STATISTICS-BASED PREDICTIONS OF CORONAVIRUS EPIDEMIC SPREADING IN MAINLAND CHINA

I. Nesteruk*

Institute of Hydromechanics, National Academy of Sciences of Ukraine, Kyiv, Ukraine
Igor Sikorsky Kyiv Polytechnic Institute, Kyiv, Ukraine

*Corresponding author: inesteruk@yahoo.com

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Background. The epidemic outbreak caused by coronavirus COVID-19 is of great interest to researchers because of the high rate of the infection spread and the significant number of fatalities. A detailed scientific analysis of the phenomenon is yet to come, but the public is already interested in the questions of the epidemic duration, the expected number of patients and deaths. Long-time predictions require complicated mathematical models that need a lot of effort to identify and calculate unknown parameters. This article will present some preliminary estimates.

Objective. Since the long-time data are available only for mainland China, we will try to predict the epidemic characteristics only in this area. We will estimate some of the epidemic characteristics and present the dependencies for victim numbers, infected and removed persons versus time.

Methods. In this study we use the known SIR model for the dynamics of an epidemic, the known exact solution of the linear differential equations and statistical approach developed before for investigation of the children disease, which occurred in Chernivtsi (Ukraine) in 1988–1989.

Results. The optimal values of the SIR model parameters were identified with the use of statistical approach. The numbers of infected, susceptible and removed persons versus time were predicted and compared with the new data obtained after February 10, 2020, when the calculations were completed.

Conclusions. The simple mathematical model was used to predict the characteristics of the epidemic caused by coronavirus in mainland China. Unfortunately, the number of coronavirus victims is expected to be much higher than that predicted on February 10, 2020, since 12289 new cases (not previously included in official counts) have been added two days later. Further research should focus on updating the predictions with the use of up-to-date data and using more complicated mathematical models.

Keywords: coronavirus epidemic in China; coronavirus COVID-19; coronavirus 2019-nCoV; mathematical modeling of infection diseases; SIR model; parameter identification; statistical methods.

Introduction

Here, we consider the development of an epidemic outbreak caused by coronavirus COVID-19 (the previous name was 2019-nCoV) (see e.g., [1–3]). Since long-term data are available only for mainland China, we will try to predict the number of coronavirus victims V (number of persons who caught the infection and got sick) only in this area. The first estimations of V(t) exponential growth versus time t, typical for the initial stages of every epidemic (see e.g., [4]) have been done in [3]. For long-time predictions, more complicated mathematical models are necessary. For example, a susceptible-exposed-infectious-recovered (SEIR) model was used in [2]. Nevertheless, complicated models need more effort for unknown parameters identification. This procedure may be especially difficult if reliable data are limited.

In this study, we use the known SIR model for the dynamics of an epidemic [4–8]. For the parameter identification, we will use the exact solution of the SIR set of linear equations and statistical approach developed in [4] (tested also in [9]). These methods were applied for investigation of the children disease, which occurred in Chernivtsi (Ukraine) in 1988–1989. We will estimate some of the epidemic characteristics and present the dependencies for victim numbers, infected and removed persons versus time.

Materials and Methods

Data

We shall analyze the daily data for the number of confirmed cases in mainland China, which origins from the National Health Commission of the People’s Republic of China [1]. A part of the official
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The diagram (its version, presented on February 15, 2020) is shown in Fig. 1. For calculations, we have used the data for the period of time from January 16 to February 9, 2020. The numbers shown after February 9 were used for verification of predictions.

On February 12, 2020, the National Health Commission of the People’s Republic of China has added 12289 new cases (not previously included in official counts) as “clinically diagnosed cases”. The cases, reported by this official organization before, have the name of “tested confirmed cases” [1]. To avoid confusion, we will denote “tested confirmed cases” as $W_j$; $j$ corresponds to the different time moments $t_j$ (see the Table). Let us denote the “clinically diagnosed cases” as $Q_j$. The sum of $W_j$ and $Q_j$ is shown in the last column in Fig. 1 and in the Table.

The Table shows that the precise time of the epidemic beginning $t_0$ is unknown. Therefore, the optimization procedures have to determine the optimal value of this parameter as well as for other parameters of SIR model.

