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A Combined Model for Simulating the Spatial Dynamics of Epidemic Spread: Integrating Stochastic Compartmentalization and Cellular Automata Approach

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Abstract
This research focuses on a combined simulation model for analyzing the spatial distribution of epidemics by combining the global mixing assumption of individuals with two-dimensional probabilistic cellular automata (CA). The model presented in this paper is designed to simulate the spatial distribution of diseases in a spatially structured population. It incorporates a stochastic compartment model that uses the mixing regime, a two-dimensional probabilistic CA for constructing a decision support system for controlling epidemics. The model positions elementary populations in a regular two-dimensional lattice, whereas the compartment model applies to sets of persons who have the same epidemic regime in the community. Previous epidemic models involved dynamic compartment models with global mixing and are incorporated into most decision support systems but are more limited in their representation of the geographic spread of diseases. Alternatively, CA as individual dynamic systems can capture the spatial and temporal pattern of the epidemics through local near-neighbor interactions. They consist of rather separate cells in one or multi-dimensional space, where each cell has a constant number of neighbors. Since CA can predict the geographic distribution of some epidemics through proper mathematical models, they have the potential of improving epidemic prediction and preventive measures in public health management. The results of the study show the improvement of the quality of epidemic response management through numerical modeling and epidemic spread studies using the ensemble simulation model based on random partition models and numerical analysis.

Keywords- Cellular automata, Simulation modeling, Mathematical models, Stochastic model, Epidemic diseases.

1. Introduction

Rapid globalization, frequent travel, and the ability for people to come into contact with people across the state can cause infectious diseases to spread at an incredible rate. Throughout history, infectious diseases have led to higher human deaths and social panic (Dai et al., 2020). The global economy and society were affected by disruptions and serious consequences due to the increased frequency of natural disasters and public health emergencies in recent years. An emergency is defined as a sudden occurrence that puts public safety in jeopardy and is likely to result in significant casualties, property damage, ecological destruction, and considerable social impact (Shan et al., 2024). The world's health, economic stability, and social systems have all continuously faced serious threats from infectious diseases (Zhao et al., 2024). Global health crises, including pandemics and communicable diseases, now require an urgent call for effective prediction, control, and mitigation tools. These occasions adversely affect public health; they increase the burden on healthcare systems, bringing the possibility of societal disruption. Comprehensive and innovative approaches in this endeavor will require a combination of traditional and modern computational epidemiological methods. This research aims to address the gap through the development of improved mathematical models combined with CA for increased understanding and response to epidemic dynamics.

Epidemiology has been described as the branch of medical science that examines the patterns, causes, and effects of health events and diseases in specific populations by Samal (2016). It includes understanding disease distribution and importance, identifying species at risk, and developing prevention and control strategies, which may include affected individuals, their populations, geographical location, lifestyle factors, and environmental factors and details of their surroundings. Epidemiology, which is renowned as the fundamental science of public health, studies the distribution and determinants of health and illness factors in populations. It is important in studying and defining risk indicators for diseases and generating information for purposeful preventive health care and evidence-based medicine (Friis and Sellers, 2020). Epidemiology is able to use statistical and observational means to study the antecedents of conditions or events that affect health in an identified population group and then applies such knowledge in dealing with and controlling health issues (Bray and Regmi, 2016). Moreover, its interaction with recently developed technologies, including Geographic Information Systems (GIS) and computational modeling, has improved the knowledge of disease outbreaks and health changes in various populations (Neilan et al., 2010).

Stang et al. (2012) highlighted the significance of epidemiology in comprehending infectious and chronic diseases, environmental health issues, and the impact of lifestyle factors on health. Factor findings from epidemiological studies give useful insights for evidence-based treatment and public health policy. There are also enhancements. Mathematical epidemiology is a specialized field that uses mathematical models and computer methods to analyze the spread and prevention of infectious diseases and other health-related issues. It has to be noted that mathematical models have been used in handling issues to do with the transmission of infectious diseases and diffusion. Nevertheless, selecting the right model and correct physically relevant signatures has always been an issue in discerning and predicting the progress of a disease (Ghosh and Bhattacharya, 2021).

The goal of mathematical epidemiology is to model the spread of infectious diseases in populations. Understanding the timeline of the disease is an important goal to prevent its spread. The evolution of spatially structured populations has been modeled by a variety of different approaches. Patch-structured models and feedback diffusion models are examples of traditional modeling approaches. Such models have the advantage of enabling statistical analysis. However, these advantages always come at the expense of a number of oversimplified parameters that limit the applicability of these models, especially in development environments. A cellular automata (CA) model was created to investigate the development of an infectious nucleus under several epidemiologically diverse illness situations. CA model developed to study the evolution of an infectivity nucleus in several conditions of epidemiologically different diseases by Fuentes and Kuperman (1999). The CA model is now the more often used epidemiological modeling technique (Fan et al., 2024).

Kermack and McKendrick (1927) highlighted that mathematical models are created to reflect the interactions of individuals in a population as well as how infectious diseases travel from person to person. These models are often built around differential equations that describe how the number of susceptible, infected, and recovered individuals changes over time. The compartmental model is a popular kind of mathematical model used in epidemiology. It divides the population into different compartments, including susceptible (S), infected (I), and recovered (R). Depending on the disease being studied, additional compartments may be included to represent exposed individuals, those with partial immunity, or other relevant categories. A mathematical model refers to the characterization of a phenomenon or an object by mathematical concepts or words. The act creating of mathematically based models is known as mathematical modeling. Models are created to describe a system, analyze its components impact, and forecast the system's response (Martcheva, 2015).

