DISCUSSION PAPERS, LECTURES, NEW TRENDS IN MEDICAL SCIENCE

# ASSESSMENT OF THE EFFECTIVENESS OF RESTRICTIVE EPIDEMIC CONTROL MEASURES USING ORIGINAL MODELS OF CELLULAR AUTOMATON

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## ABSTRACT

***Background.*** *The ongoing COVID-19 pandemic, the human casualties caused by it, and the possibility of new epidemical threats make the search for effective countermeasures actual. One of the most effective tools, as the experience of the COVID-19 pandemic has shown, is restrictive measures of various types, which are especially significant with medical countermeasures being unavailable or insufficient. At the same time, the topic of restrictive measures and their mathematical modeling, especially given its importance, is not sufficiently disclosed in the scientific literature.*

***The aim.*** *To determine the possibility of assessing the effectiveness of restrictive epidemic control measures using original models of cellular automata with intercellular boundaries.*

***Methods.*** *To determine the impact of restrictive measures on the dynamics of the daily increase in infected people, an original cellular automaton with intercellular boundaries was developed, which makes it possible to simulate epidemic control measures of varying stringency. In the simulations carried out using the Monte Carlo method with subsequent statistical processing, we studied the impact of restrictive measures of varying stringency on the number of infected people, the duration of the epidemic, and the quality of forecasting. The final series of experiments simulated the spread of the COVID-19 virus in Germany in the first half of 2020.*

***The results*** *show that even a simple cellular automaton model with boundaries successfully describes the course of the epidemic and allows us to assess the effectiveness of restrictive measures. The dependence of the daily increase in infected people on the stringency of measures is presented; it is shown what characteristics of the population can influence this dependence. It was found that the measures of medium severity (40–50 % according to the Stringency Index) have the least predictable effect; they can cause both rapid localization of the focus and the spread of the epidemic to a large part of the population. Weak and strong measures give a more predictable effect.*

***Conclusion.*** *Cellular automaton models with intercellular boundaries have great potential for modeling the impact of restrictive measures on the course of an epidemic, making it possible to predict the dynamics of infected people based on the population data and the restrictive measures being introduced.*

***Key words:*** *COVID-19, epidemic, restrictive measures, mathematical modeling, agent-based models, cellular automaton*

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# ОЦЕНКА ЭФФЕКТИВНОСТИ ПРОТИВОЭПИДЕМИЧЕСКИХ ОГРАНИЧИТЕЛЬНЫХ МЕР С ПОМОЩЬЮ ОРИГИНАЛЬНЫХ МОДЕЛЕЙ КЛЕТОЧНЫХ АВТОМАТОВ

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## РЕЗЮМЕ

***Обоснование.*** *Продолжающаяся пандемия COVID-19, связанные с нею человеческие жертвы, возможность возникновения новых эпидемических угроз актуализируют поиск эффективных мер противодействия. Одним из наиболее эффективных инструментов борьбы, как показал опыт пандемии COVID-19, оказались ограничительные меры различного характера, особенно значимые в условиях, когда медицинские меры противодействия отсутствуют или недостаточны. Вместе с тем тема ограничительных мер и их математического моделирования, особенно с учётом её важности, раскрыта в недостаточной степени.*

***Цель исследования.*** *Определение возможности оценки эффективности противоэпидемических ограничительных мер с помощью применения оригинальных моделей клеточных автоматов с межклеточными границами.*

***Методы.*** *Для определения влияния ограничительных мер на динамику ежедневного прироста инфицированных разработан оригинальный клеточный автомат с межклеточными границами, позволяющий моделировать противоэпидемические меры различной строгости. В проведённых численных экспериментах по методу Монте-Карло с последующей статистической обработкой изучалось воздействие ограничительных мер различной строгости на количество инфицированных, продолжительность эпидемии, качество прогнозирования. В заключительной серии экспериментов моделировалось распространение вируса COVID-19 в Германии в первой половине 2020 года.*

***Результаты*** *показывают, что даже простая модель клеточного автомата с границами успешно описывает ход эпидемии и позволяет оценить эффективность ограничительных мер. Представлена зависимость ежедневного прироста инфицированных от строгости мер; показано, какие характеристики популяции могут влиять на эту зависимость. Выявлено, что наименее предсказуемый эффект имеют меры средней строгости (40–50 %, согласно Stringency Index), при которых может наступить как быстрая локализация очага, так и распространение эпидемии на большую часть популяции. Слабые и строгие ограничения дают более предсказуемый эффект.*

***Заключение.*** *Модели клеточных автоматов с межклеточными границами имеют большой потенциал для моделирования влияния ограничительных мер на ход эпидемии, позволяя прогнозировать динамику инфицированных на основе данных о популяции и вводимых ограничительных мерах.*

***Ключевые слова:*** *COVID-19, эпидемия, ограничительные меры, математическое моделирование, агентно-ориентированные модели, клеточный автомат*

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The ongoing COVID-19 pandemic, the associated deaths, economic and non-economic losses, and the possibility of new epidemic threats make the issue of finding effective measures to counter such threats urgent. The experience of the COVID-19 pandemic has shown that restrictive measures of various kinds are one of the most effective tools for control. These measures are particularly important when new viruses emerge that have no medical countermeasures or they are inadequate. It is therefore not surprising that countries that were leading in international rankings of The Most Efficient Health Care (Bloomberg), The Global Health Security Index (Nuclear Threat Initiative, Johns Hopkins University, The Economist Intelligence Unit) and counting on their institutional capacity were not at their best during the pandemic [1]. Restrictive measures have been much more successful (especially in the initial phase before vaccines and treatment protocols were developed).

Restrictive measures have already been the subject of a number of studies aimed both at identifying their main types and assessing the degree of restrictions imposed (see, for example, the Oxford University project [2]) and at examining the correlation between restrictions and the severity of the pandemic [3, 4, etc.]. However, it should be noted that the topic of restrictive measures, especially in view of its importance, has not yet been sufficiently addressed. A number of questions still need to be clarified: what is the optimal degree of constraint? What types of constraints are most effective? Does the order in which different types of restrictions are imposed matter? At the same time, it is obvious that the answers to these questions cannot be automatically transformed into solutions for specific situations. Local specificities must be considered when making decisions. This raises the following question: what country or regional characteristics influence the effectiveness of restrictive measures?

This study explores the possibility of assessing the effectiveness of restrictive measures using original models of cellular automata (CAs). Cellular automata are a type of agent-based models used, in particular, in epidemiological studies for simulating the spread of epidemics in a population consisting of individual agents (cells). The fundamental novelty of the CA discussed in this paper is the intercellular boundaries by which the restrictive measures introduced are modeled.

