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FORECASTING OF THE EPIDEMIC PROPAGATION BASED ON SOLVING THE INVERSE PROBLEM FOR DISCRETE AND CONTINUOUS MATHEMATICAL MODELS OF EPIDEMICS WITH VACCINATION

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Abstract. Discrete and continuous compartmental models of the spread of the epidemic are considered, taking into account vaccination and limited time spent in groups. Models include the following groups of people: susceptible, contacted, three categories of patients that are undetected, isolated and hospitalized, immunized, vaccinated, and contact vaccinated. Conducted qualitative and quantitative proposed models. The influence of process parameters is investigated. The problems of restoring the coefficients of the equations under consideration are set based on the results of measuring the number of registered patients, vaccinated and deceased. The inverse problems under consideration are solved using the corresponding optimization methods. As an example, the spread of the COVID-19 epidemic in Kazakhstan is being studied.

Keywords: inverse problem, mathematical model of an epidemic, continuous model, discrete model, vaccination.
AMS Subject Classification: 35Q62.

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1 Introduction

Mathematical epidemiology has a rich history (Bacaër, 2021). The use of mathematical methods for the analysis of epidemics goes back to the works of the greatest mathematicians of the second half of the 18th and early 19th centuries D. Bernoulli, I. Lambert, and P.S. Laplace. The first serious mathematical model of the propagation of the epidemic was developed in 1911 by R. Ross to describe the propagation of malaria (Ross, 1911). The SIR model proposed in Kermack & McKendrick (1927) became even more famous. It refers to compartmental models, for which the entire population is divided into compartments of people that differ in their epidemiological state. In particular, the SIR model considers compartments of susceptible, infected, and recovered. Becoming infected by the sick, susceptible individuals move to the compartment of infected, and then after recovery to the compartment of recovered. These intercompartment transitions are described by a system of nonlinear differential equations for the sizes of all considered population compartments.

The SIR model does not take into account the presence of a latency period during which people, being already infected, are not yet themselves a source of infection. To overcome this shortcoming, SEIR was proposed, to which an 'intermediate' exposed compartment was added (often the deceased compartment is also added here, which corresponds to the SEIRD model).

Most modern epidemiological models are extended versions of the SEIR model. Thus, in Mwalili et al. (2020) an additional compartment is considered in which the disease proceeds in an asymptomatic form, and SEIRHCD models also take into account compartments of hospitalized and critically ill patients (Unlu et al., 2020; Krivorotko et al., 2020; Krivorotko & Kabanikhin, 2021).

In addition to continuous models, similar discrete models are also considered, which are described by the corresponding recurrent relations (Brauer et al., 2010; Turar & Serovajsky, 2021; Serovajsky, 2021; Turar et al., 2021). Among other types of models, we also note partial differential equations describing the propagation of an epidemic over a certain territory (Aristov et al., 2021), stochastic models (Bailey, 1975; Andersson & Britton, 2000), agent models (Krivorotko & Kabanikhin, 2021; Krivorotko et al., 2022).

Currently, the relevant models are those that take vaccination into account. At the same time, susceptible individuals who have been vaccinated can be considered immunized and in this sense are not different from those who have been ill (Scherer & McLean, 2002). However, it seems more natural to separate the vaccinated into a separate compartment. In particular, the SIRV (Schlickeiser & Kröger, 2021) and SEIRV (Cai et al., 2018) models are considered, which are extensions of the SIR and SEIR models by adding the vaccinated compartment. In Schlickeiser & Kröger (2021), vaccination in the presence of mutant strains and the phenomenon of vaccine resistance are also studied. In Ghostine et al. (2021), the SEIRQV model is proposed, in which the category of people in quarantine is additionally present, in Parolini et al. (2022) - the SUIHTER model with categories of undiagnosed and hospitalized patients, as well as with a difference in people who have received one or two doses of the vaccine, in Diagne et al. (2021), the SVEIAHR model examines vaccination in the presence of three categories of patients that are symptomatic and asymptomatic infected, as well as hospitalized. A stochastic model of the propagation of an epidemic with vaccination is considered in Zhang et al. (2018) and He et al. (2020). In Alsakaji et al. (2022) and Alshehri & Ullah (2023), the propagation of an epidemic over a certain territory with vaccination is considered. An assessment of vaccination effectiveness based on the SEIR model is given in Saharan & Tee (2023). Khan (2022) addresses the challenges of vaccination management for the COVID-19 epidemic.

Paper Serovajsky et al. (2022) proposes continuous and discrete models with compartments of vaccinated and contact vaccinated with a limited time spent in all compartments of patients and contacts, which are generalizations of the models considered in Turar & Serovajsky (2021); Serovajsky (2021); Turar et al. (2021). A significant drawback of these models is the constancy of the vaccination rate, as a result of which people continue to be vaccinated even at the final stage of the epidemic. In this paper, it is proposed to make the rate of vaccination of the population dependent on the incidence, since it is the increase in the incidence that stimulates vaccination.

It should be noted that the practical application of epidemiology models (as well as any other mathematical models) implies their identification in each specific case. In this case, inverse problems are formulated (Kabanikhin, 2011), which consist in finding such parameters of the system that are not amenable to direct experimental measurement, based on the available mathematical model and additional information about the state of the system. The methods of the theory of inverse problems and the corresponding numerical methods are also widely used in the analysis of mathematical models of the propagation of epidemics (see, for example, (Krivorotko et al., 2020; Krivorotko & Kabanikhin, 2021; Turar & Serovajsky, 2021; Turar et al., 2021).

