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AN AGENT-BASED MODEL TO STUDY THE
SPREAD AND CONTROL OF EPIDEMICS

A Thesis submitted in partial fulfillment of the requirements for the degree of Master of
Science in Mathematics at Virginia Commonwealth University.

by

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Abstract

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By Ashley Dawn Fuller, M.S.

A Thesis submitted in partial fulfillment of the requirements for the degree of Master of Science in Mathematics at Virginia Commonwealth University.

Virginia Commonwealth University, 2008

Thesis Advisor: Dr. David M. Chan
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The world continues to face outbreaks of disease due to natural causes as well as the threat of biological warfare. Mathematical modeling provides an avenue by which to predict and ultimately prevent widespread outbreaks. A wide variety of modeling tools have been used in the study of the spread of diseases, including Ordinary Differential Equations, Partial Differential Equations, and Difference Equations. In this study, an agent-based model is used to study the spread and control of epidemics and is based on

Sirakoulis, et al. [1]. The computer program NetLogo [2] is used for simulation. The development and set-up procedures for this model are fully discussed.

The model is used to study the effectiveness of vaccination and quarantine as methods of epidemic control. It is determined that the most effective means of controlling an epidemic is to quarantine individuals with symptoms. In addition, the effect of the adjacent contact coefficient in the model is examined and further development and uses of the model are discussed.

Chapter 1--Introduction

1.1 Background Information

Disease and its spread have been a concern throughout history. From the most famous epidemic, the Black Death, that led to the death of one-third of the population of Europe, to the most recent epidemics in society today, AIDS and SARS, history is full of accounts of the horrifying effects of disease. Preventing the spread of disease is becoming increasingly important as the world grows continually ‘smaller’ with ease of travel. Advances in mathematical modeling provide ways to predict, prevent, and determine the trends of long feared epidemics [3].

Modeling of diseases can be traced back as far as the 1600’s when John Graunt first did an empirical study on the types of diseases that were killing individuals in various parishes throughout Britain. Later, more deterministic approaches were developed as individuals tried to make predictions regarding when, where, and how long a disease would progress in a community. David Bernoulli developed a more data and equation based approach in the 1700’s when he looked at the smallpox epidemic that occurred in Europe [4]. As mathematical modeling progressed, models became more sophisticated and accurate. Mathematicians now model everything from the spread of HIV, influenza, and the common cold, to the possible spread of biological weapons and how they affect society [3].

While the ability to predict the spread of disease is important, perhaps the most important aspect of this type of research is being able to prevent epidemics from occurring in the first place once a disease is introduced into society. What steps are sufficient to contain an epidemic? How helpful is it to quarantine exposed individuals to prevent the spread of disease? How much vaccination is necessary in order to save a community? These questions and many more come into play when recognizing the importance of modeling epidemics. It is not enough to wait until the problem arises to try and solve it; rather it is much more valuable to try and predict what will happen so society can be prepared.

There are several different types of models being used in this field today including Ordinary Differential Equations (ODE's), Partial Differential Equations (PDE's), Difference Equations, and Agent-Based Models (ABM's). This paper focuses on the properties and development of agent-based modeling, which will be discussed in Chapter 2. First, is a brief overview of the other types of models.

1.2 ODE Models

ODE models use differential equations to model the instantaneous rate of change of some variable. They have both positive and negative attributes. First, ODE's allow for the determination of various types of solutions including explicit and approximate when studying an epidemic system. However, a drawback is that ODE models fail to offer an adequate description of the variations in behavior of individuals or the effects of space and

location on an epidemic. They are also inadequate in terms of the mixing patterns of a population [5].

One of the most famous ODE models is the Kermack-McKendrick SIR model shown below.

$$\begin{aligned}\frac{dS}{dt} &= -rSI \\ \frac{dI}{dt} &= rSI - aI \\ \frac{dR}{dt} &= aI\end{aligned}$$

In this model, S represents the number of susceptible individuals, I is the number of infected individuals, R is the number of recovered individuals, r is the infection rate, and a is the recovery rate, which can be attributed to either death or immunity. In this particular model, it is assumed that once you recover from the disease, whether by death or other means, you obtain permanent immunity [3]. Derivations of this basic ODE model have been used to model viral infections [6], and hepatitis B [7].

More recently, Chowell, et al. [8], used the SEIR form of the model, shown below, to model the spread of influenza in the United States, France, and Australia. Compared to the SIR model, an SEIR model includes a state for individuals who have been exposed to the disease, but have not yet started to exhibit symptoms.

$$\begin{aligned}\frac{dS}{dt} &= \frac{-\beta SI}{N} \\ \frac{dE}{dT} &= \frac{\beta SI}{N} - \kappa E \\ \frac{dI}{dt} &= \kappa E - (\gamma + \delta)I \\ \frac{dP}{dt} &= \gamma I \\ \frac{dD}{dt} &= \delta I\end{aligned}$$

In this model the additional variables E , P , and D represent the number of exposed, immune or protected individuals, and dead individuals, respectively. Additionally, β represents the transmission rate of the disease, N represents the total population, κ is the rate at which individuals go from exposed to infected, and γ and δ represent the recovery rate and mortality rate, respectively. Chowell, et al. [8] use this model to estimate the reproductive number of influenza and also to study the effectiveness of current vaccination procedures in these countries. From their data, they were able to conclude that in order to reduce the spread of influenza a much higher vaccination rate of healthy individuals would be necessary as well as a plan for re-vaccination as new strains of the virus develop.

1.3 PDE Models

While ODE models serve to describe systems where the total number of people in each group is concerned, a different type of system is necessary to include additional factors in the model such as age or space. PDE models serve this purpose. While these models are not used as extensively as ODE's they do have their place in epidemic modeling.

One example of a PDE model for epidemic spread is Murray's model [9] of fox rabies shown below.

$$\begin{aligned}\frac{\partial S}{\partial t} &= -rIS \\ \frac{\partial I}{\partial t} &= rIS - aI + D \frac{\partial^2 I}{\partial x^2}\end{aligned}$$

In this very simplistic model, foxes are categorized into two groups, namely infected I and susceptible S . Murray looks at the spread of the epidemic where the foxes are allowed to move in one space dimension. In this model r represents the transmission coefficient, a the mortality rate of the foxes, and D the rate at which the foxes diffuse.

Another example of the use of PDE's in epidemic modeling is Feng's, et al. [10] system of PDE's to model a disease in varying age groups using an SIS model shown below.

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) s_i(t, a) = -\mu_i(a)s_i(t, a) - \Lambda_i(a, u(t, \cdot))s_i(t, a) + \gamma_i(a)u_i(t, a)$$

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) u_i(t, a) = -\mu_i(a)s_i(t, a) + \Lambda_i(a, u(t, \cdot))s_i(t, a) - \gamma_i(a)u_i(t, a)$$

$$\text{where } \Lambda_i(a, u(t, \cdot)) := K_i(a)u_i(a_i, t) + \sum_{j=1}^n \int_0^{\omega} K_{ij}(a, s)u_j(s, t)ds$$

In this model, for each group i , $s_i(t, a)$ represents the age specific density of susceptible individuals at time t and $u_i(t, a)$ represents the age specific density of infected individuals at time t . $\mu_i(a)$ represents the death rate and γ_i represents the recovery rate. Finally, K_i and K_{ij} represent the transmission rate of a disease within group i and between groups i and j ,

respectively. From their development and study of this model, Feng, et al. were able to draw conclusions regarding the conditions necessary for global stability of both disease-free and endemic equilibriums.

1.4 Discrete (Difference Equation) Models

Both PDE and ODE models describe a system in which the variables are considered to change on a continuous basis. Another approach to modeling an epidemic comes in the use of discrete or difference equations. This type of modeling determines the variable quantities at distinct time intervals [11]. The advantage of using discrete models is that they often provide a better representation of the data being studied, since data is normally collected in discrete time intervals as opposed to continuously [12].

Previously, an example of a continuous SIR model was described, but the same concept can be applied to a discrete system. A basic SIR model in the discrete form is shown below.

$$\begin{aligned} S_{t+1} &= S_t - \frac{B}{N} I_t S_t + b(I_t + R_t) \\ I_{t+1} &= I_t(1 - r - b) + \frac{B}{N} I_t S_t \\ R_{t+1} &= R_t(1 - b) + rI_t \end{aligned}$$

In this system of equations, S_t , I_t , and R_t represent the number of susceptible, infected, and recovered individuals, respectively, at time t . B represents the number of contacts that result in an infection, b is the birth and death rate, and r the recovery rate from the disease. It is assumed that individuals are born susceptible to the particular disease and that the

birth and death rate are equivalent. This system of equations, or similar derivations of it, can be used to model various diseases including measles [13], and other childhood diseases such as mumps, and chickenpox [11].

