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Development of Mathematical Models Taking into Account the Effect of Isolating Individuals in a Population

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Abstract—The effect of the isolation of individuals in the population on the dynamics of the epidemic is analyzed. Based on the SIR model, a SIRDi model is built that takes into account the isolation of individuals, as well as the presence of deceased patients, which is appropriate to use in cases of widespread infection, when the number of infected is comparable to the number of susceptible individuals. Simplified IRD and IRDi models are proposed for studying the spread of an infectious disease at the initial stage of an epidemic (or for the case when the rate of infection is not high). It is found that there is a threshold value of the coefficient (fraction) of isolation, which delimits the qualitatively different behavior of the epidemic indicators of the population system. A comparison is made between different models. It is shown that the simplified (IRDi) and more complex (SIRDi) models at the initial stage of the epidemic give approximately the same results.

Keywords: epidemic, reproduction indices, SIR model, isolation factor
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1. INTRODUCTION

Currently, a great deal of attention is paid to modeling epidemic processes. This issue has become especially relevant in connection with the spread of the coronavirus infection COVID-19. Simple models that approximately describe the dynamics of the epidemic are based on the principles of the "encounter theory," the foundations of which were laid in the early 20th century by the mathematicians V. Volterra [1] and A. Lotka [2].

There are now various modifications of this theory in relation to modeling the spread of epidemics. The SIR model [3–5] is among the most popular of these models, according to which the entire population is divided into three groups: those susceptible to infection, actually infected, and recovered; and differential equations are compiled that describe the interaction between different groups (the name of the model is formed from the initial letters of the names of the three population groups mentioned above). More complex models ([6–9], etc.) take into account various factors, such as natural birth and death rates, vaccination, the development or loss of immunity (SIRS model), the influence of climatic conditions, the heterogeneity of the population distribution, and the incubation period of the disease (for example, the SEIR model). The works devoted to the constructing and studying mathematical models of immunological and epidemiological processes in infectious diseases [10, 11], where the models are built based on modern knowledge about pathogenesis and epidemiology, in particular, diseases such as influenza, pneumonia, and tuberculosis, should also be noted.

Based on basic models such as SIR, many (sometimes quite complex) models have emerged recently, taking into account various factors that describe the interaction between different groups in a population. Some of them take into account the effect of quarantining infected patients (SIQR models) [12, 13]. This introduces another variable Q, the number of individuals in quarantine, which leads to an increase in the number of differential equations, and, accordingly, complicates the analysis of the system of model equations.

Considerable attention is paid to building models for studying the current problem: the COVID-19 pandemic [6, 13–16]. In [15], a kinetic model of the spread of epidemics is proposed that describes the dynamics of changes in the number of healthy, infected, and recovered (the SIR model) based on a logistic

equation with a lagging argument. It has been established that this model predicts the possibility of the existence of a quasi-stationary mode of the epidemic, in which the number of infected people is constant due to the balance of the daily increase in the infected patients and those who have recovered. Based on data from the COVID-19 pandemic, it is possible to reliably predict the spread of the epidemic for up to two months.

An analysis of the universal stages in the development of the COVID-19 viral infection epidemic is presented in [16]. It is assumed that during a pandemic, the rate of growth in the number of infected people occurs similarly to the process of reproduction of virions in the affected organism. The indicator of the rate of increase in the number of infected people reflects not only the medical and biological parameters of a viral infection but also the characteristics of the social behavior of the population. The dynamics of changes in the growth rate indicators is modeled by a system of ordinary differential equations of the relaxation type. The limit values of the rate of increase in the number of infected people are predicted based on the immersion method, using the available experimental data.

In general, there are numerous works devoted to modeling epidemic processes; however, a detailed analysis of the behavior of the system, taking into account the effect of isolation, has not been carried out.

The aim of this study is to model and study the dynamics of the epidemic in the presence of the isolation of individuals (including both healthy and infected individuals) of the population system. Moreover, unlike the SIQR model, a separate unknown variable is not introduced here for the group of isolated individuals, but the analysis is carried out using the isolation factor. Thus, the number of differential equations in the presented models is the same as in the basic SIR model (the category of those who died due to the illness, which is taken into account in this paper, can, in principle, be included in the group of those who became ill under the assumptions made in this paper). In addition, here, together with the isolation of those infected, the isolation of healthy individuals is taken into account, which also affects the rate of the spread of the infection.

Studying the behavior of the infection at an early stage is most important, since, at this stage, it is possible to effectively stop the further spread of the disease among the population and prevent it from developing into an epidemic. One such method is the isolation of individuals in a population, which is important, especially in cases where a vaccine has not yet been developed. The effect of isolating individuals in a population is very important, since with a sufficient number of isolated individuals, it leads to a decrease, and in the future, a complete decline in the epidemic. In relation to this, the paper proposes simplified models based on the basic SIR model, suitable for describing the dynamics of infection at the initial stages, when only a small fraction of the population is infected and the criteria are established (taking into account the isolation of individuals, both infected and healthy), which if maintained prevent the infection from turning into an epidemic (i.e., the number of infected individuals decreases over time).

The advantages of the proposed approaches lie in the systematic and detailed study of the effect of isolating individuals on the dynamics of the spread of an infectious disease (without increasing the number of equations). In addition, in the simplified models that are presented in this paper, the differential equations, unlike the SIQR or SIRS models, are linear, which facilitates analysis. The novelty of this study lies in the consistent consideration of the isolation effect in the entire population (both among infected and healthy individuals) using the isolation coefficient.

2. SHORT DESCRIPTION OF THE SIR MODEL

Almost all models built to study epidemic processes are based on the SIR model. If I is the number of infected people, and S is the number of those not infected (prone to infection), according to the theory of encounters, the rate of growth in the number of the former and the decrease in the latter will be greater the more encounters between the two, i.e., the greater the product IS. Let us assume that the population is closed; i.e., there is no inflow or outflow of individuals from the system, and the natural birth and death rates of the population are also neglected. Per unit of time (for example, per day), each infected individual will be in contact with k other individuals in the population. Moreover, kS/N (N is the population size) of these contacts account for uninfected individuals. If a certain proportion of contacts η leads to the transmission of infection, then each infected individual infects $\eta kS/N$ uninfected individuals per unit of time. Thus, in total, the infected individuals infect $\eta kSI/N$ individuals among the uninfected. It is considered that those who have been ill are not reinfected.

