Dynamics of the COVID-19 Comparison between Theoretical Predictions and Real Data

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April 14, 2020

Abstract

A new coronavirus, called COVID-19, appeared in the Chinese region of Wuhan at the end of last year; since then the virus spread to other countries, including most of Europe. We propose a differential equation governing the evolution of the COVID-19. This dynamic equation also describes the evolution of the number of infected people for 13 common respiratory viruses (including the COVID-19). We validate our theoretical predictions with experimental data for Italy and Belgium, and compare them with the predictions of the logistic model. We find that our predictions are in good agreement with the real world since the beginning of the appearance of the COVID-19; this is not the case for the logistic model that only applies to the first days. We use our differential equation parametrised with experimental data to make several predictions, such as the date when Italy and Belgium will reach a peak number of COVID-19 infected people.

1 Introduction

Viral infections usually affect the upper or lower respiratory tract. Although respiratory infections can be classified according to the causative agent (e.g. the flu), they are mostly clinically classified according to the type of syndrome (e.g., common cold, bronchiolitis, laryngo-tracheo-bronchitis acute, pneumonia). Although pathogens typically cause characteristic clinical manifestations (e.g., rhinovirus causes the common cold, respiratory syncytial virus [RSV] usually causes bronchiolitis), they can all cause many of the most common respiratory syndromes. The severity of viral respiratory disease is highly variable; serious illness is more frequent in elderly patients and young children. Morbidity can

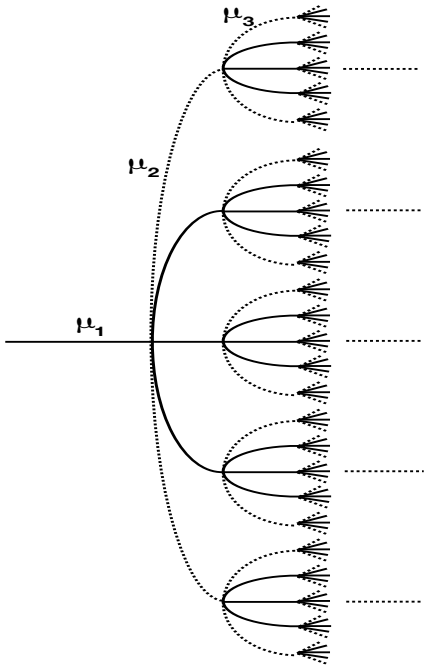

Figure 1: *Schematic dynamics of respiratory virus in the absence of the lockdown measures* (for simplicity, we illustrate the case $R = 5$) After a period of time μ_1, an infected individual is able to infect R individuals. In turn, after a period μ_2, each of them will be able to infect other R people and so on. After n steps the elapsed time is $t = \sum_{i=1}^{n} \mu_i$.

either directly result from the infecting agent, or may be indirect. The latter case can be due to the exacerbation of an underlying cardiopulmonary disease, or a bacterial superinfection of the lung, paranasal sinuses, or middle ear. The main motivation of this work is to verify, by making theoretical predictions, that political decisions are truly effective to minimise the number of infected people in order to (i) not overload local health services (such as hospitals), and to (ii) gain time to allow research institutes to deliver vaccines or the anti-virals.
Tables (1) and (2) respectively provide the experimental data for Italy [2] and for Belgium [3], [4]. They show the number of active people (i.e., people currently infected by COVID-10), the recovered people, and deaths for COVID-19.
We start our theoretical analysis by introducing the definition of R, defined as *the ability of an individual, infected by a virus, to transmit the infection to other individuals on his turn, in the absence of lockdown measures.* This parameter is strictly linked to the *replication time of a virus*, indicated with μ_i, defined as *the time interval after which the number of infected people has increased by R times.* Fig. 1 schematically represents the diffusion dynamics of the virus. By

indicating with N the number of infected people, after n steps we get:

$$N = R^n \tag{1}$$

Of course, after n steps, the elapsed time is $t = \sum_{i=1}^{n} \mu_i$ and, if there are M outbreaks of infectious viruses, Eq. (1) can be cast into the form[1]

$$N = MR^{t/<\mu>} \tag{2}$$

with $<\mu>$ indicating the *average replication time of a virus* $<\mu>= 1/n \sum_{i=1}^{n} \mu_i$. It is more convenient to work in the Euler base e rather than in base R; in the Euler base Eq. (2) provides the *law of growth of a Malthusian population*

$$N = M \exp(t/\tau) \quad \text{where} \quad \tau = \frac{<\mu>}{\log(R)} \tag{3}$$

In literature, τ refers to as the *characteristic time of the exponential trend*. So, in the absence of containment measures the number of infected people follows the exponential law (3). Let us now analyse Eq. (3) in more dept; there are three possible scenarios:

1. $R > 1$ (as is the current world's situation). For Italy, for example, before the adoption of (severe) containment measures, the value of τ was about $\tau \sim 3.88$ days (and $\mu \sim 2.6$ days). In this case the number of the infected people increases exponentially.

2. $R = 1$ If the infection-capacity of the virus is of the type *one-to-one* (i.e., a person infected by COVID-19 can in turn infects only another person), we get the stationary situation corresponding to $N = 1$. This situation is referred to as the *latent situation* i.e., the virus is still present but does not spread. In this limit case, the COVID-19 is substantially ineffective. Scenarios (1) and (2) are illustrated in Fig. 2.

