Phenomenological dynamics of COVID–19 pandemic: meta–analysis for adjustment parameters

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We present a phenomenological way of dealing with the COVID–19 data provided by government health agencies of eight different countries. Instead of using the (exact or approximate) solutions to the SIR (or other) model(s) and trying to adjust the time–independent parameters included in those models, we introduce dynamical parameters whose time–dependence may be phenomenologically obtained by adequately extrapolating a chosen subset of the daily provided data. This phenomenological approach works extremely well to properly adjust the number of infected (and removed) individuals in time, for the countries we consider.

Keywords: Time-dependent parameters; Phenomenological dynamic model; COVID-19

Mathematics Subject Classification: 92B05; 92D30

I. INTRODUCTION

Pandemic propagation models are usually described by systems of first order ordinary non–linear coupled differential equations such as it is the case for the well known SIS and SIR models, for instance. Numerous classical as well as very recent articles have been written to deal with this problem [1–8]. The dynamical variables are usually denoted by S(t), I(t) and R(t), which are functions of a single time variable t and denote the number of susceptible individuals (which may get infected), the number of infected individuals and the number of recovered or removed individuals (which some time after becoming infected are either immune or dead), respectively.

In addition to the dynamical variables, the models introduce time–independent parameters (usually denoted by greek letters) which describe the intensity of the coupling between the dynamical variables. These parameters clearly depend on the behavior of quarantined people in different countries which, in turn depend on the containment policies implemented by different governments in different countries.

It is not difficult to realize when trying to fit the data informed by health governmental institutions of different countries that they cannot be fitted by solutions of the model’s equations for time–independent parameters, due to the fact that the policies change over time and so does the behavior of the societies.

Strictly speaking, the so called parameters are really dynamical variables whose time evolution equations are difficult to hypothesize or construct due to the fact that their time evolution depends on people idiosyncrasy and government policies, which are almost impossible to foresee.

Because of these difficulties, in this work we propose an analysis on the study of the daily change of parameters in order to retrieve the dynamical information of a pandemic. The estimation of the time–dependence behavior of the parameters of epidemiological models have been an active research field in the past [9–16]. However, our procedure is different to previous ones, as it does not require any set of differential equations as a model. Instead of studying the total data set that gives origin to total structure of the pandemic, we focus in the study of time evolution of the parameters that produce such total structure, i.e., we do a meta–analysis of the data set system. Therefore, instead of solving a model described by a set of differential equations with solutions that fit the data, a meta–analysis proceeds in the opposite direction, finding the global evolution of the parameters, and thus obtaining a model. This procedure allow us to find the global dynamical behavior of data by studying the day-to-day evolution of the adjustment parameters.

In other words, we can extract the time-dependent information of the system without solving any differential equation set. Hence, we are able to solve the system in a phenomenological fashion. This proper meta–analysis of the adjustment parameters can provide the kind of information that is needed in order to have a better understanding of the evolution of the pandemic. The main goal of this work is to show that this procedure gives us global information of the changes in the spread of the disease.

The adjustment parameters in this meta–analysis, hereafter called meta–parameters, are no longer considered as constants, and they can be extracted directly from the data information. It is the purpose of this work to delineate a systematic procedure to estimate the dynamics of meta–parameters. We show how these meta–parameters substantially improve the understanding of
In this section we describe the phenomenological procedure to estimate the evolution of the infected population. We start with the data set $R_j$ for the recovered population, for time $j = 1, ..., N$ measuring lapsed days (with a final day $N$). Here, $R_j$ represents the recovered population at day $j$. The information of this data set is equivalent to the cumulative integral or sum of infected cases. The data are obtained from Ref. [19]. By using the information in $R_j$, we can infer the infected population data as

$$I_j = R_j - R_{j-1},$$

at day $j$. For this work, we have used data until May 8th, 2020.