This paper describes discrete and continuous models of the propagation of the epidemic, taking into account vaccination and the limited time spent in all compartments of contacts and patients. The properties of the solution of the resulting equations are described. The corresponding inverse problems are solved with an estimate of the accuracy of their solution. As an example, the propagation of COVID-19 in Kazakhstan is considered. The forecast results are compared with real data.

2 Used assumptions

As is known, all compartmental models differ in the choice of population compartments and acceptable intercompartment transitions. In almost all models of epidemiology, there is a susceptible compartment. It consists of healthy people who can get sick by coming into contact with the sick. The number of susceptible individuals at time t for the continuous model and on the k-th day for the discrete model are denoted respectively by $S(t)$ and S_k. A similar principle will be used later to indicate the size of other population compartments. In the case of contact with the sick, the susceptible move into the contact compartment, which can thereby become ill, although they do not necessarily become ill. The number contacted will be denoted by E, since this compartment largely corresponds to the exposed compartment of the SEIR model.

We will distinguish three categories of patients that are undetected, isolated and hospitalized, the number of which is denoted by U, I and H, respectively. As a result, there is no information about category of undetected patients in the official statistics of the disease, which significantly affects the process of setting inverse problems. This compartment consists of patients in whom the disease proceeds in an asymptomatic form, as well as mildly ill patients who have not consulted a doctor. Hospitalized (these are patients with a severe form of the disease) differ from other sick people in that they are under the watchful supervision of doctors. As a result, their influence on the propagation of the epidemic can be neglected. The isolated compartment, which is mainly made up of patients with a mild form, treated at home plays an intermediate role. On the one hand, they are taken into account in the official statistics of the disease, and, on the other hand, they can serve as sources of infection, although to a lesser extent than undetected.

Next, two compartments of vaccinated are considered that are vaccinated and contact vaccinated, the number of which is denoted by V and C, respectively. We assume (see Saharan & Tee (2023) and Olliaro (2021)) that the vaccinated may still get sick, but less likely than the unvaccinated. If they get sick, then the disease they have is milder.

Recovered people are immune and form the immunized compartment. Their number is denoted by R, since they correspond to the recovered compartment present in almost all compartmental models. The last compartment is deceased, the number of which is traditionally denoted by D.

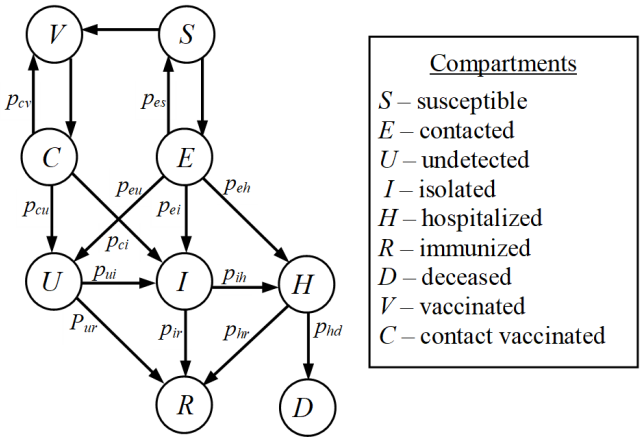

Figure 1: Characteristics of intercompartment transitions.

Figure 1 shows the considered intercompartment transitions. In particular, the susceptible move into the contacted compartment, coming into contact with the sick, and into the vaccinated compartment after vaccination. The latter, in case of contact with patients, go to the contact vaccinated compartment. Contact may get sick in any form or not at all, returning to the

susceptible compartment. Contact vaccinated may also get sick, but not severely, or return to the contacted compartment. A patient in any form can recover or his disease will go into a more severe form. The hospitalized may die. We denote by n_x the time spent in compartment X, and p_xy denotes the proportion of people from compartment X moving over time to compartment Y. Naturally, the sum of all the parts leaving this compartment will be equal to 1.

$$p_{es} + p_{eu} + p_{ei} + p_{eh} = 1,\ p_{cv} + p_{cu} + p_{ci} = 1,\ p_{ui} + p_{ur} = 1,\ \ p_{ih} + p_{ir} = 1,\ p_{hr} + p_{hd} = 1. \quad (1)$$

We will consider two models that describe the process under the assumptions made. They differ in the nature of time (discrete or continuous value) and in the way they take into account the limited time spent in contact and patient compartments.

3 Discrete model

In the discrete model, all values of X_k characterizing the number of individuals of compartment X on the k-th day are determined. If X describes all compartments of patients and contacts (i.e., takes the values E, C, U, I, H), then the value of X_k is the sum of their number at the moment of time for each of the days of being in this compartment, which corresponds to the equalities

$$X_k = \sum_{j=1}^{n_x} x_k^j, \quad (2)$$

where x_k^i denotes the number of people in the compartment X at time k on the j-th day of being in this compartment, $j = 1, \ldots, n_x$. In this case, every other day each individual of the compartment Z of the j-th day of being in this compartment passes to the category of the $j+1$-th day, if it was not the last day of being in the compartment (on the last day the person leaves the compartment altogether), which corresponds to the equalities

