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# Peculiarities of Construction and Analysis of a Complex Epidemiological Susceptible-Infected-Removed Model

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**Abstract**

This study is focused on the construction and analysis of a complex epidemiological practical model built on the basis of the Susceptible-Infected-Removed (SIR) model. The examples illustrate the behavior of the practical model in various scenarios and also compare this model and a similar model, taking into account migration. The nature of the behavior of the model is determined by parameters such as the rate of spread of infection, the coefficients of recovery, mortality, the intergroup transition and others with different values of influence. _

**KEY WORDS:** *generalized susceptible-infected-removed (SIR) model, epidemiological situation, conflict interaction*

## 1. Introduction

Throughout its history, humanity has faced various diseases. Some were commonplace and did not carry great danger, such as the common cold we all have; others, in turn, were so deadly and rapid in distribution that struck millions. To be able to cope with such situations, you need to be able to anticipate different scenarios and respond accordingly.

One of the tools that allows you to do this is mathematical modeling [1 - 10], in particular, modifications of susceptible-infected-removed SIR models [11 - 14]. It allows you to project the dissemination of infection and the possible consequences of an epidemic. The importance of this knowledge when it comes to human health and life cannot be overestimated.

Such models use basic assumptions or statistics paired with mathematical approaches to calculate disease rate, mortality, and other parameters that describe the nature of epidemics. Knowing this information, you can develop a strategy to combat, and in the same way to test its effectiveness within the model. The effectiveness of such forecasts, in addition to the correct selection of data, also depends on taking into account all important factors and rules. The more details are built into the model, the more expressive and useful it will be. At a time when the Covid-19 epidemic is raging all over the world, the relevance of such research should not be in doubt. In the generalized epidemiological model studied in this work, we tried to take into account 11 possible states of people that are not taken into account in simpler versions of the model, for example, asymptomatic infected people, people in quarantine, people in the intensive care unit.

## 2. The Mathematical Background

### 2.1. Susceptible-Infected-Removed Model

Susceptible-Infected-Removed (SIR) is one of the simplest models used to mathematically model the dissemination of infectious diseases. In this model, the population is divided into three groups: susceptible to the

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disease (S – susceptible), (I – infectious) (R – recovered).

Susceptible and Infected persons have obvious interpretation. “Recovered” can have a wider concept. Consequently, we could say that R consists of those individuals who cannot no further fall ill, or which have recovered or have gone. The values of the groups depend on time, according to the order of the illness.

The differential equations of SIR model has a form:

$$\frac{dS}{dt} = -\frac{\alpha SI}{N} \quad (1)$$

$$\frac{dI}{dt} = \frac{\alpha SI}{N} - \beta I \quad (2)$$

$$\frac{dR}{dt} = \beta I \quad (3)$$

The SIR model in its initial form describes the simplest possible version of the spread of infection, so it is not always practical. For greater practicality, this basic model is refined to take into account as many different factors as possible.

The increments in infected individuals are determined by the product of the numbers of favorable and infected individuals. Here,  is the prevalence rate of the disease and is the recovery rate. The rate at which the number of infected individuals increases over time is related to the size of some event, which corresponds to infected and susceptible individuals being in close proximity to each other and interacting. The magnitude of this event appears to be proportional to the product of the number of susceptible individuals (*S*) and infected individuals (*I*). Apparently, the number of susceptible individuals decreases at the same rate as they cease to be susceptible and become infected.

Equation (1) shows that the number of susceptible individuals decreases with the growth of the infected. And since the rate of growth of the number of infected people is never zero, it turns out that the function *S(t)* is decreasing. Equation (2) shows that the rate of infection growth apparently increases as the number of infected increases and decreases as more individuals become infected. And equation (3) shows that the number of people who have recovered is directly proportional to the number of infected people. That is, *R(t)* is increasing.