3. $0 < R < 1$. We may also imagine that the capacity of infection of COVID-19 is less than 1. This means that the virus is no longer able to be spread (e.g., thanks to protective measures, or to the production of vaccines and anti-virals, or because people who overcame the disease became auto-immune. In this case, the value of R is negative and the number of infected people decreases ever time. That is, the infection eventually disappears. The rate of decrease of the number of infected people depends on the value of τ. This scenario is depicted in Fig. 3.

[1] Actually, Eq. (2) applies only if the M outbreaks of the virus are exactly at the same conditions. In general, the correct expression reads $N = \sum_{i=1}^{M} R^{t/<\mu>_i}$, with $<\mu>_i$ indicating the average replication time of the virus for the *i-th* outbreak.

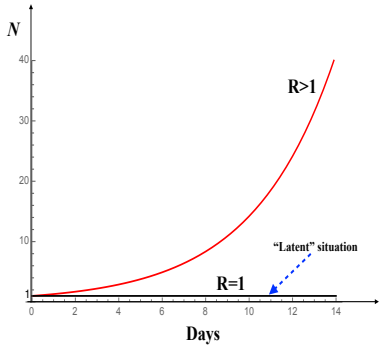

Figure 2: *Situation before the lockdown measures*. Number of infected people corresponding to the exponential law. The red line represents the case $R > 1$, such as the situation before the adoption of lockdown measures. The black line corresponds to the case $R = 1$, the *latent situation* in which the virus is substantially ineffective.

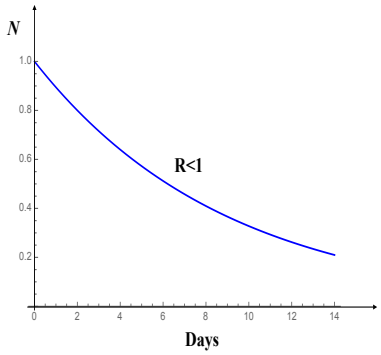

Figure 3: Number of infected people corresponding to the exponential law. The blue line represents the case $R < 1$. In this situation the number of infected people decreases exponentially and the virus disappears after a few weeks.

1.1 Comparison with the Real Data for COVID-19 before the Lockdown Measures

It is understood that the main objective of the lockdown measures established by most European governments and health organisations is to reduce the ability of a virus to spread. From a mathematical point of view, we would like to have $R = 1$ (or, better, $R < 1$), in Eq. (3) instead of $R > 1$. In practical terms, this means reducing the frequency of all involuntary contacts with a large number of people, reducing unnecessary movements to avoid encounters, and to prolong the closure of schools. Although these measures cannot prevent the spread of the infection in the long term, they can reduce the number of new infections daily. This has the benefit of leaving room for seriously-ill patients by avoiding to overload the healthcare system. We can easily realise what are the consequences if the lockdown measures are not set up. To make a comparison between the theoretical predictions and the experimental data in absence of lockdown measures, we have to consider the correct reference period. More specifically, we saw that the number of positive cases grows over time by following the law (3). Hence, at the reference time t_0, the number of people infected by the virus is

$$N_0 = M \exp(t_0/\tau) \tag{4}$$

After a period of time, say t, Eq. (3) reads

$$N = M \exp(t/\tau) \tag{5}$$

Hence,

$$N = N_0 \exp((t - t_0)/\tau) \tag{6}$$

Eq. (6) is the equation that we use for comparing the mathematical predictions with experimental data during the initial phase where the spread of COVID-19 follows the exponential law, and $(t - t_0)$ is our *reference period*. E. Bucci and E. Marinari have assumed that for the case of COVID-19 [1]

- All infectious outbreaks are exactly at the same conditions. So, Eq. (2) applies;
- All the μ_i are equal with each other: $\mu_1 = \mu_2 = \cdots = \mu_n = const.$ So, $< \mu >= const. \equiv \mu$;
- $R = 2$.

In this case, μ is referred to as the *doubling time*. E. Bucci and E. Marinari compared their theoretical assumptions with the real data for Italy, and they confirmed their brilliant intuition by showing that, if we do not apply the locking measures, the evolution over time of the number of infected people is best approximated by an exponential curve with $R = 2$ and a doubling time close to $\mu \simeq 2.6$ days. Fig. 4 and Fig. 5 respectively show the comparison between the theoretical predictions and the experimental data for Italy and Belgium before the lockdown measures. We get $\tau \simeq 3.88$ and $\mu \simeq 2.6$ for Italy, and $\tau \simeq 4.36$ and $\mu \simeq 3.0$ for Belgium.
The paper is organised as follows. Section (2) determines the dynamic differential equation for the COVID-19; Section (3) compares the theoretical predictions and experimental data for Italy and Belgium; and Section (4) concludes.

2 Modelling the COVID-19 growth

The objective of this section is to determine the coefficients of the evolutionary differential equation for the COVID-19 (see the forthcoming Eq. (13)). We also determine the generic analytical expression for the time-dependent number of infected people through fitting techniques validated by the χ^2 tests. This expression can be proposed for 13 respiratory infectious diseases caused by viruses (including the COVID-19), in addition of being solution to the Richard's differential equation.