Under the assumptions made, the equations of the SIR model have the form

$$dS/dt = -\gamma SI, \quad dI/dt = -\alpha I + \gamma SI, \quad dR/dt = \alpha I, \quad (\gamma = \delta/N, \quad \delta = \eta k).$$

Here, S, I, and R are the number of susceptible (i.e., those who may be infected), actually infected, and recovered individuals, while coefficients γ and α characterize the rates of infection and recovery, respectively. Obviously, $S + I + R = N = \text{const}$ (this relation follows from the system of equations as the first integral if they are added together and integrated), where N is the total number (size) of the population. This model has been analyzed in detail in the scientific literature (see, for example, [3]). In particular, it is shown that in the SIR model, the epidemic always disappears over time; this can be seen from the equation for R: if I does not tend to 0 over time, then R tends to infinity, which leads to a contradiction, since R should be less than N. An effective reproduction index is introduced $R_e = R_0 S(0)/N$ [3], where $S(0)$ is the initial number of uninfected individuals and $R_0 = \delta/\alpha$ is basic reproduction index. Then the "epidemic threshold theorem" is valid [3, 4], according to which, if $R_e \le 1$, the value $I(t)$ decreases monotonically to zero at $t \to \infty$, and if $R_e > 1$, $I(t)$ behaves nonmonotonically: first, it increases, reaches a maximum, then, drops to zero at $t \to \infty$ (the scenario corresponding to the condition $R_e > 1$ is called an *epidemic*). The proofs of these assertions can be found in [3]. This model underlies many studies of the processes of an epidemic disease spreading in a population [17–19].

3. SIMPLIFIED EPIDEMIC MODELS

We consider the case when the number of infected individuals I is much less than the number of uninfected individuals S, so $I \ll S \approx N$. This situation occurs when the infection spreads at a low rate, and the number of uninfected individuals S does not change much. This assumption is also fulfilled at the initial stage of the spread of the epidemic. As the statistics show, at the moment, in the case of coronavirus, a similar situation takes place.

Unlike the SIR model, together with those who have been ill R, we will also take into account the presence of deaths among the infected; the number of deaths will be denoted by D (obviously, R, and $D \ll N$). Thus, the statistics on COVID-19 show that the number of deaths among those infected can reach significant values (for example, as of May 1, 2020, in Spain, the proportion of deaths among those infected was about 11%; and in Italy, about 14%). In relation to this, the effect of the number of deaths must be taken into account. An isolated population system is considered, i.e., $S + I + R + D = N = \text{const}$. In addition, as in the SIR model, it is assumed that those who have recovered do not become reinfected.

Next, we analyze several simple models based on the principles of the SIR model.

3.1. IRD Model

Assume that infected and uninfected individuals are not isolated from each other. Then, based on the SIR model, equations can be written (within the assumptions made, we neglect the change in S)

$$dI/dt = -\alpha I - \beta I + \gamma SI, \quad dR/dt = \alpha I, \quad dD/dt = \beta I. \tag{1}$$

Here, β is the proportion of patients who died per unit of time (for example, in one day). Insofar as $S = N - I - R - D$ and I, R, and $D \ll N$, the first equation of the system can be modified and instead of (1) we obtain the following linear system:

$$dI/dt = -\alpha I - \beta I + \delta I, \quad dR/dt = \alpha I, \quad dD/dt = \beta I, \quad (\delta = \gamma N). \tag{2}$$

Let us set the initial conditions: assume that at some (initial) moment of time $t = 0$ we have $I = I(0)$, $R = R(0)$, and $D = D(0)$. The solutions of Eqs. (2), taking into account the initial conditions, have the form (at constant coefficients α, β, and δ)

$$I = I(0)\exp(\nu^\circ t), \tag{3}$$

$$R = R(0) + \frac{\alpha I(0)}{\nu^\circ}\left[\exp(\nu^\circ t) - 1\right], \tag{4}$$

$$D = D(0) + \frac{\beta I(0)}{\nu^\circ}\left[\exp(\nu^\circ t) - 1\right], \qquad \nu^\circ = \delta - (\alpha + \beta). \tag{5}$$

Three cases are possible. In the first case, when $\nu^\circ < 0$ (i.e., $\alpha + \beta > \delta$), value I tends to zero over time; and the values R and D, to the limit values $R(\infty) = R(0) + \alpha I(0)/(-\nu^\circ)$ and $D(\infty) = D(0) + \beta I(0)/(-\nu^\circ)$, respectively. In the second case, when $\nu^\circ > 0$ ($\alpha + \beta < \delta$), the number of healthy, infected, recovered, and dead individuals increases with t. In the third case, when $\nu^\circ = 0$ ($\alpha + \beta = \delta$), we have an equilibrium state $I = I(0)$, i.e., the number of newly infected is equal to the sum of recovered and deceased patients. This

case is degenerate, and the dependences $R(t)$ and $D(t)$ corresponding to this case do not follow directly from solutions (4) and (5) (the latter give uncertainties of type 0/0). The solution is obtained by substituting the value $I(0)$ instead of I in the right parts of the second and third equations of system (2). Their subsequent integration gives $R = R(0) + \alpha I(0)t$ and $D = D(0) + \beta I(0)t$; thus, in this case the dependences $R(t)$ and $D(t)$ obey a linear law. Note that, as can be seen from solution (3), this equilibrium state is unstable, since any small deviation from this state leads to an exponential increase (or decrease) in the number of infected people. From the obtained solutions, it follows that between R and D there is an obvious relation $D - D(0) = (\beta/\alpha)(R - R(0))$ (such a relationship also follows from the last two equations of system (2), if we divide them into each other and integrate the resulting equation).

In addition, system (2) has the following first integrals

$$I - \frac{\nu^\circ}{\alpha} R = \text{const} \quad \text{and} \quad I - \frac{\nu^\circ}{\beta} D = \text{const},$$

where the constants on the right-hand sides can be determined, in particular, from the initial data. From this the relation between R and D obtained above in a different way follows. The model given, by analogy with the SIR model, will be conventionally denoted as the IRD model.

