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Integrated Simulation Model of the Spatial Distribution of Dynamic Systems Using Intelligent Cellular Automaton

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ABSTRACT

This research emphasizes the versatility of cellular automata in studying the spatial and temporal aspects of disease spread. By simulating various intervention strategies, such as vaccination campaigns and social distancing measures, the model provides a platform for assessing their efficacy and optimizing resource allocation. The findings contribute to the development of informed public health policies aimed at curbing the impact of infectious diseases. Mathematical modeling using cellular automata emerges as a valuable approach in unraveling the complexities of infectious disease dynamics. The versatility of this framework allows for a nuanced exploration of diverse scenarios, fostering a deeper understanding of the interplay between individual-level interactions and broader population dynamics. The insights gained from such models hold the potential to guide evidence-based decision-making in the ongoing battle against infectious diseases.

Keywords*:* Cellular automaton, artificial intelligence, dynamical systems, simulation modeling, mathematical models, epidemic diseases.

1. INTRODUCTION

Infectious diseases can spread incredibly quickly due to rapid globalization, frequent travel, and interactions between individuals in other nations. Throughout history, infectious diseases have frequently led to a rise in human mortality and social anxiety. As this work is being assembled, countries around the world are dealing with the coronavirus disease 2019 (COVID-19) [1]. Since it is unethical to conduct experiments on the spread of infectious diseases in our society, mathematical tools—such as theoretical modeling, analysis, and data mining—offer a workable substitute for examining the mechanism of spread and devising effective control measures.

Understanding infectious diseases, chronic illnesses, environmental health concerns, and the influence of lifestyle variables on health are all made possible by epidemiology. The results of epidemiological studies support evidence-based public health and medicine, which eventually enhances community health and well-being. Within the specific discipline of epidemiology known as "mathematical epidemiology," researchers examine the transmission and management of infectious illnesses as well as other health-related phenomena using mathematical models and computational methods [2]. Its goals are to forecast the possible effects of different interventions and control measures and to comprehend the dynamics of disease transmission within populations. The goal of epidemiology is to identify the factors that cause or contribute to the development of diseases by studying how they spread.

Epidemiology is an interdisciplinary scientific area that studies biological processes, especially epidemics, in detail by using mathematical ideas like statistics. Over the course of its development, epidemiology has made significant strides, particularly in reaction to significant epidemics like the flu and the impact of computer technology improvements, which have made sophisticated numerical simulations possible [3].

The goal of the modeling technique known as "system dynamics" is to comprehend how complex systems behave over time. It represents the interactions and feedback loops between various systems components using mathematical equations [4]. One of the most important and difficult issues in the study of epidemics is predicting future trends, such as the number of people that could get infected daily [5].

Mathematical modeling stands as an indispensable tool in contemporary epidemiology, providing profound insights into the intricate dynamics of infectious disease spread. This paper elucidates the pivotal role of mathematical models in understanding, predicting, and mitigating the transmission dynamics of infectious diseases. Drawing upon historical developments and seminal models such as the susceptible–infective–recovered (SIR) model, introduced by W. O. Kermack and A. G. McKendrick in 1927, is one of the foundational models in mathematical epidemiology for studying the spread of infectious diseases, we highlight how mathematical modeling encapsulates essential parameters and variables, including transmission rates, population demographics, and intervention strategies. Important insights into the mechanics of infectious illness transmission are offered by the SIR model, such as the peak number of infections, the duration of the epidemic, the proportion of the population affected, and the impact of control measures (e.g., vaccination, social distancing, quarantine) on disease spread. Although the SIR model makes simplifying assumptions and may not capture all complexities of real-world disease dynamics, it serves as a fundamental framework for understanding and analyzing the spread of infectious diseases and has been adapted in various ways to address different epidemiological scenarios and challenges [6].

By simulating various scenarios and incorporating uncertainty, mathematical models facilitate informed decision-making, resource allocation, and policy formulation for public health authorities and policymakers. Furthermore, we discuss the challenges, limitations, and advancements in mathematical modeling approaches, emphasizing the integration of real-world data, interdisciplinary collaboration, and technological innovations. In conclusion, this abstract underscores the indispensability of mathematical modeling as a powerful and versatile tool for elucidating infectious disease dynamics, fostering global health security, and guiding proactive measures to safeguard public health [7].