2.1 General background

Letting N represent population size and t represent time, this model is formalised by the differential equation below:

$$\frac{dN}{dt} = \alpha N\Big(1 - \frac{N}{K}\Big) \tag{7}$$

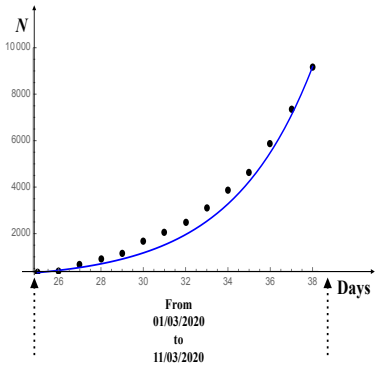

Figure 4: *Number of infected people in Italy on the 10th of March 2020 (before the adoption of lockdown measures).* The blue line corresponds to the theoretical predictions and the black dots correspond to experimental data. The values of the parameters τ and μ are $\tau \simeq 3.88$ and $\mu \simeq 2.6$.

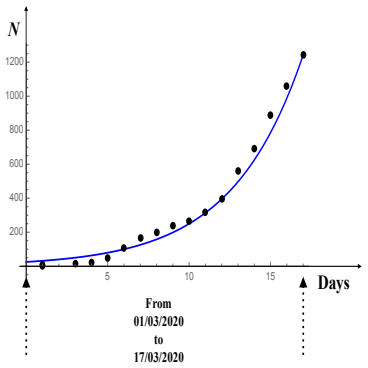

Figure 5: *Number of infected people in Belgium on the 16the of March 2020 (before the adoption of lockdown measures).* The blue line corresponds to the theoretical predictions and the black dots correspond to experimental data. The values of the parameters τ and μ are $\tau \simeq 4.36$ and $\mu \simeq 3.0$.

where $\alpha > 0$ defines the *grow rate* and $K > 0$ is the *carrying capacity*. In this equation, the early, unimpeded growth rate is modelled by the first term $+\alpha N$. The value of the rate α represents the proportional increase of the population N in one unit of time. Later, as the population grows, the modulus of the second term (which multiplied out is $-\alpha N^2/K$ becomes almost as large as the first, as some members of the population N interfere with each other by competing for some critical resource, such as food or living space. This antagonistic effect is called the *bottleneck*, and is modelled by the value of the parameter K. The competition diminishes the combined growth rate, until the value of N ceases to grow (this is called *maturity of the population*). The solution to the Eq. (7) is

$$N(t) = \frac{K}{1 + B\exp\left(-\tau t\right)} \tag{8}$$

where $B > 0$ is a constant related to the value of $N(0)$. It is more convenient to rewrite Eq. (8) in terms of the *initial Logistic time* t_{0L} defined as

$$t_{0L} = \frac{1}{\tau}\log B \tag{9}$$

So, Eq. (8) may be cast into the form

$$N(t) = \frac{K}{1 + \exp\left(-\tau(t - t_{0L})\right)} \tag{10}$$

Since the environmental conditions influence the carrying capacity, as a consequence it can be time-varying, with $K(t) > 0$, leading to the following mathematical model:

$$\frac{dN}{dt} = \alpha N\Big(1 - \frac{N}{K(t)}\Big) \tag{11}$$

More generally, the growth modelling is well described by Richards' differential equation (RDE) (also known as the *Generalised logistic differential equation*)

$$\frac{dN}{dt} = \alpha N\Big(1 - \Big(\frac{N}{K(t)}\Big)^{\nu}\Big) \tag{12}$$

where $\nu > 0$ affects near which asymptote maximum growth occurs. Now, let us suppose that the Government decides to adopt the lockdown measures. If these lockdown measures start with a log-kill effect, the equation may be revised to be

$$\frac{dN}{dt} = \alpha N\Big(1 - \Big(\frac{N}{K(t)}\Big)^{\nu}\Big) - c(t)N \tag{13}$$

where $c(t)$ takes into account the mortality rate of COVID-19, induced by the locking measures and, albeit in a small percentage, also the decreased carrying capacity $K(t)$ of the COVID-19 due to the deceased.

2.2 Determination of $K(t)$ and $c(t)$ for the COVID-19

According to Prof. Roberto Ronchetti[2] *Respiratory viruses remain quiet for months, inactive but viable, within living cells. Then suddenly they activate and become virulent as they say, the infectious capacity grows to a maximum, after which it decreases. The time duration, explains R. Ronchetti, is about of 2 or 3 months. So we can expect that the epidemic will soon die out in Italy too. So, there is no valid reason to think that this coronavirus behaves differently from others* [6]. The present work starts from the following hypothesis: *the COVID-19 behaves exactly like the other viruses that cause respiratory diseases.* As a consequence, for the COVID-19 case, functions $K(t)$ and $c(t)$ are determined by performing several *fittings* on the growth rate-trends of infection capacity of the viruses that mainly affect the respiratory system. More specifically, we considered the following 13 different diseases caused by 12 different viruses: *Whooping Cough (Pertussis)*, *Swine Flu (H1N1)*, *Bird Flu (Avian Flu H5N1)*, *Enterovirus*, *Flu in Children*, *Flu in Adults*, *Bacterial Pneumonia*, *Viral Pneumonia*, *Bronchitis*, *Common Cold (Head Cold)*, *Severe acute respiratory syndrome (SARS)*, and *MERS (Middle East Respiratory Syndrome)*. In all the examined cases, we took into account the fact that the therapy-induced death rate is greater than the baseline proliferation rate, then there is the eradication of the disease. In

