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MATHEMATICAL MODELING OF EPIDEMIC PROPAGATION WITH VACCINATION

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Abstract. Discrete and continuous models of the spread of the epidemic are considered, taking into account vaccination and limited time spent in groups. Conducted qualitative and quantitative proposed models. The influence of process parameters is investigated. As an example, the spread of the COVID-19 epidemic in Kazakhstan is being studied.

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1 Introduction

One of the consequences of the COVID-19 pandemic has been the rapid development of mathematical epidemiology. Currently, hundreds of various mathematical models of the epidemic development are known. Compartmental models are the most widespread among them, which involve the division of the entire population into parts (compartments), which differ in their epidemiological state. The source of this trend is the SIR model proposed by W. Kermack and A. McKendrick (Kermack, 1927). In this model, the population consists of susceptible, infectious, and recovered groups, and the mathematical model is a system of differential equations that describes the transition of individuals from the susceptible group to the infectious group and then recovered. Its natural extension is the SIRD model, which also introduces the deceased compartment (Bailey, 1975).

The main drawback of these models, as well as the similar SIS and SIRS models, is the ignoring of the latency period, during which individuals have been infected, but are not yet infectious themselves. As a result, the SEIR model was developed, to which the exposed compartment was added. This model, as well as its extended version SEIRD, which takes into account the deceased, became the basis of modern mathematical epidemiology (see, for example, Hethcote (2000); Keeling et al. (2007); Krivorotko et al. (2020); Sameni (2020); Krivorotko et al. (2021)). In particular, the MSEIR model also considers people maternally derived immunity (Almeida et al., 2019). In Mwalili et al. (2020), authors consider a model that additionally takes into account patients in whom the disease proceeds in an asymptomatic form, and the SEIRHCD model also

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takes into account compartments of hospitalized and critically ill patients (Krivorotko et al., 2020, 2021; Unlu et al., 2020).

To describe the spread of an epidemic over a certain territory, partial differential equations with diffusion terms are used (see, for example, Aristov et al. (2021)). Similar equations are also used to analyze the distribution of certain population compartments not only in time, but also by age (Roddam, 2001). Along with continuous models, discrete models are also used, characterized by a system of recurrent relations (Brauer et al., 2010). In particular, Serovajsky (2021); Serovajsky et al. (2021); Turar et al. (2021) consider a discrete model with a limited time spent in contact and patient compartments. We also note numerous stochastic models of epidemiology (see, for example, Bailey (1975); Andersson (2000)), as well as agent models (see, for example, Krivorotko et al. (2021, 2022)).

Models that take into account vaccination arouse particular interest. In the simplest case, vaccinated susceptible individuals are directly transferred to the recovered compartment (De La Sen et al., 2010). In the SIRV (Scherer, 2002) and SEIRV (Cai et al., 2018) models, vaccinated are already considered as an independent population group. In Ghostine et al. (2021), the SEIRQV model is proposed, with additional compartment of people in quarantine. In Parolinia et al. (2021), the SUIHTER model also includes compartments of undetected and hospitalized patients, and separately takes into account people who received one and two doses of the vaccine. In the SVEIAHR model, vaccination is studied in the presence of three compartments of patients that are symptomatic and asymptomatic infected, as well as hospitalized Diagnea et al. (2021).

In Serovajsky et al. (2022), continuous and discrete models are proposed with compartments of vaccinated and contact vaccinated people with a limited time spent in all compartments of patients and contacts, which are generalizations of the models considered in Serovajsky (2021); Serovajsky et al. (2021); Turar et al. (2021). However, in these models, the rate of vaccination is assumed to be constant and independent of the state of the epidemic. In this paper, it is proposed to consider the rate of vaccination depending on the number of sick people at a given time.

In addition, we propose, as it seems to us, a more realistic division of the population into groups compared to known works. In particular, it seems more natural to interpret the compartment E as contact; identification of three compartments of patients, among which undetected patients are not included in official statistics, and hospitalized compartments is not source of infection; dividing vaccinated people into compartments of healthy people and those who were in contact with sick people. These, in turn, predetermines the clarification of intergroup transitions. A feature of this article is also the analysis based on two types of models – discrete and continuous, which expands the possibilities of mathematical modeling.

The paper contains 7 sections. The first of them is introductory. The second section describes the assumptions made, in particular, it provides a list of compartments into which the population is divided, as well as a list of intercompartment transitions taken into account. The third and fourth sections describe, respectively, the discrete and continuous models of the considered process, and also establish their most important qualitative properties. The fifth section presents the main results of the calculation and also gives their practical interpretation. As an example, information about the spread of the COVID-19 epidemic in Kazakhstan is used. The sixth section is devoted to estimation of the model parameters' influence on the course of the epidemic based on computer analysis of both models. Finally, the last section summarizes the results of the study.

2 Used assumptions

As already noted, compartmental models differ primarily in the choice of population compartments. The corresponding mathematical models characterize the change in the size of these compartments over time. In our case, nine compartments are considered. First of all, it is

susceptible, i.e., healthy, who can become ill after contact with the sick. This compartment is invariably present in all compartmental models, starting with SIR. $S(t)$ and S_k will denote the number of susceptible individuals at time t for a continuous model and on the k-th day for a discrete model. Similar designations will be used for other population compartments.

The second compartment consists of contacted, i.e., people who have been in contact with sick people, as a result of which they can infect, although they do not necessarily infect. Since this compartment is close to the exposed compartment present in the SEIR model, we will denote the corresponding value as E.

Then there are three compartments of patients, in particular, undetected, isolated and hospitalized, the number of which is denoted, respectively, by U, I and H. The consideration of just such compartments is explained by the following circumstances. The fundamental difference between undetected patients (as a rule, these are patients in whom the disease proceeds in an asymptomatic form, as well as mildly ill patients who have not consulted a doctor) from other patients is that they are not included in the official statistics of the disease. Consequently, in the solving of inverse problems to identify the system, we do not have any information at all, unlike other categories of patients. The fundamental difference between hospitalized patients and other patients is that they are under the supervision of doctors, which means that they are practically do not act as sources of infection. Finally, isolated is, as a rule, slightly ill, consulting a doctor and undergoing treatment at home. Like hospitalized, they are included in the official statistics of the disease. However, unlike the latter, they can be a source of infection, although to a lesser extent compared to undetected, which largely continue to lead a normal life, and therefore pose the greatest threat to others.