In general, Mitchell et al. (1994) described CA as a dynamical system that is formed based upon spatial and discrete time as a model of physical process as a computational device. CA consists of spatial grids placed by cells in certain time (t) and state. At each discrete time, we perform an iteration in which cells update on certain rules. In this case we can say that CA is a perfect feedback machine, or more specifically, a finite state machine, which its state changes step by step.

Solving problems on the spatial distribution of epidemics requires a parallel or distributed architecture for its implementation. There are a number of mathematical models for parallel and distributed computing. One of the mathematical models of parallel and distributed computing is CA. The spread of an epidemic is a spatially distributed dynamic system, and to describe the spatiotemporal behavior of which it is possible to use models of the class of CA. The relevance of the development of problem-oriented systems for the management of epidemic diseases is not suspicious. The most important study of this disease is systemic adequate mathematical models for predicting the incidence of an epidemic (Bashabsheh, 2023a). To date, a significant number of such theoretically substantiated models based on a complex mathematical apparatus have been created. The total number of cases of missing prevalence includes cases of applying the incidence of a temporary epidemic disease, accounting for common forms of geographical objects and other cases of incidence of certain that presented by Bashabsheh (2023b). Vanag (1999) explained that they are often referred to as homogeneous structures. Cells can be located on a one-dimensional line, a plane, or in a multidimensional space. Each cell has a given number of "neighbors," determined by the problem statement, and can be in one of several states. Neighbors are established either by the presence of common boundaries between cells or with the help of a graph.

The study has great economic and commercial value by offering improved capabilities for modeling and forecasting the effects of epidemic diseases. CA-based models provide a low-cost substitute for disease modeling and, in turn, assist public health agencies and governments to manage and distribute resources, including vaccines, medical equipment, and human capital in an efficient and cost-effective manner without accruing unnecessary expenses. The approach is elastic and valuable in informing policymaking, allowing for the design of targeted interventions, such as mobility restrictions or vaccination campaigns that minimize disruptions to economic activities. In the commercial context, it could be incorporated into intelligent algorithms for care costs involved for health services, GIS appliances, and epidemic surveillance and monitoring systems, which will present prospects for the health technology organizations and data analysis firms. However, the proposed model may also be useful to the pharmaceutical manufacturers to optimize the logistics and distribution processes. Thus, the present paper’s finding of minimizing its economic costs and facilitating business continuity makes the study valuable for both the short-term pandemics’ health impact and the long-term economic robustness.

In this work, the author suggested a compartmental model for simulating the spread of cholera in the population, experimented with the simulation, and compared a deterministic and stochastic compartmental epidemic model. A new method for describing the spatial-temporal distribution of epidemic diseases is introduced using a CA where the rule changes are the status transitions of cells.

The contributions of our research are as follows:

- Implemented a method of modeling the dynamics of the epidemic processes and CA theory.
- Studied proposed model used by the Gnumeric spreadsheet and simulation package Any Logic.
- Developed a software tool for predicting the spatial and temporal spread of epidemics, utilizing object-oriented analysis and design principles. The implementation was carried out in C++ using the GNU GCC-4.7 compiler and Qt-4.8 libraries for development.

This study aims to improve the quality of management of epidemic response by numerical modeling and studies of the spread of epidemics using the combined simulation model based on stochastic compartment models and CA. This paper is organized into five main sections. Section 1 introduces the background and motivation of the spatial distribution of epidemics. Section 2 presents a literature review of the relevant topics. In Section 3, the proposed methodology used is described. Section 4 presents the experimental results, and Section 5 provides a conclusion.

2. Related Work

The following are studies that aim to predict the most prevalent epidemics globally. Hethcote (2000) presented compartment models, including more complex variants, such as the SEIR (Susceptible-Exposed-Infectious-Recovered) model, which are commonly used in decision support systems. These models assume that individuals interact uniformly across a large, homogeneous population, which simplifies computations but overlooks spatial heterogeneity. This limitation has led to the development of alternative modeling approaches aimed at improving spatial accuracy. Satorras and Vespignani (2001) also used graph-based models, in which networks are used to identify populations and their relationships. These examples can be used to illustrate the effects of physical barriers, mobility, and density on disease transmission. Studies have shown that network architecture plays an important role in disease transmission. Their findings suggest that basic model assumptions (such as homogenous mixes) may not hold true for scale-free real-world networks.

This work highlights how flexible CA is for examining the temporal and geographical dimensions of disease transmission. The model offers a platform for evaluating the effectiveness of different intervention tactics and allocating resources as efficiently as possible by mimicking them, such as vaccination campaigns and social distancing measures. The results aid in the creation of well-informed public health regulations meant to lessen the effects of infectious illnesses. One useful method for deciphering the intricacies of infectious illness dynamics is mathematical modeling with CA. This framework's adaptability enables a detailed investigation of many situations, leading to a better comprehension of the relationship between interactions at the individual level and larger population dynamics. In the continuous fight against illnesses, the knowledge gathered from these models may help direct evidence-based decision-making (Bashabsheh and Alzubi, 2024).