$$x_{k+1}^{j+1} = x_k^j, \qquad j = 2, \ldots, n_x - 1. \quad (3)$$

Obviously, the change in the number of all compartments of contacts and patients occurs due to the arrival of new people in the compartment, which corresponds to the number of people on the first day of being in this compartment at the next point in time and leaving it by people who are in the compartment on the last day. As a result, we obtain the equality

$$X_{k+1} = X_k + x_{k+1}^1 - x_k^{n_x}. \quad (4)$$

Let us now turn to the description of population compartments that are not related to contact and patients. Susceptible individuals leave their compartment through contact with the sick and vaccination, but their number is replenished by non-sick contacts of the last day. The number of susceptibles at a given point in time who have become contacts is proportional to the total number of susceptibles. The corresponding coefficient of proportionality is determined by the number of active carriers of the disease (to a greater extent from undetected, to a lesser extent from isolated, but not hospitalized). Similarly, the number of those currently vaccinated susceptible is also proportional to their total number, and the corresponding proportionality factor depends on the number of registered patients (mostly hospitalized, it is a large number of seriously ill patients that stimulates the vaccination of the population, to a lesser extent from isolated ones, but not from undetected, about which nothing is known). As a result, we get the formula

$$S_{k+1} = S_k - \frac{v_h H_k + v_i I_k}{N} S_k - \frac{\kappa_u U_k + \kappa_i I_k}{N} S_k + p_{es} e_k^{n_k}, \quad (5)$$

where parameters ν_h and ν_i characterizes the degree of influence of the number of hospitalized and isolated people on the desire of people to be vaccinated, and κ_u and κ_i reflect the contagiousness of undetected and isolated patients. The division by the number N of the entire population count is carried out here for reasons of normalization, as in the well-known models SIR, SEIR, etc.

The number of those vaccinated decreases due to contacts with the sick and increases due to the vaccination of the susceptible and the return to the compartment of those contact vaccinated who did not get sick. By analogy with formula (5), we have

$$V_{k+1} = V_k + \frac{v_h H_k + v_i I_k}{N} S_k - \frac{\kappa_u U_k + \kappa_i I_k}{N} V_k + p_{cv} c_k^{n_c}. \tag{6}$$

The number of immunized increases due to the recovery of all types of patients, which corresponds to the equality

$$R_{k+1} = R_k + p_{ur} u_k^{n_a} + p_{ir} i_k^{n_i} + p_{hr} h_k^{n_h}. \tag{7}$$

The number of deceased increases due to the deaths of a part of the hospitalized, which gives the formula

$$D_{k+1} = D_k + p_{hd} h_k^{n_h}. \tag{8}$$

It remains to indicate the number of people on the first day of being in the compartments of contact and all types of patients. The number of contacts and vaccinated contacts on the first day of being in compartments is exactly equal to the number, respectively, of susceptible and vaccinated contacts who had contact with patients on the previous day:

$$e_{k+1}^1 = (\kappa_u U_k + \kappa_i I_k) \frac{S_k}{N}, \quad c_{k+1}^1 = (\kappa_u U_k + \kappa_i I_k) \frac{V_k}{N}. \tag{9}$$

The number of new undetected is the sum of the number of both compartments of contacts of the last day of stay in the compartment, in which the disease developed in an undetected form:

$$u_{k+1}^1 = p_{eu} e_k^{n_e} + p_{cu} c_k^{n_c}. \tag{10}$$

The number of new isolated patients is the sum of the people of the last day of stay in both of contact compartments, who became isolated patients, as well as the number of undetected patients of the last day of stay in the compartment, in whom the disease was detected

$$i_{k+1}^1 = p_{ei} e_k^{n_e} + p_{ci} c_k^{n_c} + p_{ui} u_k^{n_u}. \tag{11}$$

The number of new hospitalizations is the sum of the number of contacts and isolated patients of the last day of stay in the compartment, who developed a severe form of the disease, as a result of which they were hospitalized

$$h_{k+1}^1 = p_{eh} e_k^{n_e} + p_{ih} i_k^{n_i}. \tag{12}$$

The initial states of the system X0 for all compartments are considered to be known, and the distribution of all forms of contact and patients at the initial moment of time by days spent in compartments is considered uniform for simplicity, i.e. the following equalities are fulfilled

$$x_0^j = X_0/n_x, j = 1, \ldots, n_x. \tag{13}$$

In this case, the sum of the initial values all population compartments (including those who died from this disease) is equal to the number of the entire population:

$$S_0 + V_0 + E_0 + C_0 + U_0 + I_0 + H_0 + R_0 + D_0 = N. \tag{14}$$

Relations (2) — (14) with equalities (1) constitute a discrete model of the propagation of the epidemic with vaccination. Note that equalities (7), (8) imply that the sequences R_k and D_k are increasing, i.e., over time, there is an increase in immunized and dead. If we add together all equalities (4) — (8) taking into account conditions (1), (2), (3), (9) — (12), then it turns out that the sum of the numbers of all compartments does not depend on time and is equal to N due to condition (14). Finally, if there are limits of all sequences X_k, then as a result of passing to the limit in equalities (4) —- (8) it turns out that the limiting values of the sizes of all compartments of contact and sick people are equal to zero, i.e. the epidemic ends with time.