The next population compartment is immunized. It is made up of people who have already been ill and have immunity. Since this compartment largely corresponds to the recovered compartment present in many models, its size is denoted by R. The use of the term "immunized" instead of "recovered" seems to be preferable, since the main thing here is not that the person recovered, but that he, being in this compartment, can no longer get sick. When generalizing the proposed model, it is possible to provide for the possibility of re-infection. In this case, a person, remaining recovered, no longer has immunity and, in fact, should be classified as susceptible.

Subsequently the deceased, which have a natural meaning, are also taken into account. Their number is denoted by D.

Finally, vaccinated and contact vaccinated are also considered, the numbers of which are denoted by V and C, respectively. Healthy people who have been vaccinated belong to the vaccinated compartment, and vaccinated people who have had a contact with sick people belong to the contact vaccinated compartment. This takes into account that vaccination does not provide complete protection against the disease, i.e., the vaccinated people fall ill, although less likely than the unvaccinated, and in the case, the disease proceeds in them in a milder form.

The second most important characteristic of compartmental models of epidemiology after the list of population compartments is the list of acceptable intercompartment transitions. For the models under consideration, the transitions indicated in Figure 1.

According to the accepted assumptions, susceptible can contact with patients (to a greater extent with undetected, to a lesser extent with isolated ones) and be vaccinated. The vaccinated may also come into contact with infected people. Contacted people may become ill in some form or not at all. Contact vaccinated can get sick and move into the undetected and isolated compartments (less likely than susceptible). A patient in any form either recovers, or his disease becomes more severe. Hospitalized may die. It is assumed that after some time a person from any compartment of contact and patients leaves it, moving to another compartment (contacted will either get sick in one form or another, or will certainly not get sick; hospitalized will either recover or die, etc.). Time spent in compartments contacted, contact vaccinated, undetected, isolated and hospitalized are denoted, respectively, as n_e, n_c, n_u, n_i and n_h.

Further two models are used to describe the process under study. They differ not only in

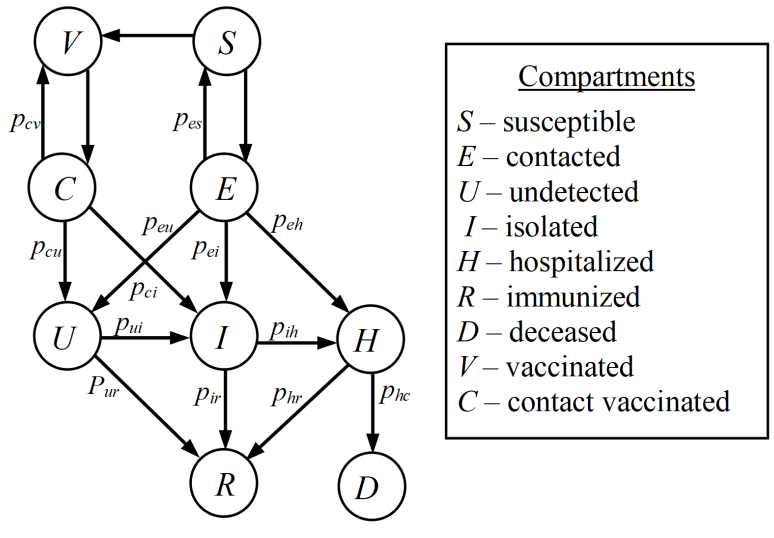

Figure 1: Characteristics of intercompartment transitions

the nature of the independent variable, i.e. time (continuous or discrete value), but also in the way they take into account the limited time spent in contact and patient compartments.

3 Discrete mathematical model of the epidemic propagation with vaccination

As already noted, the discrete model assumes the determination of all Z_k values characterizing the number of individuals corresponding to compartment Z on the kth day. At the same time, the number of people belonging to all compartments of contacts and patients can be acquired as sum of numbers, in each of the days of being in this compartment. Thus, the following equalities hold

$$Z_k = \sum_{j=1}^{n_z} z_k^j. \tag{1}$$

Here, z_k^j denotes the number of people in compartment Z at time k on the jth day of being in this compartment, $j = 1, \ldots, n_z$. Here Z can take the values E, C, U, I, H. The symbol z has a similar meaning. In this case, each individual of the jth day of being in the compartment Z passes to the category of the $j+1$-th day of being in the compartment Z when in one day, if he was not in the last day of being in this compartment, which corresponds to the equalities

$$z_{k+1}^{j+1} = z_k^j, \quad j = 1, 2, ...n_z - 1, \tag{2}$$

where z can take the values e, c, u, i, h.

Susceptible individuals can leave their compartment either through contact with the sick or after vaccinations. On the other hand, this compartment is replenished with those contacted who will certainly not get sick. Thus, the number of susceptible on the next day is equal to their number on the previous day, minus those who were vaccinated and who had contact with patients on that day, plus those contacts about whom it can be said with certainty that they will not get sick up to a day being considered. Obviously, the latter is about the contacted of being in the compartment last day. At the same time, the number of people who are naturally vaccinated at a given time is directly proportional to the number of susceptible. The corresponding coefficient of proportionality depends on the number of registered patients (to a greater extent

from hospitalized, to a lesser extent from isolated ones), because it is the incidence rate that encourages people to get vaccinated. It is clear that the number of susceptible who had contact with patients at a given time is also proportional to the existing number of susceptible; and the corresponding coefficient depends on the number of active carriers of the disease (to a greater extent from undiagnosed, to a lesser extent from isolated ones). As a result, we obtain the equality

$$S_{k+1} = S_k - \frac{v_h H_k + v_i I_k}{N} S_k - \frac{k_u U_k + k_i I_k}{N} S_k + p_{es} e_k^{n_e}. \tag{3}$$

Here, the parameters v_h and v_i characterize the degree of influence of the number of hospitalized and isolated people on the desire of people to be vaccinated; and k_u and k_i reflect the contagiousness of undetected and isolated patients. The division by the total population number is carried out for reasons of normalization. Otherwise, the numbers of two compartments are multiplied, which are sufficiently large values. The p_{es} parameter is the proportion of contacts of last day being in this compartment, moving into the compartment of susceptible, i.e. not sick. Everywhere below, p_{yz} denote the proportion of individuals from compartment Y on the last day of being in this compartment, moving into compartment Z.