It is considered that the CA concept was introduced into science in the late 1940s by J. von Neumann for modeling complex, spatially extended systems [5], based on the idea of S. Ulam [6]. It is also fair to say that “cellular automata have been invented many times under different names, and somewhat different concepts have been used under the same name” [7]. A. Burks [8], J. Holland [9], G. Hedlund [10], S. Wolfram [11, etc.] et al. have made significant contributions to the development of the cellular automaton theory and their use. CAs allow modeling mass processes of different nature: dissemination of information, opinions, protest activity (both in real life and in virtual social networks); group formation and the emergence of segregation; urban growth; territorial expansion of states; military conflicts, etc.

Cellular automata are a popular tool for modeling epidemics. N. Bailey [12, etc.] was one of the first to describe the use of CAs for modeling epidemics. He was followed by the papers of D. Mollison [13], S. Jakowitz et al. [14], and a number of other researchers [15, 16, etc.]. Of note are the papers of domestic authors: M.M. Bashabshekh and B.I. Maslennikov [17], D.K. Gorkovenko [18], A.V. Shabunin [19] and others. The COVID-19 pandemic, which triggered a wave of publications on epidemic modeling, contributed to the growing interest in models using CAs [20, 21, etc.] However, for all the abundance of publications, the potential of cellular automata for modeling restrictive measures is not actually used.

The advantages of CAs are visibility, relative ease of creating a model and conducting experiments with it. An important argument in support of the use of CAs is also the fact that simulation modeling with their contribution does not require ultra-high computing power and can be performed on an ordinary personal computer.

The basic element of a cellular automaton is a *cell*, which, most often, has the form of a square and within the framework of epidemic modeling can be interpreted as an individual, a small group (family) or a territorial community (residents of a city block, village, etc.). A set of contiguous cells form a “playing space”, or CA *grid*; most often the grid has the form shown in Figure 1. In different models, a cellular grid can be interpreted as both a geographic space and a conventionally depicted population. By using cell geometry and grid shape, it is possible to increase or decrease the number of neighbors a cell has and thus account for the density of connections between individuals (or groups) in the simulated population, as well as the infectivity of the pathogen.

A cell may be in one of several *states*; minimally, there may be only two such states (e. g., a cell may be infected or uninfected). The transition of a cell from one state to another is determined by a set of *rules* that, in the simplest case, take into account 1) the current state of the cell and 2) the current state of its neighboring cells. For example, we can set the following rule: if a cell has two or more infected neighbors, the cell itself also becomes infected (see Fig. 1). This rule can be complicated by indicating that infection occurs in the presence of two or more infected neighbors not always, but with some probability, taking into account, on the one hand, the infectiousness of the pathogen, and on the other hand, the innate or acquired resistance of the individual. In more complex models, an individual’s liability to disease may additionally be a function of age, gender, lifestyle, occupation, presence of chronic diseases, etc.

Cellular automata allow us to consider that the degree to which an infected cell is dangerous to its neighbors may change over time. This may take into account not just the average duration of the incubation period and the average duration of infectiousness, but the presence of different forms of the disease course (e. g., mild, moderate, severe), for each of which a different function of the change in infectiousness over time is defined.

Thus, the state of a cell can be influenced by a large number of factors related to both the properties of the cell itself, the properties and state of the cell's distant neighbors, and random factors.

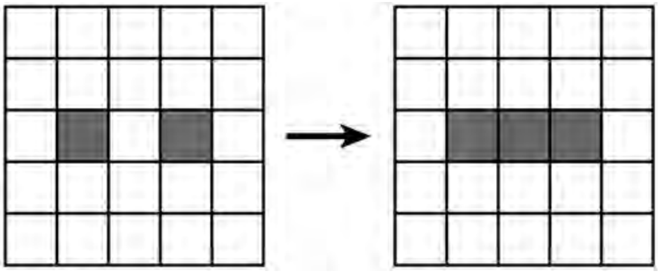

***FIG. 1.***

*Two consecutive steps of the cellular automaton leading to the infection of the central cell*

Classical CAs are *discrete* dynamic systems – that is, time in them is measured in steps, and the system life consists as if of separate static frames.

Due to their simplicity and the possibility to almost infinitely increase the set of cell properties, the set of states and the set of rules for changing states, epidemic models constructed using CAs successfully compete with classical models using systems of ordinary differential equations – SIS, SIR, SIRS, SEIRD – and similar models, the development of which began in the 1920s [22]. The use of CAs is also supported by the fact that models using ordinary differential equations are so-called *mean-field models*, i. e., models that assume a random and uniform distribution of healthy and infected individuals in the population. This assumption does not take into account that epidemics are most often focal, i.e. the distribution of infected and healthy people is not even. CA models allow us to account for the uneven distribution in the population of healthy and infected individuals.

## THE AIM OF THE STUDY

To determine the possibility of assessing the effectiveness of restrictive epidemic control measures based on original models of cellular automata with intercellular boundaries.

Achieving the objective required the following tasks to be solved:

- searching for how restrictive measures can be implemented within the CA model;
- creation of an original CA model simulating the introduction of restrictive measures, in the R language;
- carrying out numerical experiments with the created CA model;
- analyzing the results of numerical experiments.

The method proposed in this article can be used by both epidemiologists and decision-makers when planning the introduction of restrictive measures to determine their necessary level of severity, as well as when assessing the effectiveness of measures already implemented.

## MODELING OF RESTRICTIVE MEASURES

Restrictive measures introduced at the state, regional and local levels (as the experience of countering COVID-19 has clearly shown) are primarily aimed at reducing physical contacts of the population, during which the virus is transmitted. That is, it is the introduction of barriers to the virus by stopping contact or reducing its intensity. These measures include: transfer of employees to remote work; closing catering facilities; transferring students to distance learning; restrictions on visiting public places; restrictions on going outdoors, etc. Moreover, there are *targeted* restrictive measures aimed at reducing (or even eliminating) the contacts of an infected individual who poses a risk to others.

To model the restrictive measures, we used a special type of cellular grid *with boundaries* not previously encountered by the authors in the scientific literature[1]. Thus, while in the typical CA the grid consists only of cells, in the proposed CA additional objects, i. e., boundaries between neighboring cells, are introduced.

The introduction of restrictive measures can be interpreted as closing part of the boundaries between cells. If the boundary is closed, it becomes impenetrable – the pathogen cannot be transmitted through it. Closure of the boundary between two cells in practice can be expressed as the transfer of two employees to remote work, as a result of which their physical contacts are interrupted, as the cessation of face-to-face communication between two classmates when school classes are canceled, etc. It is quite obvious that in practice not all imposed restrictions are "impenetrable", just as the reverse is also true: without the imposition of restrictive measures, the boundaries between cells are not completely "transparent" either – contact between an infected individual and an uninfected one does not necessarily result in the latter becoming infected as well. In this paper, we restrict ourselves to models with fully impermeable boundaries, showing that even such simplified models allow us to describe well the effect of restrictive measures. At the same time, in more complex models it is justified to use partially permeable boundaries, i.e. those that with the introduction of restrictive measures reduce permeability, reducing the probability of virus passage from cell to cell, but not excluding it completely.

