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Agent-Based Epidemic Models: International Trends and Implementation in Russian Practice



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Abstract. The article presents an analysis of developments in the modeling of epidemiological processes, primarily conducted using a modern mapping the scientific research landscape. The authors identify the world's leading research centers and groups that have been actively working in this field in recent years, as well as the key approaches used in modeling epidemiological processes that have been tested in practice and proven their adequacy. It is noted that alongside classical compartmental models, which describe epidemiological dynamics as the transition of a population segment from one category (associated with a specific stage of an infectious disease) to another, agent-based models are becoming increasingly widespread. These models simulate the processes of person-to-person infection transmission. The advantages of the agent-based approach include the ability to reproduce population heterogeneity within an artificial society, which significantly influences infection spread processes, and to simulate direct and feedback loops between various processes, including the agents' capacity to adapt their behavior based on the current epidemiological situation. The paper presents the concept of an agent-based epidemiological model for Russia, designed for testing and evaluating the effectiveness of planned anti-epidemic measures. The concept involves simulating the spread of an epidemic through agent interactions: the population of agents replicates the real socio-demographic structure of the population, accounting for all individual characteristics that influence people's involvement in infection spread, including their social connections, spatial distribution, and regional specifics; the progression of each agent through all stages of the disease is simulated according to the features of the infectious disease causing the epidemic; a realistic picture of population movement across Russia's transport infrastructure is reproduced, represented as a graph where vertices are transport hubs and edges are the connecting routes.

Key words: epidemic modeling, scientific landscape, agent-based models, recreation of social and spatial structure in an artificial society, behavior, virus transmission, computational experiments on social process models, intelligent decision support information technologies.

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Introduction

Contemporary challenges associated with globalization, urbanization, and the constant variability of pathogens spreading within human communities require fundamentally new approaches to forecasting epidemics. Under these conditions, at the national level, a modern toolkit is needed for modeling pandemic scenarios that accounts for population mobility. This toolkit should enable forecasting the dynamics of the healthcare system's load and allow for preliminary assessment of the effectiveness of planned containment measures (e.g., quarantine, vaccination, etc.) through computer experiments.

When developing such a toolkit, it is essential to consider the achievements of global leaders in creating infection spread models, as well as the most successful examples of the practical application of modern approaches in this field to reduce the scale of epidemic outbreaks and associated negative social and economic consequences.

The aim of our research is to develop a modern toolkit for practical use within a decision support system in the context of potential new global biological threats, taking into account advanced experience and global trends in creating epidemiological models. The research objectives are:

identifying modern approaches and models, using scientific landscape mapping methods, applied in modeling epidemiological processes; determining global centers, research groups, and leading specialists in the field of epidemic modeling; designing a model based on the identified most promising epidemic modeling methods, which will ensure flexible adaptation to various (both existing and new) types of infections, transparency regarding the influence of the model's control parameters on the simulation results; and user-friendly setup of model experiments.

In both international and domestic practice, mathematical modeling methods are widely used for forecasting the spread of viral epidemics and assessing their consequences, taking into account spatial and temporal relationships. These methods are constantly being improved and developed. The main challenges facing developers of large-scale infection spread models are primarily related to selecting an adequate mathematical framework that allows for the incorporation of numerous heterogeneous factors. These factors influence both the speed of infection spread and the severity of the disease for individuals, as well as the social and socio-economic consequences of the epidemic for society as a whole and its specific groups. To achieve this, modeling must account for population heterogeneity based on age, social, and geographical differences, as well as the specifics of virus transmission in various environments (households, transport, workplaces). A separate set of problems that developers must address involves providing the model with the informational base necessary for its debugging, verification, and calibration, given that complete empirical data might be unavailable for various reasons. Finally, creating software to implement the developed mathematical model is a complex technical task. Scaling it to the level of a country, macro-regions consisting of multiple countries, or even the global level requires not only solving problems of integrating regional data

but also optimizing computational algorithms, including transitioning to parallel computing using supercomputers.

Solving such an interdisciplinary set of theoretical and practical tasks typically occurs within the framework of large scientific centers and/or large scientific projects, which define the main current trends in the field of modeling epidemiological processes. An understanding of these trends can be obtained using methods for mapping the scientific research landscape.

Building and analyzing the scientific landscape in the field of epidemiological process modeling

The process of collecting scientific and technical documents on the topic of "Infection spread modeling" was carried out in several stages. In the first stage, a set of key vocabulary in Russian and English was formed to create search queries. To compile this set of key terms, a semantic search of scientific and technical documents was conducted based on the titles and key words of the analyzed epidemiological models and methods for modeling human-to-human infection spread. Subsequently, lists of key vocabulary were built from the relevant documents found in the databases.

In the second stage, the authors of the study identified databases suitable for analysis under current conditions of restricted access to international publication databases like Web of Science and Scopus for Russian scientific organizations. All accessible publication databases were analyzed, considering characteristics such as the availability of full-text collections of foreign open-access medical journals and journals in the field of "computer science" research, sets of filters for forming database queries, limitations on the number of rows when exporting search results, and specific features of the formats for downloading the found data.

In the third stage, the search query was formulated based on the identified key vocabulary. Within the document collections, two types of scientific and technical documents were considered:

scientific articles and scientific reviews. The obtained sample was expertly checked for the relevance of the article titles, key words, and abstracts.

