

# The Concept of Developing a Decision Support System for the Epidemic Morbidity Control

Sergiy Yakovlev<sup>a</sup>, Kseniia Bazilevych<sup>a</sup>, Dmytro Chumachenko<sup>a</sup>, Tetyana Chumachenko<sup>b</sup>, Leonid Hulianytskyi<sup>c</sup>, Ievgen Meniailov<sup>a</sup> and Anton Tkachenko<sup>b</sup>

<sup>a</sup> National Aerospace University "Kharkiv Aviation Institute", Chkalov str., 17, Kharkiv, Ukraine

<sup>b</sup> Kharkiv National Medical University, Nauky ave., 4, Kharkiv, Ukraine

<sup>c</sup> V.M. Glushkov Institute of Cybernetics, Kyiv, Ukraine

## Abstract

Paper presents concept model of intelligent information technology of epidemic process control. The project is an interdisciplinary research that combines scientific results obtained by specialists in the field of biosafety, systems and means of artificial intelligence, mathematical modeling, epidemiology, information technology, and public health. The development of a conceptual model provides the analysis of epidemic threats and problems of the biosafety of society; preprocessing of the initial data; development of machine learning models for analyzing the epidemic process; creation of a bank of simulation models; improvement of methods of intelligent interaction of agents of multiagent systems of population dynamics; predicting morbidity; analysis of factors influencing the epidemic process; development of information technology specification and testing of an intelligent decision support system in the field of biosafety. The implementation of the research results will increase the efficiency of management decisions to ensure the biosafety of the population and the development of scientifically based strategies for anti-epidemic and preventive measures.

## Keywords 1

Public Health, Epidemic Process, Epidemics Control, Intelligent Information Technologies, Decision Support System, Machine Learning, Simulation.

## 1. Introduction

The growth of biological threats both in the world and in Ukraine is a significant challenge for scientists, society and government [1]. The existing biological threats are primarily associated with massive outbreaks of especially dangerous infections, new and emerging infections in humans and animals [2]; activation of natural foci of zoonotic diseases, the possibility of overcoming the interspecies barrier by causative agents of animal infectious diseases [3]; the risk of using pathogens as biological weapons [4]; development of genetic engineering technologies without adequate control of their safety and proper expertise [5]; the growth of population migration, tourism [6], etc. 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 the development of the epidemic process of a certain infectious disease. Assess the leading risk factors for its occurrence and intensification. Have an adequate tool for predicting and controlling the

---

IDDM'2020: 3rd International Conference on Informatics & Data-Driven Medicine, November 19–21, 2020, Växjö, Sweden  
EMAIL: svsyak7@gmail.com (S. Yakovlev); ksenia.bazilevich@gmail.com (K. Bazilevych); dichumachenko@gmail.com (D. Chumachenko); tatalchum@gmail.com (T. Chumachenko); lh\_dar@hotmail.com (L. Hulianytskyi); evgenii.menyailov@gmail.com (I. Meniailov); antontkachenko555@gmail.com (A. Tkachenko).  
ORCID: 0000-0003-1707-843X (S. Yakovlev); 0000-0001-5332-9545 (K. Bazilevych); 0000-0003-2623-3294 (D. Chumachenko); 0000-0002-4175-2941 (T. Chumachenko); 0000-0002-1379-4132 (L. Hulianytskyi); 0000-0002-9440-8378 (I. Meniailov); 0000-0002-1029-1636 (A. Tkachenko).



© 2020 Copyright for this paper by its authors.  
Use permitted under Creative Commons License Attribution 4.0 International (CC BY 4.0).  
CEUR Workshop Proceedings (CEUR-WS.org)

spread of infections among society, creating conditions for a timely response, warning and warning of the population.

Despite the developed international documents on the system of measures in response to biological threats, including within the framework of the emergency response program [7], the existence of the International Health Regulations (IHR-2005) to protect the population from the spread of infectious diseases [8], the latest pandemic of the coronavirus infection COVID-19 showed the inconsistency of the world community to adequately respond to biological threats on a planetary scale, to resist epidemic complications and ensure the biological safety of the population. Countries of the world introduced a number of measures, which included sanitary and quarantine measures [9], large-scale restrictions on the movement of people and international passenger traffic [10], etc. to contain the spread of COVID-19. However, no country in the world was able to predict the development of the epidemic on 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.

