Multicentral Agent-Based Model of Four Waves of COVID-19 Spreading in Nizhny Novgorod Region of Russian Federation

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Abstract. To study the characteristics of the spread of the COVID-19 pandemic and introduce timely and effective measures, there is a need for models that can predict the impact of various restrictive factors on COVID-19 disease dynamics. In this regard, it seems expedient to employ agent-based models that can take into account various characteristics of the population (for example, age distribution and social activity) and restrictive measures, testing, etc., as well as random factors that are usually omitted in traditionally used modifications of Susceptible-Infected-Recovered (SIR) type models. This paper presents the development of the previously proposed agent model for numerical simulation of the spread of COVID-19, namely, the transition from a single-center model, in which all agents interact within one common pool, to a multi-center model, in which the agents under consideration are distributed over several centers of interactions, and are also redistributed over time to other pools. This model allows us to more accurately simulate the epidemic dynamic within one region, when the patient zero usually arrives at the regional center, after which the distribution chains capture the periphery of the region due to pendulum migration. This paper demonstrates the application of the developed model to analyze the epidemic spread in the Nizhny Novgorod region of Russian Federation. Simulated dynamics of the daily number of newly detected cases and COVID-19-associated deaths is in good agreement with official statistics. Modeling results suggest that the actual number of COVID-19 cases is 1.5–3 times higher than the number of reported cases. The developed model also takes into account the process of vaccination. It is shown that with the same modeling parameters, but without vaccination, the third and fourth waves of the pandemic would be characterized by a significant increase in the incidence and the formation of natural immunity, but the number of deaths would exceed the real one by about 9 times. © 2023 Journal of Biomedical Photonics & Engineering.

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1 Introduction

The COVID-19 pandemic has become a real global challenge, which requires reliable methods for modeling the epidemiological process in order to take timely restrictive and preventive measures. Currently, there are several classes of models used to calculate and predict the spread of infections.

Logistic models operate with ordinary differential equations of the first order. Despite their simplicity, such models made it possible to obtain a very correct description of the first wave of the spread of COVID-19 [1]. Generalized logistic models make it possible to take into account a power-law, rather than exponential, increase in the number of cases [2, 3]. Methods of mathematical statistics and machine learning make it possible to build regression [4] and network models [5] of the spread of the disease.

More complex, so-called compartmental models are based on systems of differential equations. In such models, the population is divided into several groups. In the classical SIR model proposed in Ref. [6], three groups are distinguished, namely, susceptible (S), infected (I), recovered (R), and the interaction between them is described in terms of differential equations. In more complex modern models, an even greater number of groups are distinguished. In particular, exposed (E), hospitalized (H), deceased (D), in critical state (C) and others are added [7–9].

A significant drawback of the SIR model and its modifications is the inability to take into account both random factors in the epidemic dynamics and the individual characteristics of specific people. In this regard, to model the spread of an epidemic, it is rational to use agent-based models. Within the framework of such models, the entire population is considered as a set of agents with a selected number of both constant and variable characteristics that determine the strategy of behavior and interaction with other agents in the considered population. The characteristics of the disease (incubation period, probability of infection, etc.), restrictive and preventive measures (self-isolation, social distancing, contact tracing, etc.) are also included as parameters of the model. Agent-based models have demonstrated their effectiveness in calculating the spread of infection in a population of various sizes, for example, among visitors to a supermarket [10], residents of a relatively small [11] or large city [12], and an entire country [13]. In Ref. [14], an agent-based model was developed for modeling the spread of COVID-19 in Russia, taking into account transport routes. The mean-field-type game model is actually a combination of the SIR model (or its modifications) and the agent model, which take into account the rationality of agents: each member of the population seeks to reduce the risk of hospitalization and limit its economic consequences, firms seek to maximize profits while reducing the risk of exposing workers to the risk of infection, public authorities seek to reduce the number of deaths based on cost-effectiveness considerations [15].