Similarly, the number of vaccinated on the following day is the sum of their number on the previous day, the number of susceptible ones who were vaccinated that day, and the number of contact vaccinated people who can now be said to certainly not get sick, minus the number of vaccinated who had contact with infection on a given day. As a result, by analogy with formula (3), we obtain the equality

$$V_{k+1} = V_k + \frac{v_h H_k + v_i I_k}{N} S_k - \frac{k_u U_k + k_i I_k}{N} V_k + p_{cv} c_k^{n_c}. \tag{4}$$

The number of all contact and infected compartments on the next day is equal to their number on the previous day plus the number of people who entered this compartment on new day, minus the number of people who left the compartment on the previous day. Thus, we have

$$Z_{k+1} = Z_k + z_{k+1}^1 - z_k^{n_z}, \tag{5}$$

where Z can take the values E, C, U, I, H.

The number of immunized at a subsequent day is equal to their number on the previous day plus the number of patients in all compartments who recovered on the previous day. As a result, we obtain the equality

$$R_{k+1} = R_k + p_{ur} u_k^{n_u} + p_{ir} i_k^{n_i} + p_{hr} h_k^{n_h}. \tag{6}$$

The number of deaths at a subsequent time point is equal to their number on the previous day plus the number of deceased on that day

$$D_{k+1} = D_k + p_{hd} h_k^{n_h}. \tag{7}$$

Relations (1) – (7) are supplemented by formulas for determining the number of new contacts and patients, i.e., the number of relevant compartments of people related to the first day they were in the compartments. In particular, the number of contacts, both vaccinated and unvaccinated, is exactly equal to the number of vaccinated and susceptible, respectively, who had contact with patients on the previous day. Thus, there are the equalities

$$e_{k+1}^1 = (k_u U_k + k_i I_k)\frac{S_k}{N}, \quad c_{k+1}^1 = (k_u U_k + k_i I_k)\frac{V_k}{N}. \tag{8}$$

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

$$u_{k+1}^1 = p_{eu} e_k^{n_e} + p_{cu} c_k^{n_c}. \tag{9}$$

The number of new isolated contacts is the sum of the number of both compartments of contacts of the last day of being the compartment who fell ill with an isolated form of the disease, as well as the number of undiagnosed contacts of the last day of being in the compartment in whom the disease was detected

$$i_{k+1}^1 = p_{ei} e_k^{n_e} + p_{ci} c_k^{n_c} + p_{ui} u_k^{n_u}. \tag{10}$$

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

$$h_{k+1}^1 = p_{eh} e_k^{n_e} + p_{ih} i_k^{n_i}. \tag{11}$$

The initial states of the system Z_0, i.e. $S_0, E_0, U_0, V_0, C_0, I_0, H_0, R_0, D_0$ are considered to be known. For all forms of contact people and patients the distribution by days of being in compartments at the initial moment of time is considered uniform for simplicity, i.e. we have the equalities

$$z_0^j = \frac{Z_0}{n_z}, \quad j = 1, ..., n_z, \tag{12}$$

where z takes the values e, c, u, i, h.

Note that the parameters of the system have some relations. In particular, the sum of the size of all population compartments at the initial moment of time (including those who died from a given disease) is equal to the total population number, which corresponds to the condition

$$S_0 + V_0 + E_0 + C_0 + U_0 + I_0 + H_0 + R_0 + D_0 = N. \tag{13}$$

The proportions of the number of all contact and patient compartments passing into one or another compartment are related by natural factors.

$$\begin{aligned} p_{es} + p_{eu} + p_{ei} + p_{eh} = 1, \qquad p_{cv} + p_{cu} + p_{ci} = 1, \\ p_{ui} + p_{ur} = 1, \qquad p_{ih} + p_{ir} = 1, \qquad p_{hr} + p_{hd} = 1. \end{aligned} \tag{14}$$

For vaccinated contacts, the time spent in the compartment is assumed to be the same as for unvaccinated contacts, i.e.

$$n_c = n_e. \tag{15}$$

The contagiousness of undetected patients is higher than that of isolated ones, which corresponds to the inequality

$$k_u > k_i. \tag{16}$$

The degree of influence of the number of hospitalized patients on the rate of vaccination is higher than the number of isolated, which corresponds to the inequality

$$v_i < v_h. \tag{17}$$

Those vaccinated are significantly less likely to get sick than those who are susceptible, in line with the inequalities

$$p_{cu} < p_{eu}, \quad p_{ci} < p_{ei}. \tag{18}$$

Vaccinated people are more likely not to get sick at all and less likely to become isolated

$$p_{ci} < p_{cu} < p_{cv}. \tag{19}$$

The above formulas constitute a discrete model of the epidemic development with vaccination.

Theorem 1. *The following properties are fulfilled for the discrete mathematical model:*
i) the sequences R_k and D_k are increasing;
ii) the following equality holds

$$S_k + V_k + E_k + C_k + U_k + I_k + H_k + R_k + D_k = N, \quad k = 1, 2, ...; \tag{20}$$

iii) the system has an equilibrium position such that

$$E = 0,\ U = 0,\ C = 0,\ I = 0,\ H = 0. \tag{21}$$

To prove the first property, it suffices to pay attention to the fact that the increment of the functions of the discrete argument R and D (the difference between their values on the next and previous day) is positive because of equalities (6) and (7). To prove the second property, it suffices to add equalities (3) – (7) together, taking into account conditions (8) – (11), (14) and make sure that the sum of the values of all functions at the next and previous time is the same. This value is equal to N by equality (13). To verify the validity of the third assertion, it is required to pass to the limit for $k \to \infty$ in the available recurrence relations under the assumption that limits of the sequences of the considered quantities exist, taking into account the fact that the limits of each considered nine functions coincide at the next and the previous moment of time.

Presented results have a rather natural meaning. The monotonous increase in the number of immunized and dead is explained by the fact that none of these compartments of people decreases, i.e., according to the accepted assumptions, the immunized will no longer get sick, and the dead, of course, remain so. The second statement is equally natural: in the balance of natural birth and death rates (i.e. as many were born in a unit of time, that many died naturally during that time), as well as the isolation of the population (the absence of inflow and outflow of the population from outside), the total population does not change. Finally, when the system reaches the indicated equilibrium position, it means that the epidemic ends with time, i.e., the number of all compartments of contacts and patients tends to zero over time: all contacts will either get sick or not get sick, and all patients will either recover or die.