For bioethical reasons, experiments with pathogens in the human population are impossible. At the same time, only a trial can assess the actual impact of a particular factor on the improvement or worsening of the epidemic situation. In these cases, mathematical modeling and computational experiments can come to the rescue. In public health and epidemiology, such models are used to quantify the effectiveness of various methods of disease control and prevention, such as isolation and restriction measures, vaccination and selection of contingents for immunization, identification of groups at risk of morbidity, etc. [11]. This is necessary so that health authorities can implement the most rational and effective measures to combat infections [12]. Only correctly formulated mathematical models allow one to approach a thorough study of all aspects of this problem, regardless of whether it is about epidemiological diagnostics, assessing the effectiveness of existing preventive and anti-epidemic measures [13], or measures planned by health authorities and public health services [14].

Thus, the purpose of this work is to create a conceptual model of intelligent information technology of decision-making support for the control of epidemic morbidity.

## **2. Analysis of current stage of epidemic simulation**

The effectiveness of the use of mathematical methods in the field of health care is scientifically substantiated. For example, one of the main conclusions of the general meeting of specialists from the US National Academy of Engineering and the US Institute of Medicine was the need to shape modern approaches to disease control through collaboration between engineers and epidemiologists [15]. The models and methods used to model the epidemic process, for the most part, are based on systems of integro-differential equations and the concept of using SIR (Susceptible-Infected-Recovered) states, which has many modifications for various diseases [16]. Such approaches have a number of limitations and drawbacks: modeling the dynamics of large populations requires large computing power; it is impossible to take into account the heterogeneity of the population (age, sex, profession, etc.); it is impossible to take into account the peculiarities of the territories, are being investigated; to change the modeled process, it is necessary to completely rebuild the model, etc.

The existing shortcomings do not allow the use of such models on-line, as well as taking into account the stochastic nature of the epidemic process [17], taking into account the spatial-geographical distribution and mobility of the population [18]. Thus, the existing methods for modeling epidemic processes are not structurally adaptive and do not provide an opportunity to solve with their help the problems of predicting the development of the epidemic, the need for resources, identifying red zones, etc.

Within the framework of this study, the analysis of models of epidemic processes has been done (table 1).

The first group includes models using a statistical approach [19]. These models allow us to calculate only a short-term forecast for a sufficiently large population.

The second group of approaches to the modeling of epidemic processes is based on the use of the theory of differential equations [20]. These models provide an opportunity to consider the

characteristics of the population and the environment, but still cannot be transferred to small populations.

**Table 1**

Results of analysis of epidemic processes simulation

Model	Short-term forecast	Long-term forecast	Small population	Big population	Taking into account specifics of population	Taking into account specifics of environment	Taking into account process factors	Approach
Grount-Petty [21]	+	-	-	+	-	-	-	Mortality tables
Bernoulli [22]	+	-	-	+	-	-	-	Statistical approach
Farr [23]	+	-	-	+	-	-	-	Statistical approach
Brownly [24]	+	-	-	+	-	-	-	Statistical approach
Hamer-Ross [25]	+	-	-	+	-	-	-	Differential equations (DE)
Kermak-McKendrick [26]	+	-	-	+	-	-	-	DE
Kauffman-Edlund-Douglas [27]	+	-	-	+	-	-	-	DE
Baroyan-Rvachev [28]	+	-	-	+	-	-	-	DE
Kendall [29]	+	-	-	+	-	+	-	DE
Eichner-Schwehm-Duerr-Brockmann [30]	+	-	-	+	+	+	-	DE
Reed-Frost-Greenwood [31]	+	-	+	+	-	-	-	Binomial chains
Bailey [32]	+	-	+	+	-	-	-	Cellular automata
Longini-Halorran-Nizam-Yang [33]	+	-	+	+	+	-	+	Population model
FluTE [34]	+	-	+	+	+	+	+	Population model
MIDAS [35]	+	-	+	+	+	+	-	Agent-based (AB)
De Guchi [36]	+	-	+	+	+	+	-	AB
Okhusa-Sugawara [37]	+	-	+	-	+	+	+	AB
Das-Savochkin-Zhu [38]	+	-	+	+	+	+	+	AB

