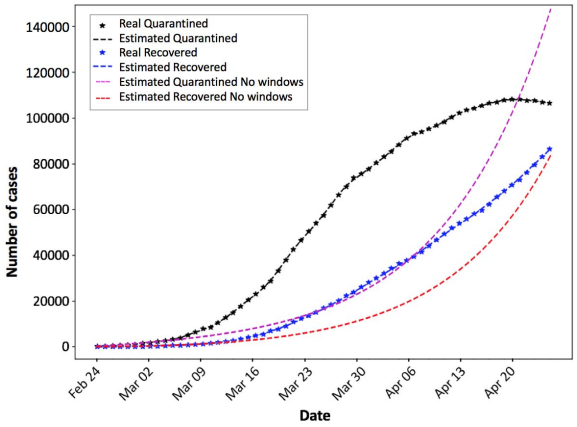


Fig. 5: SIQR predicted and real Quarantined and Recovered with and without the windowing approach.

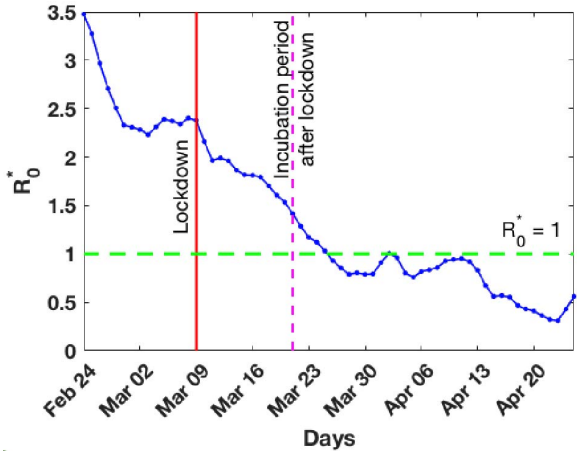


Fig. 6: Time evolution of the basic reproduction number R_0^*, computed according to algorithm 1.

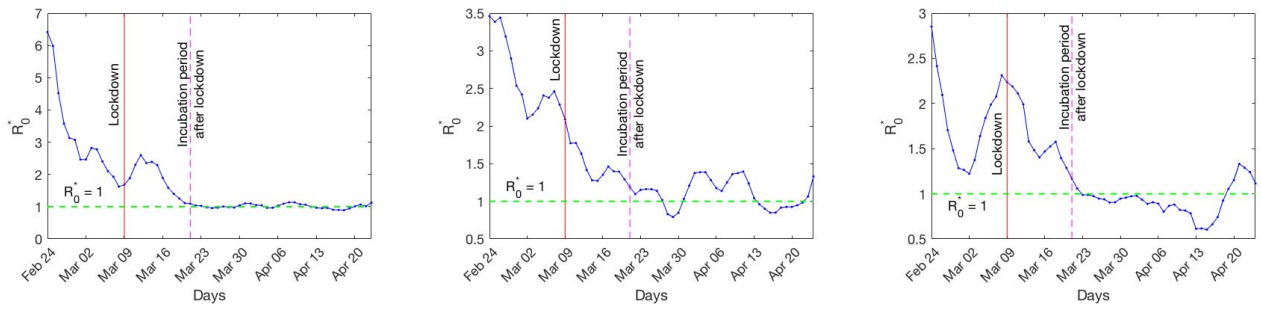
over consecutive sliding windows. This approach accounts for two parameters to set: the window length w and the overlap o. Fig. 3 reports a box plot of the normalised sum of the residual sum of squares (NRSS) computed on the estimations of R and Q provided by our model with different combinations of window length and overlap. The average NRSS appears to be lower for small window sizes, but with a larger standard deviation. We deem this is related to the fact that there isn't enough data available to build a stable model, or rather that any model could fit these few samples.