[2]Prof. Roberto Ronchetti is currently working at the Pediatric Clinic of *La Sapienza* of the University of Rome, at the *Policlinico Umberto I* and at the *S. Andrea 24 MarchHospital* where he helped to found, dealt with childhood respiratory diseases, and studied bronchiolitis in particular. In these days he has studied (with his collaborators) the data available on SARS-Covid-19 in China, in South Korea and now in Italy.

other words, the function $c(t)$ in Eq. (13) represents the therapy-induced death rate [7]-[14]. Of course, this is an oversimplified model of both the growth and the therapy (e.g., it does not take into account the phenomenon of clonal resistance). We empirically noticed (according to the χ^2 test) that all these viruses have in common the same growth rate-trend of infected people (of course, each of these behaviours have their own growth rate parameters). In particular, we noticed that the trends of the infected people by respiratory viruses versus time follow the function

$$N = At\exp(-(t-t_0)^2/\sigma) \tag{14}$$

where the values of parameters A, t_0 and σ depend on the virus in question and on the external conditions (e.g., the lockdown measures) to which the population is subject. It is not difficult to check that Eq. (14) is a particular solution of the differential equation (13) where

$$\nu = 1; \quad \alpha = \frac{2t_0}{\sigma}; \quad K(t) = \frac{2A}{t_0}t^2; \quad c(t) = \frac{2t^2-\sigma}{\sigma t} - \frac{t_0^2}{\sigma t}\exp(-(t-t_0)^2/\sigma) \tag{15}$$

Finally, the dynamic differential equation for the COVID-19 can be brought into the general form

$$\frac{dN}{dt} = \alpha N\Big(1 - \frac{N}{\eta t^2}\Big) - \left(\frac{2\lambda t^2 - 1}{t} - \frac{\lambda t_0^2}{t}\exp\big(-\lambda(t-t_0)^2\big)\right)N \tag{16}$$

and expression (14) is solution of the RDE in presence of the lockdown measures. According to the literature nomenclature, we shall refer differential equation (16) to as *COVID-19 dynamic model*[3]. The *average replication time of a virus* $<\mu>$ is defined as

$$<\mu> \equiv \frac{(t-t_0)\log(R)}{\log(N/N_0)} \tag{17}$$

where N is solution of Eq. (16). Notice that λ is linked to $<\mu>$. Indeed, as shown in Section 1, the COVID-19 grows according to the law (see Eq. (6)) during the exponential period:

$$\frac{dN}{dt} \simeq \tau^{-1}N \tag{18}$$

Hence, we get

$$\lambda \simeq \frac{1}{2t_0\tau} = \frac{\log(R)}{2t_0 <\mu>} \tag{19}$$

The curves reach the peaks at the time $t_{\max}$ given by the expression

$$t_{Max} = \frac{1}{2}\left(t_0 + (t_0^2 + 2/\lambda)^{1/2}\right) \tag{20}$$

By summarising, the ascending behaviour of the total number of infected people by COVID-19 (i.e., the number of of positive cases plus the cumulative number

[3]Viral dynamics is a field of applied mathematics concerned with describing the progression of viral infections within a host organism (see, for example, [15].)

of healed people plus the cumulative number of deaths) is given by the solution of Eq. (16) for $0 \leq t \leq t_{Max}$.
It is also worth noticing that for large values of time Eq. (16) simply reads

$$\frac{dN_p}{dt} = \alpha N_p \left(1 - \frac{N_p}{\eta t^2}\right) - 2\lambda t N_p \tag{21}$$

with N_p indicating the number of positive cases. Eq. (21) may be used to study the descent-phase for the number of people infected (positive cases) by COVID-19.

2.3 Behaviour of the function $c(t)$

In this Section we deal with the COVID-19 for Italy and Belgium. So, from now on, we set $R = 2$ and $< \mu >= \mu = const.$ in our expressions. As we will see in Section (3), λ and t_0 are of the order of $\lambda \simeq 10^{-3}$ days^{-2} and $t_0 \simeq 10$ days for Italy and Belgium, respectively. In particular, we found $\lambda_{IT} = 0.00263$ days^{-2}, $t_{0IT} = 70.6$ days and $\lambda_{BE} = 0.00185$ days^{-2}, $t_{0BE} = 48$ days. Hence $c(t)$ is of the order of 10^{-1} days^{-1}. Fig. 6 and Fig. 7 show the behaviours of the functions $c(t)$ for Italy and Belgium, respectively. As we can see, the

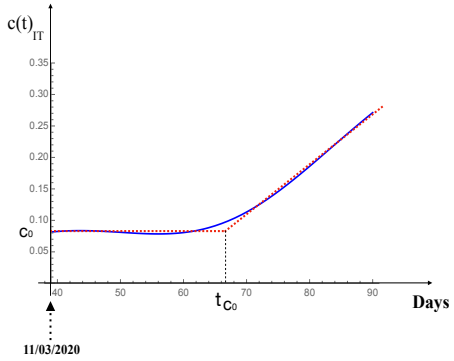

Figure 6: *Mortality rate of COVID-19 induced by the locking measures for Italy.* $c(t)$ is almost constant until t_{c_0}. After t_{c_0} it starts to grow linearly, with slope 2λ, over time.

