Modelling the epidemiological trend and behavior of COVID-19 in Italy

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Abstract

As of March 16, 2020, over 185,000 across the world, Italy became the red hotspot for the COVID-19 pandemic after China. With over 35,000 cases and 2900 deaths reported in the month of March in Italy, it is necessary to stimulate epidemic trend to understand the behavior of COVID-19 in Italy. By S.E.I.R. simulation, we estimated the most representative epidemic parameters occurred from March 1 to 14, 2020, thus being able to evaluate the consistency of the containment rules and identify possible Sars-Cov-2 local mutations. Our estimations are based on some assumptions and limitations exited.

Keywords: *COVID-19, coronavirus, contamination, novel coronavirus, Sars-Cov-2, Europe, Italy.*

Introduction

The current surge of COVID-19 pandemic is devastating globally, with over 200,000 cases and more than 8600 deaths reported [1]. In Europe, COVID-19 cases are most dramatically started to increase from the first week of March 2020. Of these, Italy is grappling with the worst outbreak, with over 35,713 confirmed cases and around 3000 deaths by March 18, 2020 [1-5]. This exponential increase in COVID-19 positive cases in Italy raised turmoil, and the government decree to a lockdown of the entire country [1]. Given the seriousness of the situation, it is absolutely necessary not only an immediate intervention but also a criterion for assessing its effectiveness.

Article on modeling epidemic transition of COVID-19 have been published [1-8] and based on the previous publication from China, South Korea, Iran, and Japan presented the estimation of epidemic trends and transmission rates [1-8]. Through this research, we evaluated the consistency of the containment rules and identified possible SARS-CoV-2 local mutation using the S.E.I.R mathematical model. We used the most representative epidemic parameters that occurred during the first half of March 2020 to predict the trend of infections. Therefore, to assess the effectiveness of the containment measures, it will signal the presence of an evolutionary mutation. To do this, it will be sufficient to compare the general trend foreseen by the S.E.I.R. with the real Italian population.

Methods

To carry out this study, we used the most recent data, found in the scientific literature relating to COVID-19 total and active cases, deaths, recoveries, and all epidemic parameters, have been used. Since the Chinese situation has provided the most information, great statistical importance

was given to the Sars-Cov-2 evolution in the Hubei region, with the implicit assumption of "very significant local mutations" absence necessary for generalizing the reports through classical inference. The statistics collected on virus mortality were first divided by age group and then recalibrated on the Italian demography, in order to be as representative as possible. To do this, we considered the most representative population of COVID-19 cases reported between March, 1-14, 2020, the number of infected persons necessary to approach the required mortality rate was added to the correct values.

S.E.I.R Modelling

To obtain a more realistic trend and assuming true the probable "patients non-relapse", and we applied S.E.I.R. model to predict the virus progress in Italy. As a note, it is not possible to estimate the containment measures taken by the government. However, at the same time, assuming that only half of the population was susceptible to the virus precisely due to the above containment measures. Thanks to the comparison between real and theoretical evolution, it is likely to estimate the presence of essential mutations and/or the limitation strategy effectiveness through similarities, anomalies, or substantial deviations from each other. We used S.E.I.R. differential equations and non-linear methods to resolve the gaps analytically. An interactive algorithm was developed using C++ software (version) to find a solution through a finite discretization method. The total population number has been considered constant because of the very low deaths/population ratio.

Software iterative algorithm

By entering the initial values for the incubation time $1/\sigma$, recovery time $1/\gamma$, basic reproduction number R0, and number of infected I0 on March 1, 2020, the software prints the S.E.I.R. values

day by day. The best epidemic parameters were estimated through continuous iteration until the "closest values to the real ones" were reached until March 14, 2020. The number of initial incubates was calculated with the formula E0=R0·I0.

Results

Epidemic parameters

After the reconstruction of the real data on COVID-19 in Italy in the period March 2020, 1-14, through the above methods, the best estimates obtained for the Italian epidemic parameters are $1/\sigma = (3\pm1)$ days, $1/\gamma = (15\pm3)$ days, $R0 = 3.51 \pm 5\%$, $I0 = 3350 \pm 20\%$.

