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A Multiagent Model of the Spread of Epidemics Based on Prefractal Graphs.

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ABSTRACT

As of today, infectious diseases remain one of the leading causes of premature peoples' death on the Earth. According to the World Health Organization, over 1 billion people carry infectious diseases every year. The goal of preventive measures is to influence the source of the infection in order to reduce the contamination of the external environment, localize the spread of microbes, and increase the resistance of the population to diseases. Agent modeling can play a very important role in predicting the spread of diseases and in assessing containment and prevention measures. I consider the processes of spatial distribution and temporary change of these two groups of epidemics as infectious dynamics. As a rule, the topology of the prefractal graph in the proposed models takes on the hard-to-implement spatial components of the dynamics. The topology is expanded by volumetric graphs, and the dynamics of the accumulation of the prefractal graph, called its recognition, is responsible for the temporal component of the process. An elementary participant in the study is understood as an agent. The agent is active, in a certain state that can change under the influence of certain factors. Agent's properties include characteristics that form the level of immunity: height, weight, sex, income, marital status, education, geography, etc.

Keywords: modeling, agent, epidemic, distribution, graph.

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INTRODUCTION

The mechanism of infection has epidemiological significance and is the basis for the classification of infectious diseases: intestinal infections, respiratory tract infections, blood infections, infections of external covers, infections with different transmission mechanisms. There are air, water, food, and contact-household ways of transmission of infection. There are many models describing the spread of infectious diseases, but they do not take into account the demographic structure of the megalopolis and the system of contacts between their residents. Simulating the epidemiological situation allows one to test the effectiveness. Knowing the pathways of transmission, authorities can influence the network through closure of institutions, the introduction of quarantine, isolation, and treatment [3].

Consider the situation when the spread of the epidemic began in a city, and the authorities must take preventive measures. To carry out mass vaccination, to introduce quarantine, or to prescribe antibiotics? If you send antiviral drugs to the city, donor countries will not be able to protect the population from infections. Not only people's lives depend on the choice of authorities, but also the economic and social well-being of the country. To choose the optimal management strategy, you need to model the scenarios. Simulation of the epidemiological situation allows to test the effectiveness of measures in the fight against outbreaks of infectious diseases on the model. Modeling the ways of city inhabitants' moving gives a dynamic picture of a social network. An infectious agent uses a similar chain of contacts while spreading in a population. The technique of *sociometry* was first proposed by J. Moreno [1]. The term "social network" was introduced in 1954 by the sociologist J. Barnes [2]. At present, there is a shortage of systematic presentation of the methods and algorithms in the field of network analysis suitable for modern applied research. Agent modeling can play an important role in predicting the spread of the disease, as well as in evaluating localization measures.

MATERIALS AND METHODS

The paper has the following research questions: (i) building a mathematical model that simulates the epidemiological situation, calculate the epidemic threshold and percolation threshold, and selects quarantine measures to destroy the network; (ii) studying the properties of the model; (iii) simulation with the use of an agent approach. The aim of the work is to build an imitative multiagent model of spreading the epidemic to formulate measures in order to effectively reduce the incidence rate. The use of the simulation is a multiagent approach in the modeling of epidemics, is it possible to conduct numerical experiments.

RESULTS AND DISCUSSION

The use of the simulation multiagent approach in the modeling of epidemics is due to the fact that this approach allows to consider many factors that affect the epidemic process, which, eventually, makes it possible to conduct numerical experiments. A social *network* on a qualitative level is understood as a structure consisting of a multitude of *agents* (individual or collective subjects, for example, individuals, families, groups, and organizations) and a set of relations defined on it (an aggregate of relations between agents, for example, acquaintance, friendship, or cooperation). Formally, the social network represents the graph $G=(V,E)$, in which V is a set of vertices (agents) and E is a set of edges corresponding to the interaction of agents. So, in epidemiology, let's consider an agent as an elementary participant of our study. The agent is active, in a certain state, which can change under the influence of certain factors. Properties of the agent include the following characteristics, which all together form a level of immunity: height (h), weight (w), sex (s), income (d), marital status (q), education (e), geography (g) [5].

