



## A simple epidemic model of COVID-19 and its application to Ukrainian, Indonesian, and the global data

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### ABSTRACT

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At the beginning of 2020, one of the most significant health problems for humanity is the pandemic of coronavirus disease 2019 (COVID-19). Here, we identify features and develop simple epidemic model of COVID-19 on the basis of available epidemiological data and existing trends worldwide. Modeling of COVID-19 epidemic process was based on a classic model. A key parameter of the model, i.e. transmission parameter of *severe acute respiratory syndrome coronavirus 2* (SARS-CoV-2), was determined numerically with the use of available epidemiological daily reports of COVID-19 from 17 April to 23 May 2020. Numerical determination of transmission parameter of SARS-CoV-2 according to the absolute number of COVID-19 cases in Ukraine, Indonesia and worldwide data showed its global tendency to decrease over time. Approximation of the obtained numerical values of the transmission parameter of SARS-CoV-2 was carried out using the exponential function. The results of prognostic modeling showed that by the end of summer 2020, above 30 thousand COVID-19 cases are expected in Ukraine, 100 thousand COVID-19 cases in Indonesia, and 12 million COVID-19 cases worldwide. Thus, predicting the possible consequences of the implementation of various health care control programs COVID-19 involves a comprehensive study of the epidemic process of the disease as a whole and for certain periods of time with the subsequent construction of an adequate prediction model.

### ABSTRAK

Pada awal tahun 2020, salah satu masalah utama kesehatan masyarakat di dunia adalah epidemi *coronavirus disease 2019* (COVID-19). Dalam studi ini, kami mengidentifikasi karakteristik dan mengembangkan model epidemi sederhana berdasarkan data epidemiologis yang tersedia. Permodelan epidemi COVID-19 dibuat berdasarkan model klasik. Parameter utama model tersebut, yaitu parameter transmisi *severe acute respiratory syndrome coronavirus 2* (SARS-CoV-2), ditentukan secara numerik berdasarkan data epidemiologis laporan kasus harian COVID-19 dari tanggal 17 April sampai dengan 23 Mei 2020. Penentuan parameter transmisi secara numerik berdasarkan jumlah absolut kasus COVID-19 di Ukraina, Indonesia, dan dunia menunjukkan adanya tren penurunan kasus. Hasil dari permodelan prognostik menunjukkan bahwa pada akhir musim panas tahun 2020, diperkirakan terdapat 30 ribu kasus di Ukraina, 100 ribu kasus di Indonesia, dan 12 juta kasus di seluruh dunia. Jadi, memprediksi hasil dari langkah-langkah kebijakan untuk menghentikan dan mengontrol pandemi COVID-19 memerlukan analisis yang komprehensif berkaitan dengan bagaimana perjalanan pandemi secara keseluruhan dan pada rentang waktu tertentu, diikuti dengan permodelan prediksi yang sesuai.

**Keywords:**  
COVID-19;  
epidemiology;  
mathematical modeling;  
prediction;

## INTRODUCTION

The role of viruses is constantly growing in the occurrence and development of infectious diseases of the human respiratory system. At the beginning of 21<sup>st</sup> century, 11 new respiratory viruses were discovered, that can cause severe respiratory diseases, often with fatal outcome. Among them are new human coronaviruses, *severe acute respiratory syndrome coronavirus* (SARS-CoV) and *middle east respiratory syndrome coronavirus* (MERS-CoV). Both of them cause acute respiratory diseases with high mortality rates. Since the discovery of SARS in 2002 and then MERS in 2012, the World Health Organization (WHO) experts have significantly increased epidemic safety against pathogens of these serious human diseases, and intensive studies of new members of the family Coronaviridae have resulted in a rapid accumulation of scientific data on their molecular biology, epidemiological and clinical features, diagnosis as well as treatment.<sup>1-4</sup>