Best statistical forecasts

The model predicts the following values for the next 7 days (March 2020, 15-22) with "D " deaths number:

March, 15: $S = 2.99308 \cdot 10^{7}$; $E = 21504$; $I = 40651$; $R = 18854$; $D = 1904$;

March, 16: $S = 2.99207 \cdot 10^{7}$; $E = 23988$; $I = 45363$; $R = 21719$; $D = 2124$;

March, 17: $S = 2.99095 \cdot 10^{7}$; $E = 26759$; $I = 50619$; $R = 24917$; $D = 2417$;

March, 18: $S = 2.98970 \cdot 10^{7}$; $E = 29849$; $I = 56481$; $R = 28486$; $D = 2719$;

March, 19: $S = 2.98830 \cdot 10^{7}$; $E = 33293$; $I = 63019$; $R = 32467$; $D = 3056$;

March, 20: $S = 2.98674 \cdot 10^{7}$; $E = 37132$; $I = 70308$; $R = 36909$; $D = 3431$;

March, 21: $S = 2.98501 \cdot 10^{7}$; $E = 41410$; $I = 78437$; $R = 41865$; $D = 3850$;

March, 22: $S = 2.98307 \cdot 10^{7}$; $E = 47394$; $I = 87500$; $R = 47394$; $D = 4317$;

These values obviously refer to the population with the constant mortality rate of 3.2%; however, the real number of deaths must be strictly less than the theoretical one expected or we will talk about mutation. Thus, thanks to the results obtained from the application of the S.E.I.R. model we can foresee three possible scenarios: -If, in Italy, the real next-days trend of the total infected number will be lower than that shown in figure 1, we can assume the following events set out in order of probability: the containment measures adopted 10 days ago are taking effect; Sars-Cov-2 has undergone a significant anti-evolutionary mutation. If, in Italy, the real next-days trend of the total infected number will be equal than that shown in figure 1. We assume the following events set out in order of probability: the containment measures adopted 10 days ago are not taking effect; the containment measures adopted 10 days ago are taking effect and Sars-Cov-2 has undergone a significant evolutionary mutation. If, in Italy, the real next-days trend of the total infected number will be higher than that shown in figure 1. We assume the following events set out in order of probability: the containment measures adopted 10 days ago are not taking effect and Sars-Cov-2 has undergone a significant evolutionary mutation; the S.E.I.R model is no-more representative of the COVID-19 Italian case and we should utilize the S.E.I.R. model.

Comparison with real national and per provinces data

Based primarily on the deaths number i.e. data with the lower margin of error, we compare real and theoretical data [14]:

March Days	15	16	17	18
Real Deaths	1809	2158	2503	2978
Theorical Deahts	1904	2124	2417	2719
Difference (%)	-5,3	+1,6	+3,4	+8,7

Even considering an admissible "theoretical-estimates statistical error" of ± 5% these values could not be accepted since the trend indicates a faster growth than that predicted by the model with a breakeven point between 15 and 16 March and a percentage difference in net growth. Deepening the discussion and going to analyze the cases region by region, a very significant result turns out: with the exception of Lombardy, the trend in the number of infected is very good [18]. Unfortunately, this figure is extremely negative since it indicates the possible presence of a much more aggressive and/or contagious evolutionary mutation in Lombardy: in fact, the weight of Lombardy in the national statistics of total dead and infected is very high and, moreover, the slope of the growth curve of both it is much greater even than in the second region with the most infected. Quantifying, Lombardy went from 5791 cases on March 10 to 17713 on March 18, i.e. a slope of 1490 cases/day; Emilia Romagna, second region by growth and number of cases, has an average slope over the same period of time equal to 374 cases/day (1533 to 4525 cases). Going further, we can see how three cities in particular are causing alarm: Brescia, Bergamo and Milan, with similar angular coefficients. As if that were not enough, Lombardy holds 66% of national deaths despite representing "only" 49% of national cases; in addition, the number of Deaths and Infections grow at a rate much higher than the S.E.I.R. model, despite all government restrictions.

1. Choice of model

Given that

- It seems unlikely that the virus, without significantly changing, could infect a patient again [1,2] [12],

- the mortality rate in Italy is too low to be significant in the short term [8],

- young children appear to have a secondary role in the spread of the infection [8][17],

We will investigate the possible scenarios through S.E.I.R. model.

1.1   S.E.I.R. model: Italy's COVID-19 evolution

Using the discretization carried out in the previous study "Mathematical- statistical modeling of COVID- 19 on the restricted population" [8], a new C++ software was created to print the values of the S.E.I.R. day by day until a specific date and/or situation(2). However, unlike the aforementioned study, the prediction period will be extended to a certain number of days in order to verify the effectiveness of the containment measures in Italy.

