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Research article

Generalized Models of the Seir Epidemiological Model and Their Discrete Analogues

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Abstract

The paper considers a discrete analogue of the $SEIR$ model, which, unlike SIR, includes a group of infected individuals in the incubation (latent) period. This model is based on Lotka-Volterra mappings operating in a three-dimensional simplex with degenerate skew-symmetric matrices, which correspond to mixed graphs. The models considered in this paper are intended to study the course of viral diseases transmitted by the air-capillary route without a repeated effect.

Keywords: *The SEIR model; Lotka-Volterra mapping; simplex; graph; trajectory; skew-symmetric matrix; viral diseases.*

AMS Subject Classification (2020): *Primary: 37B25 ; Secondary: 37C25; 37C27.*

1. Introduction

The history of widespread diseases that have engulfed peoples for many centuries is not only the history of innumerable disasters and severe social upheavals, accompanied by a huge number of victims carried away by these diseases, but it is also the history of the hard work of human thought, striving to know the essence of the phenomena occurring at the same time and to find measures to combat them. The scientific study of any phenomenon presupposes at least its description and explanation. The first descriptions of epidemics are given in historical writings. Among them, descriptions of the first historically proven plague (the Justinian plague, 527-565), epidemics of the plague of the XIV century (the "black death") and later times have been preserved. In the VI century A.D., an epidemic of plague and, probably, other contagious diseases, which began in the reign of Justinian, raged for 62 years. This was facilitated by strong earthquakes and volcanic eruptions and the famine and other disasters that accompanied them. According to historians, the plague epidemic shook the withering Byzantine Empire more than anything else. During the plague pandemic in the XIV century . In Europe, about 25 million people died from the plague, that is, a quarter of the entire population.

At the end of the XVII - beginning of the XVIII century. In Europe, more than 10 million people were sick with smallpox every year and about 1.5 million died from this disease alone. There are numerous historical descriptions of epidemics of syphilis, smallpox (rash diseases), typhoid fevers, cholera. It should be recognized that only smallpox, leprosy and plague have a history that almost coincides with the history of human culture, and the history of other infectious diseases is the history of three or four centuries at best, and for most a little more than 100 years. Naturally, epidemics of various contagious diseases, which often covered ancient cities and countries and often assumed the dimensions of widespread disasters, provided extensive material for observations on the conditions of their spread. This already in ancient times allowed us to draw many reasonable empirical conclusions [1]. In the writings of Hippocrates (460-377 BC), there are already

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generalizations regarding the signs of epidemics ("Seven Books on Epidemics"). The largest physician of ancient antiquity after Hippocrates, Claudius Galen (about 138-201) wrote that the most dangerous diseases are called pestilence. As we can see, despite the fact that the science of the epidemic originated a very long time ago, mathematical analysis about the study of diseases and their spread is about 350 years old. Modeling of infectious diseases is a tool that has been used to study the mechanisms of disease spread, predict the future development of the outbreak and evaluate strategies to combat the epidemic [2]. The first statistical studies of infectious diseases were made by John Graunt. In 1662, J. Graunt published the book "Natural and Political Observations on the Lists of the Dead" (Natural and Political Observations Made upon the Bills of Mortal), which is devoted mainly to statistics on social hygiene and statistics of diseases. The accounts he studied were lists of numbers and causes of death published weekly. Graunt's analysis of the causes of death is considered the beginning of the "theory of competing risks", which, according to Daly and Ghani [2] is "a theory that is now firmly entrenched among modern epidemiologists."

A hundred years later, in 1760, Daniel Bernoulli used mathematical methods to analyze smallpox mortality [3]. Bernoulli argued that inoculation with a live virus would reduce the mortality rate and, consequently, increase the population, regardless of the fact that the inoculation itself could be fatal. D. Bernoulli created a mathematical model to protect the practice of inoculation against smallpox [3]. Calculations based on this model have shown that universal vaccination against smallpox will increase life expectancy from 26 years 7 months to 29 years 9 months [3]. At the beginning of the 20th century, William Hamer [4] and Ronald Ross [5] applied the law of mass actions to explain epidemic behavior. In the 20s of the last century, Kermak-McKendrick (1927), as well as Reed-Frost (1928), considered epidemiological models that describe the relationship between susceptible, infected and recovered people in the population. The Kermak-McKendrick epidemic model successfully predicted the behavior of outbreaks very similar to those observed in many recorded epidemics [10].

2. Main Part

Consider a discrete analogue of the SEIR model, which, unlike the SIR model, includes a group of infected individuals in the incubation (latent) period, this group is denoted by E.

Let the quadratic stochastic Lotka-Volterra operator have the form:

$$x_k^{(n+1)} = x_k^{(n)} \left(1 + \sum_{i=1}^{m} a_{ki} x_i^{(n)}\right), \ k = \overline{1,m}, \tag{2.1}$$

moreover, the coefficients of this system satisfy the following conditions:

$$a_{ki} = -a_{ik}, \ |a_{ki}| \leq 1. \tag{2.2}$$

This mapping displays the $(m-1)$-dimensional simplex

$$S^{m-1} = \left\{ x = (x_1, ..., x_m) : \ x_i \geq 0; \ \sum_{i=1}^{m} x_i = 1 \right\} \tag{2.3}$$

into itself. Note that from (2.1) equality, that there is a one-to-one correspondence between the Lotka-Volterra operators and skew-symmetric matrices with coefficients satisfying the conditions (2.2).