In the presented figure (Figure 2), the closed boundaries are shown as black rectangles. Assume that the virus can only transmit to the nearest cells in 4 directions (up, down, left, right), but not diagonally – i. e., we will use the so-called von Neumann's neighborhood of range $r = 1$. The center cell in the figure has two open (top and right) and two closed (left and bottom) boundaries. Direct infec-

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[1] The concept of boundary is found in some papers on CAs, but most often it is a matter of distinguishing different zones of cells on the cellular space, so that the boundary in this case is not a significant element of the model (see, for example, [23]). In our case, the boundaries are a crucial element of the model, affecting the states of the cells and thus the dynamics of the whole system.

tion of the left and lower cells from the center cell is not possible in this case. The pathogen can only be transmitted to the top and right cells. However, there is nothing to prevent the use of other types of neighborhoods, such as the Moore's neighborhood (virus transmission also goes diagonally) or the Margolus neighbourhood (the geometry of which is not static, i.e. at one step the neighbors are some cells, and at another step – others; this type of neighborhood successfully describes periodic changes in the circle of contacts, which is typical, for example, for a working individual, when on weekdays they actively interact with colleagues at work, and on weekends – with family and friends).

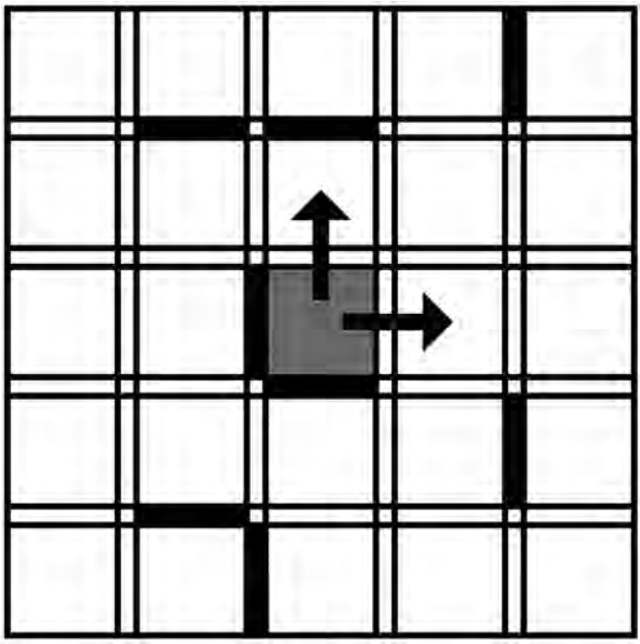

***FIG. 2.***

*Cellular automaton with closed boundaries: the arrows show the directions in which the virus can be transmitted*

The severity degree of restrictive measures is described in the model as the proportion of closed boundaries. It is obvious that an increase in the proportion of closed boundaries affects the virus spread rate and the possibility of epidemic outbreaks localization. In applied research, the percentage of closed boundaries can be taken as equal to, for example, the percentage of reduced activity, which is calculated for major world cities [24], or the self-isolation index [25], or taken from sources such as the COVID-19 Government Response Tracker [2].

An important question is which boundaries on the cellular space should be closed. Figure 2 shows a cellular space with 25 cells and 40 boundaries between them, 8 of which (i. e., 20 %) are closed. In the simplest case, the location of closed boundaries can be set randomly, based on the idea that when restrictive measures are imposed, unless they are targeted, it is impossible to predict exactly which individuals will break physical contact.

The random location of closed boundaries (where the only control parameter is the severity of restrictive measures, i. e., the proportion of closed boundaries) creates certain difficulties in modeling the impact of measures on epidemic spread. Closed boundaries can be distributed unevenly over the space, form (or not) extended structures, localize (or not) foci. All this makes it necessary to conduct a series of experiments with the model using the Monte Carlo method with further statistical processing of the findings.

As the experience of COVID-19 and other epidemics shows, restriction policies can be preventive, when restrictions are imposed before the emergence of infected people in a country or region, or reactive (situational, catch-up), when restrictions are imposed after the emergence of infected people. Both of these scenarios can be realized in models using CAs. The first scenario models the spread of an epidemic on a cellular space with already closed boundaries, while the second scenario simulates the epidemic evolving unconstrained until a certain point.

## EXPERIMENTAL MODEL DESCRIPTION OF A CELLULAR AUTOMATON

A cellular automaton with the following characteristics was used in the experiments:

- the CA grid is made up of identical square cells;
- a cell can be in two states, uninfected or infected;
- cell neighborhood is Neumann's neighborhood of range $r = 1$ (i. e., the virus from an infected cell can be transmitted only to its four neighbors – top, bottom, left, and right);
- there are 4 boundaries between a cell and the cells that make up its neighborhood, and each boundary can be in two states, open or closed;
- virus transmission from an infected cell to an uninfected cell occurs when there is an open boundary between these cells. To simplify the model and to obtain a clearer dependence of the epidemic on restrictive measures, we consider the option of unconditional infection with an open boundary;
- cell begins to pose a risk to its neighbors in the next step after infection (incubation period is equal to one step), the risk of transmission from an infected cell remains for 5 steps;
- a cellular space has a square shape, its size is 59 × 59 cells (total 3,481 cells and 6,844 cell boundaries);
- the spread of the virus starts from the center cell.

The given space size allows us to trace, first, the nature of the epidemic spread in a closed population, and second, the nature of the epidemic in an unclosed population, since for at least 30 steps (or, interpreting 1 step as 1 day, for 30 days) the spread of the epidemic is affected only by the restrictive measures introduced and is not affected by the edge effect (i. e., there is no edge effect on the cellular space). An example of the described CA functioning is shown in Figure 3.

## DESCRIPTION OF EXPERIMENTS

3 series of experiments were conducted aimed at assessing how restrictive measures affect the progression of the epidemic and the severity of its consequences.

The first series of experiments examined what nature, depending on the stringency of restrictive measures (i.e., the proportion of closed cell-to-cell boundaries), the epidemic progression has in a closed population of 59 × 59 cells. First of all, emphasis was placed on studying the rate of virus spread, duration of the epidemic, daily increase in infected persons and peak values.

9 variants of the restrictive measures stringency were considered: the proportion of closed boundaries varied from 0 to 80 % in increments of 10 %. The distribution of closed boundaries on the cellular space was set randomly in each experiment. For each of the 9 variants, 100 experiments were performed, the results of which were then subjected to statistical processing.