2. Data analysis

Since no European or international standard for data collection has been established, one of the crucial points of this analysis is the interpretation of the information available. On February 27, in Italy, a real "communicative turnaround" was announced so that only the most important symptomatic cases would be publicly counted from then on [6]. Since there do not appear to have been significant large-scale mutations and that a good amount of data is now available, we expect the WHO mortality data to be valid in Italy as well [13] [Table 1].

The more recent study about Sars-Cov- 2 mortality on symptomatic and asymptomatic COVID-19 patients in the Hubei region shows the following Sars-Cov-2 mortality per age-groups [3] [Table 2].

Since the Italian population is distributed according to the following age-percentages [15][3] [Table 3]

$\Sigma i \ P \ i \cdot DR \ i \ / \ 100 = 3,2\%$

For this reason, it makes sense to conclude that the Italian COVID-19 death rate is exaggeratedly overestimated if we rely on Ministry of Health data. On the other side, the true-infect number (as the aforementioned "communicative turn" announced) must necessarily be higher. Trying to respect the percentage just calculated we obtain the following table 4.

3 Application of the S.E.I.R. predictive model

Citing the adapted system of non-linear differential equations and their discretization [8] and and using the WHO estimated values for incubation and recovery times respectively equal to $1/\sigma \in$ [3;6] days range[9] and a generous $1/\gamma \in$ [15;35] days range (since you can infect even after being healed [5]), with a R0 $\in$ [2;4] [7] [10] [4] we have the following plausible results from our C++ software:

$$S'(t) = \beta \cdot I \cdot S/N$$
$$E'(t) = \beta \cdot I \cdot S/N - \sigma E$$
$$I'(t) = \sigma E - \gamma I$$
$$R'(t) = \gamma I$$
$$N'(t) = 0$$
$$S_{i+1} = \beta \cdot I_i \cdot S_i/N_i \cdot \delta t + S_i$$
$$E_{i+1} = \beta \cdot I_i \cdot S_i \cdot \delta t + E_i$$
$$I_{i+1} = (\sigma \cdot E_i - \gamma \cdot I_i) \cdot \delta t + I_i$$
$$R_{i+1} = \gamma \cdot I_i \cdot \delta t + R_i$$
$$N_i = S_i + E_i + I_i + R_i$$

Legend:

- $1/\gamma$ is the asymptomatic incubation time;

- $1/\sigma$ is the recovery time;

- R0 is the basic reproduction number;

- *S* is the number of susceptible people;

- *E* is the number of active exposed people (people in incubation);

- *I* is the number of active infected people;

- *R* is the number of recovered people (no longer infectable).

- X_n is the number of day-n "X-category" people;

- X_t is the number of table 4 "X-category" people;

Significant Test-Collection 1

Assumptions: $1/\sigma \in [3;6]$ days, $1/\gamma = 35$ days, $R0 \in [3;4]$

Significant results: $I0 \in [5;8] \cdot 10^3 >> I0t = 2202$, $R14 \in [8;9] \cdot 10^3 >> R14t = 3327$.

Discussion

In order for the supposed data to be representative of reality, we should admit the existence of many more cases than expected. All this is consistent both with the idea the infection had been present on the territory for some time, in the form of a less aggressive strain, than with the time course of the disease [1]. The number of people healed is also in line with international percentages [16].

Validity grade: plausible and supported by empirical evidences.

Warning level: high.

Significant Test-Collection 2

Assumptions: $1/\sigma = 3$ days, $1/\gamma = 35$ days, $R0 = 6.05$.

Significant results: $I0 = I0t = 2202$, $R14 = 7169 >> R14t = 3327$.

Another possible scenario that describes the table 4 data. In this case the value of R0 would mean an extremely more aggressive/infective genetic mutation.

Validity grade: not excludable, but improbable.

Warning level: extremely high.

Significant Test-Collection 3

Assumptions: $1/\sigma = 3$ days, $1/\gamma = 15$ days, $R0 = 3.51$.

Significant results: $I0 = 3350 > I0t = 2202$, $R14 = 16219 >> R14t = 3327$.

Discussion: a third notable possible scenario that describes the table 4 infections. This latter case fits the estimated theoretical data almost perfectly and ranks first as a representative model.

Validity grade: very plausible and supported by empirical evidences.

Warning level: high.