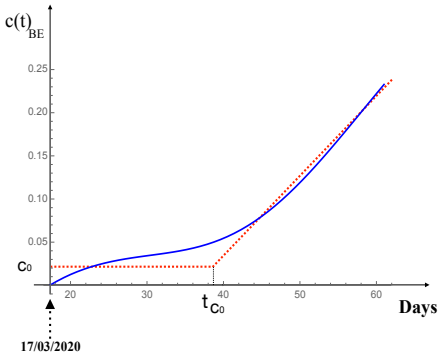

Figure 7: *Mortality rate of COVID-19 induced by the locking measures for Belgium.*

mortality rate $c(t)$ is almost constant in the first days after the application of the lockdown measures, and successively it grows, almost linearly - with slope $\sim 2\lambda$, over time. In other words, over time, the contribution of $c(t)$ becomes more and more relevant. In brief,

$$\begin{aligned} c(t) &\simeq c_0 > 0 \qquad \text{for} \quad t_{LM} \leq t \leq t_{c_0} \\ c(t) &\simeq 2\lambda t \qquad \text{for} \quad t > t_{c_0} \end{aligned} \tag{22}$$

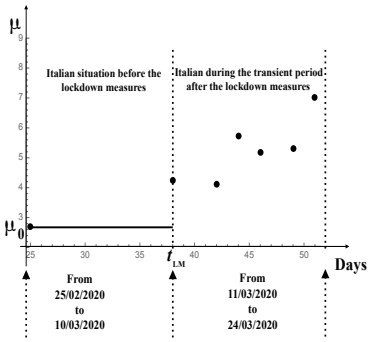

Figure 8: *Italian transient period (from the 10th of March 2020 to the 24th of March 2020).* During this period, the doubling time μ oscillates over time. μ_0 indicates the (constant) doubling time during the exponential period (for Italy $\mu_0 \simeq 2.6$ days).

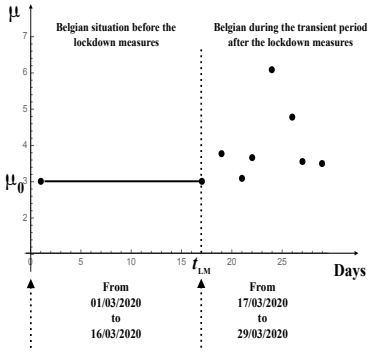

Figure 9: *Belgian transient period (from the 17th of March 2020 to the 29th of March 2020).* During this period, the doubling time μ oscillates over time. μ_0 indicates the (constant) doubling time during the exponential period (for Belgium $\mu_0 \simeq 3.0$ days).

with t_{LM} and t_{c_0} indicating the *time when the lockdown measures are applied* and the *time when function $c(t)$ starts to grow linearly over time starting from the constant value c_0*, respectively.

3 Comparison between the Theoretical Predictions and Experimental Data

For Italy and Belgium we observed three phases related to the dynamics of the COVID-19, which we classify as follows:

1. The *exponential period*. As seen in Section 1, before the application of lockdown measures, the *exponential trend* is the intrinsic behaviour of the grow rate of the COVID-19. In this period the doubling time μ is a *constant parameter* versus time.

2. The *transient period*. The transient period *starts* after having applied the severe lockdown measures. In this period we observe a sort of oscillations (or fluctuations) of μ versus time. Fig. 8 and Fig. 9 show the behaviour of the parameter μ versus time for Italy and Belgium, respectively. The transient period *ends* when the last step of the exponential trend fits real data as good as the linear trend[4].

[4] A numerical condition may be established by using the χ^2 test: the fittings of the two trends are considered both *good* if, for example, for both trends, the χ^2-tests get values ≥ 0.9.

3. The *bell-shaped period* (or the *post-transient period*). In the bell-shaped period parameter μ is a (typical) function of time, given by Eq. (17) and Eq. (16). Several theoretical models can be used to study the post-transient period (e.g., by using Gompertz's law). Here, we use two mathematical models: the solution of the differential equation (16) and the *logistic model* (see, for example, ref. [5]), and we compare these two theoretical models with real data for Italy and Belgium.

