CSCI 154 Project 3 Report - Infectious Disease Simulation

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Abstract

This project analyzes a basic setup for an infectious disease simulation. The simulation takes into account a scenario where healthy agents are infected as they move randomly and pass by each other on a grid. The project makes observations based on collected data from running this simulation to create some hypothetical black-box policies for future work, with an ultimate goal of reducing the spread of infection in a basic environment using simple movement-based policies.

Contents

1 Motivation

Infectious disease modeling is a popular topic in the realm of simulations. Many approaches have been made to analyze infectious diseases and their spread, such as: mathematically modeling population fluctuation, statistical prediction of outbreaks, dynamics of disease transmission, and plenty more. While many simulations use a variety of data to inform policies, our goal is to develop policies that reduce infection spread without any assumed knowledge of infection spread or whether an agent is sick or healthy.

2 Problem Statement

The goal of this project is not to go deep into any one of these robust prior works or methods, but instead to analyze a simple model based only on the movement of agents and how an infection spreads among a population, and make observations of collected data in order to develop policies for future work that may reduce the rate of infection.

3 Related Work

Our work for this project is based on a simplified version of W. O. Kermack and A G. McKendrick's SIR Model, as well as the general study of stochastic modeling of infectious diseases of which there are many examples, such as the famous Reed-Frost mathematical model.

These models appear to be loose inspirations for the general project guideline provided to us in class which we've chosen to use for the following experimentation.

4 Experiment Setup

For our approach, we've set up a simulation of 240 agents that are randomly placed on a 20x20 grid of cells. At the beginning of our simulation, we randomly choose one healthy agent and make them our infected patient zero. During discrete time steps of the simulation, each agent randomly moves in an orthagonal direction, and any infected agents spread the disease to any healthy agents that are orthagonally adjacent to them. This continues until all our healthy agents become infected.

This simulation was run in two separate experiments. One in which 10 separate instances of the simulation were conducted with random starting

positions, and one with 1000 different instances.

5 Results

As per our project guidelines, data was gathered from two separate metrics: one where the simulation was run 10 times (Figure 1), versus another where the simulation was run 1000 times (Figure 2). From these results we can see that the law of large numbers gives us a much clearer picture of accurate metrics and averages. From here on out we will be discussing the metrics from (Figure 2) exclusively.

We can see from our graph that the average rate of infections peaks around time step 12 or so. A majority of infections happen prior to time step 15, and by this time almost 80% of our population is infected. Although there are a good deal of simulation runs that make it past turn 25. I wanted to analyze what causes these particular instances and see if favorable positioning could lead us to further development of policies.

Another graph, (Figure 3), was created from the data of the n = 1000 simulation. This is a heatmap representing the starting positions of patient zero in each run, with the color of the cell representing how long it took runs with that starting position to become fully infected. The more saturated blue represents the more runs that started on that grid cell which lasted longer than 25 turns, while red represents the more runs that lasted under 20 turns. We can see clearly from this heatmap that runs in which the patient zero starts towards the center of the grid tended to end prematurely, while starting positions towards the edge, and especially the corners, lasted much longer.

6 Proposed Policies

Based on the information gathered from our results, it makes me wonder whether guiding agents towards or away from particular regions of the grid will have a similar effect as the starting positions. Modifying the starting positions itself would be an unreasonable policy to implement, since in real outbreaks this represents an uncontrolled variable, but perhaps if policies were made to divide the population into quarantines or herd the infected away from healthy agents, then the population as a whole would last much longer. For these reasons in future work I would like to test the following policies:

Policy 1: Each agent is assigned a quadrant of the available space, closest

to their starting position. The agents wander randomly, but must stay within 2 tiles of the borders of the other quadrants.

Policy 2: When an agent is infected, have them move to the nearest corner, and constrain their movement so they cannot leave a small area in that corner. Healthy agents will instead remain near the center.

Policy 3: Split the available space into two sections, with a line dividing the population in which no agent is allowed to remain. Infected agents go to one section, and healthy agents remain in the opposite section.

7 Conclusion

In this project we implemented a simple, movement-based infectious disease simulation on a discrete grid and analyzed how the infection spreads over time and space. Our results demonstrate that, even under purely random movement, the initial placement of patient zero has a pronounced effect on outbreak duration: central starting positions yield rapid, widespread infection, whereas edge and corner positions substantially delay full infection (Figure 3).

These findings suggest that spatial policies and boundary effects alone can slow epidemic progression. Building on this baseline, our proposed policies—partitioning the grid into quarantined regions, routing infected agents toward corners, or enforcing a barrier between healthy and infected populations—aim to exploit these geometric effects to further reduce transmission rates.

Going forward, we plan to implement and compare these candidate movement policies. Ultimately, this work underscores how simple, local movement rules can inform more sophisticated interventions in epidemiological modeling.