At the beginning of 2020, one of the most significant global health problems for humanity is a novel coronavirus infection (coronavirus disease 2019 or COVID-19), which human population has not been previously encountered yet. Thus, it was began from an outbreak of SARS caused by an unknown type of coronavirus, previously called novel coronavirus (2019-nCoV) in December 2019 in the Chinese city of Wuhan.<sup>5,6</sup> Subsequently, genetic analysis showed that this novel coronavirus belonged to the genus *Betacoronavirus* and was officially renamed as SARS-CoV-2.<sup>7</sup> A very quickspread of SARS-CoV-2 beyond China to all continents (except Antarctica) was observed and affected the population of developed countries, including the United States, Italy, Spain, Germany, and France.<sup>8</sup> On March 11, 2020, WHO declared the COVID-19 as pandemic and assessed the event as “public health

emergency of international concern (PHEIC)”.<sup>9</sup> During a period of less than 5 months from the first report of cases of new respiratory disease, as of May 6, 2020, the incidence of COVID-19 in the world reached 3,778,016 cases with a mortality rate of about 7%, from 4.17 % in Germany to 13.8% in Italy.<sup>10</sup> According to the Center for Public Health (CPH) in Ukraine on the same date, 13,184 cases of COVID-19 were registered, 327 people died, mostly of respectable age with chronic comorbidities (mortality 2.48%).<sup>11</sup>

It is important to emphasize that SARS-CoV-2 is genetically closely related to the original SARS-CoV.<sup>5,6</sup> However, no effective vaccines and antiviral drugs are available at this moment. Given this critical situation, the only way to prevent the spread of COVID-19 is to impose strict quarantine and containment measures aimed at isolating patients, contacts and virus carriers, social distancing, and the use of antiseptics and disinfectants.<sup>12</sup>

Most studies of COVID-19 epidemic modeling started in March 2020 in many countries. In particular, such modeling was performed on the basis of the susceptibility-infected-recovered (SIR) model parameterized with the use of statistical morbidity and mortality data.<sup>13,14</sup> Other modeling approaches were based on neural networks. Within such model, analysts have developed two scenarios for the future spread of the COVID-19 pandemic. They showed that countries with rapid government interventions and strict public health measures were successful in halting the exponential spread of infection.<sup>15</sup> Principle of similarity for COVID-19 modeling was used in the Center for Systems Science and Engineering, Johns Hopkins University. It was based on statistics of countries with the most characteristic manifestations of the pandemic.<sup>16</sup> However, the above studies have an excessive mathematical component, some of them introduce

conditions and parameters, which are difficult to assess in practice.

The peak incidence of COVID-19 pandemic in the world has not yet passed. It is also not known for how long the COVID-19 pandemic will last. WHO experts predict a new wave of SARS-CoV-2 in the second half of 2020. This situation fully applies to Ukraine and Indonesia. Thus, an extremely important and urgent task for the healthcare system is to build a prediction of the possible further development and features of the COVID-19 epidemic process based on available (official) epidemiological data. Therefore, we would like to identify features and develop simple epidemic model of COVID-19 on the basis of available epidemiological data and existing trends in several countries (Ukraine and Indonesia) and

worldwide. The aim was to develop simple mathematical model that allows calculations in the available information packages without loss of quality.

## MATERIALS AND METHODS

The scenario of COVID-19 epidemic process as an acute respiratory viral infection from a mathematical point of view is based on the basic epidemiological model proposed by W. Kermak and A. McKendrick in 1927.<sup>17</sup> According to this model, individuals in the population can be divided into “susceptible” (S), who have not previously been exposed to SARS-CoV-2, “infectious” (I), who have COVID-19 with clinical manifestations, and those who recovered or died after COVID-19 (R) (FIGURE 1).