The second series of experiments examined the effect of restrictions during the initial phase of the epidemic (lasting for 30 steps) in an unclosed population. Following on from this time, the CA used allows us to model the spread of the virus without the influence of edge effects and to compare the epidemic development under different stringency of restrictions.

In this series, the emphasis was on examining the number of cells affected by the virus over a limited period of time and on the accuracy of estimating the effect of restrictive measures.

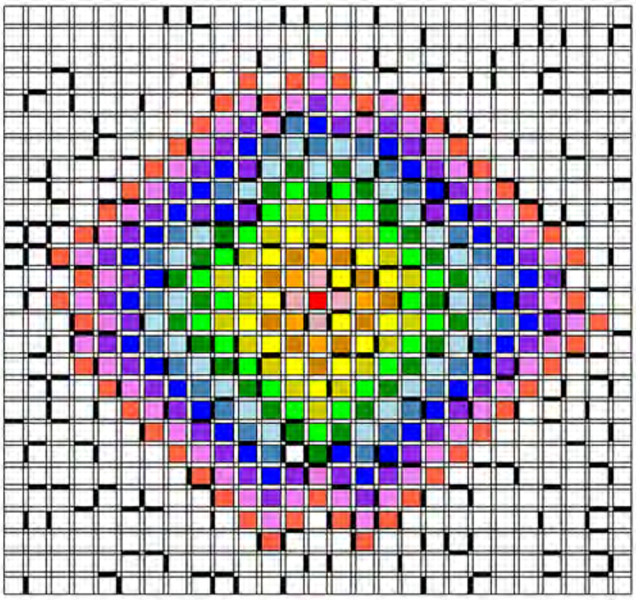

***FIG. 3.***

*An example of the cellular automaton operation indicating the spread of an epidemic with 20 % of closed boundaries at the step 14 (the central part of the cellular space is shown). Cells infected at the same step have the same color. Cells surrounded by closed boundaries from all sides remain uninfected throughout the epidemic*

16 variants of the restrictive measures stringency were considered: the proportion of closed boundaries varied from 0 to 80 % in 5 % increments. The distribution of closed boundaries on the cellular space was set randomly in each experiment. For each of the 16 variants, 100 experiments were performed, the results of which were then subjected to statistical processing.

In a third series of 100 experiments, the proposed cellular automaton with boundaries was used to simulate the spread of COVID-19 virus in Germany in the first half of 2020.

The R environment, version 3.4.3, was used to build the model and perform numerical experiments with it. Data statistical processing was performed using R environment and MS Excel 2016 (Microsoft Corp., USA) using standard methods of variation statistics. Hardware: PC with Intel Core i5-1035G1 1.19 GHz processor, 8 GB RAM.

## DATA ANALYSIS AND RESULTS

In the absence of restrictions, there is a steady increase in the daily increment of infected from day 1 to day 30. At the same time, visually the zone of infected cells represents a rhombus growing with each step. Starting from day 31, the daily growth rate is reduced due to the edge effect, and the zone of infected cells turns from a rhombus into an octagon and gradually fills the entire cellular space. This results in a population of 3,481 cells being completely infected in 59 days.

The imposition of weak restrictions (10–30 % of closed boundaries) has almost no effect on this pattern, only slightly pushing the peak forward in time. Imposing tighter restrictions (40–50 % of closed boundaries) reduces the peak, lengthens the course of the epidemic, and protects some part of the population (usually not very significant) from infection. Strict restrictions (60 % or more closed boundaries) allow in a large number of cases to localize the epidemic focus, protecting an appreciable part of the population.

Figure 4 shows typical plots (graphs) of the number of daily infections at different levels of restrictive measures stringency.

As can be seen from the graphs, the nature of the epidemic progression does not change much at 10, 20, 30 % restrictions, not very different from the situation of complete absence of restrictions. The fact is that, while making it more difficult for the virus to spread, weak restrictive measures do little to shield the population from the virus, but only slightly reduce the rate of spread. The proportion of cells isolated from the virus is very small, amounting to only 1.5 % at 30 % restriction (see Table 1). In other words, the probability of avoiding infection under such restrictions is only 1.5 % for a cell.

However, even these weak measures have a clear positive effect: they shift the peak of the epidemic to the right, and the end of the epidemic also comes later, reducing the burden on the health system. For instance, a 30 % restriction reduces the burden in the first 30 days of the epidemic by an average of 28 % (see Table 1). Along with this,

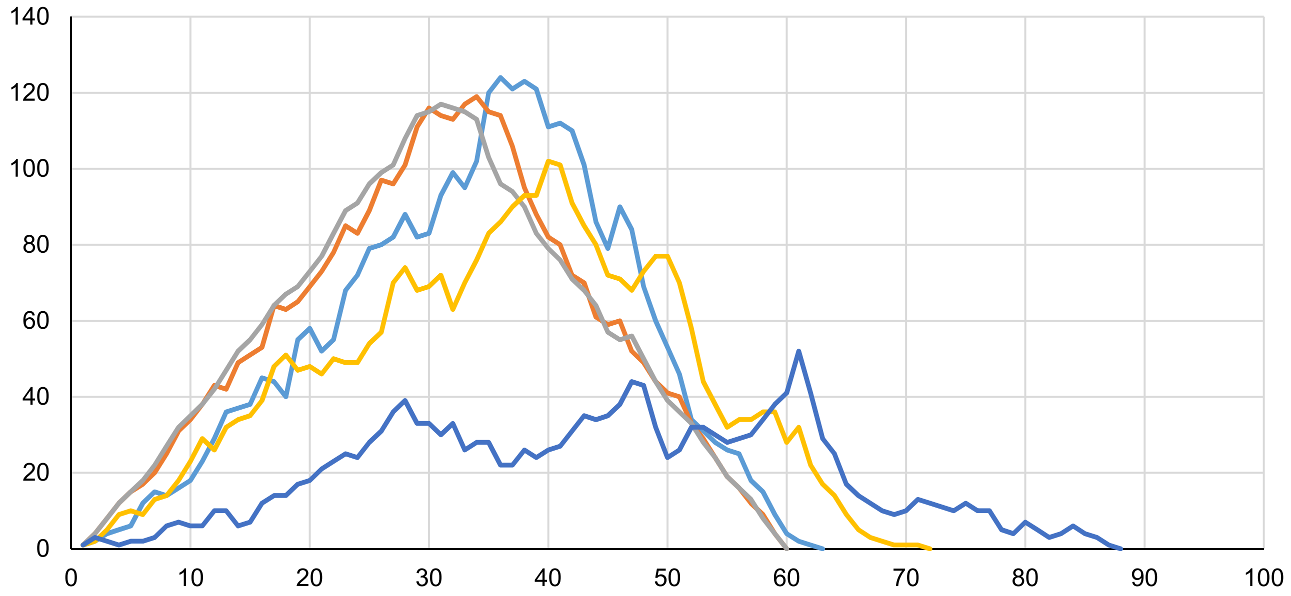

**FIG. 4.**

*Examples of typical dynamics of the incremental growth of infected cells under restrictions of varying stringency. Horizontal axis represents steps; vertical axis – growth of infected cells. Gray – 10 % stringency; orange – 20 % stringency; blue – 30 % stringency; yellow – 40 % stringency; cyan – 50 % stringency*

it is also worth noting the possible negative consequences of introducing weak restrictions: in some cases, the peak value may be even higher than in the absence of restrictions (see Fig. 4). Although this excess is usually no more than 10 %, this negative effect should be taken into account when imposing restrictions and forecasting the burden on the health care system.

