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Infectious Disease: An agent-based simulation.

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Infectious Disease: An agent-based simulation

Honors Thesis

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The Honors College

Honors-in-Discipline: Biology

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Abstract:

One of the primary reasons for studying infectious diseases is to improve control and ultimately eradicate the infection from the population (Keeling 2008). An agent base model was designed to observe the spread of disease and the effect of vaccination using the program known as StarLogo- TNG. Experiments were designed, not having a particular disease in mind, and simulations were run to determine the effects of different variables on the vaccination process of a certain population. Goals included observation of how infections spread and how vaccination plays a role in various situations such as, root of the infection, population size, number of providers for vaccination, and the longevity of vaccination.

Introduction:

The Oxford Dictionary (Oxford, 2003) defines disease as "a condition of the body, or of some part or organ of the body, in which its functions are disturbed or deranged; a morbid physical condition; a departure from the state of health, especially when caused by structural change." Disease can be either infectious or noninfectious. Infectious disease has the potential to be passed between individuals, whereas noninfectious diseases are those that develop over an individual's lifespan.

The primary risk factor for catching an infectious disease is the presence of infection in the local population. The infecting pathogen can be either a microparasite or a macroparasite (Boots, 2004). The progress of an infectious microparasitic disease is defined qualitatively in terms of the level of pathogen within the host, which in turn is determined by the growth rate of the pathogen and the interaction between the pathogen and the host's immune response.

When trying to understand the spread of an infectious disease through a population, many different factors are important (Eames, 2007). One of the primary reasons for studying infectious disease is to improve control and ultimately to eradicate the infection from the population. Models can be highly effective tools in this approach, allowing us to optimize the use of limited resources or simply target measures more efficiently. Models have been proven to have great predictive power at the population scale and over relatively short periods of time. They have two distinct roles— prediction and understanding, which are related to the model properties of accuracy and transparency.

The practice of vaccination began with Edward Jenner in 1796 who developed a vaccine against smallpox, which remains the only disease to date that that has been eradicated worldwide (Anderson, 1992). Vaccination acts by stimulating a host immune response, such that immunized individuals are protected against infection. It is generally applied prophylactically to a large proportion of the population, so as to greatly reduce the number of susceptible individuals (Rand, 1997).

In the current study, a model was designed using the program known as *StarLogo-TNG*. One of the goals for developing this program was to observe how infection spreads. Another goal was to notice how vaccination plays a role in different situations and different types of populations. Many factors were taken into consideration and observed during this experiment. Some of these included the root of the infection, the population, the number of providers that were able to cure and vaccinate, and the amount of time an individual was vaccinated. It was predicted that if the infectors were in a specific closed area, rather than spread randomly, it would take a longer time to eradiate the infection. Thus, in turn, it was predicted that as the population grows, it would also take a longer time period to cure the infection and vaccinate the population. It was hypothesized that the higher the number of doctors and the longer the vaccinations lasts, the faster individuals are cured and vaccinated.

Materials and Methods:

Program Used

StarLogo TNG: A modeling system created by Michigan Institute of Technology was used. This was downloaded from http://education.mit.edu/projects/starlogo-tng. *StarLogo* is an agent-based simulation language developed by Mitchel Resnick, Eric Klopfer, and others at MIT Media Lab and MIT Teacher Education Program in Massachusetts. It is an extension of the Logo programming language, a dialect of Lisp. Designed for education, *StarLogo* can be used by students to model the behavior of decentralized systems. The programming is done with graphical programming blocks instead of text-base commands. This innovation adds a powerful visual component to the otherwise abstract process of programming. The programming blocks are arranged by color based on their function, which enables students to associate semantically similar programming blocks with each other. Procedures are made from blocks that are snapped together, forming a visual chunk, which helps students chunk the goals of the procedures in their mental models of the program (Klopfer, 2007). This is shown in the figure below.
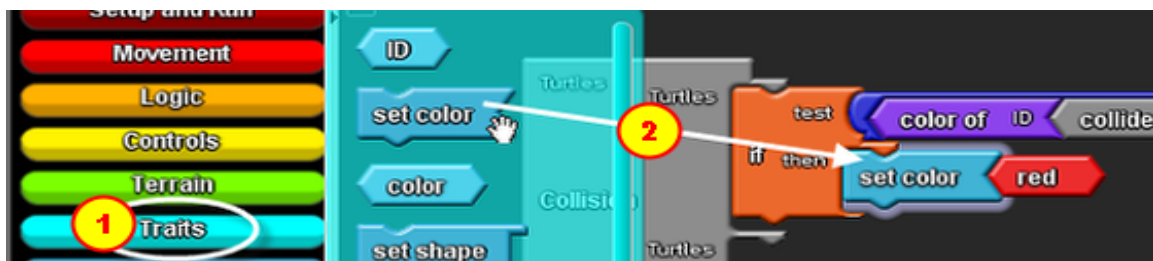

Figure 1. Blocks arranged by color in the *StarLogo TNG* program
http://education.mit.edu/projects/starlogo-tng.

StarLogo TNG spatially organizes block programs into breed drawers, which affords an object-oriented style of programming. It is a 3D representation of the agent world which provides the ability to model new kinds of physical phenomena, and allows

students to take the perspective of an individual agent in the environment, which helps them bridge the description of individual behaviors with system level outcomes.

The program was downloaded onto a laptop (MacBook 2.4GHz Intel Core 2 Duo P8600). Next, using *StarLogo TNG* and the blocks technique, a model was built.

Model:

A model was designed in which the population consisted of 200 uninfected individuals, 5 infectors, and 5 doctors. Every individual is programmed to have random movement. The doctors are set in a specific area of the plane and they are restricted from leaving that area (Figure 2). When a yellow uninfected individual collided with an infector, the yellow individual got infected, represented by a color change from yellow to red. This is how the spread of the disease begins. A collision process was set up using the block system that helps with the spreading of the infection. If a red infected individual collided with a yellow uninfected individual, the yellow individual, having become infected, will turn red. Once an individual is infected, they are programmed to go towards the doctors to be cured and then vaccinated, simultaneously infecting other individuals on their way. This set up was used as the control. This simulation was run for a time of 200 years, for 15 times to average out the affect of random fluctuations. 200 years of simulation time is chosen in order to have the simulation run for an amount of time where change can be observed. The control set up is shown in Figure 2.
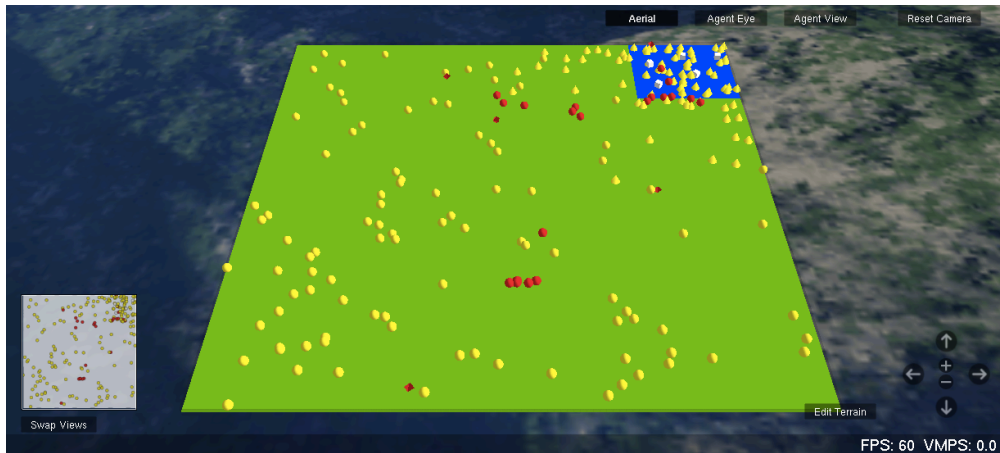
Figure 2. Screen shot of population at time: 50 years. 5 doctors are in the blue plane. Infected individual are seen making way towards the doctors.

