COVID-19 spreading: a model
Sergey O. Ilyin

A.V. Topchiev Institute of Petrochemical Synthesis, Russian Academy of Sciences,
29 Leninsky prospect, 119991 Moscow, Russia; s.o.ilyin@gmail.com

Abstract: This communication describes a recursive mathematical model of the spreading COVID-19 infection, which allows estimating the effectiveness of quarantine measures. The model was used to analyze the situation in eight countries and to find the viral transmissibility, which made it possible to give a brief prediction of the COVID-19 spreading.

Most predictions of the spread of coronavirus infection are based on opinions, speculation, assumptions, and hopes. The situation is developing rapidly and this requires responsible decisions from both the authorities and ordinary citizens. Fortunately, an accurate forecast can easily be made using a simple mathematical model.

The COVID-19 spreading model is based on a set of parameters whose values are unique for each country due to differences in population density and humans’ behavior, date of virus penetration and government actions. The set includes the following parameters:

- $d_0$ is the date of the initiation of the epidemic; it is not the date of detection of the first infected person but the date of appearance of the first undetected (or detected too late) one;
- $d_1, d_2, d_3$ are dates of change in the behavior of the population, e.g., due to the awareness of the reality of what is happening, the introduction of quarantine and its tightening;
- $t_D$ – is the average time from infecting to isolating the infected person, which is equal to the incubation period that I assume to be six days (from 5.2 to 6.4 days according to different sources);\(^{1,2}\) theoretically, this parameter can be reduced by total testing of the entire population, but it is feasible only for small communities;
- $R_0, R_1, R_2, R_3$ – are the viral transmissibilities that are equal to the average number of people who will be infected by one person before its isolation and depend on the behavior of the population at different stages of the epidemic; when $R$ is less than 1.0 the epidemic fades, and vice versa;
- $r_0, r_1, r_2, r_3$ – are the reduced transmissibilities that are equal to the average number of people who will be infected by one person per day: $r = R/t_D$; to suppress the COVID-19 spreading, $r$ should be less than 0.167.

The evaluation of the virus spreading is based on the calculation of the following data:

- $N_D(d_i)$ is the number of detected infected persons on $d_i$ date, which equals the total number of infected persons six days earlier:

$$N_D(d_i) = N_T(d_i-t_D);$$
\( N_T(d_i) \) is the total number of infected persons on \( d_i \) date, which is the sum of the total number of infected persons the day before and the number of new infected persons that, in turns, is equal to the product of the reduced transmissibility and the number of active infected persons the day before (taking into account that those who have been previously infected cannot re-infected):

\[
    N_T(d_i) = N_T(d_{i-1}) + r_0 \times N_A(d_{i-1}) \times (1 - N_T(d_{i-1})/N_P),
\]

where \( N_P \) is the total population;

\( N_A(d_i) \) is the total number of active (undetected) infected persons on \( d_i \) date, which equals the difference between the total number of infected persons the day before and the number of detected infected persons also the day before:

\[
    N_A(d_i) = N_T(d_{i-1}) - N_D(d_{i-1}).
\]

At the start of the epidemic (\( d_0 \) date), \( N_A(d_0) = 1, N_T(d_0) = 1, \) and \( N_D(d_0) = 0. \)

Thus, in order to calculate the virus spreading dynamics it is necessary to know the values of only two parameters – \( d_0 \) and \( r_0 \). In case of changing the behavior of the population from the date \( d_i \), parameter \( r_0 \) changes its value from this date to become \( r_1 \). If the behavior changes again, a pair of \( d_2 \) and \( r_2 \) will appear, etc.

It is more difficult to model human losses correctly. Two more parameters appear:

\( L \) is the apparent lethality rate that is equal to the ratio of the number of deaths to the sum of those who died and recovered;

\( t_L \) is the average time from infection to death.

These two parameters depend on the efficacy of treatment and may vary as physicians gain experience and as hospitals overflow. Number of deaths on \( d_i \) date equals total number of people infected \( t_L \) days earlier multiplied by the lethality rate:

\[
    N_L(d_i) = N_T(d_i-t_L) \times L.
\]

Due to the presence in the equation of two parameters \( (t_L \) and \( L \)) that have the same effect on the resulting value, the precision of their evaluation is lower than that of transmissibility.

The situation with predicting the number of recovered persons is even worse due to the appearance of an even greater number of independent parameters:

\[
    N_R(d_i) = N_T(d_i-t_M) \times k_M + N_T(d_i-t_S) \times k_S
\]

where \( k_M, k_S, t_M, \) and \( t_S \) are the shares of mild and serious ill patients as well as the times from their infection to healing respectively; \( k_M + k_S + L = 1. \)
Based on historical data on disease development in eight countries, the model was tested and most of its parameters were found (Figure). These parameters allow making a forecast of the situation development and the conclusion about the effectiveness of quarantine measures. By way of example, determine the current number of active infected persons ($N_A(d_i)$), the approximate date of isolation of the last infected person ($d_E$), and the number of people that could eventually be infected under the current quarantine ($N_{T,max}$). According to the calculations, the efforts made by many European countries, the USA and Japan to stop the spread of the COVID-19 infection are not as effective as those implemented previously in the People's Republic of China. Most countries were able to achieve a daily reduction in the number of infected people, but even in these cases, the viral transmissibility remains high enough, which does not allow to defeat the epidemic within a reasonable time. At the same time, suppressing the epidemic, albeit slowly, allows time for vaccine development.

**References**

1. Backer JA, Klinkenberg D, Wallinga J. Incubation period of 2019 novel coronavirus (2019-nCoV) infections among travellers from Wuhan, China, 20–28 January 2020. Euro Surveill 2020; 25: 200062.

2. Li Q, Guan X, Wu P, et al. Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia. N Engl J Med 2020; 382: 1199–207.