3.2. IRDi Model

We consider the case when some part of the population can be isolated. Assume σ_I and σ_S are fractions of isolated individuals among infected and uninfected individuals, which can be called isolation coefficients (obviously, $0 \le \sigma_I, \sigma_S \le 1$). Then the numbers of non-isolated individuals among infected and non-infected groups that can contact each other are $(1 - \sigma_I)I$ and $(1 - \sigma_S)S$, respectively. In this case, the first equation of system (2) is modified, and the remaining equations do not change; thus, we have

$$dI/dt = -(\alpha + \beta)I + (1 - \sigma_I)(1 - \sigma_S)\delta I, \quad dR/dt = \alpha I, \quad \text{and} \quad dD/dt = \beta I. \tag{6}$$

The product of $(1 - \sigma_I)(1 - \sigma_S)$ can be equated to $(1 - \sigma)$, i.e., we get the equation $(1 - \sigma_I)(1 - \sigma_S) = (1 - \sigma)$, where σ can be called the generalized isolation factor. Hence,

$$\sigma = 1 - (1 - \sigma_I)(1 - \sigma_S). \tag{7}$$

Obviously, the relations that follow from (7) are satisfied:

$$\sigma = \begin{cases} 1, & \text{if} \quad (\sigma_I = 1 \text{ or } \sigma_S = 1) \quad \text{or} \quad (\sigma_I = 1 \text{ and } \sigma_S = 1), \\ \sigma_I, & \text{if} \quad (\sigma_S = 0), \\ \sigma_S, & \text{if} \quad (\sigma_I = 0), \\ 0, & \text{if} \quad (\sigma_I = 0 \quad \text{and} \quad \sigma_S = 0). \end{cases}$$

Lines of equal values of parameter σ satisfying relation (7) are shown in Fig. 1.

Now, system (6) is rewritten in the form

$$dI/dt = -(\alpha + \beta)I + (1 - \sigma)\delta I, \quad dR/dt = \alpha I, \quad dD/dt = \beta I. \tag{8}$$

System (8) under the condition of constant coefficients and taking into account the initial conditions (for $t = 0$, $I = I(0)$, $R = R(0)$, $D = D(0)$) has the following solutions:

$$I = I(0)\exp(\nu t), \tag{9}$$

$$R = R(0) + \frac{\alpha I(0)}{\nu}[\exp(\nu t) - 1], \quad D = D(0) + \frac{\beta I(0)}{\nu}[\exp(\nu t) - 1], \tag{10}$$
$$\nu = (1 - \sigma)\delta - (\alpha + \beta).$$

At $\alpha + \beta > \delta$, as in the IRD model, the number of infected individuals I decreases to 0, while R and D increase over time (regardless of the value of σ). In this case, the limit values R and D will be

$$R(\infty) = R(0) + \alpha I(0)/(-\nu) \quad \text{and} \quad D(\infty) = D(0) + \beta I(0)/(-\nu) \big(\text{where } \nu < 0\big), \tag{11}$$

and they are less than the corresponding values in the IRD model ($\sigma = 0$). Obviously, with an increase in the isolation coefficient σ, the limit values $R(\infty)$ and $D(\infty)$ will decrease, reaching their minimum values

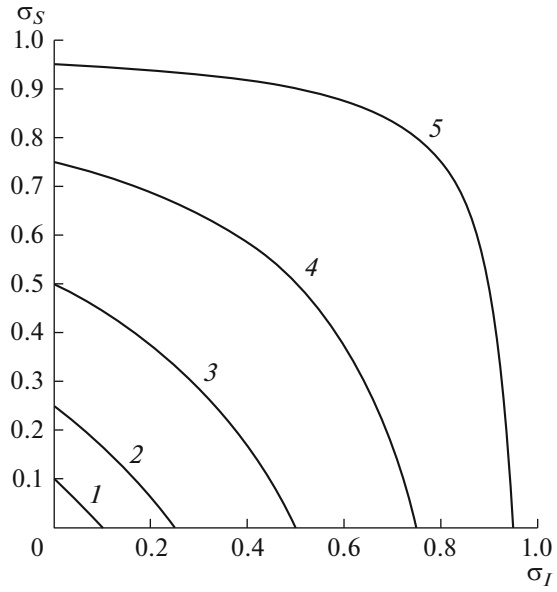

Fig. 1. Lines of equal values of the generalized coefficient σ on the plane (σ_I, σ_S): *1*, $\sigma = 0.1$; *2*, 0.25; *3*, 0.5; *4*, 0.75; and *5*, 0.95.

at $\sigma = 1$: $R(\infty) = R(0) + \alpha I(0)/(\alpha + \beta)$, $D(\infty) = D(0) + \beta I(0)/(\alpha + \beta)$, and $R(\infty) + D(\infty) = I(0) + R(0) + D(0)$. As in the IRD model, system (8) has the first integrals

$$I - (\nu/\alpha)R = \text{const}, \quad I - (\nu/\beta)D = \text{const},$$

from which the same relationship follows between quantities R and D, as in the IRD model,

$$D - D(0) = (\beta/\alpha)(R - R(0)).$$

As an example, when $\alpha + \beta > \delta$, we consider the characteristic behavior of the quantities $I(t)$ and $R(t)$ (assigned to $I(0)$) for the values of the defining parameters $\alpha = 0.05$, $\beta = 0.005$, and $\delta = 0.01$, for which the condition $\alpha + \beta > \delta$ is satisfied, are illustrated in Fig. 2 (in the case $R(0) = D(0) = 0$). When changing the parameter σ from 0 to 1, all curves $I(t)$ and $R(t)$ will be located between the corresponding limit dashed curves and curves *5*.

In the case when $\alpha + \beta < \delta$, the sign of the coefficient before t in the exponent in (9) depends on parameter σ. At $\sigma > \sigma_*$, where

$$\sigma_* = 1 - (\alpha + \beta)/\delta \quad (\alpha + \beta < \delta), \tag{12}$$

we have $\nu < 0$; i.e., in this case, the number of infected individuals I will decrease over time. At $\sigma < \sigma_*$ from (9) we obtain $\nu > 0$, so that value I will grow. When $\sigma = \sigma_*$ ($\nu = 0$), the number of infected individuals over time remains unchanged and equal to the initial value $I = I(0)$ (equilibrium state). Note that in the degenerate case $\sigma = \sigma_*$, the solutions for R and D in the considered model have the same linear form as in the IRD model.

Thus, there is a threshold value of the isolation factor σ_*, which delimits the qualitatively different behavior of dependence $I(t)$: at $\sigma < \sigma_*$ the number of infected people increases over time; at $\sigma > \sigma_*$, in contrast, it decreases; and in the case $\sigma = \sigma_*$, the system enters an equilibrium state when the number of infected individuals remains constant, and the number of recoveries and deaths grows linearly.

For known values of parameters α, β, and δ, the value σ_* can be interpreted as the threshold value of the isolation coefficient, upon reaching which the infection does not develop into an epidemic.

By analogy with the previous model, this model will be conditionally called the IRDi model (additional symbol *i* from *isolation*).

