# Intelligent System of Epidemic Situation Monitoring and Control

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#### Abstract

The paper presents concept of intelligent system of epidemic situation control. An intelligent information technology has been developed to support decision-making in the field of biosafety, which will make it possible to develop a scientifically grounded basis for the implementation of effective preventive and anti-epidemic measures of the Ministry of Health of Ukraine, an epidemiologist and public health specialists. Agent-based model has been developed for COVID-19 epidemic process in Ukraine. The experiments carried out not only speak about the effectiveness of self-isolation. They also tell us how many, how many people need to stick to it to be effective, and that there isn't much difference between 88 and 100%. But it also tells us that isolation alone cannot eradicate disease.

#### **Keywords 1**

Public Health, epidemic process, epidemics control, intelligent information technologies, decision support system, COVID-19, simulation.

## 1. Introduction

On December 31, 2019, the Chinese government first reported the emergence of a new pathogen – the coronavirus, later called COVID-19. On January 30, WHO declared the outbreak of the new coronavirus as a public health emergency of international concern. [1, 2]. The virus was rather contagious, according to [3] the basic reproductive number R0=2.2 and Liu Y. et al. [4] estimated R0 to be between 2.76 and 3.25, i.e., one person can infect 2-4 susceptible individuals. Despite the fact that the mortality rate of coronavirus disease is lower than that of SARS and MERS, by the time of submitting this report (April 22, 2020), the disease has claimed the lives of more than 177 thousand people, and about 2.5 million people in the whole world have been infected [5].

All forecasting models have different initial assumptions and use historical data differently. Models based on well-grounded theoretical understanding and available evidence are critical to formulating viable observational policies, but shifts in distribution can lead to systematic false predictions [6-10].

Ukraine became involved in the current COVID-19 pandemic later than other countries outside of China. The first confirmed case was reported on March 3, 2020 with a man who returned from Italy on February 26. The first death was reported on March 13 with a woman who returned from Poland. On March 24, 2020 the number of cases exceeded 100, on April 3, 2020 – 1000. On April 22, 2020 – 6592 cases and 174 deaths were reported. The peculiarity of the outbreak in Ukraine was that after the announcement of shutdown and lockdown in many EU/EEA countries, primarily Italy, citizens who in large numbers were employed in Italy, Poland and other EU countries began returning to Ukraine. This way a flood of potential sources of infection poured into Ukraine from countries where the epidemic was already raging.

On March 12, the first restriction measures were implemented in the country. All educational institutions were closed, and all public events and mass gatherings were banned. On March 17, the maximal number of passengers in the public transport was limited to 10, and the metro was closed.

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Catering enterprises and shopping centers were closed. On March 18, the intercity movement of trains and buses inside the country was stopped. From April 6, the population was obliged to cover their faces with masks or respirators in public places, visiting the parks and recreations areas was prohibited. From April 7, 2020, it became possible to only cross the Ukrainian border only by car at 19 checkpoints. However, the increase in the incidence of COVID-19 continued.

Leading experts in the medical community have also recognized the need to develop new approaches to solving biosafety problems. Thus, the health ministers of the G20 countries, at their meeting, which took place online on April 19, 2020, acknowledged that the COVID-19 pandemic revealed systemic deficiencies in health systems and showed the inability of the world community to prevent and respond to the threats of a pandemic. Also, the G20 countries agreed that human health and well-being should be at the heart of all decisions and measures taken to combat infection. Participants in the meeting of G20 health ministers also discussed the importance of using digital solutions in current and future pandemics. One of the promising areas among the set of measures aimed at preventing the development of epidemics (including COVID-19) is the systematic use of digital contact tracing (DCT) technology. For example, there are such initiatives focused on this technology: Pan-European Privacy-Preserving Proximity Tracing (proposed by a number of European research centers), Privacy-Preserving Contact Tracing Project (proposed by Apple and Google), Decentralized Privacy-Preserving Proximity Tracing (proposed by a number of British and Italian research centers) and others. The basic method of this technology is the use of geolocation data of mobile devices, which are collected by mobile operators to support their technological process. However, the use of these data should be based on complex epidemiological models, the development of which is a challenge for the world scientific community. Unfortunately, for a number of reasons, all the possibilities of modern information and communication technologies were not used to collect and process information about the epidemiological state in regional, national and supranational communities.

Thus, we see that the organizational systems and, in particular, the systems of anti-epidemic protection of the population, in different countries were unable to counteract the explosive spread of the SARS-CoV-2 virus, which led to a high mortality rate of certain categories of infected people, as well as to a wide range of long-term negative consequences of inadequate management decisions, such as unjustified restriction of civil rights, deterioration of the national and global economies, narrowing of the labor market, decline in the quality of education, increased violence in families, negative impact of isolation and quarantine measures on the mental state and mental health of the population, and the like [11].