The spatial distribution of epidemics can be solved using a variety of parallel and distributed computing mathematical models, which is realized on cellular automata. Cellular automata (CA) represent a powerful mathematical model of parallel and distributed computing for studying the spatial distribution of epidemics. By simulating the complex interactions and dynamics of infectious diseases within spatially explicit environments, CA models provide a versatile framework for exploring epidemic patterns, evaluating intervention strategies, and enhancing our understanding of the spatial aspects of infectious disease transmission and control [8, 9].

First conceived by von Neumann [10], CA are computational algorithms that are realized by parallel computation and rely on a small number of very basic local rules. The spread of infectious illnesses is one well-known scientific domain where CA computing has been shown to be helpful for complex systems [11]. A two-dimensional spatial progression of the infection was simulated by White et al. [12]. In order to mimic population mobility and model the population in various patches, Athithanet al. [13] used a dynamic CA. Pfeiferet al. [14] simulated the spread of disease by introducing real geographic data into CA.

One of the key characteristics of a CA is the kind of grid that is utilized to calculate the cell's state. A one-dimensional line is the most basic type of grid. Grids that are square, triangular, or hexagonal can be analyzed in two dimensions. The grid can have any limited number of dimensions. A CA is composed of an endless or finite regular grid of cells, each in one of a limited number of states. A cell's condition at time t depends on the conditions of the cells that surround it at time $t - 1$. Within our framework, the grid can be viewed as a geographical area that is segmented into smaller areas, or cells. The Moore neighborhood [15] and the von Newmann neighborhood [16] are the two types of neighborhoods that are frequently employed for the computation of cellular automata on the square grid. For the purpose of updating its state based on the values in this neighborhood, each cell has its own set of rules.

The behaviors of ongoing dynamic systems, like populations grappling with spreading epidemic diseases,

can be defined using CA [17]. According to statistical data, the epidemiological situation aligns with the conventional SIR model. In the initial phase of the modeling procedure, we specific the independent and dependent variables. The independent variable is time denoted as t in days. The early models of epidemics outline three demographic groups: the count of susceptible individuals (S), the count of infected individuals (I), and the count of individuals who have recovered with lasting immunity (R).

It is commonly acknowledged that automation of AI holds great promise in simulating the processes of epidemics and making a major contribution to tackling global issues. The key advantage of AnyLogic that motivated the choice of this environment is its capacity to create hybrid models, which fuse an agent-based methodology with a discrete or continuous description of the surroundings. Through simulations, users can explore various algorithms and configurations to improve task distribution, path planning, and overall system performance [18 - 20].

In this paper, we introduce a CA model designed for simulating the transmission of influenza. The proposed simulation model integrates stochastic models with the assumption of global individual mixing and employs a two-dimensional CA to model the spatial dissemination of influenza within dispersed populations. Within the CA simulation, migration takes place, capturing the dynamics of migratory flows and the interaction of populations between elementary units [21].

2. METHODOLOGY

CA represents an ideal platform for capturing the complex interactions between individuals within a population. Leveraging a lattice-like structure, each cell represents an individual, and state transitions emulate the progression of the disease. This paradigm makes it possible to describe temporal and geographical dynamics, which sheds light on how illnesses spread and change over time within a population. Researchers can simulate different scenarios and use the results to guide public health plans and actions by changing the settings and regulations. The model integrates key epidemiological parameters, such as transmission rates, recovery periods, and spatial factors, to simulate realistic scenarios [22].

The SIR model is a mathematical model that divides a population into these three categories, and it is commonly used to study the dynamics of epidemics. Susceptible (S) denotes individuals vulnerable to the infectious disease, susceptible to becoming infected upon contact with an infected person. Infected (I) refers to those who have contracted the disease and can transmit it to susceptible individuals. Infected individuals may exhibit symptoms or remain asymptomatic. Recovered (R) encompasses individuals who have successfully overcome the infection and acquired immunity. Having recovered, they are no longer susceptible to the disease and are incapable of transmitting it to others [23].

The stochastic compartment model of an epidemic disease based on CA is shown in Figure 1.

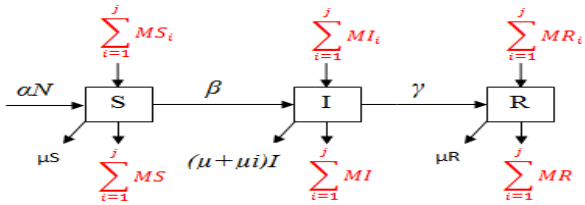

Figure 1. The stochastic compartment model of an epidemic disease based on CA

N represents the total population, while α signifies the rate of new susceptible populations, β represents the infection rate, γ represents the recovery rate, μ represents the death rate, μ_i represents the death rate from the disease, M represents the migration rate coefficient, j represents the number of neighbors.

