

A Cellular Automata SIR Model for Landscape Epidemiology

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Abstract

A stochastic cellular automata (CA) model is proposed to simulate susceptible-infected-removed populations over space and time. Three initial grid configurations are used to compare and contrast the spatiotemporal dynamics of this system; random, center, and patchy. The simulations show that random configurations infect more of the population, but quickly dissipating through the space. The center case slowly propagates through space and infects less of the population, while the patchy configuration shows to be a middle case between random and center.

1 Introduction

Landscape epidemiology studies the disease patterns across the landscape that arise from abiotic and/or biotic conditions that support a particular pathogen [1]. In addition, the proximity to susceptible individuals directly influences disease transmission, making the process inherently spatial. The objective of this project is to simulate the spatiotemporal dynamics of an infectious disease propagation on various landscapes using a stochastic cellular automata (CA) susceptible-infected-removed (SIR) model.

2 Background

CA applied to grid-based modeling is a means to model disease propagation over time and space [2-7]. CA models provide rules that are biologically motivated and easily programmable. In this approach, a gridded array of cells represents a landscape. Each cell contains an embedded mini-model composed of state variables describing its condition, a means of communicating with surrounding cells (neighborhood), and rules dictating the cell's response to its own state and communications from its neighbors through a series of time-steps. The imposition of relatively simple rules can generate complex emergent behaviors as the landscape evolves through time.

3 Dynamical System

The CA rules can be extracted from the ideas behind the classical SIR models based on differential equations (e.g. [8]). The set of ordinary differential equations corresponding to the CA model is:

$$\frac{dS}{dt} = -aSI, \quad (1)$$

$$\frac{dI}{dt} = aSI - bI, \quad (2)$$

$$\frac{dR}{dt} = bI, \quad (3)$$

where a is the infection rate, and b the recovering rate. The system is then divided into three groups, where each cell represents an individual that can be in one of three states: S, when the individual is susceptible to infection by neighbors; I, when the individual is infected and can transmit the disease for neighboring susceptible cells; and R, when the individual is recovered. Figure 1 shows the ODE system plotted against time.

4 Methods

Scientific python was used to visualize the CA model depiction of the spatial disease propagation. The disease will propagate through the landscape based on a set of probabilities of state transitions. At each time step, there is a probability of a S cell becoming infected according to $P_i(v) = 1 - e^{-Kv}$, where v is the number of neighbor cells infected

and K is a measure of how infectious the disease is. Likewise, each I-cell can become recovered based on probability P_c or parameter b from the previous ODE model. The spatial and temporal dynamics were examined with simulations of various initial landscape population configurations, i.e., random, center, and patchy. The grid size used was 128×128 with 1% of the cells initially infected, $K = 0.17$, and $b = 0.3$. Figures 3-5 show an example of each of the initial grid configurations.

5 Results

Each initial case (random, center, and patchy) were initiated and simulated over 100 time steps and averaged over 30 runs. Figures 6-8 show an example snapshot of each case after 10 time steps. Here, it is clear that the random case infects the population more quickly than the center or patchy cases. Table 1 shows the averaged maximum infected populations and time steps with their corresponding standard deviations. In combination with Figures 9-11, which show the example runs S, I, and R populations plotted against time, we see that the center case takes the longest time to propagate through the population while infecting the least amount of individuals. The random case infects the most individuals, but relatively quickly. And finally, the patchy case fits somewhere in between the random and center cases.

Table 1: Each initial case with its average maximum infected cells and corresponding time step over 30 simulations \pm standard deviations.

Initial Case	Maximum Infected (cells/16348)	Time Step Maximum Infected
Random	(3886 ± 198.5)	(9.6 ± 0.61)
Center	(1201.5 ± 85.39)	(56.85 ± 4.470)
Patchy	(1588.4 ± 233.41)	(29 ± 4.0)

This model can be extended by including environmental layers, thus incorporating actual landscape barriers into the rules. It can also be improved to consider long-range interactions between CA cells that would incorporate metapopulation dynamics.

