Epidemiological Simulation Based on Cellular Automata: Modeling Disease Spread in a Two-Dimensional Grid

LINALDO QUIRINO DE ALBUQUERQUE NETO[1]

[1]Department of Computer Science, University Federal Rural de Pernambuco, Brazil

Abstract

This paper presents a computational model for simulating the spread of infectious diseases using cellular automata (CA) in a two-dimensional grid. The model captures the dynamics of disease transmission, recovery, and immunity, providing insights into how infections propagate in a population. By varying parameters such as infection probability and recovery rate, we explore different scenarios and their impact on the spread of the disease. The results demonstrate the utility of cellular automata as a tool for understanding epidemiological processes and informing public health strategies.

Introduction

The study of disease spread is critical for public health planning and response. Computational models, such as those based on cellular automata, offer a simplified yet powerful framework for simulating complex epidemiological dynamics. Cellular automata are discrete models that represent space as a grid of cells, each of which can be in a finite number of states. In this work, we use a CA-based model to simulate the spread of an infectious disease in a population, where individuals are represented as cells in a two-dimensional grid. The model incorporates key factors such as infection probability, recovery rate, and immunity, allowing us to observe how these parameters influence the progression of an outbreak.

Methods

Model Design

The simulation is implemented using a two-dimensional grid of size
$L \times L$
$L \times L$, where each cell represents an individual. The cells can be in one of three states:

1. **Healthy (0)**: Susceptible to infection.

2. **Infected (1)**: Capable of transmitting the disease.
3. **Recovered (2)**: Immune to further infection.

Rules of the Simulation

1. **Infection**: A healthy cell becomes infected if it has at least one infected neighbor, with a probability
2. pinfect
3. *p*
4. infect
5.
6. .
7. **Recovery**: An infected cell recovers with a probability
8. **precover**
9. *p*
10. recover
11.
12. , transitioning to the recovered state.
13. **Immunity**: Recovered cells remain immune and cannot be reinfected.

Implementation

The simulation was implemented in Python using the NumPy library for grid manipulation and Matplotlib for visualization. The grid is updated iteratively, and the state of each cell is determined by the rules described above.

Parameters

- Grid size:
- L=50
- L=50
- Infection probability:
- pinfect=0.3
- p
- infect
-
- =0.3
- Recovery probability:
- precover=0.1
- p
- recover
-
- =0.1
- Number of iterations: 100

Results

The simulation results illustrate the spread of the disease over time. Initially, the infection is localized to a single cell at the center of the grid. Over successive iterations, the infection spreads to neighboring cells, creating clusters of infected individuals. As the simulation progresses, some infected cells recover, leading to the formation of immune regions. The final state of the grid shows a mix of healthy, infected, and recovered cells, with the distribution depending on the parameters used.

Key observations:

1. Higher infection probabilities lead to faster spread of the disease.
2. Higher recovery rates result in smaller outbreaks and quicker containment.
3. The spatial structure of the grid influences the clustering of infected and recovered individuals.

Discussion

The CA-based model provides a simple yet effective way to study disease spread. By capturing the spatial interactions between individuals, the model highlights the importance of local transmission dynamics in shaping the overall progression of an outbreak. The results align with epidemiological principles, demonstrating that reducing infection probability (e.g., through social distancing) and increasing recovery rates (e.g., through medical interventions) can significantly mitigate the impact of a disease.

However, the model has limitations. It assumes a homogeneous population and does not account for factors such as age, mobility, or vaccination. Future work could extend the model to include these variables, providing a more comprehensive understanding of disease dynamics.

Conclusion

This study demonstrates the utility of cellular automata for simulating epidemiological processes. The model successfully captures the spread, recovery, and immunity dynamics of an infectious disease, offering insights into how different parameters influence the course of an outbreak. While simplified, the model serves as a valuable tool for exploring public health strategies and understanding the fundamental principles of disease transmission.

References

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