The research aims to develop an universal intelligent system for simulation infectious morbidity in given territory.

#### 2. Formalization of epidemic processes

In the modern period of human development, there are constant social changes in society that affect the evolution of the epidemic process, and which should be taken into account when carrying out measures aimed at curbing the spread of infections among the population.

The direct driving forces of the epidemic process are the source of infection, the transmission mechanism and the susceptible human body, which create a chain of successive infections with infections [12]. Without these links, the existence of the epidemic process is impossible. The biological hazard of the population is determined by the possibility of the emergence and spread of biological agents that are pathogenic for humans. At the same time, the process of spreading pathogens in space and time, the distribution of cases among various groups of the population and the dependence of these events on various phenomena and processes occurring in nature and society are important. Therefore, no less significant are the secondary driving forces of the epidemic process - social and natural factors that affect the intensity and manifestation of the epidemic process, slowing down or accelerating its development.

The main tasks of practical epidemiology are to assess the existing epidemic situation, identify causal relationships due to which it has developed, and analyze risk factors, that is, factors whose action on the epidemic situation determines the likelihood of its complication [13]. In order to

rationally control the epidemic process, one should take into account the direction of evolution of the epidemic process and evaluate the most influential factors affecting the incidence of the population.

Gromashevsky proposed an epidemiological classification of infectious diseases based on the determination of the transmission mechanism, which is of great practical importance for public health [12]. The transmission mechanism is most often influenced by social events taking place in the life of the population. Under the influence of social conditions, the leading factors of transmission of the pathogen (for example, evolutionary changes in the transmission pathways of shigellosis) or the population of vectors (tick-borne infections) can change, the transmission routes that existed earlier (the use of shared water for washing with trachoma) or new transmission routes appear (for example, artifactual pathway for viral hepatitis B, C, HIV). The specificity of the mechanism and routes of transmission determine the range of social factors, the most significant, which play a decisive role as regulators of the epidemic process in any infection. For example, in respiratory tract infections, migration processes are important, which contribute to the exchange of strains of pathogens, the introduction of strains into new territories that have not previously circulated in this area, this in turn leads to changes in the immunological structure of the population. Also, for the group of respiratory tract infections, for which there are effective vaccines, it is important to organize and conduct vaccinations for the population. With a group of intestinal infections, the condition of the water supply, the organization and characteristics of nutrition, the removal of garbage, and the like can be of decisive importance. In infections with a vector-borne transmission mechanism, the processes of anthropogenic transformation of nature, the presence and number of vectors and conditions for their reproduction and distribution, etc., are important. In infections with a contact mechanism of transmission, the biological behavior and the characteristics of certain groups of the population, the possibility of implementing artifacts of transmission in medical institutions, in public service institutions (beauty salons, hairdressing salons, tattoo studios, etc.) are important.

Each state may have its own characteristics of the spread of infectious diseases, which differ from other countries, which is associated with the characteristics of the socio-economic, ecological, religious, cultural and other conditions of the population's existence [14]. The basis for the prevention of infectious diseases on a national scale is an increase in the material well-being of the population, the provision of quality water and food, quality housing, qualified medical care, available, etc.

To prevent the intensification of epidemic processes of infectious diseases, it is necessary to determine the driving forces characteristic of a certain time and a certain territory. For Ukraine, we have identified the most relevant infections with each of the groups of infections according to the epidemiological classification of Gromashevsky.

## 3. Concept of intelligent system of epidemiological control

The growth of biological threats both in the world and in Ukraine is a significant challenge for scientists, society and government. Existing biological threats are primarily associated with massive outbreaks of especially dangerous infections, new and emerging infections in humans and animals; activation of natural foci of zoonotic diseases, the possibility of overcoming the interspecies barrier by causative agents of animal infectious diseases; the risk of using pathogens as biological weapons; development of genetic engineering technologies without appropriate control of their safety and proper expertise; the growth of population migration, tourism and the like. Meanwhile, ensuring biological safety is an essential component of national security and the key to sustainable development of the country.

To solve the problem of biological safety, it is necessary to clearly understand the mechanisms of development of the epidemic process of a certain infectious disease, assess the leading risk factors for its occurrence and intensification, and have an adequate tool for predicting and controlling the spread of infections among communities, creating conditions for timely response, warning and alerting the population, and the implementation of effective and effective anti-epidemic and preventive measures.