Within the framework of agent-based models, it is assumed that all agents belonging to a certain group, for example, an age group, behave in the same way. The effectiveness of such models can be increased by introducing new data, such as demographic or transport data, and transition to the so-called multicenter agent model, in which the population is considered as a set of several separate pools of agents with different behavioral characteristics. Thus, in Ref. [16], a simulation of the spread of COVID-19 in several schools was performed, taking into account, for example, kinship (brothers, sisters) and friendships between students from various educational institutions. The paper [17] considers four Chinese cities with the interaction of agents both within each of the cities and between them. The paper [14] presents the country model like a combination of a city models set and a matrix of population flows defined for each day, considering different types of transport links.

The aim of this work is to develop the previously proposed agent model [18, 19] to simulate the spread of COVID-19 in various regions of the Russian Federation. The development is associated with the transition to a multicenter model, which allows considering a separate region of the Russian Federation as a set of regions with population movement between them, as well as taking into account the vaccination process as one of the measures to prevent the spread of the disease.

2 Materials and Methods

2.1 Multicentral Agent-Based COVID-19 Spread Model

The previously developed single-center agent-based COVID-19 spread model with the Monte Carlo method implementation is described in detail in Ref. [19]. Within the framework of the proposed approach, a set of agents $\mathfrak{N}$ representing the population of the chosen region is considered. Each agent $a_n \in \mathfrak{N}$ is characterized by a set of daily changing Boolean states ("alive", "infected", "contagious", "with symptoms of a disease", etc.) that determine its behavior (interaction with a common pool of agents, self-isolation, etc.). The model presented in Ref. [19] assumes that every agent interacts with all the others, and the probability of spreading the disease is determined by the total number of non-isolated agents. Table 1 presents the main parameters of the previously proposed single-center model.

In order to generalize the developed model to the multi-center case, all agents from the common pool are distributed among n_c pools of smaller size, which correspond to the districts of the region (regional center and peripheral cities). The number of agents N_i in each i-th pool corresponds to the population of the i-th district or city, and the total number of agents in these pools is equaled to the population of the region N: $N = \sum_{i=1}^{n_c} N_i$. For each agent, the index i of its initial pool (i.e. hometown or district) is stored. During the modeling a certain percentage p_t of agents aged from 18 to 65 in each pool, excepting the population of regional center, receive

the binary status of "pendulum migrant", which means that they periodically move from native city to the regional center for working purpose. The p_t value distribution by pools (districts of the region) is chosen empirically, taking into account the distance of a particular city/district from the regional center, while the percentage of commuting migrants among the agents of the general pool is 15%, which is consistent with information available in open sources.

In the simulation, all agents that initially have the "infected" status are assigned to the regional center, and agents with the "pendulum migrant" status change their pool to the regional center from Monday to Friday, returning to the original pool on Saturday and Sunday. Thus, the mechanism of spreading the disease from the regional center to the entire region is implemented. This assumption is consistent with the general trends in the spread of imported epidemics, when the "patient zero" usually appears in the regional center.

Table 1 Values of main parameters employed for Nizhny Novgorod Region in single-center model in paper [19].