![Diagram](https://example.com/diagram.png)

**Figure 1:** A part of official diagram with the numbers of $W_j + Q_j$ (last column) and $W_j$ (previous column) [1]

<table>
<thead>
<tr>
<th>Day in January, 2020</th>
<th>Time moment $t_j$</th>
<th>“Tested confirmed cases” $W_j$</th>
<th>Day in February, 2020</th>
<th>Time moment $t_j$</th>
<th>“Tested confirmed cases” $W_j$</th>
<th>The sum of “tested confirmed cases” and “clinically diagnosed cases” $W_j + Q_j$</th>
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</thead>
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<td>45</td>
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<td>11791</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

**Table:** The information from the official table of the National Health Commission of the People’s Republic of China [1]. The corresponding time moments $t_j$ and the number of $W_j$ and $Q_j$ which were used for calculations and verification.
**Exact solution of SIR equations**

The SIR model for an infectious disease can be written as follows [6, 7]:

\[ \dot{S} = -\alpha SI, \quad I = \alpha SI - \rho I, \quad R = \rho I. \tag{1} \]

The number of susceptible persons is \( S \), infected (persons who are sick and spread the infection) – \( I \), removed (persons who do not spread the infection anymore, this number is the sum of isolated, recovered and dead people) – \( R \); the infection and immunization rates are \( \alpha \) and \( \rho \) respectively. Since \( \dot{S} + I + R = 0 \) (see, eqs. (1)–(3)), the sum \( N = S + I + R \) must be constant for all moments of time and can be treated as the amount on susceptible persons before the outbreak of an epidemic, since \( I = R = 0 \) at \( t < t_0 \). It must be noted that the constant \( N \) is not the volume of population \( N_{\text{total}} \) but only the initial number of people sensitive and not protected to some specific disease. In particular, the ratio \( N/N_{\text{total}} \) may be rather small.

To determine the initial conditions for the set of eqs. (1)–(3), let us suppose that
\[ I(t_0) = 1, \quad R(t_0) = 0, \quad S(t_0) = N - 1. \tag{4} \]

It follows from (1) and (2) that
\[ \frac{dI}{dS} = \frac{\nu}{S} - 1, \quad \nu = \frac{\rho}{\alpha}. \tag{5} \]

Integration of (5) with the initial conditions (4) yields:
\[ I = \nu \ln S - S + N - \nu \ln(N - 1). \tag{6} \]

Function \( I \) has a maximum at \( S = \nu \) and tends to zero at infinity, see [6, 7]. In comparison, the number of susceptible persons at infinity \( S_\infty > 0 \), and can be calculated with the use of (6) from a non-linear equation
\[ S_\infty = (N - 1) e^{-\frac{\nu}{\nu}}. \tag{7} \]

In [4] the equations (1)–(3) were solved by introducing the function \( \dot{V}(t) = I(t) + R(t) \), corresponding to the number of victims. The integration of corresponding equation
\[ \dot{V} = \alpha SI = \alpha(N - V) \times [\nu \ln(N - V) + V - \nu \ln(N - 1)] \tag{8} \]

yields:
\[ t = \frac{F_1(V, N, \nu) + \alpha t_0}{\alpha}, \tag{9} \]
\[ F_1 = \int_{\nu}^{V} \frac{dU}{(N - U)[\nu \ln(N - U) + U - \nu \ln(N - 1)]}. \tag{10} \]

Thus, for every set of parameters \( N, \nu, \alpha, t_0 \) and a fixed value of \( V \) the integral (10) can be calculated and the corresponding moment of time can be determined from (9). Then \( I \) can be calculated from (6) by putting \( S = N - V \) and function \( R \) from \( R = V - I \).

**Statistical approach for parameter identification. Linear regression**

As in paper [4], we shall use the fact that the random function \( F_1(V, N, \nu) \) has a linear distribution (see (9)). Then we can apply the linear regression (see [10]) for every pair of parameters \( N \) and \( \nu \) and calculate the corresponding values of \( t_0 \) and \( \alpha \). The optimal (the most reliable) values of \( N \) and \( \nu \) correspond to the maximum value of the correlation coefficient \( r \) (see [4, 9]).