Bowness et al. (2018) proposed a hybrid, individual-based approach that analyzes spatial-temporal dynamics at the cellular level, linking the behavior of individual bacteria and host cells with the macroscopic behavior of the microenvironment. The individual elements (bacteria, macrophages, and T cells) are modeled using CA rules, and the evolution of oxygen, drugs, and chemokine dynamics is incorporated in order to study the effects of the microenvironment in the pathological lesion. That allowed bacteria to switch states depending on oxygen concentration, which affects how they respond to treatment. This is the first multi-scale model of its type to consider both oxygen-driven phenotypic switching of Mycobacterium tuberculosis and antibiotic treatment.

Recent studies have investigated the combination of stochastic methods and CA models to increase the accuracy of epidemiological models. This hybrid approach exploits the strengths of both approaches: the spatial dynamics of CA and the probabilistic nature of stochastic models. For example, Perez and Dragicevic (2009) developed a stochastic CA model to simulate the spread of influenza, where the probability of transmission between countries was determined by stochastic methods. Their model showed how random changes in individual motion patterns of disease rates may lead to different outcomes of the epidemic.

Another example is the work of Medeiros et al. (2011), which used CA with a stochastic compartment model to simulate the onset of viral diseases such as dengue fever. Their method took into account both vector behavior and environmental factors, which is crucial for accurately predicting the spread of insect-borne diseases. The model did an outstanding job of portraying how the disease spread across different areas and giving data on the effectiveness of intervention approaches like targeted spraying and vaccination.

The current research brings an extension to epidemic modeling literature in which CA is introduced to rectify the shortcomings found in both compartment-based models such as SEIR and graph-based approaches. Little previous work has been done on the spatial distribution of disease transmission; Hethcote (2000) and Satorras and Vespignani (2001) have explored transmission in homogeneous population and network-based models but did not account for critical heterogeneities instrumental in real-life projections. The current study builds on this by utilizing CA to describe the interaction of the individuals within a defined spatial framework, enhancing spatial resolution and enabling the simulation of various intervention strategies. Furthermore, the intervention of Bowness et al. (2018) and Perez and Dragicevic (2009) has informed this work that adopts the CA integrated with stochastic estimation to enhance model precision. The contribution of this paper is to add greater practical realism and flexibility into disease models by accounting for such factors as space, time, and probability of intervention, and therefore offers a more flexible and realistic analytical platform for policymaking and resource allocation in epidemic combat. This combined approach allows for topological representations of disease transmission through the surrounding environment and movement of disease vectors or infected individuals, which has been missing in the majority of the models. It is not merely in formulating a new method to blend the strengths of two modeling techniques in epidemic predicting but also in constructing a model that might become a valuable tool in the decision-making process of future public health solutions.

3. Methodology

This section is divided into three distinct subsections. The first part shows a description of the problem of the spread of the epidemic. In the second part, the proposed method of modeling the spatial spread of cholera in a spatially distributed population is to use the combined simulation model using probabilistic CA. In the third part, it shows the architecture and implementation of the software package for the proposed simulation model.

3.1 Problem Description

Review of the modern state of the problem of the spread of cholera in developing countries indicates that the epidemic of this disease is a complex process that is caused by a large number of factors of different natures. The epidemic process, or the process of the spread of infectious diseases among the population, is a complex, socially conditioned phenomenon, composed of the interaction of three main elements: the source of infection, transmission, and susceptibility to infection of the microorganism.

For forecasting the spread of epidemics, a compartment model is often used. Known models of cholera epidemics using the principle of a global mixing of individuals when all susceptible to infection are exposed to equal risk of infection. However, populations with diseases such as cholera, where great importance for the transmission of infection is not only the direct contact of individuals but also the environment, are spatially distributed dynamic systems. In this connection it is appropriate to use for modeling the epidemic process in such a population the method of CA. A CA is a mathematical object with a discrete space and time. Space is a field consisting of a set of cells forming some periodic lattice. Time is the sequence of steps or generations.

3.2 Proposed Model

The proposed model employs a probabilistic cellular automaton, where each cell represents an elementary population, incorporating global mixing within a population characterized by a discrete spatial structure. The cell's state dynamics are governed by a stochastic compartmental model, capturing the spread of the disease while accounting for migration processes between adjacent elementary populations. A schematic of a compartmental model developed to represent the spread of cholera within an elementary population is shown in **Figure 1**.

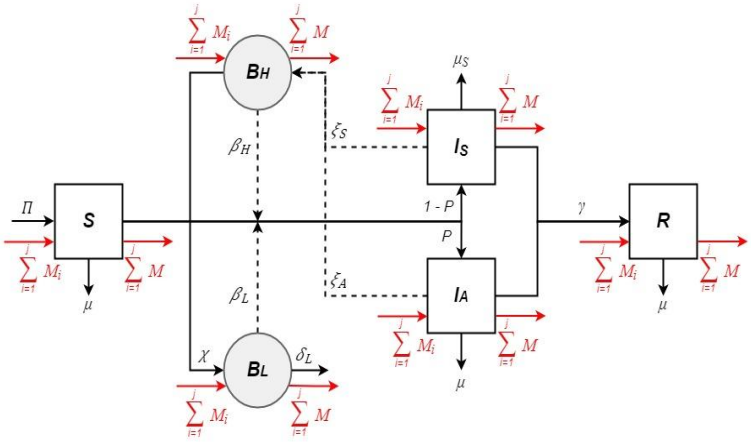


Figure 1. Graph compartment of simulation model of the spread of cholera using CA.

