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. 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.

2. Methodology

A two-dimensional Cellular Automata (CA) framework was developed to simulate the dynamics of a discrete-time SEIR (Susceptible–Exposed–Infectious–Recovered) epidemiological model.

2.1 Model Structure and Parameters

The model uses the following parameters, inspired by real-world infectious disease dynamics:

- **β**: Transmission rate
- **σ**: Latency period
- **D**: Duration of infection
- **γ**: Recovery probability

Transitions follow SEIR dynamics:

- **Susceptible (S)** cells may become **Exposed (E)** based on the number of infectious neighbors and the calculated infection probability:

$$P(infection) = 1 - (1 - \beta)$$

  where *n* is the number of infectious neighbors.

- **Exposed (E)** cells transition to **Infectious (I)** after σ time steps.
- **Infectious (I)** cells remain infected for D steps, after which they may become **Recovered (R)** with probability γ.
- **Recovered (R)** cells remain immune indefinitely.

2.2 Visualization and Analysis

Real-time visualization was implemented using the SDL2 library. For quantitative post-processing, Python libraries such as *NumPy*, *Pandas*, *Seaborn*, and *Matplotlib* were used to generate graphs and heatmaps of compartment transitions and population distributions.

2.3 Fractal Dimension Analysis

To assess the spatial structure of infected clusters, a similarity (fractal) dimension was estimated using the box-counting method. The relationship between box size and infection cluster count was plotted using a log–log scale, with linear regression applied to valid (non-zero) data points. The resulting slope estimates the fractal dimension of the infection pattern, providing insight into the heterogeneity of spread.

2.4 Implementation Notes

Key elements of the CA logic, including state definitions, infection rules, latency progression, and recovery conditions, were implemented in C. Model constants were defined in a configuration header file. Modular functions supported cell updates, movement, probability evaluation, and infection tracking.

3. Epidemic Simulation Results

3.1 Quantitative analysis

The epidemic was simulated on a $32x32$ 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.

3.2 Visual Analysis

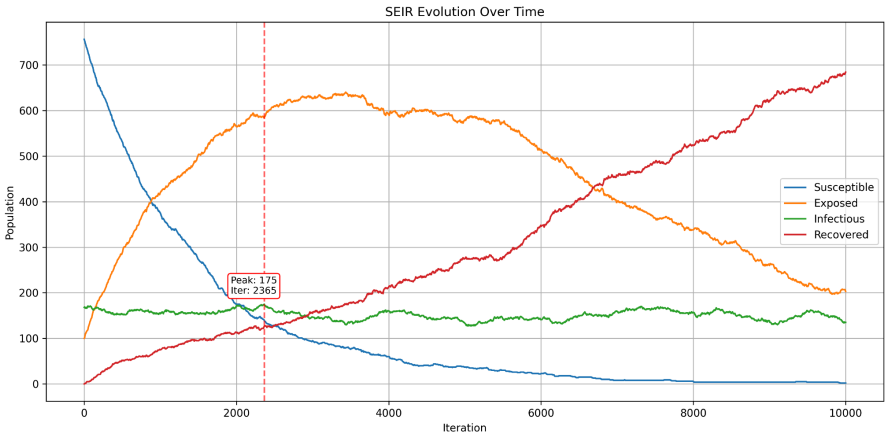

Figure 1: Evolution of the SEIR model through the CA iterations

Analyzing the SEIR evolution over time, we observe the temporal dynamics of each compartment (Susceptible, Exposed, Infectious, and Recovered) throughout the simulation. This allows us to understand how the epidemic progresses and transitions between states.

The **Susceptible (S)** population declines as individuals become exposed and infected, which is a typical pattern during an outbreak. The **Exposed (E)** group rises sharply before the **Infectious (I)** peak, reflecting the incubation period characteristic of many diseases. The **Infectious (I)** curve indicates the period of highest transmission and can help estimate healthcare system burden. Finally, the **Recovered (R)** population increases steadily, reflecting recovery and, in more complex models, the development of immunity can also be a factor.

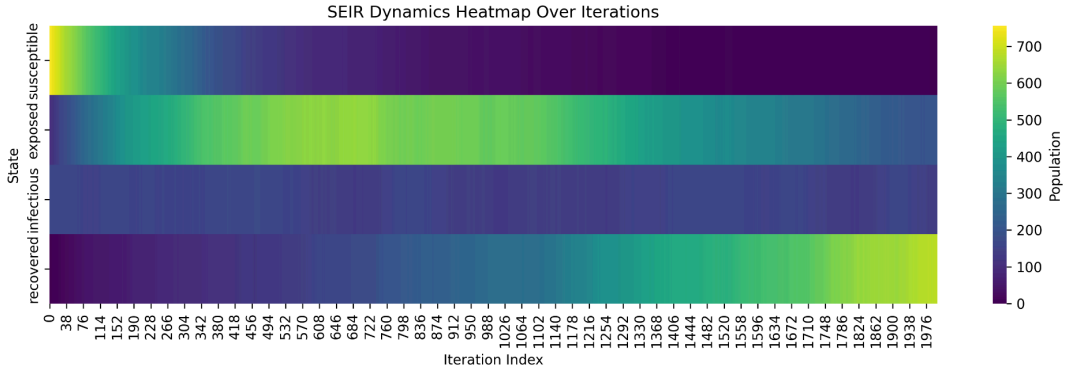

Figure 2: Dynamics of each iterations as a heatmap

The heatmap visualizes the proportion of the population in each SEIR state across time, using color intensity to represent magnitude. Rows correspond to SEIR compartments, and columns to time steps.

