

1. (i) Let $\mu = \mathbb{E}[Y] = 0 \cdot 0.4 + 2 \cdot 0.6 = 1.2$, then $\mathbb{E}[Z_n] = \mu^n Z_0 = 1.2^n$. Then $\mathbb{E}[Z_n] \geq 10000 \implies n \geq \log_{1.2}(10000) \approx 50.5$, so we expect the number of infected individuals to reach 10000 after about 51 generations.
- (ii) The probability of extinction is the smallest non-negative solution of $G_Y(\gamma) = \gamma$. Since

$$G_Y(s) = \sum_{k=0}^{\infty} s^k p_k = s^0 p_0 + s^2 p_2 = 0.4 + 0.6s^2,$$

we have

$$\gamma = G_Y(\gamma) \implies \gamma = 0.4 + 0.6\gamma^2 \implies \gamma = \frac{1 \pm 0.2}{1.2} = 1, 2/3.$$

Thus the probability of extinction is $2/3$.

- (iii) A histogram of the simulation is shown below.

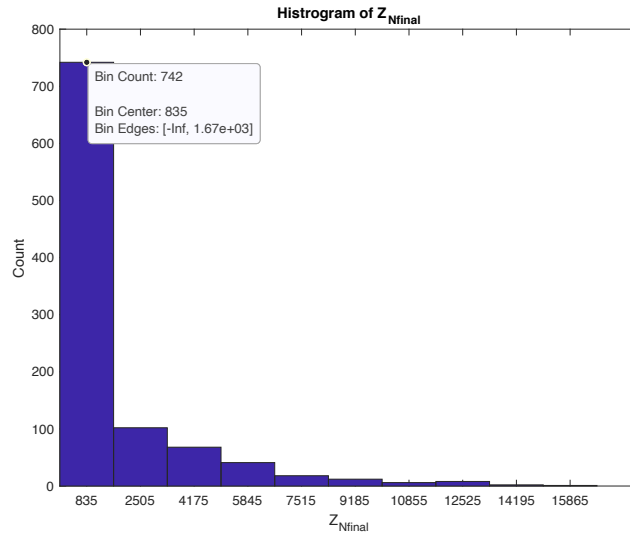


Figure 1: 1000 samples with final time $n = 40$.

This shows 742 simulated trajectories going extinct, or 74.2% of the simulations. The empirical mean of the 1000 samples of Z_{40} is approximately 1295. Since $\mu = 1.2$, the actual mean is $\mathbb{E}[Z_{40}] = \mu^{40} \approx 1469$.

2. (i) The offspring distribution should be a weighted average of the moderate and super spreader distributions.

$$\{p_k\}_{k=0}^{\infty} = \{p_0 = 0.88\alpha + 0.4(1 - \alpha), p_2 = 0.6(1 - \alpha), p_{10} = 0.12\alpha\}.$$

- (ii) Below are simulated cumulative infectious cases for $\alpha = 0$ and $\alpha = 1/2$. Note the different scales of each graph. From this we can see
 - i. When $\alpha = 1/2$, the largest outbreaks are significantly larger than the largest outbreaks when $\alpha = 0$, and
 - ii. Fewer of these large outbreaks occur. A larger percentage of outbreaks die out early on when $\alpha = 1/2$.

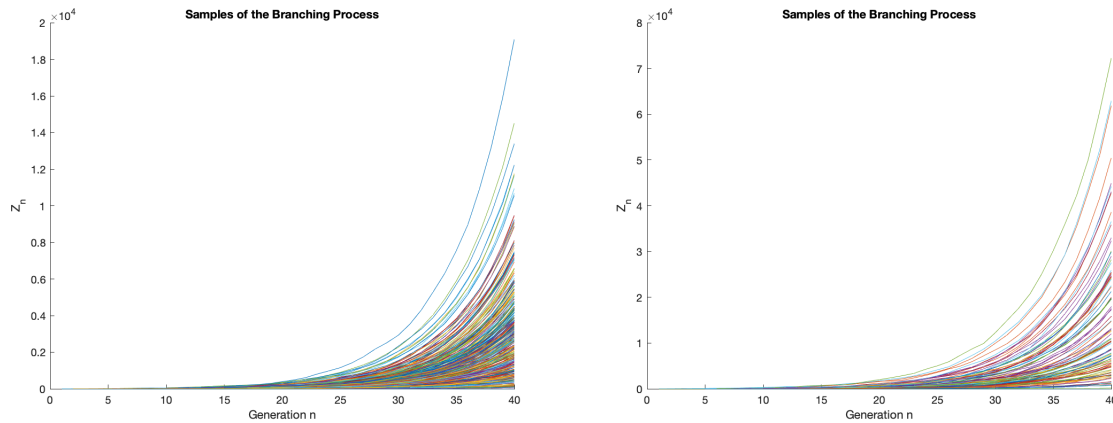


Figure 2: Left: $\alpha = 0$, Right: $\alpha = 1/2$.

Since the growth of these outbreaks is exponential when viewed at a large scale, we can infer that when $\alpha = 1/2$, the behavior at early generations is comparable to a highly variant choice of initial condition. With low probability, the disease is initially spread to many people and a large outbreak occurs because the probability of many branches all dying out is small (akin to starting an exponential growth model with a higher initial condition). With high probability, few people contract the disease and it dies out quickly.

3. (i) The generating function for Y is

$$G_Y(s) = \sum_{k=0}^{\infty} s^k p_k = s^0 p_0 + s^2 p_2 = 0.53 + 0.47s^2,$$

so we have

$$\gamma = G_Y(\gamma) \implies \gamma = 0.53 + 0.47\gamma^2 \implies \gamma = 1 \text{ or } \gamma \approx 1.1.$$

The minimum of these two roots is 1, so the extinction probability is 1.

- (ii) In this example, the outbreak begins with a single infection. This one person is assumed to infect Y people. Since branching process assume that branches grow independently of one another, each of these individuals can then be treated as the original infectious individual of a “new” outbreak. Suppose the original infected person infects people 1 through Y . Let D_i denote the number of people that newly-infected person i infects, then the total number of infected D can be written recursively as

$$D = 1 + D_1 + D_2 + \cdots + D_Y.$$

In words, this says that the total number of infected people is equal to the 1 original person infected person plus the number of infected individuals in each of the original Y branches.

- (iii) We can partition this expectation over all possible values of Y .

$$\begin{aligned} \mathbb{E}[D] &= \sum_{y=0}^{\infty} \mathbb{E}[D \mid Y = y] \mathcal{P}(Y = y) \\ &= \mathbb{E}[D \mid Y = 0] p_0 + \mathbb{E}[D \mid Y = 2] p_2 \\ &= p_0 + p_2 \cdot \mathbb{E}[1 + D_1 + D_2]. \end{aligned}$$

Then since each D_i has the same distribution as D , and by linearity of expectation, this becomes

$$\begin{aligned}\mathbb{E}[D] &= p_0 + p_2 + 2p_2 \cdot \mathbb{E}[D] \\ \mathbb{E}[D] &= \frac{p_0 + p_2}{1 - 2p_2} \\ \mathbb{E}[D] &= \frac{0.53 + 0.47}{1 - 0.94} = \frac{1}{0.06} \approx 16.7.\end{aligned}$$

Thus we expect between 16 and 17 people to become infected during this outbreak.