The proposed method of modeling the spatial spread of cholera in a spatially distributed population is to use the combined simulation model based on a stochastic compartment model assuming global mixing of individuals and two-dimensional probabilistic CA. Elementary populations form a regular two-dimensional spatial lattice, and their sizes allow you to use a compartment model. Compartment models are known as models in the state space where the state variables are the values of groups of individuals with the same epidemic status. The key parameters involved in modeling the spread of cholera are present, as indicated in **Table 1**. The table shows the description of the key elements that determine how the disease propagates through a population and its interaction with the environment (Codeço, 2001; Hartley et al., 2006; Neilan et al., 2010; Merrell et al., 2002; King et al., 2008).

Table 1. Description of model parameters

Parameter	Description	Value	Range
α	Proportion of population drinking contaminated water	different	0-1
β_H	Rate of drinking contaminated B_H vibrio cholera water	1/day	1/day – 1.5/day
β_L	Rate of drinking contaminated B_L vibrio cholera water	1/day	1/day – 1.5/day
K_H	The concentration of high infectious vibrio cholera	k_L/ 50	k_L/ 700 - k_L/ 10
K_L	The concentration of the low infectious vibrio cholera	10^6 cells/ml	--
χ	Rate of decay of BH to BL vibrio cholera	$(5\ h)^{-1}$	--
δ_L	Death rate of vibrio cholera in the environment	$(30\ d)^{-1}$	$(15\ d)^{-1}$ - $(90\ d)^{-1}$
μ	Rate natural death	$(61\ yr)^{-1}$	--
μ_S	the death rate from symptomatic cholera	$0.005(d)^{-1}$	$0.001(d)^{-1}$ - $0.05(d)^{-1}$
γ	Recovery rate	$(5\ d)^{-1}$	$(3\ d)^{-1}$ - $(10\ d)^{-1}$
P	The probability of symptomatic or asymptomatic infection	0.76	0.5 – 0.98
ξ_S	Rate of excretion of vibrio cholera, symptomatic patient	50cells/ml-d	10 - 50
ξ_A	Rate of excretion of vibrio cholera, asymptomatic patient	0.5cells/ml-d	0.5 - 10
$\prod$	The rate of new susceptible populations	--	--
M	Coefficient speed migration	--	--

The deterministic of the model is described by non-linear systems of differential Equations (1-6):

$$\frac{dS}{dt} = \Pi - \alpha\beta_H \frac{S.B_H}{K_H.B_H} - \alpha\beta_L \frac{S.B_L}{K_L.B_L} - \mu S + M\sum_{i=1}^{j} S_i - M\sum_{i=1}^{j} S \quad (1)$$

$$\frac{dI_S}{dt} = (1-P)\alpha\beta_H \frac{S.B_H}{K_H.B_H} + (1-P)\alpha\beta_L \frac{S.B_L}{K_L.B_L} - (\mu_S + \gamma)I_S + M\sum_{i=1}^{j} I_{S_i} - M\sum_{i=1}^{j} I_S \quad (2)$$

$$\frac{dI_S}{dt} = P\alpha\beta_H \frac{S.B_H}{K_H.B_H} + P\alpha\beta_L \frac{S.B_L}{K_L.B_L} - (\mu + \gamma)I_A + M\sum_{i=1}^{j} I_{A_i} - M\sum_{i=1}^{j} I_A \quad (3)$$

$$\frac{dR}{dt} = \gamma(I_S + I_A) - \mu R + M\sum_{i=1}^{j} R_i - M\sum_{i=1}^{j} R \quad (4)$$

$$\frac{dB_H}{dt} = \xi_S I_S + \xi_A I_A - \chi B_H + M\sum_{i=1}^{j} B_{H_i} - M\sum_{i=1}^{j} B_H \quad (5)$$

$$\frac{dB_L}{dt} = \chi B_H - \delta_L B_H + M\sum_{i=1}^{j} B_{L_i} - M\sum_{i=1}^{j} B_L \quad (6)$$

These equations model the interaction between the human population and the cholera bacteria, capturing the dynamics of how the disease spreads, how individuals recover, and how the bacteria persist in the environment. Models of cholera transmission dynamics, which describe the four states for population and two states for vibrio cholera: susceptible to the disease (S); symptomatic infection (I_S) and asymptomatic infection (I_A); recovered (R); highly infectious vibrio cholera (B_H); low-infectious vibrio cholera (B_L).

The main difference of this model is the introduction of migration flows between neighboring elementary populations, allowing you to use it as a transition rule of an algorithm for CA. Described model in discrete stochastic option:

- The state variables are considered to be integral, that is, consistent with their dimension (pers.);
- Introduce a single discrete time interval, to the dimensions of which are parameters of the model;
- Flows individuals between compartments considered discrete random variables distributed according to a binomial law; the flow rate in the deterministic version of the model is the probability of success in one experiment for a given distribution, and the volume of the compartment is the number of experiments.