To get a deeper insight on this phenomenon, Fig. 4 reports the average standard deviation for each window size with the related standard deviation (grey area). For values $w < 4$ and $w > 5$ the NRSS shows an unstable behaviour, with more fluctuations. For small size windows this happens for the aforementioned reasons of lack of data for a proper fitting, whereas for $w > 5$ this is probably due to the presence of noise in the data. It is clear, now, that the best compromise lies with $w = 5$ which allows to have lower values for NRSS standard deviation and also a grater amount of data to fit the model. Consequently the overlap value is $o = 4$, which is the maximum one and allows the to gain the smallest granularity in parameters estimation, as mentioned in section II.

Fig. 5 shows in black and blue the values estimated by our model setting $w = 5$ and $o = 4$ with respect to the real values of Q and R. The qualitative inspection of the figure indicates that the proposed SIQR-PSO windowing approach is able to follow the real values trend, and this is also corroborated by the NRSS, equal to $1.4e^{-10}$ (95% C.I. $[1.1e^{-10}; 1.7e^{-10}]$). The same figure shows in purple and red the Q and R estimates attained fitting the data without the time-window approach, i.e. assuming that the coefficients of the SIQR model are constant over time. Straightforwardly, the results in this latter case are not satisfactory (NRSS = $1.9e^{-5}$).

Fig. 6 reports the time variation of the basic reproduction number R_0^* computed with the procedure in presented in algorithm 1. The curve trend drops after the lockdown, confirming its efficacy. It is worth noticing that the first estimated of R_0^* is equal to 3.5, coherently with previous work that found R_0 falling between 2 and 4 [1], [4], [5], [6], [7], [8]. In the specific case of the Italian situation, the work in [1] found $R_0 = 2.78$ fitting a SIQR model, too. However, our approach significantly differs from [1] because we use a global optimisation strategy to fit the data, and because we analyse the epidemic for a longer period. Indeed, differently from what presented here, in such a work the authors first solved the SIQR model under some assumptions; then they fit an exponential model on $Q+R$ using log-transformed data, whilst γ was estimated by linear regression on step-wise unitary differences on R [1].

As a further observation still referring to Fig. 6, the basic reproduction number drops after the lockdown (red line) and reaches the threshold value ($R_0^* = 1$) 14 days after, due to the incubation time of the virus. After this threshold the basic reproduction number assumes values lower than 1, meaning



(a) Piemonte (b) Lombardia (c) Veneto

Fig. 7: Basic reproduction number estimation over time on three Italian regions. All plots show both the lockdown (red line) and the threshold R0=1 (green line) under which the disease is likely to disappear (R0<1).

that the disease is likely to decline and eventually disappear. Although these results seem to indicate that Italy should be out of this emergency situation, the overall evaluation on the whole country does not take into account the lack of homogeneity of the real situation in the Italian regions. To get a closer look into this phenomenon, we performed the same analysis on the regional data provided by the Civil Protection Department. Fig. 7 shows the basic reproduction number over time of the three regions most affected by the virus, i.e. Piemonte, Lombardia and Veneto. As it is possible to notice in these cases, R_0^* fluctuates around the threshold. This indicates that these regions still need to stick to the containment measures to further reduce the disease impact.

V. Conclusion

In this work we presented an analysis of the COVID-19 pandemic, modelling the spread dynamic on the Italian territory. We used a SIQR model fitted exploiting a global optimisation strategy and a time windowing approach. This takes into account the variability over time of the SIQR model parameters, due to the change in people habits and societal behaviour introduced by the lockdown containment measures. The results show a satisfactory fitting of the model and an interesting trend of the basic reproduction number, which differs from the entire country to the specific regions. Indeed, on the one hand, the overall Italian R_0 falls under 1 after 14 days since the lockdown; on the other hand, for some of the most affected Italian regions it is still over the desired threshold.

To further investigate this phenomenon a step forward for this work could be the prediction of future model parameters trends, applying a regressive approach on the reconstructed time varying data. This could provide insights about the future dynamics of the disease and the regions which are out of danger or rather at greater risk, building an country heatmap. Moreover, we plan to apply our approach to other countries.

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