A Simplified SEIR Epidemic Model Based on Cellular Automata for Spatial Analysis

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Abstract

This article presents a cellular automata (CA) framework for simulating epidemiological dynamics using a discrete-time SEIR (Susceptible-Exposed-Infectious-Recovered) model. Each cell represents an individual whose state evolves based on interactions with neighbors, incorporating realistic transition probabilities such as infection rate, latency period, and recovery likelihood. The CA grid captures spatial heterogeneity and movement, allowing study of disease spread under varying conditions including a simulated mobility. To quantitatively analyze infection patterns, a box-counting method estimates the similarity dimension of the infected clusters, providing insights into the spatial structure of outbreaks. Real-time (RT) visualization is implemented via SDL2, facilitating RT observation of epidemic progression. This approach demonstrates the potential of CAs as accessible and versatile tools for epidemiological studies.

Key-words: Cellular Automata. Epidemiology Models. SEIR Model. Similarity Dimension. Spatial Dynamics.

1. Introduction

Modeling infectious disease dynamics is crucial for understanding and controlling epidemics. Cellular automata (CA) provide a simple yet effective computational approach for simulating the spatial and temporal progression of diseases within populations. Due to their straightforward implementation and low computational demands, CA models are particularly suited for preliminary epidemiological assessments and educational purposes when more complex models are impractical.

In this study, we present a two-dimensional CA implementation of the SEIR (Susceptible–Exposed–Infectious–Recovered) model developed in C. The system's state transitions are driven by epidemiological parameters including infection rate, latency period, and recovery probability. Visualization and graph-based analyses were performed using Python to investigate spatial patterns of disease spread. Although CA models lack the detailed complexity of advanced epidemiological frameworks, they offer a valuable balance between simplicity and insight, making them well-suited for rapid scenario evaluation and teaching.

Key model parameters such as latency period and transmission rate were calibrated using real-world epidemiological data, predominantly from COVID-19 studies. These data reflect the biological and transmission characteristics of the virus and ensure realistic simulation outcomes. The latency period represents the interval between exposure and infectiousness, while the transmission rate quantifies the probability of disease spread between individuals.

2. Epidemic Simulation Results

The epidemic was simulated on a 32 × 32 grid over 10,000 iterations to analyze the spatial and temporal dynamics of infection spread. The **Area Under the Infectious Curve (AUC)** was calculated as 1,423,055, representing the cumulative infectious load throughout the simulation period.

The **peak infection** occurred at iteration 2,005, with 176 infectious individuals recorded. The epidemic persisted for the entire 10,000 iterations, indicating a prolonged, low-level presence of the infection.

An **approximate basic reproduction number (R_0)** of 0.02 was estimated, suggesting limited transmissibility under the current model parameters. This low R_0 indicates that, on average, each infected individual transmits the disease to significantly less than one other person, preventing sustained exponential spread.

It is important to recognize that the SEIR model employed here is a simplified framework. It does not incorporate factors such as reinfection, vaccination, governmental lockdown measures, or natural and partial immunity. Therefore, it cannot capture the full complexity or duration of real-world epidemics, such as the COVID-19 outbreak.

Yet, despite these limitations, cellular automata are capable of simulating basic disease spread dynamics and provide useful visualizations of approximate epidemic behavior without requiring extensive parameterization. These quantitative results illustrate the capacity of the CA-based SEIR model to simulate both the intensity and duration of epidemic outbreaks under constrained transmission conditions.

References

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