In the model, there is an entire artificial city of agents possessing the same set of properties, but different in values, i.e. some agent database (AD). These data are needed not only for modeling on existing epidemics, but we must have this kind of database for any sudden appearance of new viruses. Through the vertices $v_i \in V, i=\overline{1,n}$, we denote individual family members consisting of n persons who live together. We connect the vertices $v_i (i=\overline{1,n})$ and $v_j (j=\overline{1,n}) i \neq j$ by an edge $e=(v_i, v_j)$ in a case when there is a close household contact between family members, which is, in turn, sufficient for infection with an investigated infectious disease. In case when one of the family members gets infected, he/she can infect the rest of the family with a respiratory infection. The model of contacts between family members consisting of 4 persons will be represented by the following

graph $H_1 = (W_1, Q_1)$. If the number of people in the family is 5, then we have a 5-vertex complete graph: $H_2 = (W_2, Q_2)$ (see Fig. 1).

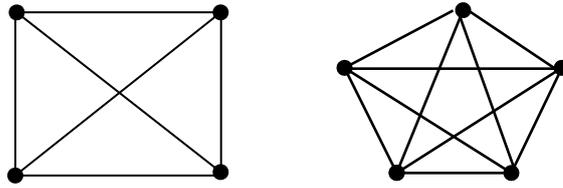


Fig 1: Contact Models $H_1 = (W_1, Q_1)$ and $H_2 = (W_2, Q_2)$

The graph-model has an increasing number of vertices and edges, but its structure remains surprisingly stable, consisting of different-scale and self-similar parts with different number of vertices in these parts. It remains for us to name the parts as the seeds, and the graph model - as the prefractal graph. Thus, at the stage $l = 1$, the model describing contacts in the family will be a n_1 -vertex complete graph $G_1 = (V_1, E_1)$. At the stage $l = 2$, the model describing contacts of families living on one entryway is represented by the graph $G_2 = (V_2, E_2)$ that can be obtained from the graph $G_1 = (V_1, E_1)$ by applying the ZWZ operation to each of its vertices. Moreover, this operation can be performed randomly by graphs $H_1 = (W_1, Q_1)$ or $H_2 = (W_2, Q_2)$. Continuing the process, you can describe the contacts of a multi-storey building, a residential block, a city, etc.

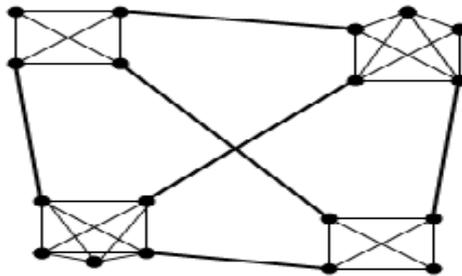


Fig 2. The model of household contacts of people living on the same staircase in apartments numbered 1-4.

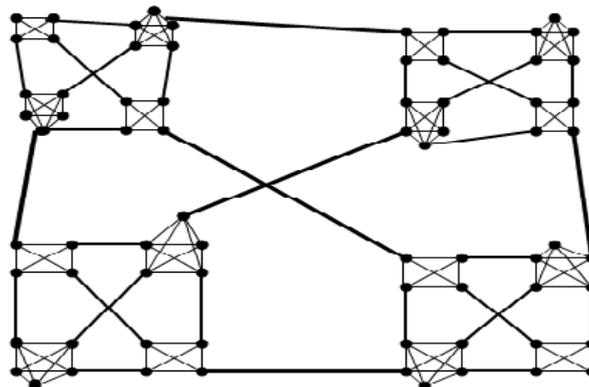


Fig 3: Model of more complex connections between the residents of one entrance.