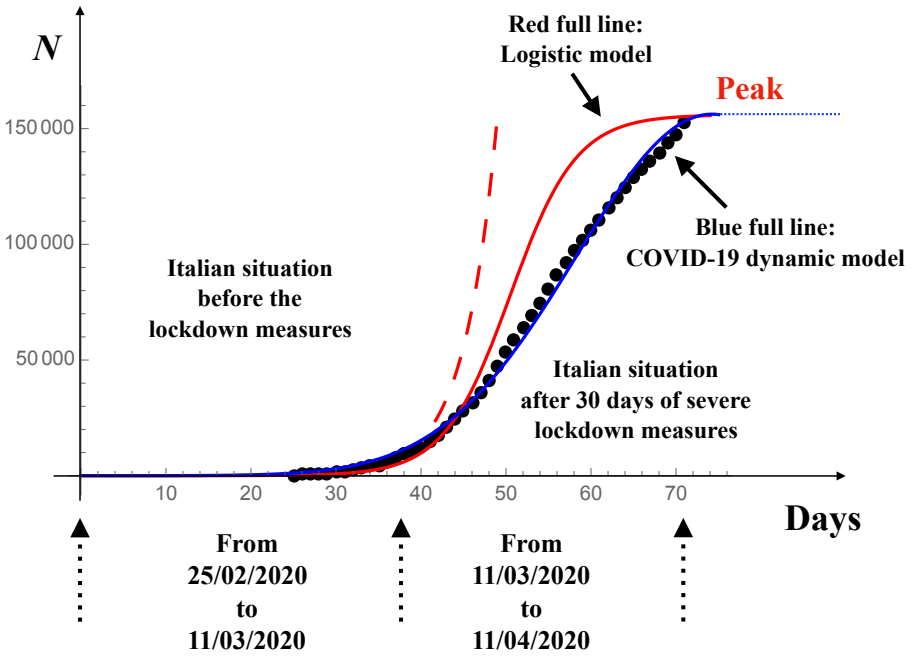

Figure 10: *Situation in Italy on 11 April 2020—before and 30 days after the adoption of lockdown measures.* The black dots correspond to experimental data. The blue dotted line corresponds to the situation in Italy before the adoption of the lockdown measures. The blue and the solid lines, in the zone II, correspond to the theoretical predictions for Belgium according to the solution of Eq. (16) and the logistic model, respectively. Solution of Eq. (16) fits well all the experimental data from the initial days (i.e., from the 1st of February 2020), while the logistic model applies only to the first days. The values of the parameters of Eq. (16) and the logistic function (10) are: $\alpha_{IT} \simeq 0.261$ days^{-1}, $\lambda_{IT} \simeq 0.00185$ days^{-2}, $\eta_{IT} \simeq 61.10$ days^{-2} and $t_{0IT} \simeq 70.6$ days for Eq. (16), and $t_{0LIT} \simeq 50.5$ days and $K_{IT} \simeq 156000$ for the Logistic function, respectively.

Fig. 10 and Fig. 11 respectively compare the theoretical predictions, with the experimental data for Italy and Belgium updated to the 11th of April 2020. The values of the parameters α, η, λ and t_0 for Eq. (16) and the parameters

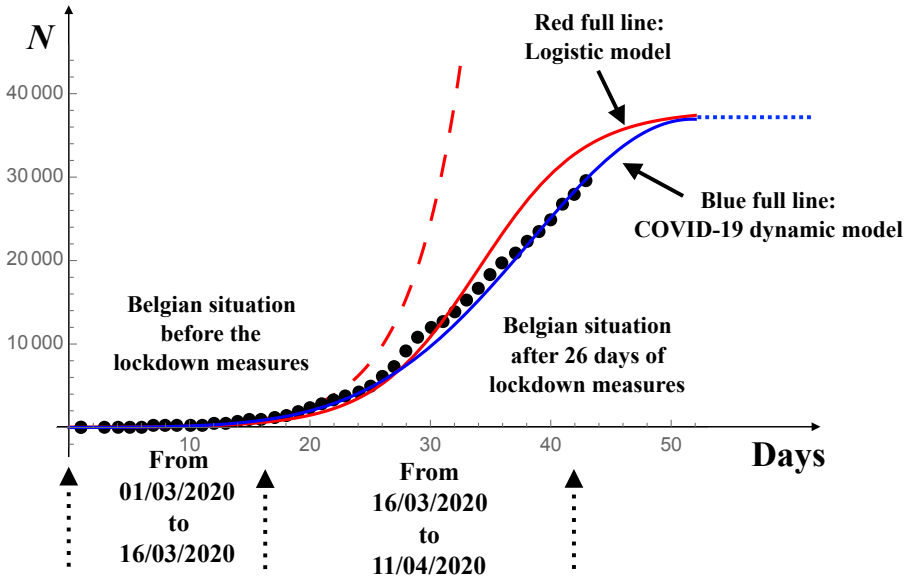

Figure 11: *Situation in Belgium on 11 April 2020—before and 26 days after the adoption of lockdown measures.* The black dots correspond to real data. The blue dotted line corresponds to the situation in Belgium before the adoption of the lockdown measures. The blue and the red solid lines, in the zone II, correspond to the theoretical predictions for Belgium according to the solution of Eq. (16) and the logistic model, respectively. Solution of Eq. (16) fits well all the experimental data from the initial days (i.e., from the 29th of February 2020), while the logistic model applies only to the first data. The values of the parameters of Eq. (16) and the logistic function (10) are: $\alpha_{BE} \simeq 0.245$ days^{-1}, $\lambda_{BE} \simeq 0.00255$ days^{-2}, $\eta_{BE} \simeq 30.83$ days^{-2} and $t_{0BE} \simeq 48$ for Eq. (16), and $t_{0LBE} = 34$ days and $K_{BE} = 38000$ for the Logistic function, respectively.

t_0 and K for the Logistic function are reported in the figure captions. As we can see, for both Countries Eq. (16) fits well all the real data from the initial days, while the logistic model applies only to the first data. The theoretical predictions seem to confirm that Italy reaching the *plateau* while Belgium is in the *bell-shaped* period. The curves reach the peaks at the time t_{Max} given by Eq. (20). By inserting the values of the parameters, we get

$$t_{MaxIT} \simeq 68 \text{ days} \quad \text{and} \quad t_{MaxBE} \simeq 53 \text{ days} \tag{23}$$

corresponding to $t_{MaxIT} \simeq 8$ April 2020 and $t_{MaxBE} \simeq 22$ April 2020 for Italy and Belgium, respectively.