Ramani, et al. [12] used discrete time models, specifically an SIRS model, to look at the oscillating behavior of epidemics over time. They looked at two cases, one with a constant population where no death occurs, and another where the population had the ability to gain permanent immunity either by recovery or death. When the population remained constant, the epidemic approached a fixed point, where at least part of the population remained infected. However, when individuals were allowed to leave the population by means of death or permanent immunity, this oscillating effect was at first present, but eventually the epidemic died out completely.

The models discussed above all fall into the category of classical models. Each type has several advantages and disadvantages depending on the purpose of the model. This study now looks to examine and develop a more recent approach to modeling, agent-based modeling.

Chapter 2--Agent-Based Modeling

Agent-based, or individual based modeling, is a relatively new area of study as compared to the classical models. While ABM's were present prior to computers, their popularity increased with the advent of computers which helps with the speed and complexity of simulation work. Two particular models, while not the first ABM's developed, are historically recognized for their contribution to this field of study. They are Botkin's JABOWA forest model in the early 1970's and DeAngelis, Cox, and Coutant's model on fish cohort growth in 1980 [14].

In order to develop an ABM, it is important to clearly define the purpose or goals of the model. What information is to be gained by using the model? What data is going to be collected? Once this is established, the overall structure of the model is then defined. This is where an ABM starts to separate itself from classical models. In an ABM there are two basic components, the environment and the agents.

The environment is composed of a grid of cells, or patches, where individuals reside. These patches are where the agents interact with the environment and other agents. For example, patches may have resources that agents consume. The patches themselves have certain characteristics or attributes that are defined within the model [14].

Similarly, the agents may have many of their own attributes. Each agent is given certain characteristics such as location on the grid, an age, the ability to move, and any other characteristics deemed necessary by the purpose of the model. There can be many

different agents within a model, each with its own set of characteristics; however, the more agents there are and the greater their differences, the more complex the model becomes. Once defined, these agents proceed through a series of rules that allow them to interact with other agents in the model and the environment [14].

The range of interactions between agents and/or patches is dependent upon the type of model. For example, in a social science model focused on segregation, differences between agents can cause them to relocate; in predator-prey models, one type of agent may feed off another; in competition models, different types of agents may compete for the same resources located in a patch; in disease models, individuals may come into contact with each other resulting in infection. Based on these interactions, the characteristics of each agent are transformed during the simulations [15].

In order to study these models, a computer program of some type is necessary. Without effective technology, these models quickly become cumbersome and lose their usefulness. Gilbert [15] recommends several pre-formatted programs for ABM's and ranks them according to ease of use and several other criteria. The four programs he evaluates are *Swarm* [16], *Repast* [17], *Mason* [18], and *NetLogo*[2]. While all four programs have advantages, the model in this paper is developed using NetLogo for its ease of use, adequate speed, and simple programming language.

The use of ABM's has grown in recent years, and their value is quickly becoming evident in many areas. In epidemic modeling ABM's are currently being used to develop prevention plans to keep both naturally occurring epidemics such as avian-flu [19] from spreading as well as to provide response plans for biological warfare [20].

Two key examples of the use of real data in ABM come from the desire to have a preparedness plan for pandemic influenza or bioterrorism. Germann, et al. [19] use an ABM and U.S. Census data on population distributions as well as Department of Transportation data to develop a model to study ways to control the spread of influenza in the United States. From their model they are able to make predictions regarding the spread of influenza and how to appropriately vaccinate the population based on how often individuals are in contact with one another and the stockpile of vaccinations that is available. Their model also provides recommendations regarding how to best slow the epidemic spread if vaccination availability drops below a certain amount.

A second example of the use of ABM's looks at the diffusion of a disease through Tokyo. Ohkusa and Sugawara [20] used real "Person Trip" data for the city of Tokyo to simulate how an epidemic would spread in this city. Using the agent-based approach and real data, they were able to simulate contact at home with the family, during transportation, and through social contact to determine how the epidemic will spread.

ABM provides a method of modeling by which to simulate complex situations and account for the differences among individuals. With increasing improvements in technology and computer programming, they continue to grow in popularity as a way to study complex interactions.

Chapter 3--Description of the Model

3.1 *The Model:*

The goals of this study are to look at the spread of an epidemic and ways to control it. An ABM is developed to study the ability to control an epidemic using vaccination and quarantine. The effect of the contact coefficient is also examined.

The basis for this research is a model developed by Sirakoulis, Karafyllidis, and Thanailakis [1]. Their article, describes a model which studies the spread of an epidemic based on neighborhood interactions. After developing the model, the authors look briefly at the effects of population movement and vaccination on total spread of an epidemic.

The model uses a two-dimensional grid with individual agents, or turtles, dispersed homogeneously throughout. The model makes several important assumptions. Each turtle falls into one of three states: sick, susceptible, or immune. Based on the state into which they fall, turtles are able to interact with other turtles in neighboring cells to spread the disease.

Each cell is described by the characteristics of its population. Each turtle starts the model susceptible to the disease with the exception of a certain percentage of turtles that start off sick in the center cell. As the turtles interact with one another, their state, and their cells' state, will change over time. On a given day, if any turtle in a patch is infected, the patch is considered infected. Only if the entire population of the cell is immune, the patch is considered immune. If the entire population is neither sick nor immune, the patch is considered susceptible.

The infection being modeled, while not specified for this study, is assumed to have several characteristics as well. There are both an infectious time as well as an immune time for the disease. The infectious time determines how long an individual remains infected after first acquiring the disease and the immune time determines how long the individual remains immune after recovering from the disease. Once the immune time passes, the individual is again susceptible to the disease. It is assumed that the disease is not lethal; however, the model could be easily modified to account for the death of turtles and the effect this has on epidemic spread. Figure 3.1.1 gives a basic schematic of how the characteristics of the patches and turtles are determined throughout the simulation. A full description of these characteristics and their definitions is provided in Appendix 1.

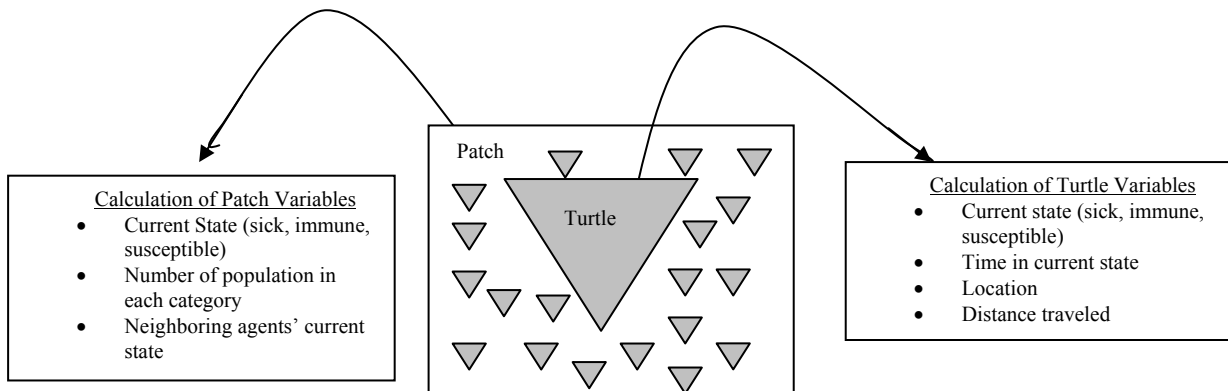


Figure 3.1.1: Schematic of attributes of turtles and patches.

At the beginning of each simulation, the disease is introduced to some percentage of the population in the center patch. The disease is then allowed to progress to the turtles of neighboring patches. The percentage of each patch at (i, j) infected at time $t + 1$, denoted $P_{i,j}^{t+1}$, is dependent upon the percentage sick of each of its neighboring patches at

time t . Patches that are adjacent to a patch have a greater effect than those located diagonally from the patch. This can be seen in Figure 3.1.2 where it is assumed that the adjacent contact coefficient, s , is greater than the diagonal contact coefficient w .

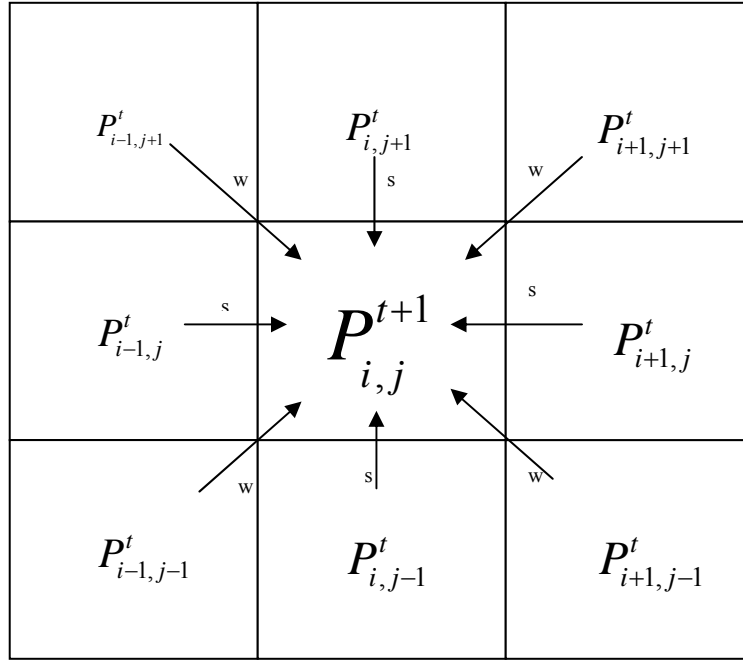


Figure 3.1.2: Effect of neighboring patches on sick percentage.

