Epidemiological Modeling of Measles with a Long Incubation Period using Cellular Automata

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ABSTRACT

Infectious diseases have significantly impacted human populations, with their spread influenced by factors such as density, mobility, and social interactions. Traditional epidemiological models, such as SIR and its extensions (SEIR, SEIRS), provide insights into outbreak dynamics but often overlook spatial heterogeneity. This study employs cellular automata to simulate the spread of measles, incorporating Moore neighborhood to SEIR model transmission through close contact. The simulation accounts for variable incubation periods and the development of herd immunity, capturing key aspects of disease propagation. By analyzing the spatial evolution of outbreaks, the model enhances the understanding of transmission patterns and contributes to the development of effective containment strategies in epidemiological research.

Introduction

Rapid globalization, frequent travel, and interactions among people from different countries contribute to the astonishing rate at which infectious diseases can spread. However, the dissemination of pathogens is not a phenomenon exclusive to modern times. Since prehistoric times, infectious diseases have played a crucial role in human history, influencing not only population health but also social organization, demographic growth, and the evolution of civilizations [1]. Throughout history, the expansion of human populations and increased interactions among individuals have created favorable conditions for the emergence and spread of new pathogens, leading to heightened risks of outbreaks, epidemics, and pandemics [2]. Documented since antiquity — such as the plagues mentioned in biblical records — epidemic outbreaks have frequently emerged during periods of population growth and intensified human contact, often driven by trade, wars, or migrations.

In the current scenario, international travel plays a similar role, facilitating the rapid spread of diseases across continents. Given the recurring nature of pathogens throughout history, researchers have sought ways to model the dissemination of infectious diseases in society. A significant milestone in this field was the study by Kermack and McKendrick in 1927, which developed the Susceptible–Infected–Recovered (SIR) model to analyze the spread of the Black Death in London [3]. This model introduced the important threshold theory, used to determine whether a disease could reach epidemic proportions, laying the groundwork for the study of infection dynamics.

However, many infectious diseases exhibit high complexity, influenced by factors such as prophylaxis, medical treatments, transmission rates, incubation periods, population movement, quarantine measures, and vaccine availability. To address these complexities, the SIR model has been modified to account for additional epidemiological characteristics. The Susceptible–Exposed–Infected–Recovered (SEIR) model was developed to incorporate the incubation period before an individual becomes infectious [4], while the Susceptible–Exposed–Infected–Recovered–Susceptible (SEIRS) model extends this by considering the possibility of reinfection after immunity wanes [5].

In this context, this study aims to develop a computational epidemiological model using cellular automata to simulate the spread of measles, a highly contagious disease caused by the Measles morbillivirus. Although measles has been eliminated in some countries, outbreaks continue to occur due to declining vaccination coverage and viral circulation in regions with low immunization rates. Through this analysis, the goal of this study is not only to gain a better understanding of measles transmission patterns but also to evaluate preventive strategies, such as the impact of vaccination and herd immunity, thereby contributing to the formulation of effective containment measures and supporting future research on infectious disease control.

Methods

The proposed modelling for studying the spread of measles uses cellular automata based on the SEIR model, incorporating a two-dimensional representation, as discussed in the book *Modeling Infectious Diseases in Humans and Animals* [6]. This approach allows the simulation of disease spread in a spatially distributed population, where each individual is represented by a cell within the matrix. The SEIR model was chosen because of the natural dynamics of measles, which is characterised by an incubation period before the onset of symptoms and permanent immunity acquired after recovery.

Initially, the model simulates a grid of size N × N, where each cell represents an individual that interacts only with those in its immediate neighbourhood. Initially, all individuals are in a susceptible state, i.e. they are at risk of contracting the disease if they come into contact with an infected individual. When such contact occurs, the susceptible cell transitions to the exposed state, indicating that the individual has been infected but is not yet symptomatic or capable of transmitting the virus. This incubation period is crucial for realistically representing the dynamics of measles and its variability within the population. After a certain incubation period, the cell transitions to the infected state, at which point it becomes a carrier. This phase corresponds to the symptomatic period, during which the individual can infect other susceptible individuals in its neighbourhood. Finally, at the end of the infectious period, the cell enters the recovered state and acquires permanent immunity against future infections.