4 Continuous model

The continuous mathematical model is derived under the same assumptions and using the same notation as the discrete model described earlier. The state of the system is described here by the same functions, but with a continuously changing time t. In particular, the number of susceptible people decreases due to contacts with patients and vaccination, and increases due to the fact that some people who have been in contact with patients in the past do not get sick. This corresponds to the equation

$$\frac{dS(t)}{dt} = -\frac{v_h H(t) + v_i I(t)}{N} S(t) - \frac{\kappa_u U(t) + \kappa_i I(t)}{N} S(t) + p_{es} \frac{E(t)}{n_e}. \tag{15}$$

The first and second terms on its right side have the same meaning as similar summands in equality (5), and the third term says that the longer the time n_e spent in the contact compartment, the less those of them that did not get sick, will return to the susceptible compartment per unit of time.

The change in the number of vaccinated is associated with their decrease due to contacts with patients, and an increase due to the vaccination of susceptible and the fact that some of the vaccinated contacts did not get sick. The corresponding equation is similar to formula (6) and can be written as

$$\frac{dV(t)}{dt} = \frac{v_h H(t) + v_i I(t)}{N} S(t) - \frac{\kappa_u U(t) + \kappa_i I(t)}{N} V(t) + p_{cv} \frac{C(t)}{n_c}. \tag{16}$$

The change in the number of both contact compartments grows due to contacts of susceptible and vaccinated with patients, and decreases due to the limited time spent in compartments. The result is the equations

$$\frac{dE(t)}{dt} = \frac{\kappa_u U(t) + \kappa_i I(t)}{N} S(t) - \frac{E(t)}{n_e} \tag{17}$$

$$\frac{dC(t)}{dt} = \frac{\kappa_u U(t) + \kappa_i I(t)}{N} V(t) - \frac{C(t)}{n_e} \tag{18}$$

similar to conditions (4) for X equal to E and C, taking into account formulas (9).

The number of undetected increases due to the undetected diseases occurred in both contact compartments and decreases due to the limited time spent in the compartment. This gives the equation

$$\frac{dU(t)}{dt} = p_{eu} \frac{E(t)}{n_e} + p_{cu} \frac{C(t)}{n_e} - \frac{U(t)}{n_u} \tag{19}$$

similar to equality (4) for $X = U$ with formula (10) taken into account.

The number of isolated patients increases due to the diseases occurred both contact compartments and the detection of the disease in some of the undetected patients, and decreases due to the limited time spent in the compartment. Thus we get the equation

$$\frac{dI(t)}{dt} = p_{ei}\frac{E(t)}{n_e} + p_{ci}\frac{C(t)}{n_c} + p_{ui}\frac{U(t)}{n_u} - \frac{I(t)}{n_i} \tag{20}$$

similar to formula (4) for $X = I$, taking into account condition (11).

The number of hospitalized increases due to the severe form of the disease in some of the contacts and hospitalization of the isolated ones and decreases due to the limited time spent in the compartment. As a result, we obtain the equation

$$\frac{dH(t)}{dt} = p_{eh}\frac{E(t)}{n_e} + p_{ih}\frac{I(t)}{n_i} - \frac{H(t)}{n_h} \tag{21}$$

similar to formula (4) for $X = H$, taking into account condition (12).

The number of immunized increases due to the recovery of patients of all categories, and the number of deceased increases due to the death of a part of the hospitalized. As a result, we obtain the equations

$$\frac{dR(t)}{dt} = p_{ur}\frac{U(t)}{n_u} + p_{ir}\frac{I(t)}{n_i} + p_{hr}\frac{H(t)}{n_h} \tag{22}$$

$$\frac{dD(t)}{dt} = p_{hd}\frac{H(t)}{n_h} \tag{23}$$

similar to equalities (7) and (8).

The resulting differential equations are considered with the initial conditions

$$X(0) = X_0, \tag{24}$$

where X_0 covers all available populations. The Cauchy problem (15) — (24), taking into account equalities (1), constitutes a continuous mathematical model of the process under study.

Note that since all the quantities on the right-hand sides of equations (22) and (23) are positive, the functions R and D are increasing. As a result of adding all equalities (15) — (23), taking into account formulas (1), we conclude that the sum of all considered functions is constant, and therefore represents the first integral of the system. Thus, the total population size (including those who died from the disease) does not change with time and is equal to N, since equality (14), which relates the initial values of all population compartments, is assumed to be satisfied. Equating all derivatives of the functions under consideration to zero and solving the resulting system of algebraic equations, we conclude that in the state of equilibrium numbers of all compartments of contact and patients is equal to zero. Thus, the equilibrium position of the system corresponds to the end of the epidemic. Thus, main qualitative characteristics of both models coincide.

5 Numerical analysis of the mathematical models

For numerical analysis of the system, we assume that the parameters of the system are bound by certain conditions. In particular, time spent in the compartment of vaccinated contacts is assumed to be the same as for unvaccinated contacts, i.e. $n_c = n_e$. The contagiousness of undetected patients is considered higher than that of isolated ones, which corresponds to the inequality $\kappa_u > \kappa_i$. The influence of the number of hospitalized patients on the rate of vaccination is higher than that of those isolated, i.e. $\nu_i < \nu_h$. The probability of getting is significantly lower for vaccinated than for susceptible, which corresponds to the inequalities

$p_c u < p_e u, p_c i < p_e i$. Those vaccinated are more likely not to get sick at all and less likely to become isolated $p_c i < p_c u < p_c v$.