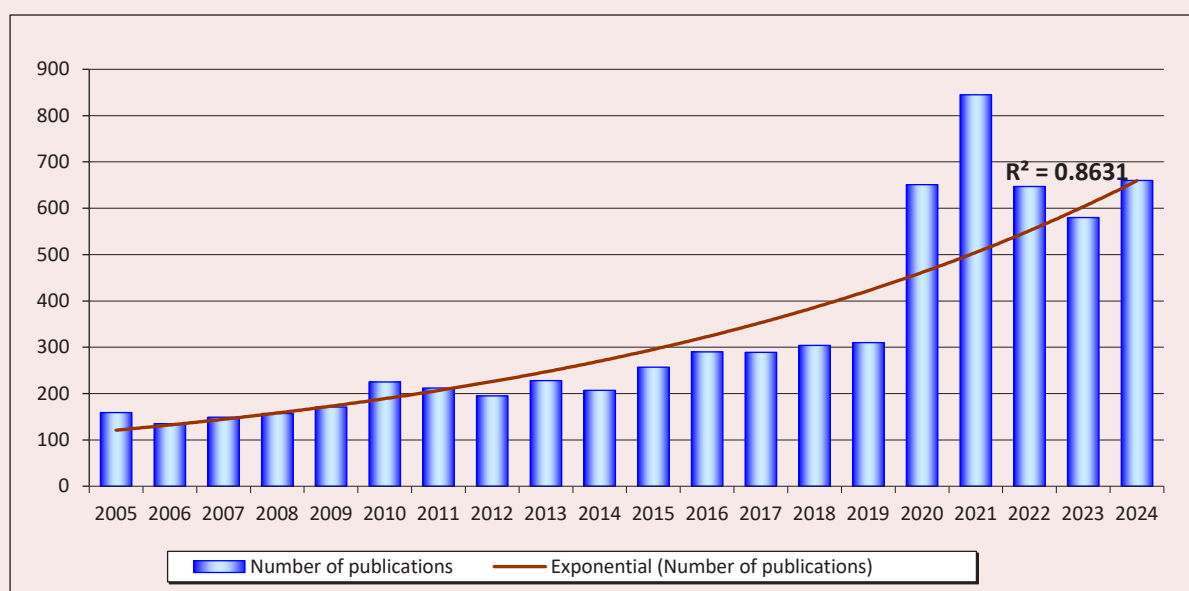
For scientific articles and reviews, the authors used The Lens publication database¹, the flagship project of the social enterprise Cambia, built on the open web platform Lens.org and comprising 272 million scientific publications of various types, as well as global public resources such as PubMed, Microsoft Academic, CrossRef, ORCID, OpenAlex, and others.

When forming the search query, after numerous test runs of the sample of scientific and technical documents, the following combination was determined: epidemic, model, agent, virus, transmission, which allowed for the selection of a manageable number of relevant scientific documents. The research period covered 2005–2024.

As a result of applying the methodology described above, the authors of the study formed an information base of documents in English on the topic of “Infection spread modeling,” which included 7,021 scientific and technical documents, comprising 6,997 scientific articles and 24 scientific reviews. The information base in Russian included collections of open full-text documents from Russian scientific journals, including those on medical topics, formed using the Russian intellectual digital platform for aggregating and analyzing scientific and technical information, SciApp² (used to identify the scientific groundwork of leading organizations in the field of epidemiological modeling, taking into account actually created models).

During the study period, a growth close to exponential is observed in the number of publications related to methods and models of epidemiological modeling, indicating increasing

Figure 1. Dynamics of publication activity on the topic of “epidemic modeling” for 2005–2024, number of publications



Compiled from: The Lens publication database data, data current as of July 15, 2025.

¹ The Lens. Available at: <https://www.lens.org> (accessed: 17.07.2025).

² An intelligent digital platform for the aggregation and analysis of scientific and technical information. Available at: <https://sciapp.ru> (accessed: 17.07.2025).

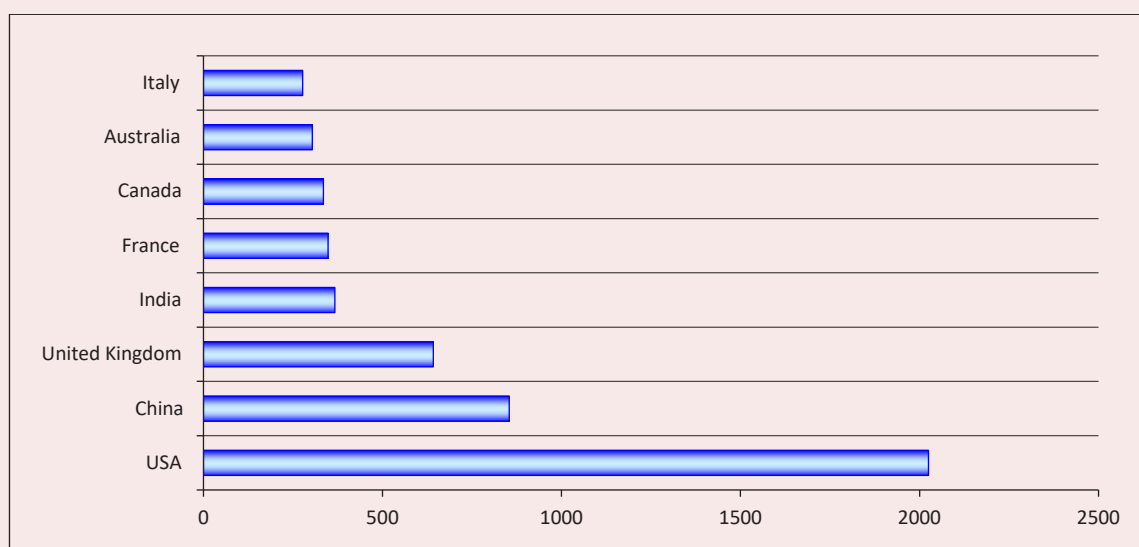
interest from the global scientific community in studying this research topic. *Figure 1* clearly shows a surge in publication activity in 2020–2021, associated with the COVID-19 pandemic. Furthermore, methods for modeling epidemics and their consequences continue to be constantly refined and developed, which explains the significant number of publications on the topic in 2023–2025.