For such given data set, a global dynamical behavior can be found by fitting the curve $R_j \rightarrow R(t)$, where now the continuous recovered population function is given by

$$R(t) = a \left( \tanh\left( b \left( t + c \right) - \tanh \left( c \right) \right) + R_0 \right),$$

where $a$, $b$ and $c$ are global constant adjustment parameters, and we have assumed that the relevant data to perform any analysis start with $R_0 \neq 0$, by properly setting the initial time $t = 0$ of our analysis. By global we refer that the adjustment is for the total lapsed time $N$. Notice that recovered population curve (2) is not equal to the approximated solution emerging from SIR system. We show below that (2) is a good global fitting for the recovered population. On the other hand, the infected population dynamics is assumed to be found as $I_j \rightarrow I(t) = R(t)$, which gives

$$I(t) = a \text{sech}^2 (b(t + c)),$$

Now, let us perform the meta–analysis of fitting (2) for the recovered population. Let us promote the three parameters used in (2) to meta–parameters $a \rightarrow a_1(t)$, $b \rightarrow a_2(t)$, and $c \rightarrow a_3(t)$. This meta–parameters are no longer globally constants. Their dynamics must be obtained considering the new information that brings any new day that it is added to the data set of recovered population. For each time $j$ ($j = 1, ..., N$), the meta–parameters $a_i$ ($i = 1, 2, 3$) are found by fitting the curve (2) to the data, by using them as constant adjustment parameters for such time. As the amount of data grows with time, the value of each meta–parameter varies, taking into account the different behavior that the governments or the society may have at different times. After that several iterations are performed for different times and fitting curves (2), a regular and dynamical behavior of each meta–parameter starts to emerge. This regularity starts at some time $\zeta \neq 1$ for the three meta–parameters, and it depends on each particular studied case. All of this implies that meta–parameters are not globally constant in time, and now their global time–dependent $a_i = a_i(t)$ is apparent. Once this stage is reached, the complete dynamical solution for each meta–parameter is established, and a solution (2) for the recovered population can now be promoted to the function

$$R_{M}(t) = a_1(t) \left[ \tanh \left( a_2(t) t - a_3(t) \right) - \tanh \left( a_3(t) \right) \right] - R_0,$$

II. PHENOMENOLOGICAL TREATMENT FOR PANDEMIC DYNAMICS

In this section we describe the phenomenological procedure for pandemic evolution. This is exemplified for the case of actual current data from eight countries. These are Italy, United States, Canada, United Kingdom, Spain, Poland, Austria and Germany.

In order to put in context our proposal, let us consider first the SIR model as an example for pandemic evolution. This model considers three kind of populations, the susceptible $S = S(t)$, the infected $I = I(t)$ and the recovered $R = R(t)$ population, respectively, all of them evolving in time. Besides, the total population $N = S + I + R$, is constant in time. The three variables are related by the differential system $\dot{S} = -\alpha SI$, $\dot{I} = \alpha SI - \beta I$, and $\dot{R} = \beta I$, where ‘’ symbol time derivation. Here, $\alpha$ and $\beta$ are constant parameters, that contain the relevant information for pandemic evolution. Our lack of knowledge on how the pandemic evolves, is hidden in such parameters. Although no explicit exact solution for $R = R(t)$ is known, it is straightforward to show that at second order in an expansion around $\alpha R / \beta$, we can obtain the solution for the recovered population as a function of time [17][18], given by $R(t) = r_1 \tanh(r_2 t - r_3) + r_4$. Here, $r_1 = \gamma \beta^2 / (\alpha^2 S_0)$, $r_2 = \beta \gamma / 2$, $r_3 = \tanh^{-1} (\alpha S_0 / (\beta \gamma) - 1 / \gamma)$, and $r_4 = \beta / \alpha - \beta^2 / (\alpha^2 S_0)$, are all constants, in terms of $\gamma = [(\alpha S_0 / \beta - 1)^2 + 2 S_0 I_0 \alpha^2 / \beta^2]^{1/2}$, where $S_0$ and $I_0$ are the initial values of susceptible and infected populations in $t = 0$. It has been assumed that initial value of recovered population $R_0 = 0$. It is important to realize that the system is now completely solved, as the infected population can be readily obtained by $I(t) = \dot{R} / \beta \approx (r_1 \gamma / 2) \text{sech}^2 (r_2 t - r_3)$, while the susceptible population is $S(t) = N - I(t) - R(t)$. Those solutions are often used to study in an approximated manner the pandemic evolution. However, they fail to describe correctly its dynamics when social conditions change or different governmental decisions are taken along the progress of the pandemic.

In the following sections we show how better fitting results can be achieved by the procedure of using a hyperbolic tangent function to fit the data of recovered population during the pandemic, using meta–parameters. The evolution of these meta–parameters is obtained by analyzing day-by-day the same data that they adjust. This procedure gives a precise figure of the increment of infected individuals. Therefore, the meta–analysis produces a better fitting of the estimation of the temporal behavior of infected population, thus solving the pandemic dynamics in a phenomenological way. The final solution obtained from the data fitting procedure will not be a solution of the SIR model, neither of any other simple model described by first-order differential equations with constant parameters.
which produces a dramatic departure from solution (2).