Since the total number of persons must remain the same, an additional condition is imposed. *S(t) + I(t) + R(t) = N*

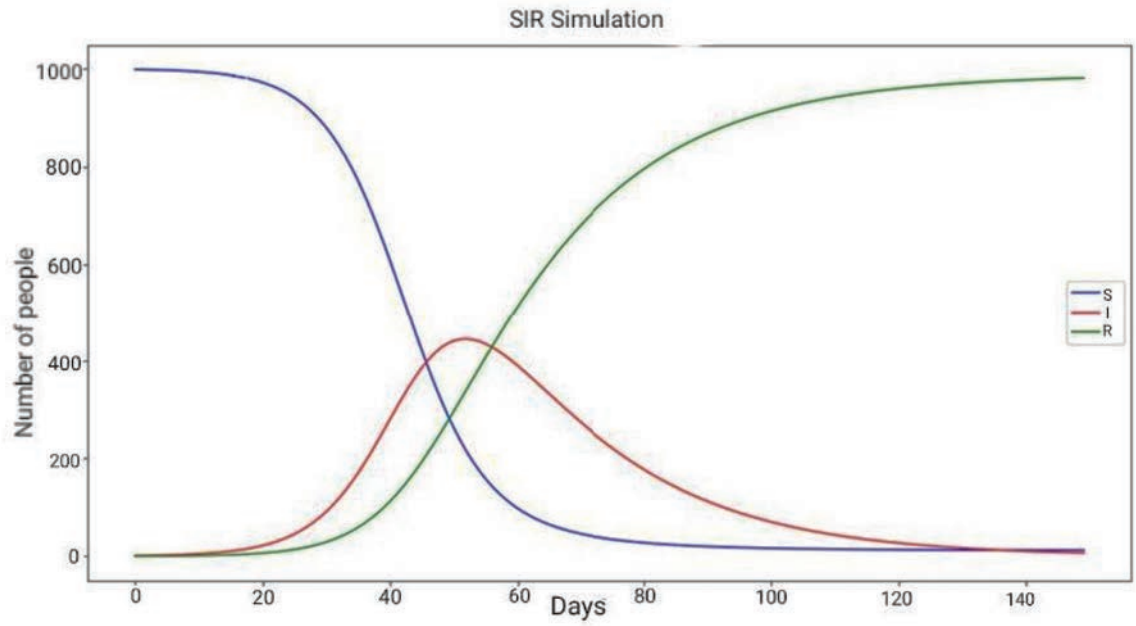


Fig.1. Graph of the behavior of the model for 150 days with the given initial parameters.

For clarity, Figure 1 shows a graph of the behavior of the model for 150 days with the initial parameters: α=0.218, *β*=0.05, N=1000, S(*0*)=999, *I*(0)=1, *R*(0)=0. It should be noted that the epidemic reached its peak on the 52nd day and only 18 people did not avoid infection throughout the period.

### 2.2. Solutions of the SIR Model

**Exact analytical solution**

Despite the fact that the SIR model was formulated back in 1927, until recently only numerical methods were used to solve it. However, in 2014, T. Kharko and his co-authors proposed the first analytical solution [5]:

$$t(u) - t_0 = \int_0^u \frac{N}{s(c_1 N - \beta N log(s) + \alpha S_0 s)} ds$$

From this solution, we can draw some conclusions about the time dependence of the model. But, despite this, such a solution remains useful only in the framework of academic curiosity, since it is difficult to generalize it for use in computer calculations.

### 3. Brief Description of Numerical Methods

***The method of differential transformation***

When applying such models in practice, it is much more convenient to consider time as discrete, since the data used are often recorded no more than once a day, or even less often. Taking this into account, let us rewrite equations (1)-(3) in discrete form:

$$S(k+1) = \frac{1}{k+1}\left[-\frac{\alpha}{N}\sum_{n=0}^{k} S(k)I(k-n)\right] \quad (5)$$

$$I(k+1) = \frac{1}{k+1}\left[\frac{\alpha}{N}\sum_{n=0}^{k} S(k)I(k-n) - \beta I(k)\right] \quad (6)$$

$$R(k+1) = \frac{1}{k+1}[\beta I(k)] \quad (7)$$

Such equations can be easily used to find results by programming on a computer.