Thus, a stochastic version of the cholera model used in CA is described by a system of finite-difference Equations (7-12):

$$S^{t+1} = S^t + \Pi - rb\left(\beta_H, \alpha\frac{S^t.B_H^t}{K_H.B_H^t}\right) - rb\left(\beta_L, \alpha\frac{S^t.B_L^t}{K_L.B_L^t}\right) - rb(\mu, S^t) + \sum_{i=1}^{j} rb(M, S_i^t) - \sum_{i=1}^{j} rb(M, S^t) \quad (7)$$

$$I_S^{t+1} = I_S^t + rb\left(\beta_H, (1-P)\alpha\frac{S^t.B_H^t}{K_H.B_H^t}\right) - rb\left(\beta_L, (1-P)\alpha\frac{S^t.B_L^t}{K_L.B_L^t}\right) - rb(\mu_S + \gamma, I_S^t) + \sum_{i=1}^{j} rb(M, I_{S_i}^t) - \sum_{i=1}^{j} rb(M, I_S^t) \quad (8)$$

$$I_A^{t+1} = I_A^t + rb\left(\beta_H, P\alpha\frac{S^t.B_H^t}{K_H.B_H^t}\right) - rb\left(\beta_L, P\alpha\frac{S^t.B_L^t}{K_L.B_L^t}\right) - rb(\mu + \gamma, I_A^t) + \sum_{i=1}^{j} rb(M, I_{A_i}^t) - \sum_{i=1}^{j} rb(M, I_A^t) \quad (9)$$

$$R^{t+1} = R^t + rb(\gamma, (I_S^t + I_A^t)) - rb(\mu, R^t) + \sum_{i=1}^{j} rb\left(M, R_i^t\right) - \sum_{i=1}^{j} rb(M, R^t) \quad (10)$$

$$B_H^{t+1} = B_H^t + rb(\xi_S, I_S^t) + rb(\xi_A, I_A^t) - rb(\chi, B_H^t) + \sum_{i=1}^{j} rb(M, B_{H_i}^t) - \sum_{i=1}^{j} rb(M, B_H^t) \quad (11)$$

$$B_L^{t+1} = B_L^t + rb(\chi, B_H^t) - rb(\delta_L, B_L^t) + \sum_{i=1}^{j} rb(M, B_{L_i}^t) - \sum_{i=1}^{j} rb(M, B_L^t) \quad (12)$$

These equations represent the evolution of the system over discrete time steps, capturing the probabilistic nature of disease transmission and recovery. Where, rb (A, B) - the operator receiving the item sample of a random variable distributed according to the binomial distribution with probability of success in one trial (A) and the number of experiments (B).

Analysis of the spread of epidemic diseases, the spatial transmission of infection, primarily associated with migration flows in a population of various levels, plays a significant role in this process. Important features of CA are the following rules:

- The ability of elements to move in space and the application of the concept of state to a new position.
- The state of each cell is updated as a result of a sequence of discrete constant steps in time.
- The variables in each cell are changed simultaneously ("synchronously"), based on the values of the variables in the previous step.
- The rule for determining the new state of a cell depends only on the local values of cells from some neighborhood of the given cell.

3.3 Architecture and Implementation of the Software Package

This section describes the calculation algorithm for the proposed simulation model, architecture, and realization of the program complex of forecasting spatiotemporal spread of epidemic diseases. Software implementation of the proposed model is made in C++ using the cross-platform toolkit Qt-4.7 and the graphs visualization library QwtPlot.

Figure 2 shows a diagram of objects that developed software tools in the category of Unified Modeling Language (UML).

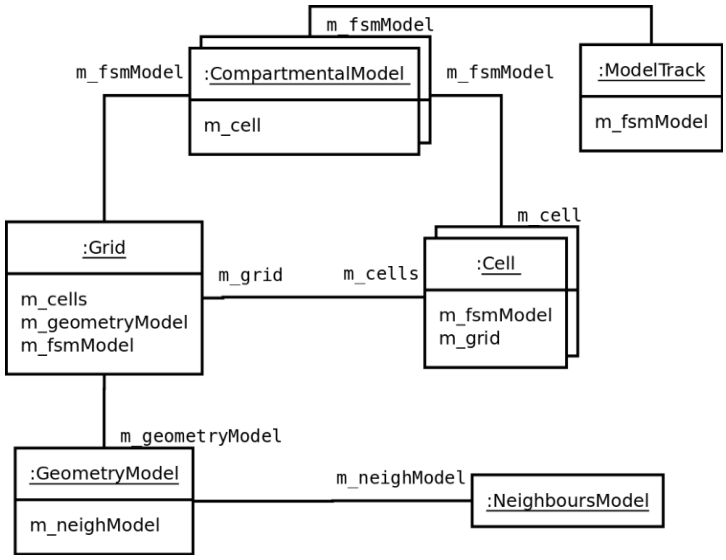


Figure 2. Diagram objects software tool space-time forecasting of epidemic situation.