This process of disease propagation is described mathematically as,

$$P_{i,j}^{t+1} = \text{current sick percentage} + s(\text{adjacent neighbors}) + w(\text{diagonal neighbors}) \quad (1)$$

$$P_{i,j}^{t+1} = P_{i,j}^t + s(P_{i-1,j}^t + P_{i,j-1}^t + P_{i,j+1}^t + P_{i+1,j}^t) + w(P_{i-1,j-1}^t + P_{i-1,j+1}^t + P_{i+1,j-1}^t + P_{i+1,j+1}^t)$$

Within this equation it should be noted that the percentage of infected turtles is affected only by the adjacent and diagonal neighbors. The term $s(P_{i-1,j}^t + P_{i,j-1}^t + P_{i,j+1}^t + P_{i+1,j}^t)$, shows the affect of turtles in adjacent patches on the percentage sick in a patch, and the term $w(P_{i-1,j-1}^t + P_{i-1,j+1}^t + P_{i+1,j-1}^t + P_{i+1,j+1}^t)$, shows the affect turtles located in diagonal patches have on the percentage sick in a given patch.

3.2 Simulation Model Set-up and Procedures:

To obtain the results discussed in Chapter 4, simulations were run using the program NetLogo [2]. The initial patch population is considered to be homogeneous, where each patch contains twenty turtles. Initially, all turtles are considered to be susceptible with the exception of 60% of the center patch being infected. The only exception to this occurs when testing the effect of vaccination, where different percentages of the population are vaccinated, and thus permanently immune.

As the simulation progresses, turtles undergo certain procedures to mimic the spread of an epidemic. The model runs through each procedure once each time step, which can be considered as any discrete unit the user chooses relating to the disease. For this study each time step is considered to be one day.

Turtles age with each day, and based on the infectious time and susceptible time these turtles are also able to contract, spread, or recover from the disease. After thirty days, a certain percentage of turtles in each patch are allowed to move within a certain radius of their starting location. The size of the grid is chosen such that boundary conditions do not affect the area of infection. This progression of these steps can be seen in Figure 3.2.1 with a complete explanation in Appendix 1.

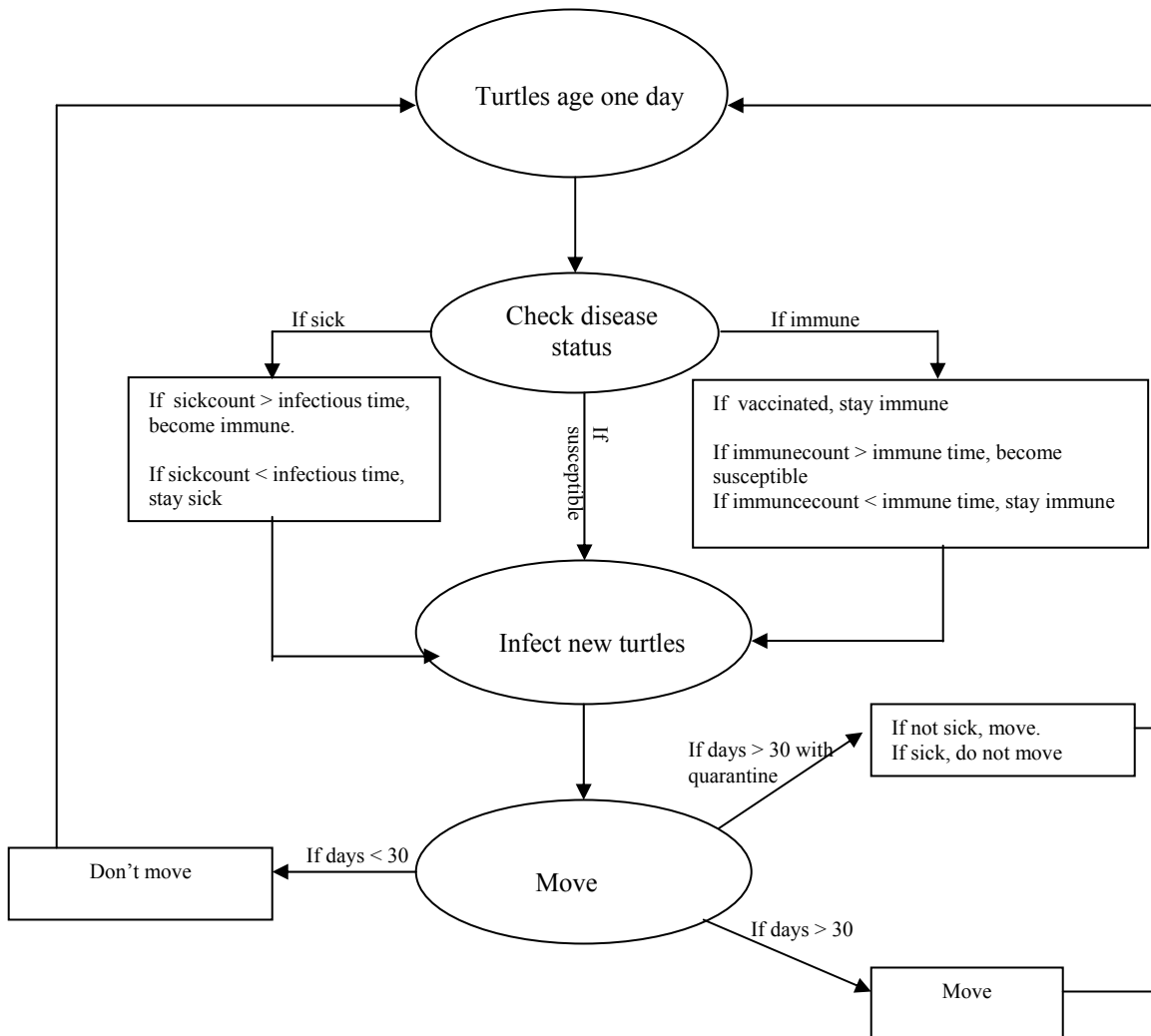


Figure 3.2.1: Flow chart of model procedures as run by NetLogo.

Chapter 4--Results

Using this model, several areas were studied regarding the spread of an epidemic. Initially, the results of Sirakoulis, et al. [1] were recreated in regard to the spread of the epidemic without movement, the effect of population movement, and the effect of vaccinating a small region of the population. Once these results were verified, additional simulations were run to test the effect of vaccination of varying percentages of the population, quarantine, and the effect of the adjacent contact coefficient.

The infection time was chosen to be five days, and the immune time was chosen to be ten days when no population movement was present. When movement was permitted, the infection time was increased to fifteen days and the immune time to thirty days. When movement did occur, it began after thirty days. The parameter values s and w for (1) were chosen to be 0.44 and 0.04, respectively, and were maintained for all stimulations testing vaccination and quarantine. Each simulation was allowed to run for forty-one days. The array size was chosen to be 22801 patches, a grid of (151 x 151) cells in order to avoid boundary effects, and the population of each patch was set at twenty turtles. The center cell was infected at a 60% infection rate at the beginning of each simulation. These values were chosen to provide an adequate sample size while also allowing for a reasonable simulation time.

4.1 Epidemic Spread with no Population Movement:

In order to obtain a basis for comparison of epidemic spread, the percentage of patches infected at some point during the simulation when no movement was allowed was obtained. Figure 4.2.1a, generated by Netlogo, clearly shows the spread of the epidemic and the three regions A: susceptible, B: immune, C: infected can be easily distinguished. Under these conditions 11.76% of the patches became infected at some point during the simulation. This was the number used for comparison in all subsequent simulations.

4.2 The effect of population movement with no preventative measures

While epidemics in the distant past were perhaps easier to contain due to the lack of travel outside of one's own community, this is certainly not the case today. In just forty-five years travel within the United States has increased dramatically. According to the U.S. Department of Transportation Bureau of Transportation Statistics, in 1960 there were 33,399 million passenger miles traveled by car in the US. Air travel in 1960 resulted in 1,272,078 million passenger miles. In comparison, in 2005 there were 583,689 million passenger miles traveled by car and 4,884,557 million passenger miles traveled by air [21]. Given these trends, it is important to determine how great of an impact movement will have on the spread of an epidemic.

In order to test the model in terms of population movement, a series of simulations were run varying the maximum distance traveled by each turtle as well as the percentage of turtles per patch that were allowed to move after thirty days. Maximum distances moved were varied between five and fifteen patches from the turtles' starting location. A random

number generator chose the actual distance each turtle moved. The percentage of each patch that was allowed to move varied between ten and forty percent, in increments of ten. All of these values were chosen to be the same as those of Sirakoulis, et al. [1].