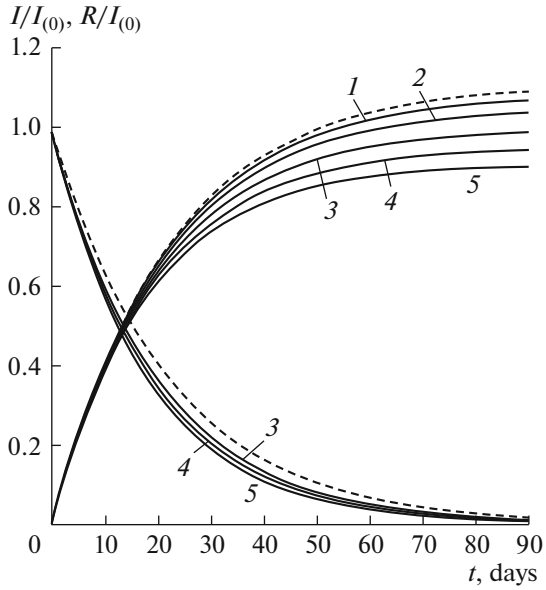

Fig. 2. Change in the number of infected $I/I(0)$ (decreasing curves) and recovered $R/I(0)$ (increasing curves) individuals in the case $\alpha + \beta > \delta$ for different values of the isolation factor: *1*, $\sigma = 0.1$; *2*, 0.25; *3*, 0.5; *4*, 0.75; *5*, 1.0; dashed curves, $\sigma = 0$.

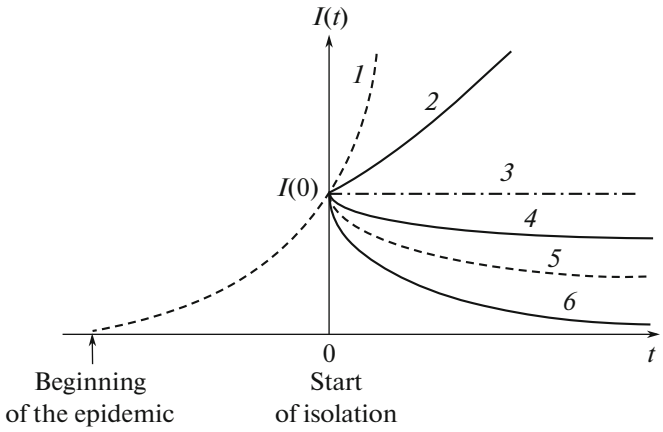

Fig. 3. The nature of behavior of dependence $I(t)$ in different models: curve *1*, IRD (for $\alpha + \beta < \delta$); *2*, IRDi (for $0 < \sigma < \sigma_*$); *3*, IRDi (for $\sigma = \sigma_* > 0$) or IRD (for $\alpha + \beta = \delta$); *4,* IRDi (at $0 < \sigma_* < \sigma$); *5*, IRD (for $\alpha + \beta > \delta$); *6*, IRDi (for $\alpha + \beta > \delta$, $\forall\sigma$).

Using the expression for the critical quantity σ_*, parameter ν in solutions (9) and (10) can be rewritten in another form

$$\nu = \delta(\sigma_* - \sigma),$$

in which the role of the critical parameter σ_* is more clearly visible.

The nature of the behavior of the number of infected individuals $I(t)$ in different models is schematically illustrated in Fig. 3. The dashed curve corresponds to the IRD model (in the absence of isolation, $\sigma = 0$), while the dashed line corresponds to the state of equilibrium $\sigma = \sigma_*$ in the IRDi model and $\alpha + \beta = \delta$ in the IRD model.

As can be seen from the presented diagram, at first value I (the number of infected patients) rises to the value $I(0)$ by the moment of the introduction of isolation; then, depending on the value of the degree of isolation (coefficient σ), the number of infected people may increase (in the case $\sigma < \sigma_*$) or decrease (if

$\sigma > \sigma_*$). Note that the equations in the considered models describe the dynamics of the infectious process, starting from the moment of the introduction of isolation. It should also be noted that the system takes on an equilibrium state in two cases: first, when the equality $\alpha + \beta = \delta$ is fulfilled in the case of no isolation ($\sigma = 0$, IRD model), and second, in the case of isolation with coefficient $\sigma = \sigma_*$ in the IRDi model. In general, the point corresponding to the moment of the introduction of isolation ($t = 0$, $I = I(0)$), can be interpreted as a bifurcation point, since, starting from this point, the behavior of the population system, depending on the values of the defining parameters, branches out.

3.3. Reproduction Indices

Note that the critical value σ_* can be written in terms of the well-known reproduction index [20–23], which characterizes the rate at which an infectious disease spreads. To this end, we introduce reproduction indices for different situations: in the absence of dead and isolated individuals ($\beta = 0$, $\sigma = 0$), the reproduction index will be $R_0 = \delta/\alpha$ (which is often called basic), and in the presence of deceased individuals ($\beta \neq 0$) but the absence of isolation ($\sigma = 0$), we have $R_1 = \delta/(\alpha + \beta)$; similarly, for the case $\beta = 0$, but $\sigma \neq 0$, we get $R_2 = (1 - \sigma)\delta/\alpha$, and in the general case, when $\beta \neq 0$ and $\sigma \neq 0$, we have $R_3 = (1 - \sigma)\delta/(\alpha + \beta)$. For the introduced reproduction indices, the relations $R_3 \leq (R_1, R_2) \leq R_0$ are satisfied (i.e., the presence of isolation leads to a decrease in the reproduction index), and there is an obvious relationship between them $R_0 R_3 = R_1 R_2$. As we can see, the definition of the reproduction index depends on the model.

Now expression (12) for σ_* is rewritten in the form

$$\sigma_* = 1 - 1/R_1.$$

At the same time, the critical value $\sigma = \sigma_*$ corresponds to the threshold value of the reproduction index $R_3 = 1$. In the case of $\beta = 0$, we have $\sigma_* = 1 - 1/R_0$.

Thus, the lower the reproduction index the lower the critical value of the isolation coefficient. At $R_1 = 1$ (or $R_0 = 1$ in the case $\beta = 0$), we have $\sigma_* = 0$, which means that, in this case, any level of isolation leads to a decrease in the epidemic.