Next, the program was set to where the original infectors were not spread throughout the population. They were located in a specific area as shown in Figure 3. This simulation was also run for 200 years, 15 times.
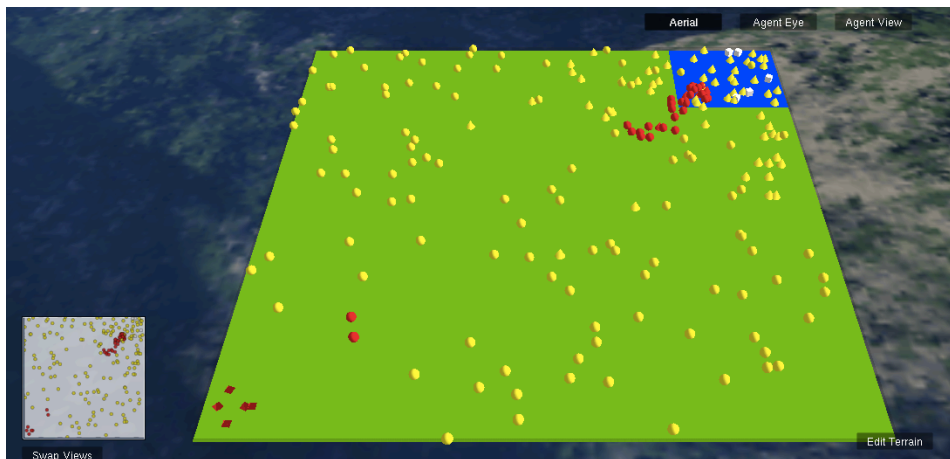

Figure 3. Screen shot taken at time: 50 years. Notice infectors are located in the bottom left corner.

The next variable that was changed in order to observe the effects on infected individuals was the population size where the infectors were not restricted to a specific area. Simulations were run with a population of 50, 100, 400, and 600. Again, the simulation was run for duration of 200 years, 15 times.
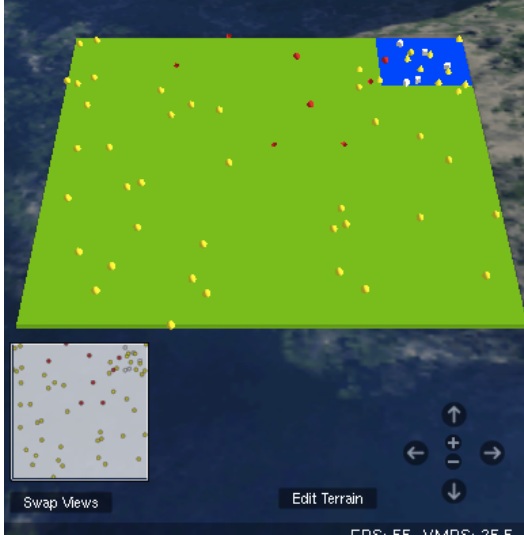
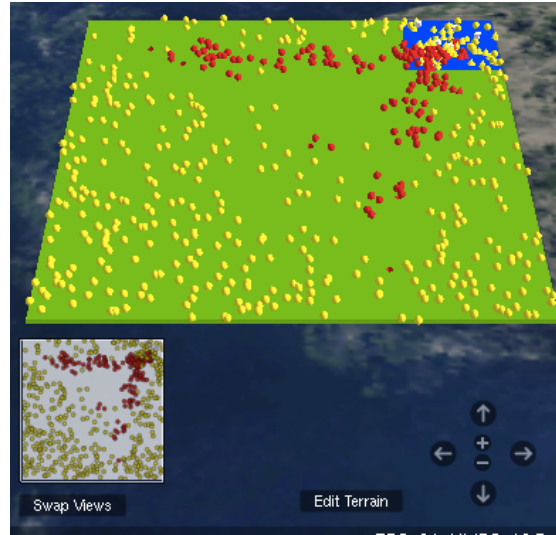Figure 4. Screen shot taken at time: 50 years; population size: 50.

Figure 5. Screen shot taken at time: 50 years; population size: 600.

After observing the spread of infection in different population sizes, the number of doctors was changed. The number of doctors, located on the blue plane, was set to 1, 2, 4, 8, and 16 respectively. Each simulation was run for a time of 200 years, 15 times each.
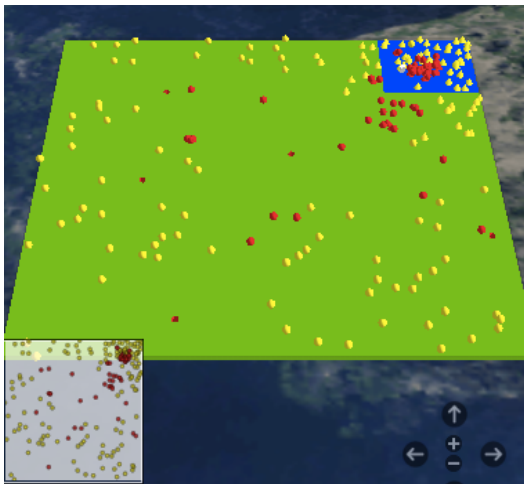

Figure 6. Screen shot taken at time: 50 years; population size: 200; number of doctors: 1.
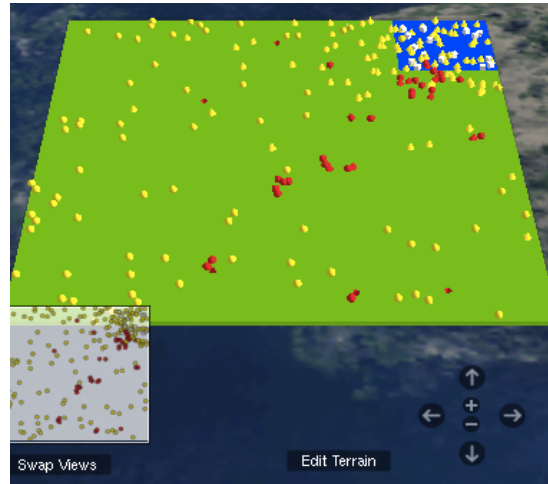

Figure 7. Screen shot taken at time: 50 years; population size: 200; number of doctors: 16.

The last variable that was taken into consideration was the time period the vaccination lasted. In all previous simulations the vaccination lasted for an infinite period of time. But, in many cases, vaccinations are effective only for a limited period of time. Therefore, for the next five simulations the vaccinations were programmed to last for 6

years, 8 years, 10 years, 12 years, and 14 years respectively. The numbers infected was
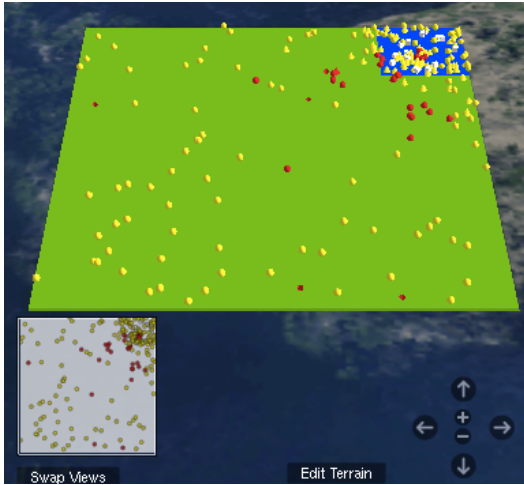
observed.