***Variational-iterative method***

Let there be some (nonlinear) simple differential equation:

$$x'(t) = f\big(x, x(t)\big);\ x(t_0) = x_0;\ t_0 < t < t_f$$

The idea of the method is to select some sequence of functions $u_n(t)$ such that $\lim_{n\to\infty} u_n(t) \equiv x(t)$. This sequence has a form

$$u_{n+1}(t) = u_n(t) + \int_{t_0}^{t} \lambda_n(s)(u_n'(s) - f(s, u_n(s)))ds \quad (8)$$

Next, we need to choose $\lambda(s)$, which is called the Lagrange multiplier, in such a way that $\lim_{n\to\infty} u_n(t) \equiv x(t)$ is always fulfilled.

Applying the variational iteration method to equations (1)-(3), we obtain:

$$s_{n+1}(t) = s_n(t) + \int_0^t \lambda_1 \left[s_n'(w) + \frac{\alpha}{n} x_n(w) y_n(w)\right] dw \quad (9)$$

$$i_{n+1}(t) = i_n(t) + \int_0^t \lambda_2 \left[i_n'(w) - \frac{\alpha}{n} x_n(w) y_n(w) + \beta y_n(w)\right] dw \quad (10)$$

$$r_{n+1}(t) = r_n(t) + \int_0^t \lambda_3 [r_n'(w) - \beta y_n(w)] dw \quad (11)$$

## 4. Simple Modifications of the Basic Susceptible-Infected-Removed SIR Model

Further, the main options for modifying the SIR model will be considered, on the basis of which more complex options are built, the behavior of which allows us to predict real scenarios of the spread of the disease.

### Susceptible-Infected-Susceptible (SIS) model

As we know, there are many diseases, including the common cold, after which a person does not have long-term immunity and can become sick again.


Fig. 2. Shema for Susceptible-Infected-Susceptible (SIS model).

To model this behavior, the group of recovered individuals (R) is removed from the SIR model.

$$\frac{dS}{dt} = -\frac{\alpha SI}{N} + \beta I; \quad (12)$$

$$\frac{dI}{dt} = \frac{\alpha SI}{N} - \beta I \quad (13)$$

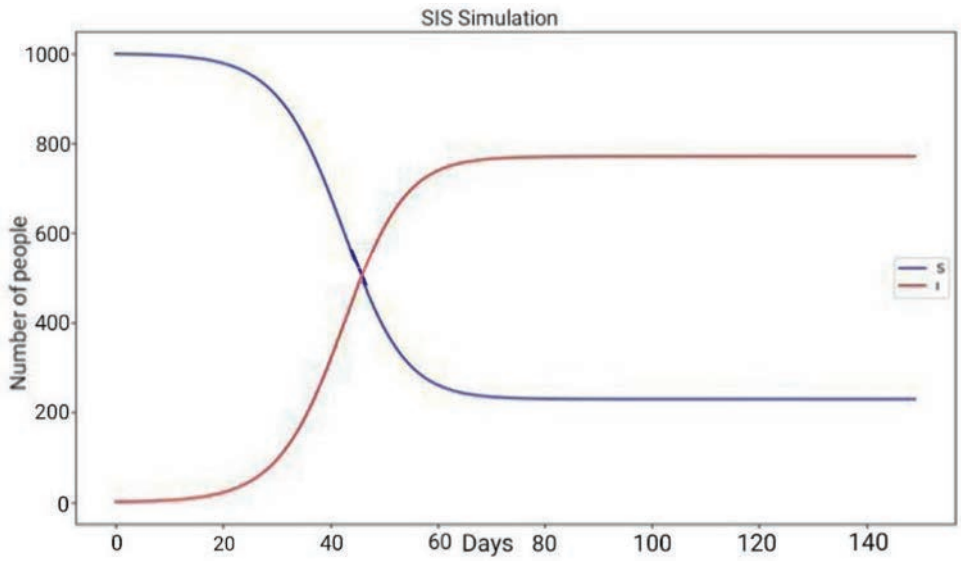


Fig. 3. Behavior of the SIS model over 150 days.