Often, in the problems of population genetics and epidemiological models, there is an interest in degenerate cases that more accurately correspond to the real situation.

Therefore, we will give the necessary definitions for the further presentation of our work.

Definition 2.1 A skew-symmetric matrix is called degenerate if some coefficients of the matrix are equal to zero, i.e. $a_{ki} = 0$.

In cases where the skew-symmetric matrix is non-degenerate, we can introduce the concept of a tournament ([6],[7],[11],[12]) but since we are considering Lotka-Volterra maps with a degenerate skew-symmetric matrix, we will introduce the concept of a mixed graph. To do this, we give classical definitions from graph theory [9]:

Definition 2.2. A directed graph or digraph is a finite nonempty set of vertices and of the given set of ordered pairs of different vertices.

The definition implies that every orientation of a graph generates a directed graph.

From the name, one can understand that a mixed graph is a graph that contains both oriented and undirected edges.

Definition 2.3. An undirected graph is a graph that does not have oriented edges, and, generally speaking, it can be considered as a mixed graph. The digraph can be considered as a mixed graph, in which each symmetric pair of oriented edges is replaced by an undirected edge.

Choose an arbitrary interior point from the simplex: $x^0 \in S^{m-1}$. If $x^0 \in S^{m-1}$, then the sequence $\{x^{(n)}\} \subset S^{m-1}$, defined by the recurrent formula $x^{(n+1)} = Vx^{(n)}$, $n = 0, 1, ...$, is called a trajectory starting from the point x^0.

Let $\omega(x^0) = \{x^0, x^{(1)}, ...\}'$ the set of limit points of a given trajectory. Obviously, $\omega(x^0)$ is a nonempty closed and invariant subset of S^{m-1}, i.e. $V(\omega(x^0)) \subset \omega(x^0)$.

We know from [8] that the Lotka-Volterra mapping V is always a homeomorphism of the simplex S^{m-1}.

Since V is a homeomorphism for $|a_{ki}| \leq 1$, for any internal point of the simplex $x^0 \in S^{m-1}$, there is a negative trajectory

$$x^{(-n-1)} = V^{-1}(x^{(-n)}),\ n = 0, 1, ...$$

We donate by $\alpha(x^0) = \{x^0, x^{-1}, ..., x^{-n}, ..., \}'$ the set of limit points of the negative trajectories.

An arbitrary point of the simplex determines the state of the individual in which it is located, and its positive trajectory determines the course of the disease. The meaning of the negative trajectory is to describe the individual's medical history.

To determine the location of the set of negative trajectory $\alpha(x^0)$ and the set of positive trajectory $\omega(x^0)$, we give a theorem from [8]:

Theorem 2.4. If A is a skew-symmetric matrix, then the sets of solutions of linear inequality systems

$$P = \{x \in S^{m-1} : Ax \geq 0\} \text{ and } Q = \{x \in S^{m-1} : Ax \leq 0\}$$

are convex nonempty polyhedra.

The set P corresponds to $\alpha(x^0)$ – negative trajectory, and the set Q corresponds to $\omega(x^0)$ – positive trajectory. The epidemiological meaning of these sets lies in the set of P the epidemic of viral diseases begins, i.e. the epidemic flares up in the set of Q, the disease is on the decline.

Let the Lotka-Volterra mapping acting in a three-dimensional simplex have the form:

$$V : \begin{cases} x_1' = x_1(1 - a_{12}x_2 + a_{13}x_3 + a_{14}x_4), \\ x_2' = x_2(1 + a_{21}x_1 + a_{23}x_3 + a_{24}x_4), \\ x_3' = x_3(1 + a_{31}x_1 + a_{32}x_2 + a_{34}x_4), \\ x_4' = x_4(1 + a_{41}x_1 + a_{42}x_2 + a_{43}x_3). \end{cases}$$

where the coefficients a_{ki} satisfy the conditions (2.2).

If the skew-symmetric matrix is in the general position, then as we indicated above we will get the non-degenerate case. For such cases, the concept of a tournament corresponds. But we are interested in degenerate cases of mappings, since they correspond to the course of viral diseases. For degenerate cases, we have introduced the concept of a mixed graph.

The total number of mixed graphs corresponding to Lotka-Volterra mappings operating in the three-dimensional simplex S^3 is 42 cases. Among them, those that describe the course of viral diseases that do not have a repeat effect are four cases. Viral diseases that do not have a repeated effect are measles, chickenpox, rubella, scarlet fever, mumps, whooping cough and others.

Let us move on to the description of these four models (See Figure 1).