Repeating this process if $l \rightarrow \infty$, the contact structure will be the fractal graph $G = (V, E)$ generated by two complete seeds, $H_1 = (W_1, Q_1)$ and $H_2 = (W_2, Q_2)$. If families consist of a different number of people, then the seeds will be of different types. Any prefractal graph $G_l = (V_l, E_l)$, $l = 1, 2, \dots$ from the trajectory of the construction of the fractal graph $G_l = (V_l, E_l)$ is the structure of the contacts at the l -stage. The process of

constructing the fractal graph $G_l = (V_l, E_l)$ can be generalized to the case when the ZWZ operation is performed by a set of seeds $H = \{H_1, H_2, \dots, H_s\}$, $s \in Z$. The resulting model will be more adequate if we additionally take into account a number of factors:

1. An important feature is that human contacts with family members are more frequent, close and prolonged than with a neighbor, and contacts with residents of neighboring entrances are even weaker, etc. These characteristics change in proportion with time, so it is logical that all the edges of the prefractal graph $G_l = (V_l, E_l)$, $l = \overline{1, L}$, depending on their rank, need to be determined by the rule $w_r(e_{s_r}) \in (k^{r-1}a, k^{r-1}b)$, where $r = \overline{1, L}$ is the edge rank, s_r is the edge number of r -rank; $k(k > 1)$ is the coefficient of proportionality, which affects the change in the weight of the edge.

2. It is well known from the theory of epidemics that each person has a certain level of immunity from infectious diseases. Some people make vaccinations against infectious diseases, become unaffected by infection, and have the maximum level of immunity. In turn, people with weakened immunity are more prone to infection. To take into account this fact, we assign the vertices of the graph $G = (V, E)$, representing the model of household contacts, the weights $w(v_i), v_i \in V, i = \overline{1, n}$, $0 \leq w(v_i) \leq 1$. The weight of the top $w(v_i)$ is a coefficient proportional to the degree of protection from an infectious disease. If a person comes in contact with an infected person, in a mathematical interpretation he/she becomes infected with the disease with some probability $w(v_i) = \beta$, $0 \leq \beta \leq 1$. There are several cases possible:

- $w(v_j) = 1$ - a person is not susceptible to the disease, he/she has been vaccinated or already overcome this disease, and, as a result, is no longer susceptible;
- $w(v_j) = 0$ - a person will necessarily be infected when making household contacts sufficient for infection;
- $0 < w(v_j) < 1$ - a person is susceptible to the disease, and infection is possible due to household contacts [18].

For social networks, the key indicator in the process of infection is the “epidemic threshold” (threshold of percolation), λ_n , i.e. the critical probability of infection of a neighbor, if exceeded, the “infection” spreads throughout the network. If the social network is represented by a random prefractal graph, then this infection with the probability of getting infected being above the percolation threshold multiplies exponentially. In turn, the virus with the probability of infection being below the percolation threshold, “dies out” exponentially. Suppose that if a person with the $\beta > \lambda_n$ probability of getting infected with a disease has some kind of household contact with an infected person, then he/she becomes infected; if $\beta < \lambda_n$, than the contactee remains healthy. For the simplicity of the study, taking into account the general randomness of infection of weight $w(v_i), v_i \in V, i = \overline{1, n}$, $0 \leq w(v_i) \leq 1$, the vertices of the graph are assigned arbitrarily by a random number generator.

In percolation theory, percolation processes are considered left-to-right or bottom-up. Let’s define the concept of “percolation” on the prefractal graph with weighted vertices, which must be taken as the *source* and *sink*. We assume that there is a flow between different fixed seeds of the same rank $S_1 = H_1 = (W_1, Q_1)$ and $S_2 = H_2 = (W_2, Q_2)$, representing the *source* and *sink* if there is a route (u_i, v_j) from the vertices $w(v) > \lambda_c$ connecting the two vertices, where $u_i \in W_1$ and $v_j \in W_2$, $u_i, v_j \in I \cup R$, $i, j = \overline{1, n}$.

