

Cholera Transmission Model - NetLogo

Introduction

Cholera is an infectious disease that targets a victim's small intestine. It is primarily spread through contaminated drinking water or food, and when caught, can lead to vomiting, diarrhea, and if left untreated, can kill within hours. One of the biggest factors on a person's survival chances is their access to adequate healthcare. If an infected individual can get proper fluids and antibiotics, then their survival chances go up greatly. The theoretical situation being used in this model will be a large outbreak of people with no access to hospitals. In the absence of hospitals, there is still a much more cost effective and resourceful way to fight the disease, which is vaccination. This raises another question, which is cost. In an ideal world, governments could buy enough vaccines for everyone. In the case of a lot of third world countries, this is not always an option. With this in mind, the model needs to be able to focus on maximizing lives saved, while minimizing vaccines used to hopefully find a sweet spot.

Explanation of Model

One approach to modeling a population of people infected by cholera could be a top down approach using equations to calculate the best approach of vaccination. This model takes a bottom up approach by modeling a complex system using an agent based model. The complex system in this case would be a population of people. This population of people can be put in a Netlogo program as agents following simple instructions to model a very complex real world problem.

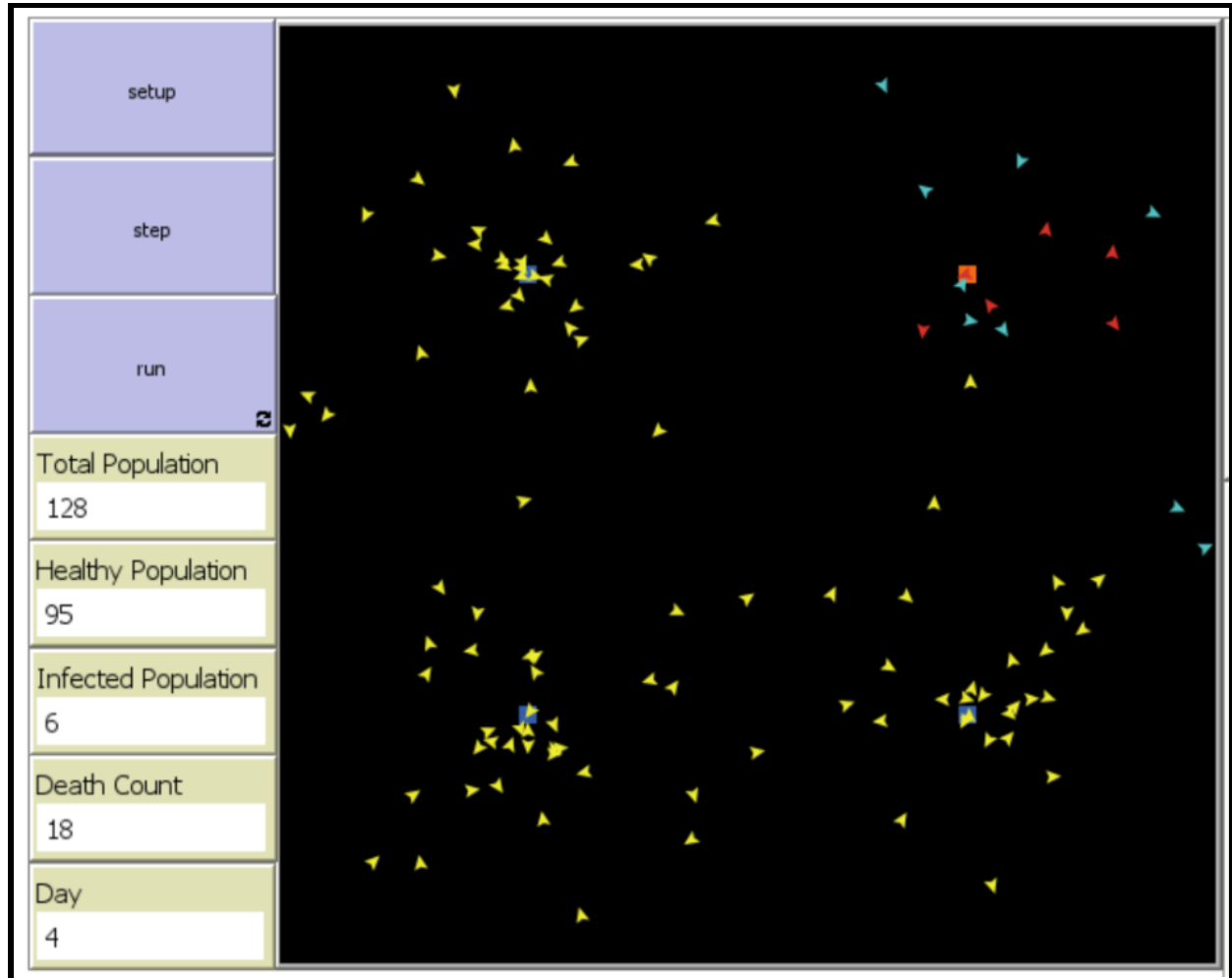


Figure 1: Netlogo Simulation Screen