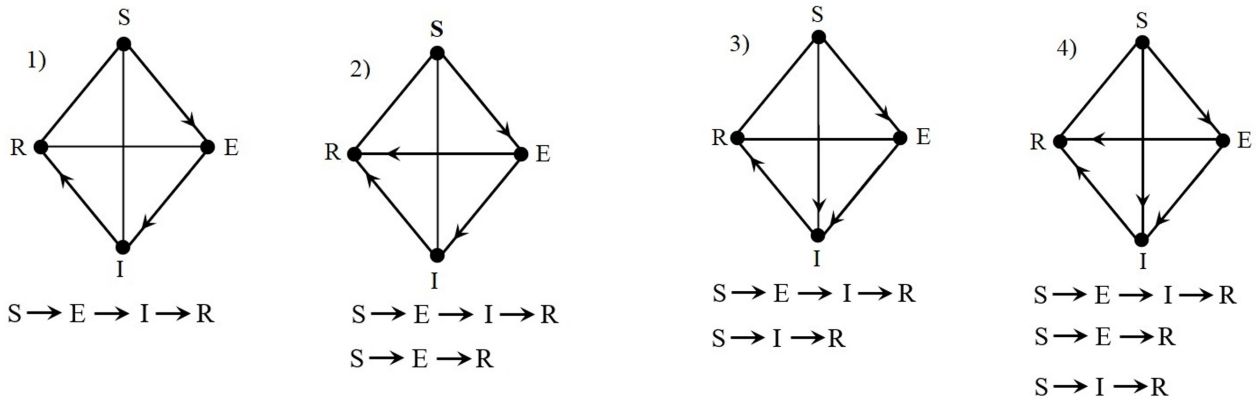

Figure 1. Discrete SEIR models.

Let us turn to the consideration of the first case. Here, as shown in Figure 1, there is only one transition from groups to groups, i.e.

$$V_1 : \begin{cases} S' = S(1 - aE), \\ E' = E(1 + aS - dI), \\ I' = I(1 + dE - fR), \\ R' = R(1 + fI). \end{cases} \tag{2.4}$$

Theorem 2.5. If the course of the disease is described by model 1, then the set P and Q correspond to the following

$$P = \left\{ \frac{d}{a+d} \le S \le 1 \right\} \quad \text{or} \quad P = \left\{ 0 \le I \le \frac{a}{a+d} \right\}$$

$$Q = \left\{ 0 \le E \le \frac{f}{f+d} \right\} \quad \text{or} \quad Q = \left\{ \frac{d}{f+d} \le R \le 1 \right\}.$$

The meaning of the theorem in epidemiology lies in the fact that an individual passes all stages over time, that is, from a susceptible class to a latent one, from a latent to an open form of the disease, and only then recovers.This path is typical for diseases such as chicken pox, the incubation period of which is 3-5 days, at this stage it is not possible to identify the disease, with scarlet fever it ranges from 1 to 12 days, more often 2-7 days. The incubation period for measles (the period when a person is contagious to others, but does not have symptoms of the disease) averages 9-11 days, the maximum incubation period is 21 days, the signs of the disease appear gradually, not immediately. There is a very long incubation period for mumps, the time from infection to the onset of the first symptoms, which usually takes 12 to 19 days.

Now let us move on to the case describing diseases that pass from the susceptible to the latent and then recover. One of the features of infectious diseases is the presence of an incubation period, that is, the period from the time of infection to the appearance of the first signs. The duration of this period depends on the method of infection and the type of pathogen and can last from several hours to several years (the latter is rare). This model also includes a generalized complete transition of individuals from each category. As an

example of such viral diseases, we can cite COVID-19. Despite all the epidemic danger, most patients suffer from coronavirus infection in a mild form, that is, they recover from a latent period when the disease does not manifest itself clearly. At the moment, it is recorded that the mild form (there is no viral pneumonia or pneumonia passes in mild form) is 81 percent of cases.

$$V_2 : \begin{cases} S' = S(1 - aE), \\ E' = E(1 + aS - dI - eR), \\ I' = I(1 + dE - fR), \\ R' = R(1 + eE + fI). \end{cases} \tag{2.5}$$

Theorem 2.6. If the epidemiological model describes diseases in which there are two transitions

$$S \to E \to R$$

$$S \to E \to I \to R$$

then the following conditions are met for each of them:

1) $S \to E \to R$ This transition corresponds to those individuals for whom the disease does not show itself clearly, i.e., the individual is in the latent period (the disease passes in a mild form), the situation occurs on the edge Γ_{SER} of the graph. Then there is a neutral point $N_1(\frac{e}{a+e}, 0, \frac{a}{a+e})$ on the edge of Γ_{SR}. Then we get

$$P = \left\{ \frac{e}{a+e} \le S \le 1 \right\} \text{ or } P = \left\{ 0 \le R \le \frac{a}{a+e} \right\}$$

$$Q = \left\{ 0 \le S \le \frac{e}{a+e} \right\} \text{ or } Q = \left\{ \frac{a}{a+e} \le R \le 1 \right\}.$$

If the starting point lies to the left of the curve connecting the vertex E and the neutral point N_1, then the disease progresses, but up to a certain time, and as soon as the trajectory crosses this curve, then the epidemic is on the decline in the set Q.

2) $S \to E \to I \to R$. This situation occurs for those individuals who completely go through all stages of the disease. Here the picture corresponds to the entire graph, the onset of the disease on the edge Γ_{SI}

$$P = \left\{ \frac{d}{a+d} \le S \le 1 \right\} \text{ or } P = \left\{ 0 \le I \le \frac{a}{a+d} \right\}$$

the end of the disease on the edge

$$Q = \left\{ 0 \le S \le \frac{e}{a+e} \right\} \text{ or } Q = \left\{ \frac{a}{a+e} \le R \le 1 \right\}.$$

Let us move on to the third model, it describes diseases that either immediately show themselves clearly, ignoring the latent period, or go from latent to open form and only then go to recovery. As the situation around the world has shown since November 2019, this is an infection called COVID-19. In most cases, as the COVID-19 clinic shows, individuals who have chronic diseases, the disease progresses immediately, affecting the vulnerable organs of the patient.