The *Grid* class object is an aggregate class of Cell objects that represent the elementary population compartment model. Class objects *Compartmental Model*—replaceable compartment implementation of various models. The paper describes a model for cholera. *Model Track* objects are created for all instances of the model state variables, which should be preserved for display on the graphs. Objects *Geometry*

Model—replaceable realization of the geometric properties of lattices CA-model. The paper describes a model of rectangular and hexagonal two-dimensional lattices, CA. Class objects *Neighbors Model*—replaceable rules for determining the proximity of cells.

Figure 3 shows the user interface of a software tool developed to visualize the spatial dynamics of epidemic spread using the CA method. The interface contains various controls and visualization fields that allow users to set model parameters internally, start simulations, and observe results. Real-time simulation network description, epidemic spread visualization, and adjustable model parameter settings are some of the key features of the tool.

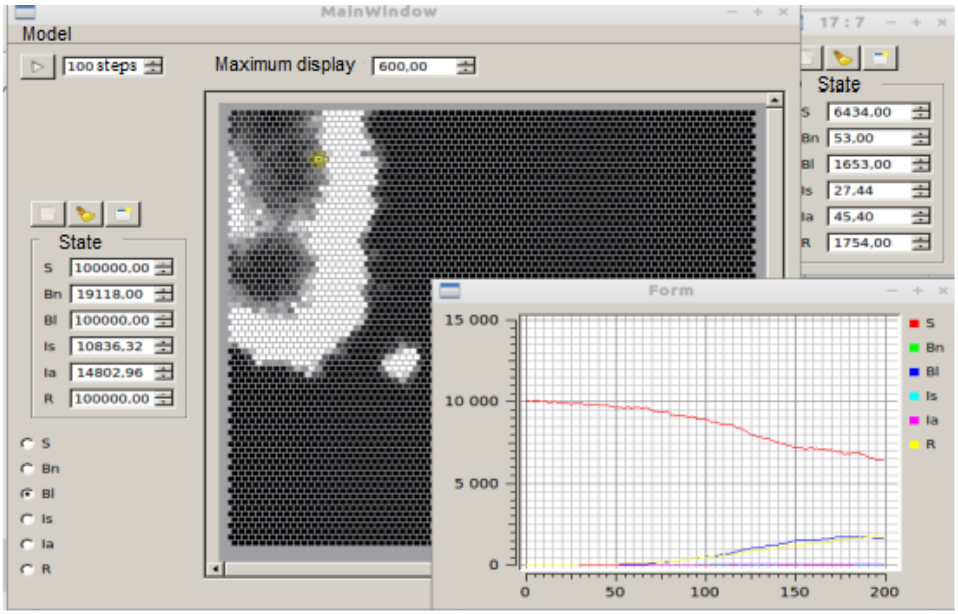


Figure 3. The software modeling of epidemic processes.

The functions of the developed software tools include:

- Modeling of the dynamics of two-dimensional CA models;
- Visualization of the simulation results in the form of raster maps states of cells. Charts change the values of the state variables of cells and the entire model;
- Providing the interface expansion a set of models by connecting external modules that implement:
  - Geometries, lattices, and CA models;
  - Options Neighborhoods cells CA-models;
  - Variants of models of states and transitions of cells.

The application of the proposed simulation model of the spatiotemporal spread of epidemic disease on the example of cholera in medical practice will allow us to control and analyze regularities of the spread of disease, thus enhancing the quality of management of anti-epidemic operations.

4. Results and Discussion

This section describes the experiments on the comparative analysis of results of modeling the dynamics of the epidemic process for cholera using compartment simulation of the model and developing a combined model, as well as modeling the spatial spread of the disease.

4.1 Experiment 1

The experiment was conducted to simulate the spatial dynamics of an epidemic using a combined model implemented in a CA framework. The simulation was set up with the following conditions:

- Lattice Configuration: Compared to the square lattice, the regular hexagonal lattice provided a more organic lattice structure for the interaction structure of the CA model.
- Neighborhood Algorithm: Using the 1st-order neighborhood algorithm, each cell communicated with its cell that was directly adjacent to it.
- Initial Conditions: The average number of individuals susceptible to the disease (S) was set to 10^5. This parameter sets the initial population at risk in the simulation.

Figure 4 shows the results of the visualization simulation experiment for the state variables S, I_S, and B_H in three steps of discrete time.