3.1   Best Test forecast and graphs: Test 3

Since test 3 turned out to be the most likely, we focus on it.

Peak-day: 80.

Peak value: $Imax = 8.86694 \cdot 10^5$ people (almost 9 million people);

$I < 10 - $ day: 333 (almost one year);

$I = 0$ – day: 386.

We can also fit the curve through a convenient Gaussian $f(x) = y0 + Gauss(A,x0,\sigma)$ (x) function, useful for modeling the initial trend of the virus.

Conclusions

The model is approximate as a direct consequence of the uncertainty of the data it was supposed to fit but it can act as a valid comparison for the identification of any Sars-Cov-2 genetic mutations as well as for the evaluation of the containment measures effectiveness. Observed the comparison between the predictions of the S.E.I.R. and the actual trends highlighted above, as well as between the trends of Lombardy and the other Italian regions, there are valid reasons to assert that in Lombardy, in particular in the cities of Brescia, Bergamo and Milan, a very significant evolutionary mutation of the virus is taking place, which requires immediate containment.

Authors contribution

AR and ASB designed the study, collected the data, analyzed the data, prepared the manuscript. All the author read and approved the final manuscript.

Available data and materials: All the materials are attached as supplementary and information related to the study are in the manuscript.

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Competing interests: The authors declare that they have no competing interests.

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Table 1: Italy Ministry of Health March 2020, 1-14 official data [14].

March Day	Total Cases	Deaths	Recoveries	Active Cases	Recovery (%)	Death (%)
1	1101	41	83	977	7,5	3,7
2	1436	52	149	1235	10,4	3,6
3	1902	79	160	1663	8,4	4,2
4	2489	107	276	2106	11,1	4,3
5	3258	148	414	2696	12,7	4,5
6	4036	197	523	3316	13,0	4,9
7	5283	233	589	4461	11,1	4,4
8	6775	366	622	5787	9,2	5,4
9	8572	463	724	7385	8,4	5,4
10	10749	631	1004	9114	9,3	5,9
11	12462	827	1045	10590	8,4	6,6
12	15113	1016	1258	12839	8,3	6,7
13	17660	1266	1439	14955	8,1	7,2
14	21157	1441	1996	17720	9,4	6,8

Table 2: The more recent Hubei death-rate per age.

Age-groups (years)		Death Rate (%) = DR i
80 ++		18
70	– 79	9,8
60	– 69	4,6
50	– 59	1,3
40	– 49	0,4
30	– 39	0,18
20	– 29	0,09
10	– 19	0,02
0	– 9	0

Table 3: Italian population per age**.**

Age-groups (years)		Population (%) = P i
80++		7,2
70	79	9,9
60	69	12,2
50	59	15,5
40	49	15,3
30	39	11,7
20	29	10,3
10	19	9,6
0	9	8,3