Remarkably, we show below that when meta-parameters have achieved a regular dynamics, they all behave in the following quadratic form with respect to time \((i = 1, 2, 3)\)

\[
a_i(t) \approx a_{0i} + a_{1i}t + a_{2i}t^2, \tag{5}
\]

with constant coefficients \(a_{0i}, a_{1i},\) and \(a_{2i}\). This very simple behavior is manifested by the meta-analysis. It shows that any change in the information of the data evolves in an ordered form and it can be recovered through the study of the meta-parameters.

With all the above, the new meta-parameter fitting function (4) contains more precise information of the daily changes of the recovered population compared with the fitting function (2). In other words, its derivative represents a more accurate description of the infected population curve, which can be calculated as

\[
I_M(t) = \dot{R}_M(t), \tag{6}
\]

which anew, results to be different from function (3).

In order to quantify how both infected population fittings differ from each other, we define the global function \(\epsilon = E_M/E_C\), as the ratio between the error function \(E_M = \sqrt{\sum_{j=2}^{N} [I_M(j) - I_j]^2}\) for the meta-analysis of infected population (6), and the error function \(E_C = \sqrt{\sum_{j=2}^{N} [I(j) - I_j]^2}\) for the global fitting of infected population (3) with constant adjustment parameters. The case of \(\epsilon < 1\) implies a better fitting curve for the infected population dynamics due to the meta-analysis.

Below, we present examples for different countries that explicitly show the strength of this phenomenological dynamical analysis, and its better fitting to the existence data. It is the goal of this work to search for the explicit form of each meta-parameter for the studied countries, finding in this way the underlying dynamical structure of their pandemic scenarios, and thus determine \(R_M\) and \(I_M\). With all this in mind, let us discuss the pandemic data for cumulative infectious cases as evolving in time for eight different countries, and how the phenomenological dynamical procedure applies to each of them. We use the case of Italy to carefully explain each step in the procedure, as it is straightforwardly replicated for the other country cases.

\[\text{A. Italy}\]

The data for the recovered population in Italy is shown by the dotted line in Fig. 1(a), with \(N = 77\). The red-dashed line shows the fitting of function (2), with parameters given in Table I.

Consider now the blue solid line in Fig. 1(a). It describes the meta-analysis fitting (4) for the recovered population since the day \(\zeta = 33\). This is the day in which the meta-parameters start to be regular, as they can be easily seen in Fig. 2(a). The meta-parameters are calculated for each day (from \(R_0\)), taking into account all previous days. Thus, each new calculated meta-parameter contains the information of any previous change. Before day \(\zeta\), there is no regular pattern in the evolution of meta-parameter. But, after day \(\zeta\) a very distinctive regular dynamical behavior emerge. For the current case, after day \(\zeta = 33\), the meta-parameters \(a_1(t), a_2(t),\) and \(a_3(t)\) time-dependence behavior is almost quadratic, shown by red lines in Fig. 2(a). The coefficients of the quadratic form (5) are given in Table II.

These meta-parameters are used in (4) to obtain the solid blue fit in Fig. 1(a). Notice that the fitting precision for the slope of the recovered population becomes more accurate as it grows, i.e., a better fit for its derivative is achieved, compared to fitting (2). This implies that it contains better information on the the number of infected individuals. This is shown in Fig. 1(b), where the data represented by dots is the infected population calculated according to Eq. 1. The red dashed line is the infected population fit (3), with their respectively parameters. Notice also that this fit is just proportional to the approximated solution for infected population in the SIR model.

On the other hand, the solid blue line in Fig. 1(b) correspond to the meta-analysis fitting (4) for infected population, with meta-parameters with coefficients from Table I. This fitting reproduces better the global behavior of the evolution of infected population in Italy, just by considering the last part (for times \(t > \zeta\)) of the growing on recovered cases. This also coincide with the evaluation of \(\epsilon = 0.66156\), allowing us to establish that the meta-parameter fitting for infected population is superior to (3).

\[\text{B. United States}\]

The recovered population for United States is shown in Fig. 1(c). Again, the data with \(N = 78\) is represented by a dotted line, while the red dashed line shows the fitting (2), with parameters described in Table I. The blue solid line is the fitting (4) since \(\zeta = 45\), when the meta-parameters start to have a regular evolution, a quadratic form, as it can be seen in Fig. 2(b) in red lines. The meta-parameters coefficients are given in Table I.