The SIR model (Figure 1) is specified by a system of differential equations for a stochastic epidemic model has the form (at Δt=1):

$$\begin{cases} S_{t+1} = S_t + rb(\alpha; N_t) - rb(\beta I_t; S_t) - rb(\mu; S_t) \\ I_{t+1} = I_t + rb(\beta I_t; S_t) - rb(\gamma; I_t) - rb((\mu + \mu_i); I_t) \\ R_{t+1} = R_t + rb(\gamma; I_t) - rb(\mu; R_t) \end{cases} \quad (1)$$

Let St represent the count of susceptible individuals in the population at time t, It denote the count of infected individuals at time t, and Rt signify the count of recovered individuals at time t. The operator rb signifies the action of assigning a random variable following the binomial distribution law. When rb = Randbinom (p; n), p denotes the intensity, the probability of success, and n represents the number of trials in the binomial distribution.

The term "RandBinom" suggests the use of a random binomial distribution in the context of a model. In the SIR (Susceptible-Infectious-Recovered) model, this could be related to introducing randomness in the transmission of the disease. The binomial distribution is often used to model the number of successes in a fixed number of independent Bernoulli trials, where each trial has the same probability of success.

The use of a random binomial distribution introduces stochasticity into the model, reflecting the inherent randomness in the transmission of infectious diseases. In deterministic SIR models, the number of new infections is often calculated using fixed parameters. Introducing randomness through a binomial distribution allows for a more probabilistic and realistic representation of disease transmission in certain scenarios.

When CA is used, they are commonly referred to as homogenous structures. Cells can be found in multidimensional space, on a plane, or on a one-dimensional line. The problem statement specifies how many "neighbors" each cell has, and they can be in any of multiple states. Either a graph or the existence of shared cell boundaries is used to identify neighbors. A cell's state at a given time in the future is determined by its current state as well as the states of its neighbors.

The differential equations for the SIR model based on CA are as follows:

$$\begin{cases} S_{t+1} = S_t + rb(\alpha; N_t) - rb(\beta I_t; S_t) - rb(\mu; S_t) + rb(M; S_t^i) - rb(M; S_t) \\ I_{t+1} = I_t + rb(\beta I_t; S_t) - rb(\gamma; I_t) - rb((\mu + \mu_i); I_t) + rb(M; I_t^i) - rb(M; I_t) \\ R_{t+1} = R_t + rb(\gamma; I_t) - rb(\mu; R_t) + rb(M; R_t^i) - rb(M; R_t) \end{cases} \quad (2)$$

Migration takes place between elementary populations that correspond to the cell when population mixing and migration processes are modeled using cellular automata. Individuals may be chosen for migration in the manner described below (supposition): For the whole population, the rate of migration remains constant. Every group experiences equal migration.

The impact of epidemiological disaster variables on the process of implementing preventive measures and suitable responses in real time is reflected in an epidemiological model based on CA dynamics that dynamically combines epidemiological system data and occurrence prediction.

3. RESULTS AND DISCUSSION

In CA as computational models are not considered input and output actions. Rather, the emphasis is on the fundamental local rules that control the state transitions of individual cells as a function of neighboring states. Due to its decentralized design, CA is an effective tool for mimicking a variety of events, including the spread of illness, without requiring external inputs or outputs. This is because it enables the creation of complex global behaviors from simple local interactions.Cells can be placed on a one-dimensional line, plane or in a multidimensional space. The next state of a cell is defined as the time function of the state of its own and neighbor states at the current time. The creation of problem-oriented management systems reduced the spread of epidemics and diseases, which are dynamic, spatially dispersed systems in the environment.

Data visualization tool in the developed format is a local application. The application can be launched on any hardware and software platform that is available as a target platform in this development environment. Figure 2 shows the appearance of the working copy of the software tool.