Solutions (3)–(5), corresponding to the absence of isolation ($\sigma = 0$), as well as (9) and (10), taking into account the effect of isolation ($\sigma > 0$), in the reproduction indices will be written as

$$I = I(0)\exp\left[(\alpha + \beta)(R_i - 1)t\right],$$

$$R = R(0) + \frac{\alpha}{\alpha + \beta}\frac{I(0)}{R_i - 1}\left\{\exp\left[(\alpha + \beta)(R_i - 1)t\right] - 1\right\},$$

$$D = D(0) + \frac{\beta}{\alpha + \beta}\frac{I(0)}{R_i - 1}\left\{\exp\left[(\alpha + \beta)(R_i - 1)t\right] - 1\right\}, \quad i = \begin{cases} 1, & \sigma = 0, \\ 3, & \sigma > 0. \end{cases}$$

From these expressions it follows that the values $R_i = 1$ ($i = 1, 3$) are threshold values; i.e., they separate cases of epidemic growth or attenuation of the spread of the disease in different situations: in the absence of isolation ($i = 1$) or in the presence of isolation ($i = 3$). The same values correspond to the equilibrium state of the system in these situations. From the formulas given above, we can obtain expressions relating quantities I, R, and D:

$$R = R(0) + \frac{\alpha}{\alpha + \beta}\frac{I - I(0)}{R_i - 1}, \quad D = D(0) + \frac{\beta}{\alpha + \beta}\frac{I - I(0)}{R_i - 1};$$

moreover, the following relation exists:

$$R_i = 1 + \frac{\Delta I}{\Delta R + \Delta D}, \tag{13}$$

where $\Delta I = I - I(0)$, $\Delta R = R - R(0)$, and $\Delta D = D - D(0)$, from which it follows that, in the simplified models discussed above, the reproduction index can be determined based on the numbers of infected, recovered, and deceased individuals (without using coefficients α, β, δ, and σ). Thus, at the early stage of the spread of the epidemic, formula (13) can be used to quickly calculate the reproduction index. Note that the reproduction index is determined not only by the increment in the number of infected people but also by the increments in the number of those who have recovered and died. Moreover, $R_i < 1$ (a condition

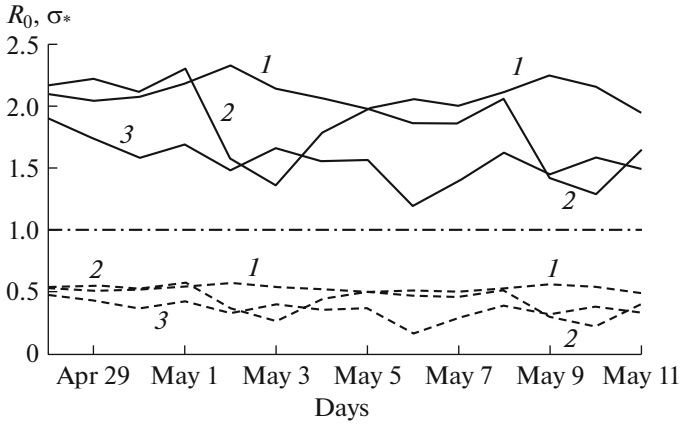

Fig. 4. Change in the reproduction index (solid lines) and the critical value of the isolation factor (dashed lines) for COVID-19 in Russia (curves *1*), Germany (*2*), and United States (*3*) from April 28 to May 11, 2021.

corresponding to a decline of the epidemic), unless $\Delta I < 0$. Obviously, the increments ΔR and ΔD are always greater than zero.

As an example of using formula (13), Fig. 4 shows the results of calculating the reproduction index using the specified formula in the case of the COVID-19 epidemic for Russia, Germany, and the United States. The calculations were carried out with an interval of one day from April 28 to May 11, 2021. For convenience, it is assumed that $D = D(0) = 0$. At the same time, the reproduction index R_1 turns into the base reproduction index R_0. It also shows the changes over the considered period of time of the critical value of the isolation coefficient corresponding to the calculated reproduction index. It can be seen that for Russia there are two peak values of the reproduction index: 2 and 9 May. In this case, the critical value of the isolation coefficient is slightly more than 0.5. In the case of the United States, the reproduction index is generally lower than in Russia and Germany. The smallest value of the critical isolation factor ($\sigma_* \approx 0.3$) in the United States is reached on May 6th. If, starting from this day, approximately at least a third of the population went into quarantine (isolation), then the epidemic would decline (the reproduction index would be less than 1).

The equations of the simplified models proposed above are solved analytically, and, thus, it becomes possible to study in more detail the behavior of the population system during the spread of the epidemic within the accepted assumptions.

4. SIRDi MODEL OF THE EPIDEMIC

In the previous section, we analyzed the case when the number of infected individuals I is much less than the number of uninfected individuals S; thus, $I \ll S$ ($\approx N$). This situation occurs when the infection spreads at a low rate (or at the initial stage of the spread of the epidemic), and the number of people not infected does not change much. In particular, as noted above, for the coronavirus infection, such a situation is currently being observed. If the epidemic reaches alarming proportions, when value I is comparable to value S, then in order to describe the spread of the epidemic, we need to use a more complex model, which should take into account the change in S. Let us consider such a model.

4.1. SIRDi Model Equations

We consider the case when the change in S cannot be neglected. In this case, it is necessary to add an equation for S (similar to the SIR model, but taking into account the effect of isolation) to the equations of the IRDi model (see above). We have

$$dS/dt = -(1-\sigma)\gamma SI, \tag{14}$$

$$dI/dt = -\alpha I - \beta I + (1-\sigma)\gamma SI, \tag{15}$$

$$dR/dt = \alpha I, \tag{16}$$

$$dD/dt = \beta I, \tag{17}$$

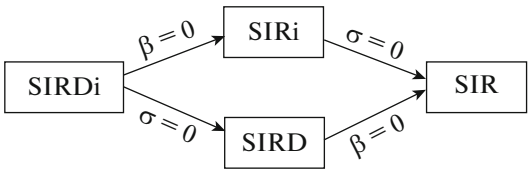

Fig. 5. Diagram of the relationship between different models.

Parameters α, β, γ, and σ have the same meaning as in the previous sections. The proposed model can be referred to as the SIRDi model. With $\sigma = 0$ we get the SIRD model, and with $\beta = 0$, but with $\sigma \neq 0$, we get the SIRi model. In the event that at the same time $\sigma = 0$ and $\beta = 0$, the SIRDi model changes into the SIR model. The relationship between different models is conveniently presented schematically (Fig. 5).

