

On agent-based approach to influenza and acute respiratory virus infection simulation

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Abstract—The paper analyzes existing approaches of mathematical modeling of morbidity spreading by the example of the dynamics of influenza and ARVI. The analysis showed that the most perspective approach is an agent-based. Agent-based model with SEIR type which takes into account behavior, age groups, as well as special features of the influenza and ARVI has been developed. Software implementation of model allows forecasting the morbidity, as well as calculating the epidemic threshold has been realized using C# programming language. The relevance of the model has been tested on real statistics.

Keywords—simulation; agent-based simulation; epidemic process.

I. INTRODUCTION

The preservation and strengthening of population health is an important socio-economic issue. The reduction of infectious morbidity is an essential aspect of that. In this task, preventive measures are crucial. Forecasting of the disease spreading dynamics allows developing and applying appropriate countermeasures and ensuring the rational use of material and human resources.

Methods of infectious morbidity forecasting are actively developing since the beginning of the twenties century. In recent years, the number of works on this subject is growing rapidly due to the deployment of information supervision systems and the appearance of large amounts of statistics available for analysis. Epidemiological forecasts are carried out for different periods and depending on them serve different purposes. Thus, the short-term forecast for a few weeks in advance is used in the operational management and the detection of epidemic outbreaks.

The medium-term forecast for the period from two to six months used in the tactical management can be considered the most useful [1]. Of course, it is less accurate than short-term, but leaves enough time to prepare for a possible emergency situations and the implementation of preventive measures. You cannot do without long-term forecasts for the year ahead and more in case of making strategic decisions. Achieving high quality of such forecasts is not possible in most cases, however, they are required, for example, in assessing the necessary

volumes of production of medicines and vaccines, equipping of medical facilities and staff training.

Qualitative forecast of the disease spreading is achievable only on the basis of adequate mathematical models. Taking into account recent advances in the field of mathematical modeling and simulation the formation of accurate and comprehensive models is now quite feasible task.

II. BACKGROUND

A. Problem of morbidity by influenza and acute respiratory viral infections (ARVI)

Influenza and other acute respiratory viral infections (ARVI) are the large-scale diseases occurring throughout the year, but more often in the fall and winter. According to the World Health Organization, ARVI took first place in the structure of infectious diseases and account for 80 - 90% of all infectious pathology [2].

Influenza is an acute infectious disease with viral etiology, which is accompanied by lesions of the upper respiratory tract. Influenza reduces the body's defenses, so a variety of diseases of the upper and lower respiratory tract, central nervous system, heart, kidneys and other organs can appear. Taking into account the ability of influenza to cause annual epidemics and pandemics across the globe, we can say that influenza is world value problem. From 5% to 20% of population are sick during epidemics [3]. Every second person is sick in case of a pandemic when there is a sharp change of virus properties. Generally, new influenza strains first appear in China and Southeast Asia and then spread rapidly throughout the world.

Economic damage from influenza is huge. And it damages both human (lost working days, expenses for medicines), and society. Seasonal influenza outbreaks bring direct and indirect losses of billions of dollars [4]. In addition to direct harm to human health, influenza is able to aggravate other diseases, which is especially dangerous for people with chronic pathologies and weakened immune system especially for the elderly, newborns, patients with cardiovascular clinics, etc. Other acute respiratory infections caused by parainfluenza, respiratory syncytial, adenoviruses, coronary, enteroviruses, rhinoviruses, and other pathogens.

Reliable protection against these diseases may be reached by using specific (vaccines against influenza) and non-specific protection. Modern medications can significantly increase the body's defenses and create a barrier to the penetration of respiratory viruses, including influenza. Thus, nowadays healthcare practitioner has a sufficiently wide range of preparations of different spectrum of activity and action mechanism, which can be used for the treatment and prevention of ARVI. Their proper and timely use can significantly reduce the infection rate of these diseases.