To identify the countries where the most active research on epidemic modeling is conducted, the authors analyzed the structure and compared the volumes of national publication portfolios for 2005–2025. According to the conducted analysis, the combined contribution of countries such as the USA, the UK, China, France, Germany, India, Italy, Canada, and Australia amounted to over 73% of the global publication volume. Among these, the USA demonstrates the highest level of publication activity and the largest contribution to the study of this topic (29% of the global publication volume; *Fig. 2*).

An analysis of author affiliations with global centers of competence revealed the leading universities and research centers in the USA, China, the UK, and France that are flagships in terms of the number of publications in the field of infection spread modeling: National Institutes of Health, USA; Centers of Disease Control and Prevention, USA; Harvard University, USA; Chinese Academy of Science, China; French Institute of Health and Medical Research, France; Johns Hopkins University, USA; University of Oxford, UK; Imperial College London, UK; University of London, UK; University of Washington, USA. The results of the publication activity analysis for the identified organizations are presented in *Figure 3*.

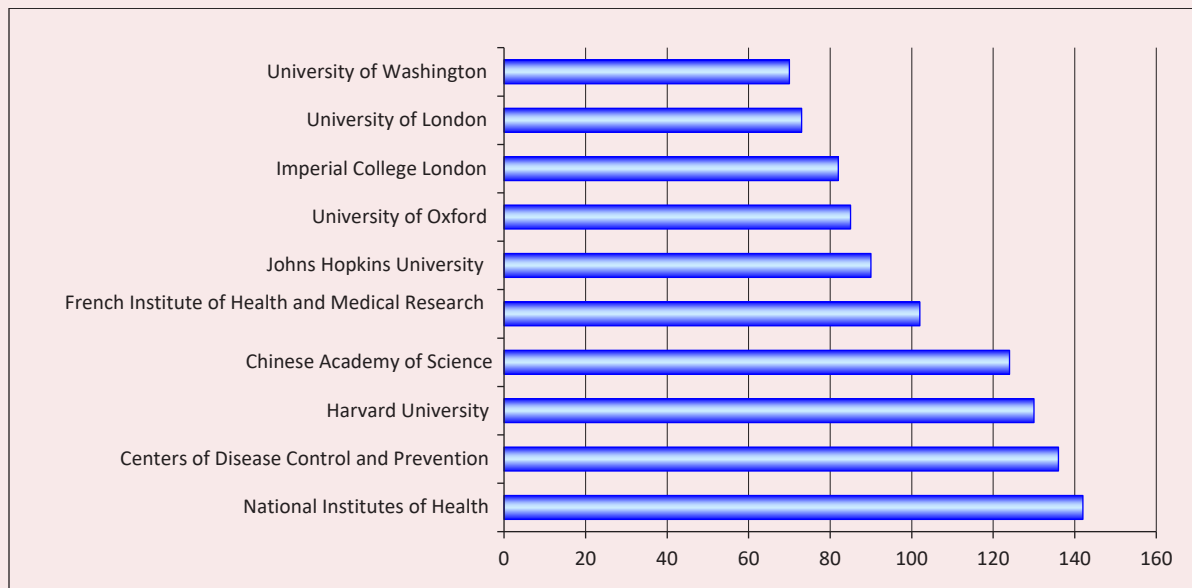
The analysis showed that a substantial proportion of highly cited publications on epidemic modeling (especially concerning the COVID-19 pandemic) include a significant number of authors (11–83 people), and the number of author affiliations can reach up to 49, as seen, for example, in the article (Howerton et al., 2023) published in the prestigious journal “Nature Communications”.

Figure 2. Volume of national publication portfolios of leading countries in epidemic modeling research for 2005–2025, number of publications



Compiled from: The Lens publication database data, data current as of July 15, 2025.

Figure 3. Top 10 leading organizations by number of publications on epidemic modeling for 2005–2025, number of publications



Compiled from: The Lens publication database data, data current as of July 15, 2025.

A clearly discernible increased interest in applying the agent-based approach to designing models for the spread of various viruses is evident starting from 2009, for example, for the Dengue virus (Kang, Aldstadt, 2019); the Measles virus (Perez, Dragicevic, 2009); and the COVID-19 virus (Silva et al., 2020; Truszkowska et al., 2021; Zhu et al., 2024).

The prospects of using computer modeling capabilities for forecasting the spread of infections are discussed in leading global science journals from the “Nature” publishing group (Syrowatka et al., 2021).

Publications by Russian authors are also represented in the obtained article sample, indicating the integration of this research direction into Russia’s national research agenda. Within the sample with Russian affiliation from The Lens database, a joint article “Agent-based modeling of COVID-19 outbreaks in New York state and the United Kingdom: parameter identification algorithm” (Krivorotko et al., 2022) by Russian

researchers from the Institute of Computational Mathematics and Mathematical Geophysics of the Siberian Branch of the Russian Academy of Sciences and Novosibirsk State University, in collaboration with scientists from the USA and the UK, stands out with the highest citation level. In this article, the authors used the Covasim agent-based model to assess and develop epidemic spread scenarios.

To identify Russian research teams with competencies in this thematic area, in addition to the body of domestic works indexed in The Lens, data from the Russian Science Citation Index (RSCI) and a database of Russian medical journals (678 scientific articles) were additionally considered, using SciApp, the Russian intellectual digital platform for aggregating and analyzing scientific and technical information.

Based on the analysis of publications in foreign and Russian journals using the method of author affiliations, considering contextual search of full-text publications and key words for the period

2005–2025, we identified the main research centers that develop infection spread models. For a detailed examination of such experience, taking into account the characteristics of infection spread in Russia, a fairly wide range of domestic research teams was identified. Taking into account a comprehensive analysis of the relevance of the contextual search results, the citation level of articles and journals, and the quality of the models, we singled out three foreign and five Russian research groups.