The third group of models uses the discrete-event approach of population dynamics [39], allows considering the characteristics of the population, the environment and the factors of the epidemic process. However, this approach has the main disadvantage of high complexity of making changes to the model, which significantly complicates the possibility to transfer models to new areas of knowledge.

The fourth group of models uses the multiagent approach [40], which allows taking into account the features of the population, environment and factors of the epidemic process. The effective use of the multiagent approach involves the consideration of intelligent social communications of the objects of the population and expansion to other areas, what makes such kinds of model complex and decrease accuracy of simulation.

Also, recent works include modern methods of modeling and analyzing the behavior of society, however, there is still no model of the spread of the epidemic process, in which all the possibilities of the multi-agent approach would be fully realized.

### **3. Novel concept of epidemic process control**

The emergence of new pathogens and the rapid spread of new emerging diseases pose serious challenges to the world community, requiring adequate methods and means of controlling the epidemic process. On the one hand, with the rapid development of the epidemic process of dangerous diseases, epidemics pose a very significant threat to human life and health. On the other hand, the introduction of long-term quarantines and restrictive measures causes colossal economic losses, stopping the economic life of countries and continents. Therefore, decisions to control the spread of the disease require special consideration, because on the one side of the scale is the life and health of a large number of people, on the other – significant economic losses and potential impoverishment of the population.

In such conditions, the need for modeling and decision support tools based on mathematical calculations of their consequences increases. Such tools 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, etc. [41-43]. It is also necessary to take into account the various risks and uncertainties that arise when simulating such complex processes with a stochastic uncertain nature of their components. Such modeling requires the use of an appropriate mathematical apparatus, in particular, machine learning and operation research methods, fuzzy logic, etc. [44-49].

As a result of the project, 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.

The developed intelligent information technology to support decision-making in the field of biosafety will make it possible to develop a scientifically grounded basis for the implementation of effective preventive and anti-epidemic measures by the Ministry of Health of Ukraine, epidemiologists and public health specialists. The implementation 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 prophylactic institutions will ensure the adoption of effective preventive decisions, reduce the negative economic, medical and social impact on society and the state.

### **4. Methodology**

The development of models and methods for assessing the epidemic process is based on the concept of the epidemic process by L.V. Gromashevsky [50], according to which the epidemic process exists with the continuous interaction of three main components: the source of infection, the transmission mechanism and the susceptible organism, which are the primary driving forces of the epidemic process. Secondary driving forces include social and natural factors. Social factors include the quality of medical care, the availability of drugs, the organization of vaccine prevention, the

availability and equipment (capacity) of laboratories, the state of water supply and sewerage, population density, age structure of the population, public catering, etc.

Natural factors include climatic conditions and landscape zones, which determine the distribution area of animals are the main sources of infection, and carriers of infectious agents.

For different groups of infections, both natural and social factors affecting the epidemic process are different, while the leading role always belongs to the social factor, which can both inhibit the development of the epidemic process (for example, properly organized immunization), and contribute to its intensification (for example, an increase in population density in winter contributes to the spread of respiratory tract infections, the organization of new teams in preschool institutions contributes to the spread of intestinal and respiratory tract infections, an increase in the number of injecting drug users leads to the spread of HIV infection, hepatitis B and C, etc.).

Among the factors there are those that cannot be changed (for example, gender, age), but there are those that can be regulated (maintenance of water supply networks and sewerage systems, ensuring safe water supply, vaccine availability, availability of medical care, etc.). Analysis of the factors influencing the epidemic process, with the identification of those that have the greatest influence, which can be eliminated or regulated, as well as the identification of groups at increased risk of infection or severe outcomes, is important for making a rational management decision to contain or stop the development of the epidemic process.