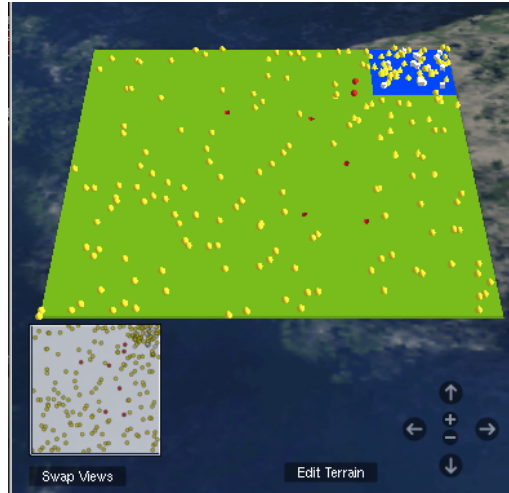Figure 8. Screen shot taken at time: 50 years, in which infection lasted for 6 years.

Figure 9. Screen shot at time: 50 years, in which infection lasted for 14 years.

Results:

After running each simulation a total of 15 times, the average of all 15 runs was taken. After collecting the data line graphs were made, showing the total number infected, the total number vaccinated, the total number uninfected, and the number of normal individuals. Normal individuals are not infected or vaccinated. These lines provide a visual that is easier to comprehend and composes the data in such a way that it is facilitates the process of comparing and contrasting the results.

Also, the standard deviation was taken of the total number infected to see the variation of the numbers infected over time. Standard deviation helps with the measurement of how the data or numbers are spread out.
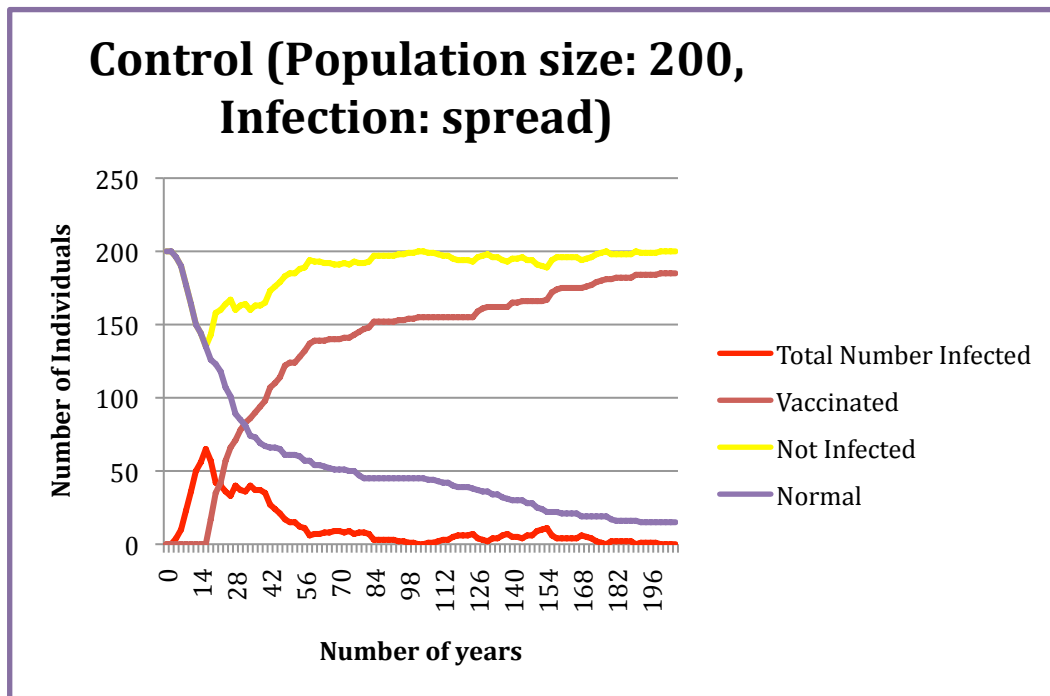

Figure 10. Shows the control. Population size: 200, the infection was spread randomly; doctors: 5 in specific location, and infected individuals move toward doctors.

Descriptive Statistics					
	N	Minimum	Maximum	Mean	Std. Deviation

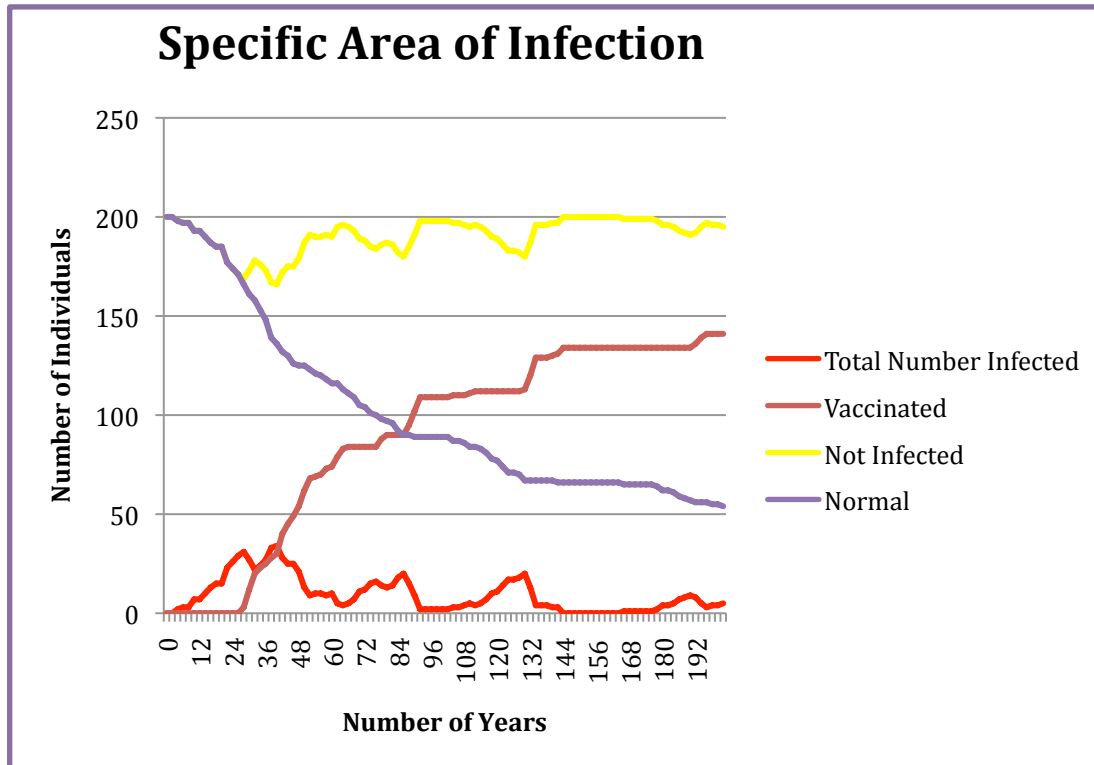|					
Total Number Infected	101	.00	65.00	11.5050	14.78961

Specific Area of Infection

Figure 11. Shows a line graph where the original infectors are located in one specific area. In this case the infection was located diagonal from the doctors. Population: 200; number of doctors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	34.00	9.2970	8.91913

The standard deviation for the total number infected, when the infection was only in a specific location is 8.9, compared to the control where the standard deviation was 14.8. It is also evident that the number of infected individuals in figure 11 keep

reappearing, therefore suggesting that it may be harder to eradicate the spread of an

infection if it starts from a specific location.

