Branching Processes

1 Introduction

Branching processes are a classic concept that presents itself in many real-world applications. We can use Martingale's systems to express how infections spread since the number of infections in each generation can be modeled as related random variables in a sequence.

2 Problem Statement

The problem we considered is that of a disease spreading in some hypothetical population. Our goal is to see the progression of infections through the population to see how many time-steps it would take for the total population to become infected. We will visualize the infections as a tree since new infections must be borne out of pre-existing ones.

3 Simulation

To test out the theory of branching processes, we ran some simulations using a variety of parameters. The simulation was set up as follows: given a population of N people, one person is randomly selected to have an infectious disease at time t=0. At each successive timestep, each pair of persons is likely to meet modeled by a Poisson process with parameter λ . If an infected person meets a non-infected person at time t, the non-infected person will catch the disease with parameter p in[0,1). If the non-infected person catches the disease, then that person is able to infect others at time t+1. Additionally, if person A infects person B, then A is the parent of B.

We primarily wanted to see (1) visually how the disease would spread with small populations across different parameters, and (2) how changing the parameters would affect the average number of iterations to spread the disease to all people in the simulation. Below, we show some visualizations of our simulations and a graph showing the average number of iterations as a function of N and the Poisson parameter, λ Note that these graphs used a fixed p=0.3.

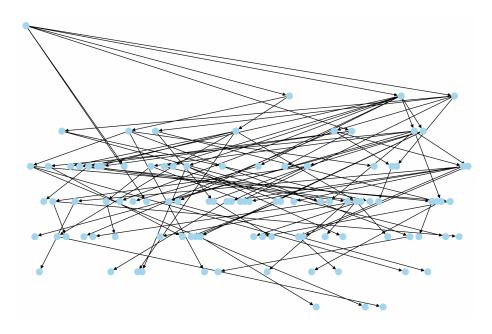


Figure 1: Figure 1: N = 100, lambda = 0.2, p = 0.1. Num generations = 8

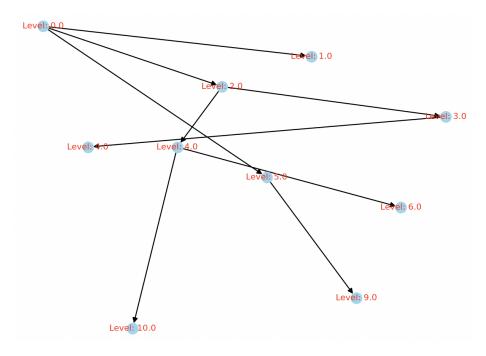


Figure 2: Figure 2: N = 10, lambda = 0.5, p = 0.2. Num generations = 10

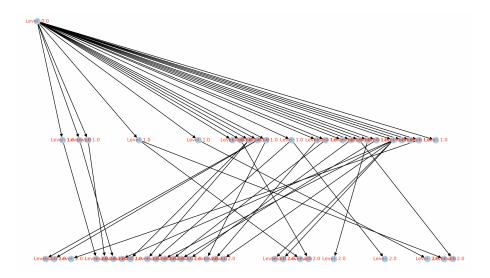


Figure 3: Figure 3: N = 100, lambda = 1, p = 0.5. Num generations = 2

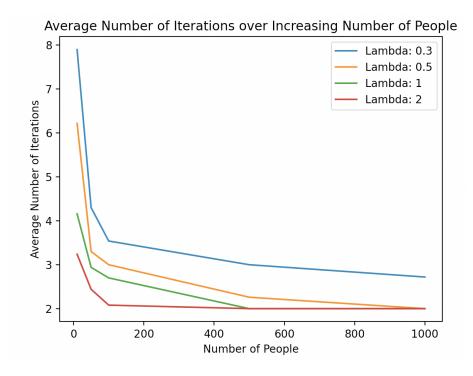


Figure 4: Figure 4: Average number of iterations taken to spread disease to all N people across different lambda and number of people. Averaged across 50 iterations per setting.