Figure 3 describes the behavior of the SIS model over 150 days with parameters.

$$\alpha = 0.218, \beta = 0.05, N = 1000, S(0) = 999, I(0) = 1,$$

With such parameters, the peak of the epidemic was reached on day 72. A total of 770 people were infected and, accordingly, 130 never got sick.

### Maternal immunity-susceptible-infected-removed model (MSIR)

Many infectious diseases are often not found in young children, due to inherited immunity, because antibodies were passed on from the mother (see Fig. 3).


Fig.4. Scheme for the Maternal Immunity-Susceptible-Infected-Removed (MSIR) model.

To simulate this factor, an additional group is introduced, maternal immunity (*M* - maternally-derived immunity). With the loss of this immunity, the individuals in group *M* will transition to group *S*. Then, over time, some proportion of these individuals will transition to the infected group.

However, obviously not all children receive this immunity. To account for this, suppose that a fraction *q* of all born children inherited the required antibodies, then, accordingly, a fraction 1 q were born susceptible to infection.

The differential equations that describe this model are as follows:

$$\frac{dM}{dt} = q\Omega - \gamma M - \delta M; \quad (14)$$

$$\frac{dS}{dt} = (1-q)\Omega - \frac{\alpha SI}{N} + \gamma M - \delta S; \quad (15)$$

$$\frac{dI}{dt} = \frac{\alpha SI}{N} - \beta I - \delta I; \quad (16)$$

$$\frac{dR}{dt} = \beta I - \delta R \quad (17)$$

Here, Ω is the birth rate, $\delta$ is the death rate, and $\gamma$ is the rate of loss of immunity. Since the main difference of this model is the consideration of immunity in born children, modeling without taking into account vital dynamics would not make sense. Therefore, the birth rate was added to equation (15) and the death rate was taken into account for each group.

**State Carrier**

In the case of certain infections, such as tuberculosis, some individuals may never fully recover, thus remaining carriers. That is, over time, they can get sick again or infect other susceptible persons. Schematical view of this kind

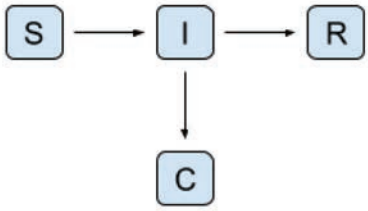


Fig. 5. Scheme for the Susceptible-Infected-Removed (SIR) model with state carrier.

The model can be presented by strite connections of four groups (see Figure 5) To model such behavior, a group of "Carriers" is introduced (*C* - carriers).

**Susceptible-Exposed-Infected-Removed (SEIR) model**

Many infectious diseases have a so-called incubation period, after infection, during which there are no symptoms and the possibility of infecting others. To take this into account, an intermediate group of people (E - exposed) is introduced (see Figure 6).


Fig. 6. The scheme for the Susceptible-Exposed-Infected-Removed (SEIR) model.

If the average incubation period is assumed to be $1/\mu$, then the differential equations to describe the model have a form

$$\frac{dS}{dt} = -\frac{\alpha SI}{N}; \quad (18)$$

$$\frac{dE}{dt} = \frac{\alpha SI}{N} - \mu E; \quad (19)$$

$$\frac{dI}{dt} = \mu E - \beta I; \quad (20)$$

$$\frac{dR}{dt} = \beta I \quad (21)$$

**Susceptible-Exposed-Infected- Susceptible (SEIS) model**

Some infections have distribution characteristics common to both SIS and SEIR models. The schematic view of the Susceptible-Exposed-Infected-Susceptible (SEIS) model is presented below in Figure 7.


Fig.7. The schema for the Susceptible-Exposed-Infected-Susceptible (SEIS) model.

That is, there is an intermediate group (E) and no long-term immunity acquisition occurs. The equations that describe an intermediate group (E) have a form presented by equations:

$$\frac{dS}{dt} = -\frac{\alpha SI}{N} + \beta I; \quad (22)$$

$$\frac{dE}{dt} = \frac{\alpha SI}{N} - \mu E; \quad (23)$$

$$\frac{dI}{dt} = \mu E - \beta I \quad (24)$$

Next, we examine the pattern of spread behavior of COVID-19 during April 2020 in India.