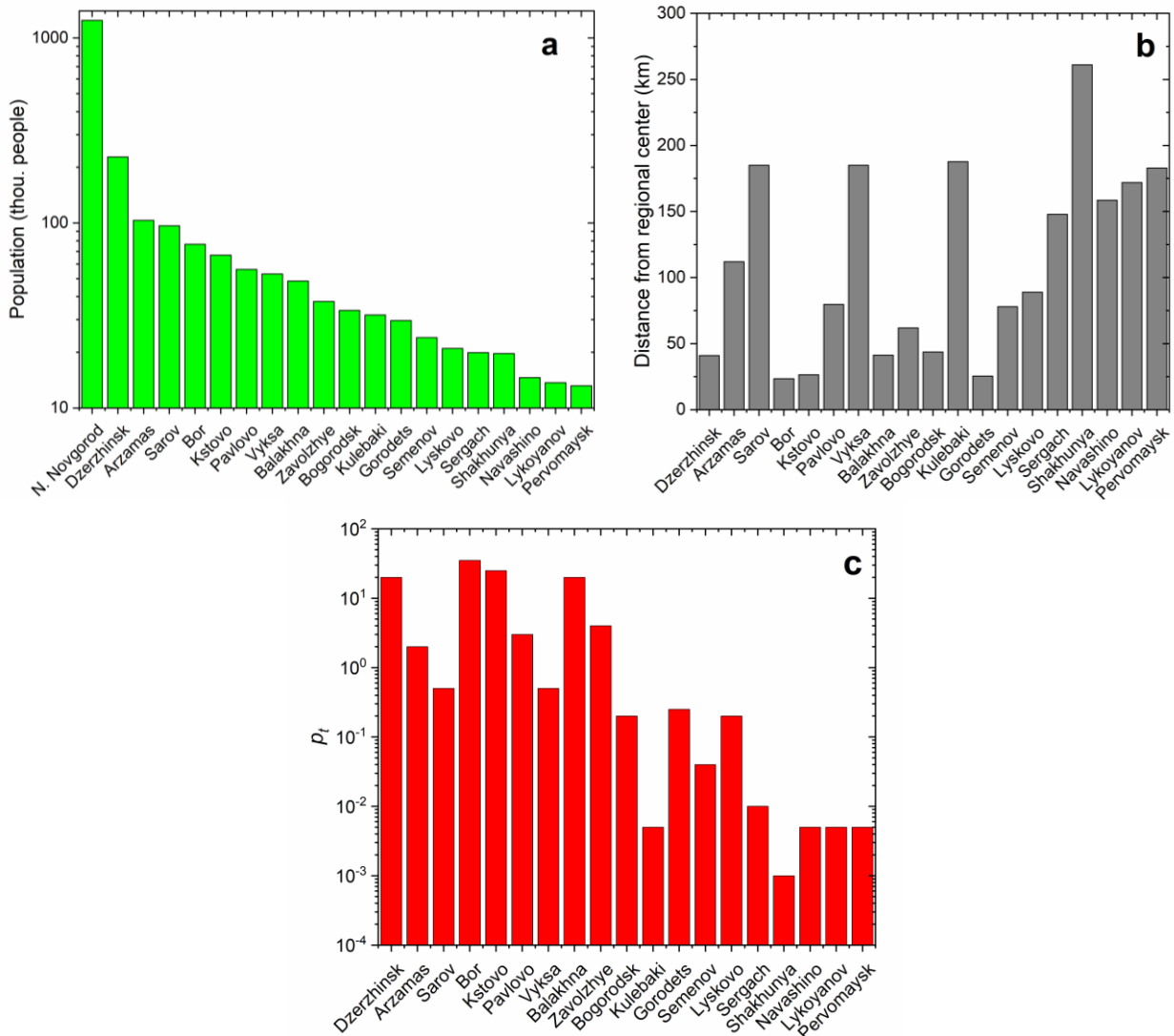| Parameter	Value
Probability of symptoms manifestation	0.3
Daily death probability in critical state	0.06–0.10
Average weekly number of agents infested by a spreader	4.6
Probability of isolation decision for agents with symptoms manifestation	0.5
Self-isolation index	1.0–3.0

Fig. 1 (a) Population of Nizhny Novgorod Region districts and cities included into modeling; (b) distance from chosen district/city to regional center (Nizhny Novgorod); (c) distribution of agents with "pendulum migrant" status with the respect to chosen districts/cities in modeling.

2.2 Accounting for Vaccination in Modeling

For more precise modeling of the 3rd and 4th waves of the spread of COVID-19, the ability to account for the vaccination process was implemented into developed model. For this purpose, data on partial vaccination of the population in the Russian Federation from January 1, 2021 to December 31, 2021 was taken from open sources [20]. The daily number of partially vaccinated people N_i^{vacc} is calculated in proportion to the share of the region population in the population of the country.

Following the nomenclature previously suggested in Ref. [19], we introduce the additional Boolean state "vaccinated" (α_n^9) that is also set as 'false' (0) at the initialization of the simulation for all agents.