$$V_3 : \begin{cases} S' = S(1 - aE - bI), \\ E' = E(1 + aS - dI), \\ I' = I(1 + bS + dE - fR), \\ R' = R(1 + fI). \end{cases} \tag{2.6}$$

Theorem 2.7. If the epidemiological model describes diseases in which there are the following transitions

$$S \to I \to R,$$

$$S \to E \to I \to R,$$

then the following conditions are met for each of them:

1) $S \to I \to R$

In this transition, the disease progresses immediately, the situation occurs on the edge Γ_{SIR} of the graph. Then there is a neutral point $N_2(\frac{f}{b+f}, 0, \frac{b}{b+f})$ on the edge of Γ_{SR}. Then we get

$$P = \left\{ \frac{f}{b+f} \le S \le 1 \right\} \quad \text{or} \quad P = \left\{ 0 \le R \le \frac{b}{b+f} \right\}$$

$$Q = \left\{ 0 \le S \le \frac{b}{b+f} \right\} \quad \text{or} \quad Q = \left\{ \frac{f}{b+f} \le R \le 1 \right\}.$$

If the starting point lies to the left of the curve connecting the vertex I and the neutral point N_2, then the disease progresses, but up to a certain time, and as soon as the trajectory crosses this curve, then the epidemic is on the decline in the set Q.

2) $S \to E \to I \to R$. This situation occurs for those individuals who completely go through all stages of the disease. Here the picture corresponds to the entire graph, the onset of the disease on the edge Γ_{SR}.

$$P = \left\{ \frac{f}{b+f} \le S \le 1 \right\} \quad \text{or} \quad P = \left\{ 0 \le R \le \frac{b}{b+f} \right\}$$

the end of the disease on the edge Γ_{RE}.

$$Q = \left\{ 0 \le E \le \frac{f}{f+d} \right\} \quad \text{or} \quad Q = \left\{ \frac{d}{d+f} \le R \le 1 \right\}.$$

Finally, let us move on to the last model, which includes all three possible transitions, and for this model we obtain the following theorem:

In the model, there are three transitions from a state to a state of individuals in the population:

$$V_4 : \begin{cases} S' = S(1 - aE - bI), \\ E' = E(1 + aS - dI - eR), \\ I' = I(1 + bS + dE - fR), \\ R' = R(1 + eE + fI). \end{cases} \tag{2.7}$$

1) $S \to E \to R$; 2) $S \to I \to R$; 3) $S \to E \to I \to R$.

Theorem 2.8. If there are three transitions in the epidemiological situation

$$1) S \to E \to R,\ 2) S \to I \to R,\ 3) S \to E \to I \to R.$$

then the following conditions are satisfied for each of them:

1) $S \to I \to R$;

This corresponds to the situation on the verge Γ_{SIR}. Here there is a neutral point $N_1(\frac{f}{f+b}, 0, \frac{b}{f+b})$ on the edge Γ_{SR}, then we get

$$P = \left\{ \frac{f}{f+b} \le S \le 1 \right\} \text{ and } Q = \left\{ 0 \le S \le \frac{f}{f+b} \right\},$$

or

$$P = \left\{0 \le R \le \frac{b}{f+b}\right\} \text{ and } Q = \left\{\frac{b}{f+b} \le R \le 1\right\},$$

If the starting point lies to the left of the curve connecting the vertex I and the neutral point N_1, then the disease progresses, but up to a certain time, and as soon as the trajectory crosses this curve, then the epidemic is on the decline in the set Q.

2) $S \to E \to R$;

This transition corresponds to those individuals, for which the disease does not manifest itself explicitly, i.e., this situation is on the face Γ_{SER}. Then on the same edge Γ_{SR}, there is a neutral point $N_2\left(\frac{e}{a+e}; 0; \frac{a}{a+e}\right)$. At the same time, either

$$P = \left\{\frac{e}{a+e} \le S \le 1\right\} \text{ and } Q = \left\{0 \le S \le \frac{e}{a+e}\right\},$$

or

$$P = \left\{0 \le R \le \frac{a}{a+e}\right\} \text{ and } Q = \left\{\frac{a}{a+e} \le R \le 1\right\},$$

If the starting point lies to the left of the curve (straight line) connecting the vertex E and neutral point N_2, then the disease progresses, but up to a certain time, and as soon as the trajectory crosses this curve, then the epidemic is on the decline in the set Q.

3) $S \to E \to I \to R$. This situation occurs for those individuals who completely go through all stages of the disease.

If $eb < af$, then

$$P = \left\{\frac{f}{f+b} \le S \le 1\right\} \text{ and } Q = \left\{0 \le S \le \frac{e}{a+e}\right\},$$

or

$$P = \left\{0 \le R \le \frac{b}{f+b}\right\} \text{ and } Q = \left\{\frac{a}{a+e} \le R \le 1\right\}.$$

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$$P = \left\{\frac{e}{a+e} \le S \le 1\right\} \text{ and } Q = \left\{0 \le S \le \frac{f}{f+b}\right\},$$

or

$$P = \left\{0 \le R \le \frac{a}{a+e}\right\} \text{ and } Q = \left\{\frac{b}{f+b} \le R \le 1\right\}.$$

Corollary 1. If the epidemiological situation is described by a discrete dynamic system (3), then for any transition from a group to a group (i.e., for any course of the disease), the disease begins and ends at the edge Γ_{SR}. The boundaries of the beginning and end of the disease depend on the coefficients of transition a, b, e, f from groups to groups. The boundaries of the beginning and end of the disease depend on the coefficients of transition from groups to groups S, E, I, R.