The NetLogo program running this model is named [“Cholera-Transmission-Model-V3.nlogo”](#) and can be downloaded and run at the link provided. Looking at figure 1, we have a main screen with a lot of spots. These little triangles are people. The color they are represents their status. Yellow means healthy, blue is immune/vaccinated, and red is infected. When the model is set up, the people will wander around and occasionally drink from the four water patches. If the water patch is blue, then the water is clean, but if the patch is orange, then it is infected and will cause the people who drink it to become infected. When the model is started, every person has a home water patch, every turtle will only drink from one patch, but they do have a random chance to switch water patches, which represents them going to a different area. This is how the disease spreads. Looking at the left side, there are monitors for various population variables.

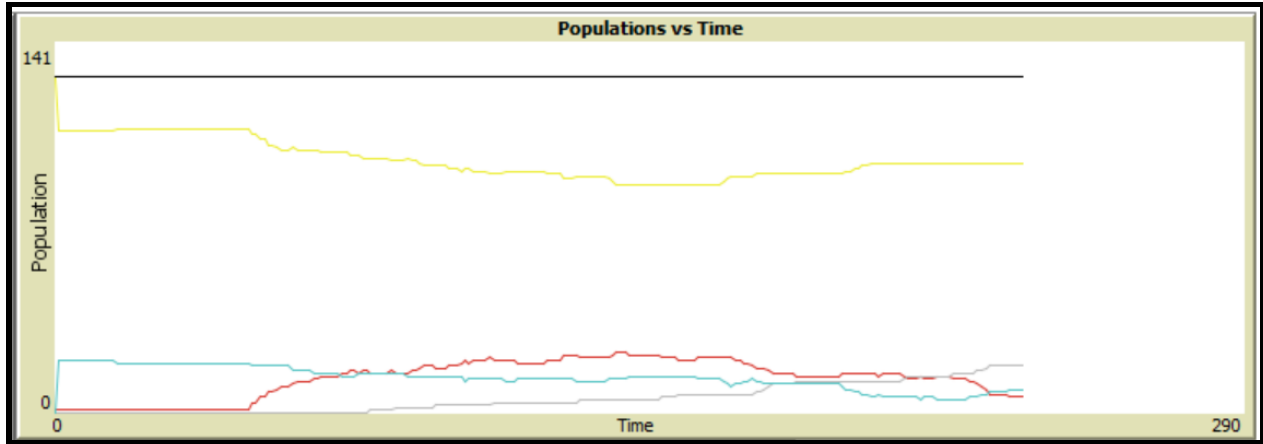


Figure 2: Population Graph

The second aspect of the program is the Population vs. Time graph. This graph will automatically update as the program is running. It is important to have the “Run-Multiple” switch turned off when running this program or there will be multiple graphs plotted. The variables being plotted are the total population including the dead population (black), healthy (yellow), immune (blue), sick (red), and dead (gray).

VARIABLES

DEFAULT VARIABLES

HUMAN

Initial-Population

128

Initial-People-Infected

1

Initial-People-Immune

20

Max-Immunity

200

Infection-Duration

150

Travelers-Per-Day

5

WATER

Decontamination-Chance

15

ENVIRONMENT

Day-Length

75 Days

DOWNLOAD PLOT

download-path

c:/Users/wesmu/Desktop/plot.csv

Figure 3: Variables

The third section of the program is the variables portion. This includes various sliders that will adjust the initial conditions of the program. There is a default variables button which will set the sliders back to their default values. There is also a download button which will download the data points from the plot shown in Figure 4 to a specified location.