Preparation for modeling includes a detailed system analysis and classification of epidemic threats and biosafety problems in society. The development of machine learning models requires data preparation, for which it is necessary to analyze them and organize them by data type. It is planned to use the data on the actual incidence of infectious diseases in Ukraine, obtained from the State Institution "Center for Public Health under the Ministry of Health of Ukraine" and laboratory centers in different cities and regions of the country. These data have a different structure, distribution and determinism for various diseases, which necessitates their detailed analysis, as well as the development of infrastructure, data storage and design of the architecture of the information system for epidemiological diagnostics.

To achieve high accuracy in constructing forecasts of the dynamics of epidemic processes, it is advisable to use machine learning methods. For this, the development and comparative analysis of a number of machine learning methods for forecasting time series are planned. Models of epidemic processes based on machine learning do not allow identifying factors influencing the epidemic process, however, high-precision forecasts obtained using such models will be needed at subsequent stages to assess the adequacy of multiagent models.

To identify the control effects on the dynamics of the epidemic process, it is advisable to use a multi-agent approach. But to take into account the complex nature of the population, the determinism of the population and the stochastic nature of the spread of infectious diseases, it is necessary to develop methods for the intelligent interaction of agents that are objects of multi-agent systems. To solve this problem, it is planned to use game theory, including Bayesian methods for partially observable systems, as well as fuzzy logic.

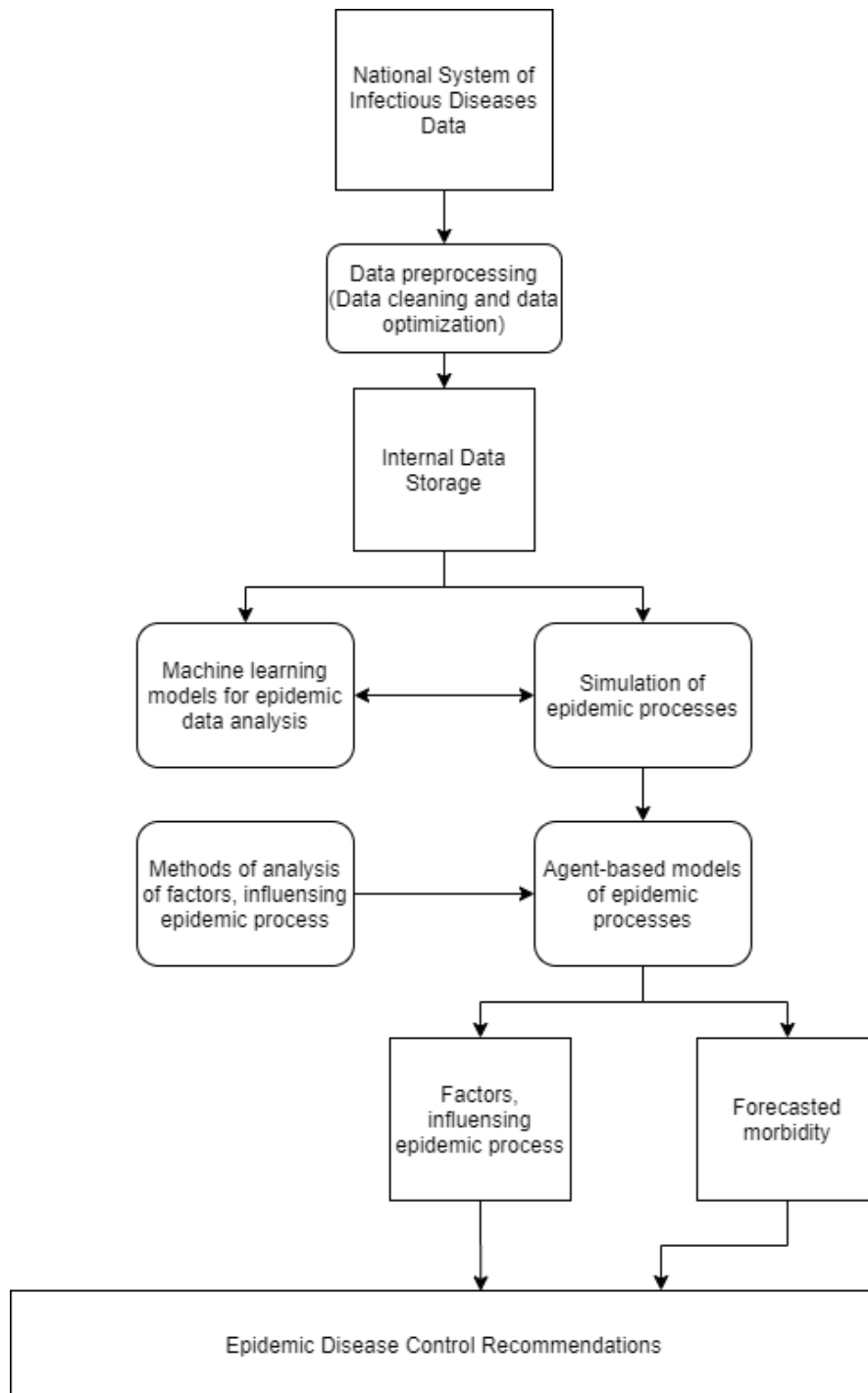
The next step will be the development of an integrated universal multiagent model of the epidemic process. The development of the model, in addition to creating the rules for the interaction of agents and the spread of the epidemic process, includes a number of major stages:

- determination of the mortality rate from infectious diseases (the information of the State Statistics Committee of Ukraine is analyzed regarding the general mortality rate, statistics in other countries, etc.);
- assessment of the number of asymptomatic infected (the correlation of testing and the number of patients in Ukraine and in other countries is analyzed, the type of tests and testing methods);
- calculation of the base reproductive number (the scenarios of the development of epidemics in different countries are compared, the changes in virulence and the rate of mutation of the pathogen are determined);
- calculation of the index of recovery (determined by statistical methods based on statistics on morbidity);
- calculation of the percentage of cases detected (determined by comparative analysis of statistical data on morbidity in Ukraine and other countries, taking into account testing methods).

Adjustment, verification and verification of the developed multiagent models for adequacy will be carried out on the basis of real statistical data on morbidity in Ukraine. With the help of the developed models, forecasts of morbidity are constructed and experimental studies are carried out, which will reveal the factors affecting the development of the epidemic process.

For convenient use of intelligent decision support technology in the field of biosafety, it is planned to implement it in the form of a web application. To be able to be used by users who do not have special mathematical training, a user-friendly interface and documentation of the software product is being developed.

The structure of intelligent information technology for the control of epidemic morbidity, as well as data flows are shown in Fig. 1.



**Figure 1:** Intelligent information system data flow diagram.

## 5. Conclusions

Thus, the conceptual model of intelligent information technology for decision-making support for the control of epidemic morbidity involves the creation of the following scientific and scientific-technical products: models and methods of machine learning for the analysis of epidemic processes; multiagent models of epidemic processes; methods of intelligent interaction of objects of multiagent systems of population dynamics with an epidemic nature; models and methods for predicting the dynamics of infectious morbidity; bank of models of dynamics of epidemic processes and methods of epidemiological diagnostics; methods for assessing the information content of factors affecting the epidemic process; methods for assessing the effectiveness of strategies for managing epidemic processes; infrastructure and architecture of epidemiological data warehouses; functional model of the decision support system in the field of biosafety; specification of an intelligent information system for decision support in the field of biosafety; intelligent information system for decision-making support in the field of biosafety; documentation of an intelligent information system for decision support in the field of biosafety.

Scientific and technical products, which will be created within the framework of the study, are a complex intelligent decision support system in the field of biosafety, which, unlike the existing ones, will make it possible to identify the factors influencing the epidemic process, quickly adapt to emerging diseases and the spread of new dangerous pathogens. Unlike the existing ones, new models of epidemic processes and methods of epidemiological diagnostics will make it possible to develop effective scientifically grounded strategies for the prevention of morbidity and countering epidemic dynamics.