4 Continuous mathematical model of the epidemic propagation with vaccination

The continuous mathematical model is derived under the same assumptions as the discrete model described above. The state of the system is described by the same functions as before, but depending on the continuously changing time t. At the same time, the previously adopted designations remain valid.

The change in the number of susceptibles is due to their decrease due to vaccination and the fact that some part of the susceptible came into contact with the sick, and an increase, since some of the contacts do not get sick. As a result, we have a differential equation

$$\frac{dS(t)}{dt} = -\frac{v_h H(t) + v_i I(t)}{N} S(t) - \frac{k_u U(t) + k_i I(t)}{N} S(t) + p_{es} \frac{E(t)}{n_e}. \tag{22}$$

The first and second terms on its right side coincide with the corresponding summands of formula (3). According to the last term, the longer the time n_e of being in the contact compartment, the fewer of them (those who did not get sick) will return to the susceptible compartment per time unit. Thus, the last terms in equalities (3) and (22) have the same meaning, although expressed in different ways.

The change in the number of vaccinated is due to their decrease because some of them encountered the infection, and the increase due to vaccination and the fact that part of the contact vaccinated does not fall ill. The corresponding quantities are determined in the same way as in the previous formula. As a result, by analogy with equality (4), we obtain the equation

$$\frac{dV(t)}{dt} = \frac{v_h H(t) + v_i I(t)}{N} S(t) - \frac{k_u U(t) + k_i I(t)}{N} V(t) + p_{cv} \frac{C(t)}{n_c}. \tag{23}$$

The change in the number of contacts, both unvaccinated and vaccinated, increases due to, respectively, susceptible and vaccinated, who had contact with patients, and decreases due to the limited time spent in these compartments. Thus, we have the equalities

$$\frac{dE(t)}{dt} = \frac{k_u U(t) + k_i I(t)}{N} S(t) - \frac{E(t)}{n_e}, \tag{24}$$

$$\frac{dC(t)}{dt} = \frac{k_u U(t) + k_i I(t)}{N} V(t) - \frac{C(t)}{n_c}, \tag{25}$$

similar to formula (5), when Z takes the values E and C, taking into account formulas (8).

The number of undetected increases due to the disease of both contact compartments and decreases due to the limited time spent in this compartment. As a result, we obtain the equation

$$\frac{dU(t)}{dt} = p_{eu} \frac{E(t)}{n_e} + p_{cu} \frac{C(t)}{n_e} - \frac{U(t)}{n_u}, \tag{26}$$

which is similar to equality (5) with $Z = U$ considering formula (9).

The number of isolated patients increases due to the disease of both contact compartments and the detection of the disease in some of the undetected patients and decreases due to the limited time spent in this compartment. This corresponds to the equality

$$\frac{dI(t)}{dt} = p_{ei} \frac{E(t)}{n_e} + p_{ci} \frac{C(t)}{n_c} + p_{ui} \frac{U(t)}{n_u} - \frac{I(t)}{n_i}, \tag{27}$$

which is similar to formula (5) with $Z = I$, considering condition (10).

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

$$\frac{dH(t)}{dt} = p_{eh} \frac{E(t)}{n_e} + p_{ih} \frac{I(t)}{n_i} - \frac{H(t)}{n_h}, \tag{28}$$

which is similar to formula (5) with $Z = H$, considering condition (11).

The number of immunized is increasing due to the recovery of patients of all categories. Then, by analogy with formula (6), we have the equation

$$\frac{dR(t)}{dt} = p_{ur} \frac{U(t)}{n_u} + p_{ir} \frac{I(t)}{n_i} + p_{hr} \frac{H(t)}{n_h}. \tag{29}$$

The number of deceased increases due to the death of a part of the hospitalized, which corresponds to the equation

$$\frac{dD(t)}{dt} = p_{hd}\frac{H(t)}{n_h}, \tag{30}$$

similar to formula (7).

The system of differential equations (22) – (30) is supplemented by the initial conditions

$$Z(0) = Z_0, \tag{31}$$

where Z takes the values $S, V, E, C, U, I, H, R, D$. Formulas (22) – (31) are a continuous model of the epidemic development with vaccination. It is assumed that relations (13) – (19) are also satisfied for continuous model.

The following assertion is true, which is an analogue of Theorem 1.

Theorem 2. *The following properties are fulfilled for the continuous mathematical model of the epidemic propagation with vaccination:*
i) functions R and D are increasing;
ii) the system under consideration has a first integral characterized by the equality

$$S(t) + V(t) + E(t) + C(t) + U(t) + I(t) + H(t) + R(t) + D(t) = N, \quad t > 0; \tag{32}$$

iii) the system has an equilibrium position such that

$$E = 0,\ U = 0,\ C = 0,\ I = 0,\ H = 0. \tag{33}$$

Here the first condition follows from the positiveness of the corresponding derivatives in equalities (29) and (30). To prove the validity of the second assertion, it suffices to add all equalities (22) – (30) taking into account conditions (14). To substantiate the third assertion, it suffices to equate the expressions on the right-hand sides of the existing equations to zero and analyze the resulting system of algebraic equations.

5 Numerical analysis of the mathematical models of the epidemic propagation with vaccination

The quantitative analysis of both models was carried out at the same parameter values, and the continuous model was implemented using the 4th order Runge–Kutta method. The following number of days spent in groups was assumed: $n_e = 14$, $n_u = 3$, $n_i = 5$, $n_h = 7$, $n_c = n_e = 14$. The coefficients of the equations take the following values as main set: $k_u = 3.18$, $k_i = 0.171$, $v_h = 0.3$, $v_i = 0.01$, $p_{es} = 0.679$, $p_{eu} = 0.154$, $p_{ei} = 0.145$, $p_{eh} = 0.022$, $p_{cv} = 0.9$, $p_{cu} = 0.05$, $p_{ci} = 0.05$, $p_{ui} = 0.03$, $p_{ur} = 0.97$, $p_{ih} = 0.021$, $p_{ir} = 0.979$, $p_{hr} = 0.982$, $p_{hd} = 0.018$. The 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 all infected people, as well as the number of recovered, deceased and vaccinated on a given day.