Summing the first three equations (14)–(16) gives

$$d(S + I + R)/dt = -\beta I;$$

i.e., the living population will decrease on account of those who die due to the consequences of infection. Thus, in contrast to the SIR model, in the SIRD and SIRDi models, the living population does not remain constant, although the total number of individuals, taking into account the dead, is maintained: $S + I + R + D = N = \text{const}$. Note that in system (14)–(17) the first two equations can be considered separately from the rest, because they do not include quantities R and D. In addition, from Eqs. (16) and (17), (as in the IRD and IRDi models) the relationship between the numbers of recovered and deceased patients $D - D(0) = (\beta/\alpha)(R - R(0))$ immediately follows.

As in the SIR model (see above), it is easy to show that the SIRDi model also has the asymptotic property $I(\infty) = 0$.

4.2. Critical Value of the Isolation Factor

Similarly to [3], we determine the effective reproduction index $R_e^{(\lambda)} = \lambda R_0 S(0)/N = \lambda R_e$, which differs from the number determined in the SIR model [3] $R_e = R_0 S(0)/N$ by the presence of the multiplier $\lambda = (1 - \sigma)\alpha/(\alpha + \beta)$. Note that the statements of the epidemic threshold theorem formulated for the SIR model (see above) are also valid in this case (but only instead of R_e we have to take $R_e^{(\lambda)}$). In particular, if $R_e^{(\lambda)} \leq 1$, then $I(t)$ decreases monotonically to zero as $t \to \infty$, and in the case $R_e^{(\lambda)} > 1$ $I(t)$ first increases, then after reaching its maximum decreases to zero at $t \to \infty$, i.e., $I(\infty) = 0$. The proofs of these assertions are similar to those in [3]. The threshold value $R_e^{(\lambda)} = 1$ corresponds to the critical value of the isolation factor

$$\sigma_* = 1 - \left(\frac{\alpha + \beta}{\alpha}\frac{1}{R_e}\right). \tag{18}$$

Thus, the statements of the epidemic threshold theorem can be reformulated in terms of the critical value of the isolation coefficient: at $\sigma \geq \sigma_*$ the number of infected individuals drops to zero over time; i.e., the infectious disease does not turn into an epidemic, and in the case of $\sigma < \sigma_*$, the number of infected people first increases, then after reaching the maximum it decreases to 0.

We can usually assume $S(0) \approx N$, then expression (18) for σ_* transforms into the same form as in the IRDi model, $\sigma_* = 1 - 1/R_1$.

4.3. The maximum Number of Infected Individuals

Equating the right side of Eq. (15) to zero, we obtain the critical point at which I takes on its maximum value $I_{\max}$

$$S_c = (\alpha + \beta)/[(1 - \sigma)\gamma].$$

Another critical point $I = 0$, corresponds to the trivial situation when the system remains in an unchanged state (the initial state, at $t = 0$ in the absence of infected individuals, or the final state at $t = \infty$,

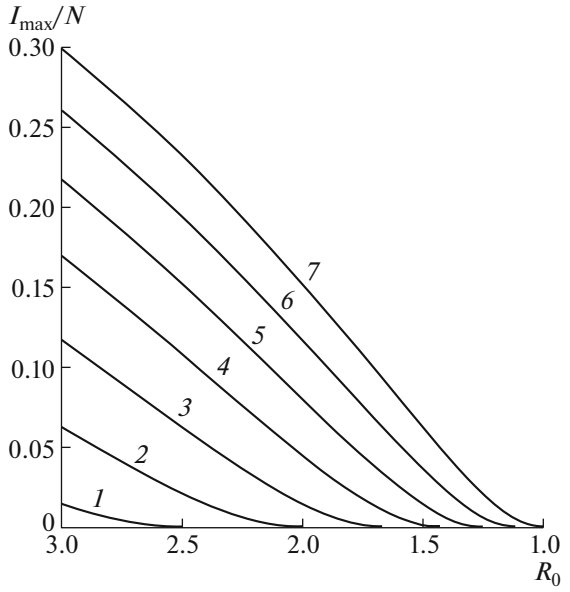

Fig. 6. Dependence of value I_{max}/N on R_0 at different values of parameter $\lambda = 0.4$ (curve *1*), 0.5 (*2*), 0.6 (*3*), 0.7 (*4*), 0.8 (*5*), 0.9 (*6*), and 1 (*7*).

when the epidemic subsides completely). For I_{max} it is not difficult to find a formula (the method of obtaining it is similar to [3])

$$I_{max} = I(0) + S(0) - S_c \ln S(0) - S_c + S_c \ln S_c.$$

If at the initial time $R(0) = 0$ and $D(0) = 0$, then $I(0) + S(0) = N$. Then we have

$$I_{max} = N - S_c\{1 + \ln[(N - I(0))/S_c]\}.$$

In the case when there are very few infected individuals at the beginning, $I(0) \ll N$, we get

$$\frac{I_{max}}{N} = 1 - \frac{1}{R_3}(1 + \ln R_3) = 1 - \frac{1}{\lambda R_0}(1 + \ln \lambda R_0),$$

insofar as $S_c/N = 1/R_3$, and $R_3 = \lambda R_0$. Dependences I_{max}/N on R_0 for different λ are shown in Fig. 6. The curve constructed for $\lambda = 1$ corresponds to the SIR model and is extreme (or limiting) for other values of $\lambda < 1$. The points where the curves touch the lower axis correspond to the threshold value $\lambda R_0 = R_3 = 1$, to the right of which $R_3 < 1$, and according to the first statement of the threshold theorem [3], the quantity I in this case decreases monotonically with time (i.e., it has no maximum). As parameter R_0 decreases, magnitude I_{max} also decreases.

4.4. Limit Values of Variables

Similarly to the SIR model, in the case of the SIRDi model, it can also be shown that $S(\infty) > 0$. To do this, we divide Eq. (14) by Eq. (16) and obtain

$$dS/dR = -\kappa S, \quad \kappa = (1 - \sigma)\gamma/\alpha, \quad (\gamma = \delta/N).$$

Separating the variables and integrating, we find

$$S(t) = S(0)\exp\{-\kappa[R(t) - R(0)]\}. \tag{19}$$

Hence, given that $0 \le R(t) - R(0) \le N$, we have $S(t) \ge S(0)\exp(-\kappa N)$ or

$$S(\infty) \ge S(0)\exp[-(1 - \sigma)R_0] > 0,$$

which needed to be proved.