8 References

- Kermack, W.O., McKendrick, A.G. Contributions to the mathematical theory of epidemics—I. Bltn Mathcal Biology 53, 33–55 (1991). https://doi.org/10.1007/BF02464423

- Fine, P. E. M. (1977). A commentary on the mechanical analogue to the Reed-Frost epidemic model. American Journal of Epidemiology, 106(2), 87–100.

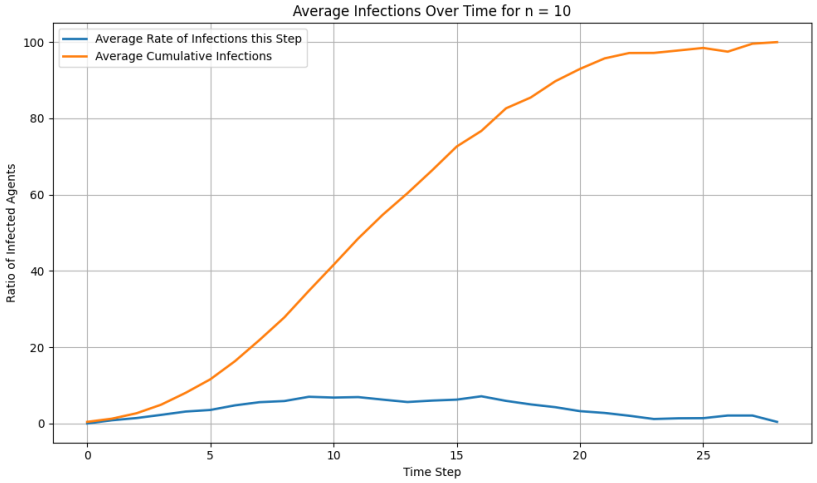

Figure 1: Infections over Time and Cumulative for n = 10 run.

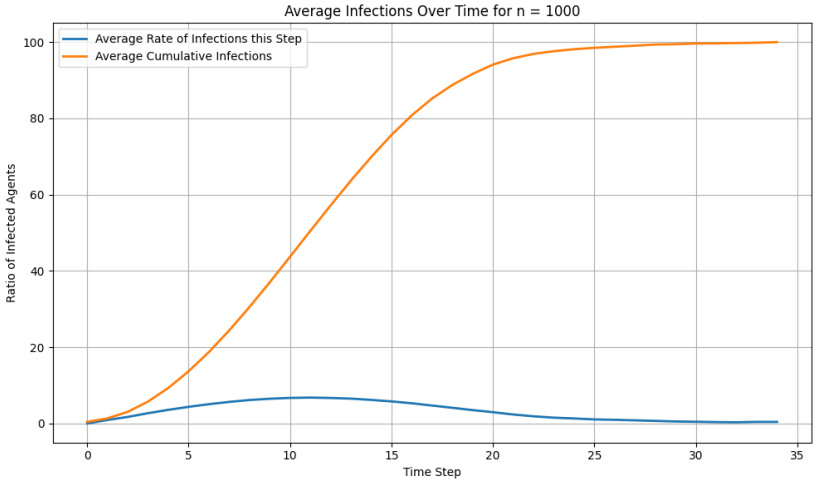

Figure 2: Infections over Time and Cumulative for n = 1000 run.

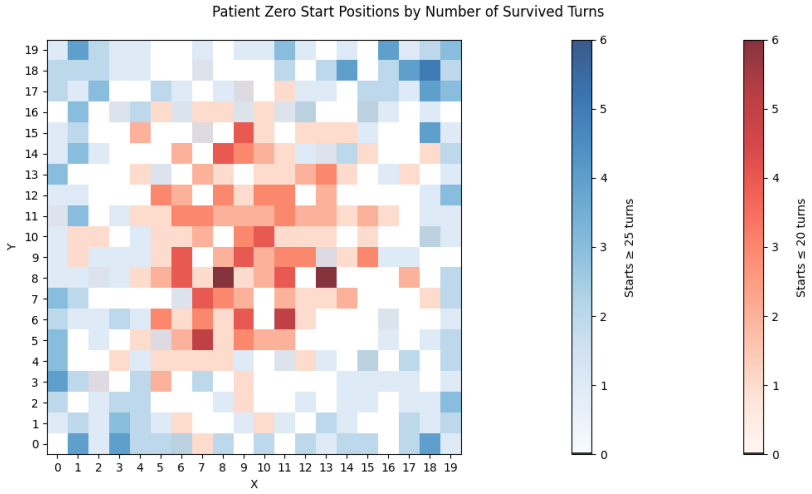

Figure 3: Heatmap of n = 1000 simulation run representing patient zero starting positions and the amount of turns before each simulation finished.