First of all, we note that both models give close results. This can be explained by the fact that both models were obtained on the basis of the same hypotheses. However, these results do not completely match. In particular, the curves for the continuous model turn out to be smoother than those for the discrete model. In addition, there are certain deviations in the

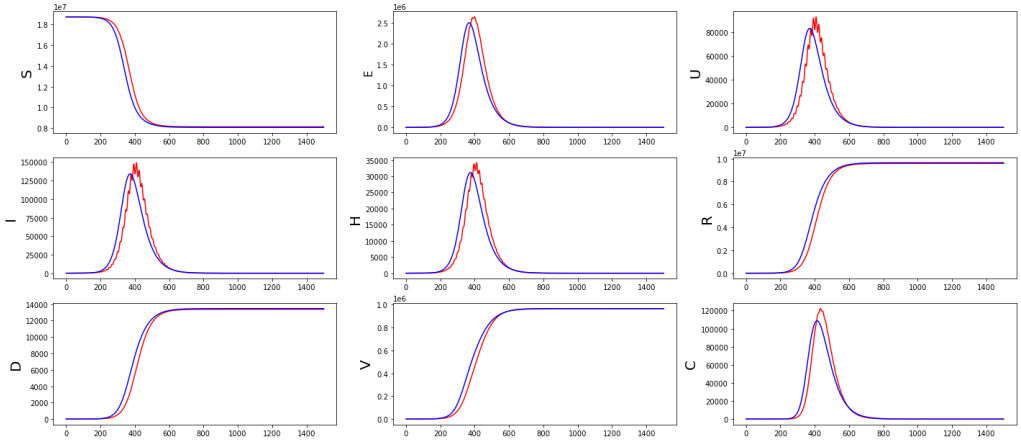

Figure 2: Change in the sizes of population compartments for the main set of parameters

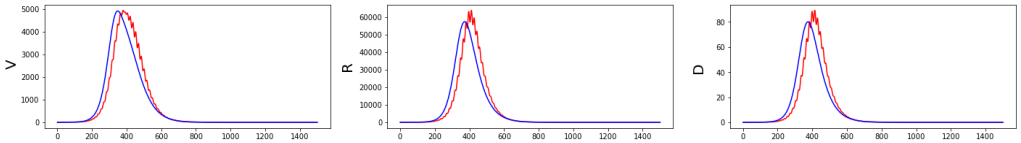

Figure 3: The number of infected, recovered, dead and vaccinated on a given day

maximum values of individual functions and the time to reach these values. These discrepancies are explained by the fact that individual effects in these models are described by different means.

Calculations show that five out of nine functions tend to zero over time. They correspond to all groups of contact and patients. The remaining four functions reach the equilibrium position, taking positive values. The results obtained are consistent with the statements of the theorems formulated above and indicate that the epidemic ends eventually.

Among the most important quantitative characteristics of the system there are the duration of the epidemic (up to the point in time at which the number of all simultaneously ill is close enough to zero), the peak time of the epidemic (the point in time at which the number of all simultaneously ill reaches its maximum value), the total number of infected, recovered and deceased at the end of the epidemic and the maximum number of patients at a time. The relevant information for the specified calculation option is given in Table 1.

Table 1: The most important characteristics of the system for the main variant of calculation

	Discrete Model	**Continuous Model**
Peak time of the epidemic	409	372
The maximum number of patients at the same time	275620 (1.47%)	248302 (1.33%)
Epidemic end time	1070	1144
Total number of sick people and % of the total population	9598590 (51.33%)	9659525 (51.66%)
Total number of recovered and % of the total number of sick people	9585214 (99.86%)	9646064 (99.86%)
Total number of deceased and % of the total number of sick people	13376 (0.14%)	13460 (0.14%)

As it can be seen from the these results, according to the discrete model, the epidemic reaches

its peak about a month later than according to the continuous model (difference is 9.9%), and the maximum number of sick people at the same time turns out to be more by 27.3 thousand people (difference is 11%). At the same time, the end of the epidemic comes about 2.5 months earlier than according to the continuous model (discrepancy is 6.46%), and the total number of sick people and recoveries is less by about 60 thousand people (difference is 0.63% in both), the total number of deceased is less by 84 people (difference is 0.62%). Thus, according to the discrete model, the epidemic is more intense, as long as there is a higher value of the maximum incidence with a shorter duration of the epidemic.

6 Analysis of the influence of system parameters

We investigate the influence of individual parameters on the course of the process. In particular, Table 2 describes the effect of the k_u contagiousness coefficient of undiagnosed patients. Here and in whole paper, d-model denotes the discrete model, and c-model denotes the continuous model. As it can be seen from the table, with an increase in the contagiousness coefficient, both the peak time and the duration of the epidemic are reduced, and both the maximum number of patients at a time and the total number of those who have been ill increase, i.e. the epidemic is intensifying. At the same time, according to both models, these changes have practically no effect on the ratio between the recovered and the deceased (about 0.14% of the number of cases die). We also note that the increase in the contagiousness coefficient from 2.88 to 3.48, i.e. on 20,8% leads to a decrease in the peak time and duration of the epidemic, respectively by 29.59% and 22.28% for a discrete model, and by 31.52% and 27.27% for the continuous model. At the same time, the maximum number of simultaneously ill people and the total number of recovered patients increase by 0.84% and 0.72%, respectively, for the discrete model, and by 11.39% and 11.56% for the continuous model (here and in the analysis of subsequent tables, the percentage of people count is taken from the total population size).

Table 3 describes the impact of the contagiousness coefficient k_i of isolated patients. Actually, it affects the same way as the contagiousness rate of undiagnosed patients. However, increasing this parameter by 281% leads to a decrease in the peak time and duration of the epidemic, respectively, by 14.09% and 12.11% for the discrete model, and on 17.23% and 11.60% for the continuous model. At the same time, the maximum number of simultaneously ill people and the total number of recovered patients increase by 1.05% and 0.91% of the total population for the discrete model, and by 6.12% and 6.21% of the total population for the continuous model, respectively. Mortality again does not undergo any changes and is 0.14%.