Theorem 2.9 The set of limit points of the positive trajectory $\omega^+(x^0) \subset Q$ and the set of limit points of the negative trajectory $\omega^-(x^0) \subset P$. That is, the medical history begins in the set P, and ends in the set Q.

In other words, any trajectory in this case converges for an arbitrary initial point but converges to a point belonging to the set Q, and the whole situation depends on the initial point.

Theorems 2.5 - 2.9 are proved using Theorem 2.4.

3. Numerical analysis

In order to verify the compliance of the mathematical description of the above-analyzed models, for diseases transmitted by the air-capillary route, we have compiled a package of application programs in the Python

programming language 10. For each model, in accordance with the numerical analysis of the data, a phase portrait of the course of the disease was obtained.

For the first model described by mapping V_1 (see Figure 1, Example 1), as well as, according to the Theorem 2.5, the location of individuals and the phase portrait looks as follows:

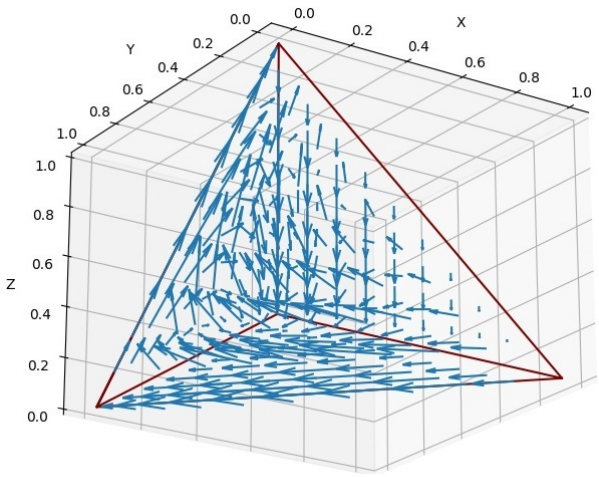

Figure 2. Phase portrait of trajectories of internal mapping points V_1.

The trajectory of the inner points of the first model is shown in Table 1.

$S^{(i)}$	$E^{(i)}$	$I^{(i)}$	$R^{(i)}$
0.7	**0.1**	**0.1**	**0.1**
0.6300000000000001	0.16000000000000003	0.1	0.11000000000000001
0.5292000000000001	0.24480000000000005	0.10500000000000001	0.12100000000000002
0.3996518400000001	0.3486441600000001	0.11799900000000002	0.13370500000000002
0.2603155599507456	0.4468407778134146	0.14336160594084005	0.14948205629500003
0.1439959526654199	0.4991005735915551 3	0.18599142979823496	0.1709120439447903
0.07212749009524641	0.4781406068663161	0.24703168367061717	0.20270021936782062
0.03764040820936109	0.39451180960672466	0.3150741863452577	0.25277359583865683
0.01629405005874072 5	0.18901208182541437	0.34269707426417556	0.4519967938516696
0.013214277735770625	0.12731796670623402	0.25257298287657115	0.6068947726814244
0.011531862762960851	0.0968433030542703	0.1314448384729987	0.7601799957097704
0.010415079082627178	0.08523053440744374	0.044252654053683324	0.860101732456246
0.009527396326519074	0.08234653980960868	0.009962546990266543	0.898163516873606
0.008742848205635452	0.08231070665815321	0.001834932020809267	0.9071115131154023
0.008023218191624631	0.08287930212086154	0.0003214786102515538	0.9087760010772625
0.007358259467139381	0.08351761692248237	5.5970487259704123e-05	0.9090681531231187

Table 1. The trajectory of internal points in the entire simplex for mapping V_1.

Let us move on to the second model described by the mapping V_2 (see Figure 1, Example 2), and also, according to Theorem 2.6, the location of individuals and the phase portrait describes Figure 3.

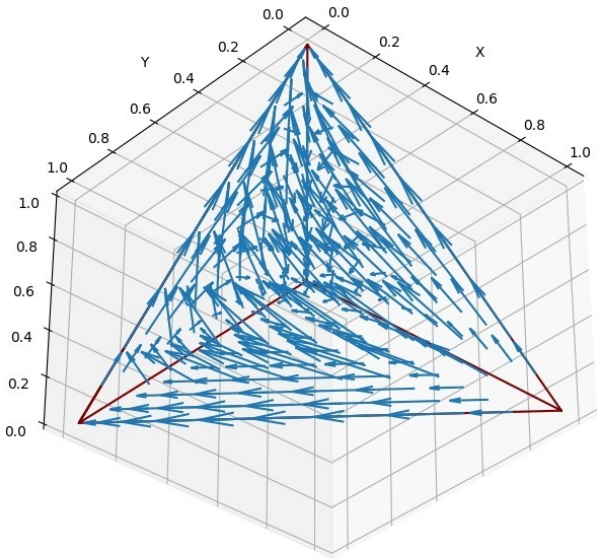

Figure 3. Phase portrait of trajectories of internal mapping points V_2.

