Epidemic Simulation Using Cellular Automata

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ABSTRACT

Infectious disease modeling is a crucial tool for understanding and predicting disease dynamics within populations. This study presents a computational model that integrates the SIR (Susceptible-Infected-Recovered) framework with cellular automata, allowing for a spatially structured simulation of epidemic spread. By incorporating local interactions between individuals, this model enhances the realism of disease transmission patterns compared to traditional compartmental models. The simulation enables visualization of epidemic propagation and evaluation of key epidemiological parameters such as infection rate and recovery probability.

Introduction

Mathematical models play an essential role in epidemiology, providing insights into disease spread and informing public health strategies. Classical compartmental models, such as SIR, assume homogeneous mixing within populations, which may oversimplify real-world interactions. Cellular automata (CA) provide a powerful alternative by incorporating local interactions, capturing spatial heterogeneity in transmission dynamics. Here, we introduce a computational approach that integrates a discrete SIR model within a cellular automaton framework to simulate infectious disease spread in a structured population.

Methods

The proposed model employs a two-dimensional cellular automaton, where each cell represents an individual characterized by one of three possible states: susceptible, infected, or recovered. The evolution of the system follows a discrete-time update rule that governs state transitions based on probabilistic interactions between neighboring cells.

At each time step, an infected cell has a defined probability of transmitting the infection to adjacent susceptible cells, modeled through a stochastic process that accounts for localized interactions. This formulation introduces a spatially explicit mechanism for disease spread, diverging from classical compartmental models that assume homogeneous mixing. The transition from an infected to a recovered state is governed by a recovery probability, encapsulating the natural progression of disease resolution. The cellular automaton thus enables emergent behavior that mirrors real-world epidemic diffusion patterns, such as clustering and wave propagation.

The model can be further parameterized to incorporate heterogeneities in transmission rates, recovery probabilities, and interaction neighborhoods, allowing for adaptability to different epidemiological contexts. The simulation is iterated over multiple time steps to capture the dynamic evolution of the epidemic, with results visualized as spatiotemporal distributions of disease spread.

Results

The simulation demonstrates characteristic epidemic waves, where infection initially spreads rapidly, peaks, and eventually declines as individuals recover. Spatial clustering of infections emerges due to localized interactions, providing a more nu-

anced understanding of disease diffusion patterns compared to well-mixed models. Key epidemiological insights, such as the effects of varying infection and recovery rates, can be explored through parameter adjustments.

Discussion

The integration of cellular automata with epidemiological modeling offers significant advantages in capturing spatial dependencies in disease transmission. This approach can be extended to study the impact of non-pharmaceutical interventions, such as social distancing or quarantine, by modifying interaction rules. Future work may incorporate additional complexity, such as mobility patterns or heterogeneous population structures, to further refine predictive capabilities.

Conclusion

This study presents a computationally efficient and visually intuitive model for epidemic simulation using cellular automata. By bridging the gap between classical SIR models and spatially explicit frameworks, this approach provides valuable insights into infectious disease dynamics, supporting both theoretical research and practical decision-making in epidemiology.

References

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