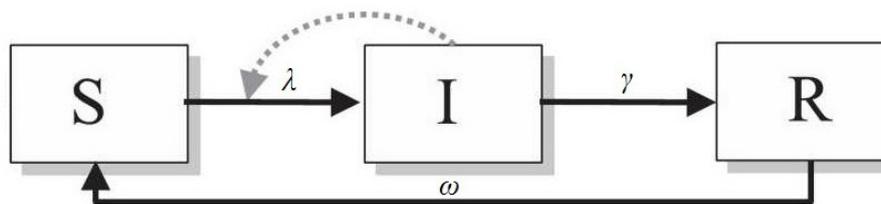


FIGURE 1. Basic epidemiological model of COVID-19

The transition from state S to state I represents new cases of COVID-19, and it is determined by the force of infection  $\lambda$  (rate of SARS-CoV-2 infection). For acute infections, the period during which a individual is infected (infection period) is distributed around some average value that can be accurately estimated from retrospective epidemiological data. Mathematically, this is expressed in the probability of transition of individuals from state I to state R, which depends on how long they were in state I. However, epidemiologists often assume that the recovery rate  $\gamma$  is a value inverse to the

average infectious period. The loss of acquired immunity over time is reflected in the transition from the state R to the state S at a rate of  $\omega$ .

In practice, it is impossible to determine such parameters of the epidemiological model as the recovery rate, the rate of acquired immunity loss, as well as the number of people who have recovered and acquired immunity. Since the purpose of the study was only to predict the number of new cases (incidence) of COVID-19, this allowed to identify a simplified model that describes only this process (FIGURE 2).

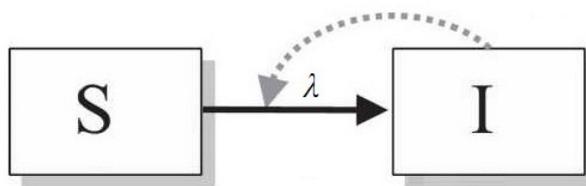


FIGURE 2. The incidence model of COVID-19

Mathematically, the incidence model of COVID-19 can be described by the following equation, according to which the number of individuals with COVID-19 at each time depends on the number of all individuals with COVID-19 before.

$$I_{t+1} = I_t + \lambda_t S_t \tag{1}$$

where  $I_t$  – the total number of individuals with COVID-19 at a given time;  
 $I_{t+1}$  – the total number of individuals with COVID-19 in the next time;  
 $S_t$  – the total number of susceptible individuals in the population at a given time;

The force of the infection  $\lambda$  (rate of SARS-CoV-2 infection) depends on three different factors: the prevalence of infected individuals, the structure of population contacts, and probability of infection through contact with a sick individual:

$$\lambda_t = \beta_t I_t / N_t \tag{2}$$

where  $I_t$  – the total number of patients with COVID-19 at given time;  
 $N_t$  – the total number of people in the population at given time;  
 $\beta_t$  – the transmission parameter of the SARS-CoV-2 pathogen at given time.

Substitution of formula (2) into formula (1) allows to determine transmission parameter of SARS-CoV-2 as the main parameter of the epidemic process of COVID-19 at any time on the basis of available epidemiological data:

$$\beta_t = (I_{t+1} - I_t) / (I_t / N_t \cdot S_t) \tag{3}$$

Given the fact that  $I_t \ll N_t$ , a  $S_t \approx N_t$ , formula (3) can be simplified without loss of accuracy:

$$\beta_t = (I_{t+1} - I_t) / I_t \tag{4}$$

Without reliable data, we can not understand the pandemic. Only based on good data can we know how the disease is spreading, what impact the pandemic has on the live of people around the world, and whether the counter measures are successful or not. However, even the best available data on the coronavirus pandemic is far from perfect. In the website Our World in Data, we found the latest accumulated data together with detailed explanations of its origin, European Centre for Disease Prevention and Control (ECDC). To determine initial values of the SARS-CoV-2 transmission parameter, the daily reports COVID-19 cases in Ukraine, Indonesia and worldwide were used from 17 April to 23 May 2020.<sup>18</sup>

## RESULTS AND DISCUSSION

The first step of the study was the numerical determination of transmission parameter of SARS-CoV-2 according to the absolute number of COVID-19 cases in Ukraine, Indonesia and worldwide that showed its tendency to decrease over time and ability of its approximation using the exponential function of the general form (FIGURE 3-5).