In the simulation the vaccinated group $\mathfrak{B}$ is determined each simulation day in the following way:

$$\mathfrak{B}: R_p(N_i^{vacc}, \{a_n | h_n \geq 18\} \backslash \mathfrak{P}), \qquad (1)$$

where $R_p(j, \mathfrak{A})$ is a random permutation of j elements from set $\mathfrak{A}$: N_i^{vacc} is the total number of vaccinated taken at day i corresponding to the official statistics data; h_n is

an agent age parameter; $\mathfrak{P}$ is the group of agents, who are unavailable for vaccination. The latter group contains agents with states "symptomatic" (α_n^3), "in critical state" (α_n^4), "dead" (α_n^5) or "positive test" (α_n^8):

$$\mathfrak{P}: (\{a_n | \alpha_n^3 = 1\} \cup \{a_n | \alpha_n^4 = 1\} \cup$$
$$\cup \{a_n | \alpha_n^5 = 1\} \cup \{a_n | \alpha_n^8 = 1\}). \qquad (2)$$

On each simulation day agents from the vaccinated group change the status to "vaccinated":

$$\alpha_n^9 = 1 | a_n \in \mathfrak{B}. \qquad (3)$$

For each vaccinated agent, the day of vaccination t_n^{vac} is stored. After a period of vaccination and antibodies formation T_a equaled 42 days (21 days is the interval between two stages of vaccination and 21 days is the period of antibodies formation), the probability of infection p_{is} for a vaccinated agent during the interaction with a pool of other agents is artificially reduced by 20 times (immunity formation). Duration of immunity T_i chosen in the model is 6 months.
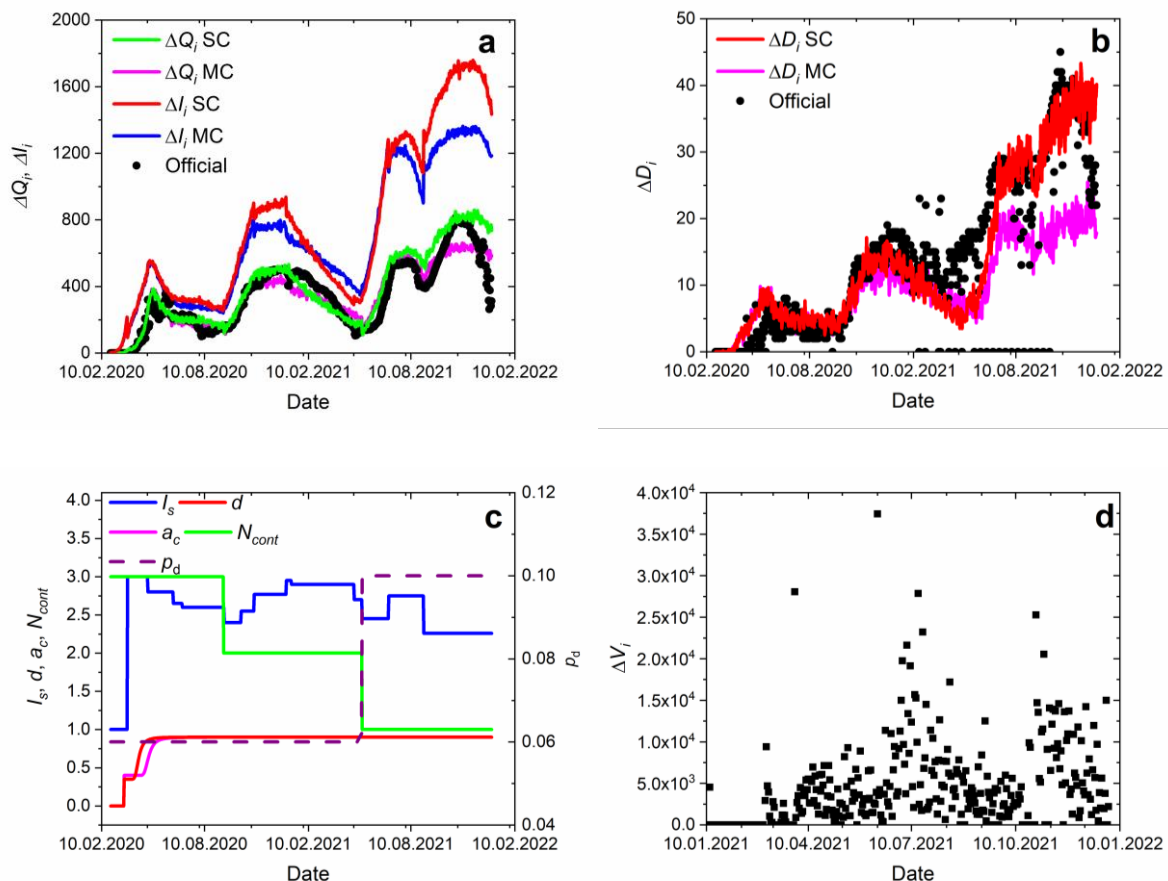

