2-бөлім **Раздел 2** **Section 2**

Қолданбалы математика **Прикладная математика** **Applied Mathematics**

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S.I. Kabanikhin[1], **M.A. Bektemesov**[2], **Zh.M. Bektemessov**[3*]
[1]The Institute of Computational Mathematics and Mathematical Geophysics Siberian Branch of Russian Academy of Science, Russia, Novosibirsk
[2]Abai Kazakh National Pedagogical University, Kazakhstan, Almaty
[3]Al-Farabi Kazakh National University, Kazakhstan, Almaty
*e-mail: jolaman252@gmail.com

MATHEMATICAL MODEL FOR MEDIUM-TERM COVID-19 FORECASTS IN KAZAKHSTAN

In this paper has been formulated and solved the problem of identifying unknown parameters of the mathematical model describing the spread of COVID-19 infection in Kazakhstan, based on additional statistical information about infected, recovered and fatal cases. The considered model, which is part of the family of modified models based on the SIR model developed by W. Kermak and A. McKendrick in 1927, is presented as a system of 5 nonlinear ordinary differential equations describing the variational transition of individuals from one group to another. By solving the inverse problem, reduced to solving the optimization problem of minimizing the functional, using the differential evolution algorithm proposed by Rainer Storn and Kenneth Price in 1995 on the basis of simple evolutionary problems in biology, the model parameters were refined and made a forecast and predicted a peak of infected, recovered and deaths among the population of the country. The differential evolution algorithm includes the generation of populations of probable solutions randomly created in a predetermined space, sampling of the algorithm's stopping criterion, mutation, crossing and selection.

Key words: COVID-19, ODE, inverse problems, identification, differential evolution.

С.И. Кабанихин[1], М.А. Бектемесов[2], Ж.М. Бектемесов[3]
[1]Есептеу математикасы және математикалық геофизика институты, Ресей ғылым академиясының Сібір бөлімі, Ресей, Новосибирск қ.
[2]Абай атындағы Қазақ ұлттық педагогикалық университеті, Қазақстан, Алматы қ.
[3]Әл-Фараби атындағы Қазақ ұлттық университеті, Қазақстан, Алматы қ.
*e-mail: jolaman252@gmail.com

Қазақстандағы COVID-19 орта мерзімді болжамдарының математикалық моделі

Берілген жұмыста жұқтырылған, қалпына келтірілген және өліммен аяқталған жағдайлар туралы қосымша статистикалық ақпарат негізінде Қазақстандағы COVID-19 инфекциясының таралуын сипаттайтын математикалық моделінің белгісіз параметрлерін анықтау мәселесі тұжырымдалған және шешілген. 1927 жылы В.Кермак пен А.Маккендрик жасаған SIR моделі негізінде модификацияланған моделдер отбасының бөлігі болып табылатын қарастырылып отырған модель, индивидтердің вариациялық бір топтан екінші топқа ауысуын сипаттайтын 5 сызықтық қарапайым дифференциалдық теңдеулер жүйесі ретінде ұсынылған. Биологиядағы қарапайым эволюциялық есептер негізінде 1995 жылы Рейнер Сторн мен Кеннет Прайс ұсынған функционалды минимизациялаудың дифференциалды эволюциялық алгоритмі, кері есепті шеше отырып, модель параметрлері нақтыланып, ел тұрғындарының арасында жұқтырылған, қалпына келтірілген және өлім-жітімнің болжамдадық. Дифференциалды эволюцияның алгоритміне алдын ала анықталған кеңістікте кездейсоқ құрылған ықтимал шешімдер популяциясының генерациясы, алгоритмнің тоқтау критерийінен сынамалар алу, мутация, қиылысу және таңдау жатады.

Түйін сөздер: COVID-19, қарапайым дифференциалдық теңдеулер, кері есептер, сәйкестендіру, дифференциалдық эволюция.