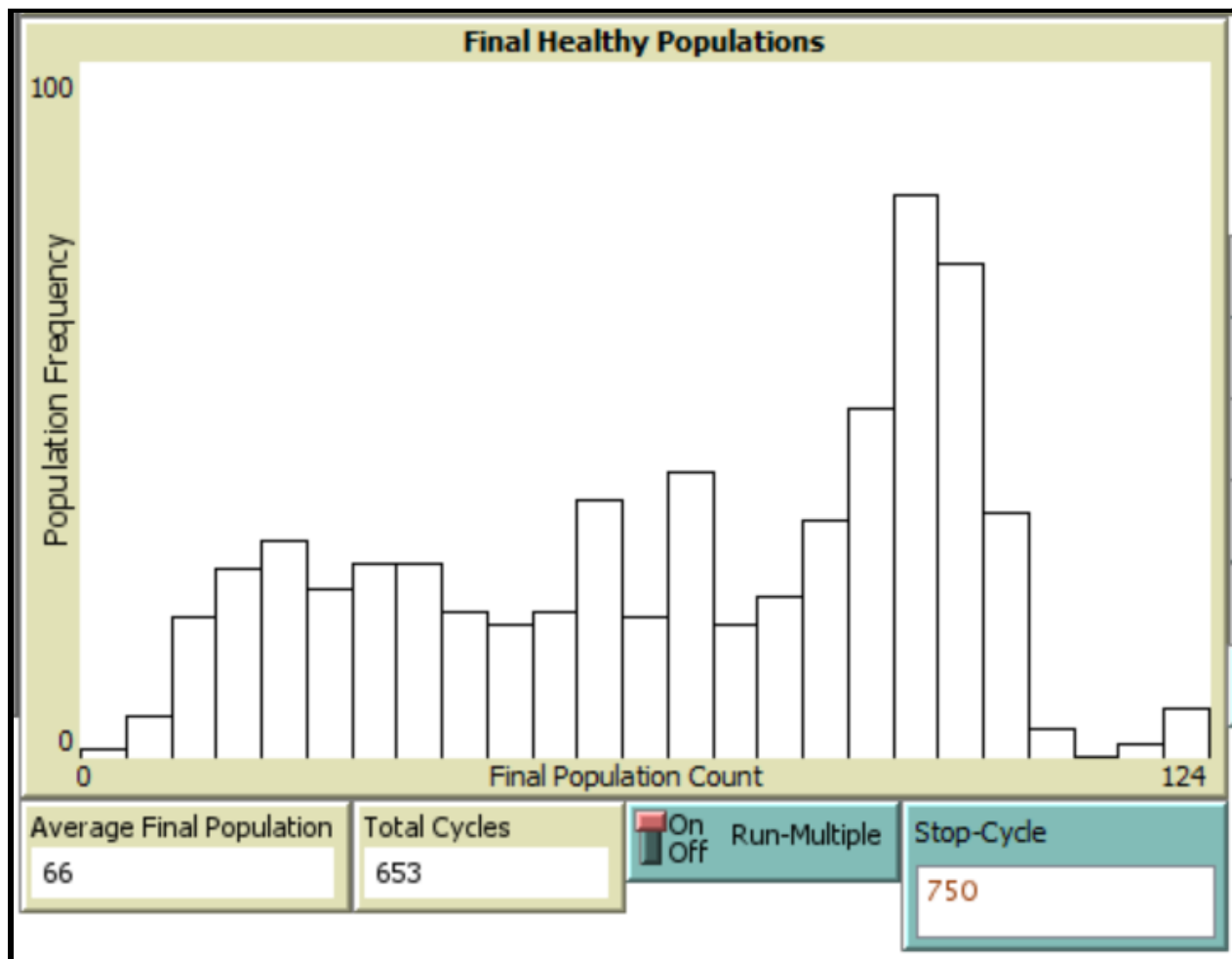


Figure 4: Histogram of Final Surviving Populations

The final part of the program is the final healthy population histogram. When “Run-Multiple” is selected, the model will run continuously and reset when there are no more infected people i.e. the Cholera was eradicated. This count is represented by the variable “Total Cycles”. Looking at this graph, we can see that the most often final population was around 91 people that survived (x-axis) which happened 81 times (y-axis).

Experiment and Results

For the experiment, I wanted to test the effect initial immunization had on survivability of the population. There are three simulations that were run. The first one was where the population was almost completely vaccinated where 190 of the initial 200 people were vaccinated. The second simulation was run where about half the population was vaccinated (100/200 people vaccinated). The final simulation run was where almost no one was vaccinated (10/100 people vaccinated).