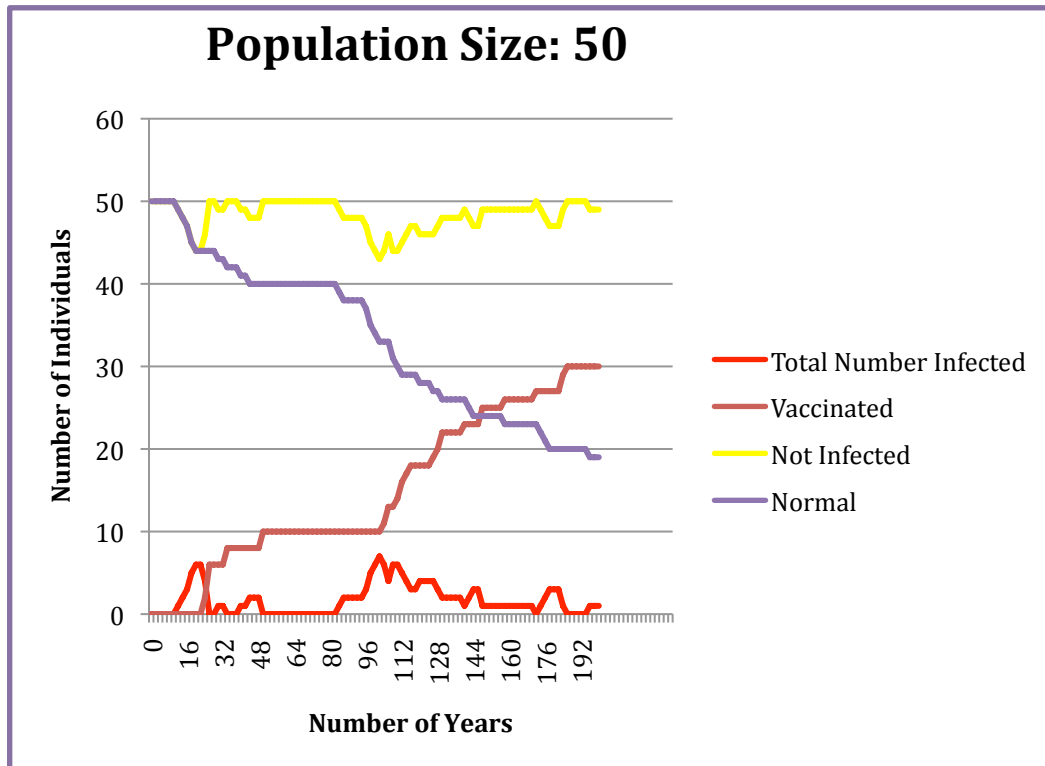Figure 12. Shows a line graph that has population size: 50; doctors: 5; infectors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	7.00	1.7030	1.83600

Figure 13. Shows a line graph that has population size: 100; doctors: 5; infectors: 5.

Descriptive Statistics

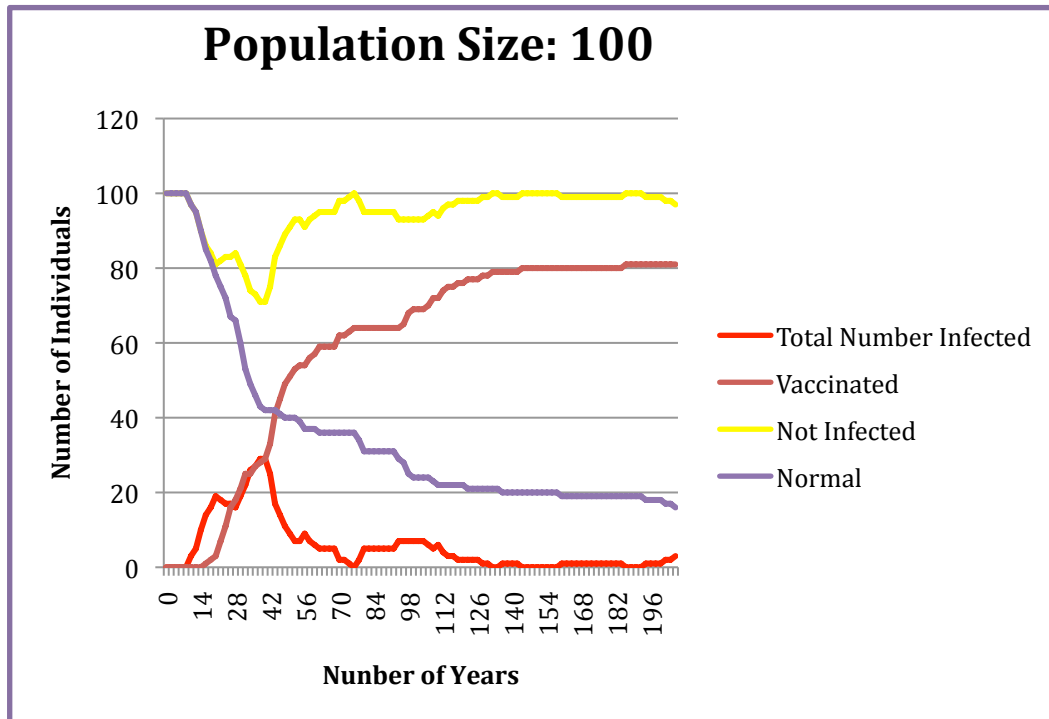|	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	29.00	5.5743	7.23235

Figure 14. Shows a line graph that has population size: 400; doctors: 5; infectors: 5.

Descriptive Statistics

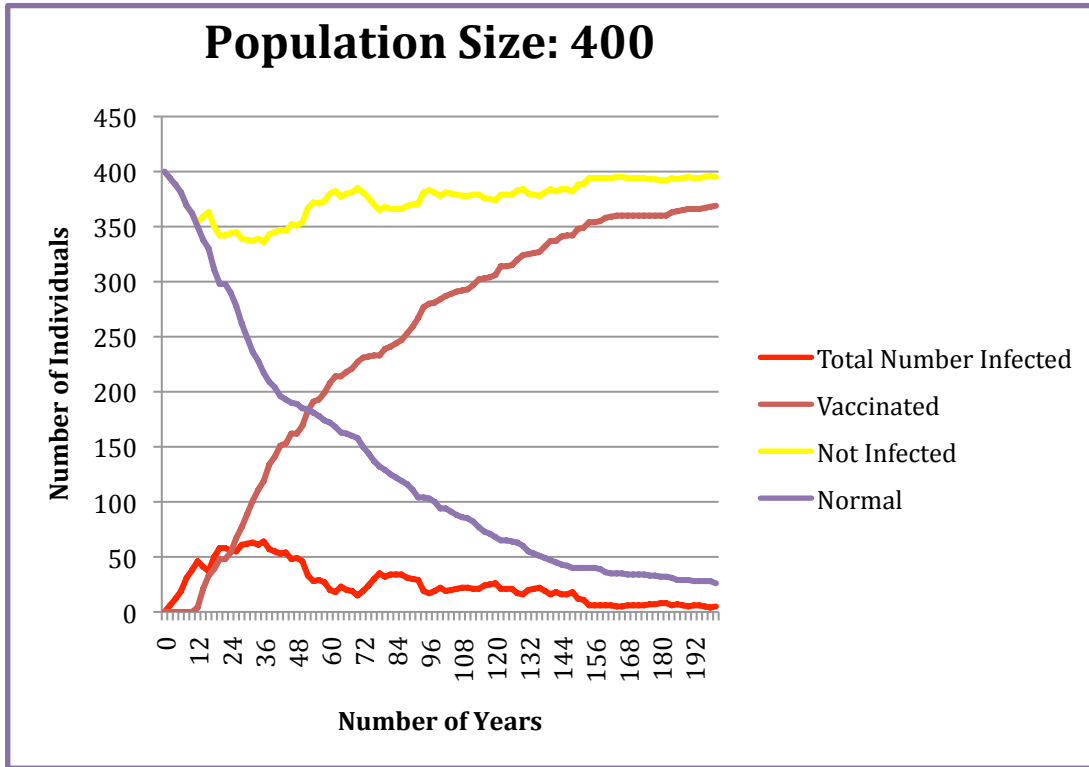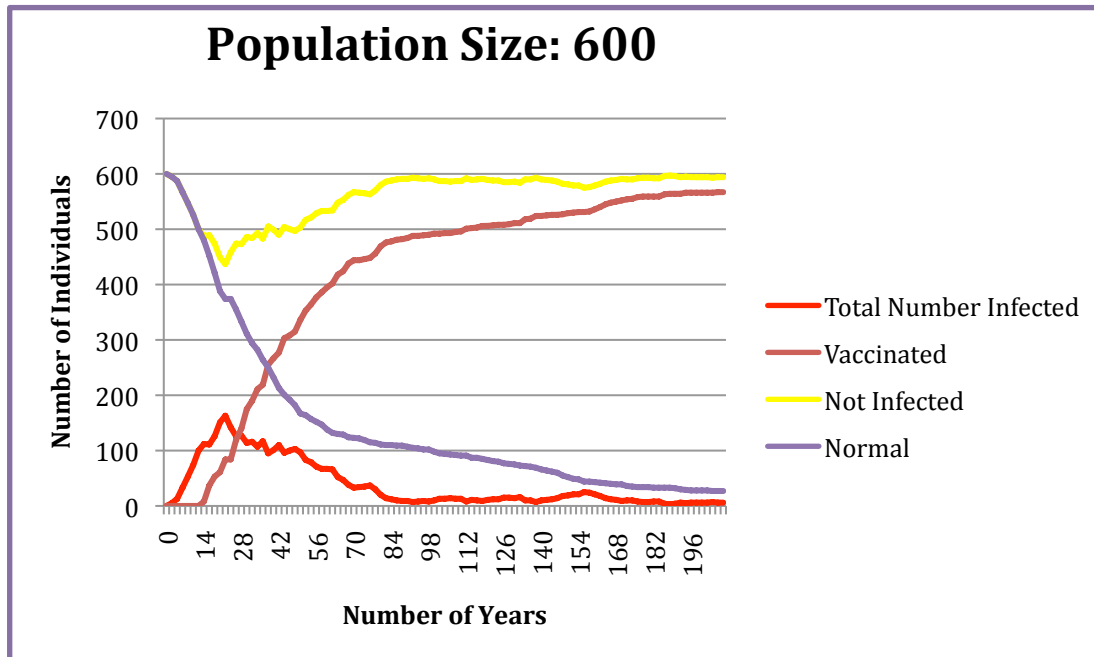|	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	64.00	24.4653	17.23344