The practical value of the project results consists not only of a social and medical component due to a decrease in epidemic morbidity, but also an important economic component due to the scientific justification of anti-epidemic measures, in particular restrictive and isolation measures, which will significantly reduce economic losses as a result of epidemics of infectious diseases.

The results of the study can be used to scientifically substantiate a complex of preventive and anti-epidemic measures for emergent and other infections, taking into account the current socio-economic, ecological and epidemiological situation; to create a national system for epidemiological surveillance of emerging infectious diseases that pose a threat to the biosafety of the population; to improve the efficiency of management decisions on the implementation of preventive and anti-epidemic measures; to ensure the efficiency of preventive measures by health services; to increase the level of safety of the population and the country in terms of epidemic morbidity; to reduce the economic costs of epidemic morbidity and its consequences; to improve the efficiency of management decisions regarding government policy in the field of biosafety in Ukraine; as a component (or subsystem) of the biosafety system of Ukraine.

## 6. Acknowledgements

The study was funded by the National Research Foundation of Ukraine in the framework of the research project 2020.02/0404 on the topic “Development of intelligent technologies for assessing the epidemic situation to support decision-making in the population biosafety management”.

## 7. References

- [1] V.K. Singh, et. al., Medical countermeasures for unwanted CBRN exposures: Part I chemical and biological threats with review of recent countermeasure patents, *Expert Opinion on Therapeutic Patents* 26 (12) (2016) 1431-1447. doi:10.1080/13543776.2017.1233178
- [2] D.M. Morens, A.S. Fauci, Emerging Pandemic Diseases: How We Got to COVID-19, *Cell* 182 (5) (2020) 1077-1092.

- [3] S. Madison-Antenucci, et. al., Emerging Tick-Borne Diseases, *Clinical Microbiological Review* 33 (2) (2020) e00083-18. doi:10.1128/CMR.00083-18
- [4] R.A. Zilinskas, A brief history of biological weapons programmes and the use of animal pathogens as biological warfare agents, *Revue scientifique et technique* 36 (2) (2017) 415-422. doi:10.20506/rst.36.2.2662
- [5] D.H.M. Steffin, E.M. Hsieh, R.H. Rouse, Gene Therapy: Current Applications and Future Possibilities, *Advances in pediatrics* 66 (2019) 37-54.
- [6] M.Z. Hossin, International migration and health: it is time to go beyond conventional theoretical frameworks, *BMJ Global Health* 5 (2) (2020) e001938.
- [7] D.A. Rose, S. Murthy, J. Brooks, J. Bryant, The Evolution of Public Health Emergency Management as a Field of Practice, *American Journal of Public Health* 107 (S2) (2017) S126-S133.
- [8] International Health Regulations, Third edition, World Health Organization, (2005), 75.
- [9] H. Lau, et al. The positive impact of lockdown in Wuhan on containing the COVID-19 outbreak in China, *Journal of Travel Medicine* 27 (3) (2020) taaa037.