The values of the complete transition of individuals from groups to groups $S \to E \to I \to R$ are given in Table 2 (mapping V_2).

$S^{(t)}$	$E^{(t)}$	$I^{(t)}$	$R^{(t)}$
0.7	**0.1**	**0.1**	**0.1**
0.6300000000000001	0.15000000000000002	0.1	0.12000000000000002
0.5355000000000001	0.21150000000000002	0.10299999999999998	0.15000000000000002
0.4222417500000001	0.2712487500000001	0.10933449999999999	0.19717500000000002
0.3077092031146875	0.3026409781471876	0.11743331641937498	0.27221650231875
0.21458378889916688	0.2778423900849278	0.1210061635162295	0.3865676574996759
0.15496331611794276	0.19643733929055335	0 0.10784973602909471	0 0.5407496085624093
0.12452273461209315	0.09946879127925114	0.07071574867654648	0.7052927254321093
0.11213660871344128	0.03466629223585898	0.027874455606756318	0.8253226434439435
0.10824924826544295	0.008976472713378626	0.005835340244806634	0.8769389387763717
0.10727755184214445	0.002023969908971026	0.0007704839356076375	0.8899279943132767
0.10706042530530788	0.0004383495278655796 3	8.6368148442748 22e-05	0.8924148570183837
0.107013495418422 2	9.405192407991973e-05	9.329789036363018e-06	0.8928831228684613
0.10700343059327558	2.0138496057663705e-05	1.0002553504814046e-06	0.8929754306553161

Table 2. Transition values of individuals S→E→I→R

In Table 3, we present the trajectory of the inner points on the SER face, that is, the transition $S \to E \to R$.

$S^{(t)}$	$E^{(t)}$	$I^{(t)}$	$R^{(t)}$
0.7	**0.2**	**0.0**	**0.1**
0.56	0.32000000000000006	0.0	0.12
0.3808	0.4608000000000001	0.0	0.1584
0.20532736	0.5632819200000001	0.0	0.23139072000000002
0.08967017043066877	0.548600900537549	0.0	0.36172892903178244
0.04047703418104839	0.3993492205698504	0.0	0.5601737452491015
0.024312562129867522	0.19180874407210863	0.0	0.783878693798024
0.019649200122562525	0.04611731831712962	0.0	0.9342334815603079
0.018743031705833326	0.0039391438822218 53	0.0	0.97731782441 1945
0.018669200207155002	0.0001631798518814918	0.0	0.9811676199409637
0.01866615376983045	6.119502313158958e-06	0.0	0.9813277267278566
0.018666039542259278	2.2849259065307614e-07	0.0	0.9813337319651503
0.018666035277207546	8.530155673351109e-09	0.0	0.981333956192637
0.018666035117983 36	3.184484462012411e-10	0.0	0.9813339645635684
0.018666035112039188	1.1888339861528531e-11	0.0	0.9813339648760726
0.01866603511181728	4.438163386996236e-13	0.0	0.9813339648877389

Table 3. The trajectory of the inner points, on the SER edge, that is, the transition S→E→R.

As we pointed out above, the third model describes diseases that either immediately manifest themselves vividly, ignoring the latent period, or move from a hidden form to an open one and only then proceed to recovery. For such a course of the disease, the phase portrait is shown in Figure 3, the numerical analysis of the transition $S \to I \to R$ in Table 4, and the complete transition $S \to E \to I \to R$ in Table 5.

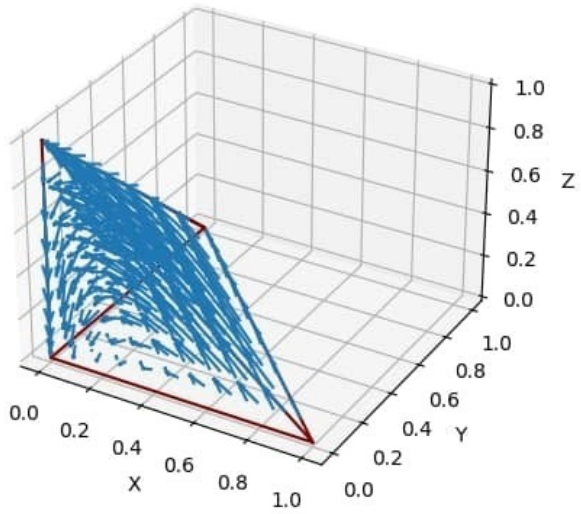

Figure 4. Phase portrait of trajectories of internal mapping points V3.

$S^{(t)}$	$E^{(t)}$	$I^{(t)}$	$R^{(t)}$
0.7	**0.0**	**0.2**	**0.1**
0.56	0.0	0.32000000000000006	0.11000000000000001
0.3808	0.0	0.4640000000000001	0.12210000000000003
0.20410879999999998	0.0	0.5840368	0.13700841000000005
0.08490174959615998	0.0	0.623225897054352	0.15577971441072816
0.0319887805426092	0.0	0.579052913851406	0.1800470338326162
0.013465583958858184	0.0	0.49331935086407785	0.21246396822453942
0.006822750821268525	0.0	0.3951495971151317	0.25760490601825753
0.004126743583027333 4	0.0	0.296053129525377 1	0.3239651936229328
0.002905008230523 3237	0.0	0.20136395544851707	0.42891864030207716

Table 4. Trajectories of internal points of the operator V3, on the SIR edge.