B. Agent-based simulation of epidemic processes

Classical models of disease spreading describe the dynamics of infection spreading using systems of differential equations. First works that laid the foundation of modern mathematical epidemiology, were published at the beginning of the twenties century [5]. The most known and used is the SIR model, which was proposed by Kermack and McKendrick in 1920, as well as its expansions (compartmental models). In such models, the studied population is divided into groups, for example, in susceptible (S), infected (I) and recovered (R). SIR type models are based on the analogy between the contacts of people in a large population and the law of mass action in chemical kinetics. The dynamics of the SIR model can be described by the following system of differential equations:

$$\begin{cases} \frac{dS}{dt} = -\beta IS, \\ \frac{dI}{dt} = \beta IS - \gamma I, \\ \frac{dR}{dt} = \gamma I. \end{cases} \quad (1)$$

where β is transmission rate between S and I states, γ is transmission rate between I and R.

Application of SIR models limits the assumption of a sufficiently large number of the analyzed population, and that all individuals in it continuously and uniformly mixed [6]. A variety of diseases spreading models are developed. They are designed to detail the SIR models and to enable their practical use. The most significant model of disease spreading, which takes into account the dynamic nature of the epidemic is the Baroyan-Rvachev model [7], which was developed in the USSR in the 1960s. It describes the epidemic process by the system of integral-differential equations:

$$\begin{aligned} \frac{dS(t)}{dt} &= -\frac{\lambda}{p(t)} S(t) \int I(t, \tau) d\tau, \frac{\partial E(t, \tau)}{\partial t} + \frac{\partial E(t, \tau)}{\partial \tau} = -\gamma(\tau) E(t, \tau), \\ \frac{\partial I(t, \tau)}{\partial t} + \frac{\partial I(t, \tau)}{\partial \tau} &= \gamma(\tau) E(t, \tau) - \delta(\tau) I(t, \tau), \frac{dR(t)}{dt} = \int \delta(\tau) I(t, \tau) d\tau. \end{aligned} \quad (2)$$

where p is population quantity, λ , γ , δ are functions of infection process development, t is global calendar time, τ is local time, which counts from the moment when person is infected. Baroyan-Rvachev model has used to predict epidemics of influenza on the territory of the USSR successfully.

A significant advantage of the models based on the apparatus of differential equations is the possibility of their analytical studies. Nevertheless, all these models are characterized by one more assumption which is that the characteristics and behavior of all individuals classified as a subgroup are considered the same. This assumption can be weakened by modern computer simulation models.

The paradigm of system-dynamic simulation proposed by Forrester in the 1950s [8] is the graphical diagrams links and global influences of some parameters on the other which are built in time for the studied system. Built model is simulated on the computer on the basis of these diagrams. This type of modeling provides insights into what is happening in the system and identifying of causal relationships between objects and phenomena better than all other paradigms. However, parametric identification of detailed epidemic diseases models of system dynamics represents difficulties [9].

Agent-based modeling is a relatively new (1990s-2000s.) direction in simulation, which is used to study the decentralized systems, the dynamics of functioning of which is determined not by global rules and laws (as in other paradigms of simulation), but on the contrary, global rules and laws are the result of the individual activity of the group members. The aim of agent-based modeling is to obtain understanding of these global rules, the general behavior of the system based on the assumptions of the individual, private behavior of its individual active objects and the interaction of these objects in the system [10].

Agent-based models allow to transfer the social structure of the simulated population by the most natural and easy way. Each agent has its own state variables and behavior, which allows detailing model almost unlimited. There is no need for the formation of complex formulas for calculating the probability of transmission of the disease, because the probabilities of infection are defined parametrically (but still require justification and calibration). Based on the above analysis the agent-based approach in simulation has been chosen as an instrument for morbidity by influenza and ARVI modeling in this research.

III. CONSTRUCTION OF AGENT-BASED MODEL

The developed model of influenza and ARVI spreading is based on the traditional SIR model with its expansion by adding the state Exposed (E), which means people who are staying in the incubation period. Agents are located in the incubation period from 1 to 14 days in case of influenza and ARVI. The scheme of transitions between states of the model is shown in Figure 1.