6 References

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7 Figures

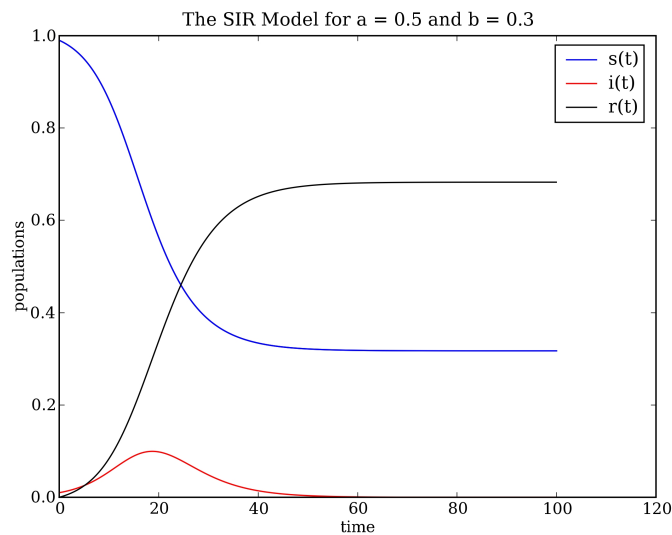


Figure 1: Normalized concentrations of S, I and R-individuals obtained by numerically integrating the ODE model using Runge-Kutta Order 4 ($dt = 0.01$). Parameter values: $a = 0.5$, $b = 0.3$. Initial conditions: $S(0) = 99.0\%$, $I(0) = 1.0\%$, and $R(0) = 0.0\%$.

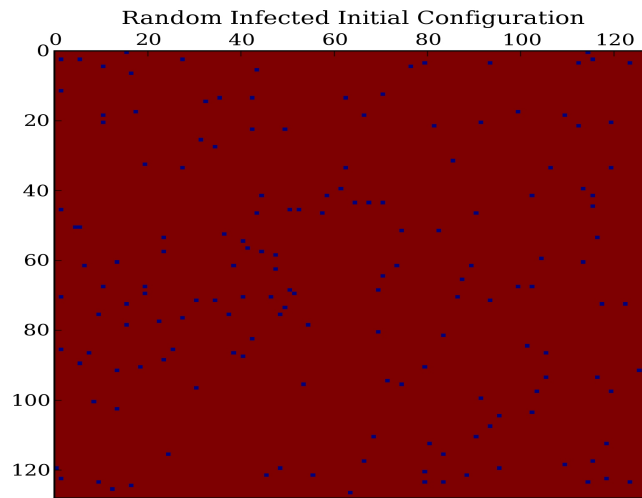


Figure 2: 128x128 grid with 1% of the cells initially infected and spaced randomly. Parameter values: $K = 0.17$, $b = 0.3$ (S-Red cells, I-Blue cells, and R-Green cells).

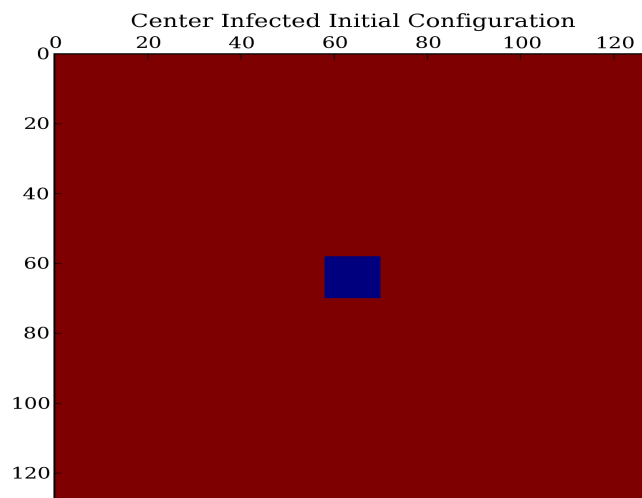


Figure 3: 128x128 grid with 1% of the cells initially infected and spaced in the center. Parameter values: $K = 0.17$, $b = 0.3$ (S-Red cells, I-Blue cells, and R-Green cells).

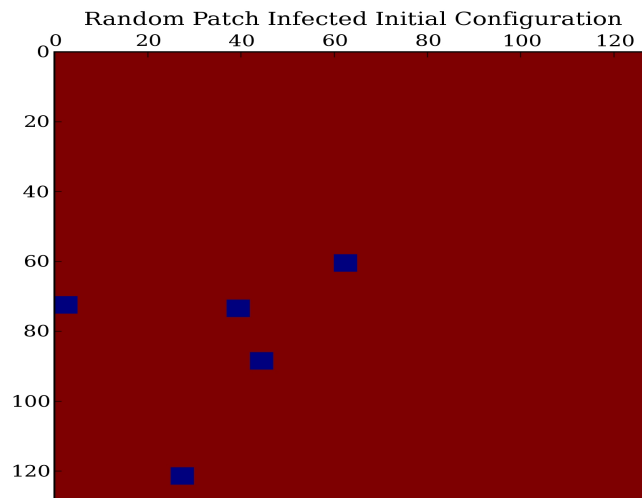


Figure 4: 128x128 grid with 1% of the cells initially infected and spaced in 5 randomly placed patches. Parameter values: $K = 0.17$, $b = 0.3$ (S-Red cells, I-Blue cells, and R-Green cells).