For preliminary calculations, we used the following values of the system parameters, which were selected based on expert assessments, as well as earlier studies based on solving inverse problems for simpler models that do not take into account vaccination (**?**). Number of days spent in compartments: $n_e = 14$, $n_u = 3$, $n_i = 5$, $n_h = 7$, $n_c = n_e = 7$. The coefficients of the equations take the following values: $\kappa_u = 3.180$, $\kappa_i = 0.171$, $\nu_h = 0.3$, $\nu_i = 0.01$, $p_{es} = 0.679$, $p_{eu} = 0.154$, $p_{ei} = 0.145$, $p_{eh} = 0.022$, $p_{cv} = 0.9$, $p_{cu} = 0.05$, $p_{ci} = 0.05$, $p_{ui} = 0.03$, $p_{ur} = 0.97$, $p_{ih} = 0.021$, $p_{ir} = 0.979$, $p_{hr} = 0.982$, $p_{hd} = 0.01$. Calculations were carried out at the initial stage of the epidemic, and N=18699640, which corresponded to the population of Kazakhstan at the time of the start of the COVID-19 epidemic. The change in the numbers of all considered population compartments obtained as a result of the calculation is shown in figure 2, here and everywhere below, the red curves correspond to the discrete model, and the blue curves to the continuous one. Figure 3 shows the total number of sick people, as well as the number of recovered, dead and vaccinated on a given day.

As can be seen from the graphs, both models lead to fairly close, although not identical, results. This can be explained by the fact that the models were derived based on the same hypotheses, although individual effects are described by different methods. According to the results obtained, the number of people in all contact and patient compartments tends to zero over time, which corresponds to the end of the epidemic and is consistent with the previously noted properties of the models.

Naturally, the practical application of the proposed models in each specific case is possible only after the system has been identified on the basis of solving the corresponding inverse problems.

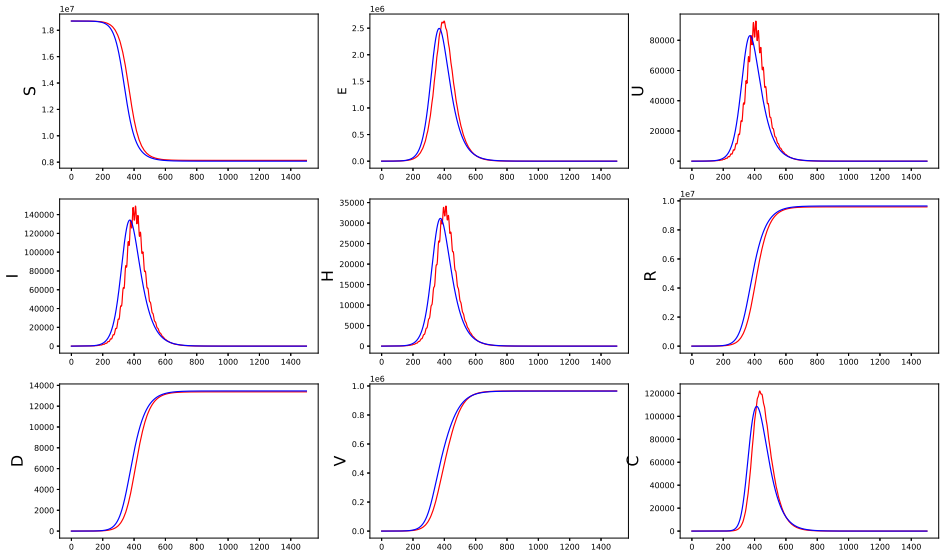

Figure 2: Change in the sizes of population compartments for the main set of parameters.

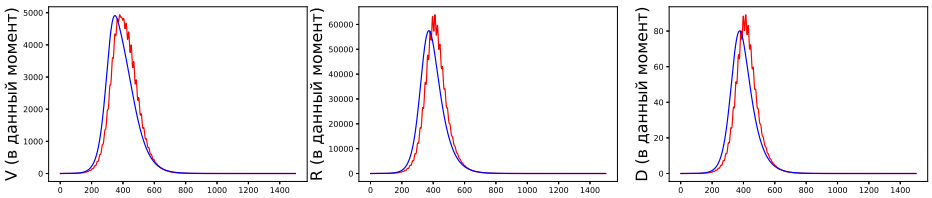

Figure 3: The number of sick, recovered, deceased and vaccinated people on a given day.

6 Inverse problems

The practical use of the considered models for forecasting the epidemiological situation requires knowledge of all the parameters included in the system. The number of these parameters is too large, and the available more or less reliable statistical information on the development of the epidemic is not very much. Under these conditions, the corresponding inverse problems turn out to be essentially ill-posed (Kabanikhin (2011)). As a result, it is not necessary to rely on the restoration of all unknown parameters directly with a reasonable degree of accuracy.

In connection with stated above, we divided all system parameters into three groups. The first part consisted of those characteristics for which there is some information based on expert assessments of specialists. This includes the number of days spent in compartments, as well as some of the parameters characterizing intercompartment transitions. It is true for all the parameters that are not related to the exit from the compartments of contact and undiagnosed patients (they belong to the second group of parameters) and contact vaccinated (we attributed them to the third group of parameters). We simply consider them given. The second part of the parameters (the initial values of the number of undetected and contact patients and the other part of the parameters characterizing intercompartment transitions) are in no way related to vaccination. In this regard, they can be found by solving the corresponding inverse problems for analogs of the considered models in the absence of vaccination. The corresponding results were obtained earlier, see Turar et al. (2021). The use of this information in the model is justified by the fact that it refers exclusively to people who have not been vaccinated. Thus, in this case, we also consider this group of parameters to be known (they correspond to the values discussed in the previous section of the article). As a result, the parameters characterizing the rate of vaccination ν_i and ν_h are unknown, as well as the characteristics of transitions from the compartment of vaccinated contacts p_{cv} and p_{cu} (the p_{ci} is determined by them in (1)). In addition, we also consider the coefficients of contagiousness unknown κ_u and κ_i, which, although not related to vaccination, and therefore can be found in the process of solving inverse problems for simplified models, but, as preliminary calculations show, have a significant effect on the process under study (Serovajsky et al., 2022) and are less amenable to recovery (Turar et al., 2021).

