# Epidemiological Simulation Using Cellular Automata: A Computational Approach to the SIR Model

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## Abstract

This document presents an epidemiological simulation based on the Susceptible-Infected-Recovered (SIR) model using cellular automata. The simulation is performed on a two-dimensional grid, where cells represent individuals, and disease spread follows local interaction rules. The model incorporates a fixed infection probability and a defined recovery period for each infected individual. The results illustrate how an epidemic spreads and how recovery time influences its progression. This study highlights the utility of computational models in predicting epidemic behavior, offering valuable insights for public health decision-making.

**Keywords:** Epidemiological Simulation, SIR Model, Cellular Automata, Disease Propagation, Computational Modeling.

## Introduction

Epidemiological modeling is a crucial tool for understanding the transmission of infectious diseases. Traditional models, such as the SIR model, use differential equations and assume homogeneous population mixing. However, these approaches often fail to capture localized interactions.

In contrast, cellular automata-based models offer a spatially explicit approach, accounting for local heterogeneity in disease spread. This study implements an SIR-based simulation using cellular automata to analyze epidemic propagation. The simulation occurs on a discrete two-dimensional grid, where individuals interact only with their neighbors. Each individual transitions through three states—susceptible, infected, and recovered—based on predefined rules governing infection probability and recovery time. The primary goal is to observe the emergence of infection patterns over multiple time steps.

## Methods

The simulation was developed in Python, utilizing NumPy and Matplotlib for efficient data handling and visualization. The methodology includes the following steps:

- **Grid Initialization:** A 50×50 matrix represents the population, with each cell corresponding to an individual.
- **State Definitions:** Each individual can be in one of three states:
    - **Susceptible (S):** Healthy individuals at risk of infection.
    - **Infected (I):** Individuals who spread the disease to susceptible neighbors.
    - **Recovered (R):** Individuals who have recovered and gained immunity.
- **Infection Dynamics:**
    - One randomly selected cell starts as infected.
    - Susceptible individuals have a 30% chance of infection if they have at least one infected neighbor.
    - Infected individuals recover after 10 time steps, transitioning to the recovered state.
- **Simulation Execution:**
    - The grid updates at each time step based on transition rules.
    - Color-coded visualization represents different states: blue (susceptible), red (infected), and yellow(recovered).

# Results

The simulation ran for 100 time steps, revealing the following observations:

- **Initial Spread:** The infection rapidly propagates to neighboring cells, forming localized clusters.
- **Peak Infection Period:** Around time step 20, the number of infected individuals reaches its peak before declining as recovery rates increase.
- **Disease Saturation:** By time step 40, most individuals have recovered, signaling the epidemic's conclusion.
- **Effect of Recovery Time:** A shorter recovery period leads to a quicker decline in infection, whereas a longer recovery period prolongs disease transmission.

# Discussion

The simulation results underscore the role of local interactions in epidemic dynamics. Unlike compartmental models assuming homogeneous population mixing, cellular automata allow for spatial heterogeneity, leading to more realistic epidemic behavior. Observations include the formation of infection clusters, non-uniform disease spread, and the emergence of immune zones post-recovery.

Future improvements could integrate factors such as individual mobility, vaccination strategies, and external interventions to assess their impact on epidemic control. Additionally, incorporating stochastic variations in recovery time and immunity duration could enhance the model's accuracy in reflecting real-world disease spread.

# Conclusion

This study demonstrates that cellular automata effectively model epidemic spread using local interaction rules. Findings highlight the significance of infection probability and recovery time in shaping epidemic dynamics. Compared to traditional SIR models, cellular automata provide a finer-grained representation of disease propagation, accounting for spatial variations. Future work may explore additional factors such as reinfection, vaccination strategies, and mobility patterns to further refine the model.

# References


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