As the percentage of the population allowed to move increased, as well as the maximum distance traveled, the spread of the epidemic increased. Figure 4.2.1a-d shows a sample of this increased spread with 4.2.1a representing no movement, and 4.2.1b-d representing 40% of the population moving a maximum of five, ten, or fifteen patches, respectively. The diameters of the epidemic spread in each of these diagrams were approximated to be 60, 80, 112, and 142 patches, respectively. This shows how an increase in distance traveled leads directly to an increase in epidemic spread. The amount of increase in spread will be discussed in detail in future sections.

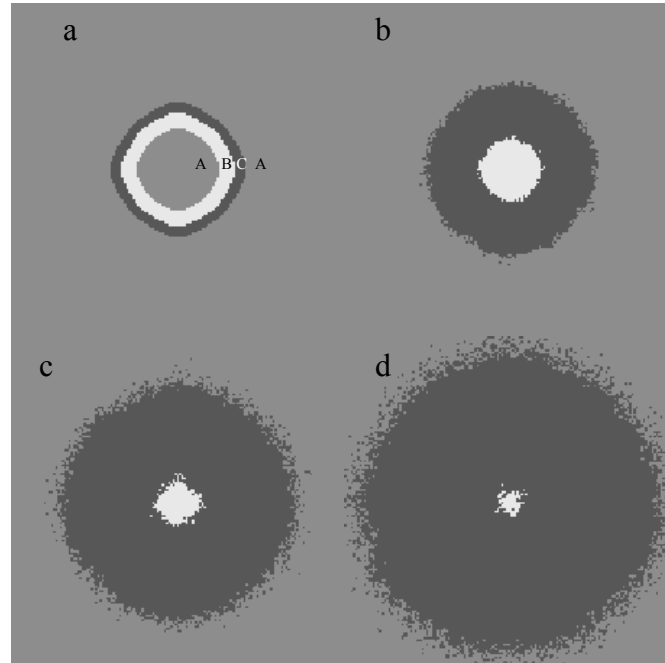


Figure 4.2.1: Effect of movement on epidemic spread. The representations above are for a) no movement, b) 40% moving 5 patches, c) 40% moving 10 patches, and d) 40% moving 15 patches. Simulations ran for 41 days. Regions are represented as A-susceptible, B-immune, and C-infected.

The effect of population movement can be seen by looking at Figures 4.2.2-4 which compare the amount of area covered by the epidemic versus the maximum distance traveled, and the percentage of population moving. In all of these simulations, no restrictions were placed on movement regardless of the state of the turtle. Plot 4.2.2 shows the effect the percentage of the population moving had on the spread of epidemic when the maximum distance traveled was five patches. Plot 4.2.3 shows the effect when the maximum distance traveled was ten patches, and plot 4.2.4 shows the effect when the maximum distance was fifteen patches. Notice that as the percentage of the population moving increases, the spread of the epidemic increases regardless of distance traveled. The greatest increase in epidemic spread as compared to no movement was when the maximum distance traveled was fifteen patches. The line showing the spread the epidemic when no movement was allowed is included for comparison. All data is presented as a percentage of total patches infected at some point during the simulation.

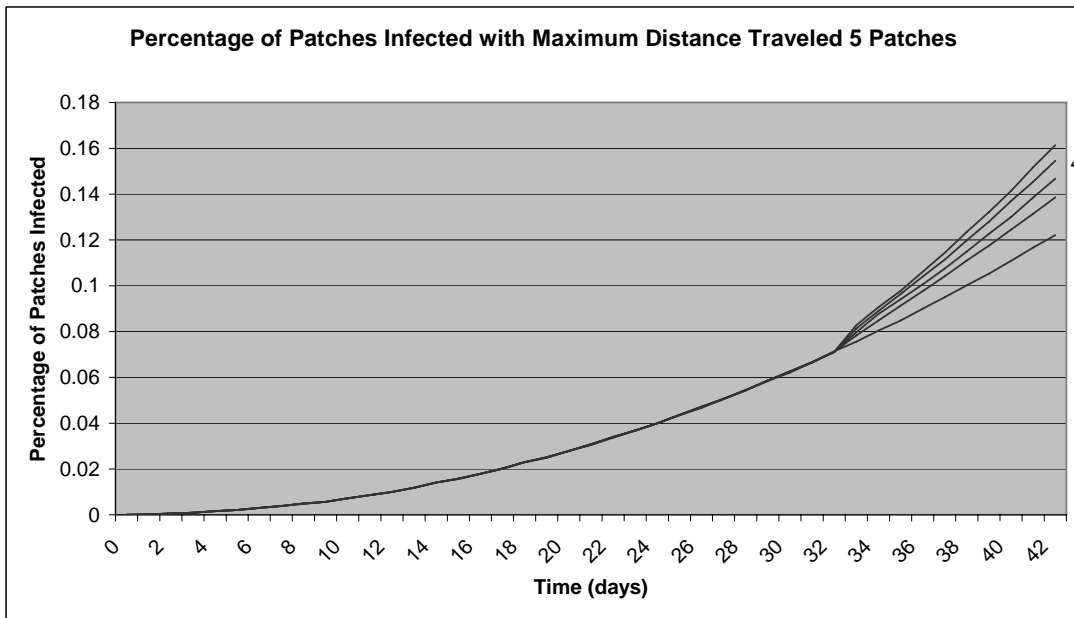


Figure 4.2.2: Effect of varying percentages of the population moving a maximum of 5 patches. Line 0 corresponds to no movement, and lines 1-4 correspond to 10%, 20%, 30%, and 40% of the population moving a maximum of 5 patches, respectively.

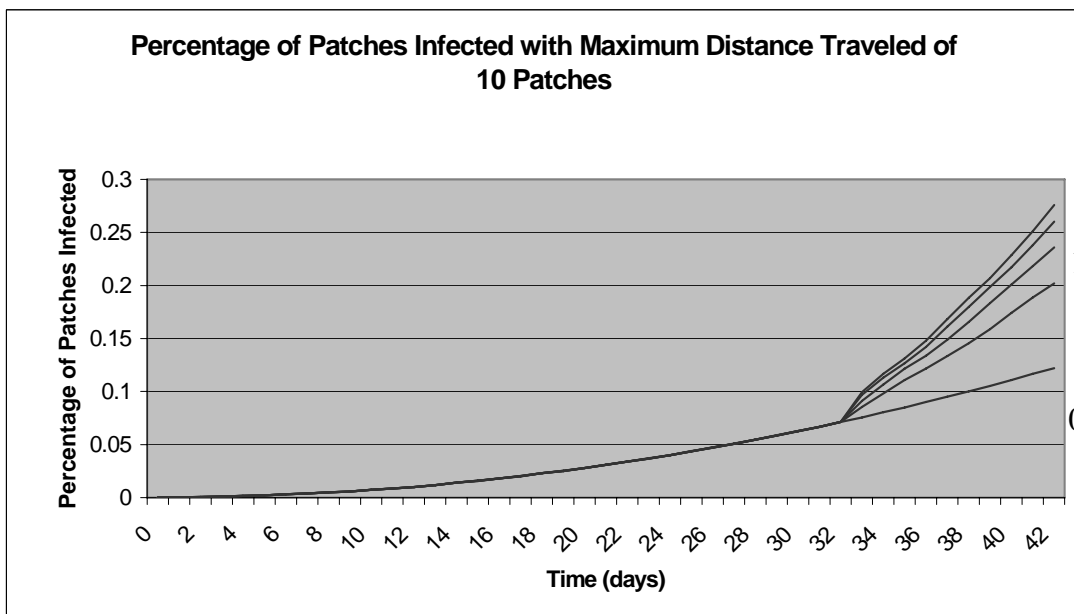


Figure 4.2.3: Effect of varying percentages of the population moving a maximum of 10 patches. Line 0 corresponds to no movement, and lines 1-4 correspond to 10%, 20%, 30%, and 40% of the population moving a maximum of 10 patches, respectively.