Brighter colors (e.g., yellow or red) indicate a higher proportion of individuals in that state at a given moment. Initially, **Susceptible (S)** individuals dominate, but their proportion declines rapidly as they transition to the **Exposed (E)** state—visible through shifting color intensity. Before reaching the midpoint of the timeline, most individuals have left the S compartment, highlighting the fast spread of the pathogen. The **Infectious (I)** compartment remains relatively stable in intensity, rarely becoming dominant.

In more detailed models, abrupt changes in color patterns could signal interventions like lockdowns or policy shifts.

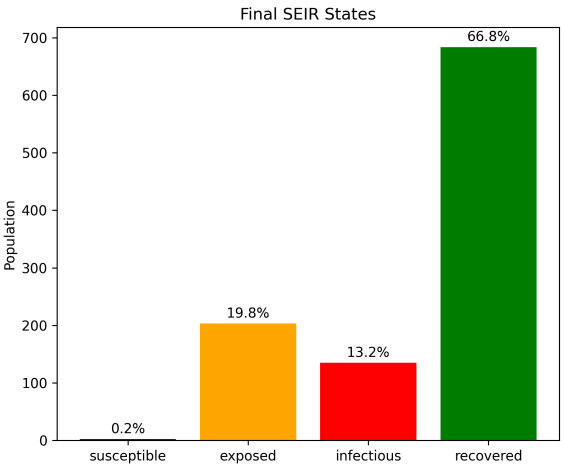

Figure 3: Final states for each cell

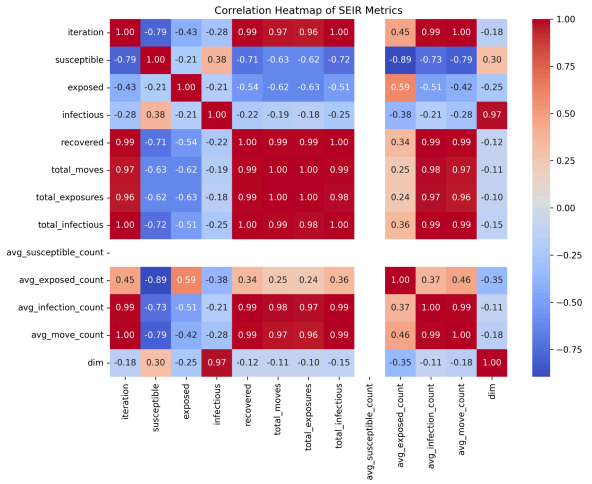

Figure 4: Correlation heatmap using SEIR metrics

In figure 3, the bar chart summarizes the **final distribution of the population across SEIR compartments at the end of the simulation.** A high **Recovered (R)** rate of 66.8% suggests widespread exposure and the development of natural immunity, assuming no reinfection in the SEIR framework. The remaining **Susceptible (S)** individuals indicate a potential for future outbreaks if preventive measures, such as vaccination or public awareness, are not maintained.

Any residual **Exposed (E)** or **Infectious (I)** populations suggest that the epidemic has not yet been fully eradicated and may still be active in limited pockets.

In figure 4, the heatmap displays the **Pearson correlation coefficients** between key **SEIR variables** and **the simulation time (iterations).** Strong correlations are visualized through color intensity, helping to reveal linear relationships among the states.

A strong **positive correlation** between iteration and **Recovered (R)** confirms that recovery accumulates steadily over time. A negative correlation between **Susceptible (S)** and **Infectious (I)** reflects the natural epidemic dynamic where rising infections reduce the susceptible pool.

Weaker or unexpected correlations could point to nonlinear effects, delayed transitions, or emergent dynamics not explicitly programmed into the model. This type of analysis helps in identifying **inter-variable dependencies** and may guide further model refinement or policy parameter adjustments.

4. Conclusion

- A cellular automata (CA) framework was successfully implemented to simulate the spatial and temporal dynamics of an SEIR-based epidemic model.

- The model used realistic parameters (e.g., latency period, transmission rate) based on COVID-19 data, ensuring a balance between simplicity and epidemiological relevance.

- Despite being simplified and not accounting for factors such as reinfection, vaccination, governmental interventions, or immunity variations, the model captured essential features of epidemic behavior.

- Quantitative results included metrics such as peak infection, area under the infectious curve (AUC), and approximate R_0, offering a numerical view of epidemic intensity and duration.

- Visual tools—such as compartment evolution plots, heatmaps, and correlation matrices—helped reveal patterns of spread, state transitions, and spatial heterogeneity.

- The CA model proved valuable for low-cost simulation, educational purposes, and rapid scenario testing without requiring large parameter sets or high computational resources.

- This work reinforces the potential of cellular automata as intuitive and accessible tools for early-stage epidemiological modeling and analysis.

References

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