С.И. Кабанихин[1], М.А. Бектемесов[2], Ж.М. Бектемесов[3]
[1]Институт вычислительной математики и математической геофизики СО РАН, Россия, г.Новосибирск
[2]Казахский национальный педагогический университет имени Абая, Казахстан, г.Алматы
[3]Казахский национальный университет имени аль-Фараби, Казахстан, г.Алматы
*e-mail: jolaman252@gmail.com

Математическая модель по среднесрочным прогнозам COVID-19 в Казахстане

В работе сформулирована и решена задача идентификации неизвестных параметров математической модели распространения инфекции COVID-19 в Казахстане, по дополнительной статистической информации об инфицированных, выздоровевших и летальных случаях. Рассматриваемая модель, входящая в семейство модифицированных моделей на базе модели SIR, разработанной У. Кермаком и А. Маккендриком в 1927 году, представлена в виде системы из 5 нелинейных обыкновенных дифференциальных уравнений, описывающая вариационный переход индивидуумов из одной группы в другую. За счет решения обратной задачи, сведенной к решению оптимизационной задачи минимизации функционала, алгоритмом дифференциальной эволюции, предложенной Райнером Сторном и Кеннетом Прайсом в 1995 году на основе простых эволюционной задач биологии, были уточнены параметры модели и построен прогноз инфицированных, выздоровевших и умерших индивидуумов среди населения страны. Алгоритм дифференциальной эволюции включает в себя генерацию популяций вероятных решений случайно созданных в предварительно определенном пространстве, выборку критерия остановки алгоритма, мутацию, скрещивание и отбор.

Ключевые слова: COVID-19, ОДУ, обратные задачи, идентификация, дифференциальная эволюция.

1 Introduction

In December 2019, there was an outbreak of pneumonia, where the COVID-19 strain was first detected, and after 4 months, more precisely on March 11, 2020, the World Health Organization (WHO) announced the global COVID-19 pandemic. In the first months of the pandemic, the countries of Europe with the most high rates of morbidity and mortality of the population become its center. To date, despite the efforts of health systems to counter the pandemic, the exponential growth of infection and mortality of the population of 187 countries of the world continues, the number of confirmed cases has reached 55.7 million, the number of deaths is 1 340 thousand. USA, Brazil, India, France and Russia are leaders in these positions (Fig. 1). In the Republic of Kazakhstan, within seven months of the epidemic (March - August 2020), 128 thousand were identified and 1.8 thousand people died from COVID-19. The introduction of an emergency, classified as a threat to national security, and the response actions led to a decrease in new cases (less than 200 per day) and deaths (less than 5 per day).

The inability to stop the spread of COVID-19 in the world and its further impact has shown the unpreparedness and inconsistency of the previous organizational approaches of states, including Kazakhstan, to combat this disease using of non-pharmaceutical interventions, and requires new approaches using mathematical methods to assess the epidemic pro-