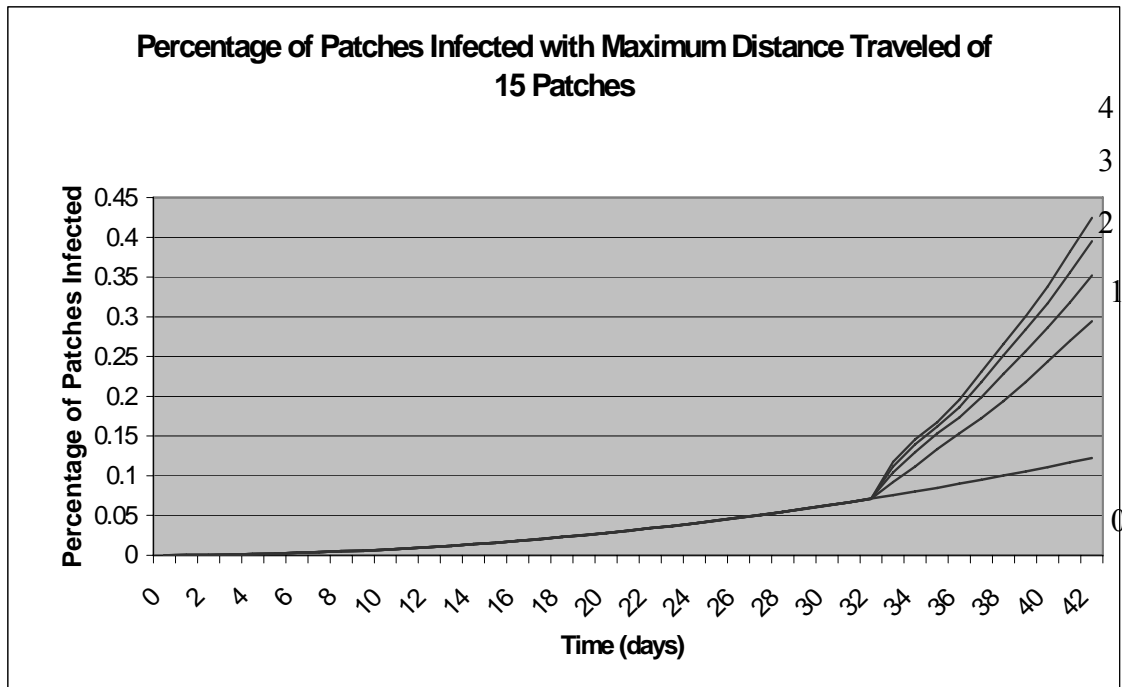


Figure 4.2.4: Effect of varying percentages of the population moving a maximum of 15 patches. Line 0 corresponds to no movement, and lines 1-4 correspond to 10%, 20%, 30%, and 40% of the population moving a maximum of 15 patches, respectively.

It can be seen from the data above that increasing the distance the population was allowed to travel increased the percentage of patches infected. When the maximum distance traveled was five patches, the percentage of patches infected as compared to no movement increased as much as 1.7 times, from 11.76% to 20.28% when forty percent of the population moved five patches. Increasing the maximum distance to ten patches caused the percentage of infected patches to increase 3.4 times, up to 39.57% of the patches, when forty percent of the population was moving. Finally, a maximum of fifteen patches resulted in 65.44% of the patches being infected when forty percent of the population moved, 5.5 times that of the percentage of patches infected when no one moved. The differences in percentages are summarized in Table 4.2.1.

While distance plays an important role in the spread of an epidemic, the percentage of the population moving also has an effect. When the distance was restricted to five patches and the percentage of the population moving was varied, the percentage of the population ranged between 15.56%, for ten percent of the population moving, 1.3 times that of the percentage of patches infected with no movement, up to 20.28% for forty percent of the population moving, 1.7 times that of no movement. Once the distance was increased to ten patches 2.5 as many patches were infected when ten percent of the population moved as compared to no movement, and 3.4 times as many when forty percent of the population moved ten patches. Finally, a distance of fifteen patches saw an increase in the percentage of patches infected to 3.4 times that of no movement when ten percent of the population moved up to 5.5 times as many when forty percent of the population moved.

It can be concluded that restricting distance or the percentage of the population allowed to move during an epidemic would be beneficial in terms of decreasing the spread. When the population was only allowed to move five patches the greatest percentage infected was 20.28% as opposed to a 40.39% when only ten percent of the population moving was allowed to move fifteen patches, indicating that distance traveled played a key role in epidemic spread. Likewise, when the population was allowed to move fifteen patches and the percentage increased, the percent of patches infected went from 40.49% to 65.44%. This trend was seen regardless of the distance traveled indicating that both distance traveled and percentage of the population moving increase the spread of the epidemic.

Maximum Distance Traveled	Percentage of population moving	Percentage of Patches Infected	Increase in Percentage of Infected Patches as Compared to No Movement
0	0	11.76	0
5	10	15.56	3.80
5	20	17.54	5.78
5	30	19.04	7.28
5	40	20.28	8.52
10	10	26.55	14.79
10	20	32.17	20.41
10	30	36.42	24.66
10	40	39.57	27.81
15	10	40.39	28.63
15	20	51.02	39.26
15	30	59.06	47.30
15	40	65.44	53.68

Table 4.2.1 Comparison of epidemic spread as movement and percentage of population moving increase.

4.3 The effect of vaccination of the population

Throughout the world, vaccination is one of the ways that countries choose to prevent epidemics. In the United States several epidemics have been eliminated through the use of vaccinations. According to the Center for Disease Control (CDC), in 1916 over 6,000 people in the United States died of polio and an additional 27,000 were left paralyzed. Over the course of time, a vaccination for polio was developed and since vaccination began in 1955 the cases of polio have dropped dramatically. In fact, in 1979 there were only ten reported cases of polio in the United States. Vaccination is an effective way to control an epidemic. The CDC's website has an entire section devoted to Emergency Preparedness and Response, that includes plans for vaccination procedures in the event of disease outbreaks and biological warfare [22].

It is important for the effectiveness of vaccination to be tested in order to develop a plan for implementation should a disease outbreak occur. The model was tested for the

effectiveness of vaccination using the same parameters discussed above. Specifically, the effect of vaccinating varying percentages of the population was tested. Appendix 2 gives reference to changes in the code regarding vaccination.

The higher the percentage of each patch that was vaccinated, the less the epidemic spread. When ten percent of the population was vaccinated, and no movement allowed, 10.50% of patches were infected as compared to 11.76% when there was no movement and no vaccination. When the percentage of the population vaccinated increased to twenty, thirty, and forty percent, the percentage of patches infected was reduced to 9.26%, 7.87%, and 6.43%, respectively. This indicates that with no movement and a vaccination percentage of up to forty percent, the spread of the epidemic can be cut by more than 1/3.

When movement was allowed, vaccination helped control the spread of the epidemic, but not as effectively as when there was no movement. With a maximum distance of five patches traveled and no vaccination, epidemic spread increased between 3.80-8.52% depending on the percentage of the population moving as compared to no movement. Vaccinating ten percent of the population when movement was restricted to five patches, showed an increase in epidemic spread between 2.07-6.20% as compared to no movement. However, increasing the vaccination rate to forty percent of the population with movement restricted to five patches, actually decreased epidemic spread between 3.52% and 0.85%, as compared to no movement and no vaccination. This shows that when the distance traveled was small, vaccination was an effective way to control the epidemic while still allowing for movement.

After the distance traveled was increased to ten or more patches, even a vaccination rate of forty percent was no longer sufficient to decrease the spread of the epidemic as compared to no movement, regardless of what percentage of the population was moving. However, vaccination was still successful in decreasing the percentage of patches infected as compared to when there was no vaccination. When ten percent of the population moved ten patches, a forty percent vaccination rate brought the percentage of patches infected within 2.20% of the percentage of patches infected with no movement and no vaccination. When no vaccination was present and ten percent of the population was moving ten patches, there was a difference of 14.79% as compared to no movement. As the vaccination rate increased to forty percent of the population, and forty percent of the population moved ten patches, vaccination was able to bring the percentage of patches infected within 8.02% of the percentage of patches with no movement and no vaccination, as compared to a 27.81% increase with no vaccination.

A distance of fifteen patches traveled made it more difficult for the vaccination to control the epidemic, but significant decreases were seen regardless. When forty percent of the population was permitted to move fifteen patches, a forty percent vaccination rate led to 24.06% more of the patches being infected as compared to 53.68% more when no vaccination was implemented.

This shows that vaccination can significantly reduce the spread of an epidemic even when movement is permitted. The vaccination data in its entirety is shown in Table 4.3.1.