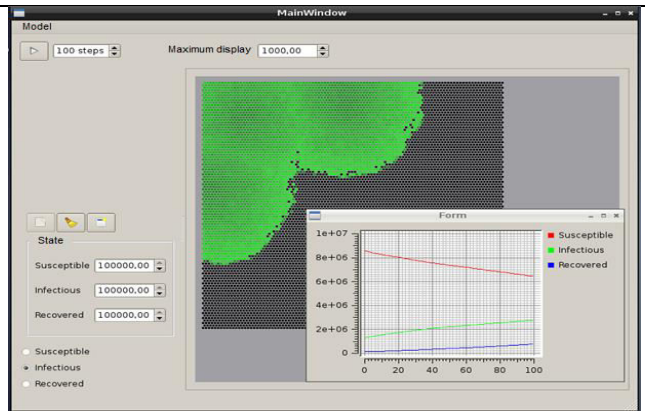

Figure 2. The software modeling of epidemic processes

The application supports zooming and scrolling the image of a two-dimensional (2D) lattice of a CA. In this case, the color of the cells may be associated with their state and parameters.

CA is well-suited for illustrating the spatial progression of epidemics. Figure 3 shows the visualization results for modeling epidemic diseases with an interval of 20 steps. In this case, the area with size (test grid) 100 × 100 cells is considered. Initially, five infected individuals are dispersed randomly within this area.Over time, the CA model simulates how the disease spreads through interactions between neighboring cells, providing valuable insights into the dynamics of epidemic progression within a defined spatial domain.

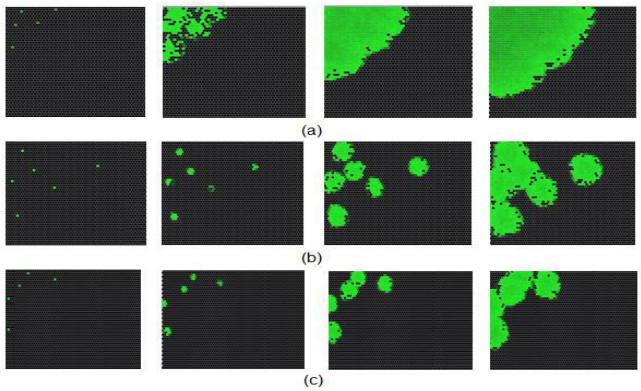

Figure 3. An illustrative example showcasing the spatial progression of the epidemic (time = 20, 40, 60, and 100 day).

We conducted three experiments (a, b, c) in several areas at multiple times that measured in days (d). A simulation of the propagation process shows that the infected region (I) keeps spreading outward and that the infected individuals recover (R) after a certain amount of time. Government control and medical reaction stop the spread of infectious disease.

Model results indicate that the transmission of epidemic diseases is retarded when the intensity of migration flows between cells under all conditions decreases. As illustrated in the picture, the migration rate coefficient determines how an infection spreads from the initial cell to the other cells.

The graphs show that the simulated epidemic situation's development in nearby healthy cells is significantly influenced by the value of this coefficient. The state of each cell is determined by the proportion of the population that is infected at each time step.

4. CONCLUSIONS

In this paper, we introduce a CA model designed for the modeling and evaluation of epidemic evolution. The model represents a simplified social community on a two-dimensional plane, accounting for individual heterogeneity by incorporating factors such as sex ratio, age structure, individual immunity, incubation and

treatment periods, and population movement.

The author genuinely hopes that this work will offer a different perspective on how infectious diseases propagate and ultimately aid in the global control of infections in the future. Exploring more practical strategies, including partitioned management and the synergy of multiple strategies, can be investigated to enhance decision-making informed by the model developed in this study. In addition to infection-related problems, symptoms may vary widely, reflecting variations in the underlying mechanism of infection. Determining the spread's current evolution condition via data analysis from a systematic perspective is also beneficial and doable. Future research can examine the transmission of all infectious illnesses within a given area as a complicated system with an underlying mechanism.

The proposed CA model is well-suited for incorporating and simulating the dynamics of mobility and interaction between vectors and hosts (individuals susceptible to the disease). Here's a breakdown of the key points:

- The modeling framework being discussed is based on CA. Cellular automata involve a grid of cells, each with a state that can evolve over discrete time steps based on predefined rules. In this context, the cells likely represent spatial locations or compartments.
- The strength of the proposed CA model lies in its ability to seamlessly incorporate and simulate the movement and interactions between disease vectors and hosts.
- The primary purpose of the model is to not only describe the ongoing spread of diseases but also to identify and predict outbreaks. By considering the mobility and interaction between vectors and hosts, the model is better equipped to simulate and anticipate the spatial and temporal patterns of epidemic outbreaks.
- The use of CA, with its ability to represent local interactions and discrete spatial entities, provides a flexible and intuitive framework for studying complex systems like epidemic dynamics. It allows for the incorporation of various parameters influencing disease spread, making it a valuable tool for decision-makers in public health.

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