The imposition of more severe restrictions (40–50 % of closed boundaries) fundamentally changes the picture of the epidemic course: the proportion of isolated population increases significantly (up to 75 %); on average, the public health burden decreases by 83 % in the first 30 days (with 50 % restrictions); the peak value is markedly reduced. The epidemic itself can lengthen considerably. Thus, at 50 % restrictions, the duration of the epidemic doubled or more in 15 % of the experiments.

The most significant effect of more severe restrictions is to increase the likelihood of epidemic localization, so that a significant proportion of the population is protected from infection by the measures. To some extent, as shown above, isolated cells can also occur under weak restrictions. Moreover, with weak restrictions, there is also the possibility of focal suppression, but it is very low, so it is not necessary to rely on such a scenario with weak restrictions. It is at moderate restrictions that a scenario of focal suppression can be considered: at 40 % restrictions, localization occurs in about 10 % of cases, and at 50 % restrictions, in about 30 % of cases[1].

An important feature identified in numerical experiments with the model is a wide scatter of the results when introducing moderate severity measures (see Table 1). In particular, while the standard deviation of the isolated cells proportion at weak restrictions did not exceed 0.5 %, at moderate restrictions the standard deviation reaches 25 %, markedly reducing the ability to predict the performance of the measures implemented. Thus, in 100 experiments with 40 % closed boundaries, the minimum proportion of isolated cells was 5.08 % and the maximum was 99.97 %.

Similar scatter is observed for other parameters. At 40 % restrictions, both cases of focus localization within the first week and an increase in the duration of the epidemic up to 100 days are observed. At 50 % restrictions, the difference between the maximum and minimum duration increases even further to almost 200 days.

Thus, one of the main disadvantages of moderate severity measures is the poorly predictable effect of their introduction. Analyzing the behavior of the constructed CA, it can be observed that, as in real life, restrictive measures perform two main functions: isolating a part of the population (1) and reducing the rate of virus spread (2). Both of these functions have positive effects, one by protecting part of the population from infection, the other by reducing the burden on the health system and helping to buy time to mobilize additional resources, develop vaccines, and so on. Under weak restrictions, a scenario is implemented in which the effect of reducing the virus spread rate is more important, since weak restrictions (i. e., a small number of closed boundaries) are unable to protect an appreciable part of the population from infection – single cells are protected. As the number of closed boundaries increases, another scenario is increasingly implemented, in which

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[1] In the context of the experiments, focal localization (suppression) was understood as a situation in which the spread of the virus was stopped by the measures introduced in 25 days or less. This value was chosen based on the fact that if the virus stops spreading during this period, more than 65 % of the population will be protected from it. It is possible to choose a different number of days, which, however, does not change the main conclusion about the marked increase in the cases of focal suppression with increasing stringency of restrictions starting from 40 % restrictions.

the configuration of the closed boundaries is such that a significant part of cells can be shielded from the virus (up to localization of the epidemic focus in the first few steps of CA operation). The higher the number of closed boundaries, the more likely this scenario is to occur.

The wide scatter of indicators and poor predictability of the effect when introducing measures of moderate severity are related to the fact that both the first scenario discussed above and the second one can be implemented with almost equal probability. Such unpredictability is well illustrated by the distribution histogram (Fig. 5). The percentage of isolated cells at 50 % restrictions is shown horizontally, and the occurrence frequency of this result is shown vertically. Focal localization (rightmost column) occurs in one-third of cases, but in a large number of cases localization does not occur and the epidemic affects a significant number of cells. In 21 % of cases, the epidemic covers more than half of the population (leftmost four columns).

Especially important to note is that in such a distribution, focusing on average values can lead to significant errors in predicting the impact of restrictive measures. The average proportion of isolated cells at 50 % restrictions is 74.95 %, but as can be seen from the histogram, the probability of obtaining such a result (let's take the interval from 70 % to 80 %) is only 7 %, which is much lower than the probability of focus localization or spreading the epidemic to a large part of the population.

This finding appears to be one of the most important in our work, allowing us to explain, in particular, the high variability in the results from similar restrictions across countries when dealing with COVID-19.

Moderate restrictive measures make it much more difficult for the virus to spread in a population. Closed boundaries create complex structures on the cellular space, similar to a maze; rather large spaces emerge, partially or completely walled off from the epidemic focus. As a result, the spread of the virus often proceeds in leaps and bounds – sometimes slowly, with small increments of infected people per step, and sometimes rapidly. Wave-like graphs of the infected are typical of moderate restrictions (see Figure 4).

Severe restrictions (60 % or more closed boundaries) turn out to be, as one would expect, the most effective. Al-

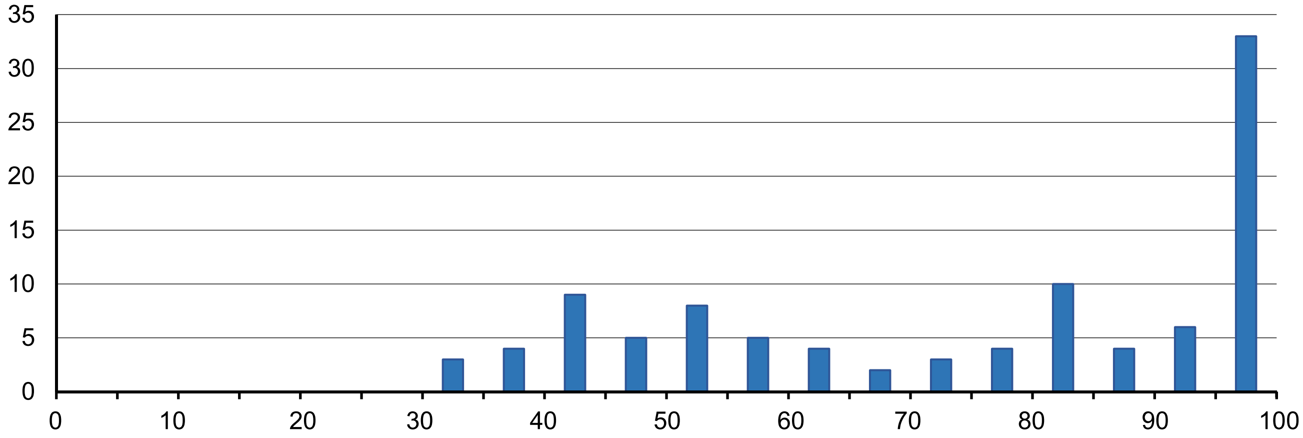

***FIG. 5.***

*Distribution of results of numerical experiments under 50 % restrictions. Horizontal axis represents the proportion of cells (%) that turned out to be isolated by the end of the spread of the epidemic in the population; vertical axis – frequency of occurrence (%)*