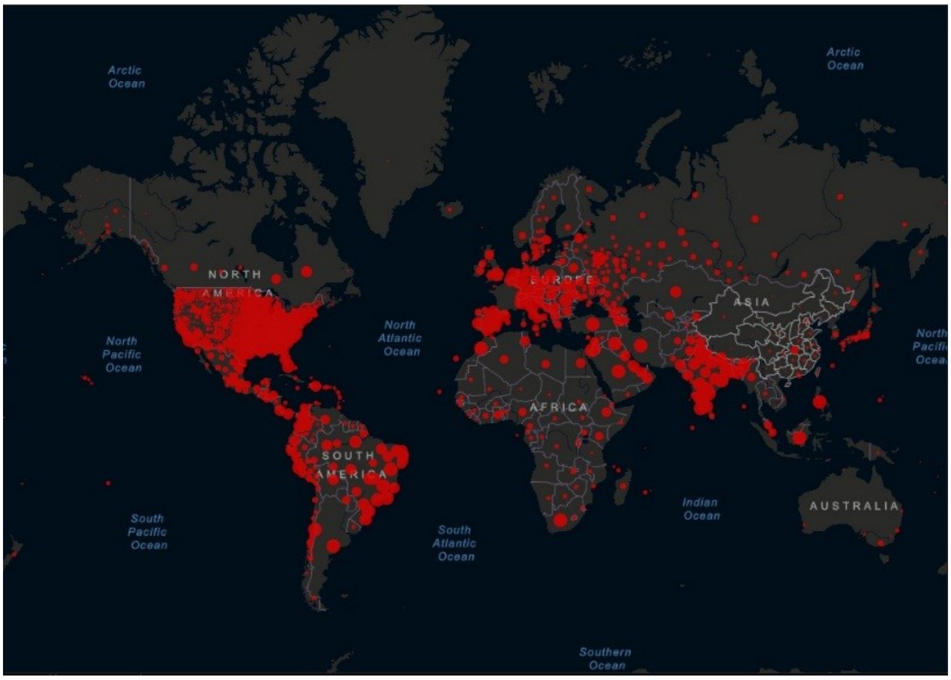

Figure 1: The number of detected cases of COVID-19 worldwide

cess, affecting not only health, but also all spheres of human activity (medical, social, economic, environmental). To analyze the COVID-19 situation, WHO experts recommended using assessment indicators: the number of confirmed cases (cumulative and new), the number of deaths (cumulative and new), the percentage of recovered, the number and percentage of tests. One of the most effective methods of monitoring and managing epidemic processes is mathematical modeling, namely the development and identification of mathematical models. Such models are described by systems of differential equations, the coefficients of which characterize the features of the spread of the disease and epidemic processes in the country. To draw up an optimal plan of measures to control epidemiological processes, it is necessary to refine the coefficients of the models using some additional information (inverse problem). One of the ways to solve the problem of specifying the coefficients is to reduce the inverse problem to a variational formulation, where the functional characterizes the quadratic deviation of the model data from the statistical data.

2 Material and methods

2.1 The statement of the problem

In most mathematical models [1–6], [7–10], [17, 18], attention is paid to the structure of the model and the results of numerical experiments, and the values of the model parameters are taken averaged and, often, from extraneous literary sources. Therefore, forecasts and recommendations based on these models are of an average nature and do not take into account regional and social specifics.

Mathematical methods in the study of diseases were first applied by D. Bernoulli in

1760 when analyzing the effectiveness of vaccination against smallpox. In the middle of the 19th century, a number of researchers used statistical methods to describe the spread of various diseases. Modern mathematical models in epidemiology originate from the SIR model developed by W. Kermak and A. McKendrick in 1927 [1]. It involves dividing the entire population under consideration into Susceptible, Infected and Recovered groups. The mathematical model of the process is a system of differential or difference equations describing the change in the size of each of the indicated population groups. The SIR model stops working if it is necessary to take into account more data, such as: population density in different regions or different transmission routes [19, 20]. In view of the shortcomings, the SIR model was repeatedly refined, because of which a whole family of models appeared on its basis: SIRS, SEIR, SIS, MSEIR.

There are also a number of models where the differentiation of the diseased is carried out, i.e. among the infected, groups of easily sick, seriously ill, etc. are distinguished, and a group of deceased is added [3–10].

In this work, the SEIR-D model is used, where the population is divided into 5 groups. The population of deaths from infection (D) is added to the four base SEIR populations. This choice of the model is based on the fact that the COVID-19 disease has a rather long incubation period (5-14 days), where the infected person does not show any symptoms for a long time, while being the carrier of this disease. Also, the choice of a model is determined by the available data. The study was carried out on the basis of official data on the current state of the health care system and the measures taken to protect human health.

Thus in the article [11] the authors conducted a sensitivity-based identifiability analysis for various models of the spread of the COVID-19 pandemic. This analysis made it possible to determine the most and least sensitive parameters to data changes. The authors, using the methods to solve the inverse problem, described the main trends in the spread of the virus. The more precise results and deeper investigation was made in [12] by using stochastic methods for solving the inverse problems of mathematical models SEIR-HCD and SEIR-D for forecasting of COVID-19 spread in Moscow and Novosibirsk region.

The authors of [13] solved the inverse problem to simulate the spread of COVID-19 in Bulgaria using the SEIR mathematical model, presenting a two-week forecast of the number of new infections, active cases and recovered people. While in [14], the authors, using the SIR model, investigated the spread of coronavirus infection in different countries, such as the USA, Italy, China, India and others. In addition, to calculate the dynamics of COVID-19 in Brazil, the author [15] used a stochastic differential equation (SDE) corresponding to the nonlinear Fokker-Planck equation. In the article [16], a semi-supervised neural network is used to study the solution of differential equations for various parameters of modeling the evolution of COVID-19 propagation and its initial conditions, and then methods of solving inverse problems for evaluating the optimal conditions corresponding to statistical data.

This paper clarifies the coefficients of the transition from one group to another by solving the inverse problem using data on the number of registered infected, recovered and died. After that, the direct problem is solved and the scenario of the development of the epidemic is calculated. It should be noted that the model does not take into account climatic conditions, seasonal diseases, population growth and age characteristics.