Table 4 describes the effect of the parameter v_h characterizing the effect of hospitalized patients on the rate of vaccination. Doubling it had practically no effect not only on mortality, but also on the time of the peak of the epidemic, and on the maximum number of patients at the same time. At the same time, the duration of the epidemic decreased by 0.84% for the discrete model and on 0.87% for the continuous model, and the total number of recovered patients decreased by 1.72% for the discrete model and 1.71% for the continuous model. Thus, an increase in the rate of vaccination leads to a reduction in both the duration of the epidemic and the number of those who have been ill. The influence of a similar parameter associated with isolated patients is approximately the same, but weaker.

Table 5 and Table 6 characterize the impact of changing the proportion of contacts who moved to other compartments. According to Table 5, when the parameter p_{eu} is increased by 13.9% with a corresponding decrease in the p_{es} parameter (more contacts get sick in an undetected form and fewer do not get sick at all), the time of the peak of the epidemic and its duration decrease, respectively, by 21.18% and by 17.82% for the discrete model, and by 23.08% and 17.53% for the continuous model, while the maximum number of patients and the total number of recovered patients increase, respectively, by 0.61% and 8.34% for the discrete model, and by 0.51% and 8.4% for the continuous model. Thus, an increase in the proportion

of cases in an undiagnosed form due to a decrease in the proportion of those who are not ill leads to a more intense course of the epidemic (the duration of the epidemic is reduced, but the incidence increases). According to Table 6, when the parameter p_{ei} is increased by 32% with a corresponding decrease in the parameter p_{eh} (more contacts become isolated patients and fewer are hospitalized), the peak time of the epidemic and its duration decrease, respectively, by 3.91% and 1.3% for discrete model, and by 3.68% and 1.3% for continuous model, while the maximum number of patients and the total number of recovered patients increase by 0.12% and 5.33%, respectively, for the discrete model, and by 0.1% and 5.32% for the continuous model. Thus, an increase in the proportion of those isolated with a decrease in the proportion of those hospitalized again leads to a more intense course of the epidemic (although to a lesser extent than after previous changes). This can be explained by the fact that in this case there are fewer sources of infection.

Table 2: Influence of the contagiousness coefficient of undiagnosed patients

k_u	**peak time of the epidemic in days**		**maximum number simultaneously ill**		**duration of the epidemic in days**		**number of recoveries**	
	d-model	c-model	d-model	c-model	d-model	c-model	d-model	c-model
2.88	490	460	195696	179107	1239	1324	8398573	8447761
3.18	409	372	275620	248302	1070	1144	9598590	9659525
3.48	345	315	353940	314178	963	1032	10528004	10597509

Table 3: Influence of the contagiousness coefficient of isolated patients

k_i	**peak time of the epidemic in days**		**maximum number simultaneously ill**		**duration of the epidemic in days**		**number of recoveries**	
	d-model	c-model	d-model	c-model	d-model	c-model	d-model	c-model
0.071	440	412	236356	212193	1148	1224	8987477	9040028
0.171	409	372	275620	248302	1070	1144	9598590	9659525
0.271	378	341	315671	283280	1009	1082	10131894	10200517

Table 4: Influence of the parameter v_h

v_h	**duration of the epidemic in days**		**number of recoveries in % of the population**	
	d-model	c-model	d-model	c-model
0.02	1074	1150	9763287	9823445
0.03	1070	1144	9598590	9659525
0.04	1065	1140	9440601	9502245

Table 5: Influence of the proportion of contacts who become undetected patients

k_u	**peak time of the epidemic in days**		**maximum number simultaneously ill**		**duration of the epidemic in days**		**number of recoveries**	
	d-model	c-model	d-model	c-model	d-model	c-model	d-model	c-model
0.669	458	429	220245	199973	1190	1272	8760111	8814914
0.679	409	372	275620	248302	1070	1144	9598590	9659525
0.689	361	330	333908	296014	978	1048	10320519	10385997

Table 6: Influence of the proportion of contacts who become isolated patients

k_u	**peak time of the epidemic in days**		**maximum number simultaneously ill**		**duration of the epidemic in days**		**number of recoveries**	
	d-model	*c*-model	*d*-model	*c*-model	*d*-model	*c*-model	*d*-model	*c*-model
0.071	409	380	265991	238713	1078	1153	9118258	9178938
0.171	409	372	275620	248302	1070	1144	9598590	9659525
0.271	393	366	287406	257818	1064	1138	10113994	10174574

Table 7 describes the impact of the proportion p_{ci} of vaccinated contacts who become ill and isolated. In particular, a fourfold increase in this proportion (with a corresponding decrease in p_{cv}, the proportion of vaccinated contacts who did not get sick at all), the time characteristics of the epidemic remained practically unchanged, and the maximum number of sick and the number of recoveries decreased by less than 0.01%.

Table 7: Influence of the proportion of vaccinated contacts who become isolated patients

p_{ci}	**maximum number simultaneously ill**		**number of recoveries**	
	d-model	*c*-model	*d*-model	*c*-model
0.02	275668	248342	9606348	9667555
0.05	275620	248302	9598590	9659525
0.08	275572	248263	9591068	9651754

Table 8 evaluates the impact of the proportion of undiagnosed p_{ui} patients who were subsequently diagnosed with disease and isolated. A five-fold increase in this parameter had little effect on the time characteristics of the epidemic (the duration of the epidemic is reduced by several days). At the same time, the maximum number of sick people decreased by 0.03% for the discrete model and by 0.04% for the continuous model, and the total number of infected decreased by 0.19% for both models. According to (14), the sum of the parameters p_{ui} and p_{ur} is equal to 1, as a result of which the latter has the opposite effect on the system.

Table 8: Impact of the proportion of undiagnosed patients whose disease was subsequently detected

p_{ui}	**the maximum number of sick people**		**number of recoveries**	
	d-model	*c*-model	*d*-model	*c*-model
0.01	278882	252297	9616295	9677493
0.03	275620	248302	9598590	9659525
0.05	272256	244335	9580793	9641461

Table 9 contains information on the impact of the proportion of isolated patients who were subsequently hospitalized p_{ih}. An increase in this parameter by six times had practically no effect on the time characteristics of the epidemic. At the same time, the maximum number of simultaneously sick people increased by 0.2%, and the total number of sick people increased by 0.45% for both the discrete model and the continuous model. According to (14), the sum of the parameters p_{ih} and p_{ir} is equal to 1, because of this the latter has the opposite effect on the system.