In this case, something similar to the previous case occurs. The fitting (4), with their respective meta-parameters, is not much better than fit (2) for the recovered population. However, its slope is in much better agreement with the growing rate for the recovered data. This implies that our meta-analysis gives a better fit for the infected population, compared to the extracted data from Eq. 1. This can be seen in Fig. 1(d). In this case, the red dashed line represents the fitting (3) for infected population, while blue solid line is our meta-analysis fitting (6) using meta-parameters (5) with coefficients given in Table II. The fit due to meta-parameters...
TABLE I: Parameters for fittings of recovered population (2) and infected population (3), for different countries.

| Country      | $R_0$ | $a$ | $b$  | $c$     |
|--------------|-------|-----|------|---------|
| Italy        | 17    | 109659 | 0.04946 | -1.97906 |
| United States| 16    | 657278 | 0.05523 | -3.07358 |
| Canada       | 12    | 37629.5 | 0.04928 | -2.66134 |
| United Kingdom| 16   | 110064 | 0.05478 | -2.75723 |
| Spain        | 7     | 83879.7 | 0.10154 | -3.41748 |
| Poland       | 5     | 8258.58 | 0.05047 | -2.07227 |
| Austria      | 5     | 7600.84 | 0.09253 | -2.74671 |
| Germany      | 17    | 81777.8 | 0.06773 | -2.57146 |

TABLE II: Values for $a_{0i}$, $a_{1i}$ and $a_{2i}$ for meta–parameters (5), shown in Figs. 2 and 4, for different countries.

is so dramatic, that when the global solution (3) shows a decreasing on infected population, the meta–analysis shows that the rate is not slowed down. For this case, the meta–analysis fitting is better as $\epsilon = 0.64328$.

C. Canada

The recovered population data for Canada is shown with the dotted line in Fig. 1(e). The red dashed line is the fit of Eq. (2) with $N = 72$ and parameters given in Table I. Anew, the blue solid line is our meta–analysis fitting (4), using the meta–parameters that are described by a regular dynamics starting in $\zeta = 33$, as red lines in Figs. 2(c). The meta–parameters coefficients are given in Table II. The blue solid line for recovered cases indicates a better approximation to the growing of such data.

The infected population is depicted in Fig. 1(f), where the data is obtained from (1), while in red dashed line is the fitting (3) with parameters from Table I and in blue solid line we have the fitting (6) with the meta–parameters coefficients given in Table II. Once again, with $\epsilon = 0.75349$, the meta–analysis represents a better fit to the global evolution of infected population.

D. United Kingdom

The recovered population data is shown in Fig. 1(g), while the infected population data is shown in Fig. 1(h), both of them in dotted lines. The recovered population data fit (2), in red line in Fig. 1(g), is achieved with $N = 71$ and parameters from Table I. The blue solid line in Fig. 1(g), represents the fit of meta–analysis (4) for meta–parameters (5) that have achieved regular evolution for $\zeta = 31$ [see Figs. 2(d)]. Those have coefficients given in Table II. The information in the meta–analysis is used for infected population in comparison with data (1). In Fig. 1(h), the solid blue line for meta–parameters fitting (6) shows a better correspondence than fit (3) with constant parameters. This is confirmed by evaluating $\epsilon = 0.70413$. Notice how the $\text{sech}^2$ approach fails to describe the global dynamical behavior of the infected population, which is indeed well–described by our meta–analysis.

E. Spain

In Fig. 3(a) we show the recovered population data (in dotted line). The red dashed line is the fitting (2) for recovered population with $N = 72$, and parameters given in Table I. Similarly, the blue solid line is fitting (4) with meta–parameters (5) starting in $\zeta = 35$, and with coefficients given in Table II. We can see in Fig. 4(a) that the
meta–parameters are described by quadratic functions again.

Using this, we can calculate the behavior of the number of the infected individuals, shown in Fig. 3(b). The infected population data (dotted line) is given by Eq. (1), while fit (3) is in red dashed line and meta–analysis fit (4) is in solid blue line. We obtain that \( \epsilon = 0.84965 \), showing that the fit based in meta–parameters is again superior to a time–independent one.