Next, we find an equation for $S(\infty)$. From (19) with $R(0) = 0$, it follows

$$S(\infty)/N = [S(0)/N]\exp\{-(1 - \sigma)R_0 R(\infty)/N\},$$

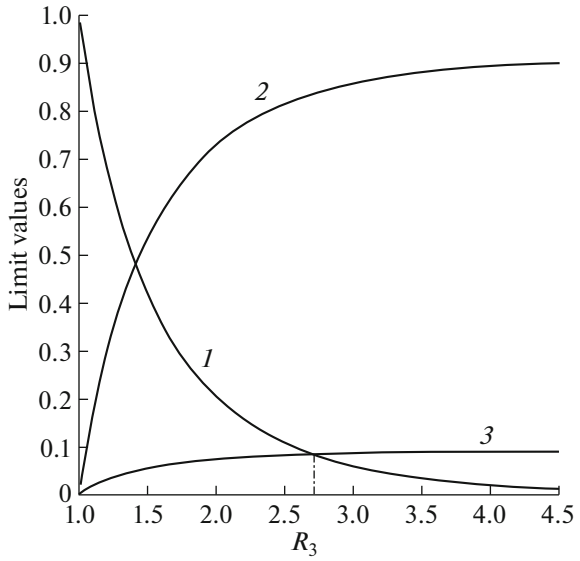

Fig. 7. Dependences of limit values of $S(\infty)/N$ (curve *1*), $R(\infty)/N$ (*2*), $D(\infty)/N$ (*3*) on parameter R_3.

or

$$\ln[S(\infty)/N] = -(1-\sigma)R_0[R(\infty)/N], \tag{20}$$

as we can usually take $S(0) \cong N$. Dividing Eq. (14) by Eq. (17), we obtain

$$dS/dD = -\theta S, \quad \theta = (1-\sigma)\gamma/\beta.$$

Separating the variables and integrating, we find

$$S(t) = S(0)\exp\{-\theta[D(t) - D(0)]\}.$$

Given that $D(0) = 0$, from above expression at $t \to \infty$ we have

$$S(\infty)/N = [S(0)/N]\exp\{-(1-\sigma)(\alpha/\beta)R_0 D(\infty)/N\}.$$

Usually $S(0) \cong N$, so that the last expression implies

$$\ln[S(\infty)/N] = -(1-\sigma)(\alpha/\beta)R_0 D(\infty)/N. \tag{21}$$

Insofar as $I(\infty) = 0$ (according to the threshold theorem, see above), the following relation is obviously satisfied:

$$S(\infty) + R(\infty) + D(\infty) = N. \tag{22}$$

Solving Eqs. (20)–(22) jointly, we arrive at a transcendental equation with respect to $S(\infty)$:

$$\ln[S(\infty)/N] = \lambda R_0[S(\infty)/N - 1],$$

or

$$\ln[S(\infty)/N] = R_3[S(\infty)/N - 1]. \tag{23}$$

Computing $S(\infty)$ from (23), it is easy to find the values $R(\infty)$, $D(\infty)$ according to the formulas

$$\frac{R(\infty)}{N} = \frac{\alpha}{\alpha+\beta}\left[1 - \frac{S(\infty)}{N}\right], \quad \frac{D(\infty)}{N} = \frac{\beta}{\alpha+\beta}\left[1 - \frac{S(\infty)}{N}\right].$$

Figure 7 shows the dependences of the quantities $S(\infty)/N$, $R(\infty)/N$, and $D(\infty)/N$ from parameter R_3. Values $R(\infty)/N$ and $D(\infty)/N$ are calculated at $\beta = 0.1\alpha$, so $D(\infty)$ is smaller than $R(\infty)$ by a factor of 10. As parameter R_3 increases, magnitude $S(\infty)$ decreases, while $R(\infty)$ and $D(\infty)$, in contrast, increase. Note that for the values $R_3 \geq 2.7$ the limit number of not infected individuals will be less than the number of deaths from infection, i.e., $S(\infty) < D(\infty)$. The main changes in the limit values are observed with R_3 increasing in the range from 1 to 3. The further growth of R_3 only weakly affects these values.

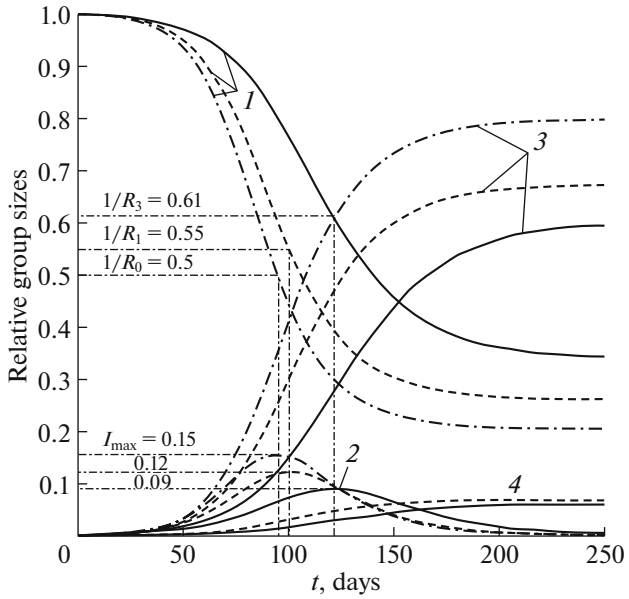

Fig. 8. The change in $\bar{S}$ (curves *1*), $\bar{I}$ (*2*), $\bar{R}$ (*3*), $\bar{D}$ (*4*) in time at $R_0 = 2$ and $1/\alpha = 14$ days. Solid curves, SIRDi model ($\sigma = 0.1$, $\beta = 0.1\alpha$); dashed curves, SIRD model ($\sigma = 0$, $\beta = 0.1\alpha$); dashed-dotted curves, SIR model ($\sigma = 0$, $\beta = 0$).