Such models are usually used to monitor the development of events, the possibility of assessing the consequences and developing a countermeasure plan. It is obvious that the scenario of the development of the epidemic is constantly changing, and it is difficult to take into account all scenarios, therefore, for the adequacy of the model, it is often modified to obtain new data and consider only small-time intervals (from a week to several months). Thus, the model corresponds to the real course of events only for a few months.

We will make some simplifications and modifications to better understand the basic principles and ideas of our modeling approach.

The population is divided into 11 states: Susceptible (*S*), 'noncontagious' (*E*), Infected people who ignore the symptoms (), Infected (*I*), Asymptomatic infected (), In quarantine (*Q*), In the intensive care unit (*Q'*), Carriers (*C*), Recovered (*R*), Recovered immobilized (), Deaths (*D*), the detailed description of the presented states can be found in [13].

The differential equations together with the presented considerations (from 25 to 35) have the form:

$$\frac{dS}{dt} = -\alpha\frac{S(I + I_s + I_w + C)}{N} + gR \quad (25)$$

$$\frac{dE}{dt} = \alpha\frac{S(I + I_s + I_w + C)}{N} - \mu E \quad (26)$$

$$\frac{dI_s}{dt} = r(1 - s)\mu E - hI_s \quad (27)$$

$$\frac{dI}{dt} = rs\mu E - \varepsilon I + fC - \xi_1 I - \eta_1 I - \beta_5 I + hI_s \quad (28)$$

$$\frac{dI_w}{dt} = (1-r)\mu E - \xi_3 I_w - \eta_3 I_w - \beta_3 I_w - \lambda I_w \quad (29)$$

$$\frac{dQ}{dt} = \varepsilon I - \beta_1 Q - vQ - \rho Q - \xi_2 Q - \eta_2 Q + \lambda I_w \quad (30)$$

$$\frac{dQ'}{dt} = \rho Q - \beta_4 Q' - \xi_5 Q' - \eta_5 Q' \quad (31)$$

$$\frac{dC}{dt} = vQ - fC - \beta_2 C - \xi_4 C - \eta_4 C \quad (32)$$

$$\frac{dR}{dt} = \beta_1 Q + \beta_2 C + \beta_3 I_w + \beta_4 Q' + \beta_5 I - gR \quad (33)$$

$$\frac{dR_d}{dt} = \eta_1 I + \eta_2 Q + \eta_3 I_w + \eta_4 C + \eta_5 Q' \quad (34)$$

$$\frac{dD}{dt} = \xi_1 I + \xi_2 Q + \xi_3 I_w + \xi_4 C + \xi_5 Q' \quad (35)$$

Table 1.

Parameters of the complex generalized SIR model.

| Parameter | Value | Parameter | Value |
|---|---|---|---|
| (total number of persons) | 1.400.000.000 | (proportion of carriers who again get relapsed) | 0.2 |
| (rate of recovery) | 0.5 | (disease spread rate) | 0.53 |
| (rate of recovery) | 0.1458 | (the coefficient of deterioration of the condition of people who ignore the disease) | 0.6 |
| (rate of recovery) | 0.1458 | (rate of recovery of infected people with subsequent immobilization) | 0.1 |
| (rate of recovery) | 0.05 | (rate of recovery) | 0.1 |
| (rate of recovery) | 0.09 | (rate of recovery) | 0.05 |
| (coefficient of transition from group (E) to one of the infected states) | 0.5 | (rate of recovery) | 0.01 |
| (the proportions of persons in quarantine who did not recover but left from quarantine (became carriers) | 0.05 | (rate of recovery) | 0.1 |
| (proportion of infected people who will be quarantined) | 0.5 | (mortality of infected people) | 0.25 |
| (rate that determines what proportion of individuals when transitioning from the group (E) will be infected)) | 0.3 | (rate of mortality) | 0.2 |
| (rate of loss of immunity in recovered persons) | 0.0001 | (mortality of asymptomatic infected people) | 0.1 |
| (the rate of worsening of the condition and transfer to intensive care) | 0.01 | (rate of mortality) | 0.05 |
| (proportion of infected people for next quarantine among people without symptoms) | 0.025 | (rate of mortality) | 0.2 |
| (proportion of infected persons with symptoms who do not ignore them) | 0.5 | | |

Parameters of the complex generalized SIR model are presented in Table 1. Specific parameters were selected mainly on the basis of previous presented scientific investigations focused on INDSCI-SIM [2], in which the spread of COVID-19 was simulated.