As a result, the leading organizations in the field of epidemic modeling, leading researchers, and the most interesting works were identified:

1) Imperial College London (UK), Neil Ferguson, agent-based modeling methods (Ferguson et al., 2006; Kraemer et al., 2025);

2) Johns Hopkins University (USA), Joshua M. Epstein, agent-based modeling methods (Parker, Epstein, 2011; McCabe et al., 2021; Bedson et al., 2021; Epstein, 2023);

3) University of Oxford (UK), Christophe Fraser, agent-based modeling methods, OpenABM-Covid19 project (Pellis et al., 2020; Hinch et al., 2021; Ferretti et al., 2024).

Among Russian organizations, the leaders in the field of epidemiological modeling, considering actually created human-to-human virus transmission models, are:

1) Institute for Information Transmission Problems of the Russian Academy of Sciences (IITP RAS) and Skolkovo Institute of Science and Technology (Skoltech), G.A. Bazykin, methods of genomic epidemiology (Komissarov et al., 2021; Matsvay et al., 2023);

2) Russian Federal Nuclear Center – All-Russian Research Institute of Technical Physics (RFNC-VNIITF), V.V. Vlasov, O.V. Zatsypin, S.N. Lebedev, agent-based modeling methods (Vlasov et al., 2023; Taranik et al., 2023);

3) Central Economics and Mathematics Institute of the Russian Academy of Sciences (CEMI RAS), A.R. Bakhtizin, V.L. Makarov,

E.D. Sushko, agent-based modeling methods (Makarov et al., 2020);

4) Institute of Computational Mathematics and Mathematical Geophysics of the Siberian Branch of the Russian Academy of Sciences and Novosibirsk State University, O.I. Krivorotko, S.N. Kabanikhin, agent-based modeling methods (Krivorotko et al., 2022; Krivorotko, Kabanikhin, 2024);

5) Keldysh Institute of Applied Mathematics of the Russian Academy of Sciences and Institute of Applied Physics of the Russian Academy of Sciences (IAP RAS), V.I. Baluta, V.P. Osipov, agent-based modeling methods (Baluta et al., 2020; Baluta et al., 2022).

As noted above, recent years have seen increased interest in applying the agent-based approach when designing models for the spread of various viruses. Let us consider the advantages of this approach that contribute to its growing popularity.

Analysis of the application of the agent-based approach in modeling epidemiological processes

In classical compartmental epidemiological models, based on the SIR model (Susceptible – Infected – Recovered) by A. McKendrick and W. Kermack (Kermack, McKendrick, 1927), where the population is divided into corresponding groups (“susceptible”, “infected,” and “recovered”), the mathematical apparatus of differential equations is used to describe how these groups change. This implies population homogeneity regarding its participation in the spread of epidemics. To account for the real existing population heterogeneity and increase the realism of these models (and the estimates of epidemiological process development obtained with their help), developers of practically used models are forced to divide the population into groups (for example, by age categories) (Noll et al., 2020). Unlike classical models, in agent-based epidemiological models (ABM), the processes of epidemic development are simulated “from the bottom up” by simulating the movement of

individuals in an artificial society, their contacts with sick people, infection, and the subsequent course of the disease in those who fall ill as a change of states over time. Thus, the agent-based approach allows for the creation of adequate models of epidemiological processes, relying on expert knowledge about the progression of a particular disease and its modes of transmission, even in the absence of reliable data on the dynamics of the state of society as a whole. This was observed, for example, during epidemics caused by the spread of a new infection, particularly during the COVID-19 pandemic.

Time in ABM is discrete, and the simulation of changes occurring with each human agent is carried out in stages (step-by-step), where the step duration corresponds to the chosen unit of model time. At the end of a simulation step, changes in agent states are recorded, and statistics are collected for the population of agents, similar to how it is done in real life. This reflects the dynamics of epidemiological indicators at the level of the entire population and at the level of its individual groups. This approach allows for the natural incorporation of all aspects of population differentiation into groups based on any combination of properties affecting epidemiological processes, up to and including accounting for individual characteristics of specific people.

Due to the advantages of the agent-based approach, its growing popularity in modeling many processes that are formed at the individual level – such as, for example, natural population movement, migration, and the spread of infection – is natural. Therefore, the number of epidemiological ABMs and their representing publications has recently been growing exponentially, with the COVID-19 pandemic causing a particularly vigorous surge. Simultaneously, the number of publications dedicated to reviewing these models, their design features, and application areas is increasing. Thus, the work (Hunter et al., 2017) lists the main constructive blocks that should be implemented in

an ABM to simulate the development of epidemics (possibly with varying degrees of detail):

- simulation of infection transmission and the progression through stages of the disease caused by the infection in agents;
- simulation of the population of agents (society), including recreating the structure of this society;
- simulation of agent movement in space, considering the transport component;
- simulation of the environment as the space for agent interaction.

Among the most successful review works, the publication in the leading journal on modeling artificial societies – “Journal of Artificial Societies and Social Simulation (JASSS)” (Lorig et al., 2021) – should be primarily noted. It presents a large-scale and detailed study of 126 agent-based models dedicated to the COVID-19 epidemic and published during the height of the pandemic. A strength of the sample of these models is that they were filtered by specialists from over 500 ABMs found by the search engine COVIDScholar.org, which model the spread of infection through agent interaction (the search query included the words “simulation”, “agent”, and “transmission”). The selection considered both the quality of the models themselves and the quality of their presentation according to the following criteria:

- works are published in a journal or conference proceedings, or are available as a preprint in a recognized archive (e.g., PubMed³, arXiv⁴, medRxiv⁵);
- the work uses the Agent-based Social Simulation (ABSS) approach, allowing for the

³ PubMed® contains over 38 million links to biomedical literature from MEDLINE, natural sciences journals, and online books (available at: <https://pubmed.ncbi.nlm.nih.gov>).

⁴ arXiv – is an electronic archive with open access to scientific articles and preprints in physics, mathematics, astronomy, computer science, biology, electrical engineering, statistics, financial mathematics and economics (available at: <https://arxiv.org>).