$S^{(t)}$	$E^{(t)}$	$I^{(t)}$	$R^{(t)}$
0.6	**0.2**	**0.1**	**0.1**
0.4200000000000001	0.30000000000000004	0.17	0.11000000000000001
0.22260000000000002	0.3750000000000001	0.27370000000000005	0.12210000000000003
0.07819937999999997	0.35583750000000003	0.40384435	0.13700841000000005
0.01879273033274699	0.2399608079876 2504	0.5237976193986446	0.15577971441072816
0.0044396241675139034	0.11877942676967133	0.5777350632228913	0.1800470338326162
0.0013473616047193016	0.05068372314900657	0.5449035449319701	0.21246396822453942
0.0005448901874473319	0.02313427203731753	0.4574830980050661	0.25760490601825753
0.00028300649859449374	0.012563339233420406	0.3504660240312798	0.323965193622 9328
0.0001802668296099624	0.008163871190374476	0.24142943840975728	0.42891864030207716
0.0001352734349964888 8	0.006194344028809603	0.13989037251432845	0.612889840300 6597
0.0001155120535892101 9	0.005328652865331848	0.055038436989306924	0.9885237966444279

Table 5. Trajectories of internal points of the operator V3, in the entire simplex.

Let us move on to the numerical analysis of the latest model, which includes all transitions simultaneously. This model describes those viral diseases, the course of which may be different for each individual. A separate numerical analysis is made for each transition and a phase portrait of the trajectory of internal points is shown. This model corresponds to the V_4 mapping.

For the transition $S \to E \to R$:

$S^{(i)}$	$E^{(i)}$	$I^{(i)}$	$R^{(i)}$
0.1	**0.8**	**0.0**	**0.1**
0.019999999999999997	0.8	0.0	0.18000000000000002
0.003999999999999998	0.672	0.0	0.32400000000000007
0.0013119999999999994	0.45696	0.0	0.5417280000000002
0.0007124684799999997	0.21001150463999987	0.0	0.7892760268800003
0.0005628419025066261	0.044404085236143385	0.0	0.9550330728613502
0.0005378494226932487	0.002021707745285429	0.0	0.9974404428320215
0.0005367620483495925	6.262050894659341e-06	0.0	0.999456975900756
0.0005367586871183274	6.761675811579 46e-09	0.0	0.9994632345512061
0.0005367586834889392	7.258822182944388e-12	0.0	0.9994632413092526
0.0005367586834850429	7.792471729883707e-15	0.0	0.9994632413165075
0.0005367586834850388	8.365353733711145e-18	0.0	0.9994632413165153
0.0005367586834850388	8.980352513983743e-21	0.0	0.9994632413165153
0.0005367586834850388	9.64056438527156e-24	0.0	0.9994632413165153
0.0005367586834850388	1.0349313294978596e-26	0.0	0.9994632413165153
0.0005367586834850388	1.111016755836994e-29	0.0	0.9994632413165153

Table 6. The trajectory of internal points for mapping V_4 on the SER edge.

Phase portrait on this face:

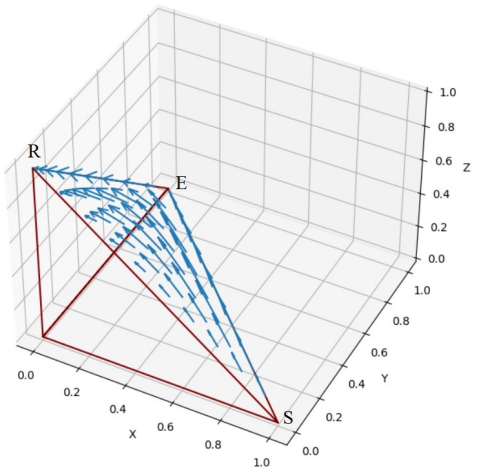

Figure 5. Phase portrait of trajectories of internal V_4 mapping points on the edge Γ_{SER}.

The values of the transition $S \to I \to R$ are shown in Table 7, and the phase portrait on the SIR edge is shown in the Figure 6.

$S^{(i)}$	$E^{(i)}$	$I^{(i)}$	$R^{(i)}$
0.2	**0.0**	**0.4**	**0.4**
0.12	0.0	0.32	0.5599999999999999
0.08159999999999999	0.0	0.17920000000000005	0.7392
0.06697727999999999	0.0	0.06135808	0.87166464
0.06286768269557759	0.0	0.011984008590131197	0.9251483087142912
0.06211427584611215	0.0	0.0016504301608192273	0.9362352939930687
0.06201176057183828	0.0	0.00020775446826347914	0.9377804849598982
0.06199887735149459	0.0	2.5809602606452324e-05	0.9379753130458989
0.06199727185108106	0.0	3.2009989085632098e-06	0.9379995218159832
0.0619970787318915	0.0	3.969166796008565e-07	0.9380025243514288
0.06199705412421687	0.0	4.921550681328109e-08	0.9380028966602761
0.06199705107300043	0.0	6.102435301473628e-09	0.9380029428245641
0.06199705069466743	0.0	7.566660233499998e-10	0.9380029485486663
0.06199705064775637	0.0	9.382212418966837e-11	0.9380029492584213
0.06199705064139666	0.0	1.1633389979336518e-11	0.9380029493464267
0.06199705064121843	0.0	1.442471735508057e-12	0.9380029493573389

Table 7. The trajectory of internal points for mapping V_4 on the SIR edge.