Population Size: 600

Figure 15. Shows a line graph that has population size: 600; doctors: 5; infectors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	163.00	38.9208	42.90634

Obviously, the larger the population, the higher the number of individuals who will be affected. But as the population size grew, the standard deviation became larger. In other words, the data was spread out more as the population went from a size of 50 (Std. dev.= 1.8) to a size of 600 (Std. dev.= 42.9). The percentage of infected individuals stays pretty similar throughout the different population sizes.

Figure 16. Shows a line graph in which there is only 1 doctor to cure and vaccinate-population size: 200; infectors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	61.00	20.2871	17.77602

Figure 17. Shows a line graph during which there are 2 doctors to cure and vaccinate-population size: 200; infectors: 5.

Descriptive Statistics

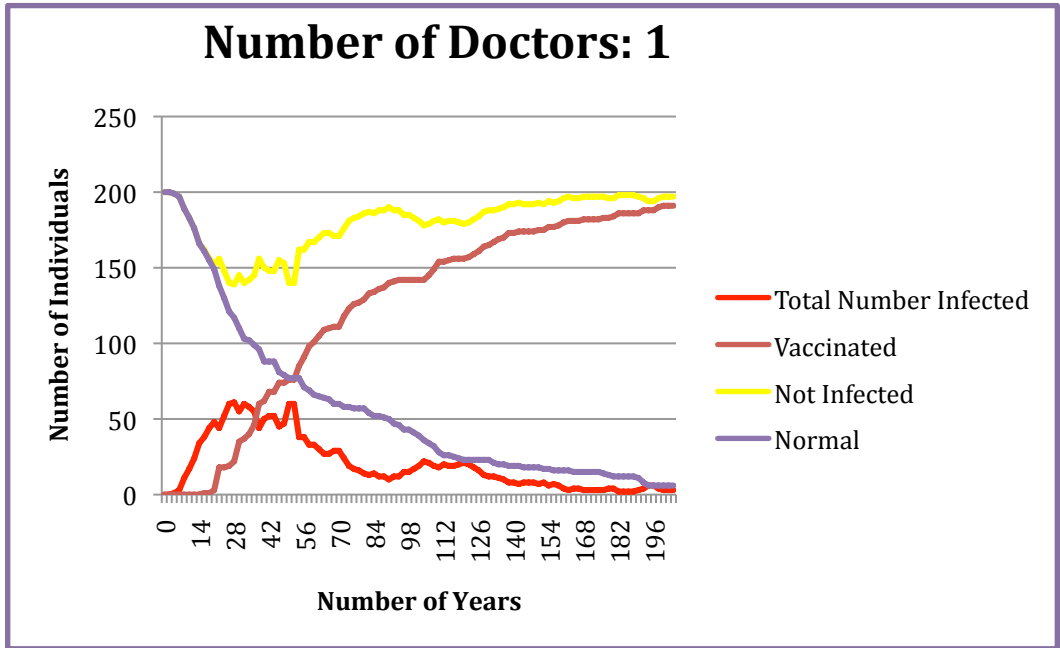|	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	51.00	15.7921	15.47664

Figure 18. Shows a line graph during which there are 4 doctors to cure and vaccinate-population size: 200; infectors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	51.00	12.5545	12.29510

Number of Doctors: 8
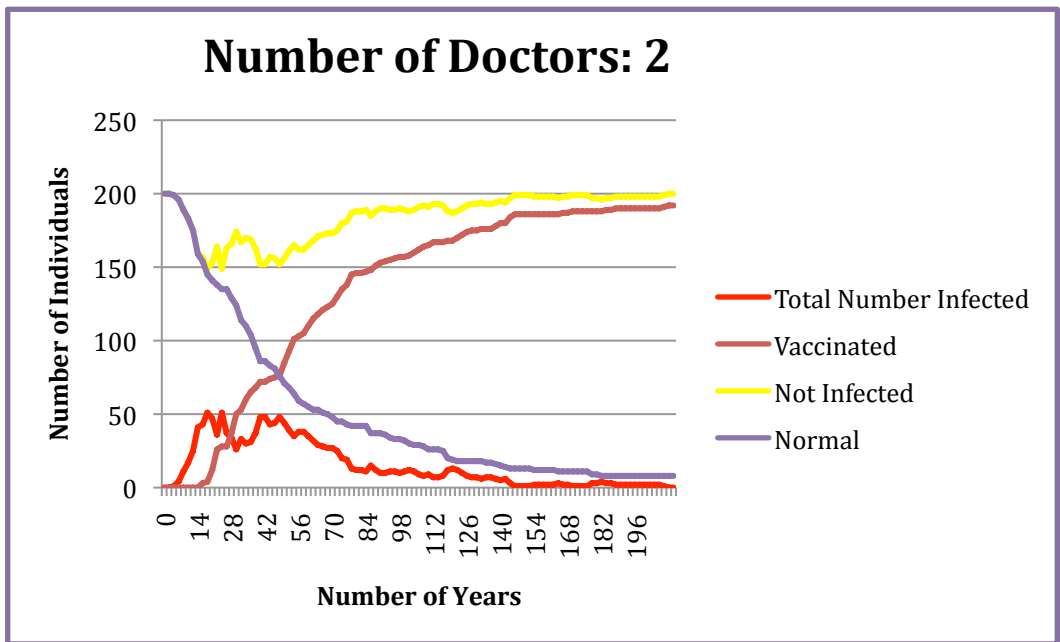
Figure 19. Shows a line graph during which there are 8 doctors to cure and vaccinate-population size: 200; infectors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	37.00	11.7129	9.30090