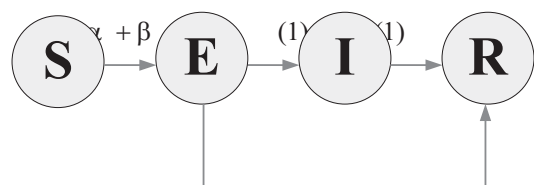


Fig. 1. The scheme of state changes in agent-based model.

Also, the proposed structure of the agent-based model can be expanded by adding a state Dead (D) for the agents who died due to disease. However, since the mortality rate from influenza and ARVI is low in comparison with other diseases, this specification of the model can be neglected.

Two types of agents have been defined in developed model.

Agent-human: agent is simulating behavior of one person.
Agent-location: location is the environment for the agent and it simulates location in which the infection spreads.

Also, agents-people in addition to the states described above have age. On to this property, according to collected statistics and data received regarding to the incidence of influenza and ARVI five age groups were identified in model:

- children from 0 to 4 years;
- teens from 5 to 14 years;
- youth from 15 to 24 years;
- adults from 25 to 54 years;
- elderly people older than 55 years.

Age groups determine the probability of contact with other agents. These conclusions relate to the hypothesis that children and elderly people are in contact with fewer people than younger people. Proportion of agent distribution by age is determined by demographic data and depends on the modeled area.

The dynamics of the model is described by the combined actions of the agents, and events generated by them. The rules of agents' interaction are described by the system (3). Transitions events are generated by agents. Agents' states duration parameters are agreed with the characteristics of the disease. The transition and interactions probabilities between agents tailored to the developed model and based on the results of the experiments.

Being in the same location, the agents are in contact with each other. The result of contact between sick and healthy agent may cause infection of healthy agent. The simulated area is split on cells. To reduce the computational complexity of the model, the contact between the agents is considered to their affiliation of the same cell.

Processes of the developed model are configured parametrically during setup and calibration of the simulation process. In the case of all agents will be in the «Susceptible» state at the initial time, what means they are healthy, infected agents do not appear and simulation of disease does not occur. Therefore, at the initial moment of the model time it is necessary to present sick agents («Exposed» and «Infected») in the model.

The result of the model of influenza and ARVI morbidity dynamics is the morbidity level: the percentage of susceptible, infected and recovered agents in every moment of model time.

IV. PROGRAM REALIZATION AND SIMULATION RESULTS

The prototype of model of morbidity by influenza and ARVI dynamics is developed by programming language

NetLogo (fig. 2) [11]. NetLogo is a cross-platform modeling environment based on the programming language Logo. But despite this NetLogo allows using external procedures written in other programming languages, e.g., Java. Language Logo was created to teach children using the computer. So NetLogo modeling environment is still focused on learning, so it is suitable for the construction of not complex models, though it allows making full analysis of them using third-party tools.

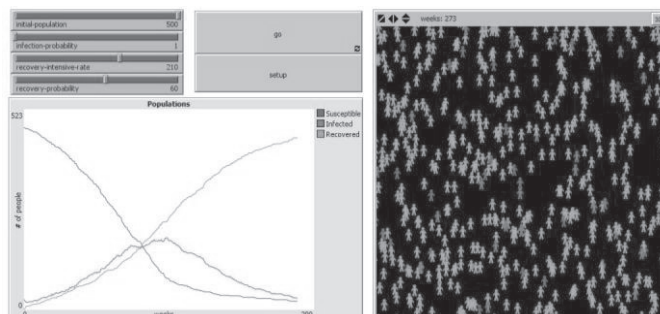


Fig. 2. Interface of model of influenza and ARVI spreading in NetLogo.

Because of the inability of the model in NetLogo with a large number of agents, quantitative data and forecasts do not correspond to the actual. Despite this, the dynamic behavior of the model coincides with the actual dynamics. To increase the accuracy and availability of adequate quantitative data model of influenza and ARVI spreading has been realized in the programming language C # (Fig. 3). The developed model consists not only of simulation and calculation of forecasted morbidity, but also has a possibility of calculation of epidemic thresholds of morbidity by influenza and ARVI for convenient work and analysis of software by epidemiologists. Algorithm of calculation of the epidemic thresholds is based on probability calculations based on existing statistics for the past years.

