Modeling Infectious Disease Spread Using Cellular Automata: A Case Study with the SIR Model

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ABSTRACT

Understanding the dynamics of infectious disease spread is crucial for epidemiological research. In this study, we implement a computational model based on cellular automata to simulate the propagation of an infectious disease using the Susceptible-Infected-Recovered (SIR) framework. Our approach leverages a two-dimensional grid where each cell represents an individual, with state transitions governed by local interactions and probabilistic rules. The simulation captures the effects of infection probability, recovery time, and spatial distribution on disease dynamics. The results highlight the potential of cellular automata as a powerful tool for modeling epidemiological processes.

Introduction

The spread of infectious diseases has been extensively studied through mathematical models such as compartmental frameworks (e.g., SIR, SEIR). However, traditional differential equation models often assume homogenous mixing, which may not accurately represent real-world spatial dynamics. Cellular automata (CA) offer an alternative by incorporating local interactions and spatial heterogeneity. In this study, we develop a CA-based model to simulate the spread of an infectious disease within a structured population.

Results and Discussion

Preliminary simulations indicate that the spread of infection is highly sensitive to the probability $t_$infection and the duration of infectiousness t_{recovery}. Key findings include:

- Higher $t_$infection leads to faster outbreaks, with nearly all individuals infected within a few time steps.
- Longer t_{recovery} increases the total number of infected individuals at peak infection.
- Spatial clustering of initially infected individuals affects the speed of disease propagation.

Model Validation and Limitations

Our CA-based model captures essential epidemiological patterns but has limitations, including the assumption of a static population. Future extensions could incorporate individual mobility, vaccination, and reinfection dynamics.

Methods

Model Framework

We employ a two-dimensional cellular automaton where each cell represents an individual in one of three states:

- S (Susceptible): Healthy individuals who may become infected upon contact with an infected neighbor.
- I (Infected): Individuals carrying the disease who can spread it to susceptible neighbors.
- R (Recovered): Individuals who have recovered and are immune.

State transitions occur based on probabilistic rules:

- A susceptible individual becomes infected with probability $t_$infection if at least one neighboring cell is infected.
- An infected individual transitions to recovered after t_{recovery} time steps.

Implementation

We simulate the CA model on a 50×50 grid, initialized with a small fraction of infected individuals randomly distributed. The grid updates synchronously at each time step, applying the transition rules globally. We use Python with NumPy and Matplotlib for implementation and visualization.

Conclusion

Cellular automata provide an intuitive and flexible approach to modeling infectious disease dynamics. This study demonstrates their applicability in simulating localized interactions and spatial effects. Further refinements could enhance predictive power for real-world epidemiological applications.

References

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