A Note on the Evolution of Covid-19 in Italy

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Abstract

We employ methods largely exploited in Physics, in the analysis of the evolution of dynamical systems, to study the pattern of the Covid-19 infection in Italy. The techniques we employ are based on the use of logistic function and of its derivative, namely the Hubbert function. The latter is exploited to give a prediction on the number of infected per day. We also mention the possibility of taking advantage from other mathematical tools based e.g. on the Gompertz equation and make some comparison on the different predictive capabilities.

1 Introduction

The Covid-19 Pandemia, which is worldwide raging, does not allow the development of multiple strategic defensive scenarios. Viruses are entering the human body, cause an infection and there is no available anti-virus drugs to contrast Covid-19.

The restriction of social contacts is therefore the only (hopefully) efficient mean to slow down the diffusion of the infectious disease, thus allowing the sanitary structures to operate without the pressure of an emergency stress.

We have therefore asked ourselves whether tools, borrowed from other disciplines, may be exploited as a predictive mean to understand how the number of Covid-19 infections increases with time, what is the maximum number of expected infections and when the rate of infections is expected to decrease.

In recent times the point of view, we are going to propose has been exploited for the understanding of bacterial growth [1] or of other mechanisms mediated

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by bacterial growth, such as global biogeochemical cycles \[2\], human gut health \[3\], wastewater treatment \[4\] or in totally different fields like cancer growth and metastasis dissemination \[5\] and in the physics of Free Electron Laser \[6\] as well.

In the following we will make use of the logistic function \[7\] and of its variants \[8\], to get a reasonable fit of the data provided by the Italian Department of health\[1\] and develop some previsions. Before getting into the specific details of the discussion, we give a short resume of the mathematical tools we will employ.

The logistic function (Fig. 1) describing the evolution of a given population \(N(\tau)\) is

\[
N(\tau) = N_0 \frac{e^{r\tau}}{1 + \frac{N_0}{K}(e^{r\tau} - 1)},
\]

where \(\tau\) is the time, measured in some units to be specified. Furthermore \(r\) and \(K\) accounts for the growth rate and the carrying capacity respectively. Regarding bacteria or viruses, \(K\) represents the maximum number of individuals which can be infected. In absence of an ad hoc developed infectious model it cannot be easily specified (see the concluding section for further comments), it (and \(r\) as well) will be inferred from the “experimental data”.

The logistic equation provides a good model for the exponential growth and it does include the so called saturation mechanism leading to the equilibrium, where the population saturates. It is the solution of the first order non-linear equation \[9\]

\[
\partial_\tau N = rN \left(1 - \frac{N}{K}\right)
\]

which states that the growth rate is not simply \(r\) but \(r \left(1 - \frac{N}{K}\right)\). The logistic curve describes the total number of infections and its derivative yields the number of infections per unit time, namely

\[
N'(\tau) = \frac{e^{r\tau}r \left(\frac{N_0}{1 - \frac{N_0}{K}}\right)}{\left(1 + \frac{1}{K} \left(\frac{N_0}{1 - \frac{N_0}{K}}\right)e^{r\tau}\right)^2} = \frac{e^{r\tau}rN_0(K - N_0)}{K \left(1 + \frac{N_0}{K}(e^{r\tau} - 1)\right)^2}.
\]

It is a bell shaped curve and it is known as the Hubbert curve, initially exploited as an approximation of the production rate of a resource over time \[10\]. The location of the peak depends on growth rate and carrying capacity according to the identity

\[
\tau^* = \ln \left(\sqrt{\frac{K}{N_0}} - 1\right).
\]

\[1\]Data taken from https : //lab24.ilsole24ore.com/coronavirus/.
At this time we find for the infected rate

$$N'(\tau^*) = \frac{rK}{4}$$

(5)

corresponding to a total number of infected

$$N(\tau^*) = \frac{K}{2}.$$  

(6)

The figures reported below yields a better idea of what has been worded so far.

In Fig. 1 we have shown the growth of infected individual $N(\tau)$ vs. the number of days ($\tau = 0$ has been arbitrarily chosen) for different values of the growth rate $r$ and for the same value of the carrying capacity $K$.