⁵ medRxiv – is an archive of free distributed articles in the field of medicine and clinical research (available at: <https://www.medrxiv.org>).

investigation of COVID-19 spread, meaning it is a micro-level model where the identity and status of each person can be tracked throughout the entire simulation period;

- the work describes the implemented mechanisms for simulating infection transmission processes and disease progression.

At the same time, the sample was significantly limited by conditions that prevent it from being considered fully representative in terms of assessing the participation of scientific centers from different countries in the development of this field. This is because only works published in English and only before October 1, 2020, were considered. The latter circumstance also affects the representativeness of the model sample, which is related to the labor-intensive nature of developing agent-based models. In practice, primarily scientific teams that already possessed previously developed epidemiological ABMs, which could be adapted to the characteristics of the new epidemic, were able to create such models, test them, and, moreover, publish the results within such tight deadlines. However, this very circumstance ensured a sufficiently high quality of the models selected for the review, although there is at least one regrettable exception: the ABM developed under the guidance of epidemiologist and professor of mathematical biology from Imperial College London, Neil Ferguson (Ferguson et al., 2020), which was subsequently subjected to severe criticism by specialists⁶. However, the criticism mainly related to the software implementation of the model and the resulting overestimated assessments of the epidemic's consequences⁷, rather

than the substantive part of the problem statement, which in Ferguson's model is quite realistic. Despite the limitations of the ABM sample, we, like the authors of the work (Lorig et al., 2021), believe that this study provides a general overview of existing approaches to modeling epidemiological processes through the simulation of social interactions.

The presented study examined in detail the purpose of each model, the managed parameters (including pharmaceutical and non-pharmaceutical intervention measures), input and output data, mechanisms for simulating infection transmission from agent to agent, mechanisms for simulating state changes (disease stages) of an infected agent, etc. – a total of 72 attributes were identified and analyzed for each model. This allowed for the classification of the sample models from the perspective of approaches to implementing the main blocks of epidemiological ABMs listed above.

The common goal of all models in the sample was to assess the spread of COVID-19 over time and the impact of implemented intervention measures on this process. At the same time, the vast majority of models considered one or two types of non-pharmaceutical interventions (119.9%), which included quarantine (in 60% of articles), isolation of (potentially) infected individuals (47.6%), social distancing (44.4%), and the closure of various facilities such as schools, workplaces, recreational venues, and shops (in 25% of articles, the closure of at least one type of such facilities is analyzed).

Let us consider the classification of ABMs in the sample from the perspective of the methods for implementing the main constructive blocks within them.

1. Simulation of infection transmission and disease progression stages in agents.

In agent-based modeling, probabilities are used to simulate agent infection. In 29.4% of the models in the sample, either a single probability, equal for all people and contacts, is used, or this mechanism is not described. In the remaining models, the

⁶ Magness P. The failure of imperial college modeling is far worse than we knew. Available at: <https://thedailyeconomy.org/article/the-failure-of-imperial-college-modeling-is-far-worse-than-we-knew/>.

⁷ Chalmers V., May L. Computer code for Prof Lockdown's model which predicted 500,000 would die from Covid-19 and inspired Britain's 'Stay Home' plan is a 'mess which would get you fired in private industry' say data experts. Available at: <https://www.dailymail.co.uk/news/article-8327641/Coronavirus-modelling-Professor-Neil-Ferguson-branded-mess-experts.html>.

calculation of individual probabilities of infection transmission may consider personal characteristics or circumstances such as the health status of the recipient (27%), their age (17.5%), population density (13.5%), and others. Furthermore, most models simulate people's social connections or gathering places to model interactions between them.

To simulate disease progression at the agent level, the transition of each agent from one state related to the infection in question to another is modeled. In the vast majority of models, the list of states corresponds to the classical SIR model. However, various extensions of the classical model with additional states are also encountered, allowing for a more detailed representation of disease development. For example, 63.5% of models account for an incubation period after contact with the virus (stage E – Exposed); 23% of models account for a critical state of ill patients requiring treatment in a hospital or intensive care unit (C – Critical ill); and 40.5% of models include a separate state for deceased individuals (D – Dead).

2. Simulation of the agent population (society), including recreating the structure of this society.

In 43.7% of the models in the sample, real statistical data are used to create an artificial society whose socio-demographic characteristics correspond to the characteristics of the population of the modeled region or country.

To make the agent population more realistic, models most often assign the following individual characteristics to agents: age or age group (44.4%); household affiliation (42.1%); workplace (35.7%); current location of the person (35.7%). Some models define specific sets of other people with whom an agent can or will have contacts (39.7%), sometimes subdivided into contacts at home, at work, or chance encounters.

Approaches to modeling agent behavior vary significantly – ranging from homogeneous models of reactive behavior based on rules, to complex

decision-making processes based on individual needs or the perceived utility of possible actions (Russell, Norvig, 2020), although such complex models constitute less than 5% of the sample. In most models (75.4%), individual behavior is modeled using either social networks (37.3%), spatial networks (16.7%), or both (7.1%), meaning agents can only infect other people when meeting within the framework of social relationships.

Another element of agent behavior is their compliance or non-compliance with various intervention measures – both pharmaceutical and non-pharmaceutical. In most simulations, it is assumed that all people without exception will comply with any given control measure.

It is also worth noting successful later developments dedicated to the COVID-19 pandemic that were not included in the reviewed analysis. For instance, the publication (Kerr et al., 2021) details the aforementioned Covasim ABM, which includes demographic information on age structure and population size, realistic transmission networks within various social groups (households, schools, workplaces, etc.), age-specific disease progression characteristics, and the dynamics of the virus within the body, including susceptibility to infection depending on viral load. Covasim also supports a wide range of measures: non-pharmaceutical, such as physical distancing and the use of protective equipment; pharmaceutical measures, including vaccination; as well as testing (symptomatic and asymptomatic), isolation, contact tracing, and quarantine. The work (Zhang et al., 2025) is interesting for us because it presents a simulation of the connection between the epidemiological situation, individual risk assessment by people, and the level of human interaction activity. In this model, human agents can change their decisions about movement within a densely populated city based on perceived risks associated with the probability of infection or death.