The values of the transition from groups to groups $S \to E \to I \to R$ are given in the Table 8.

The phase portrait of the trajectories of the interior points in the entire simplex of the V_4 mapping is shown in the Figure 7.

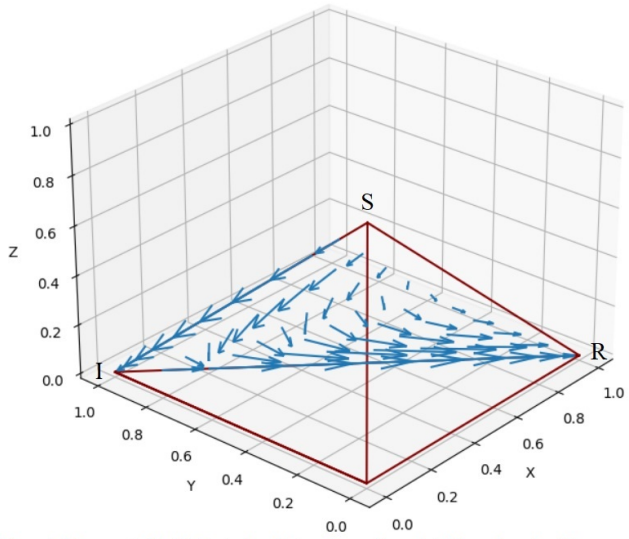

Figure 6. Phase portrait of trajectories of internal mapping points V_4, on the edge Γ_{SIR}.

$S^{(t)}$	$E^{(t)}$	$I^{(t)}$	$R^{(t)}$
0.2	**0.2**	**0.1**	**0.5**
0.14	0.11999999999999998	0.09	0.65
0.11060000000000002	0.047999999999999994	0.0549	0.7865
0.09921926000000002	0.012921600000000004	0.020428290000000005	0.86743085
0.09591030859311862	0.002731110926592001	0.004999007050182902	0.8963595734301064
0.09516891059250494	0.0005313423504363043	0.0010112083747259434	0.9032885386823327
0.09502210772045758	0.0001014168699787353	0.00019456833685570248	0.9046819070727079
0.09499398258225009	1.9283974869098355e-05	3.7053908788534226e-05	0.904949679534092
0.0949886308223112	3.6640950173501116e-06	7.042598817572789e-06	0.9050006624838537
0.09498761380812318	6.961081633941756e-07	1.338034845924733e-06	0.9050103520488675
0.09498742058973257	1.3224379135291078e-07	2.541971275842274e-07	0.9050121929693485
0.09498738388270647	2.5123010747659895e-08	4.829119078925327e-08	0.905012542703092
0.09498737690928352	4.772738763520 33e-09	9.17411251378296e-09	0.9050126091438652
0.0949873755845087	9.066998944191418e-10	1.7428499380453792e-09	0.9050126217659415
0.09498737533283491	1.7225008764935555e-10	3.310974895031178e-10	0.9050126241638174

Table 8. The trajectory of the internal mapping points V_4 throughout the simplex, i.e. the complete transition of individuals from groups to groups.

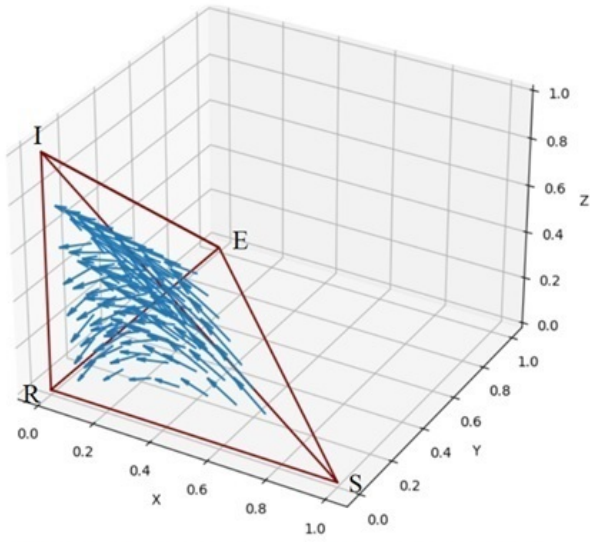

Figure 7. Phase portrait of trajectories of internal mapping points V_4.

4. Conclusion

The paper identifies a class of mixed graphs described by Lotka-Volterra mappings with degenerate skew-symmetric matrices, presented as discrete analogues of the $SEIR$ model of viral diseases transmitted by the air capillary route. If we compare the results of the previously studied continuous models and the discrete models proposed by us, then in the continuous case when an individual becomes ill, either absolutely recovers or dies [4], since the solution of differential equations is either unique or tends to infinity. Finding the set P and Q gives us the opportunity to determine the history of the epidemiological situation and its decline. In other words, the set P corresponds to the history of the disease, i.e. it consists of a set of limit points of the negative trajectory, the set Q corresponds to the end of the epidemiological situation, i.e. the set of limit points of the positive trajectory. In the work, a specific focus of the disease is shown in each model, a numerical analysis is made and a phase portrait is constructed. That is, the initial state of the population is shown, and specifically the end of the epidemiological situation. All these models are designed to study viral diseases that do not have a repeat effect, i.e. an individual who has recovered receives temporary or permanent immunity.

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