## 5. Simulations results with specified parameters and conditions

To simulate a typical pandemic, we will use a discrete-time model. To convert the previously described differential equations into iterative ones, we use the following definition.

$$\frac{dX_i}{dt} = \frac{\Delta X}{\Delta t} = \frac{X^{(n-1)} - X^{(n)}}{1}, \tag{36}$$

where $n \in (0, \infty)$ is a time. Then:

$$X^{(n+1)} = \Delta X + X^{(n)} \tag{37}$$

### 5.1. Simulation Example 1

Next we consider the solution of the previously described equations. Figure 8 shows, with the specified parameters, as well as the initial conditions: E(0)=25; $I_s$(0)=2; $I_w$(0)=2; I(0)=0; Q(0)=2; S(0)=1399999969, the rest are 0.

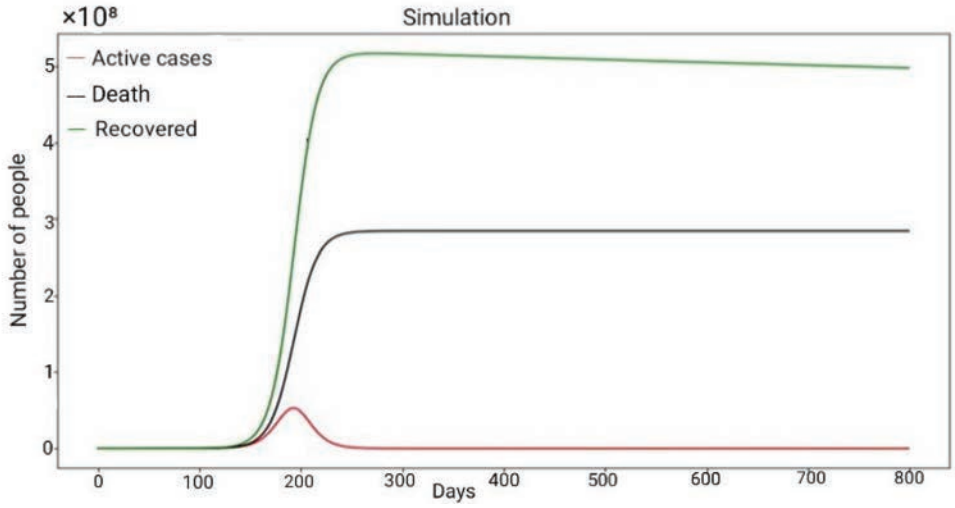


Fig. 8. Simulation results of Example 1, when initial conditions are chosen.

In this configuration, the epidemic covered almost 801.5 million people out of 1.4 billion, which is 57.3% of the entire population. Approximately 284.4 million (20.3%) became victims of the disease and more than 517 million (37% of the total population) recovered and received immunity (including those who were immobilized). Also, as can be seen in the graph, after the peak of the epidemic, the number of people with immunity slowly decreases, according to the model. The number of active cases $(I_s + I_w + I + C + Q + Q')$ was the highest on the 193rd day and amounted to about 53 million, which corresponds to 3.8%. The average mortality rate among those infected is 35.5%.

### 5.2. Simulation Example 2

Here we take the same initial data as in Example 1, but with a 4-fold increase in the initial number of active cases.