**Results**

Since we did not know and still don’t know the values of \( Q \) before February 12, 2020, we supposed that \( V_j = W_j \) and have done the calculations with the use of data for the time period from January 16 to February 9, 2020. The optimal values of the parameters are:

\[ N = 90611; \quad \nu = 65546.5; \quad \alpha = 1.477985357571669 \times 10^{-5}; \quad t_0 = -7.720998173432072. \]

The corresponding correlation coefficient is very high \( r = 0.99796648704645 \). The solution of (7) yields the value \( S_\infty = 45579 \). The corresponding number of infected \( I \), susceptible \( S \) and removed \( R \) persons versus time (starting from January 16, 2020) were calculated and shown in Fig. 2. The blue line represents the number of victims \( V = I + R \) and is in good agreement with “tested confirmed cases” \( W_j \), reported by the National Health Commission of the People’s Republic of China [1] (blue markers).
Discussion

Unfortunately, many cases have not been included in the official counts and have appeared in the official Table from [1] only on February 12 as "clinically diagnosed cases" $Q_j$ (see Fig. 1). Since the National Health Commission of the People's Republic of China has proposed two different ways of registration of the same disease [1], $V_j$ must be the sum of $W_j$ and $Q_j$, i.e. $V_j = W_j + Q_j$ (provided that no new methods of registering the same disease would appear). Values $W_j$ after February 9 are shown in Fig. 3 by "stars". "Crosses" represent the sum $W_j + Q_j$.

Since the optimal curve was obtained only with the use of $W_j$ and the difference between $W_j$ and $V_j$ is very big (e.g., it was 12,289 persons on February 12, 2020), the predictions shown in Fig. 2 and reported in [11] are no longer relevant. To have better predictions, it is necessary to have exact $Q_j$—data for the period before February 12.

Figure 2: Results of calculations and verification

Numbers of infected $I$ (green line), susceptible $S$ (red line), and removed $R$ (black line) persons versus time in days (starting from January 16, 2020). The blue line represents the number of victims $V = I + R$. Blue markers show the "tested confirmed cases" $W_j$, reported by the National Health Commission of the People's Republic of China [1]. The "circles" correspond to the points used for calculations (it was supposed that $V_j = W_j$); "stars"—to the points used only for verification.

Figure 3: Prediction (line) and observations from [1] (markers)

"Circles" show the "tested confirmed cases" $W_j$ for the period from January 16 to February 9, 2020, [2]. These points were used to calculate the prediction curve. "Stars" correspond to the "tested confirmed cases" $W_j$ for the period from February 10 to February 14, 2020, [1]. "Crosses" represent the sum $W_j + Q_j$ from [1].
Conclusions

The simple mathematical model was used to predict the characteristics of the epidemic caused by coronavirus in mainland China. The numbers of infected, susceptible, and removed persons versus time were predicted and compared with the new data obtained after February 10, 2020, when the calculations were completed. Unfortunately, many cases have not been included in the official counts and have appeared on February 12 only. It makes the predictions reported on February 10, 2020, no longer relevant. Further research should focus on updating the predictions with the use of corrected data and more complicated mathematical models.

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References


Подальші дослідження варто зосередити на оновленні прогнозів на основі свіжих даних та з використанням більш складних математичних моделей.

Ключові слова: епідемія коронавірусу в Китаї; коронавірус COVID-19; коронавірус 2019-nCoV; математичне моделювання інфекційних захворювань; SIR-модель; ідентифікація параметрів; статистичні методи.

Основні результати: Оптимальні значення параметрів SIR-моделі були отримані з застосуванням статистичного підходу. Число інфікованих, восприимчивих і удалених людей в залежності від часу було прогнозоване з використанням статистичного підходу.

Висновки: Для прогнозування характеристик епідемії, викликаної коронавірусом в материковому Китаї, було використано просту математичну модель. К сожалению, прогнозована величина числа жертв коронавірусу в материковому Китаї була значною вище, ніж прогнозувалося 10 березня 2020 р., оскільки через два дня було відомо 12289 нових випадків (раніше не включених в офіційні подання). Дальніші дослідження повинні бути спрямовані на оновлення прогнозів на основі свіжих даних і з використанням більш складних математичних моделей.

Ключові слова: епідемія коронавірусу в Китаї; коронавірус COVID-19; коронавірус 2019-nCoV; математичное моделирование инфекционных заболеваний; SIR-модель; идентификация параметров; статистические методы.