- [10] M. Sigala, Tourism and COVID-19: Impacts and implications for advancing and resetting industry and research, *Journal of Business Research* 117 (2020) 312-321.
- [11] D. Chumachenko, et. al., Development of an intelligent agent-based model of the epidemic process of syphilis, in *IEEE 2019 14th International Scientific and Technical Conference on Computer Sciences and Information Technologies, CSIT 2019 – Proceedings, Lviv, Ukraine* (2019) 42-45. doi:10.1109/STC-CSIT.2019.8929749
- [12] N. Dotsenko, et. al., Project-oriented management of adaptive teams' formation resources in multi-project environment, *CEUR Workshop Proceedings* 2353 (2019) 911-920.
- [13] G. Giordano, et al., Modelling the COVID-19 epidemic and implementation of population-wide interventions in Italy, *Nature Medicine* 26 (6) (2020) 855-860.
- [14] Y. Fang, Y. Nie, M. Penny, Transmission dynamics of the COVID-19 outbreak and effectiveness of government interventions: A data-driven analysis, *Journal of Medical Virology* 92 (6) (2020) 645-659.
- [15] S. Ratner, M. Pignone, Quality Improvement Principles and Practice, *Primary Care* 46 (4) (2019) 505-514. doi:10.1016/j.pop.2019.07.008
- [16] S.H. Paeng, J. Lee, Continuous and discrete SIR-models with spatial distributions, *Journal of Mathematical Biology* 74 (7) (2017) 1709-1727. doi:10.1007/s00285-016-1071-8
- [17] J. Yan, S. Guha, P. Hariharan, M. Myers, Modeling the Effectiveness of Respiratory Protective Devices in Reducing Influenza Outbreak, *Risk analysis: an official publication of the Society for Risk Analysis* 39 (3) (2019) 647-661.
- [18] S. Sabesan, et al. Lymphatic filariasis transmission risk map of India, based on a geo-environmental risk model, *Vector Borne Zoonotic Diseases* 13 (9) (2013) 657-665.
- [19] K. Omata, Nonequilibrium statistical mechanics of a susceptible-infected-recovered epidemic model, *Physical Review E* 96 (2-1) (2017) 022404. doi:10.1103/PhysRevE.96.022404
- [20] R. Brinks, A. Hoyer, Illness-death model: statistical perspective and differential equations, *Lifetime Data Analysis* 24 (4) (2018) 743-754.
- [21] C.T. Urabe, G. Tanaka, K. Aihara, M. Mimura, Parameter Scaling for Epidemic Size in a Spatial Epidemic Model with Mobile Individuals, *PLoS ONE* 11 (12) (2016) e0168127. doi:10.1371/journal.pone.0168127
- [22] K. Dietz, J.A.P. Heesterbeek, Daniel Bernoulli's epidemiological model revisited, *Mathematical Biosciences* 180 (2002) 1-21.
- [23] M. Santillana, et al. Relatedness of the incidence decay with exponential adjustment (IDEA) model, "Farr's law" and SIR compartmental difference equation models, *Infectious Disease Modelling* 3 (2018) 1-12.
- [24] P.E.M. Fine, John Brownlee and the Measurement of Infectiousness: An Historical Study in Epidemic Theory, *Journal of the Royal Statistical Society. Series A (General)* 142 (3) (1979) 347-362. doi:10.2307/2982487
- [25] D.L. Smith, et al. Ross, Macdonald, and a Theory for the Dynamics and Control of Mosquito-Transmitted Pathogens, *PLoS Pathog* 8 (4) (2012) e1002588.