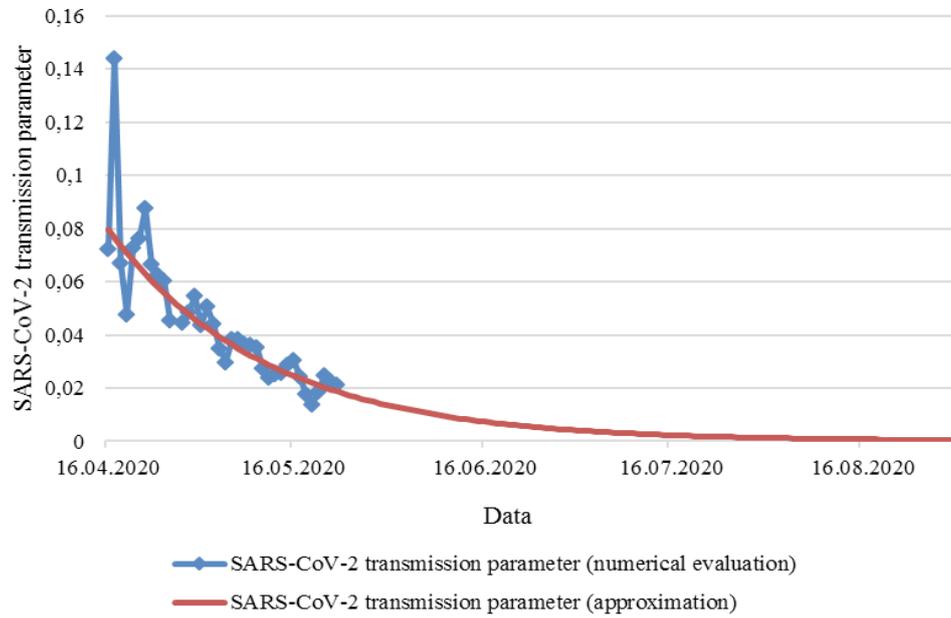


FIGURE 3. Numerical determination of SARS-CoV-2 transmission parameter by Ukrainian data ( $\beta_0 = 0.083$ ;  $\beta_1 = 0.039$ )

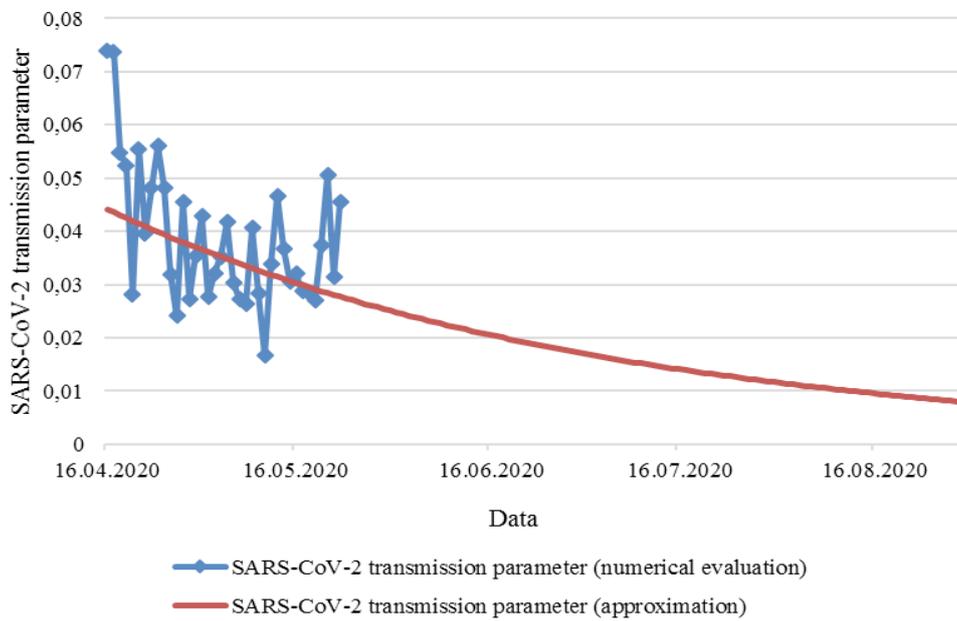


FIGURE 4. Numerical determination of SARS-CoV-2 transmission parameter by Indonesian data ( $\beta_0 = 0.045$ ;  $\beta_1 = 0.013$ )