4 Conclusions

This work proposed the differential equation governing the evolution of the COVID-19. Through fitting techniques previously performed and validated by the χ^2-tests, we proposed a general analytical expression and a three-free parameters function (see Eq. (14)) providing the number of people infected by respiratory viruses over time. We showed that this expression is solution of the Richard's differential equation subject to the adoption of lockdown measures. The differential equation (16) can be proposed for 13 respiratory infectious diseases caused by viruses, including the COVID-19. Successively, we compared the theoretical predictions, provided by the solution of Eq. (16) and by the logistic model (see Eq. (8)), with the real data for Italy and Belgium. We saw that the solution of Eq. (16) is in good agreement with the experimental data since the beginning of the appearance of the COVID-19; this is not the case for the logistic model which applies only to the few last days. We found the days where the maximum number infected people by COVID-19 will be reached in Italy and Belgium by parametrising the solution of Eq. (16) with experimental data: we get, $t_{MaxIT} \simeq 15$ April 2020 and $t_{MaxBE} \simeq 21$ April 2020 for Italy and Belgium, respectively.
We also noted, empirically, that the infection process by COVID-19 may be divided into three qualitatively different periods; i.e., the *exponential period*, the *transient period* and the *bell-shaped period* (or the *post-transient period*). The solution of Eq. (16) allows defining more precisely these three periods. Indeed, we may classify the above periods as follows

$$\begin{array}{ll} \text{The exponential period} & \text{for} \quad 0 \leq t \leq t_{LM} \\ \text{The transient period} & \text{for} \quad t_{LM} < t \leq t_{flex} \\ \text{The bell-shaped period} & \text{for} \quad t > t_{flex} \end{array} \tag{24}$$

with t_{flex} denoting the *inflection point of the solution of* Eq. (16). It is easily checked that the value of t_{flex} satisfies the following equation

$$2\lambda t_{flex}^3 - 4\lambda t_0 t_{flex}^2 + (2\lambda t_0^2 - 3)t_{flex} + 2t_0 = 0 \tag{25}$$

Hence, according to Eq. (25), the *transient period* ended on 31 March 2020 for Italy and on 7 April 2020 for Belgium, respectively.

5 Acknowledgments

I am very grateful to Alberto Sonnino from Facebook Calibra and University College London for comments on late manuscript, and to Ing. Alessandro Leone from the Italian Embassy in Belgium for his suggestions and encouragement.

References

[1] E. Bucci and E. Marinari, *Sull'evoluzione Dell'epidemia Da Covid-19*, *Patto Trasversale per la Scienza* (2020), https://www.pattoperlascienza.it/2020/03/02/lo-studio-di-enrico-bucci-ed-enzo-marinari-sullevoluzione-dellepidemia-da-covid-19/

[2] Il Sole 24 Ore, *Coronavirus in Italia, i dati e la mappa* (2020) - Website: https://lab24.ilsole24ore.com/coronavirus/

[3] Sciensano, *Epidemologie des maladies infectueuses* (2020) - Website: https://epidemio.wiv-isp.be/ID/Pages/2019-nCoV.aspx

[4] *Wikipedia, the free encyclopedia*, *2020 coronavirus pandemic in Belgium*, https://en.wikipedia.org/wiki/2020_coronavirus_pandemic_in_Belgium

[5] J. M. Hilbe, *Practical Guide to Logistic Regression*, CRC Press, Taylor & Francis Group, LLC (2015).

[6] P. Piovani, *Coronavirus, il pediatra: Questa epidemia durerà tre mesi*, *Il messaggero*, 24 March 2020.

[7] G. Sonnino, *The COVID-19 - The Infectious Disease Caused by the Latest Discovered Coronavirus (SARS-CoV-2)*, *European Commission*, ARES(2020)1530456, (March 2020).

[8] On Health, *Respiratory Illnesses: 13 Types of Lung Infections* (Reviewed by Charles Patrick Davis, MD, PhD on 3/20/2020). Website: https://www.onhealth.com/content/1/respiratory_infections_causes

[9] E. Manjarrez-Zavala *et al.*, *Pathogenesis of Viral Respiratory Infection*, (2013), DOI: 10.5772/54287. Website: https://www.intechopen.com/books/respiratory-disease-and-infection-a-new-insight/pathogenesis-of-viral-respiratory-infection

[10] C. Huang *et al.*, *Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China*, *The Lancet Journals*, **395**, Issue10223, P497-506, (Published: 24 January 2020). Website: https://doi.org/10.1016/S0140-6736(20)30183-5

[11] W. Garrett Nichols *et al.*, *Respiratory Viruses Other than Influenza Virus: Impact and Therapeutic Advances*, *American Society for Microbiology - Clinical Microbiology Review*, DOI: 10.1128/CMR.00045-07, Website: https://cmr.asm.org/content/21/2/274

[12] S. Nickbakhsh *et al.*, *Virus-virus interactions impact the population dynamics of influenza and the common cold*, *Proceedings of the National Academy of Science of the United State of America (PNAS)*, PNAS December 26, 2019 116 (52) 27142-27150; first published December 16, 2019, https://doi.org/10.1073/pnas.1911083116 Edited by Burton H. Singer,

University of Florida, Gainesville, FL, and approved November 12, 2019 (received for review June 27, 2019).