2.2 The statement of the problem

Within the framework of the SEIR-D model is considered a system of 5 nonlinear common differential equations for the time section $t \in [t_0, T]$ [21]. The models take into account the current incubation period of the disease. This is achieved at the expense of the second group of populations - contacted or exposed. Thus, in the process of infection, the susceptible to the disease, the person first turns out to be contagious and only then becomes infected. Yet the infected either recovers or expects a lethal case. So infected without symptoms can occur in a group with healthy, not even knowing about their disease. What happens to groups of healthy individuals is that they have a risk of being susceptible to disease Fig. 2.

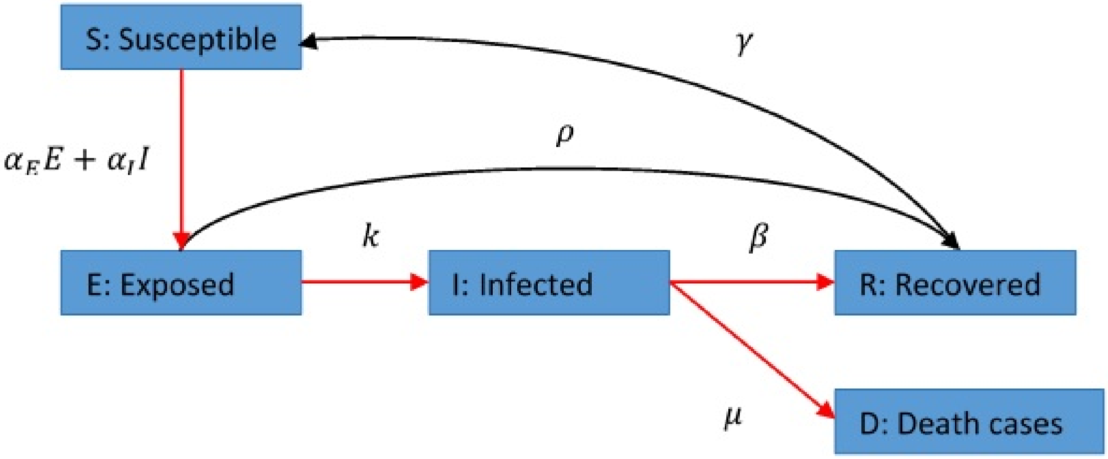

Figure 2: Scheme of mathematical model SEIR-D

$$\begin{cases} \dfrac{\partial S}{\partial t} = -\alpha_E \dfrac{S(t)E(t)}{N(t)} - \alpha_I \dfrac{S(t)I(t)}{N(t)} + \gamma R(t), \\[2ex] \dfrac{\partial E}{\partial t} = \alpha_E \dfrac{S(t)E(t)}{N(t)} + \alpha_I \dfrac{S(t)I(t)}{N(t)} - kE(t) - \rho E(t)), \\[2ex] \dfrac{\partial I}{\partial t} = kE(t) - \beta I(t) - \mu I(t)), \\[2ex] \dfrac{\partial R}{\partial t} = \beta I(t) + \rho E(t) - \gamma R(t)), \\[2ex] \dfrac{\partial D}{\partial t} = \mu I(t)). \end{cases} \tag{1}$$

where S – susceptible individuals, E – infected individuals without symptoms, I – infected individuals with symptoms, R – recovered individuals, D – deaths among the population,

N – whole population. Description of the model parameters and their average values are presented in the Table 1.

Initial data:

$$S(t_0) = S_0; E(t_0) = E_0; I(t_0) = I_0; R(t_0) = R_0; D(t_0) = D_0. \tag{2}$$

Table 1: The model parameters and their average values

Parameter	Description	Average value
α_E	Infection rate between asymptomatic and susceptible populations ($\alpha_E >> \alpha_I$)	0.65
α_I	Infection parameter between infected and susceptible populations associated with viral contagiousness and social factors	0.005
γ	Reinfection rate. This parameter is the reciprocal of the level of immunity of the virus (0 - stable immunity)	0
k	Frequency of symptom onset in open cases, leading to a shift from asymptomatic to infected population	0.05
ρ	Recovery rate of identified cases (cases that are identified but recover without any symptoms)	0.08
β	Recovery rate of infected cases	0.1
μ	Mortality rate of infected cases	0.02