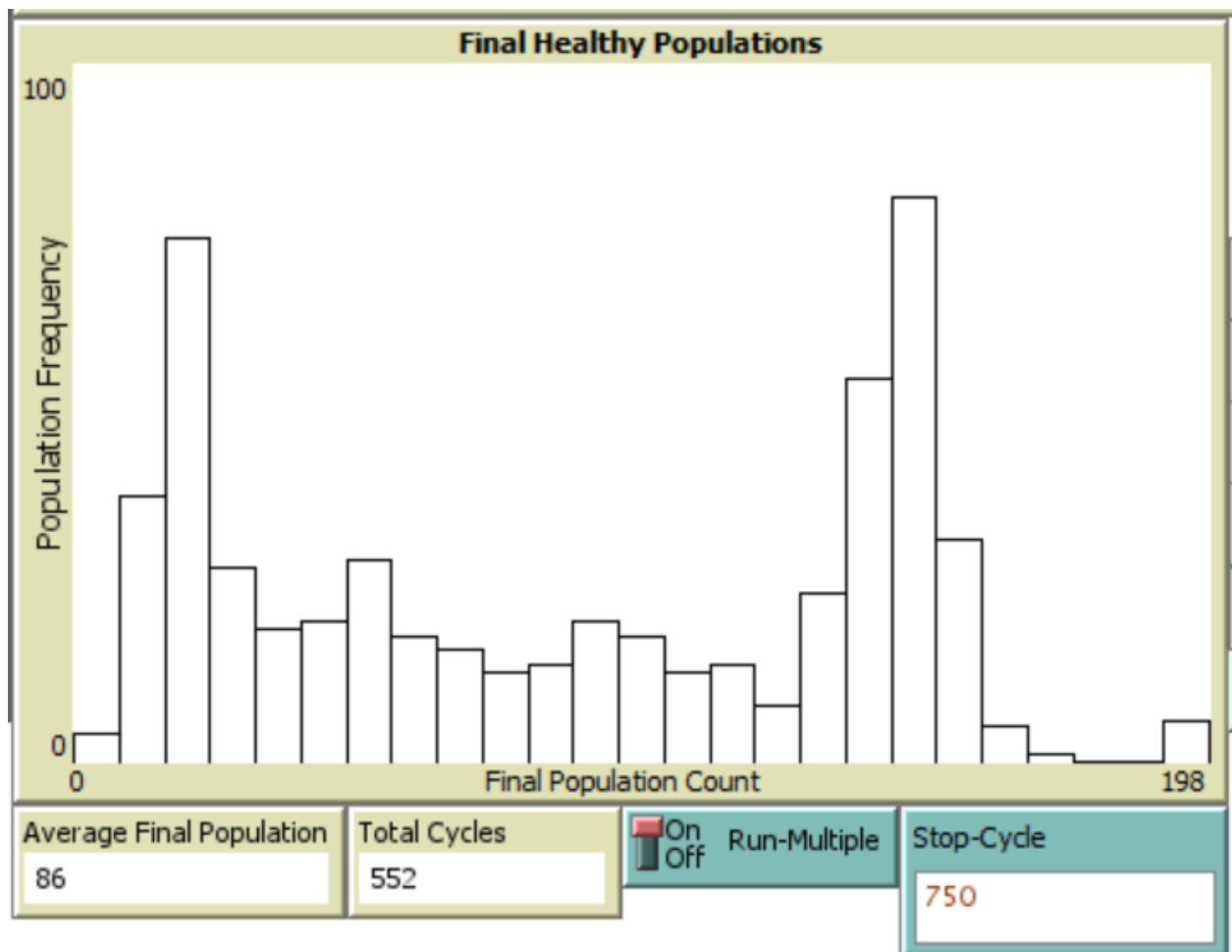


Figure 5: Histogram of 5% Initial Immunity (above)