Among domestic developments, the most interesting for us are those mentioned above (Vlasov et al., 2023; Taranik et al., 2023) and (Baluta et al., 2022).

Analysis of author experience in the general context of agent-based modeling of epidemiological processes

The authors of the present study also have experience in developing an agent-based epidemiological model, using the development of the COVID-19 epidemic in Moscow as an example (Makarov et al., 2020). The goal of the modeling was to create a tool for forecasting the epidemiological dynamics in the city depending on quarantine measures, with an assessment of peak loads on the healthcare system, based on a plausible simulation of the processes of individual people becoming infected and progressing through disease stages. For the further development of this direction, it was important to compare our approach with the identified trends in the development of agent-based modeling as applied to epidemiological processes in general and to the COVID-19 pandemic in particular.

Let us note the main design features of this model:

- model parameters: initial number of infected individuals; initial basic reproduction number R_0 ; proportion of cases with a mild form of the disease; minimum and maximum duration of the incubation period; minimum and maximum duration of the illness; two scenarios of restrictive measures: a) self-isolation of agents aged over 65 for a specified period; b) additional self-isolation of other agents, as well as the strictness of compliance with restrictive regimes by agents of the respective age groups;
- based on official statistical data, the model recreates the real age and gender structure of the population of the modeled city on the agent population; agent characteristics include: age, gender, health status, family ties, disease stage,

disease severity, number of potential infections (depends on the reproduction number R_0 for this infection);

- infection transmission from an infected agent, not in isolation, who has not yet infected the predetermined number of agents, occurs randomly to any other healthy agent (except family members) with a probability equal to the ratio of the number of possible infections to the length of the period during which they are considered contagious;

- formation of families (households), as well as accounting for family ties in the infection transmission simulation mechanism, represented as an increased probability of infection;

- the model simulates each agent progressing through all disease stages according to the SEIRD scheme, based on an individual disease progression plan generated probabilistically at the moment of infection; this plan includes disease severity (including the need for hospitalization) and its outcome (recovery or death), as well as a schedule for transitioning from one stage to another, measured in days; the simulation time step corresponds to one day;

- implementation of a mechanism linking disease severity to the agent's baseline health status, as well as a mechanism for the deterioration of overall health with increasing age.

- during experiments, the following indicators were estimated at each step: the number of agent groups at different disease stages, the number of required hospital beds (including ICU beds), and the number of deceased individuals.

Thus, it can be noted that the approach we used in developing the COVID-19 epidemic model for Moscow generally corresponds to the mainstream. As for model verification, at that time there was insufficient data to conduct it thoroughly. However, this can be done now. For instance, experiments with two scenarios for introducing restrictive measures indicate that the model adequately simulates the response of the epidemiological

situation, demonstrating an effect of reducing the values of all output indicators. At the same time, the obtained absolute values for the number of severely ill individuals requiring hospitalization, as well as the number of deceased, were clearly overestimated. This is related to the exaggerated assessments of the disease's danger provided by medical specialists⁸ at that time, which were used in the model to calculate probabilities.

Since then, the situation has changed significantly, allowing not only for a return to modeling the COVID-19 epidemic at a new level of knowledge but also for verifying and calibrating the model based on a large body of information accumulated over these years regarding the impact of this infection on the human body, the course of the epidemic, and its consequences. For example, as is now known, individuals who have recovered from a coronavirus infection acquire immunity for some time but can later fall ill again, which increases the number of people potentially susceptible to the infection. Furthermore, numerous studies have emerged on the possible long-term consequences for those who have recovered from this infection, such as an increased risk of developing or exacerbating serious chronic diseases like hypertension (Goldhaber-Fiebert et al., 2025), diabetes (Goldhaber-Fiebert et al., 2025), cognitive impairment (Amer et al., 2025), and post-COVID syndrome (Lewnard et al., 2025), with the risk of severe complications increasing in cases of severe illness. Finally, the work (Gaudet et al., 2025) systematizes research conducted to date on assessing the health consequences of SARS-CoV-2 for those who have recovered.

⁸ Prevention, diagnosis and treatment of the new coronavirus infection (COVID-19), version 5 (April 8, 2020): interim guidelines of the Ministry of Health of the Russian Federation. Ministry of Health of the Russian Federation. 2020. P. 122. Available at: https://xn--80aesfpebagmblc0a.xn--p1ai/ai/doc/114/attach/vremenniy_mr_COVID-19_versiya_5.pdf

Here it is appropriate to note another advantage of agent-based models, which can play a significant role in modeling this specific situation – the ability to simulate both direct and feedback links between various processes occurring in reality (Marshall, Galea, 2015). This is possible because connections in ABMs are implemented through specific model actors participating in several processes, and step-by-step simulation allows for accounting in agent actions of the states of the agent itself and its entire environment, including the system as a whole, established in the previous step. In real life, processes occurring both in society and in the lives of individuals, particularly everything related to the spread of infectious diseases, are interconnected. For example, a person's susceptibility to infection with a particular disease increases if they have pre-existing health problems, as well as with an increase in the number of their contacts with other people and/or with their active movement in space, which may also be related to their profession. Conversely, the presence of a high level of collective immunity in society – natural (due to an increase in the proportion of people who have recovered from the infection) or artificial (due to vaccination) – reduces the probability of infection given the same properties of the infection itself and the same lifestyle of people. The results of the aforementioned studies on the increased risk of subsequent health impairments in those who have recovered indicate the presence of not only a direct but also a feedback link between a person's health status before infection, the severity of the illness, and their general health status after recovery, which can also be simulated in an agent-based model at the level of individuals.