2.3 The statement of the inverse problem

Suppose we know measurements of 3 functions at fixed times:

$$I(t_k) = f_k; R(t_k) = g_k; D(t_k) = w_k, \qquad t_k \in (t_0, T), k = 1, ldots, K. \tag{3}$$

here f_k – number of registered patients per day k, g_k – number of recovered patients per day k, w_k – number of deaths from COVID-19 per day k, K – number of days in the period under consideration [19]. The unknown parameters are: $q = (\alpha_E, \alpha_I, k, \rho, \beta)$. Inverse problem 1 – 3 consists in determining the vector of parameters q from additional statistical information The inverse problem is reduced to the problem of minimizing the target functional:

$$J(q) = \sum_{k=1}^{K} [(I(t_k; q) - f_k)^2 + (R(t_k; q) - g_k)^2 + (D(t_k; q) - w_k)^2] \tag{4}$$

The optimization problem was solved by a stochastic global optimization algorithm based on solving simple evolutionary problems from biology. This method is called the differential evolution algorithm.

2.4 Differential evolution algorithm

Differential Evolution (DE), a class of evolutionary algorithms, was first proposed by Rainer Storn and Kenneth Price in 1995 [22–25]. The algorithm is simple to implement, but also very efficient as a meta-heuristic algorithm based on the use of populations [26]. The algorithm is easy to use, requires several control parameters, and has the characteristics of fast convergence [25]. Due to these advantages, it presents a wide range of case studies in various fields such as acoustics, biology, materials science, mechanics, medical imaging, optics, mathematics, physics, seismology, economics, etc.

The differential evolution algorithm is as follows:

1. **Generation.** Create an initial population of target parameter vectors $q_{i,G} = (q^1_{i,G}, q^2_{i,G}, q^3_{i,G}), \quad i = 1, \dots, Np$, where Np population size, G denotes the current generation. Here $q^1_{i,G} = \alpha_{1_{i,G}}, q^2_{i,G} = \alpha_{2_{i,G}}, q^3_{i,G} = p_{i,G}$. The algorithm is generated by a randomly generated population in a predefined search space, taking into account the upper (u-index) and the lower (l-index) boundaries of each parameter $q^j_{i,G} \in [q^j_l, q^j_u], j = 1, 2, 3$.

2. **Choosing a stopping criterion.** Choosing a stop parameter ε_{stop} for the functional and the maximum number of iterations G_{max}. If $J(q_{i,G}) < \varepsilon_{stop}$ for any $i = 1, \dots, Np$ or $G = G_{max}$, then the iterations are stopped and i is selected with the smallest value of the functional $J(q_{i,G})$. Otherwise, go to step (3).

3. **Mutation.** At each iteration, the algorithm generates a new generation of vectors by randomly combining vectors from the previous generation. For every new generation $(G + 1)$ vector from a given target vector q_i from the old generation (G) algorithm randomly selects three vectors $q_(r_1, G), q_(r_2, G)$ and $q_(r_3, G)$ such that i, r_1, r_2, r_3 are different and create a donor vector

   $v_{i,G+1} = q_{r_1,G} + F(q_{r_2,G} - q_{r_3,G}); F \in [0, 2]$ - differential weight

4. **Crossing.** A trial vector is created $u_{i,G}$ from the elements of the target vector $q_{i,G}$ and donor vector $v_{i,G+1}$ with $Cr \in [0, 1]$ probability using the formula

   $$u^2_{i,G+1} = \begin{cases} v^j_{i,G+1}, \text{if} \quad rand_{i,j} \le CR \quad \text{or} \quad j = j_{rand}, \\ \\ q^j_{i,G}, \quad \text{othewise} \end{cases} \qquad j = 1, 2, 3.$$

   Here $rand_{i,j}$ is a uniformly distributed random variable in the range $[0, 1)$, j_rand – a randomly selected integer in a range $[1, 3]$, to ensure that the trial vector does not duplicate the target vector.

5. **Selection.** The vector obtained after crossing is a trial vector. If it turns out to be better than the base vector, then in the new generation the base vector is replaced with a trial one, otherwise the base vector is saved in the new generation. Choosing the next generation as:

$$q_{i,G+1} = \begin{cases} u_{i,G+1}, & J(u_{i,G+1}) \le J(q_{i,G}), \\ \\ q^j_{i,G}, & \text{othewise} \end{cases} \qquad i = 1, \ldots, Np.$$

and go to step (2) until $G + 1 < G_{max}$.