As known measurable information, we choose the changing numbers of registered patients (the sum of isolated and hospitalized), vaccinated, and deceased over time. As a result, we obtain the following inverse problems.

Problem 1. Find the values of the parameters n_h, n_v, k_u, k_i, p_{cv}, p_{cu} so that the corresponding solutions I_k, H_k, V_k, D_k of problem (1) – (14) satisfy the following conditions:

$$I_k + H_k = X_k, \qquad V_k = Y_k, D_k = Z_k, \qquad k = t_0, \qquad t_{0+1}, \ldots, t_n, \tag{25}$$

where X_k, Y_k, Z_k are the known values of the sum of the isolated and hospitalized, vaccinated and deceased correspondingly at the specified points in time, t_0 and t_n are the initial and final points in time at which the problem is solved.

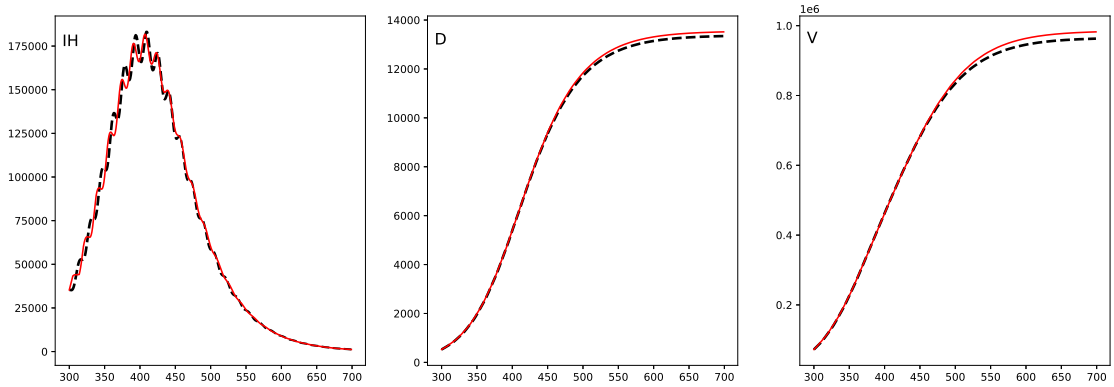

Figure 4: Exact and reconstructed values of the number of detected, vaccinated and deceased patients for a discrete model.

Problem 2. Find such values of the parameters n_h, n_v, k_u, k_i, p_{cv}, p_{cu} that the corresponding solutions I, H, V, D of problem (15) — (24) satisfy the following conditions:

$$I(t) + H(t) = X(t), \qquad V(t) = Y(t), \qquad D(t) = Z(t), \qquad t \in (t_0, t_n), \tag{26}$$

where X, Y, Z are the known values of the sum of the isolated and hospitalized, vaccinated and deceased at the specified points in time, t0 and tn are the initial and final points in time at which the problem is solved.

The obtained inverse problems are reduced in a standard way to optimization problems. In this case, the functionals being minimized are standard sums (for a discrete model) and integrals (for a continuous model), expressing the standard deviation deviations of the corresponding quantities determined from the models from their known analogues. The trust-region method (Conn et al., 2000) was used to directly solve the resulting optimization problems. In the Python programming language, it is implemented using the *scipy.optimize.minimize* module, which contains this method, as well as *scipy.optimize.LinearConstraint* to create linear constraints on the desired parameters.

To estimate the accuracy of solving inverse problems, the calculations were first carried out on model data. In this case, the unknown values of the parameters were set as in the earlier version of the calculation. In the process of numerical analysis of the corresponding models, the values of $I + H, V$, and D were determined. The values found (time functions) were included in the indicated inverse problems, after which the problem of restoring the indicated parameters was posed.

Figure 4 shows graphs of the changes over time in the number of identified patients, vaccinated and deceased, for the exact values of the parameters and for the values obtained by solving the inverse problems for discrete models. Similar information for the continuous model is shown in figure 5. In this case, the exact solution (corresponding to the given values of the parameters) is shown by a dotted line, and the solution found using the inverse problem is shown by a solid line. As can be seen from the graphs, all three curves are restored quite accurately for both models. This indicates a rather high efficiency of the optimization algorithm used.