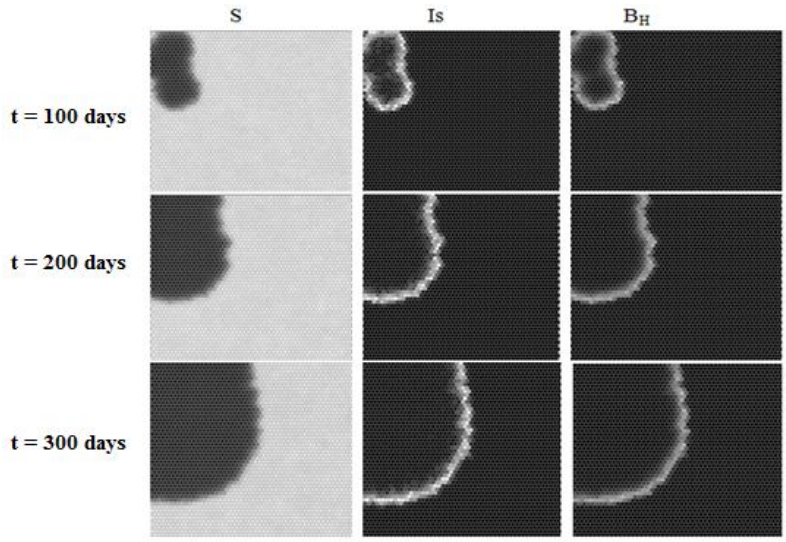
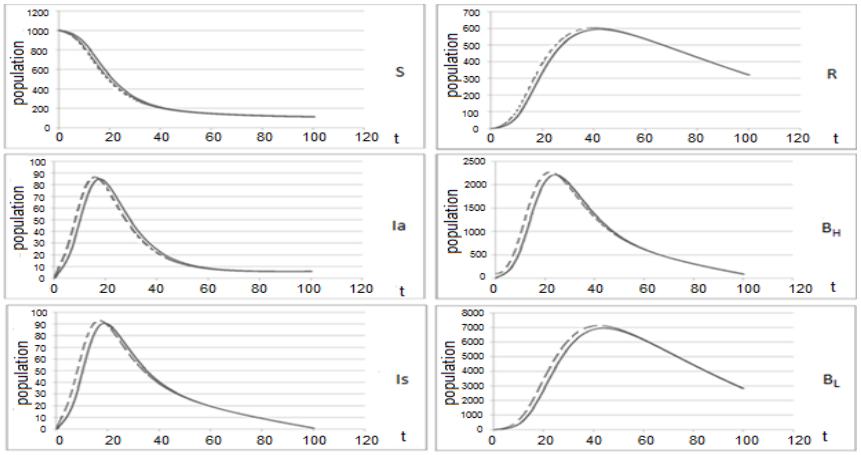


Figure 4. Visualization of the results for the three-state cholera model.

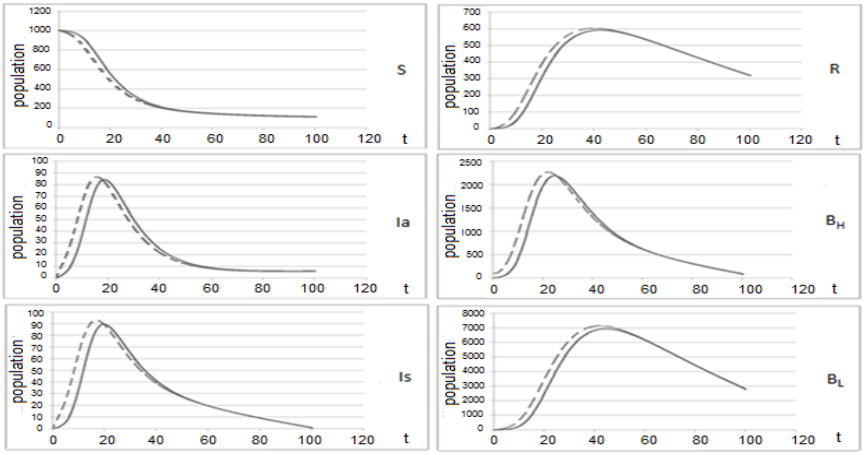
The figure represents the conclusions of the CA approach to the identification of spatial patterns of a cholera epidemic over time. It shows separate state variables in the epidemic model in three successive time points: 100, 200, and 300 days. The results indicate how the epidemic model, which works within the CA framework, describes cholera epidemic dynamics through captured and quantified interaction between a human population and bacteria in the environment. The enlarged extent of the contaminated areas shows that if not attended to, cholera can increase with time. The proliferation of contaminated areas indicates that, if not treated, cholera can spread rapidly over time.

4.2 Experiment 2

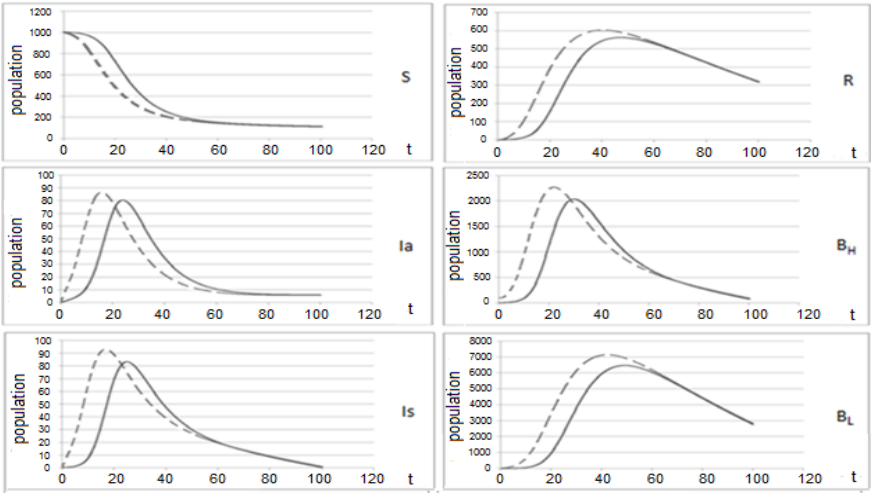
An experiment designed to compare the sensitivity of two types of models in simulating the cholera outbreak: a compartmental deterministic model and combined models that integrate CA with stochastic elements. The focus of the study is to investigate how changes in the migration coefficient (M) affect the dynamics of cholera spread over a specific period. **Figure 5 (a-c)** shows the results of a comparative study of the spread of cholera. The figure illustrates the response of the model of the migration coefficient (M) for the proposed model for three different values (M = 0.5, 0.05, and 0.005) to identify the most effective migration coefficient in the time interval [0-100] days.



a) M = 0.5



b) M = 0.05



c) M = 0.005

Figure 5. Cholera spread dynamics with sensitivity of the model to changes in coefficient speed migration (M). where, —— (solid line) is the combined model, ---- (dotted line) is the compartment model.