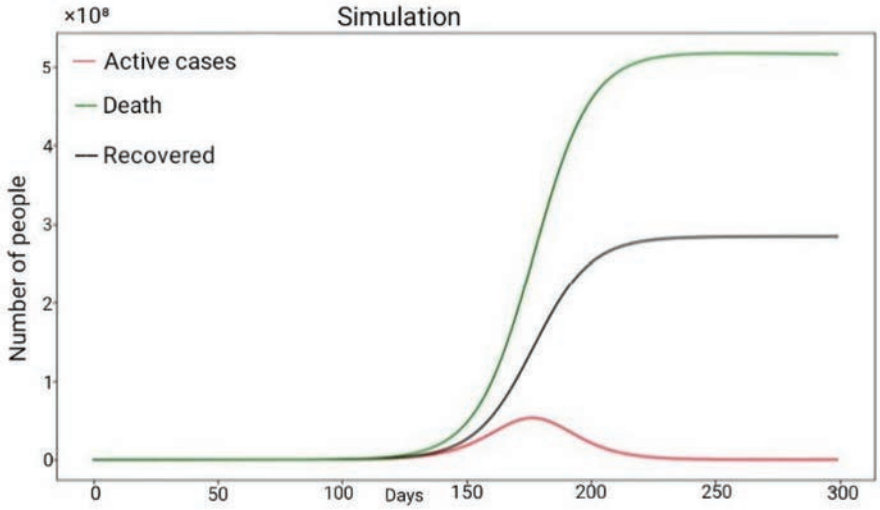


Fig. 9. Simulation results of Example 2.

Figure 9 shows the behavior of the model with $E(0)=100$; $I_s(0)=8$; $I_w(0)=8$; $Q(0)=8$; $S(0)=1399999876$. As a result, if we omit the minimal differences in the received numbers of active cases, deaths, and recoveries, the only significant difference will be the onset of the peak of the epidemic on day 176 (17 days earlier).

### 5.3. Simulation Example 3

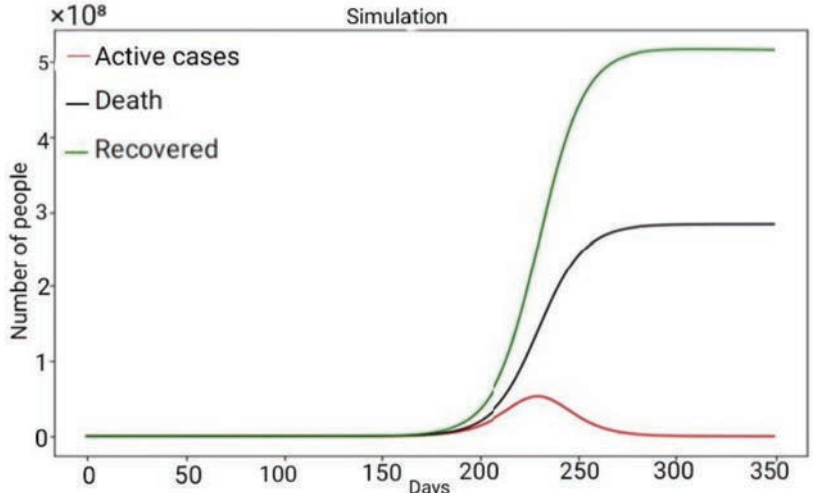


Fig. 10. Simulation results of Example 3.

Figure 10 shows the behavior of the model with a single infected person at the start of the countdown: . And again, as in Example 2, the only significant difference here was the shifted peak of the epidemic, but in the opposite direction (by 230 days).

From the simulation results obtained, it can be concluded that the epidemic simulated with the help of such a model is practically independent of the initial quantity of infected people and the only thing they impact is the time of the top of the quantity of active cases of the illness. Therefore, other rates significantly influence the behavior of the spread of the disease.

## 6. Comparison of a Complex Practical Model with a Model that takes into Account Migrations

Since the epidemiological model is described within the framework of a certain community, we are forced to impose a number of intuitive conventions in order to preserve the possibility of further complicating the model for practical application. By conflict, we will understand some interregional migration. Therefore, to begin with, it is

necessary to determine which population groups can move.