Summarizing the above, we define the goal of the present research: to develop a concept for an agent-based epidemiological model of Russia, which will be configured to simulate processes occurring during an epidemic at the level of society as a whole, at the level of its various groups, as well

as individual members, taking into account their spatial (regional) distribution, and also considering direct and feedback links between various processes.

Concept of an agent-based epidemiological model for Russia as a decision support tool for departmental and regional situation centers

In developing the concept, the experience of testing the epidemiological ABM for the city of Moscow (Makarov et al., 2020) has been taken into account. Some constructs from this model will become part of the new model, and the functionality of each of the main blocks will be expanded.

Let us formulate the conceptual provisions on the basis of which the large agent-based epidemiological model SFECTR (System for Forecasting and Epidemiological Control of Territories of Russia) will be developed.

Purpose and general characteristics of the SFECTR model

1. The ABM will be sufficiently universal to be used for modeling the development of epidemics caused by various types of human-to-human airborne infections. For this purpose, a database of such types of infections will be created, containing information about all properties characterizing each infection that are important for simulating its spread, the course of the disease it causes, and its outcome for the infected agent, including possible long-term complications.

2. The model will provide the capability to use, during computer experiments, a wide range of anti-epidemic control measures, both pharmaceutical (e.g., vaccination) and non-pharmaceutical (e.g., quarantine), for the preliminary assessment of the advisability of their practical application.

3. The model's design will reproduce all functional relationships between the specified model parameters, the current state of the agent environment, and the state and actions of the agents in the population. Based on this, the tracked simulation results are formed, which will allow for observing the effect of the chosen model parameters.

4. The simulation results will reflect aggregated information on the step-by-step change in the state of the agent population both for Russia as a whole and broken down by regions, including the level of collective immunity, morbidity and mortality rates, and indicators of the load on the healthcare system. Output indicators will be exported to external files for subsequent statistical processing, visualization, and analysis.

5. The model will be implemented as a user software product with a developed interface. Regarding experiment management, it will allow setting the time of appearance of infected individuals, their number and spatial distribution, as well as the level of collective immunity; selecting the type of infection from the database, as well as control measures and their combinations, specifying the criteria for selecting agents to which each measure applies, indicating the start and end of each intervention during the forecast period; and providing a clear representation of simulation results at each moment and dynamically throughout the simulation period, including displaying resultant indicators on a map of Russia broken down by its regions.

Main structural blocks of the SFECTR model

1. Simulation of infection transmission between agents and progression of disease stages in agents.

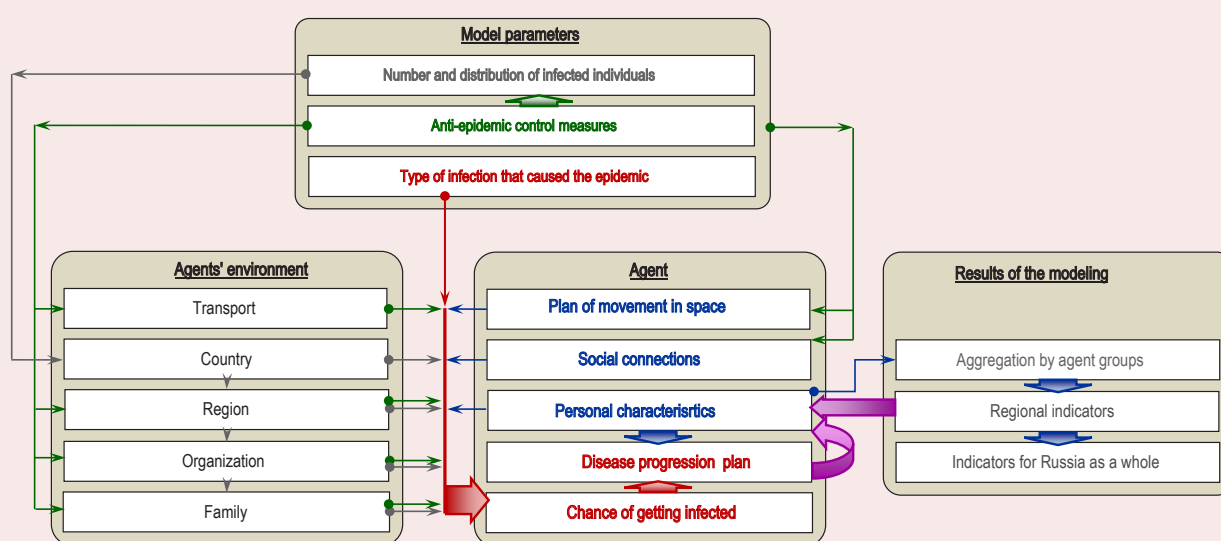
Key characteristics of model agents: age, gender, health status; place of residence; family ties; workplace/educational institution; travel schedule; disease plan; possible number of infections; compliance (willingness to adhere to implemented anti-epidemic measures). Infection transmission occurs randomly from an infected agent to a healthy, non-immune agent if they are not in isolation. The probability of infection for a recipient agent upon contact depends on the possible number of infections from the infected agent (related to the properties of the infection) and varies depending on the category of the recipient:

family member, work colleague, fellow resident, or if their meeting occurs at a transport hub. Agents progress through all disease stages according to the TSEIHCURD scheme, where added stages are: T – period of temporary immunity (Transient); H – hospitalization period (Hospitalized); C – period in critical condition (Critical ill); U – subsequent complications (Unhealthy). The disease progression plan is generated probabilistically at the moment of infection and includes the severity of the disease (including the need for hospitalization) and its outcome (including future health deterioration or death), as well as a schedule for transitioning from one stage to another, measured in days. The severity of the disease depends on the agent's current health level. The agent's compliance depends on their awareness of the disease's danger level (which increases with the number of severely ill agents in their environment). Thus, complex agent behavior is simulated, with agents dynamically assessing risks. The simulation time step corresponds to one day.