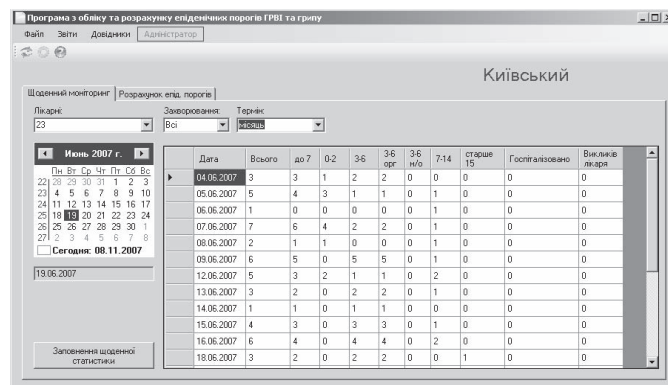


Fig. 3. Main interface of morbidity by influenza and ARVI spreading model in C#.

The following functions are realized in developed model:

- collecting daily morbidity by influenza and ARVI;
- calculation of epidemic thresholds of morbidity by influenza and ARVI in the form of upper tolerance boundaries rates of non-epidemic morbidity;
- transmission of data from districts to city or region;

- generation of reports;
- simulation of forecast morbidity by influenza and ARVI.

User of software product is available in two levels: the district level and the city level. District-level user introduces daily statistics on the morbidity by influenza and ARVI in each of the district hospitals and sends them to the city sanitary-epidemiological station using the FTP-server.

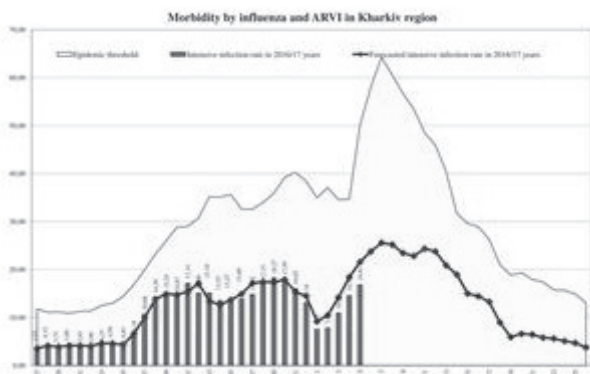


Fig. 4. Graph of morbidity by influenza and ARVI for 10 000 of population (actual and simulated).

Thus, the information is collected and systematized in real time what allows to carry out adequate measures to prevent the epidemic in time by epidemiologists. Also the information about the population assigned to each hospital of the city is updated daily. This allows making the forecast of morbidity by influenza and ARVI in the most correct way. In order to adequately calculate the simulated disease epidemiologist can mark epidemic data and the program will automatically exclude them from the calculations.

The adequacy of the obtained results has been checked by statistical data on the morbidity by influenza and ARVI in Kharkiv region (Ukraine) (Fig. 4).

V. CONCLUSIONS

Agent-based approach can be considered as the most perspective in the field of modeling of incidence, as it overcomes the limitations of classical analytical and deterministic models. Agent-based approach is applied to create a stochastic model of spreading of influenza and ARVI, which reflects the probabilistic nature of the epidemic processes.

Built agent-based model allows executing forecast for epidemic situation of influenza and ARVI on the basis of statistical data on the morbidity, as well as quantitatively calculating forecast for the morbidity by influenza and ARVI in the investigated territory. The developed model solves the problem of forecasting the dynamics of disease and the development of the epidemic of influenza and ARVI, which greatly facilitates the work of epidemiologists on prevention of epidemics of these diseases.

The developed software system implemented in city and regional sanitary and epidemiological stations in Kharkiv (Ukraine), which allowed for timely preventive measures and prevent the epidemic rise of morbidity in Kharkiv.

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