Fig. 2 Daily dynamics of (a) newly revealed (ΔQ_i) and real total number of COVID-19 cases (ΔI_i) and (b) COVID-19 associated deaths (ΔD_i) in Nizhny Novgorod Region calculated in single-center (SC) and multi-central (MC) models along with official data (Official). Simulation parameters: (c) I_s – self-isolation index, d – fraction of tested agents with symptoms, a_c – tests sensitivity, N_{cont} – number of traced contacts, p_d – death probability in critical state, (d) ΔV_i – daily dynamics of vaccinated agents.

$$\widetilde{p_{\iota s}} = \begin{cases} p_{is} \mid \alpha_n^9 = 0 \\ \frac{p_{is}}{20} \mid \alpha_n^9 = 1, \ t_{vac} + T_a \leq i < t_{vac} + T_a + T_i \end{cases} \quad (4)$$

2.3 Multicentral Modeling Parameters

Simulation of four waves of COVID-19 spread was performed for Nizhny Novgorod region ($N = 3.3 \cdot 10^6$) and included the days from February 26, 2020 to December 31, 2021. All parameters, including the temporal characteristics of the disease and the prevalence rate, the distribution of agents by age, the probability of death of an agent in critical condition, etc. corresponds to those previously used in modeling the first two waves of the spread of COVID-19 [19], while for the 3rd and 4th waves an empirical selection of parameters was performed. The number of cities and districts in the region n_c is chosen to be 20 during simulation (smaller administratively distinguished districts are combined with neighboring larger ones). Fig. 1 shows the population of selected cities and districts of the Nizhny

Novgorod region, as well as their distance from the regional center and a given percentage of commuting migrants in them.

3 Results

Fig. 2 shows the dynamics of the spread of COVID-19 in the Nizhny Novgorod region, calculated within the framework of single- and multi-center agent models, as well as the parameters used in the modeling: self-isolation index (I_s), the proportion of tested agents with symptoms of the disease (d), test sensitivity (a_c), the number of tested contact agents (N_{cont}), the probability of death of an agent in critical condition (p_d). Similar to Ref. [19], we simulate daily dynamics of daily newly revealed COVID-19 cases (ΔQ_i) which gave the positive test result on a certain day, total number of daily new cases including those that remain undetected (ΔI_i), and daily lethal COVID-19 associated cases (ΔD_i).