Number of Doctors: 16

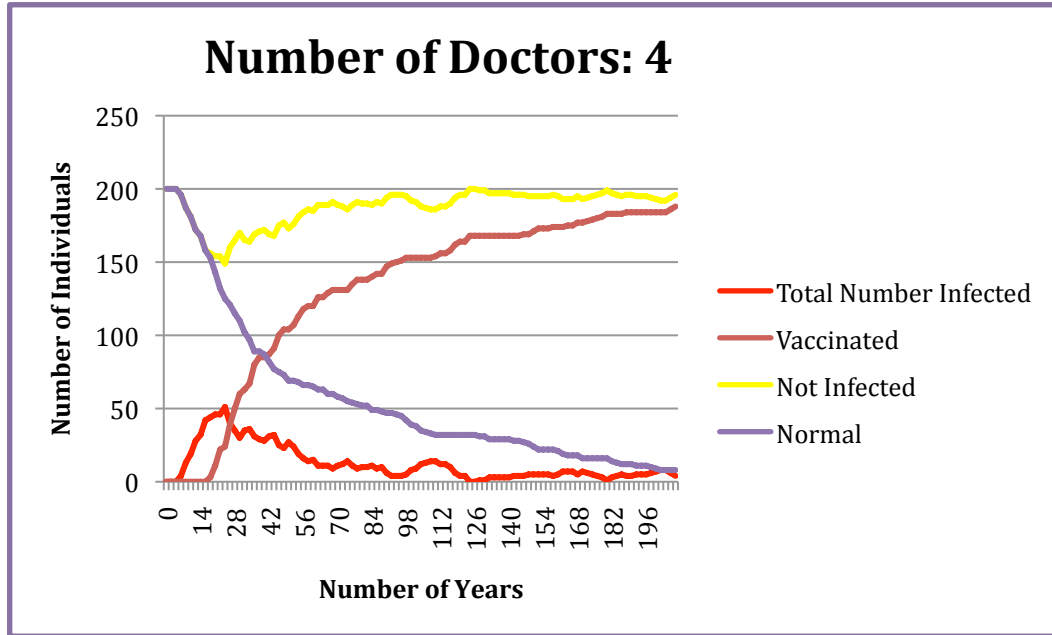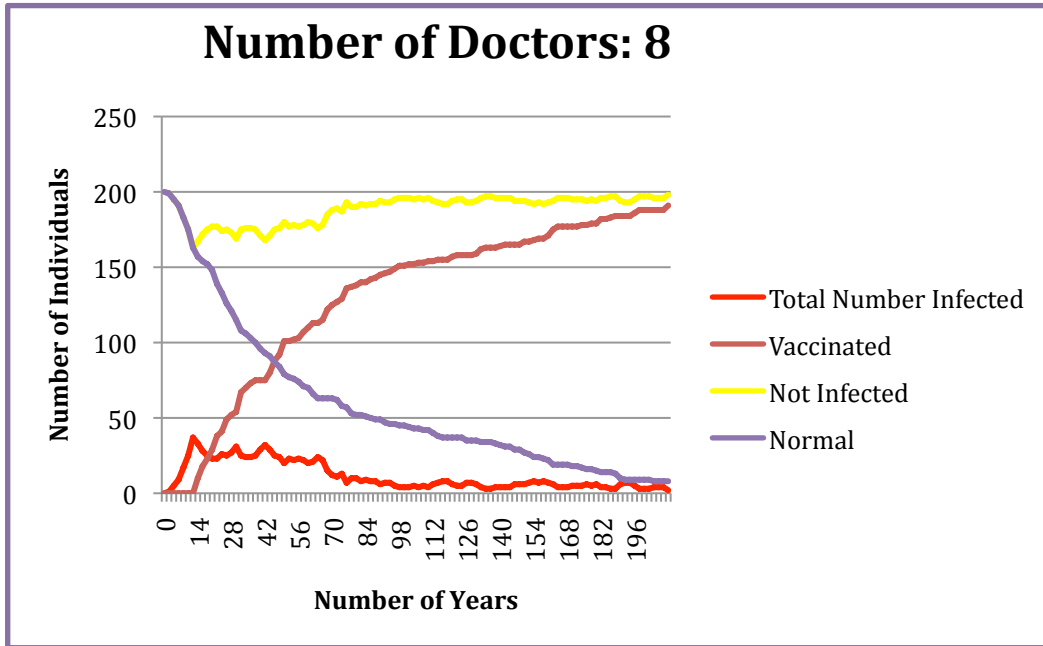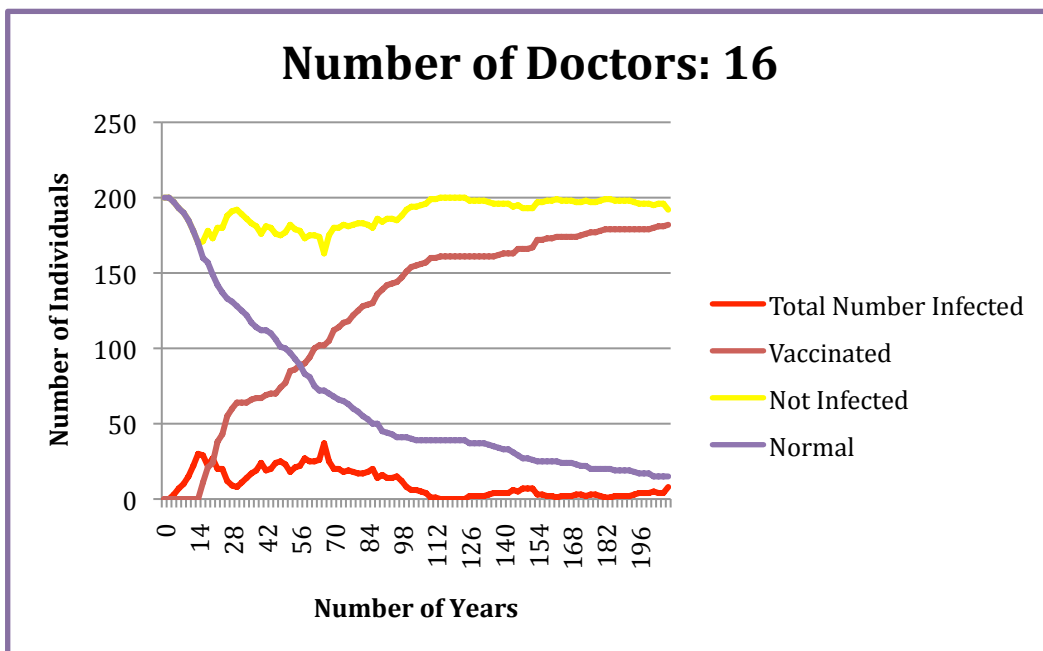Figure 20. Shows a line graph during which there are 16 doctors to cure and vaccinate-population size: 200; infectors: 5

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	37.00	10.4554	9.35898

The variation in the numbers of individuals who were infected decreases as the number of doctors increases. Even though there is not a drastic decrease in the standard deviation, the standard deviation does decrease somewhat as the doctors increase. When there was 1 doctor present the standard deviation was about 17.8, with 2 doctors 15.5, with 4 doctors 12.3, with 8 doctors 9.3. After doubling the amount of doctor from 8 to 16 the standard deviation stayed pretty much the same.

Figure 21. Shows line graph where the vaccination only lasted for 6 years. Population: 200; Doctors: 5; Infectors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	53.00	17.6733	11.60957

Figure 22. Shows line graph where the vaccination only lasted for 8 years. Population: 200; Doctors: 5; Infectors: 5.