Distance Traveled	Percentage Moving	Percentage Vaccinated	Percentage Infected	Increase from no Movement with no vaccination
0	0	0	11.76	0
0	0	10	10.50	-1.26
0	0	20	9.26	-2.50
0	0	30	7.87	-3.89
0	0	40	6.43	-5.33
5	10	0	15.56	3.80
5	10	10	13.83	2.07
5	10	20	13.49	1.73
5	10	30	10.14	-1.62
5	10	40	8.24	-3.52
5	20	0	17.54	5.78
5	20	10	14.94	3.18
5	20	20	13.79	2.03
5	20	30	11.58	-0.18
5	20	40	9.30	-2.46
5	30	0	19.04	7.28
5	30	10	16.79	5.03
5	30	20	14.84	3.08
5	30	30	12.58	0.82
5	30	40	10.36	-1.40
5	40	0	20.28	8.52
5	40	10	17.96	6.20
5	40	20	15.85	4.09
5	40	30	13.28	1.52
5	40	40	10.91	-0.85
10	10	0	26.55	14.79
10	10	10	23.26	11.50
10	10	20	20.20	8.44
10	10	30	17.08	5.32
10	10	40	13.96	2.20
10	20	0	32.17	20.41
10	20	10	28.38	16.62
10	20	20	24.82	13.06
10	20	30	21.25	9.49
10	20	40	17.02	5.26
10	30	0	36.42	24.66
10	30	10	32.44	20.68
10	30	20	28.28	16.52
10	30	30	23.84	12.08
10	30	40	19.78	8.02
10	40	0	39.57	27.81
10	40	10	35.11	23.35
10	40	20	31.05	19.29
10	40	30	26.67	14.91
10	40	40	22.01	10.25
15	10	0	40.39	28.63
15	10	10	35.88	24.12
15	10	20	30.77	19.01
15	10	30	25.65	13.89
15	10	40	21.87	10.11
15	20	0	51.02	39.26
15	20	10	45.04	33.28
15	20	20	39.21	27.45
15	20	30	33.88	22.12
15	20	40	27.36	15.60
15	30	0	59.06	47.30
15	30	10	52.52	40.76
15	30	20	46.06	34.30
15	30	30	39.00	27.24
15	30	40	31.99	20.23
15	40	0	65.44	53.68
15	40	10	58.57	46.81
15	40	20	51.61	39.85
15	40	30	43.84	32.08
15	40	40	35.82	24.06

Table 4.3.1: Effectiveness of vaccination on controlling epidemic spread.

4.4 The Effect of Quarantine

Quarantine is another method of disease control that attempts to prevent or control the spread of a disease by limiting contact between individuals. The history of quarantine

dates back many centuries and is even referenced in biblical times as a way to control the spread of leprosy. In the United States, quarantine has been used as a way to prevent diseases from entering with immigrants and/or goods. Also public places such as churches, schools, and businesses were shut down in some areas to prevent the spread of the Spanish Flu Epidemic of 1918. While quarantine has been used in the past, it is still used today, even as recently as the SARS outbreak in 2005. Before implementing such drastic measures on a society, it is important to be able to justify their effectiveness [23].

The same parameters discussed above were used in testing the effect of quarantine on containing an epidemic. The rules of the quarantine specified that no infected individuals could move, and no individuals could move into a patch that was already infected. Appendix 2 gives reference to changes in the code regarding vaccination.

The effect of quarantine was much more dramatic than that of the vaccination. As previously stated, when no movement was allowed and no other means of containing the epidemic employed, the epidemic was contained to 11.76% of the patches. With quarantine alone, and up to forty percent of the population moving as far as fifteen patches, the epidemic never spread beyond 11.96% of the population.

This data further supports the idea that the movement of infected individuals plays an important role in the spread of disease. If these individuals can be restricted in their movement, it is possible to greatly decrease the spread of the epidemic. The results of this study are summarized in Table 4.4.1.

Distance Traveled	Percentage Moving	Percent Infected without Quarantine	Percent Infected with Quarantine	Increase from no movement
0	0	11.76	11.76	0
5	10	15.56	11.81	0.05
5	20	17.54	11.89	0.13
5	30	19.04	11.90	0.14
5	40	20.28	11.93	0.17
10	10	26.55	11.82	0.06
10	20	32.17	11.9	0.14
10	30	36.42	11.94	0.18
10	40	39.57	11.96	0.20
15	10	40.39	11.81	0.05
15	20	51.02	11.89	0.13
15	30	59.06	11.93	0.17
15	40	65.44	11.96	0.20

Table 4.4.1: Effectiveness of quarantine on controlling epidemic spread

4.5 The Effect of Adjacent Contact Coefficient

All simulations up to this point were run with an s value of 0.44 as in Sirakoulis, et al. [1]. However, individual diseases have different likelihoods of being contracted upon contact with other individuals. It is important to be able to make predictions about the spread of an epidemic based on the actual likelihood that it will be transmitted upon contact. To see the effect of different diseases, the contact coefficient is varied.

In order to test the effect that the contact coefficient had on the spread of the epidemic, the adjacent contact coefficient was varied from 0.1-1.0 in increments of 0.1. All other parameter values were kept the same. For each value of s , simulations were run for no movement, as well as maximum distances and percentages tested previously. The results of this data are shown in Tables 4.5.1-4.5.3. Data is categorized by maximum distance traveled in order for ease of presentation.

Adjacent Coefficient	Percentage of Population Moving 5 Patches				
	0	10	20	30	40
0.1	3.02	4.86	5.72	6.50	7.05
0.2	5.58	8.11	9.33	10.13	11.11
0.3	8.31	11.27	12.87	13.83	14.92
0.4	10.60	14.22	16.13	17.73	18.43
0.44	11.76	15.56	17.54	19.04	20.28
0.5	12.86	17.11	19.12	20.66	20.58
0.6	13.94	19.19	21.45	23.13	24.44
0.7	14.57	20.66	23.30	25.37	26.57
0.8	14.88	17.59	24.66	26.56	28.42
0.9	15.04	23.12	26.18	28.20	29.95
1	15.11	24.60	27.60	29.74	31.75

Table 4.5.1: Percentage of infected patches with varying contact coefficient and movement of 5 patches

Adjacent Coefficient	Percentage of Population Moving 10 Patches				
	0	10	20	30	40
0.1	3.02	9.33	12.19	14.5	16.19
0.2	5.58	14.57	18.48	21.05	23.22
0.3	8.31	19.77	24.12	27.38	30.08
0.4	10.6	23.97	29.36	33.45	36.53
0.44	11.76	26.55	32.17	36.42	39.57
0.5	12.86	28.76	34.92	39.09	42.89
0.6	13.94	32.27	39.07	43.87	47.57
0.7	14.57	35.23	42.14	47.95	51.61
0.8	14.88	37.78	45.98	50.99	55.98
0.9	15.04	40.21	48.28	55.23	59.34
1.0	15.11	43.20	52.30	58.51	63.40

Table 4.5.2: Percentage of infected patches with varying contact coefficient and movement of 10 patches

Adjacent Coefficient	Percentage of Population Moving 15 Patches				
	0	10	20	30	40
0.1	3.02	15.28	20.7	24.95	28.61
0.2	5.58	22.9	29.53	35.67	39.75
0.3	8.31	30.1	38.91	45.31	50.61
0.4	10.6	36.74	47.56	54.61	60.82
0.44	11.76	40.39	51.02	59.06	65.44
0.5	12.86	43.95	55.29	63.99	70.43
0.6	13.94	49.65	61.65	71.17	77.95
0.7	14.57	53.97	67.69	76.98	82.87
0.8	14.88	58.56	72.55	80.78	86.32
0.9	15.04	62.28	77.16	84.8	89.02
1	15.11	68.65	81.96	88.2	91.82

Table 4.5.3: Percentage of infected patches with varying contact coefficient and movement of 15 patches

When the movement was restricted to five patches, allowing forty percent of the population to move caused 2.3 times as many patches to be infected when $s = 0.1$, as compared to no movement. As the contact coefficient increased, there was actually a decrease in the effect of movement with a low point being reached when $s = 0.5$. At this point, when forty percent of the population was moving five patches, there were 1.6 times as many patches infected as compared to no movement. Once s increased beyond 0.5 up to 1.0, the effect of movement again increased until there were 2.1 times as many patches infected with forty percent of the population moving five patches. This same trend was seen for ten, twenty, and thirty percent of the population moving five patches. After the distance increased to ten or fifteen patches, the effect of movement was again highest when $s = 0.1$ and lowest when $s = 0.5$. These trends indicate that increasing the percentage of agents moving was more effective, the lower the contact coefficient. It is projected that this is due to the likelihood of getting sick when $s = 0.1$ is much lower, as compared to 1.0 where coming into contact with a sick individual guarantees contraction of the disease. When contracting the disease was guaranteed, movement did not play as pivotal a role.

The data regarding contact coefficients also supported prior conclusions that distance plays a key role in epidemic spread. At a contact coefficient of 0.1, forty percent of the population moving five patches only increased the epidemic 2.3 times as opposed to 5.3 times and 9.5 times when the distances traveled were ten and fifteen patches, respectively. This same trend continued as the contact coefficient increased up to 1.0, but was again not as dramatic as with the lower contact coefficient. With $s = 1.0$ and movement restricted to five, ten, or fifteen patches, the epidemic spread to 2.1, 3.9, and 6.1

times as many patches as compared to no movement. This supports prior conclusions that restricting distance traveled is an effective way to control epidemic spread.

In order to see these trends more clearly, Figures 4.5.1a-c show the effect of the adjacent coefficient and percentage movement on epidemic spread. Figure 4.5.1a shows the effect when the population moves five patches, 4.5.1b shows the population moving ten patches, and 4.5.1c shows the population moving fifteen patches. Notice the dramatic increase in the slopes of the graph as the percentage of the population moving increases along the x-axis, as opposed to the slower increase in slope as the contact coefficient increases. The scales of each graph have been adjusted to be equivalent in order to show this more effectively.