The results of the direct recovery of the desired parameters are shown in Table 1. As can be seen from the results obtained, there are already certain discrepancies here. The fact of not very high accuracy of parameter recovery at extremely high accuracy of the state functions is quite natural and can be considered as a sign of strongly marked ill-posedness of the considered inverse problems (Kabanikhin, 2011). Indeed, in the presence of a sufficiently large amount of identifiable information and a relatively small amount of measured information, the same system state functions can correspond to different sets of system parameters. In addition, inverse

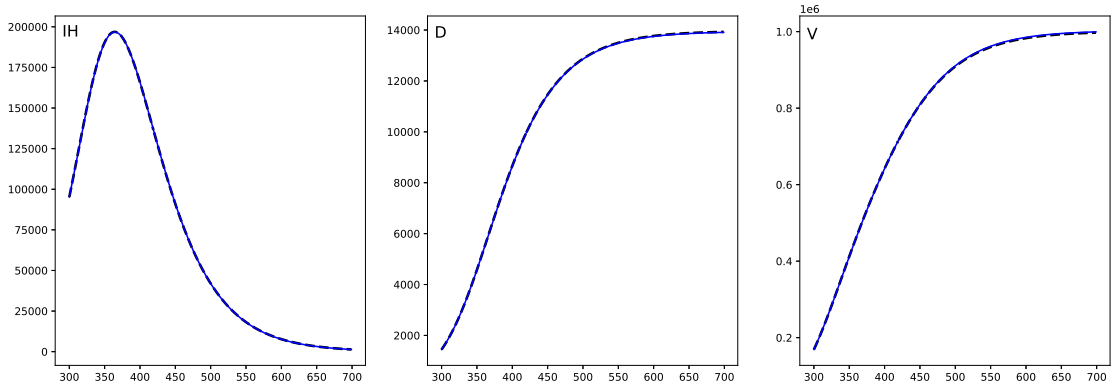

Figure 5: Exact and reconstructed values of the number of detected, vaccinated and deceased patients for a continuous model.

Table 1: Results of inverse problem calculation for previously known parameters.

Parameter	exact value	discrete model		continuous model	
		result	error	result	error
ν_h	0.300	0.320	0.020	0.169	0.131
ν_i	0.010	0.005	0.005	0.036	0.026
κ_u	3.180	0.002	3.178	2.946	0.234
κ_i	0.171	2.174	2.003	0.300	0.129
p_{cv}	0.900	0.918	0.018	0.913	0.013
p_{cu}	0.050	0.072	0.022	0.043	0.008

problems were reduced to optimization problems, which, in turn, are ill-posed in the sense of Tikhonov (Vasiliev, 2011), i.e. proximity to the minimum of the functional can be realized (see Figures 3 and 4) in the absence of sufficient proximity of the functional argument to its minimum point (see Table 2). However, from a practical point of view, i.e. to predict the course of the epidemic, it is not the coefficients of the equations that are of interest, but the curves themselves, reflecting the change in the epidemiological situation. As a result, the non-uniqueness of the approximate solution of the inverse problem is not so significant in conditions of high accuracy of reconstruction of the measured quantities; and one can hope for the possibility of practical use of the models under consideration.

Let us now turn to a more detailed analysis of the results obtained. For both models, the coefficients $p_c v$ and $p_c u$, reflecting the distribution of contact vaccinated, are best restored, and the worst are the parameters κ_u and κ_i characterizing the contagiousness of the infected. Actually, when solving inverse problems based on simplified (without vaccination) versions of the considered discrete and continuous models, the contagiousness coefficients were restored with less accuracy compared to other unknown parameters, see Turar et al. (2021). That is why we included them among the unknowns in the analysis of these models.

Let us note one more important circumstance. In all previous studies, we could not favor either of the two available models. The solution of inverse problems based on simplified (without vaccination) versions of the considered discrete and continuous models also led to approximately the same result (Turar et al., 2021). However, when estimating the accuracy of restoring parameters, the continuous model as a whole turns out to be preferable. The distribution parameters of contact vaccinated and, to an even greater extent, the contagiousness coefficients are determined more accurately on the basis of the inverse problem for the continuous model. At the same time, the reconstruction accuracy of ν_h and ν_i, expressing the rate of population vaccination, turns out to be higher on the basis of a discrete model than in continuous model. In this regard, we do not abandon the discrete model and give two forecast options below.

Table 2: Found parameters when solving inverse problems with real data.

parameter	discrete model	continuous model
ν_h	4.998	2.000
ν_i	1.164	1.476
κ_u	0.639	3.530
κ_i	3.233	0.771
p_{cv}	0.782	0.873
p_{cu}	0.218	0.127

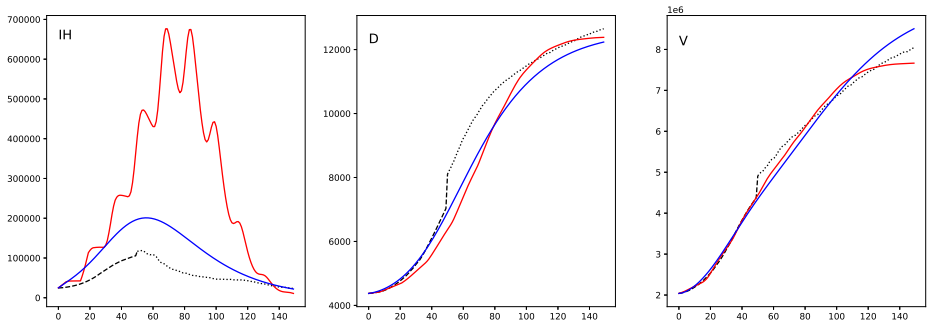

Figure 6: Comparison of inverse problem solutions based simulation with the actual data from July 1 to December 31 of 2021.