The figure shows plots of the sensitivity of state variables of the model to changes in coefficient speed migration. In this case, population mobility can be identified as high, and the migration coefficient when M = 0.5 can be attributed to the process. Frequent migration causes escalated and early transmission; hence, it is the worst situation as far as infections and diseases are concerned. However, when M = 0.05, the migration is considered average, where the number of infected patients who travel between regions is effectively controlled by the number of patients treated within a given region. Moderate migration is ideal, and this means migration to some extent but not to an extent that it gets out of hand because control can be useful in implementing gradual steps. For M = 0.005, the migration is greatly reduced due to some constraints in the movement of the individuals between regions. The transmission rates are much lower for cholera, and thus the emigration and steep rise in the infected populations are slower. Conservative migration is the most effective for containment as the outbreak slows down and the overall spread is reduced with long-lasting approaches till the disease is completely eradicated.

Together the three figures illustrate how changing the value of the migration coefficient (M) affects the transmission of cholera. Where there is higher migration, the rate of transmission increases, and the maximum infected people also increase; on the other hand, lower migration decelerates the epidemic and reduces the total affected population. The results show high importance of mobility for epidemic control and can serve as a reference point for adjusting the approaches, like mobility limitations or quarantines, to slow down the transmission of infectious diseases. Thus, M = 0.005 emerges as the best migration coefficient for managing the cholera epidemic, as it ensures slower spread, minimizes peak infection rates, and provides ample time for effective intervention strategies. The results of research models show that the decrease in the intensity of migration flows between the compartments leads to the manifestation of delay changes in the number of infected in comparison with models of global mixing.

5. Conclusions

The research is devoted to the development of the combined simulation model of the spatial spread of epidemics, which allows for modeling the spatial distribution of diseases with an assumption of global mixing of individuals and the two-dimensional probabilistic CA using a compartment model as a rule for the state transition of cells to create, on its basis, a decision support system to counter the spread of epidemics. The research received the following results:

- The structure of the stochastic compartment model spread of cholera differs in views of members of the population flows between compartments as a random variable distributed according to the binomial law that allows more accurately reflecting the dependence of the dynamics of the epidemic process of the absolute values of volume compartments compared with known deterministic models.
- A combined simulation model based on a combination of stochastic compartment models and probabilistic CA for the prognostic assessment of the spatial spread of epidemics.
- The model of two-dimensional CA and the results of imaging in simulation of the spatial distribution of epidemics using probabilistic CA based on regular hexagonal lattices. Results of the study indicate that the use of the developed model allows determining the peculiarities of this method for the prognostic assessment of the epidemiological situation.
- Develop a software modeling tool for the spatial-temporal dynamics of epidemic processes in the population that can be used as the main element of model-driven decision support systems to combat epidemics.
- The results of the study model sensitivity to a change in speed ratio compared compartment migration and combined simulation model based on stochastic compartment models and CA. The results of research models show that the decrease in the intensity of migration flows between the compartments

leads to the manifestation of delay changes in the number of infected in comparison with models of global mixing.

The proposed work has several limitations, including the assumption of homogeneous agent behavior within each grid cell, which may overlook individual-level variations that affect disease dynamics. The model's accuracy is also dependent on the availability and quality of input data, such as demographic, environmental, and mobility patterns, which could be incomplete or unreliable in real-world applications. Additionally, the computational complexity of simulating large geographic areas or high-resolution data may require significant computing resources. The intervention strategies modeled are simplified and may not fully capture the broader economic or social consequences of such measures.

These results suggest the explanatory role of the migration coefficient for cholera dynamics and bring understandings of disease control under different mobility conditions. Future studies may introduce more realistic demographic and mobility data so that the model becomes more realistic and closer to actual usage. Incorporating GIS could facilitate more accurate simulations by considering population density, migration patterns, and geographic features.

Refining the model by incorporating additional factors, such as vaccination, water sanitation measures, and access to treatment, could offer a more thorough understanding of disease dynamics. Improving epidemic preparedness through refinement of the parameters causing the model to also simulate other diseases would broaden the usage of the model for various epidemics in the preparation of public health management. Further, the identification of common factors within and between the cases of intervention strategies—quarantine zones, mobility restrictions, or improving the water hygiene of a given environment—could prove beneficial for policy-making.

The relative size of the populations and geographic resolutions that can be modeled could be some of the areas that can be improved by using high-performance computing technologies. The results could be made more policy-relevant and useful for the decision-makers and public health officials with the help of other developing techniques for creating more interactive visualizations. In this way, further developments should be made in future research on the basis of the current findings in order to enhance epidemic control and population health modeling and in responding to other important concerns of population dynamics.

Conflict of Interest
The authors confirm that there is no conflict of interest to declare for this publication.

AI Disclosure
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