3 Results and discussion

Consider the period of time from the moment of the lifting of strict quarantine measures in Kazakhstan and the moment when the Ministry of Health of the Republic of Kazakhstan (MH) calculated the statistics of cases of COVID-19 and pneumonia separately, i.e. from July 8, 2020. Data from official resources on coronavirus in Kazakhstan were used to compare with the restored function of registered infected and recovered individuals (Fig. 3).

For two weeks period from 07/08/2020, computational work was carried out to restore the parameters of the SEIR-D model and a simulation was built. That in Figure 3, you can see that the reconstructed graph of the infected completely coincides with the official data (blue line and asterisks).

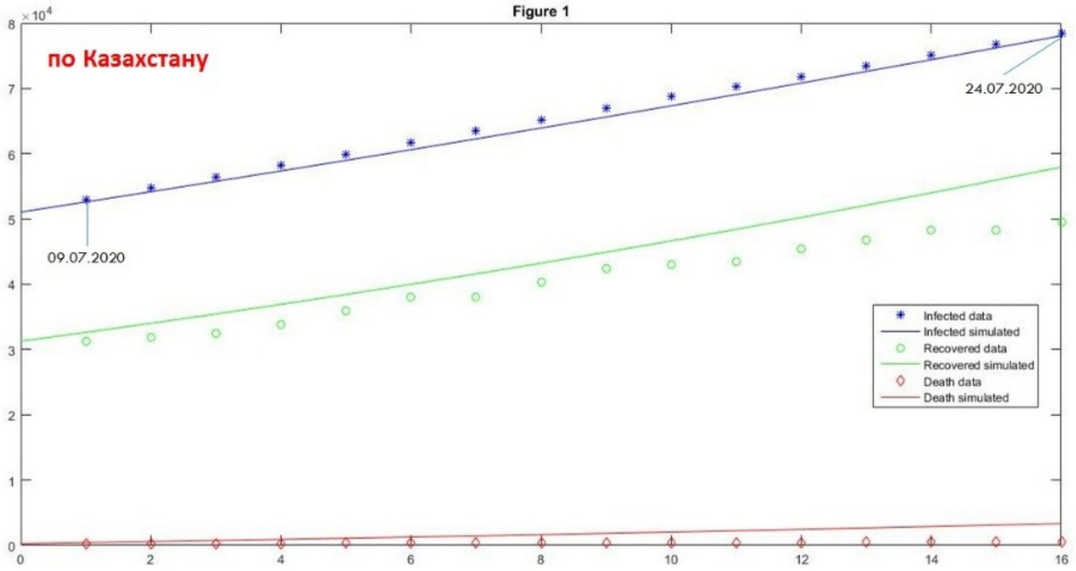

Figure 3: Comparison of model data on infected, recovered and deaths with actually registered cases in the two weeks period from 07/08/2020. Plot of simulated infected, recovered and deceased individuals due to the restored parameters - blue, green and red solid lines, respectively. Plot of registered infected, recovered and deceased individuals - blue asterisks, green rounds, and red diamonds, respectively.

The data on the recovered differ from the modeled data (green line and round circles in Fig. 3), since there are infected individuals who did not go to hospitals, clinics and ambulances, but recovered. The same applies to lethal cases of the disease (red line and diamonds in Fig. 3).

Since the method justified itself and showed more than plausible simulation results similar to real data, a forecast was made for the four weeks period from 07/08/2020 (Fig. 4).