4.5. Results of Calculations of an Epidemic's Dynamics Using the SIRDi Model

We introduce dimensionless variables

$$\bar{S} = S/N, \quad \bar{I} = I/N, \quad \bar{R} = R/N, \quad \bar{D} = D/N, \quad N = S + I + R + D = \text{const}.$$

In the new variables, system (14)–(17) takes the form

$$d\bar{S}/dt = -(1-\sigma)\delta\bar{S}\bar{I}, \quad d\bar{I}/dt = -\alpha\bar{I} - \beta\bar{I} + (1-\sigma)\delta\bar{S}\bar{I},$$
$$d\bar{R}/dt = \alpha\bar{I}, \quad d\bar{D}/dt = \beta\bar{I}. \tag{24}$$

Figure 8 shows the results of the numerical integration of system (24) under the following initial conditions: $t = 0$, $\bar{S}(0) = 0.999$, $\bar{I}(0) = 0.001$, $\bar{R}(0) = 0$, and $\bar{D}(0) = 0$ (the example is taken from [5], where the dynamics of the COVID-19 epidemic were calculated using the SIR model). The basic reproduction index $R_0 = 2$ and the isolation coefficient $\sigma = 0.1$, while the effective reproduction index $R_e^{(\lambda)} = \lambda\bar{S}(0)R_0 \approx 1.64 > 1$, which corresponds to the epidemic scenario according to the epidemic threshold theorem. The critical value of the isolation factor σ_*, calculated by (18), is equal to $\sigma_* = 0.45$; thus, in this case $\sigma < \sigma_*$. Coefficient α was considered equal to $1/14 \approx 0.07$ [5] (here, it is taken into account that the recovery time from the coronavirus infection is approximately 14 days). A ratio $\beta = 0.1\alpha$ was assumed between coefficients α and β (the observed data for COVID-19 are roughly consistent with this ratio between α and β).

For comparison, Fig. 8 also shows the results of calculations using the SIR and SIRD models. It is seen that in the SIRD and SIRDi models, the peak values I decrease compared to the SIR model but the time taken to reach them t_m increases. For example, according to the SIR model, $t_m = 95$ days, and, according to SIRD and SIRDi models, $t_m = 102$ and 120 days, respectively. The peak values $\bar{I}_{\max}$ themselves in the models given above are 0.15, 0.12, and 0.09, respectively. It should be noted that the presence of even a small proportion of isolated individuals ($\sigma = 0.1$) leads to a noticeable decrease in the maximum number of infected individuals, as well as in the number of deaths and recoveries, and an increase in the number of individuals who are not infected. Accounting for the number of deaths also leads to noticeable differences in the size of the groups.

The results obtained in the simplified IRDi model, which is valid at the initial stage of the spread of an infectious disease, and the SIRDi model, which covers the entire dynamics of the epidemic, including the later stages, are compared in Fig. 9 (the values of the determining parameters correspond to Fig. 8) for two characteristic situations: when $\sigma < \sigma_*$ (Fig. 9a) and $\sigma > \sigma_*$ (Fig. 9b). In the first case, the calculations were made for the initial stage of the epidemic. It can be seen that the dependences of the number of infected, recovered, and deceased patients on time, calculated using the models given above, differ slightly. This cir-

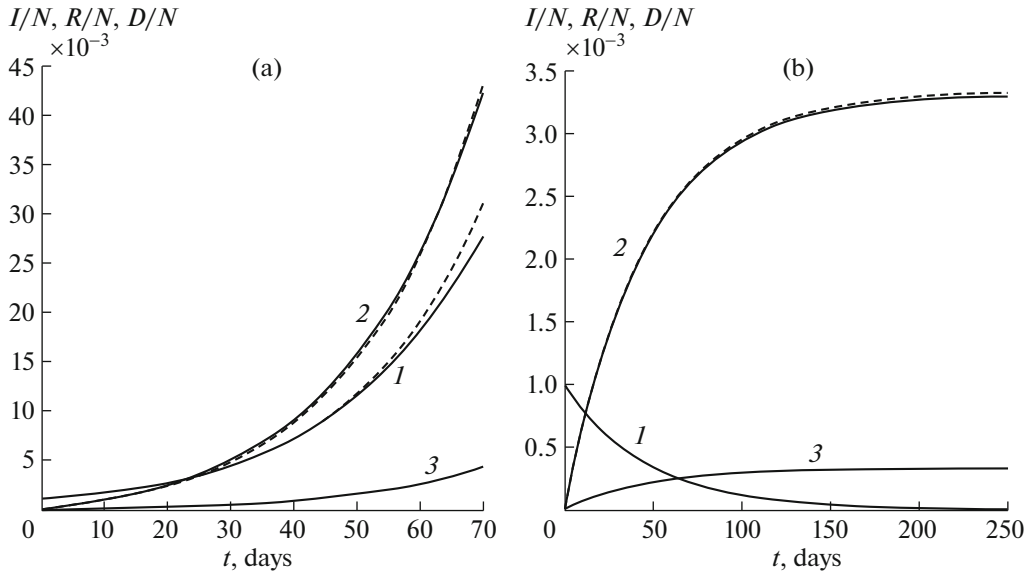

Fig. 9. Comparison of results obtained by IRDi (dashed curves) and SIRDi (solid curves) models at $\sigma = 0.1 < \sigma_* = 0.45$ (a) and $\sigma = 0.6 > \sigma_*$ (b): curves *1*, *I*/*N*; *2*, *R*/*N*; *3*, *D*/*N*.

cumstance allows us to conclude that at the initial stage of the spread of an infectious disease during an epidemic (when $\sigma < \sigma_*$), as well as in the case of preventing an epidemic (when $\sigma > \sigma_*$), it is quite possible to use a simplified IRDi model, where the solutions are expressed by simple analytical formulas (compared to the SIRDi model, where differential equations have to be solved numerically).

Thus, it has been established that the presence of isolated individuals in the population significantly affects the dynamics of the spread of an infectious disease. In particular, there is a threshold value of the isolation factor $\sigma = \sigma_*$, determined by the fact that, for values of σ exceeding this value, the number of infected people decreases over time (the infection does not turn into an epidemic), and for values less than this critical value, the number of infected people, in contrast, increases (the epidemic progresses). It is shown that at the initial stage of the epidemic, it is quite possible to use simplified models, whose equations have a linear form and have simple analytical solutions.

The constructed models make it possible to evaluate and predict the nature of the behavior of epidemic processes in the presence and absence of the isolation of individuals in a population. In particular, a fairly convenient formula has been established for calculating the average value of the reproduction index by increments over a certain period of time of the number of those individuals who were infected, recovered, and died at the initial stage of the spread of the infection.

Note that vaccination affects the interaction of individuals of different groups in the same way as isolation, since in both cases the vaccinated or isolated individuals do not participate in the process of transmitting the infection (if the effect of the vaccine is instantaneous). Obviously, when vaccinating, the generalized isolation coefficient introduced above should be considered as the proportion of those vaccinated in the group of uninfected individuals, i.e. $\sigma_I = 0$ and $\sigma = \sigma_S$. Then, all the statements given above will be true for the case of vaccination of individuals in the population.

In principle, the number of deaths, which is taken into account in these models, can be included in the number of those individuals who have been ill without distinguishing them into a separate group (which is done in most cases); however, if a situation arises when those who have been ill can be infected again (loss of immunity), then we need to account for this category.

CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

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