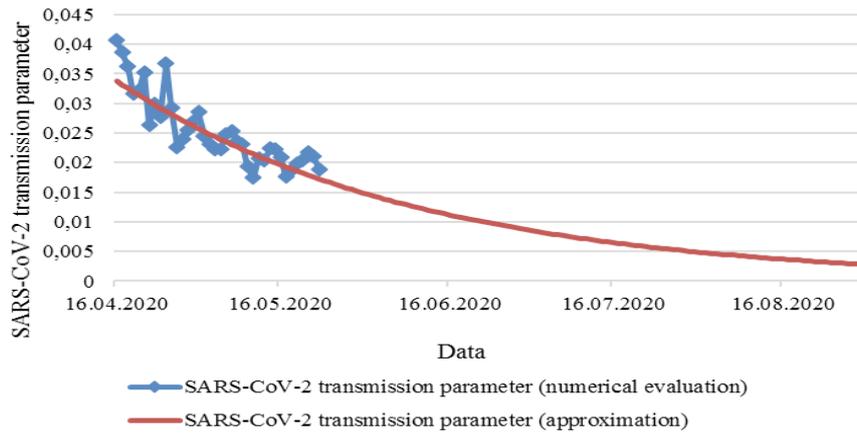


FIGURE 5. Numerical determination of SARS-CoV-2 transmission parameter by global data ( $\beta_0 = 0.034$ ;  $\beta_1 = 0.018$ )

Determination of the analytical type of SARS-CoV-2 transmission parameter allowed us to make an adequate prognosis of COVID-19 incidence in each studied region. The modeling results showed that by the end of summer 2020,

above 30 thousand COVID-19 cases are expected in Ukraine (FIGURE 6), 100 thousand COVID-19 cases in Indonesia (FIGURE 7) and 12 million COVID-19 cases worldwide (FIGURE 8).