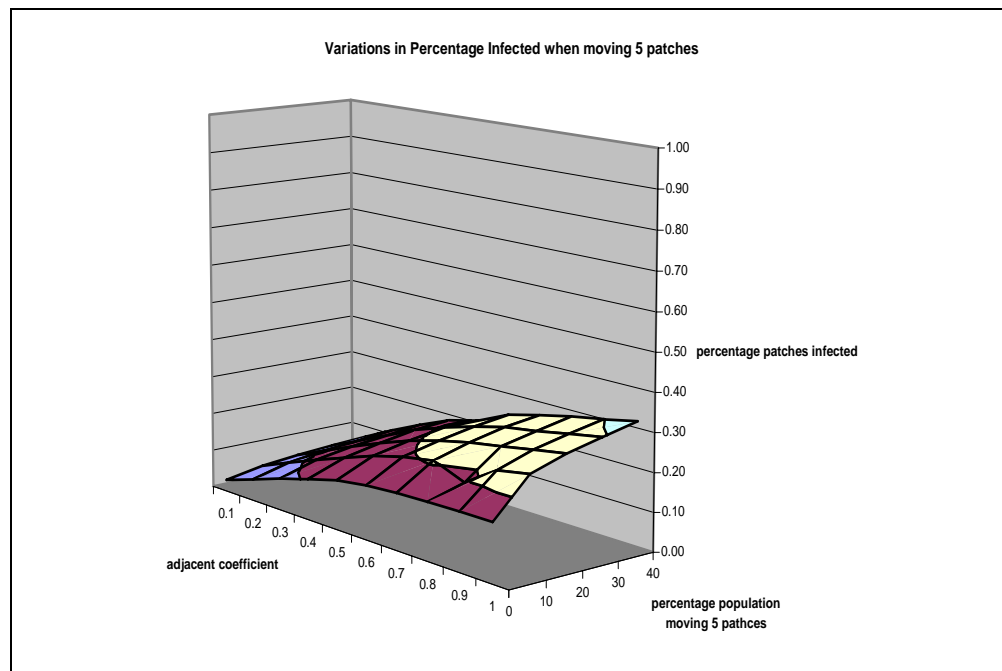


Figure 4.5.1a: Effect of adjacent coefficient on epidemic spread

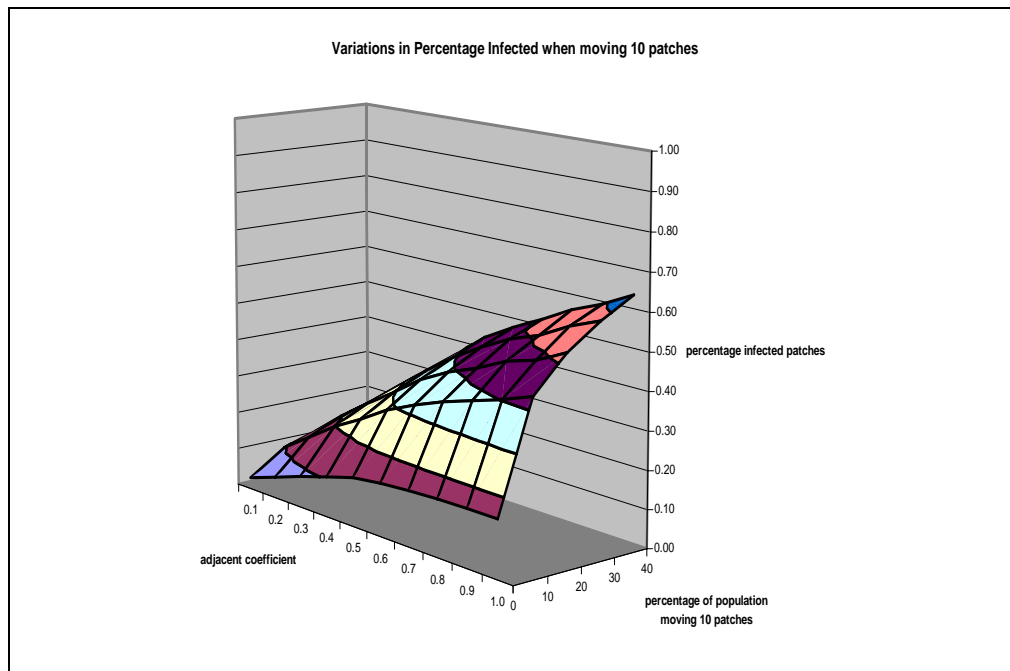


Figure 4.5.1b: Effect of adjacent coefficient on epidemic spread

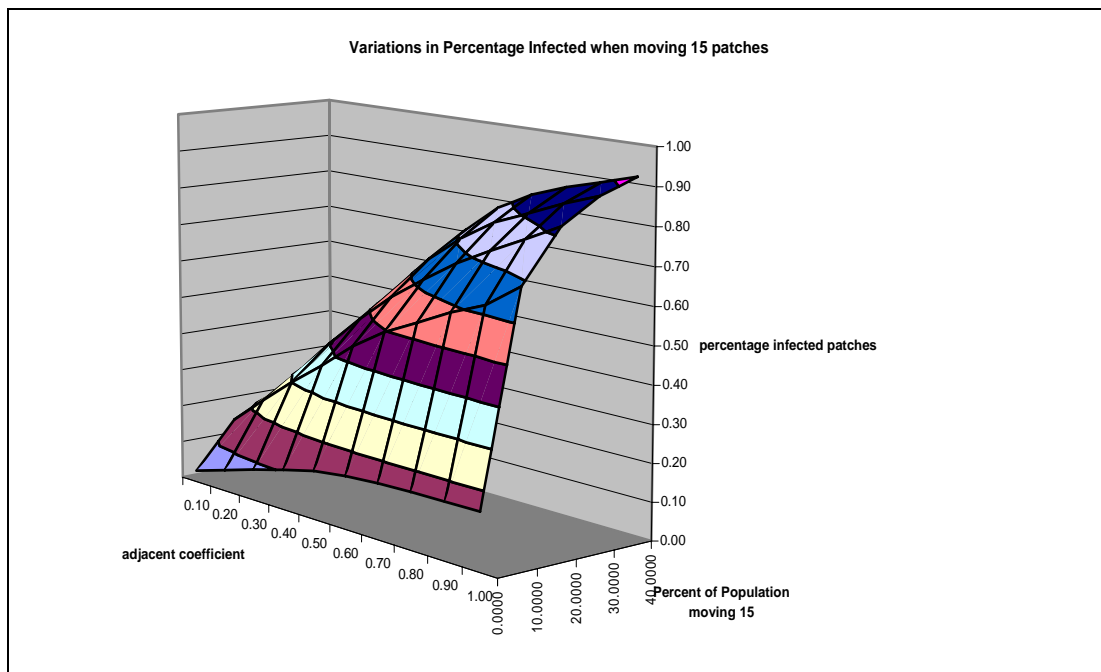


Figure 4.5.1c: Effect of adjacent coefficient on epidemic spread

Chapter 5--Conclusions and Extensions of the Model

In a world of increased travel and the growing threat of biological warfare, it is of vital importance that plans be made for the prevention and control of widespread epidemics. Understanding diseases, their likelihood of being spread, and methods to control these diseases, provide avenues by which to achieve this goal of epidemic disease prevention. One way to develop an effective plan is to create and study mathematical models which simulate various scenarios.

This study implemented an agent-based model to study a generic epidemic and the use of several options by which to control that epidemic. From the data gathered, it was evident that the spread of disease was accelerated greatly by the movement of individuals. When no one in the population was allowed to move, the epidemic spread to 11.76% of the patches at some point during the simulation. In contrast, as movement increased the epidemic spread to as many as 65.44% of the patches in the model.

One method explored for the control of the epidemic was that of vaccination. By vaccinating increasing percentages of the population it was possible to decrease the spread of the disease and still allow portions of the population to move. With a forty percent vaccination rate, it was possible for up to forty percent of the population to move up to five patches and still decrease the spread of the epidemic by 0.85%. Once movement was increased beyond five patches, vaccination did not decrease the spread of the epidemic as compared to no movement, but did still help in controlling the spread to less of the population.

By far the most effective method of disease control was quarantine. There was little increase in the spread of the epidemic when individuals who were infected were prevented from moving, regardless of how far healthy individuals were allowed to travel. When forty percent of the population was allowed to move as many as fifteen patches, still only 11.96% of the patches were infected, just 0.20% more when no one was allowed to move.

This model provided interesting results for the span of this study. There are many other areas that would be of further interest for the development of this model. One area of interest would be to examine how the spread of the epidemic changes when the disease is considered lethal to some percentage of those contracting the disease. Further extensions could also be explored by allowing turtles to infect any patch they travel through and not just those they occupy. Additionally, one could alter both the infectious and immune times to see what effect those have on the spread of the disease. NetLogo's ease of programming and the foundation built through this model offer many possibilities for further exploration.