The study aims to analyze the main threats and challenges posed by globalization facing national health systems with a focus on the current coronavirus disease 2019 (COVID-19) pandemic. The role of various factors in the emergence of outbreaks of infectious diseases, including the active development of the tourism industry, a decrease in biodiversity, which is associated with the use of

agricultural and urban lands, limited access to water resources in many regions of the world and innovative methods of genome editing, is highlighted. It also focused on the issue of antibiotic resistance and the contribution of modern approaches to the treatment of COVID-19 to exacerbate this problem. The potential of using antimicrobial peptides, nanostructured materials and bacteriophages to solve the problem of antibiotic resistance is discussed. Current advances and shortcomings in the development of COVID-19 vaccines are highlighted. Politicization and competition between governments and pharmaceutical companies have created an environment for the failure of future vaccination campaigns, heightened anti-vaccination sentiment among the population and fosters negative attitudes towards vaccination in general. International cooperation is needed to mitigate the impact of globalization-related threats to public health.

Despite the developed international documents on the system of measures for biological threats, including within the framework of the emergency response program, the existence of the International Health Regulations (IHR-2005) to protect the population from the spread of infectious diseases, the latest pandemic of coronavirus infection COVID-19 showed the inability of the world community to adequately respond to biological threats on a planetary scale, to resist epidemic complications and to ensure the biological safety of the population. The countries of the world to contain the spread of COVID-19 introduced a number of measures, which included sanitary and quarantine measures, large-scale restrictions on the movement of people and international passenger traffic, and the like. However, no country in the world was able to predict the development of the epidemic of its own territory and avoid negative economic, medical, social and other consequences due to the lack of a powerful tool for assessing various factors in the formation of the epidemic situation and its forecasting. In such conditions, the need for modeling and decision support tools based on mathematical calculations of their consequences increases. Such means should include a variety of models for assessing the epidemic situation and the volume of needs for medical care for the population, models for predicting epidemic processes, assessing factors affecting the development of infectious diseases, and the like. It is also necessary to take into account the various risks and uncertainties that arise when modeling such complex processes with a stochastic uncertain nature of their components. Such modeling requires the use of an appropriate mathematical apparatus, in particular, random processes and fields, machine learning methods, fuzzy logic, game theory, optimization methods, and the like [15]. As a result of the project implementation, for the first time, mathematical models, methods and information technology for assessing the epidemic situation will be developed, which will eliminate the existing limitations and disadvantages of existing approaches. This will improve the accuracy of forecasting the dynamics of the epidemic process.

Thus, it is proposed to build a multi-agent system for the epidemic process of infectious diseases, which allows us to identify factors that affect the dynamics of the epidemic process. Verification of the accuracy of the constructed forecast is carried out by comparing with the constructed programs of machine learning models, which show high accuracy.

## 4. Simulation of epidemic process

The real epidemic differs significantly from the idealized models, which were analyzed in detail in paper [16]. Some notable differences:

• at the beginning of the epidemic, the number of infectious diseases is small, and the model is determined, which assumes the presence of a sufficient number of infectious diseases for homogeneous mixing, is inappropriate;

• when it becomes clear that an epidemic has started, people are likely to change their behavior, avoiding crowds to reduce their contact, and being more careful about hygiene to reduce the risk of infection;

• if outbreak vaccine is available, public health measures will include vaccination of a subset of the population. Various vaccination strategies are possible, including vaccinating health workers and others responsible for a first-line epidemic, vaccinating members of the population who have been in contact with diagnosed infectious agents, or vaccinating members of the population living in close proximity to diagnosed infectious agents;

• diagnosed infectious agents can be hospitalized both for treatment and for isolation from the rest of the population;

• contact tracing with diagnosed infectious diseases can identify people at risk of infection who can be quarantined (must stay at home and avoid contact) and monitored so that they can be quarantined immediately if and when they become infected;

• for some diseases exposed, members that have not yet developed symptoms may already be infectious, and this requires inclusion in the model of new infections caused by contacts between susceptible and asymptomatic infections with those exposed to the class;

isolation may be imperfect;

• nosocomial transmission constitutes a serious risk of disease.

Taking into account the identified features and limitations, the multi-agent model is a set of agents with the following architecture:

$$Ag_i = (shmP_i, M_i) \tag{1}$$

where  $shm P_i$  – schema of the agent that originates the internal structure;  $M_i$  is the agent's method, which is the origin of the behavior.

Each agent has one of the states: S - susceptible (for agents that may be infected), I - infected (for agents that are infected), C - convalescent (for agents that are infected, but do not have external manifestations of the disease), R - recovered (for agents who have recovered and acquired immunity), D - dead (for agents who died of age or due to illness). Agents move from state to state due to interaction with each other with a certain probability. The probabilities are determined experimentally and depend on the conditions, epidemic processes and the characteristics of the spread of the incidence in a certain area.

The model implements three areas of agent interaction: safe area, risk area and treatment area. Depending on belonging to a certain zone, the probabilities of transitions between states change.

To reduce the computational complexity, interactions between agents are determined by their belonging to the same cell.

Methods of intelligent interaction of agents under conditions of uncertainty are described in article [17].