In Fig. 2 we have reported the Hubbert curve vs. $\tau$, for different values of $r$ and the same $K$. It is worth noting that, with decreasing $r$, the peak shifts towards larger $\tau$ values. We have fixed a threshold value the maximum rate that a health structure may care ($N'(\tau^*)$), the number of patients which cannot be treated is given by the total number of infected above this threshold ($\bar{N}$), namely

$$\Delta = N(\tau_+) - N(\tau_-),$$

$$\tau_{\pm} = \frac{1}{r} \ln \left\{ \frac{K - N_0}{2N_0N} \left[ rK - 2\bar{N} \pm \sqrt{rK(rK - 4\bar{N})} \right] \right\}$$

(7)

where $\tau_{\pm}$ are the times in which the Hubbert and threshold curves intercept.

In Fig. 3 we have reported the number $\Delta$ of patients potentially untreated vs $r$.

![Figure 1: Growth of infected individual vs. $\tau$ for $K = 300$ and different values of the growth rate $r$.](image)

This is the minimum Mathematica we need to start our discussion. Further information will be added once needed.
Figure 2: Hubbert curve vs. $\tau$ for $K = 300$ and different values of the growth rate $r$ and a hypothetical threshold rate.

Figure 3: Number of patients potentially untreated vs. $r$ for $K = 300$, $N = 1.5$, $N_0 = 1$.

2 Logistic Model and Covid-19 Data in Italy

In this section we apply the formalism of the previous section to the analysis of the behavior of the viral infection in Italy.

The starting point is the number of infected individuals per day, provided by the Italian Ministry of Health. The data are reported in Fig. 4 with the inclusion of the forecasting of the future trend, which foresees the saturation by the end of April.

It is evident that the plot in Fig. 4 is essentially the Hubbert curve and can be derived by a corresponding Logistic curve, as it shown in Figs. 5 where we have reported the number of infected/day. In Fig. 5 we make the comparison between the present model and that in Fig. 4. To make a correct comparison we have fitted the logistic function parameter using the data of the first 12 days.

\footnote{Data from \url{https://www.ilsole24ore.com/art/coronavirus-governo-stima-92mila-contagi-picco-18-marzo-ADfgS9C}.}
Figure 4: Real and foreseen number of infections per day from the beginning of the epidemic in Italy.

In Fig. 5b we have extended the fit to 23 days (red histogram) and included the prevision from the our model (blue histogram).

(a) Comparison between the present model (green histogram) and Fig. 4 (red).
(b) Comparison between Hubbert function and real data including 23 days of data.

Figure 5: Real and foreseen numbers of infection per day from the beginning of the epidemic in Italy.

The fit of the logistic function with the available data yields the plot in Fig. 6. It displays the evolution of the infection (number of positive individuals to Covid 19) vs. the number of days during which the morbidity has developed.

★ The zero day, coincides with that in which the number of positive cases has been started to be officially communicated.

★ The green dotted curve represents the evolution of the infected according to the official data, while the red continuous is the logistic fit. The agreement looks satisfactory.

★ The best fit procedure yields

$$N_0 = 294, \quad r = 0.2264, \quad K = 50346.$$  \hspace{1cm} (8)

The Hubbert curve, inferred from the data in Figs. 6 is shown in Fig. 7 in which the continuous and dashed curves are just the analytical derivatives of
the logistic functions, while the (noisy) black dashed curve is the increment of the data from public health ministry.

The conclusions we may draw are that, if we trust this model, the peak of the number of infected per day should be reached in the next few days and that a substantive decline could be experienced at the end of April.

It should be noted that being the baricenter of the data shifted towards those of “Regione Lombardia”, the extension of the previous conclusions to the rest of the Nation is not fully justified. In the next days we will presumably observe the impact of the lockdown restriction and have a better picture of its role on parameters like the growth rate $r$.

For further comments see the concluding section.

The number of positive cases around the peak is close to 3,000, if 10%
needs intensive cares, about 300 patient/per day are supposed to be allocated in health structures with limited resources. Further comments on these points will be given in the forthcoming section.