2. Simulation of the agent population (society), including recreating the structure of this society.

Based on official statistical data, the real age-gender structure of the Russian population, broken down by regions, is recreated in the agent population at the initial time point. Based on data on the distribution of employment by industry, the employment structure is recreated. Families are formed based on data on the distribution of births by mother's age. Initially, the probability of having immunity is calculated based on data about collective immunity at the start time. Differentiation of agents by health status (presence of chronic diseases) is carried out based on data on the actual prevalence of serious chronic diseases among different age cohorts of the population, similar to the model (Megiddo et al., 2014). Agent compliance at the initial time is distributed randomly and then recalculated at each simulation step. Also, at each step, a timer is checked, which counts down the time allocated for the current disease stage, allowing for the simulation of the transition to the next stage at the appropriate moment.

Figure 4. Generalized diagram of direct and feedback functional relationships ensuring the influence of the SFECTR agent-based epidemiological model parameters on the simulated processes and output indicators



Source: own compilation.

3. Simulation of agent movement in space, considering the transport component.

Given Russia's vast territory, the model must explicitly simulate agent movement in space to imitate the spread of infection. A trip from an agent's place of residence to another region is assigned randomly to the agent based on interregional passenger flow data. Subsequently, a trip schedule is generated, including: the trip start date; the mode of transport and route; the list of the agent's family members traveling with them; as well as the arrival date at the destination (considering the number of days required to complete the route) and the return date. Based on these trip schedules, agent movement is simulated, and their temporary groups, finding themselves at each transport hub on the same day, are determined. These groups correspond to a distinct category in terms of infection probability.

4. Simulation of the environment as the space for agent interaction.

At the initial time point, the model reproduces not only the structure of society but also the structure of Russia's transport network in the form of a graph linking regions through transport hubs (vertices of the graph) and the links between them (edges of the graph). The network is characterized by a list of transport modes for each hub, and for each transport mode at a hub – a list of neighboring vertices (i.e., vertices with a direct connection), the throughput capacity of individual hubs and links, and the time required to travel from one vertex to another. To simulate the spread of an epidemic through human interaction, it is important to ensure a realistic picture of human flows moving along the edges of the transport graph to its vertices – populated areas. Russia's transport network is not closed – infection can enter from outside (as observed, for example, during the COVID-19 pandemic). Among the inhabitants of the populated areas themselves, the infection will spread within the agents' contact groups. This

two-level approach is analogous to the approach implemented in the global model developed for simulating pandemics (Ajelli et al., 2010), which used data on the importation of infected individuals from international travel. *Figure 4* presents a generalized diagram of the functional relationships, established in the SFECTR model concept, between the specified model parameters, the current state of the agent environment, the state and actions of the agents in the population, and the tracked simulation results. These relationships ensure the simulation of the effect of the anti-epidemic measures chosen in the experiment under given conditions. The wide purple arrows in *Figure 4* denote feedback loops – the influence of the disease course on the subsequent overall health of the agent, as well as the influence of information about the current epidemiological situation on the agent's compliance with the implemented control measures.

Technical characteristics of the SFECTR model

Recreating the social structure of society in the ABM, as well as simulating the behavior of agents as individual members of this society, is based on the use of probabilistic processes. Consequently, for the stable operation of an agent-based model with such a large number of parameters and complex organization of the agents themselves, their number should be as large as possible. The desirable option is the creation of a full-scale ABM where the number of agents equals the population of Russia. Here, the ABMs developed under the guidance of Joshua Epstein serve as our benchmark: the global-scale GSAM model with 6.5 billion agents and its national sub-model for the USA with 300 million agents (Epstein, 2009; Parker, Epstein, 2011). Therefore, the software implementation of the presented SFECTR agent-based epidemiological model will be based on a supercomputer demographic model of Russia previously created by the authors, which includes 146 million human agents and simulates demographic processes in

detail (including family formation), taking into account the spatial distribution of the population and regional characteristics (Makarov et al., 2022). Testing of the model is planned using the example of simulating the COVID-19 epidemic during the 2020 period with a simulation time step of one day, which allows for the consideration of disease progression specifics.

Conclusion

The analysis of publications on the topic of epidemic modeling has shown that modern models are evolving toward interdisciplinary platforms that can integrate areas such as epidemiology, behavioral sciences, and computer modeling. Thus, in addition to the now commonplace agent-based models, the authors of the article have identified the following trends observed during the 2005–2025 period: hybrid ABMs with Machine Learning; models based on Artificial Intelligence (using Deep Reinforcement Learning methods and Transformers); multi-scale models combining data at various territorial levels (city, region, country, continent); platform models operating in real-time for instant parameter updates based on Internet of Things (IoT) integration data; and models assessing the impact of socio-economic factors on compliance with quarantine measures. The application of each of these methods can be promising for solving tasks related to managing the epidemiological situation.

In developing their own approach to formulating the concept for a full-scale agent-based epidemio-

logical model of Russia, the authors relied on the use of advanced scientific knowledge and promising models of infection spread through human interaction, while also proceeding from considerations of “reasonable sufficiency”. Since the creation of such models requires solving a complex of not only methodological but also technological tasks, it is important to consider the existing limitations of the information base and available computational power. In our view, the necessary degree of detail for the simulated processes primarily depends on the scale of the modeled object and is determined iteratively based on model validation, as the main criterion is the model’s adequacy for the assigned task. This also applies to the model’s implementation complexity: it should be defined as the minimum required to ensure adequacy.

Given the tense epidemiological situation worldwide, we believe that the identified frontiers of global science, uncovered within this research, should be more actively utilized in shaping the national research agenda. This would enable Russian researchers to create the most adequate toolkit for modeling epidemics based on the agent-based approach. The obtained results can form the foundation for a socio-economic multi-agent model to support evidence-based decision-making in the field of public health and subsequent implementation in the country’s situation centers, aiming to enhance Russia’s preparedness for potential pandemic threats.

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