

Cellular Automata Model

1 Introduction

Cellular Automata (CA) Model is a type of mathematical model used to simulate complex systems and processes in a discrete space and time framework.

2 Elements

The basic elements of CA model include:

2.1 Cells

The basic units of a cellular automaton are cells. Typically, these are arranged in a grid, which can be 1D (a line), 2D (like a chessboard), 3D, or even higher dimensions. Each cell has a state, which can change over discrete time steps.

2.2 Neighborhood

Each cell in the grid has a set of neighboring cells. The most common neighborhoods in 2D are the **Moore neighborhood** (which includes all 8 surrounding cells) and the **Von Neumann neighborhood** (which includes only the 4 direct neighbors: up, down, left, and right).

2.3 Rules

The state of a cell in the next time step is determined by a set of rules that take into account the current state of the cell and the states of its neighbors. These rules are applied simultaneously to all cells in the grid at each time step.

2.4 Initialization

The system starts from an initial configuration. This might be random, a single seed cell, or some predefined pattern, depending on the context or the problem being addressed.

2.5 Evolution

Over discrete time steps, the cellular automaton evolves. This means that, at every time step, the rules are applied to each cell, determining their next states based on their current states and those of their neighbors.

3 Case Study

Assume we want to simulate the model the spread of an infectious disease.

3.1 Case Setup

Similar with the Markov Chain model, we have the following parameters:

1. k : Duration of infection. In this case, $k = 2$.
2. t : Number of days
3. τ : Infection probability
4. Node label 0: Susceptible
5. Node label -1: Recovered
6. Node label 1 and 2: Infection date 1 and 2.

3.2 Transition

At day 0, one patient is infected, every other patients are susceptible. The N-S-E-W neighbors are exposed.



Figure 1: Day 0.

At day 1, the illness propagates randomly to the exposed and susceptible neighbors, and spreads to other neighbors:



Figure 2: Day 1.

At day 2, the first case recovers, but the infection continues to spread:



Figure 3: Day 2.

4 Data Analysis

Because there are so many possible results coming from this model, the better way to is using **Monte Carlo** simulation to conduct large amount of simulations to find the probabilities.

The basic processes of a Monte Carlo Simulation include:

1. **Define a Model:** First, you must have a model of the system you want to analyze. This could be anything from a financial model predicting the future value of an investment, to a physical model predicting the behavior of a natural system.
2. **Identity Inputs:** Determine the uncertain factors or inputs in the model. For **each uncertain factor**, you assign a **probability distribution** based on your current knowledge, historical data, or expert judgment.
3. **Random Sampling:** For each uncertain factor, draw a random sample from its probability distribution. This sample represents a possible scenario or state of the world.
4. **Run the Model and Repeat:** With the set of random samples for each of your uncertain factors, run your model to compute an outcome and repeat it millions of times.