Potential opponents of these groups can be classified as: susceptible (*S*), non-infectious infected (*E*), infected (*I*), infected who ignore symptoms ($I_S$), asymptomatic infected ($I_W$), carriers (*C*) and recovered (*R*). Next, we conditionally "place" all people on some territory and divide it into regions. Each individual can belong to one of eleven groups regardless of region. The conflict interaction will get at each moment of discrete time. Representatives of groups capable of moving will interact with each other. We notice that immobilized persons can also influence their migration.

Firstly, it was decided to unite some groups in the set according to the nature of the behavior, since it would not be quite correct to consider individuals from each group to be completely independent in their intentions, given the fact that representatives may have hidden signs of infection. Members of such groups will interact under the influence of the coefficients common to each of them. So, migration will be closer to the real one.

The group "don't want to get sick" includes all those people who find themselves healthy and are afraid of infection, that is susceptible (*S*), non-contagious infected (*E*) and asymptomatic infected ($I_W$):($S + E + I_W$).

Another group so-called "recovered" includes recovered (*R*) themselves, immobilized recovered ($R_d$), and carriers *(C):* ($C + R + R_d$). The latter was added because they do not know about the possibility of spreading the infection due to a negative test and the absence of symptoms, which makes their behavior similar to individuals with immunity obtained as a result of a full recovery. In order to take into account, the lack of ability to move among the immobilized, but still give the opportunity for moving to the rest of the recovered, we will also highlight the subset (*C*+*R*).

People in isolation *(Q)* and in the intensive care unit *(Q')*are classified as *(Q + Q')*, since the differences between these groups are insignificant.

Infected (*I*) and infected which are ignoring symptoms ($I_S$) , we assume separate, regarding the fact that (*I*) while some are aware of all the dangers of the situation, do not waste time and seek medical help or self-isolate, at the same time ($I_S$) don't understand the seriousness and don't hurry up to the hospital. The last group is the dead *(D),* is separate.

We also would like to specify that there may be two types of participants in a conflict interaction. The first one includes those aggregates and groups that are able to moving, as well as the migration of others taking place under their impact. These include ($S+E+I_W$), (*C*+*R*), (*I*), and ($I_S$). The second one ($C + R + R_d$), (*Q*+*Q'*), and (*D*) consists of representatives of those groups that cannot move but are able to impact the redistribution of others. The state of such a complex system will be fixed by the moment of time and twelve vectors – one for each group and the vector of the total quantity of populations in the region.

## 7. Conclusions

Having studied the behavior of a complex model on the example of several simulations, it can be concluded that in both cases the dynamics practically do not depend on the initial distributions that set the initial values of the number of individuals. These initial distributions affect the moment of the peak of the epidemic, therefore, by varying the starting conditions, it can be accelerated or delayed. The behavior of the models is determined by such parameters as the rate of spread of infection, recovery rates, mortality and others with different levels of impact.

In our opinion, the main result is that the integration of internal conflict into the model creates significant changes in its behavior. It turns out that both the signs of the interaction coefficients, which determine the direction of migration, and the magnitude of the values have an important influence. This was especially the case under the influence of several factors at the same time. In such cases, it is quite natural that the larger modulus of the coefficient determines the influence that has the greatest weight in determining the direction of migration.

Having studied the model with no conflict interaction, we can conclude that its behavior in the absence of external influences is proportionally scaled relative to its size. After conducting simulations with different sets of coefficients, the most interesting results were obtained. Internal conflict significantly affects the behavior of such a system and is capable of fundamentally changing the epidemiological situation. Migrations can take a wide variety of forms - from smooth migration from region to region with subsequent stabilization of the general epidemiological situation, to heterogeneous or homogeneous migration fluctuations that do not subside.

We also note that compared to the model without migration (see the corresponding graphs), the model with migration has certain fluctuations that cause epidemic waves. However, a complete ban on migration obviously leads to economic losses. Therefore, in the model, due to the qualitative selection of coefficients (that is, restrictions, and not bans on migration), it is possible to give adequate recommendations for reducing the amplitude of epidemic waves. This will allow controlling the level of morbidity, as well as the negative economic effect from the point of view of migration processes.

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