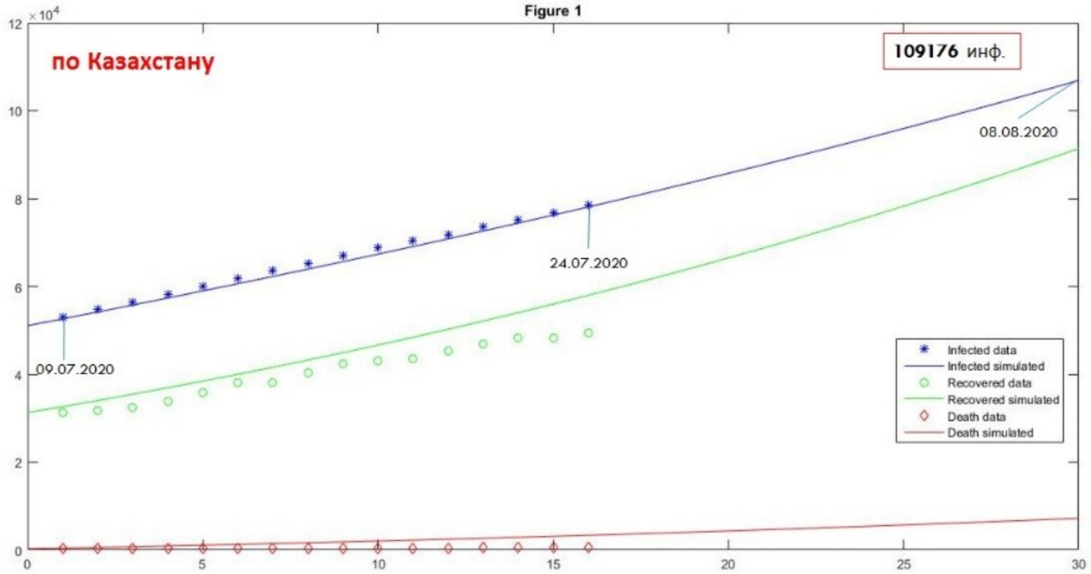

Figure 4: Forecast and comparison of model data on infected, recovered and deaths with actually registered cases in the four weeks period from 07/08/2020. Plot of simulated infected, recovered and deceased individuals due to the restored parameters - blue, green and red solid lines, respectively. Plot of registered infected, recovered and deceased individuals - blue asterisks, green rounds, and red diamonds, respectively.

According to the forecast data, modeled according to the reconstructed parameters of the SEIR-D model, by August 08, 2020, the number of infected individuals was 109, 176. Thus, the forecast was modeled for a period of up to six months. (Fig. 5).

Based on simulated data, it is projected that within six months the number of infected individuals in Kazakhstan would be 982,010. However, according to the line of the infected graph, it can be seen that the peak of infectivity has not yet been reached, in which case, further, the forecast was built for a year from the start of modeling from 07/08/2020 (Fig. 6).

Fig. 6 shows that the peak of infection occurs on February 13,2021 with 1,093,411 infected individuals, and then there is a decline, since the characteristic of the epidemic is its completion. So by 07/08/2021, it is expected to decrease to 343,565 infected individuals.

The predicted values for those infected, recovered and died for six months and one year period from 07/08/2020 are given in Table 2.