As can be seen from Fig. 2, the total number of detected cases of COVID-19 in the region is still in good agreement with official statistics during the movement from a single-center to a multicenter model.
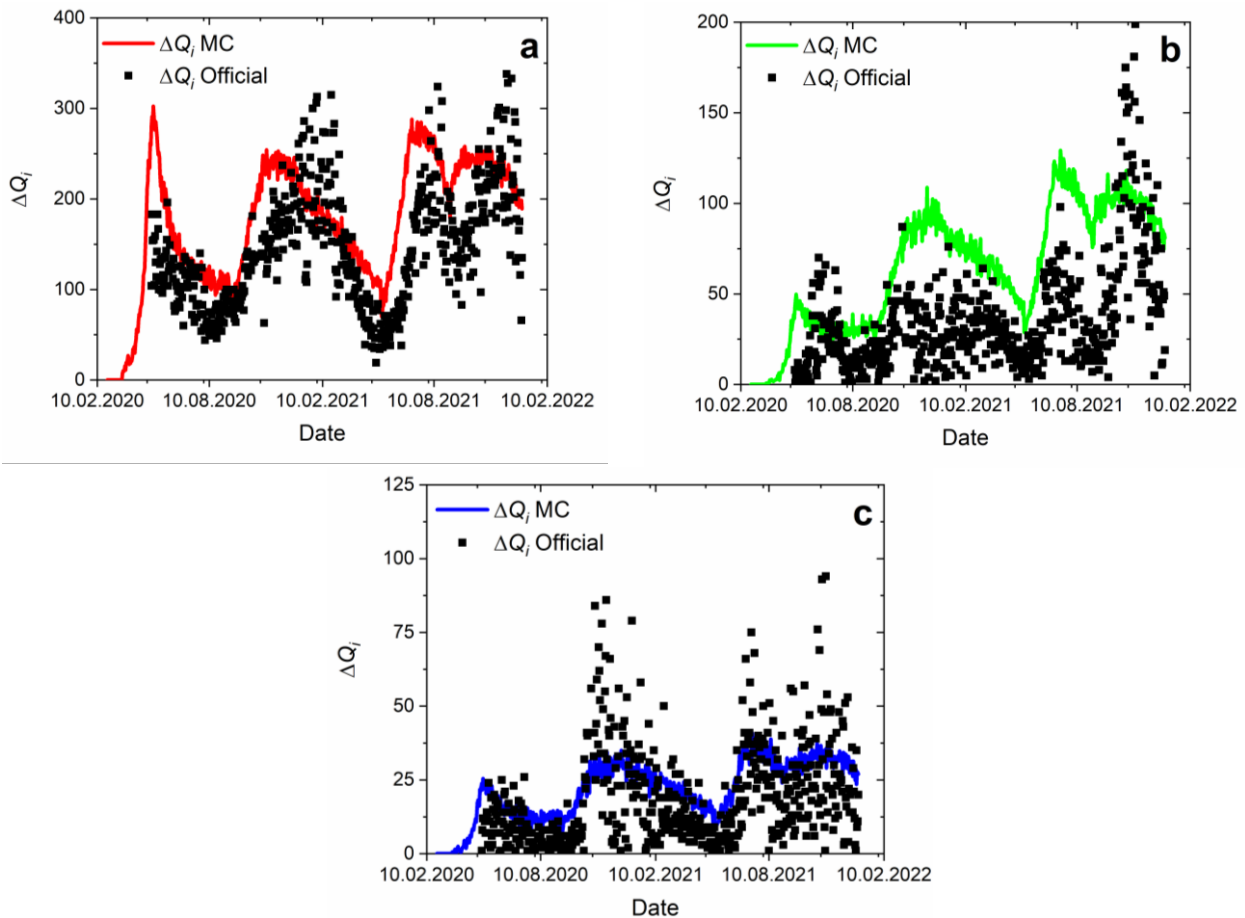

Fig. 3 Daily dynamics of newly revealed ΔQ_i COVID-19 cases, calculated with multicenter (MC) model for (a) regional center – Nizhny Novgorod, (b) Dzerzhinsk, and (c) Bor. Simulation parameters are similar to those in Figs. 2c, d.