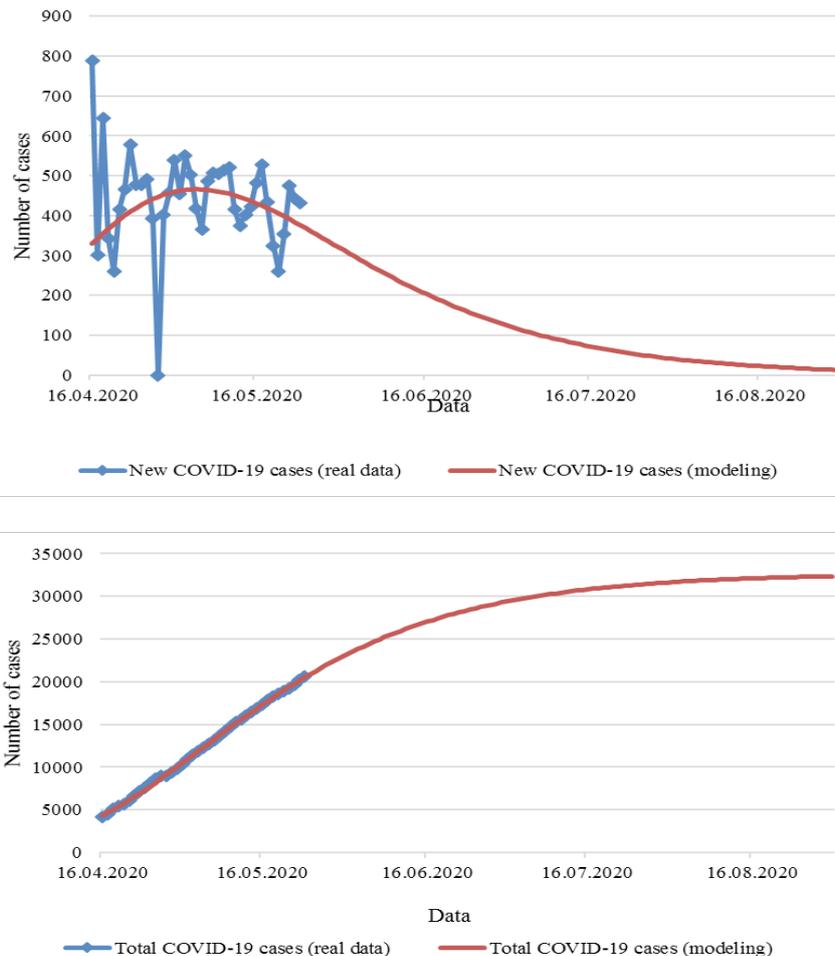


FIGURE 6. Number of new and total COVID-19 cases in Ukraine (real data and modeling)