Table 9: Impact of proportion of isolated patients that were hospitalized

p_{ih}	**the maximum number of sick people**		**number of recoveries**	
	d-model	c-model	d-model	c-model
0.006	273776	246367	9640764	9640764
0.021	275620	248302	9598590	9659525
0.036	277451	250228	9556832	9617884

Table 10 evaluates the impact of the p_{hd} parameter on the proportion of deceased among hospitalized patients. It affects only the number of deceased during the epidemic. In particular, increasing this parameter 11 times leads to an increase in the number of deaths 1000% for the for both models. According to (14), the sum of the parameters p_{hd} and p_{hr} is equal to 1, as a result of which the latter has the opposite effect on the system.

Table 10: Impact of the proportion p_{hd} of hospitalized became deceased

p_{hd}	**number of deaths**	
	d-model	c-model
0.003	2229	2243
0.018	13376	13460
0.033	24522	24677

Let us analyze the influence of the number of days spent in compartments. In particular, in Table 11 we explore changes of parameter n_e, which characterizes the number of days spent in the contact compartment. With its increase by 2.1 times, the time of the peak of the epidemic and its duration increase, respectively, by 90.75% and 89.69% for the discrete model and by 75.56% and 83.13% for the continuous model, while the maximum number of sick people and the total number of recovered patients are reduced by 0.95% and 0.75%, respectively, for the discrete model, and by 0.91% and 0.94% for the continuous model. Thus, with an increase in the number of days spent in the contact group, it slightly decreases. It is interesting that the same change in the number n_c of days spent in the compartment of vaccinated contacts has practically no effect on the time of the peak of the epidemic and the maximum number of sick people (the difference is in hundredths of a percent) and has an extremely insignificant effect on the duration of the epidemic (it increases by several days) and the total number of those who have been ill (it is reduced by about 0.05%).

Table 11: Influence of the number of days spent in the contact compartment

k_u	**peak time of the epidemic in days**		**maximum number simultaneously ill**		**duration of the epidemic in days**		**number of recoveries**	
	d-model	c-model	d-model	c-model	d-model	c-model	d-model	c-model
9	281	270	393111	358888	737	806	9691717	9775080
14	409	372	275620	248302	1070	1144	9598590	9659525
19	536	474	214795	189745	1398	1476	9551573	9599104

Table 12 examines the effect of the number of days spent in the undetected compartment n_u. Doubling this number leads to a reduction in the peak time of the epidemic and the duration of the epidemic, respectively, by 4.8 times and 3.8 times for the discrete model, and 5.5 times and 3.7 times for the continuous model. At the same time, the maximum number of patients at the same time increases, respectively, by 31 and 29 times, respectively, for discrete and

continuous models, the total number of those who have been ill is 4 times for both models, and the mortality rate does not change. Thus, this parameter has a strong influence on the intensity of the epidemic.

Table 12: Effect of the number of days spent in the undetected compartment

k_u	**peak time of the epidemic in days**		**maximum number simultaneously ill**		**duration of the epidemic in days**		**number of recoveries**	
	d-model	c-model	d-model	c-model	d-model	c-model	d-model	c-model
2	1370	1378	18090	17352	3219	3358	3002054	3006504
3	409	372	275620	248302	1070	1144	9598590	9659525
4	287	249	564311	494976	838	911	12191042	12304302

Table 13 shows the characteristics of the epidemic for different values of the number of days spent in the isolated compartment n_i. The results show that an increase in the parameter by 2.3 times leads to a reduction in the peak time of the epidemic and its duration, respectively, by 62.4% and 61.8% for the discrete model and by 54.8% and 58.6% for the continuous model, and to an increase in the maximum number of sick people and the total the number of recovered patients decreases, respectively, by 0.84% and 3.95% for the discrete model and by 0.85% and 4.06% for the continuous model of the total population. Thus, the number of days spent in the isolated compartment also affects the intensity of the epidemic, but to a lesser extent than the number of days spent in the undetected compartment. Even less influence is exerted by the number of days spent in the hospitalized compartment. In particular, the increase in this parameter by two and a half times did not affect the time to reach the peak of the epidemic, the duration of the epidemic was reduced by several days, and the maximum number of sick people and the total number of recoveries increased by about 0.05% and by 2% for both models.

Table 13: Influence of the number of days spent in the isolatied compartment

k_u	**peak time of the epidemic in days**		**maximum number simultaneously ill**		**duration of the epidemic in days**		**number of recoveries**	
	d-model	c-model	d-model	c-model	d-model	c-model	d-model	c-model
3	423	395	199025	176696	1105	1177	9213682	9266085
5	409	372	275620	248302	1070	1144	9598590	9659525
7	380	356	355300	326727	1041	1121	9952327	10025657

Based on the results obtained, it can be concluded that the process is most influenced by parameters characterizing mortality among hospitalized patients, as well as contagiousness and the number of days spent in the undetected compartment. In addition, if sufficiently accurate information about the mortality rate is available, then the characteristics of undetected patients are practically unknown. In a particular situation, they can be determined by identifying the system based on available statistical information about the course of the disease.

7 Conclusion

As a result of the study, we can come to the following conclusions. A qualitative and quantitative analysis of the considered mathematical models of the epidemic spread with vaccination and a limited time spent in compartments shows that under the assumptions made above the epidemic ends with time. The proposed two models, which differ in the structure and method of consideration of the time limit of being in compartments, lead to close results so that it is not possible to give preference to any of the models. With a change in individual parameters of the

system (an increase in the contagiousness coefficients and the proportion of contacts that were infected, a decrease in the rate and the number of days spent in compartment of vaccination), a more intense nature of the epidemic is observed. It means decrease of epidemic duration and it's peak time and increase of the amount of simultaneously ill patients.