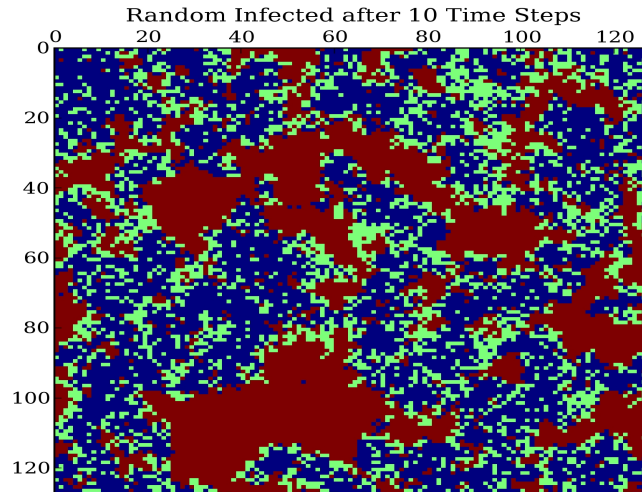


Figure 5: Randomly placed initial configuration after 10 time steps (S-Red cells, I-Blue cells, and R-Green cells).

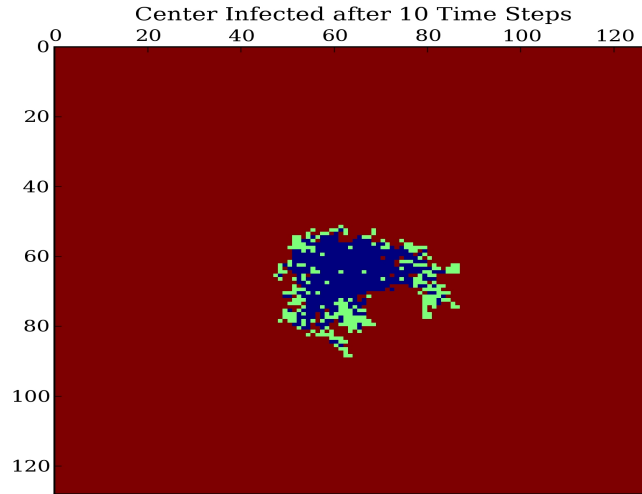


Figure 6: Center placed initial configuration after 10 time steps (S-Red cells, I-Blue cells, and R-Green cells).

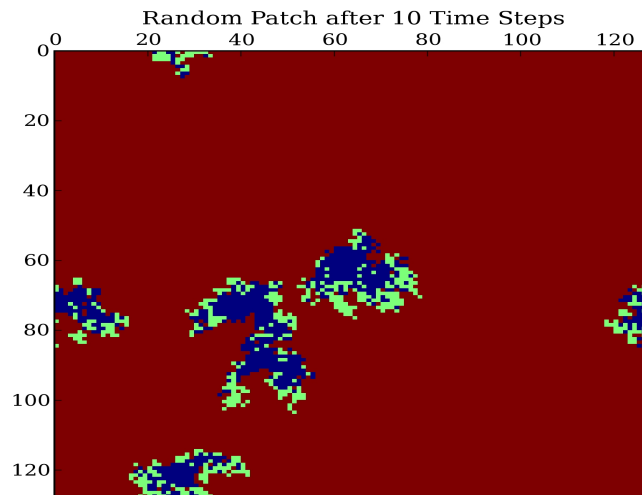


Figure 7: Patchy placed initial configuration after 10 time steps (S-Red cells, I-Blue cells, and R-Green cells).