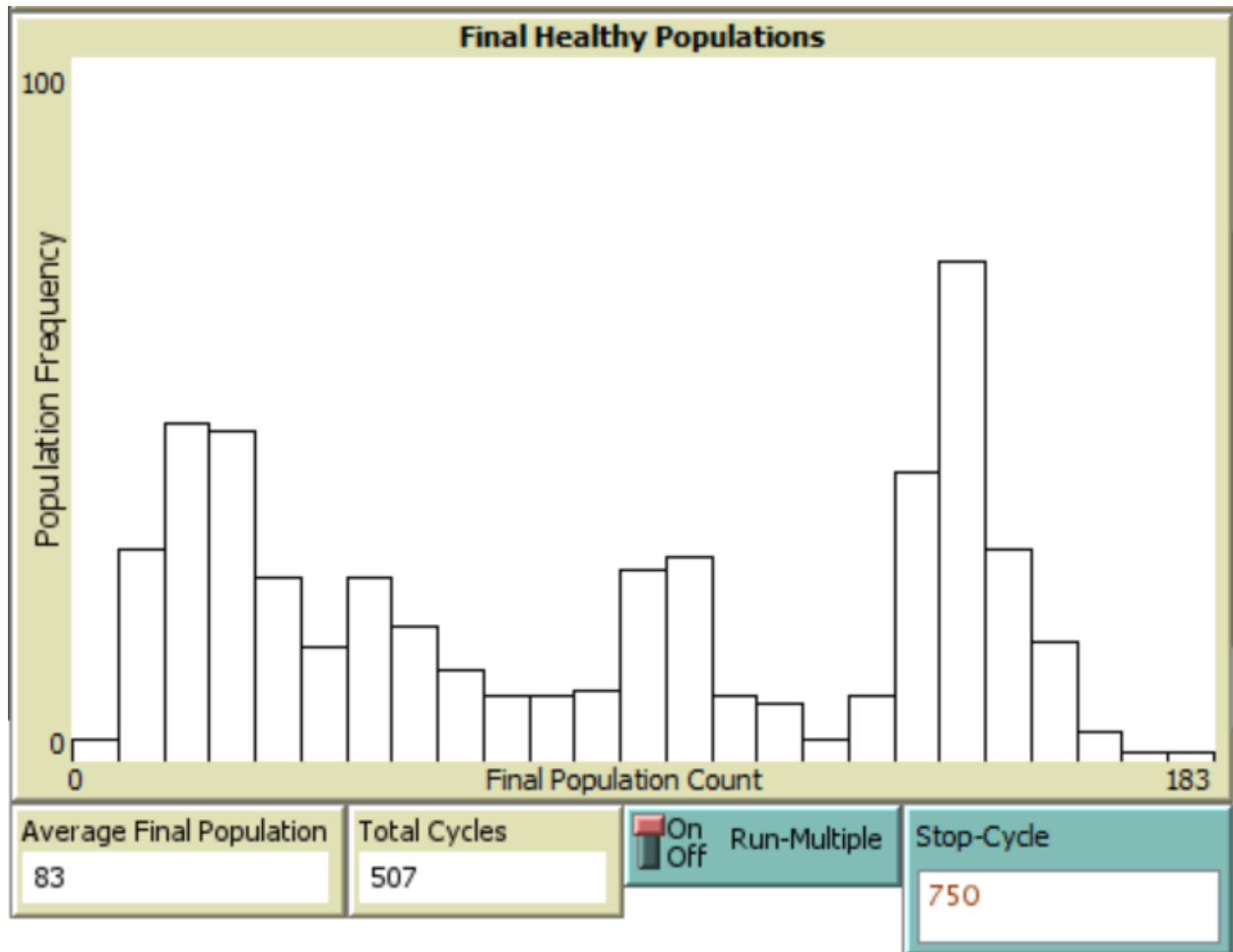


Figure 6: Histogram of 50% Initial Immunity (above)