Based on analysis performed, we indicated the following directions for further research: 1. To predict the course of an epidemic in a specific situation using the considered models, it is necessary to identify the parameters of models based on the available real information, as it is done in Krivorotko et al. (2020, 2021); Turar et al. (2021) for epidemiology models without vaccination. Based on the results of mathematical models identification, based on real information, it is possible to make a forecast about the development of the epidemic in a specific situation. 2. In case of modeling of an epidemic development over a longer period, one should take into account the possibility of re-infection of recovered people, which corresponds to a transition from compartment R (immunized) to compartment S (susceptible). 3. In case of modeling of an epidemic development over a longer period, one should take into account the limited duration of the vaccine, which corresponds to the transition from group V (vaccinated) to compartment S (susceptible). 4. Taking into account the limited duration of the vaccine, it is advisable to also consider the possibility of revaccination. 5. In the considered models, the time spent each compartment is considered fixed. However, in reality, some part of the people may leave the group either earlier or later. 6. It would also be interesting to study the influence of random factors on the process. 7. It is of interest to solve system control problems based on the models used, for example, the choice of vaccination strategy, the possibility of introducing quarantine and its parameters, etc.

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References

Andersson, H., Britton, T. (2012). *Stochastic Epidemic Models and Their Statistical Analysis* (Vol. 151). Springer Science & Business Media.

Almeida, R., Cruz, A., Martins, N., & Monteiro N. (2019). An Epidemiological MSEIR Model Described by the Caputo Fractional Derivative. *Int. J. of Dynamics and Control*, 7, 776–784.

Aristov, V.V., Stroganov, A.V., & Yastrebov, A.D. (2021). Simulation of spatial spread of the COVID-19 pandemic on the basis of the kinetic-advection model. *Physics, 3*(1), 85-102.

Bailey, N. (1975). The Mathematical Theory of Infectious Diseases and its Applications. In *Mathematics in Medicine Series*, Griffin: London, 413 p.

Brauer, F., Feng, Z., Castillo-Chavez, C. (2009). Discrete epidemic models. *Mathematical Biosciences & Engineering, 7*(1), 1-15.

Cai, L. M., Li, Z., & Song, X. (2018). Global analysis of an epidemic model with vaccination. *Journal of Applied Mathematics and Computing,* 57, 605-628.

Conn, A., Gould, N., & Toint, P. (2007). Trust-Region Methods. *MOS-SIAM Series on Optimization*, Society for Industrial and Applied Mathematics: Philadelphia.

De la Sen, M., Agarwal, R.P., Ibeas, A., & Alonso-Quesada, S. (2010). On a generalized time-varying SEIR epidemic model with mixed point and distributed time-varying delays and combined regular and impulsive vaccination controls. *Advances in Difference Equations,* 2010, 1-42.

Diagne, M.L., Rwezaura, H., Tchoumi, S.Y., & Tchuenche, J.M. (2021). A mathematical model of COVID-19 with vaccination and treatment. *Computational and Mathematical Methods in Medicine, 2021*(1), 1250129.

Ghostine, R., Gharamti, M., Hassrouny, S., & Hoteit, I. (2021). An extended SEIR model with vaccination for forecasting the COVID-19 pandemic in Saudi Arabia using an ensemble Kalman filter. *Mathematics, 9*(6), 636.

Hethcote, H.W. (2000). The Mathematics of Infectious Diseases. *SIAM Review*, *2000*(42), 599–653.

Keeling, M.J., Rohani, P. (2007). *Modeling Infectious Diseases in Humans and Animals*. Princeton University Press, Princeton, 385 p.

Kermack, W.O., McKendrick, A.G. (1927). A Contribution to the Mathematical Theory of Epidemics. In *Proceedings of the Royal Society of London. Series A*, London, GB, 700–721.

Krivorotko O.I., Kabanikhin S.I., Zyatkov N.Yu., Prikhodko A.Yu., Prokhoshin N.M., Shishlenin M.A. (2020). Mathematical modeling and forecasting of COVID-19 in Moscow and the Novosibirsk region. *Siberian J. Num. Math., 2020*(23), 395–414.

Krivorotko O.I., Kabanikhin S.I. (2021). Mathematical Models of the Spread of COVID-19. arXiv: Populations and Evolution.

Krivorotko, O., Sosnovskaia, M., Vashchenko, I., Kerr, C., & Lesnic, D. (2022). Agent-based modeling of COVID-19 outbreaks for New York state and UK: Parameter identification algorithm. *Infectious Disease Modelling, 7*(1), 30-44.

Mwalili, S., Kimathi, M., Ojiambo, V., Gathungu, D., & Mbogo, R. (2020). SEIR model for COVID-19 dynamics incorporating the environment and social distancing. *BMC Research Notes, 13*(1), 352.

Parolini, N., Ardenghi, G., & Quarteroni, A. (2022). Modelling the COVID-19 epidemic and the vaccination campaign in Italy by the SUIHTER model. *Infectious Disease Modelling, 7*(2), 45-63.

Roddam, A.W. (2001). Mathematical Epidemiology of Infectious Diseases. *International Journal of Epidemiology*, *30*, 186–186.

Sameni, R. (2020). Mathematical Modeling of Epidemic Diseases, A Case Study of the COVID-19 Coronavirus. arXiv: Populations and Evolution.

Scherer, A., McLean, A. (2002). Mathematical models of vaccination. *British Medical Bulletin, 62*(1), 187-199.

Serovajsky, S. (2021). *Mathematical Modeling.* Chapman and Hall/CRC: Boca Raton, 466 p.

Serovajsky, S., Turar, O., & Imankulov, T. (2022). Mathematical modeling of the epidemic propagation with limited time spent in compartments taking and vaccination. *Journal of Mathematics, Mechanics and Computer Science, 116*(4).

Turar, O.N., Serovaysky, S.Y. (2021). Mathematical model of the epidemic propagation with limited time spent in exposed and infected compartments. *Journal of Mathematics, Mechanics and Computer Science, 112*(4).

Turar, O., Serovajsky, S., Azimov, A., & Mustafin, M. (2021, August). Discrete and Continuous Models of the COVID-19 Pandemic Propagation with a Limited Time Spent in Compartments. In *ISAAC Congress (International Society for Analysis, its Applications and Computation*) (pp. 101-114). Cham: Springer International Publishing.

Unlu, E., Léger, H., Motornyi, O., Rukubayihunga, A., Ishacian, T., & Chouiten, M. (2020). Epidemic analysis of COVID-19 outbreak and counter-measures in France. *MedRxiv,* 2020-04.