**TABLE 1**

**STATISTICS OF NUMERICAL EXPERIMENTS**

| Parameters | Stringency of restrictive measures (%) | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | 0 | 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
| Average proportion of isolated cells (%) | 0.00 | 0.02 | 0.27 | 1.50 | 14.33 | 74.95 | 99.07 | 99.78 | 99.92 |
| Standard deviation (%) | 0.00 | 0.03 | 0.09 | 0.31 | 25.38 | 23.10 | 1.33 | 0.26 | 0.07 |
| Average change in epidemic duration (in days and %) | 0.00 | +0.2 | +0.95 | +3.32 | +9.19 | +7.51 | –48.15 | –54.28 | –56.71 |
| | 0.00 | +0.34 | +1.61 | +5.63 | +15.58 | +12.73 | –81.61 | –92.00 | –96.12 |
| Standard deviation (in days) | 0.00 | 0.53 | 1.23 | 2.14 | 20.53 | 46.60 | 12.05 | 4.45 | 1.67 |
| Average reduction in health system burden in the first 30 days of the epidemic (%) | 0.00 | 3.60 | 12.54 | 28.18 | 52.59 | 83.42 | 96.85 | 98.89 | 99.54 |

ready at 60 % restrictions the proportion of virus-free cells reaches 99 % on average, which makes further increases in the stringency of measures virtually meaningless, especially if we take into account that increasing the stringency of measures in practice is associated with economic, political and other costs. With 60 % restrictions, the burden on the health care system in the first 30 days of the epidemic is reduced by almost 97 %, and the average duration of the epidemic is strongly reduced due to the dominance of cases of epidemic focus localization – such cases were 87 %. While it is still possible that the duration of the epidemic exceeds the duration of the epidemic without restrictions, the range of values for this indicator is substantially reduced compared to the 50 % restrictions. Thus, the results of more severe restrictions are not only more efficient on average, but also more predictable; this is true for both the expected duration of the epidemic and the isolated population proportion.

The second series of experiments examined the effect of restrictions during the initial phase of the epidemic (lasting for 30 steps). Following on from this time, the CA used allows us to model the spread of the virus without the influence of edge effects (i. e., the attenuation of the epidemic in these experiments is not due to the fact that the population is limited, but only to the action of the restrictions) and to compare the epidemic development under different stringency of restrictions.

The results obtained agree with the results of the first series of experiments. Figure 6 shows how the average number of infected individuals on day 30 of the epidemic depends on the stringency of the restrictions (i. e., the proportion of closed cell boundaries). As can be observed, weak restrictions (10–30 % of closed boundaries) lead, on average, to a rather small reduction in the rate of virus spread. 30 % restrictions reduce the number of infections by about 20 %.

The introduction of more severe restrictions (40–50 % of closed boundaries) markedly reduces the rate of virus spread. At day 30, at 50 % restrictions, the number of infections is on average 10 times lower than at no restriction and 8 times lower than at 30 % restrictions.

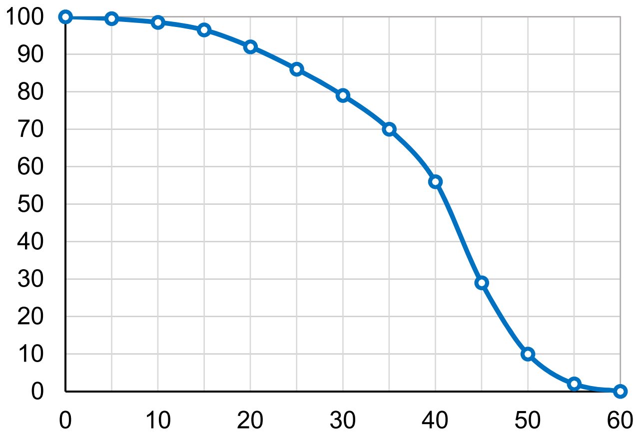

***FIG. 6.***

*Dependence of the proportion of infected cells (%) on the day 30 of the epidemic on the stringency of restrictions (%)*

Severe restrictions (60 % or more closed boundaries) almost completely stop the spread of the virus.

The effect of restrictions of varying stringency can be clearly seen in Figure 7, which shows the average number of infections by day as a function of the restrictions severity. Apparently, with 50 % of closed boundaries (and thus weaker restrictions), the number of infections tends to increase gradually. More severe restrictions (55 %) are already able to reverse this trend – the number of new cases is stable and the virus is spreading through the population at the same rate. Even more severe restrictions (60 %) can gradually reduce the rate of spread of the virus and bring the epidemic to a halt.

The high efficiency of severe restrictions demonstrated in the experiments (i. e. when 60 % of the boundaries are closed or more) is in some contradiction with real data, in particular, on the course of the COVID-19 pandemic in various countries and regions, where, according to statistics, the situation improved after the introduction of more severe restrictions (80 % and higher). At a minimum, we can point to three sources of these discrepancies:

1. An important assumption of the conducted experiments with the CA model is that virus spreading occurs in the model already *in the presence* of restrictive measures. The experience of coping with the COVID-19 pandemic and other epidemics shows that, in reality, a different scenario is more often implemented: the main set of restrictive measures is introduced not preventively, but in response to an increasingly complex epidemic situation, i. e. when the virus has already spread over a large area and/or in a significant proportion of the population. In this situation, governments are forced to go for stricter measures.
2. In the model, the closure of the cell-cell boundary completely precludes penetration of the virus. In reality, imposing restrictions does not mean that they are perfectly enforced. Under these circumstances, the introduction of, for example, 60 % restrictions may in practice lead to only 50 % or even 40 % restrictions. Thus, the lower the level of restriction compliance, the more severe the measures must be to achieve the desired effect.
3. Contemporary researchers have pointed out that the CA methodology is somewhat "outdated" for describing epidemics occurring today. Whereas in the past the key factor in the spread of epidemics was precisely "neighborhood" contacts, now, in conditions of high geographical mobility, a significant role is played by "long-distance" contacts, i. e. long-distance migrations of the population associated with recreation, business trips, etc. As a result, the transfer of a virus from one continent to another can occur faster than the transfer from one area of a city to a neighboring one. So, when building a full-fledged model of epidemic spread, it is necessary to consider distant connections, as some modifications of CAs do (see, e. g., [19]). On the other hand, as the practice of confronting epidemics shows, restrictions on movement (especially long-distance travel) are among the first to be introduced, which should significantly reduce the impact of "long-distance travel" on the spread of the virus.

