## III Міжнародна науково-практична конференція IT-професіоналів і <sup>91</sup> аналітиків комп'ютерних систем «ProfIT Conference»

## DEVELOPMENT OF INTELLIGENT MULTIAGENT MODEL OF COVID-19 EPIDEMIC PROCESS Herasymova Arina, student of group 365a National Aerospace University "Kharkiv Aviation Institute"

It is undeniable that the recent COVID-19 epidemic has changed the world in which we live. Now, more than ever, we have a constant flow falls conflicting news and inconsistent policies. Technical terms such as exponential growth, social distancing and logarithmic graphs, is now widely used on television and in social networks.

Mathematical and computational approaches are important tools for understanding epidemic patterns and evaluating disease control policies. The aim of the work was to conduct a comprehensive review of epidemic models, to get an idea of modeling and simulation of epidemics and to develop an intelligent multi-agent model of the epidemic process COVID-19.

There are 3 classifications of epidemic models for epidemic modeling: mathematical models, complex network models and agent-based models. Since our work requires an analysis of the macroscopic patterns of the spread of the epidemic, it will be appropriate to use mathematical models of the spread of the virus. Mathematical models include the SIR (susceptible, infectious and recovered) model, the SIS (susceptible, infectious and susceptible) model, and the SEIR (susceptible, infectious and recovered) model. Since people, after an illness, are immune to COVID-19 and can get sick twice, in one case because they acquire immunity, and in the other because they have died, the model that suits us is SIR.

The goal of the SIR model is to find a series of equations to calculate, at a given time t, how many people are in each compartment. So the SIR model tries to find a definition for S(t), I(t) and R(t). And it is best defined as a series of differential equations:

$$\begin{split} &\frac{\partial S}{\partial t} = -\beta \frac{SI}{N} \\ &\frac{\partial I}{\partial t} = \beta \frac{SI}{N} - \gamma I, \\ &\frac{\partial R}{\partial t} = \gamma I \\ &N = S + I + R, \end{split}$$

where  $\beta$  – determines how often the interaction between susceptible and infected people leads to a new infection;

 $\gamma$  – is the rate at which infected people recover (or die) and move to a distant compartment.

Since the rate of recovery is different for all people, we will take the average value  $\gamma = 0.1$ . Now using these formulas we can simulate the evolution of the SIR model for  $\beta = 0.6$  (fig.1) and  $\beta = 0.2$  (fig.2).





So, after simulating the epidemic process of COVID-19, you can see that in the absence of isolation measures for infected people ( $\beta = 0.6$ ), the peak of diseases will be very large and almost all people will get sick. And if isolation measures are observed ( $\beta = 0.2$ ), the peak of diseases will not be so large the number of infected will not be so significant.

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