- [26] F. Brauer, The Kermack–McKendrick epidemic model revisited, *Mathematical Biosciences* 198 (2) (2005) 119-131.
- [27] J.V. Douglas, et al. STEM: An Open Source Tool for Disease Modeling, *Health Security* 17 (4) (2019) 291-306. doi:10.1089/hs.2019.0018
- [28] O. Baroyan, L. Rvachev, et al., Computer Modelling of Influenza Epidemics for the Whole Country (USSR), *Advances in Applied Probability* 3 (2) (1971) 224-226. doi:10.2307/1426167
- [29] D.G. Kendall, Deterministic and Stochastic Epidemics in Closed Populations, in *Proceedings of the Third Berkeley Symposium on Mathematical Statistics and Probability, Vol. 4: Contributions to Biology and Problems of Health* (1956) 149-165.
- [30] M. Eichner, M. Schwehm, H.P. Duerr, S.O. Brockmann, The influenza pandemic preparedness planning tool Influsim, *BMC Infectious Disease* 7 (2007) 17. doi:10.1186/1471-2334-7-17
- [31] N. Becker, A General Chain Binomial Model for Infectious Diseases, *Biometrics* 37 (2) (1981) 251-258. doi:10.2307/2530415
- [32] N.T.J. Bailey, The simulation of stochastic epidemics in two dimensions, in *Proceedings of the Fifth Berkeley Symposium on Mathematical Statistics and Probability, Volume 4: Biology and Problems of Health* (1967) 237-257.
- [33] I.M. Longini Jr, et al., Containing a large bioterrorist smallpox attack: a computer simulation approach, *International Journal of Infectious Disease* 11 (2) (2007) 98-108.
- [34] D.L. Chao, et al. FluTE, a Publicly Available Stochastic Influenza Epidemic Simulation Model, *PLoS Computational Biology* 6 (1) (2010) e1000656.
- [35] P.C. Cooley, et al., The model repository of the models of infectious disease agent study, in *IEEE transactions on information technology in biomedicine: a publication of the IEEE Engineering in Medicine and Biology Society* 12 (4) (2008) 513-22.
- [36] D.M. Nguyen, H. Deguchi, M. Ichikawa, Agent- based simulation on avian influenza in Vietnam: Basic characteristics of the epidemic and efficiency evaluation of control measures, 2010 7th International Conference on Service Systems and Service Management, *Proceedings of ICSSSM' 10* (2010) 349-354. doi:10.1109/ICSSSM.2010.5530215
- [37] Y. Ohkusa, T. Sugawara, K. Taniguchi, N. Okabe, Real-time estimation and prediction for pandemic A/H1N1(2009) in Japan, *Journal of infection and chemotherapy: official journal of the Japan Society of Chemotherapy* 17 (2011) 468-72. 10.1007/s10156-010-0200-3.
- [38] G. Zhu, X. Fu, G. Chen, Global attractivity of a network-based epidemic SIS model with nonlinear infectivity, *Communications in Nonlinear Science and Numerical Simulation* (2012) 17.
- [39] D. Chumachenko, et. al. On-Line Data Processing, Simulation and Forecasting of the Coronavirus Disease (COVID-19) Propagation in Ukraine Based on Machine Learning Approach, *Communications in Computer and Information Science* 1158 (2020) 372-382.
- [40] N. Hoertel, et al. A stochastic agent-based model of the SARS-CoV-2 epidemic in France, *Nature Medicine* 26 (2020) 1417–1421. doi:10.1038/s41591-020-1001-6
- [41] L.F. Laker, et al., Understanding Emergency Care Delivery Through Computer Simulation Modeling, *Academic emergency medicine: official journal of the Society for Academic Emergency Medicine* 25 (2) (2018) 116–127.
- [42] D. Chumachenko, K. Chumachenko, S. Yakovlev Intelligent simulation of network worm propagation using the code red as an example, *Telecommunications and Radio Engineering* 78 (5) (2019) 443-464.
- [43] V.K. Nguyen, R. Mikolajczyk, E.A. Hernandez-Vargas, High-resolution epidemic simulation using within-host infection and contact data, *BMC public health* 18 (1) (2018) 886.
- [44] L. Williams, et al. Protection motivation theory and social distancing behaviour in response to a simulated infectious disease epidemic, *Psychology, health & medicine* 20 (7) (2015) 832–837.
- [45] D. Chumachenko, et al., On Intelligent Decision Making in Multiagent Systems in Conditions of Uncertainty, in *2019 11th International Scientific and Practical Conference on Electronics and Information Technologies, Lviv, Ukraine, (2019) 150-154. doi:10.1109/ELIT.2019.8892307*
- [46] V.P. Mashtalir, et al. Group structures on quotient sets in classification problems, *Cybernetics and Systems Analysis* 50 (4) (2014) 507-518.

- [47] L.F.Hulianytskyi, I.I. Riasna, Automatic Classification Method Based on a Fuzzy Similarity Relation. *Cybernetics and Systems Analysis* 52(1) (2016), 30-37 doi:10.1007/s10559-016-9796-3
- [48] L.F.Hulianytskyi, V.O..Rudyk, Protein structure prediction problem: Formalization using quaternions. *Cybernetics and Systems Analysis* 49(4) (2013) 597-602 doi:10.1007/s10559-013-9546-8
- [49] V.P. Mashtalir, S.V. Yakovlev, Point-set methods of clusterization of standard information. *Cybernetics and Systems Analysis* 37(3) (2001) 295-307. doi:10.1023/A:1011985908177
- [50] B.L. Cherkasskiĭ, Doctrine of the transmission of the causative agents of infections and social and ecologic concepts of the epidemic process, *Zhurnal mikrobiologii, epidemiologii i immunobiologii* 5 (2003) 54–58.