Algorithm for finding the percolation threshold of a prefractal graph:

1. $\beta_1 := 1$;

2. There is a search for all possible routes connecting the source and sink at β_1 ; if there is such a route, then we return to the beginning of step 2 at $\beta_1 := \beta_1/2$; otherwise, go to step 3;
3. $\beta_1 := \frac{\beta_1 + \beta_2}{2}$. If $|\beta_2 - \beta_1| < \xi$, suppose that $\beta := \beta_1$, and the algorithm stops working; otherwise, go back to step 2.

The resulting value will be denoted by the percolation threshold.

To identify links that need to be blocked to exclude the further development of the epidemic, it is necessary to set the rank of the seed in question and indicate the percentage of infected nodes, at which it is possible to apply quarantine measures. As soon as the percentage of infected is reached in the seed of the indicated rank, all the edges that are incident to the infected vertices get blocked. Suppose that a model is given in the form of a prefractal graph weighted over all vertices and edges. Consider the structure of the spread of an infectious disease if the primary source of infection is given.

From a mathematical point of view, the structure of infection at the stage $l = 1$ is the $(n_1 + 1)$ -vertex star $H_1 = (W_1, Q_1)$. In the terminology of graph theory, the vertex that designates the primary source of infection is called the root.

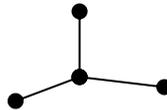


Fig 4: The structure of infection spreading in the form of a tree.

Suppose that at the stages of infection spreading $l > 1$, each “new” source is able to generate more sources of infection. The process of spreading the infection in the sense of replacing one source of infection $(n_1 + 1)$ by sources corresponds to the process of generating a fractal graph $G = (V, E)$ generated by a set of seeds $H = \{H_1, \dots, H_l, \dots, H_s\}$, each of which is the $(n_1 + 1)$ -vertex of the degree star $n_1, l = \overline{1, s}$. By matching the mathematical description to the verbal one, we will continue the next transition to the next level of distribution $r + 1$ according to the following rules:

1. The set of seeds $H = \{H_1, \dots, H_l, \dots, H_s\}$, $T \geq 2$ is involved in constructing the graph corresponds to an arbitrary number of infected individuals of the level r .
2. If the vertex $v \in V_r$ is not hanging, then it is not replaced.
3. A vertex replaced by a seed ($v \in V_r$) is selected from a subset of the hanging vertices, and the edge itself becomes incident to the center of the star.
4. If any hanging vertex was not replaced by a seed, it is called “frozen”. The ZWZ operation is not applied to it in any of the subsequent steps.

Thus, from the graph, $H_1 = (W_1, Q_1)$, applying the ZWZ operation to the hanging vertices, we obtain the graph $G_2 = (V_2, E_2)$ that is the structure of the spread of the infection in the next stage $l = 2$. Any prefractal graph $G_l = (V_l, E_l)$, $l = 1, 2, \dots$ from the trajectory of a fractal graph turns out to be the structure of the spread of infection at the l -th stage.

There is a prefractal graph $G_3 = (V_3, E_3)$ generated by a number of different star seedlings in Fig. 5. After performing L transitions, we obtain the prefractal root tree $G_L = (V_L, E_L)$, which is the tree of how an infectious disease is spreading; we denoted by $D_L = (V_L, E_L)$

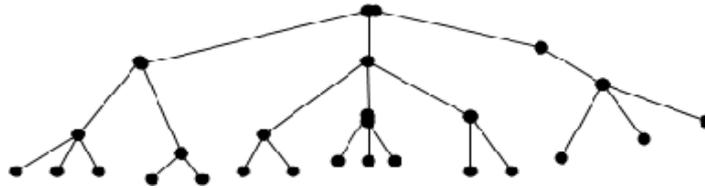


Fig 5: Structure in the form of a root tree.

CONCLUSION

I also developed a software product in the FreePascal for conducting simulations using an agent approach, which allows you to model the epidemiological situation, to calculate the epidemic threshold and the threshold of percolation, to choose quarantine measures to destroy the distribution network. Some pictures developed in the FreePascal are presented in this article.

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