At the final stage of the study, we solve the considered inverse problems based on real statistical information about the propagation of COVID-19 in Kazakhstan (Corona Virus KZ, 2022). For this purpose, the second half of 2021 was considered, when mass vaccination of the population took place in Kazakhstan. As initial information, we use data on the number of registered patients, vaccinated and deceased within fifty days, starting from July 1, 2021. Due to the fact that the available data is very noisy, we first smooth it out using moving average. Following values of the required parameters were found based on solving the corresponding inverse problems for both models, see Table 2.

Figure 6 shows graphs of the change in three recoverable functions (number of registered patients, deaths and vaccinated) obtained by inverse problems solving for discrete (red lines) and continuous (blue lines) in comparison with the actual change in the considered values (dashed lines) during second half of 2021 (July 1 to December 31) Corona Virus KZ (2022). In this case, the first 50 days correspond to the time period for which the model was identified (here we show not the actual values of real data, but the result of their smoothing; this part is depicted by dashed line), and the subsequent values are the period for which the forecast is made. Figure 7 shows the corresponding change in the number of deaths and vaccinated by day.

The results obtained show the relative realism of forecasting based on both models. In particular, in both cases, a decrease in the incidence is predicted approximately two months after the starting point, although at the end of known information usage, an increase in the incidence was still observed. Note that the largest deviations in incidence (slightly larger for a discrete model compared to a continuous one) are observed during the peak incidence (two to three months after the start of observation), and then the deviation from the actual value decreases. At the same time, both models give an overestimated incidence forecast, although the discrete model gives a slightly underestimated forecast for the last month being considered.

As it can be seen from figure 6, the curves for total mortality and vaccination are closer to the actual values of these values compared to the incidence curve. Characteristically, in both cases, the forecast is somewhat underestimated. At the same time, the continuous model reproduces mortality slightly more accurately, while the discrete model reproduces vaccinability. If we turn to these characteristics by day (see figure 7), then the following picture is observed. Naturally, in

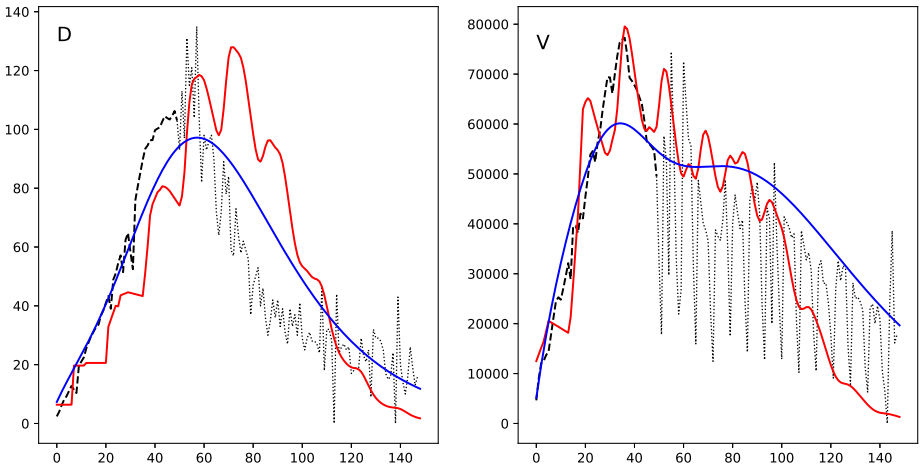

Figure 7: Change in the number of deceased and vaccinated by days.

the real picture of the disease, we observe significant jumps, which are random in nature (here, as in figure 6, the initial identification interval does not show the actual values of real data, but the result of their smoothing) and, of course, are not reproduced by models. However, the discrete model, which is characterized by sharper changes in all functions, reproduces something similar. In terms of mortality before the peak of the epidemic, the forecast for both models turns out to be underestimated, subsequently on figure 6, both forecast curves over the entire time interval are below the real curve. After the peak of the epidemic, daily mortality is predicted to be somewhat overestimated, and for the last one and a half to two months, the accuracy is quite high, especially based on a continuous model. As it can be seen from figure 7, the daily vaccination forecast curve turns out to be closer to the real one for the discrete model, while the forecast based on the continuous model gives an underestimated result, especially in the second half of the considered time interval.

The results obtained indicate that the models under consideration, preferably both at the same time, can be used to predict the development of epidemics in the state of vaccination.

7 Conclusion

In this paper, we propose two models for the development of epidemics with vaccination that are discrete and continuous, which also differ in the way they consider the limited time spent in all compartments of contacts and patients. Both models are characterized by the invariability of the size of the entire population (the population size is the first integral of the system) and predict the end of the epidemic over time (in the equilibrium position, the number of people in the contact and sick compartments is zero).

Calculations show an increase in the incidence at the initial stage of the epidemic, the achievement of a certain peak and the gradual attenuation of the process. In the process of solving the corresponding inverse problems on model data, it was found that the algorithm used provides a sufficiently high accuracy of bringing the system to the desired state and a lower accuracy of reproduction of unknown process parameters. Further, inverse problems were solved based on real information about the development of the COVID-19 epidemic in Kazakhstan. The forecast results based on the resulting parameter values correlate quite well with the available information on the actual development of the epidemic over the same period. For the practical application of the results obtained in a specific situation, similar calculations can be carried out

with real data corresponding to that situation.

To further refine the model and describe the process over a longer period of time, it would be possible to take into account the possibility of re-infection of those who have been ill, as well as the limited duration of the vaccine.

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