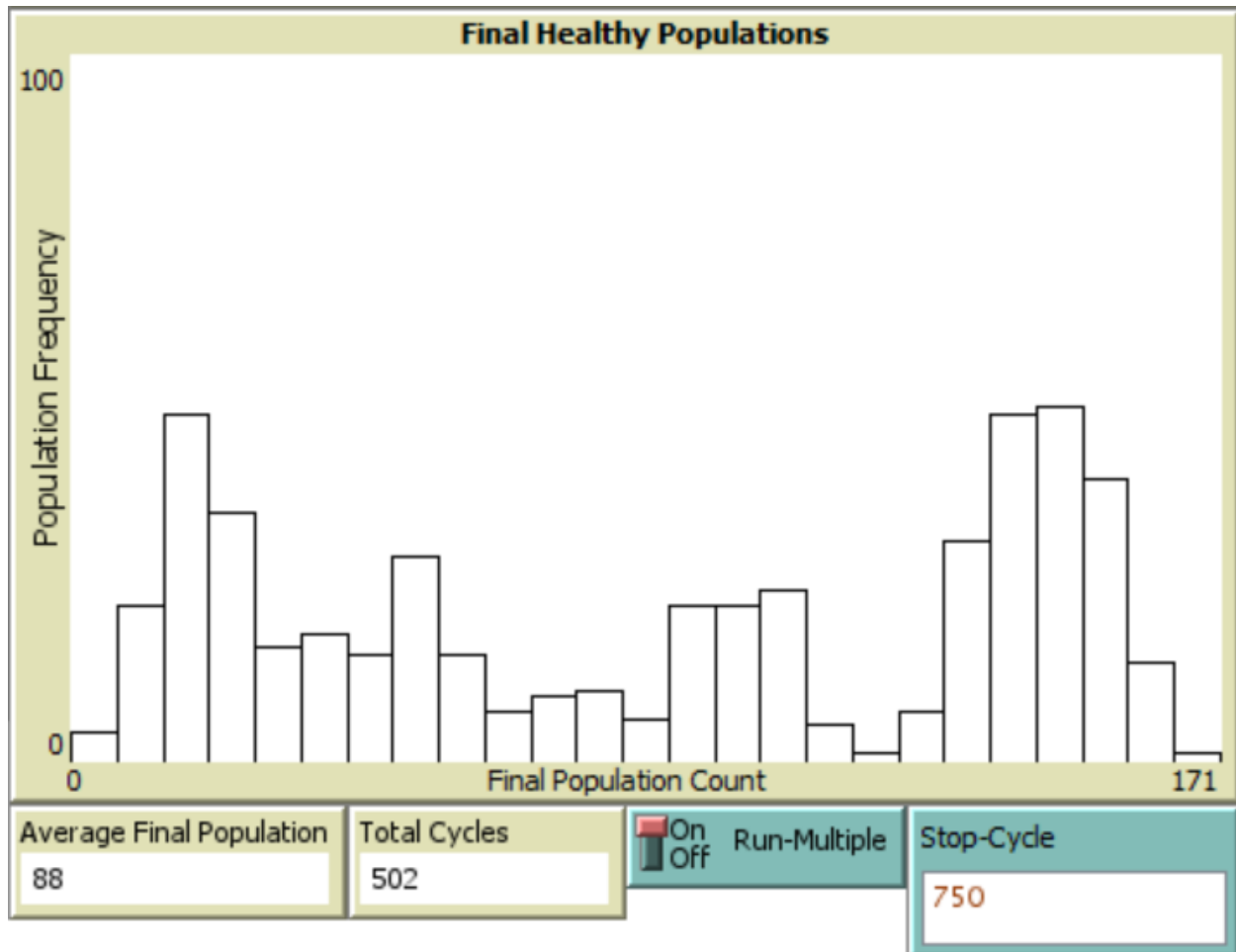


Figure 7: Histogram of 95% Initial Immunity (above)

| Histogram | 5% Initial Immunity | 50% Initial Immunity | 95% Initial Immunity |
|--|---------------------|----------------------|----------------------|
| Figure | 5 | 6 | 7 |
| Initial Population Vaccinated/Immune | 10 | 100 | 190 |
| Average Final Living Population Count | 86 | 83 | 88 |
| Most often Final Living Population Count | 125 | 140 | 147 |

Analysis and Conclusion

Looking at the results of the three models, there is no certain conclusion about how the amount of initial vaccination will affect the final surviving population. Looking at the spread of the graphs, there is a lot of variability in the spread of final populations. In all three plots, there are instances where less than 5% of people survive, and other instances where over 95% of people survive. Looking at the average final populations, we have the heavily vaccinated populations with an average of 88/200 people surviving. This is greater than both of the other models which had a less vaccinated population which makes sense. The medium vaccinated population had a slightly smaller final average population than the lightly vaccinated population which does not make sense when thinking about it. Because of how similar the three results are, it is hard to conclude that the initial vaccination rate helped the survivability of the population. Looking at the mode of the three plots, the results do check out. The greatest final living populations for the three models did correlate with the initial vaccination rate.

Although there was not a very defined correlation between final healthy populations and vaccination rates, there was a small correlation. One way that could lead to a more clear answer would be to run the program with more iterations. This simulation was only running about 500 iterations. Beyond that, it would slow down dramatically. Ideally this could be run at 10,000+ iterations at 100 different initial vaccination levels to get more accurate results. Another improvement that could be made would be to test more input combinations. Factors such as initial population, vaccine effectiveness duration, and amount of people traveling to different water sources are all variables that could be manipulated to find an optimal result.