Descriptive Statistics

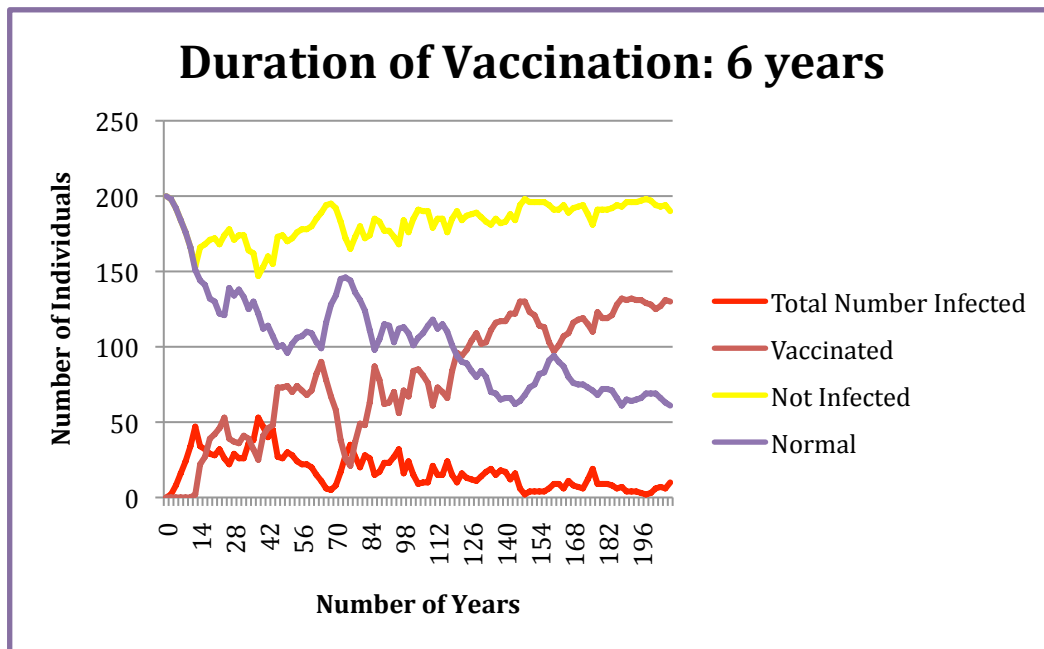|	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	30.00	10.5248	6.58118

Figure 23. Shows line graph where the vaccination lasted for 10 years.
Population: 200; Doctors: 5; Infectors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	42.00	15.7921	9.91596

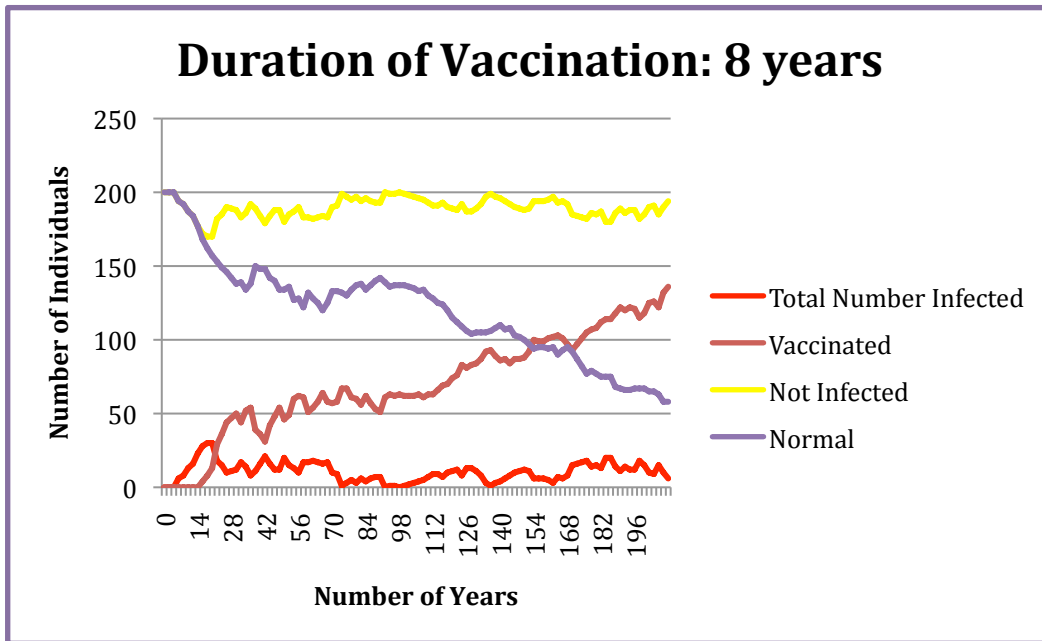Figure 24. Shows line graph where the vaccination lasted for 12 years.
Population: 200; Doctors: 5; Infectors: 5.