[13] S. A. Lauer, *The Incubation Period of Coronavirus Disease 2019 (COVID-19) From Publicly Reported Confirmed Cases: Estimation and Application*, *Annals of Internal Medicine* (ACP), (10 March 2020). Website: https://annals.org/aim/fullarticle/2762808/incubation-period-coronavirus-disease-2019-covid-19-from-publicly-reported

[14] T.-M. Chen *et al.*, *A mathematical model for simulating the phase-based transmissibility of a novel coronavirus*, *BMC Part of Springer Nature, Infectious Diseases of Poverty*, **9**, Article number: 24 (2020).

[15] M. Nowak, Martin and R. May, *Virus Dynamics: mathematical principles of immunology and virology* (2001). ISBN 9780198504177. Archived from the original on 13 February 2015. Retrieved 13 February 2015.

Date	Active	Recovered	Deceased	Total cases
25-Feb	322	1	10	333
26-Feb	400	3	12	415
27-Feb	650	45	18	713
28-Feb	888	46	21	955
29-Feb	1049	50	29	1128
01-Mar	1577	83	34	1694
02-Mar	1835	149	52	2036
03-Mar	2263	160	79	2502
04-Mar	2706	276	107	3089
05-Mar	3296	414	148	3858
06-Mar	3916	523	197	4636
07-Mar	5061	589	233	5883
08-Mar	7375	622	366	8363
09-Mar	9172	724	463	10359
10-Mar	10149	1004	631	11784
11-Mar	10590	1045	827	12462
12-Mar	12839	1258	1016	15113
13-Mar	14955	1439	1266	17660
14-Mar	17750	1966	1441	21157
15-Mar	20603	2335	1809	24747
16-Mar	23073	2749	2158	27980
17-Mar	26062	2941	2503	31506
18-Mar	28710	4025	2978	35713
19-Mar	33190	4440	3405	41035
20-Mar	37860	5129	4032	47021
21-Mar	42681	6072	4825	53578
22-Mar	46638	7024	5475	59137
23-Mar	50418	7432	6077	63927
24-Mar	54030	8326	6820	69176
25-Mar	57511	9362	7503	74376
26-Mar	62013	10361	8165	80539
27-Mar	66414	10950	9134	86498
28-Mar	70065	12384	10023	92472
29-Mar	73880	13030	10779	97689
30-Mar	75528	14620	11591	101739
31-Mar	77635	15729	12428	105792
01-Apr	80572	16847	13155	110574
02-Apr	83049	18278	13915	115242
03-Apr	85388	19758	14681	119827
04-Apr	88274	20996	15362	124632
05-Apr	91246	21815	15887	128948
06-Apr	93187	22837	16523	132547
07-Apr	94067	24392	17127	135586
08-Apr	95362	26491	17669	139422
09-Apr	96877	28470	18279	143626
10-Apr	98273	30455	18849	147577
11-Apr	100269	32534	19468	152271

Table 1: *Situation in Italy on 11 April 2020.* Columns report the number of active people (currently infected by COVID-10), the number of recovered people, and the number of deceased people.

Date	Active	Recovered	Deceased	Total cases
02-Feb	1	0	0	1
01-Mar	1	0	0	1
02-Mar	6	0	0	6
03-Mar	13	0	0	13
04-Mar	23	0	0	23
05-Mar	50	0	0	50
06-Mar	109	0	0	109
07-Mar	169	0	0	169
08-Mar	200	0	0	200
09-Mar	239	0	0	239
10-Mar	267	0	0	267
11-Mar	311	0	3	314
12-Mar	396	0	3	399
13-Mar	556	0	3	599
14-Mar	686	0	3	689
15-Mar	882	0	4	886
16-Mar	1034	14	10	1058
17-Mar	1202	31	10	1243
18-Mar	1229	243	14	1486
19-Mar	1619	155	21	1795
20-Mar	2016	204	37	2257
21-Mar	2485	263	67	2815
22-Mar	2986	340	75	3401
23-Mar	3305	350	88	3743
24-Mar	3737	410	122	4269
25-Mar	4234	547	178	4937
26-Mar	5340	675	220	6235
27-Mar	6398	858	289	7284
28-Mar	7718	1063	353	9134
29-Mar	9046	1359	431	10836
30-Mar	9859	1527	513	11899
31-Mar	10374	1696	705	12775
01-Apr	11004	2132	828	13964
02-Apr	11842	2495	1011	15348
03-Apr	12755	2872	1143	16770
04-Apr	13901	3247	1283	18431
05-Apr	14493	3751	1447	19691
06-Apr	15196	3986	1632	20814
07-Apr	16002	4157	2035	22194
08-Apr	16482	4681	2240	23403
09-Apr	17296	5164	2523	24983
10-Apr	18080	5568	3019	26667
11-Apr	18686	5986	3346	28018

Table 2: *Situation in Belgium on 11 April 2020.* Columns report the number of active people (currently infected by COVID-10), the number of recovered people, and the number of deceased people.