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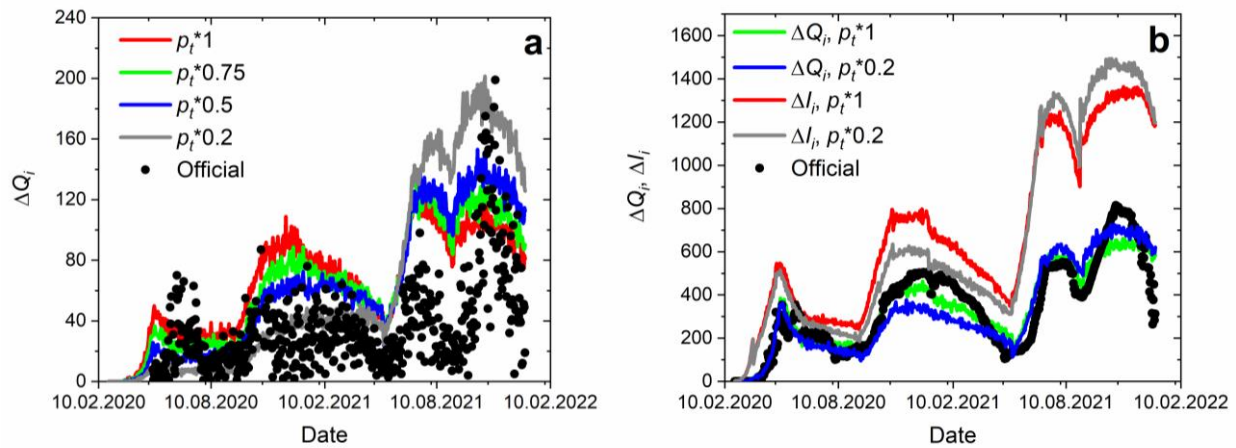
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Fig. 4 Daily dynamics of newly revealed ΔQ_i COVID-19 cases, calculated with multicenter model for (a) Dzerzhinsk and (b) Nizhny Novgorod Region with different percentage p_t of pendulum migrants along with official statistics data (Official).
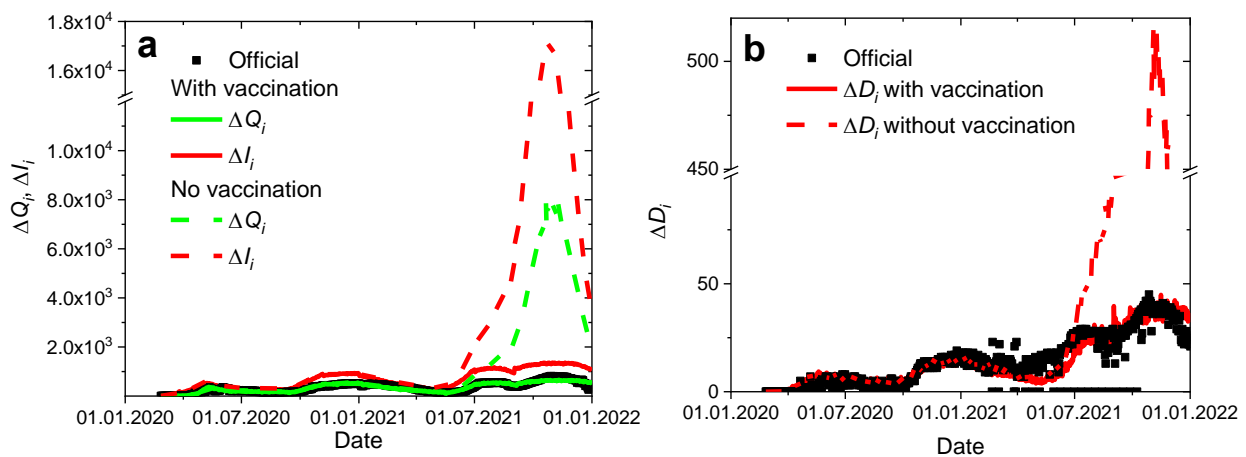

Fig. 5 Daily dynamics of (a) newly revealed (ΔQ_i) and real total number of COVID-19 cases (ΔI_i) and (b) COVID-19 associated deaths (ΔD_i) in Nizhny Novgorod Region calculated with multi-central model with and without accounting for vaccination.

The discrepancies between the curves for single- and multicenter models are due to the fact that within the framework of a single-center model, all agents participating in the modeling are affected from the very beginning, while in the case of a multicenter model, infection begins from the regional center, where the infection enters from outside the system under consideration. The resulting model scenario shows that some of the infected are not detected, and the total number of infections exceeds the number of detected cases by 1.5–3 times, and this ratio increases for later waves.

Fig. 3 shows the dynamics of the spread of COVID-19 in Nizhny Novgorod (regional center), as well as the cities of Dzerzhinsk and Bor, calculated within the multicenter model.