Table 4: Recalculated Italian data of COVID-19 cases in March, 2020

March Day	Total Cases	Deaths	Recoveries	Active Cases	% Recovery	% Death
1	2202	41	166	1995	7,5	1,9
2	2872	52	298	2522	10,4	1,8
3	3804	79	320	3405	8,4	2,1
4	4978	107	552	4319	11,1	2,1
5	6516	148	828	5540	12,7	2,3
6	8072	197	1046	6829	13,0	2,4
7	10566	233	1178	9155	11,1	2,2
8	13550	366	1244	11940	9,2	2,7
9	17144	463	1448	15233	8,4	2,7
10	21498	631	2008	18859	9,3	2,9
11	24924	827	2090	22007	8,4	3,3
12	30226	1016	2516	26694	8,3	3,4
13	35320	1266	3166	30888	9,0	3,6
14	42314	1441	3992	36881	9,4	3,4
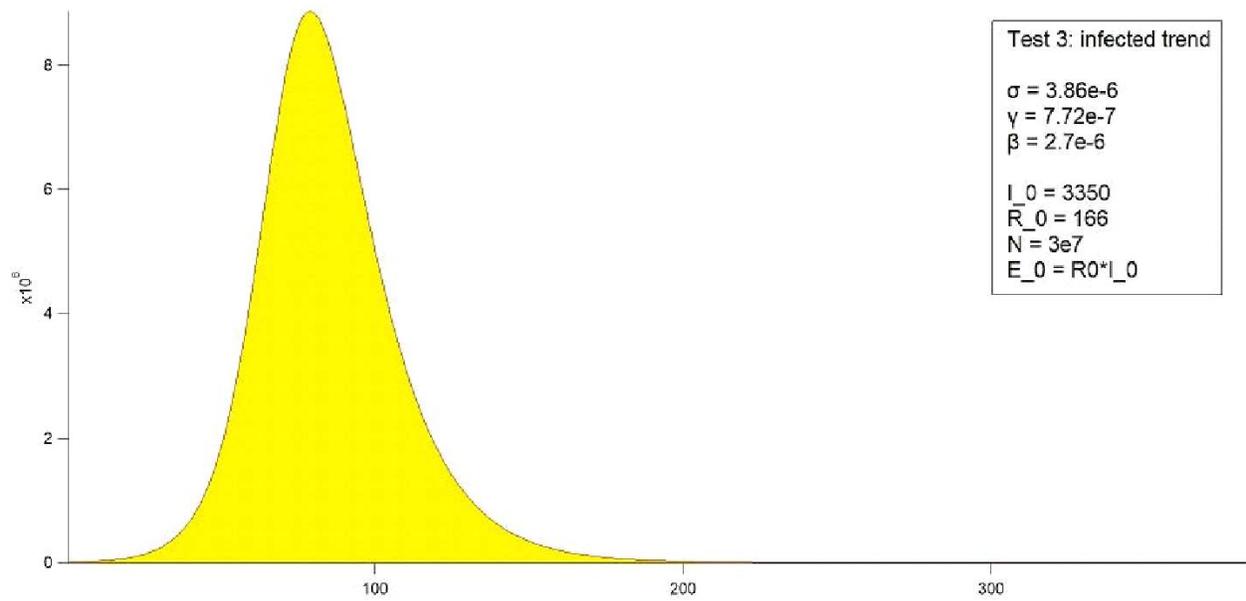
Figure 1: Test-3 – Italy infected trend.
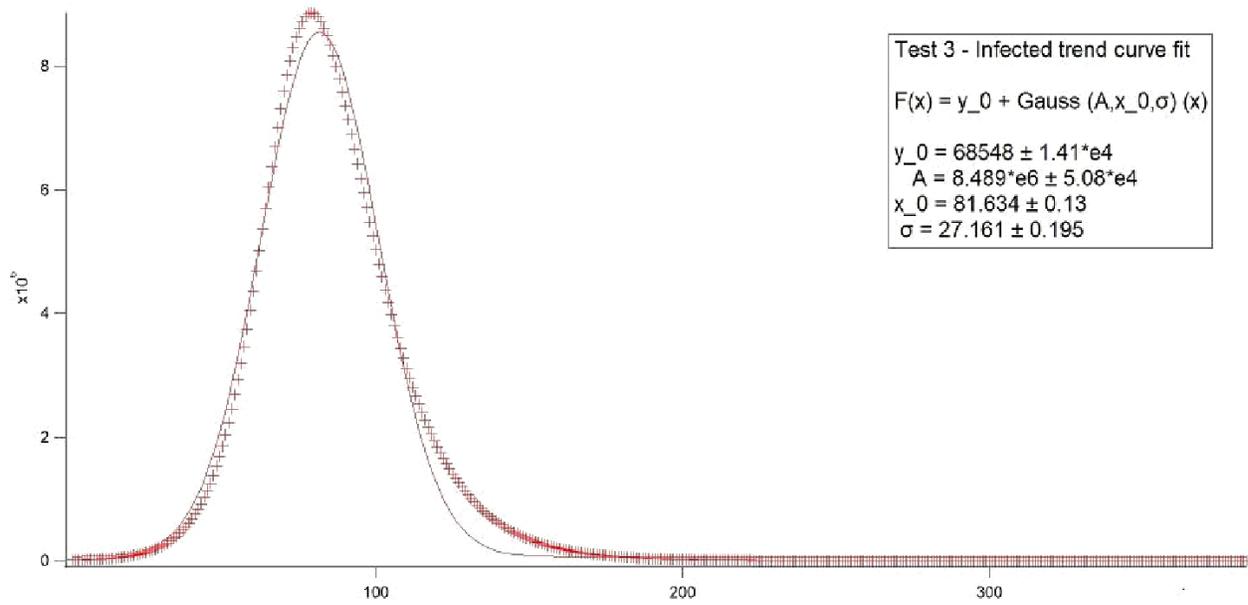
Figure 2: Test 3 – Italy infected trend, gaussian curve fit.