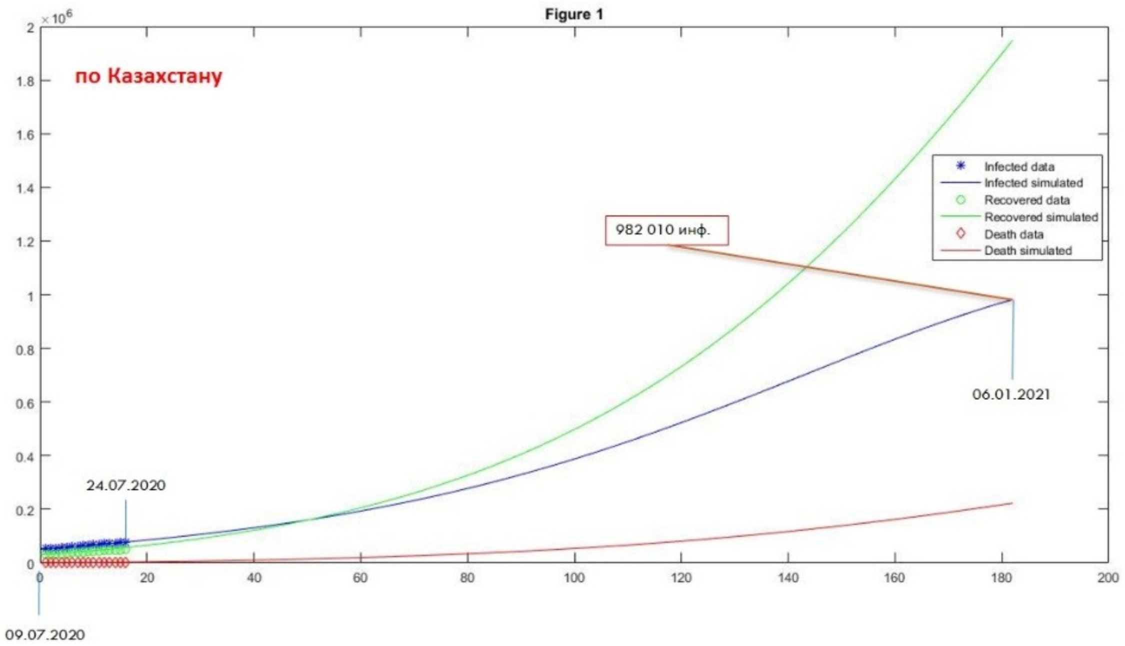

Figure 5: Forecast and comparison of model data on infected, recovered and deaths with actually registered cases in the six months period. Plot of simulated infected, recovered and deceased individuals due to the restored parameters - blue, green and red solid lines, respectively. Plot of registered infected, recovered and deceased individuals - blue asterisks, green rounds, and red diamonds, respectively.

Table 2: Forecast values for COVID-19 in Kazakhstan

	Six months period	One year period
Infected	982010	343565
Recovered	1 948 422	5 798 392
Deceased (pessimistic alignment)	223 039	674 419

4 Conclusion

This study used inverse problem solving methods and a differential evolution algorithm to determine the parameters of the SEIR-D model, which plausibly describes the current situation with the coronavirus pandemic in Kazakhstan and uses known data on infected, recovered and deceased individuals.

Thus, due to the identified model and its parameters, a forecast of the spread of COVID-19 in Kazakhstan for six months / a year was built and the peak of infectiousness was determined in the period from 07/08/2020. All the results were presented to the country authorities after which there were included new anti-covid restrictions in the country, that's why the modeling results may differ from, known from open sources, statistics.

This method allows you to make calculations for various regions and cities of the country and determine the moments for toughening or easing quarantine measures.

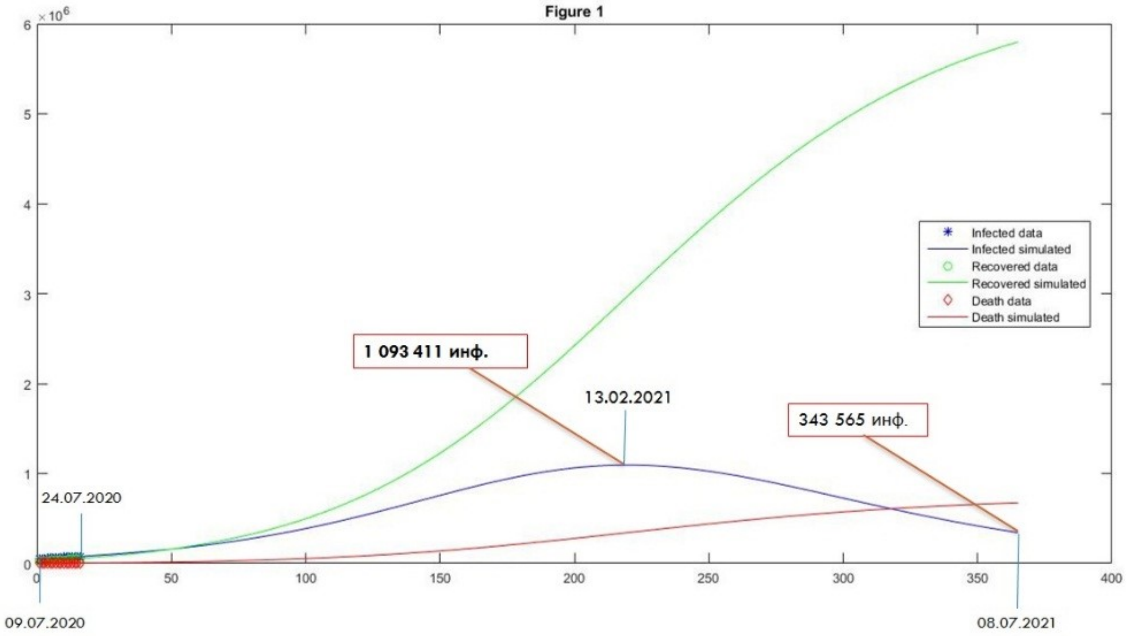

Figure 6: Forecast and comparison of model data on infected, recovered and deaths with actually registered cases in the one-year period. Plot of simulated infected, recovered and deceased individuals due to the restored parameters - blue, green and red solid lines, respectively. Plot of registered infected, recovered and deceased individuals - blue asterisks, green rounds, and red diamonds, respectively.

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