Interpolation methods were used to apply the results obtained in modeling in practice. According to the morbidity model, Lagrange interpolation polynomials were taken.

In it the lattice is formed by the intersection of straight lines;  $x = x_n$ , n = 0, ..., N;  $y = y_m$ ,

m = 0, 1, ..., M;  $f_{nm} = f(x_n, y_m)$  - the value of the function in the node  $\{x_n, y_m\}$ . Let us use, for example, the apparatus of piecewise-polynomial interpolation. To do this, we first implement by piecewise polynomial interpolation of a given degree in x on each line y. Then, for each value of x, piecewise-linear interpolation in y is implemented taking into account the values of the function obtained at the first step. So, in the case of interpolation in both variables, this method leads to an interpolation polynomial of the following form:

$$F(\mathbf{x}, \mathbf{y}) = f_{nm} \frac{(x - x_{n+1})(\mathbf{y} - \mathbf{y}_{m+1})}{(x_n - x_{n+1})(\mathbf{y}_m - \mathbf{y}_{m+1})} + f_{n+1,m} \frac{(x - x_n)(\mathbf{y} - \mathbf{y}_{m+1})}{(x_{n+1} - x_n)(\mathbf{y}_m - \mathbf{y}_{m+1})} + f_{n+1,m+1} \frac{(x - x_n)(\mathbf{y} - \mathbf{y}_m)}{(x_{n+1} - x_n)(\mathbf{y}_{m+1} - \mathbf{y}_m)} + f_{nm+1} \frac{(x - x_{n+1})(\mathbf{y} - \mathbf{y}_m)}{(x_n - x_{n+1})(\mathbf{y}_{m+1} - \mathbf{y}_m)}$$
(6)

In a similar way, you can carry out sequential Lagrange interpolation, but for each fixed value of n, taking into account the first interpolation step

$$L_{NM}(x, y) = \sum_{n=0}^{N} \sum_{m=0}^{M} f_{nm} \prod_{\substack{i=0, \ j=m\\ i \neq n}}^{N} \prod_{\substack{j=0, \ j \neq m}}^{M} \frac{(x - x_i)(y - y_j)}{(x_n - x_i)(y_m - y_j)}$$
(7)

Lagrange's formula has no restrictions on the number of interpolation nodes, or rather, an increase in the number of nodes does not entail a significant increase in calculations, since there is no need to calculate the factorial.

We used Unity to implement the model. To create a model, implemented:

- create a virtual 2D box;
- create several agents placed in a box;
- each of the agents must move continuously and randomly;
- agents can be in one of the SIR states;
- each infected agent has a fixed probability of infecting nearby susceptible agents;
- infected agents eventually recover after a fixed amount of time.

Depending on the simulated epidemic process, it is necessary to set the initial parameters of the model (Fig. 1).

Infection Infected Agents	•		6
Infection Probability	0.6	to 0.7	
Infection Radius	3	to 4	
Infection Duration	5	to 10	

Figure 1: Setting initial parameters for first case of infection.

As a result of the software product, the model adjusts the parameters depending on the real incidence statistics (Fig. 2).

0.1	to	0.2
0.75	to	2
5	to	10
•		38
	0.1 0.75 5 	0.1 to 0.75 to 5 to



As a result of work of model we will receive distribution of cases of morbidity in the chosen territories. In our case - the incidence of COVID-19 in the regions of Ukraine (Fig. 3).



Figure 3: Epidemic process distribution.

Experiments with the constructed model allow to reveal the necessary percent of immunization of the population for prevention of epidemic growth. We have provided several experiments with immunization percent -0% (Fig. 4), 80% (Fig. 5), 100% (Fig. 6).



Figure 4: Epidemic process dynamics with 0% immunization.



Figure 5: Epidemic process dynamics with 80% immunization

Figure 6: Epidemic process dynamics with 100% immunization

Also experiments has showed effect of self-isolation, on abscissa axis self-isolation coefficient is presented and on ordinate axis the incidence dynamics is presented (Fig. 7).



Figure 7: Effectiveness of self-isolation

#### 5. Conclusions

An intelligent information technology has been developed to support decision-making in the field of biosafety, which will make it possible to develop a scientifically grounded basis for the implementation of effective preventive and anti-epidemic measures of the Ministry of Health of Ukraine, an epidemiologist and public health specialists. The introduction of the scientific and applied results of the project in the highest bodies of state power, the Public Health Centers of Ukraine and medical and preventive institutions will ensure the adoption of effective preventive decisions, reduce the negative economic, medical and social impact on society and the state.

The experiments carried out not only speak about the effectiveness of self-isolation. They also tell us how many, how many people need to stick to it to be effective, and that there isn't much difference between 88 and 100%. But it also tells us that isolation alone cannot eradicate disease.

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