3 Final Comments

The model we have exploited is a simplification in many sense. It does not include all the elements of the SIR epidemic models of infections [11]. We considered infected only and we did not include the evolution of healed and mortality.

The logistic model seems to work in a reasonable way and, if further refined, may become a predictive tool. We must however underline that a sigmoid evolution curve and a bell shaped Hubbert form can be derived within different analytical frameworks. The most attractive alternative is the so called Gompertz model [8], based on the evolution curve

$$G(\tau) = \alpha e^{-\beta e^{-\gamma \tau}}.$$  \hspace{1cm} (9)

The analytical dependence on time is interesting for our purposes because it displays an exponential term, which simultaneously includes the growth rate and the saturation. Regarding the meaning of the parameters we note that

$$G_0 = G(0) = \alpha e^{-\beta}, \quad \lim_{\tau \to \infty} = \alpha.$$  \hspace{1cm} (10)

We recognize $\alpha$ as the carrying capacity so that

$$\alpha = K, \quad \beta = -\ln \left( \frac{G_0}{K} \right).$$  \hspace{1cm} (11)
and eventually, with $N_0 = G_0$, we can write Eq. (9) as

$$N(\tau) = G(\tau) = K \left( \frac{N_0}{K} \right) e^{-\gamma \tau}$$

(12)

If we keep $N_0$ and $K$ the same as those predicted by the Logistic model and derive $\gamma$ from the data, we can evaluate the corresponding Hubbert curve, as reported in Figs. 6 in which we have made a comparison with the logistic case.

The most remarkable difference is that the Gompertz-Hubbert curve is more asymmetric and wider than the Logistic counterpart, this behavior seems more similar to the case reported in Fig. 4 (which is also the result of a computational model). The drawback is that the two models predict different values of the peaks which, by using parameters from Eq. (8), in the case of the logistic is

$$\text{max}(N'(\tau)) = 2850 \quad \text{reached at } \tau^* = 23,$$

(13)

and of the Gompertz

$$G'(\tau) = \alpha \beta \gamma e^{-\gamma \tau} e^{-\beta e^{-\gamma \tau}} = -\gamma \ln \left( \frac{N_0}{K} \right) e^{-\gamma \tau} G(\tau)$$

(14)

is

$$\text{max}(G'(\tau)) = 1648 \quad \text{reached at } \tau^*_G = 18, \quad \tau^*_G = \frac{1}{\gamma} \ln \left( \ln \left( \frac{K}{N_0} \right) \right)$$

(15)

where

$$G(\tau^*_G) = K \left( \frac{N_0}{K} \right) \left( \ln \left( \frac{N_0}{K} \right) \right)^{-1},$$

$$G'(\tau^*_G) = -K \gamma \ln \left( \frac{N_0}{K} \right) \left( \frac{N_0}{K} \right) \left( \ln \left( \frac{N_0}{K} \right) \right)^{-1} \left( \ln \left( \frac{K}{N_0} \right) \right)^{-1}.$$ (16)

The conclusions we can draw confirm essentially what we have underscored in the previous section, with the caveat that the data are referring to the whole national territory, in which the infection is proceeding in a non homogeneous way.

Our analysis is strongly influenced by the growth of the disease in Lombardia (and more in general in the north of Italy). The evolution in the national territory might qualitatively reproduce that reported in Fig. 9 which refers to the world-wide landscape. The growth of the disease in other regions, owing to the lockdown, may follow a different pattern. We can foresee a kind of saturation and then a resurgence at lower increasing rate, if the government prescription are duly observed. In qualitative terms we may observe the same bi-logistic behavior \[12\], with China replacing the north of Italy and the superimposed plot
yielding the diffusion in the rest of Italy. In a forthcoming note we will analyze the evolution per individual region.

We must finally stress that the spatial diffusion of the disease, not contained in the present analysis, requires the use of models including non-linear Fisher type evolution equations [13, 14], which will be touched in forthcoming studies.

![Figure 9: World wide evolution of the disease. The pedestal of the evolution is a logistic type curve, representing the spread in China. After a certain time lag the epidemic has propagated in the rest of the world, starting a second logistic behavior (data from Johns Hopkins CSSE,WHO, CDC, NHC and DINGXIANGYUAN).](image)

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