Descriptive Statistics

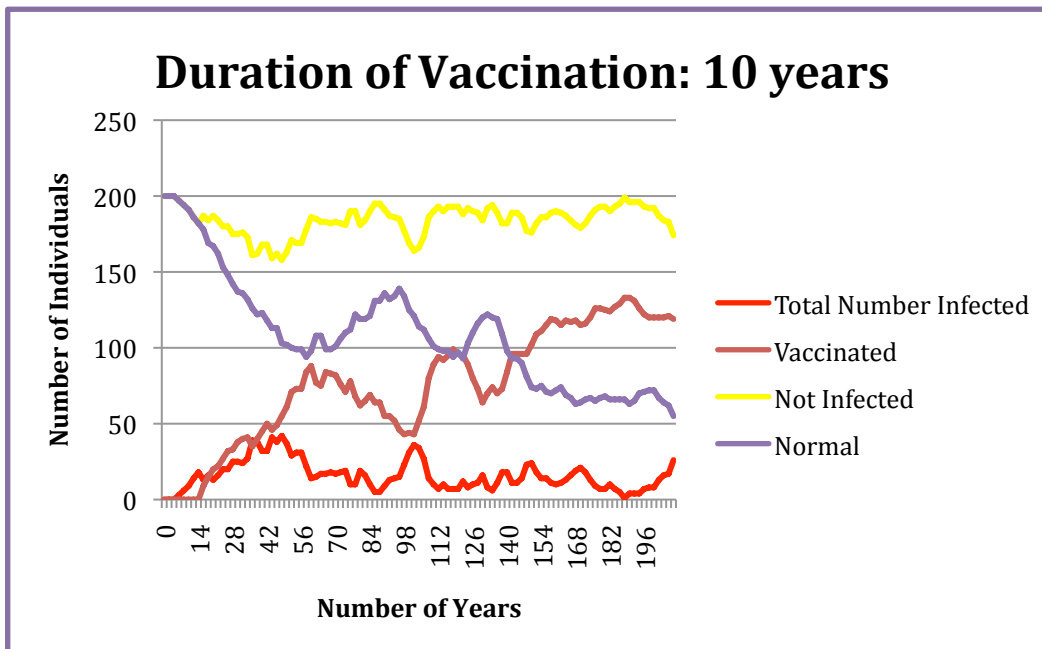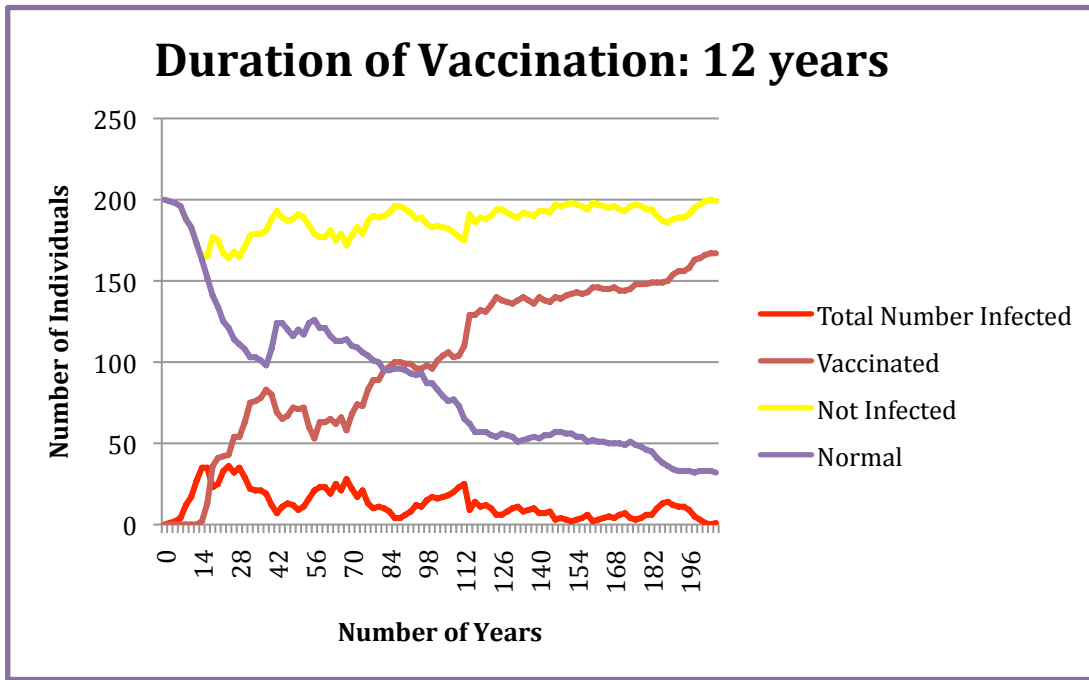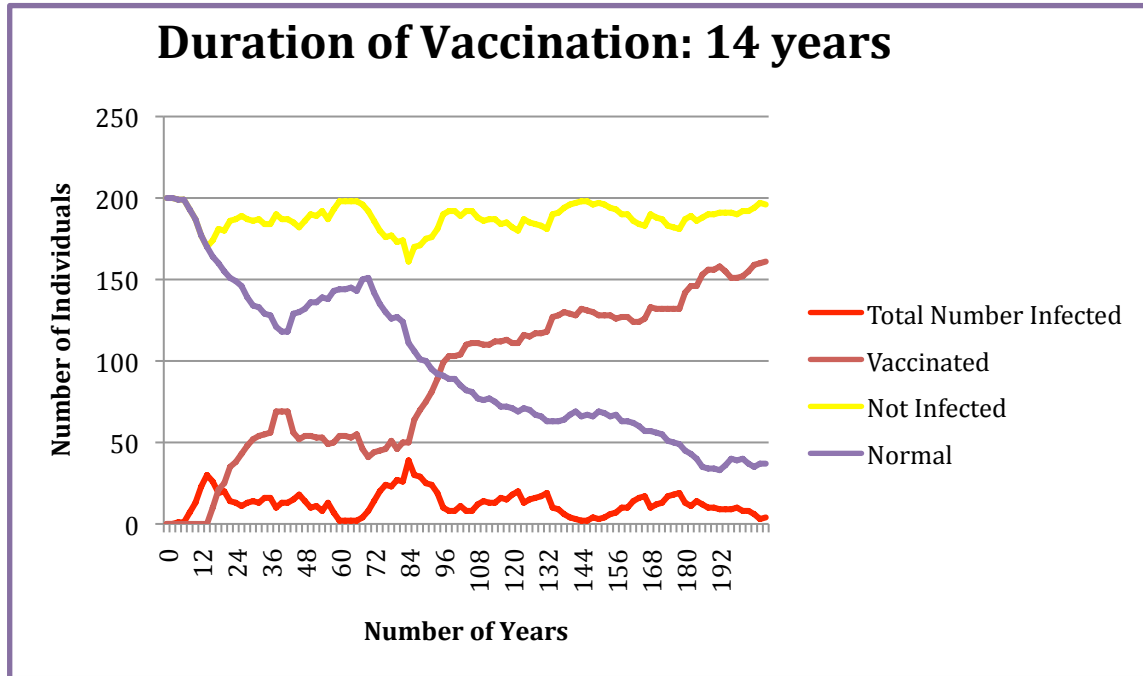|	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	36.00	12.8812	8.86937

Figure 25. Shows line graph where the vaccination lasted for 14 years.
Population: 200; Doctors: 5; Infectors: 5.

Descriptive Statistics

	N	Minimum	Maximum	Mean	Std. Deviation
Total Number Infected	101	.00	39.00	12.7426	7.43728

As the number of years an individual within the population was infected increased the standard deviation of the infected individuals did not ascend or descend. The standard deviation was sporadic. There is not a noticeable difference between the numbers of individuals infected throughout the different lengths of infection. There is a difference between the control (when vaccination was programmed to last for an infinite period of time) and when the vaccination was programmed to last a limited number of years. Looking at the line graphs in Figures 21-25 the number of infected individuals drops and rises repeated over the 200 years. Whereas, Figure 10 shows that when the vaccination was for a lifetime there

was an increase in the number of individuals infected and then a continuous

decrease in the number of individuals after 40 years.

Discussion and Future:

Although vaccination offers a very powerful method of disease control, there are many associated difficulties and challenges. In general, vaccines are not a hundred percent effective, and therefore, at times only a proportion of vaccinated individuals were protected. Comparing figures 10 and 11, it is evident that when the infectors are located in a specific area, it is harder to eradicate the infection. It is almost as if the infection comes in waves. This proves the hypothesis correct. When infectors are in a specific area, once the normal individual gets infected, they spread the infection by colliding on their way to the doctors. This cycle is repetitive. There is also a decrease in the number of individuals getting vaccinated over time when the infection is in one specific location.

A prediction was made that, if the number of doctors remained the same, the more the population grew, and the longer it would take to eradicate an infection. At least, the percentage of infected individuals would be less in the population with fewer people, because the ratio of individuals to doctors would be higher. The prediction is not necessarily true. In these experiments, it was shown that the ratio does not, in fact, have much effect. As long as individuals make a point to go to the doctors (represented by them colliding with one another), they will be vaccinated.

As predicted, there is a steady trend showing that as the number of doctors increases, there is a concomitant decrease in the number of infected individuals, and an increase in the number of individuals getting vaccinated. A model programmed with 1 doctor as compared to a model programmed with 2 or 4 doctors does not show much of a difference. But, when compared with a model programmed to have sixteen doctors, there is a noticeable impact. According to the last hypothesis the longer the vaccinations lasts,

the faster individuals are cured and vaccinated. Though, this is not always the case, as can be seen in figures 21, 22, 23,14, and 25. The difference between each vaccination time frame is only 2 years. A larger gap between years of vaccination might have given different results. For example, in comparing data from figures 21-25 to figure 10, which is the control with an undefined vaccination time, there is a noticeable difference in both the number of infected individuals and the number of individuals being vaccinated.

These simulations provide a basic understanding of how the *StarLogo* program can be beneficial. One of the accomplished goals was the observation of how infection spreads throughout a population. Another observation was the way in which vaccination plays a role in different situations and different types of populations. Influential factors such as the root of the infection, population size, the number of providers to cure and vaccinate, and the amount of time the vaccination lasted were all taken under consideration and observed during this experiment. There are numerous additional aspects that can be analyzed and altered to further explore different situations of cause and effect as relates to the spread of infectious diseases. A few examples of these types of alterations and additions might be programming death and reproduction.

Important to note is the fact that there are times in which reactive vaccination may prove to be too slow to prevent a large outbreak, and therefore, in many situations, would require alternative control measures. These alternative control measures are impossible to do on a model-based program like *StarLogo- TNG*.

In contextualizing the results of the study there are larger implications not only of the results of this one specific study, but also of programs such as StarLogo. Infectious diseases are not only a threat to one person, but to entire groups of people, animals, and

species. In cases where there are massive outbreaks of infectious disease, programs and models can prove to be a helpful tool. Models have recently been an essential part of research on infectious diseases such as, Staphlococcus aureus and AIDS which is a global disease (Why We Model, 2009). Communities not only nationwide, but all over the world can use models to prevent a future disaster in the realm of health care.

Acknowledgments:

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