State transitions occur based on epidemiological rules governing infection dynamics. Virus propagation is determined by a proximity-based criterion, using a Moore neighborhood, in which each cell interacts with its eight adjacent neighbors. This configuration reflects the nature of measles contagion, which primarily occurs through close contact in shared spaces such as schools and households. When an infected cell is near a susceptible cell, there is a defined probability of transmission, denoted as $P_{infection}$, which simulates the disease's contagion rate.

With regard to incubation time, the model considers this as a key aspect and does not assign a fixed duration to all cells. Instead, the incubation period $T_{incubation}$ varies within a predefined range, following a probabilistic distribution based on epidemiological studies. This variation provides a more realistic simulation as individuals do not show symptoms at exactly the same time. Similarly, the infectious period, referred to as $T_{recovery}$, is determined based on clinical observations of measles and defines the average length of time that an infected individual remains capable of transmitting the disease before recovering. After this period, the individual enters the recovered state, where acquired immunity prevents re-infection and further involvement in viral transmission.

The model parameters have been defined on the basis of real epidemiological data on measles [7], ensuring that the simulation accurately reflects the dynamics of the disease. The infection rate $P_{infection}$ regulates the probability of transmission between susceptible and infected individuals, while the incubation period $T_{incubation}$ varies between 7 and 14 days, capturing the statistical spread of this interval in the population. The recovery time $T_{recovery}$ is set to 10 days, which is the average time observed in the literature for the cessation of viral transmissibility.

Results

The results of the experiment were presented in graphs illustrating the spread of measles over multiple iterations, allowing a detailed analysis of the infection dynamics and the impact of the different phases of the SEIR model on the simulated population. The evolution of the infection was represented in strategic intervals, from the initial phase, in which the infection is found in isolated foci, to the final stage, in which the spread of the disease slows down as an increasing number of individuals achieve permanent immunity, as shown in Figure 1.

