Simulating Epidemic Spread Using Cellular Automata: A Spatial Approach

Marcos Leite Bezerra Neto

ABSTRACT

Epidemic modeling plays a pivotal role in understanding disease dynamics and guiding public health interventions. Traditional mathematical models, while effective, often overlook spatial heterogeneity and localized interactions, which are critical in real-world disease transmission. This study introduces a cellular automata (CA)-based framework to simulate epidemic spread, incorporating the Susceptible-Infected-Recovered (SIR) paradigm. By modeling individuals as discrete entities interacting within a spatial grid, our approach captures stochastic and localized transmission dynamics, offering a more realistic representation of epidemic behavior. This framework is versatile, serving educational, predictive, and decision-support purposes in epidemiology.

INTRODUCTION

Mathematical models have long been instrumental in studying infectious diseases, with compartmental SIR models being a cornerstone of epidemiological research. However, these models often assume homogeneous mixing, neglecting the spatial and stochastic nature of real-world interactions. Cellular automata (CA) provide a compelling alternative, enabling the simulation of individuals as discrete units interacting within a defined spatial structure. This approach allows for the incorporation of localized transmission patterns, making it particularly suitable for modeling outbreaks in spatially heterogeneous populations.

This paper presents a two-dimensional CA-based model to simulate epidemic spread, emphasizing the role of spatial dynamics in disease transmission. The model is designed to investigate localized outbreaks, evaluate control measures, and explore various transmission scenarios. By leveraging the computational efficiency and flexibility of CA, this framework offers a high-resolution tool for understanding complex epidemic dynamics, complementing traditional mathematical approaches.

METHODS

Model Design

We implemented a two-dimensional CA model where each cell represents an individual in a population. The cells transition between three states based on the SIR framework:

- Susceptible (S): Individuals who can contract the disease.
- Infected (I): Individuals who are infected and can transmit the disease.
- Recovered (R): Individuals who have recovered and are immune.

Disease transmission occurs through local interactions within a Moore neighborhood (eight surrounding cells). The transition probabilities are governed by two key parameters:

- Infection rate (τ): Probability of a susceptible individual becoming infected.
- Recovery rate (γ): Probability of an infected individual recovering.

Simulation Parameters

The model was configured with the following parameters:

- Grid size: 50x50 cells.
- Initial infection rate: 2% of the population.
- Infection rate (τ): 0.3.
- Recovery rate (γ): 0.1.
- Boundary conditions: Periodic (to eliminate edge effects).

The simulation was implemented in Python, with Matplotlib used for visualization. The state of each cell was updated iteratively over 100 time steps, and the results were analyzed by tracking the number of susceptible, infected, and recovered individuals over time. Sensitivity analyses were conducted by varying τ and γ to explore their impact on epidemic progression.

RESULTS AND DISCUSSION

Epidemic Dynamics

The simulation successfully replicated key epidemiological phenomena, including localized outbreak clusters and wave-like propagation patterns. The epidemic curve exhibited the classic SIR trend: an initial rise in infections, followed by a peak and subsequent decline as individuals recovered. Spatial heterogeneity played a significant role, with transmission dynamics varying based on population density and neighborhood connectivity.

Impact of Parameters

Sensitivity analyses revealed that altering τ and γ had profound effects on epidemic outcomes:

- Higher infection rates (τ) led to rapid outbreaks and higher peak infections.
- Increased recovery rates (γ) reduced the duration and severity of the epidemic.

Neighborhood Structures

We compared the effects of different neighborhood structures on disease propagation:

- Moore neighborhood: Resulted in faster and more widespread infections due to increased contact opportunities.
- Von Neumann neighborhood: Slower propagation rates due to fewer neighboring contacts.

These findings highlight the importance of spatial topology in epidemic modeling, suggesting that neighborhood structures should be carefully considered in public health strategies.

Validation

The simulation results were qualitatively consistent with existing epidemiological studies, demonstrating the model's validity. This alignment underscores the potential of CA-based models as tools for policy evaluation, particularly in scenarios where spatial dependencies are critical.

CONCLUSION

This study demonstrates the effectiveness of cellular automata in simulating epidemic spread, offering a spatially explicit and computationally efficient alternative to traditional models. By capturing localized interactions and stochastic processes, the CA-based framework provides valuable insights into disease dynamics, aiding in the design of targeted public health interventions.

Future work could enhance the model's realism by incorporating real-world mobility data, contact networks, and adaptive interventions. Expanding the framework to include agent-based interactions and heterogeneous population distributions could further improve its applicability in real-world epidemiological studies.

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