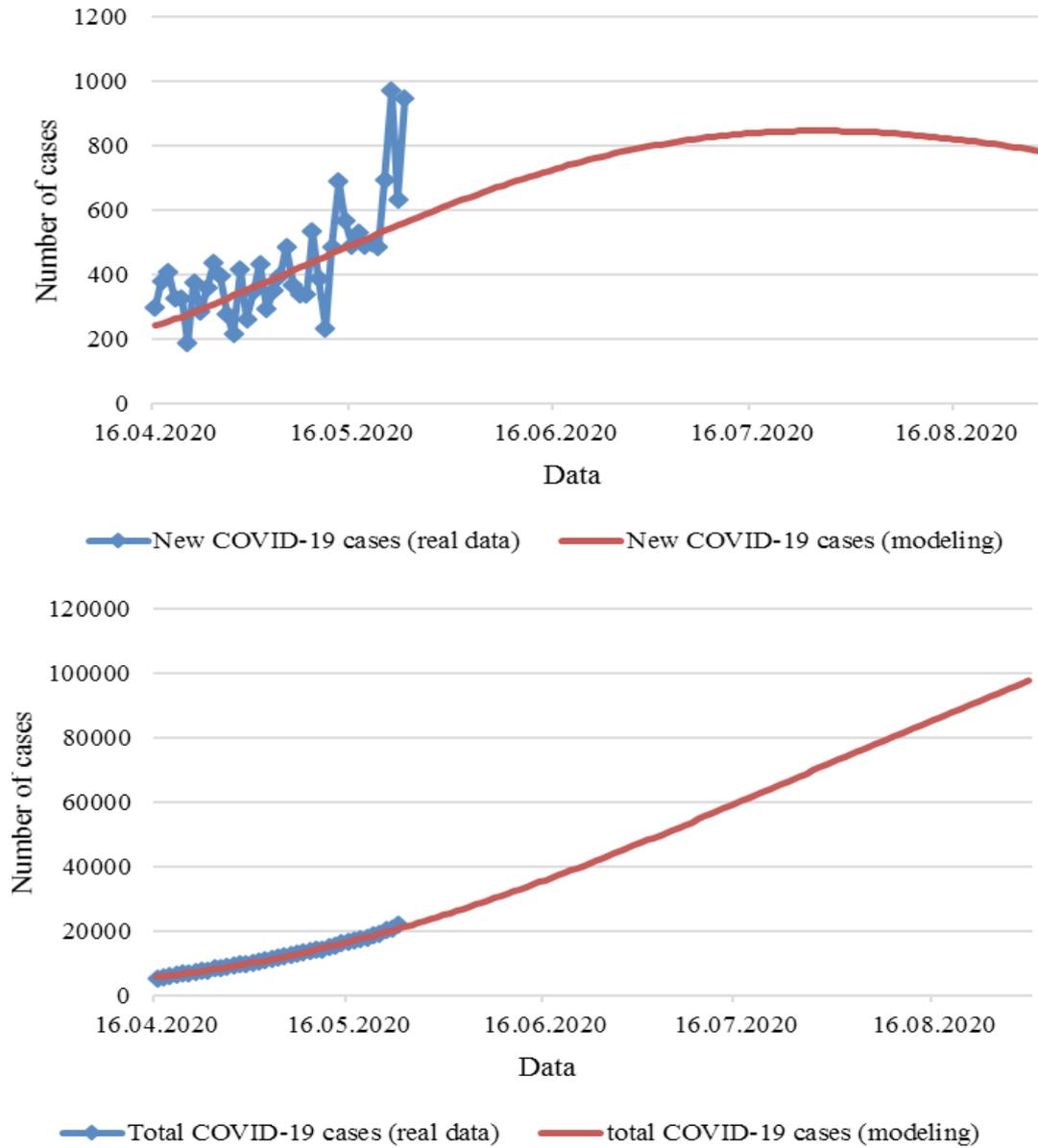


FIGURE 7. Number of new and total COVID-19 cases in Indonesia (real data and modeling)