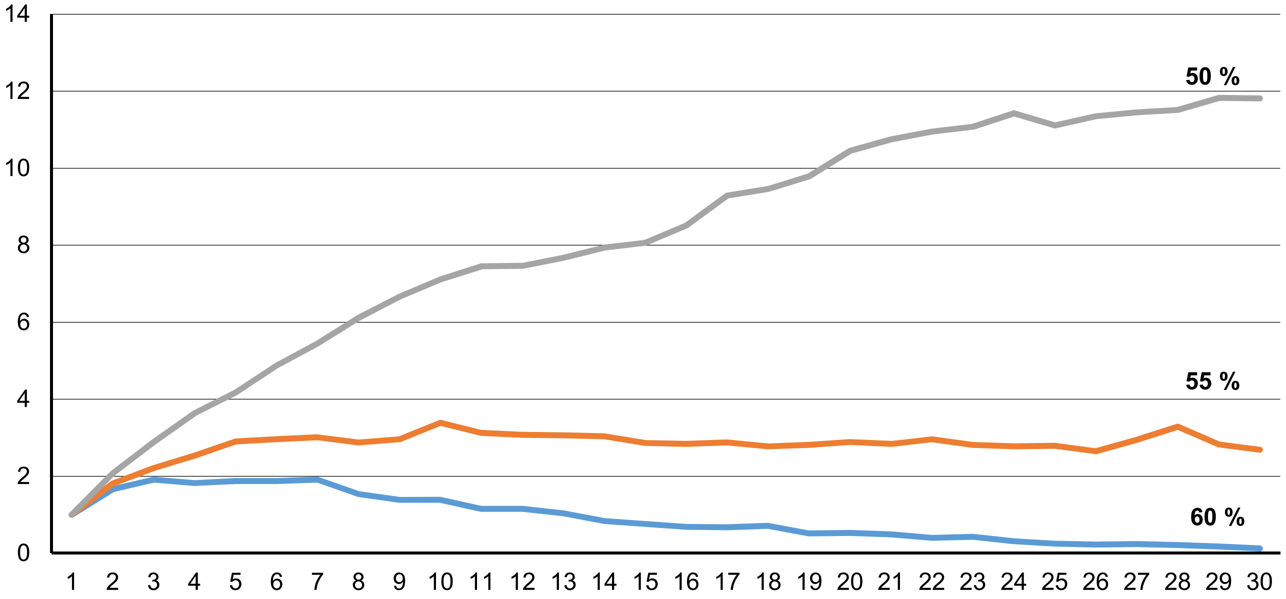

***FIG. 7.***
*Average number of infected cells per step (new cases) depending on the stringency of restrictions*

TABLE 2

**SIMPLIFIED SEQUENCE OF CHANGES IN THE STRINGENCY OF RESTRICTIONS IN GERMANY DURING THE FIRST WAVE OF THE COVID-19 PANDEMIC**

| Time period | Time period duration | Stringency Index | Percentage of closed intercellular boundaries | Long-distance connections |
|---|---|---|---|---|
| 1.03 – 9.03 | 9 days | 25 | 25 % | 87.5 % |
| 10.03 – 17.03 | 8 days | 32.87 | 32.87 % | 87.5 % |
| 18.03 – 20.03 | 3 days | 55.09 | 55.09 % | 0 % |
| 21.03 – 04.05 | 45 days | 76.85 | 76.85 % | 0 % |
| 05.05 – 16.05 | 12 days | 64.35 | 64.35 % | 0 % |
| 17.05 – 15.06 | 30 days | 59.72 | 59.72 % | 12.5 % |

The aim of the third series of experiments was to test the model on real data: a cellular automaton with boundaries was used to simulate the spread of the COVID-19 virus in Germany during the first wave. The German data were chosen because of their relative reliability and completeness[1].

During the experiments, a larger (101 × 101) CA was used to improve accuracy, which was based on the principles discussed above and included a number of additional rules to better account for the peculiarities of the epidemic in Germany.

1. The number of closed intercellular boundaries changed dynamically, according to Stringency Index (SI) data, an aggregate parameter obtained by researchers at the University of Oxford based on the COVID-19 Government Response Tracker [2]. SI takes into account the stringency of the restrictive measures imposed and is calculated for each day on a scale from 0 to 100. Slightly simplifying the real time variation of SI, the scheme shown in Table 2 was used in the experiments.

2. The closed boundaries in the model were made partially permeable, i.e. the fact that a part of the population could neglect the restrictions and some restrictions could work inefficiently was taken into account. The degree of permeability was found to be 25 %, i. e., with a 25 % probability that the virus was transmitted through a closed boundary (100 % permeability was assumed for open boundaries, as in the previous series of experiments). The degree of permeability of closed boundaries was chosen on the basis of the thesis that permeability is primarily influenced by the behavior of the population and its attitude towards restrictions, which in turn can be operationalized by the level of law-abidingness and the level of trust in the imposed measures. However, as research on the topic of COVID-19 proliferation and confrontation shows, there is currently

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[1] Germany is among the leading countries in real-time surveillance and reporting (Global Health Security Index – 2019) and at the same time Germany had one of the highest specific population testing rates during the first wave of the COVID-19 pandemic (see e. g. https://ourworldindata.org/grapher/full-list-total-tests-for-covid-19).

no objective sociological or other data reflecting law-abidingness [26], hence our study used proxy indicators from World Value Survey (WVS) studies to understand the level of non-compliance with restrictive measures [27]. In particular, the responses of German residents to questions about their trust in the World Health Organization (Q88), under whose recommendations the restrictions were imposed, and their attitudes towards tax evasion (Q180) were taken into account. For question Q88, 23.9 % of respondents stated that they do not trust or do not trust WHO at all. For question Q180, 75.7 % said that tax evasion can never be justified. As we can see, both figures allow us to assume a level of non-compliance with restrictive measures of about 25 %.

3. In addition to neighboring cell interactions, the model took into account "long-distance" connections, i. e., interactions between two non-neighboring cells that mimic long-distance travel by residents. The performance of long-distance connections was controlled in the model by two parameters: the average number of such connections per German resident and the restrictions that were imposed on long-distance travel in the relevant time period.