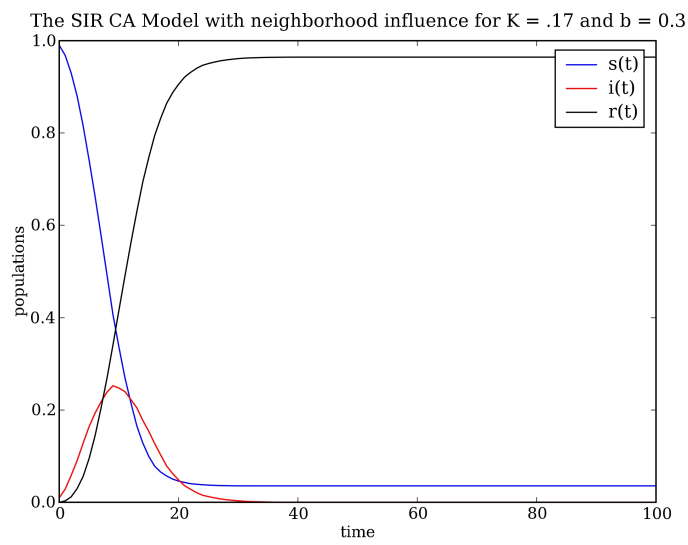


Figure 8: Normalized concentrations of S, I and R-individuals by simulating the CA model for the random initial configuration. Parameter values: $K = 0.5$, $b = 0.3$. Initial conditions: $S(0) = 99.0\%$, $I(0) = 1.0\%$, and $R(0) = 0.0\%$.

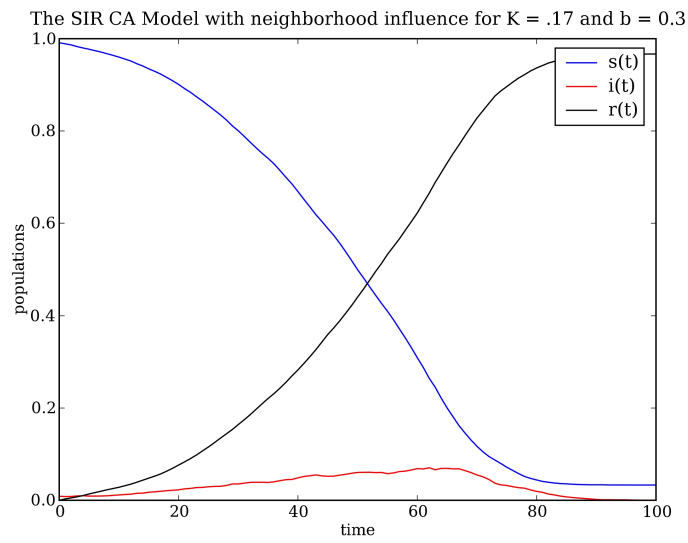


Figure 9: Normalized concentrations of S, I and R-individuals by simulating the CA model for the center initial configuration. Parameter values: $K = 0.5$, $b = 0.3$. Initial conditions: $S(0) = 99.0\%$, $I(0) = 1.0\%$, and $R(0) = 0.0\%$.

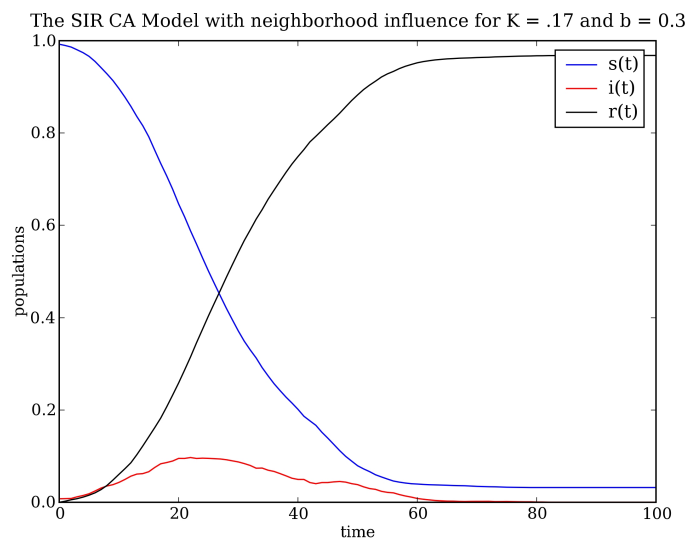


Figure 10: Normalized concentrations of S, I and R-individuals by simulating the CA model for the patchy initial configuration. Parameter values: $K = 0.5$, $b = 0.3$. Initial conditions: $S(0) = 99.0\%$, $I(0) = 1.0\%$, and $R(0) = 0.0\%$.