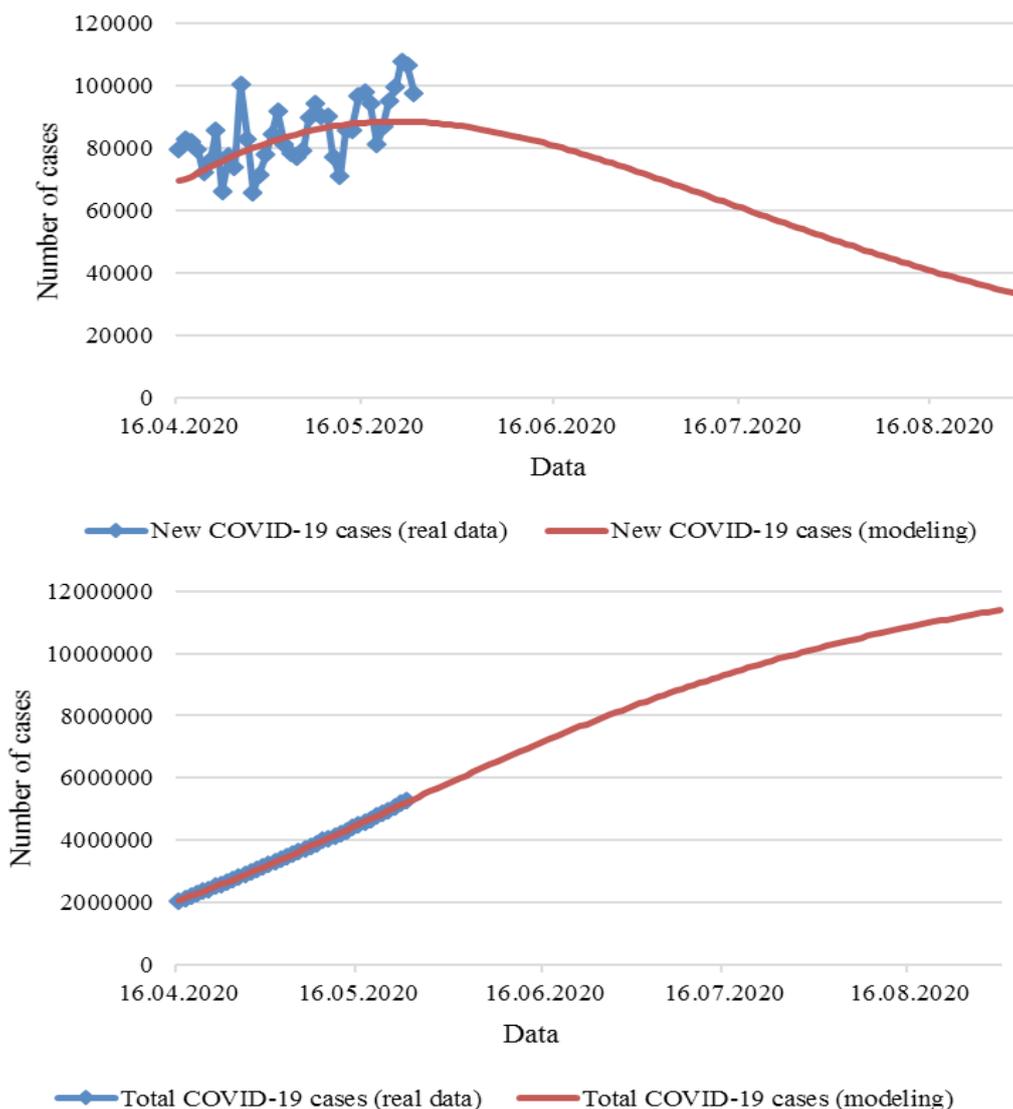


FIGURE 8. Number of new and total COVID-19 cases in the world (real data and modeling)

Thus, in our study, we developed a simple approach of epidemiological modeling of COVID-19 based on evaluation of SARS-CoV-2 transmission parameter by employing published COVID-19 cases for Ukraine, Indonesia, and worldwide. A comparative analysis showed the identity of modeling results, which further testified validity of proposed prediction model. It also showed similar trends of the epidemic progress of COVID-19 in different geographical regions, which can be a useful information for future decision making. It was found that the epidemic progress in Ukraine started more intensively than in Indonesia and

globally, but has been decreasing more rapidly. This fact could be explained by different temperature conditions, dynamics of population movement or other factors, that should be paid attention to and investigated more thoroughly in the future.

Our simple model is fully consistent with the principles of mathematical epidemiology and studies conducted by other scientists on modeling the epidemic progress of COVID-19 in other regions. Thus, a stochastic model of disease spread based on retrospective morbidity data in Wuhan was proposed. An individual-oriented model of SARS-

CoV-2 prevalence has been developed to identify potential sources of infection. Various calculations of the main number of reproductions - the average number of secondary cases of the disease - were analyzed.<sup>19,20</sup> Such works are interesting analytical studies, but usually have an excessive mathematical component, difficult numerical calculations, and some of them introduce certain conditions, such as the number of people in the incubation period, which are difficult to assess in practice. Although our work is based on similar principles, it used a simple mathematical model that allows calculations in the available information packages without loss of quality.

Despite the simplicity of our approach, our study has limitations because only confirmed COVID-19 cases with clinical manifestations were available, while the facts of asymptomatic cases are known.<sup>21,22</sup> Nevertheless, this was taken into account in the evaluation of SARS-CoV-2 transmission parameter, suggesting that this parameter already took into account involvement of asymptomatic individuals into the epidemic progress of COVID-19.

## CONCLUSION

Predicting the possible consequences of the implementation of various health care control programs of COVID-19 involves a comprehensive study of the epidemic process of the disease as a whole and for certain periods of time with the subsequent construction of an adequate prediction model. We proposed a simple mathematical model of COVID-19 epidemic process and determined its main transmission parameter of SARS-CoV-2, which is a complex characteristic of the structure of population contacts and the probability of infection after contact with a sick individual. Our calculations and analysis of their results showed that the dynamics

of SARS-CoV-2 transmission parameter is exponentially declining, indicating the gradual establishment of endemic equilibrium of COVID-19 prevalence among the population of Ukraine, Indonesia and worldwide in the nearest future while maintaining existing trends. The developed model is simple, but at the same time could be useful as a basis for future more complex approaches to COVID-19 modeling, taking into account various factors, including population density, climatic features, number of asymptomatic cases and others. Undoubtedly, our approach will require constant updating of data to adjust the prediction, taking into account possible changes in trends and the influence of other factors in the future.

## Conflict of interest

The authors declare no conflict of interest.

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