As can be seen from Fig. 3, during the first wave of the spread of COVID-19 (spring-summer 2020), the dynamics of newly detected cases is determined mainly by Nizhny Novgorod (the regional center), while the curves for regional cities show a characteristic peak

around May. During the second wave (autumn 2020–winter 2021), the self-isolation index does not reach the values of the first wave, and therefore there is a significant increase in new cases detected in the regions of the region, and the difference between them becomes quite significant. A similar trend can be traced in the case of the 3rd and 4th waves (spring 2021–December 2021).

It should be noted that the difference between the official statistics and simulated data for new cases for certain districts and cities of the Nizhny Novgorod region was not a minimization parameter of the model, but the comparison shows a fairly good agreement between simulated and official data.

Fig. 4 presents the results obtained in multicenter model with a variation in the percentage of pendulum migrants. The distribution of the percentage of pendulum migrants in Fig. 1 is taken as the initial one; the caption to Fig. 4 shows the coefficient by which the corresponding values are multiplied.

As can be seen from Fig. 4a, the developed multicenter agent model provides an adequate estimation of the spread of the disease in a particular city in the region. The discrepancy between the simulation results and official statistics is explained by the overestimated number of agents in the pool corresponding to a particular city in the framework of numerical simulation. An increase in the fraction of pendulum migrants in a particular city has a more significant impact during the first wave of the pandemic compared to the second (Fig. 4a), since restrictive measures are relaxed during the second wave (Fig. 2c). At the same time, during the first and second waves of the spread of COVID-19, an increase in the percentage of pendulum migrants expectedly leads to an increase in detected cases of the disease in a particular city, but during the third and fourth waves, an inverse relationship is observed. It is explained by the fact that in the case of a lower percentage of pendulum migrants, a significant part of infection spreading the agents remain in their pools and interact with the agents within it, and not with the rest. At the same time, the total number of newly revealed cases across the region is in good agreement with official statistics for the region, both in the case of the base percentage of commuters and for a much lower percentage (Fig. 4b).

In order to analyze the impact of the vaccination process on the spread of the disease, modeling was performed with parameters corresponding to those presented in Fig. 2c, but without vaccination of agents. The results are presented in Fig. 5 showing the comparison of the daily numbers of total and detected cases in scenarios with and without vaccination.

Fig. 5 clearly demonstrates the effectiveness of vaccination of the population as a preventive measure in the spread of the disease. It is shown that in the absence of vaccination with the same parameters of the model, a sharp increase in the incidence is observed, leading to the formation of herd immunity by the beginning of 2022, however, at the cost of high mortality (a difference of about 9 times compared to the number of deaths during the vaccination of the population). The significant difference between the curves with and without vaccination is due to the greatly relaxed restrictive measures during the third and fourth waves of the spread

of COVID-19 and the decrease in the number of contacts traced (Fig. 2c).

4 Conclusion

The paper presents the enhancement of an agent-based model that simulates the COVID-19 spread dynamics using the Monte Carlo method. The developed multicenter model considers a region as a set of separate districts in which agents interact with each other while the mechanism of interaction between districts described through consideration of pendulum migration. The proposed approach made it possible to simulate four waves of the spread of COVID-19 in the Nizhny Novgorod region and demonstrates good agreement with official statistics. In the future, the model can be improved by increasing the number of districts included in the simulation, considering the travel of agents not only from regional cities to the regional center, but also between regional cities itself, and also taking into account the different nature of restrictive measures in the regional cities. For more correct modeling results, precise information about the number of pendulum migrants in specific cities/districts of the region is required.

The developed agent-based model also includes the ability to account for the vaccination process during the spread of infection. The results obtained for the dynamics of newly detected and real total number of COVID-19 cases show that even with a significant weakening of restrictive measures, vaccination of the population can reduce the number of cases and COVID-19–associated deaths by about 9 times, which clearly demonstrates the need for vaccination and its effectiveness.

Disclosures

All authors declare that there is no conflict of interests in this paper.

Acknowledgements

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