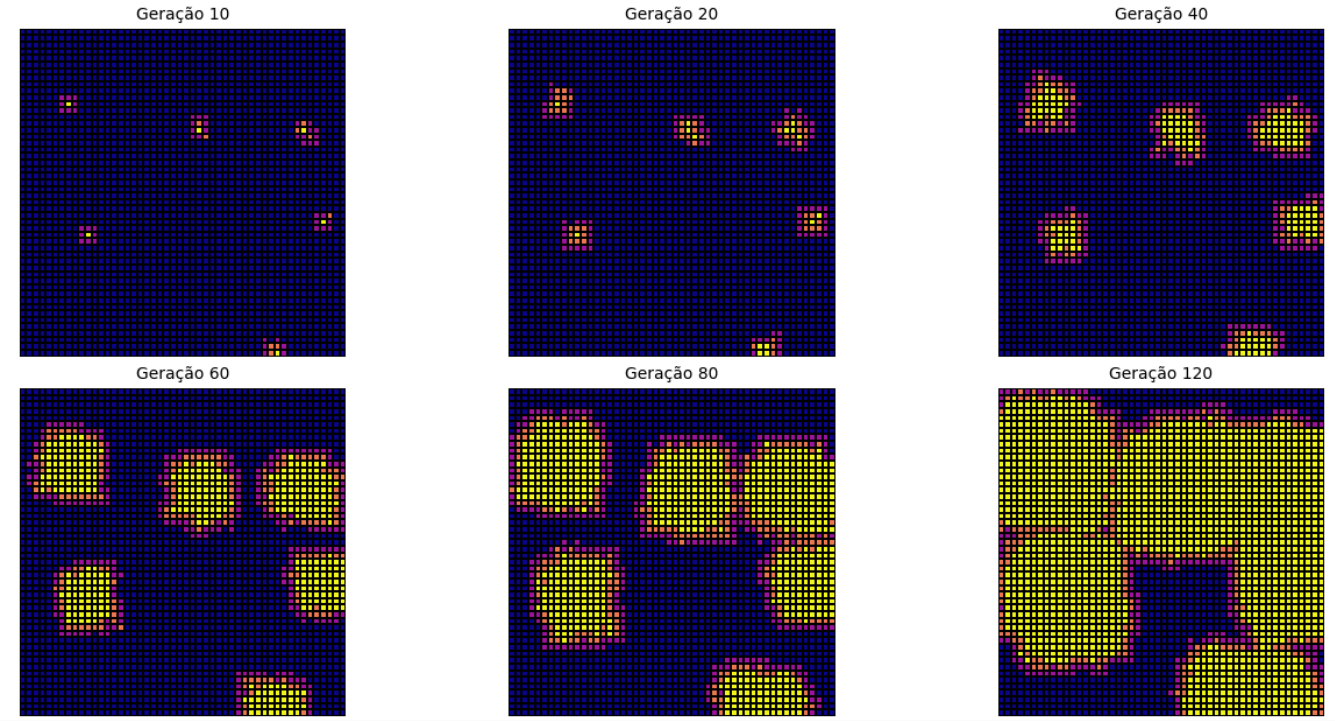

Figure 1. Spatial evolution of the spread of Measles over iterations of Cellular Automata.

To ensure accurate interpretation of the graphs, a legend table was created (Table 1), in which each epidemiological state in the model is associated with a specific colour. This approach allows the progression of the disease through the iterations to be clearly identified, making it easier to distinguish between susceptible, exposed, infected and recovered individuals within the simulated population.

State	Color
Susceptible (S)	
Exposed (E)	
Infected (I)	
Recovered (R)	

Table 1. SEIR State Table - Measles.

Discussion

In the initial iterations, there is a predominance of individuals in the **Susceptible (S)** state, with only a few infection cases appearing in a scattered manner.As time progresses, transmission intensifies, leading to a gradual increase in the number of individuals in the **Exposed (E)** state and, subsequently, in the **Infected (I)** state. This growth pattern adheres to the Moore neighbourhood logic, as articulated in the Methodology section. Individuals contract the disease upon contact with infected neighbours, reflecting the airborne transmission dynamics of measles in densely populated areas.

As more individuals complete the disease cycle and enter the **Recovered (R)** state, the infection rate commences to decline, as the increasing presence of immune individuals curtails opportunities for further contagion. This behaviour is evident in the final iterations of the experiment, where the graphs show that most of the population has reached the recovered state, effectively halting the spread of the disease.Thus, the presented results not only confirm the effectiveness of the SEIR model in simulating epidemiological outbreaks but also highlight the importance of herd immunity in controlling the virus's dissemination.

Furthermore, the simulation underscores the impact of the **variable incubation period** on the dynamics of disease transmission. Distinct values of $T_{incubation}$ exert a marked influence on the outbreak's progression, with shorter incubation periods leading to accelerated transmission, while longer periods result in delays, thereby decelerating the exponential growth of infections. This factor contributes to the variability observed among outbreaks in different regions and reinforces the importance of considering individual aspects of infection, such as immune response and the average time required for symptom onset.

Conclusion

In this study, a cellular automaton-based SEIR model was implemented and analysed to simulate the spread of measles in a spatially distributed population.This approach enabled detailed observation of the infection dynamics over time, highlighting the role of variable incubation periods in the contagion process.

Although the adopted model proved effective in representing the outbreak, simplifications were necessary due to the absence of population mobility and external interventions, factors that could influence the epidemic trajectory in real-world scenarios. Notwithstanding these limitations, the obtained results demonstrate the relevance of this approach as a tool for epidemiological modelling, allowing the analysis of disease spread patterns and the impact of herd immunity in outbreak containment.

Consequently, future studies can enhance the model by incorporating variables such as individual mobility, heterogeneous susceptibility, and control strategies, including vaccination and social distancing. Additionally, analysing different layers of social interactions may provide a deeper understanding of disease transmission patterns. Consequently, the application of cellular automata remains a promising tool for modelling infectious processes in structured populations, enabling more realistic simulations and the evaluation of epidemic mitigation strategies.

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