F. Poland

The data for the recovered population of Poland is plotted in Fig. 3(c) in dotted line. Also, the red dashed line fits Eq. (2) for the recovered population with \( N = 63 \), and the parameters of Table I. The meta–analysis fitting (4) is in blue line with the meta–parameters (5) from Fig. 3(b), starting in \( \zeta = 37 \) with coefficients of Table I. This case is interesting as the slope of meta–analysis fit (4) clearly shows that recovered population is increasing, as opposed to what can be deduced from fit (2).

Therefore, the infected population data, in Fig. 3(d), shows a better agreement with the fit (6) due to meta–parameters. While the fit (3) indicates a strong decreasing on infected population, the meta–analysis shows that infected population is decreasing slowly. A better fit of the meta–analysis is corroborated by \( \epsilon = 0.78179 \).

G. Austria

In Fig. 3(e) is the data for the recovered population in Austria. In red dashed line is the fit (2) for \( N = 71 \) and the parameters from Table I. Similarly, the fit (4), in blue solid line, requires the meta–parameters (5) show in Fig. 3(c), with coefficients in Table I starting from \( \zeta = 31 \).

The meta–analysis fit indicates a better adjustment for the infected population, as it is seen in Fig. 3(f). In that figure, the red dashed line is the fit (3), and the blue solid line is the fit (6). The global dynamical behavior of the infected population is better achieved by the meta–analysis, with \( \epsilon = 0.8802 \).

H. Germany

The last country to be studied is shown in Figs. 3(g) and 3(h) for the data (dotted lines) of recovered and infected populations, respectively. Red dashed lines represent the fitting of (2) and (3) for both cases, with \( N = 73 \) and parameters given in Table I. Blue solid lines represent the meta–parameter fittings of recovered (4) and infected (6) populations, with respect to the data (1). The meta–parameters (5) have coefficients given in Table II all of them starting from \( \zeta = 38 \).

Once more, the fit (6) is better for infected population, as \( \epsilon = 0.89286 \).

III. DISCUSSION

We have presented a new approach to deal with infection propagation data by allowing the parameters to became time–dependent. Although we are not able to produce a dynamical model for the parameters time evolution due to intrinsic difficulty associated with unforeseeable government policies and population behavior, we have been able to produce a method that may be successfully applied to the actual data informed by eight different countries which have implemented different mitigation policies to fight the COVID-19 infection with different population reactions.

All of the cases of infected populations studied above exhibit the same feature. The meta–analysis shows effectively the capture of the daily variations of cases. In other words, we have shown that using meta–parameters we can integrate the recovered population without using any pre-existing model.

Our proposal produces global results, as soon as the regular behavior of meta–parameter are found. Thus, the meta–analysis works for all data, and not only for an arbitrary particular range in the evolution of recovered cases, as for example, when the growing of recovered cases behave as a power-law [20].

On the contrary, the infection data which are informed in countries where the governments have introduced sudden infection related policy changes or where the population has not abided by the government set containment rules are difficult to describe by the approach presented here (or almost any other method).

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IV. DECLARATIONS

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(a) Recovered population for Italy  
(b) Infected population for Italy  

(c) Recovered population for United States  
(d) Infected population for United States  

(e) Recovered population for Canada  
(f) Infected population for Canada  

(g) Recovered population for United Kingdom  
(h) Infected population for United Kingdom  

FIG. 1: Recovered and Infected populations for Italy, United States, Canada and United Kingdom. Data is shown in dotted line. Fittings (2) and (3) are shown in red dashed line for recovered and infected populations, respectively. Phenomenological fittings (4) and (6), with meta-parameters, are shown in blue solid line for recovered and infected populations, respectively.
FIG. 2: Meta–parameters for Italy, United States, Canada, and United Kingdom. Data is shown in dotted line. The regular dynamical behavior of meta–parameters (starting in time ζ) is shown in red solid line. They evolve following the quadratic form (5).
FIG. 3: Recovered and Infected populations for Spain, Poland, Austria, and Germany. Data is shown in dotted line. Fittings (2) and (3) are shown in red dashed line for recovered and infected populations, respectively. Phenomenological fittings (4) and (6), with meta-parameters, are shown in blue solid line for recovered and infected populations, respectively.
FIG. 4: Meta–parameters for Spain, Poland, Austria, and Germany. Data is shown in dotted line. The regular dynamical behavior of each meta–parameter (starting in time $\zeta$) is shown in red solid line. They evolve following the quadratic form (5).