As per statistics, a German resident takes three long-distance trips per year [28]. Thus, it was calculated that per step in the model, $(101 \times 101 \times 3) / 365 = 84$ "long-distance" connections could occur. This quantity was adjusted for the restrictions that were imposed and whose numerical expressions were derived from the data on the SI components that describe restrictions on long-distance movements of residents (C7 and C8 components). As a result, the number of "long-distance" connections ranged from 73 in the initial period of the epidemic to 0 and then rose slightly to 10 (see Table 2). Cells involved in "long-distance" connections were randomly selected.

The plots of infected cell growth obtained from the experiments (Fig. 8) largely coincide with the actual plots of daily infected cell growth (Fig. 9). Similarities can be seen both in the pattern of exponential growth in the number of infected persons during the first weeks of the pandemic and in the shape of the peak apex and the shape of the relatively mild decline in the curve. This indicates that the proposed modeling method can accurately describe the dynamics of disease incidence based on population data and the degree of restrictive measures stringency and, accordingly, can be used to assess the effectiveness of anti-epidemic restrictive measures.

However, discrepancies in the plots related to the comparison of the curve scale are also noticeable. For instance, the termination of exponential growth occurs in the model about 10 days earlier than in reality (if we interpret one step of CA operation as one day). To some extent, such discrepancies can be explained by the fact that the model shows how the number of infected people changes at the time they are infected, while the statistics show the number of infected people at the time they are registered.

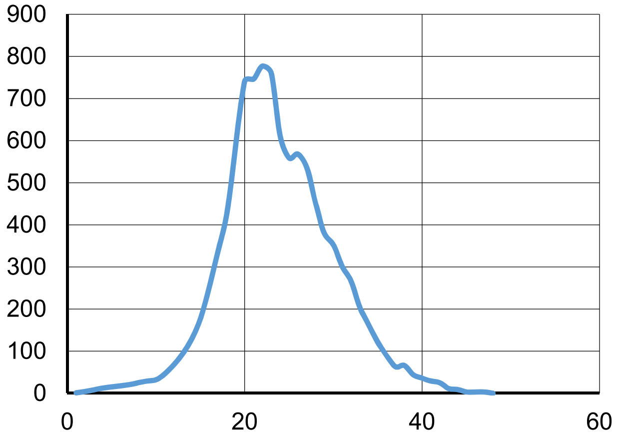

***FIG. 8.***

*An example of a typical dynamics of incremental growth of infected cells in a simulation based on German data*

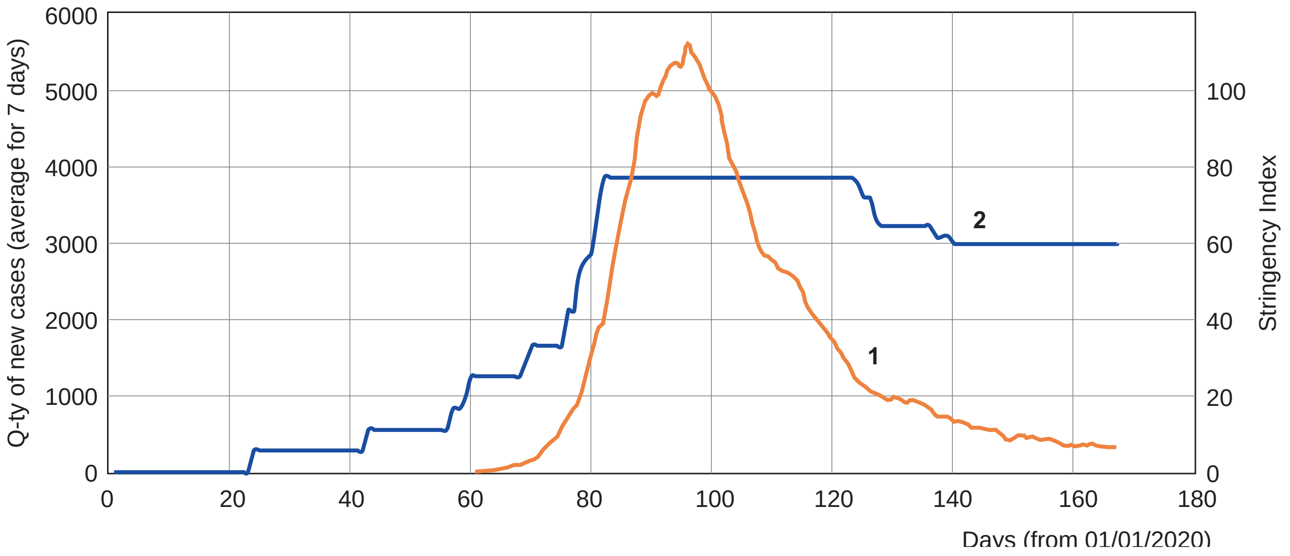

***FIG. 9.***

*The real dynamics of the daily increase in infected people in Germany:* **1** *– number of new cases;* **2** *– stringency of the restrictive measures*

Further research in this area could include the development of a model that takes into account more *population characteristics*, as well as *specific types* of restrictive measures, in order to understand the impact of these measures on the epidemic situation and, possibly, to formulate practical recommendations for their effective use, taking into account the specific characteristics of a country or region. Another major issue is the study of the relationship between the length of incubation period, duration of infectiousness and other characteristics of the pathogen (on the one hand) and the effectiveness of restrictive measures and their types (on the other hand). Besides, a number of "technical" issues related to the choice of the optimal grid size of the cellular automaton, to the determination of the CA discrete time and real time ratio, etc., need to be clarified.

## CONCLUSION

Study results show that even a rather simple cellular automaton model with boundaries can successfully describe the evolution of an epidemic and evaluate the effectiveness of restrictive measures. The proposed methodology (conducting a series of numerical experiments) makes it possible to estimate the probability of realization of one or another scenario when introducing restrictive measures. An important finding here is that with different levels of restrictions imposed, the quality of prediction is also different. Moderate severity measures (40–50 %) have the least predictable effect, with both rapid localization of the outbreak and spread of the epidemic to a large part of the population. Weak and strong measures give a more predictable effect.

CA models with intercellular boundaries have great potential for modeling epidemics and the impact of restrictive measures. Cellular automata as a kind of agent-based models potentially allow to describe with maximum completeness the population characteristics, specifying age, social, cultural, medical characteristics of each agent, which can influence both the spread of the epidemic and the effectiveness of restrictive measures. In addition, CA models allow to modify and supplement the rules of cell transition from one state to another, increase the number of these states, change the "rules of operation" of intercellular boundaries, taking into account their partial permeability.

All this makes it possible, firstly, to take into account more fully in the model the specifics of the population in a particular region or country and the specifics of its contacts, and secondly, to describe more fully the introduction of restrictive measures and their impact on the behavior of the population and the spread of the epidemic, which, in turn, makes it possible to choose the optimal degree of restrictions stringency, taking into account local characteristics.

### Conflict of interest

The authors of this article declare the absence of a conflict of interest.

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