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APPENDIX 1

The code used for the simulations discussed in this paper is included in Appendix 2. Below is a detailed explanation of the terms and variables used in that code, as well as a general overview as to how the program works. The model itself is composed of turtles residing in patches. Both turtles and patches have their own set of attributes as defined below.

Turtle Variables

Sick?	<i>Turtle is infected and will remain infected until sick-count reaches infection-time</i>
Immune?	<i>Turtle is immune and will remain immune until immune-count reaches immune-time</i>
Susceptible?	<i>Turtle is susceptible</i>
Vaccinated?	<i>Turtle is permanently immune to the infection</i>
Startingpatch	<i>Location of the turtle at the beginning of the simulation</i>
Distancetraveled	<i>Distance turtle is from starting patch</i>
Currentpatch	<i>Current location of turtle</i>
Previouspatch	<i>Previous location of turtle</i>
Sick-count	<i>Number of time steps the agent has been infected</i>
Immune-count	<i>Number of time steps the agent has been immune after recovering from the infection</i>
Susceptible-count	<i>Number of time steps the agent has been susceptible.</i>

Patch Variables

Sickpercentage	<i>Percentage of infected turtles in patch</i>
Immunepercentage	<i>Percentage of immune turtles in patch</i>
Susceptiblepercentage	<i>Percentage of susceptible turtles in patch</i>
Patchpopulation	<i>Number of turtle in patch</i>
Sickpopulation	<i>Number of sick turtles in patch</i>
Immunepopulation	<i>Number of immune turtles in patch</i>
Susceptiblepopulation	<i>Number of susceptible turtles in patch</i>

Vaccinatedpopulation	<i>Number of vaccinated turtles in patch</i>
Neighborpopulation-h	<i>Number of agents in neighboring patches</i>
Psickneighbors	<i>Factor used to calculate sick in patch based on Equation (1)</i>
New-sick	<i>Set to 1 if the sick has ever had any sick turtles, set to 0 if no sick turtles have ever occupied the patch.</i>

These attributes are defined as follows

$P_{i,j}^t$ -- Percentage of the population in cell (i, j) that is infected

$INF_{i,j}^t$ --Infection-flag. This flag is initiated if any member of the population in cell (i, j) is infected at time t

$IMF_{i,j}^t$ --Immune-flag. This flag is initiated if all members of the population in cell (i, j) are immune at time t

During the set-up procedure of the simulation, various characteristics are determined for each agent (turtle). Each agent can fall into one of three categories: “sick,” “immune,” or “susceptible.” When testing the effect of vaccinating various percentages of the population, the agents can also be characterized as “vaccinated,” which will leave them in the “immune” category permanently.

At the beginning of each simulation all agents are considered to be susceptible with the exception of the user determined percentage in the center cell that are sick and any additional agents that are designated as vaccinated. Once all the agents have been categorized appropriately, there are several other values that are calculated for each agent. These include the following:

Turtle Variables

Startingpatch	<i>Calculates and lists the x-coordinate and the y-coordinate for the location of each agent at the start of the simulation</i>
Distancetraveled	<i>Initially set at zero for each agent and then calculated in each time step of the simulation to determine how far the agent has traveled from its starting patch.</i>

Currentpatch	<i>Gives the current location of each agent. Initially set to be the starting patch and used in later calculations to determine the distance the agent has traveled.</i>
Previouspatch	<i>Lists the location the agent previously occupied in order to give the agent a location to return to if they have traveled too far.</i>
Sick-count	<i>Number of time steps the agent has been infected.</i>
Immune-count	<i>Number of time steps the agent has been immune after recovering from the infection. (Not applicable for agents that have been vaccinated)</i>
Susceptible-count	<i>Number of time steps the agent has been susceptible.</i>

The characteristics for each agent can be viewed in a list at any point during the duration of the simulation.

Patches classified according to the population of agents that occupy it. The patches can be categorized into three groups: infected, immune, or susceptible. If any agent in the patch is infected the patch is given an “infection-flag.” If all agents in the patch are immune the patch receives an “immune-flag,” and furthermore, if that immunity comes from vaccination and is thus permanent, the patch receives a “vaccinated-flag.” It should be noted that the immune and vaccinated flags only apply if 100% of the population falls into these categories. Otherwise, the patch is considered susceptible and no flags are raised.

In addition to “flagging” the various patches in the model, there are also certain calculations that are made for the patches throughout the simulation. These include the following:

Patch Calculations

Sickpercentage	<i>The percentage of agents in the patch that are infected.</i>
Immunepercentage	<i>The percentage of agents in the patch that are immune, either from vaccination or recovery from the infection.</i>

Susceptiblepercentage	<i>The percentage of agents in the patch that are susceptible.</i>
Patchpopulation	<i>Number of agents in the patch.</i>
Sickpopulation	<i>Number of agents in the patch that are sick.</i>
Immunepopulation	<i>Number of agents in the patch that are immune.</i>
Susceptiblepopulation	<i>Number of agents in the patch that are susceptible</i>
Vaccinatedpopulation	<i>Number of agents in the patch that have been vaccinated</i>
Neighborpopulation-h	<i>Number of agents in neighboring patches.</i>
Psickneighbors:	<i>Factor used to determine the sick population of each patch in the next time step. Based on Equation #1.</i>
Max-sick	<i>The maximum percentage sick in the patch at any point during the simulation.</i>
New-sick	<i>Activated and remains activated once any agent in the patch has become infected. Used to measure the spread of the epidemic.</i>

As described previously, each agent and patch has certain characteristics. Once the simulation is set-up, each of these agents and patches undergoes certain procedures that allow for the possible spread of the infection. The code for these procedures is listed in its entirety in Appendix 2, but includes several important steps as listed below:

Turtle Calculations

Aging	<i>Each agent “ages” according to the category in which they currently reside. For example, if an agent is already infected, their sick-count is increased by one, likewise if they are immune, or susceptible. No simulation assumed any definitive lifespan after which agents expired.</i>
Recovery	<i>Agents are given an opportunity to recover from the infection if they have reached the user-defined infected-time. Once they recover they become temporarily immune.</i>
Susceptibility	<i>Agents are given an opportunity to lose their immunity based on the user-defined “immune-time.”</i>
Infection:	<i>Using Equation #1, and the “psickneighbor” value calculated in each time step, the infection is spread to the appropriate number of agents in each patch.</i>
Re-calculation	<i>Patches are asked to recalculate their current populations, including those that are sick, immune, and susceptible. The new</i>

value for psickneighbors is also calculated and the appropriate flags are initiated for each patch.

Movement: *Once 30 time steps have passed (based on Sirakoulis' model) a certain percentage of agents in each patch is asked to move. The user at the beginning of the simulation determines this percentage. During simulations where the effect of quarantine is being studied, the movement of the individual agents is effected not only by percentages, but current state of the agent.*

Distance Traveled: *Each agent is asked to look at their current patch after moving and calculate the total distance it has now traveled from its starting patch. If the distance is further than then user-defined maximum distance, the agent then returns to its pervious patch. Based on this criteria, agents are free to move toward or away from their starting patch as along as they do not exceed this maximum distance.*

Data Collection: *Once all the above steps have taken place, data is collected for the simulation. This data includes area covered by the epidemic, number of patches in each classification, as well as histograms for sick, immune, and susceptible populations.*

APPENDIX 2

The following is the code, in its entirety, used for simulations on NetLogo discussed in this paper. Comments are made throughout the code regarding variations used to test different variables.

TURTLE VARIABLES

```
turtles-own
  [sick?           ;;if true, the turtle is infectious
  immune?        ;;if true, the turtle can't be infected
  susceptible?   ;;if true, the turtle can be re-infected
  vaccinated?    ;;if true, the turtle is permanently immune
  distancetraveled ;;total distance traveled by turtle
  startingpatch  ;;starting location of turtle
  currentpatch   ;;current location of turtle
  previouspatch  ;;previous location of turtle
  sick-count     ;;how long the turtle has been infected
  immune-count   ;;how long the turtle has been "recovered"
  susceptible-count] ;;how long the turtle has been re-susceptible
```

PATCH VARIABLES

```
patches-own
  [sickpercentage   ;;percentage of the population in the cell which is sick.
  immunepcentage   ;;percentage of the population in the cell that are
  immune           immune
  susceptiblepercentage ;;percentage of the population in the cell that are
  susceptible      susceptible
  patchpopulation  ;;number of turtles total in the patch
  sickpopulation   ;;number of turtles in the patch that are sick
  immunepopulation ;;number of turtles in the patch that are immune
  susceptiblepopulation ;;number of turtles in the patch that are
  susceptible      susceptible
  vaccinatedpopulation ;;number of turtles in the patch that are vaccinated
  neighborpopulationa ;;number of turtles on patches at-points (0,1)
  neighborpopulationb ;;number of turtles on patches at-points (0,-1)
  neighborpopulationc ;;number of turtles on patches at-points (1,0)
  neighborpopulationd ;;number of turtles on patches at-points (-1,0)
  neighborpopulationf ;;number of turtles on patches at-points (1,1)
  neighborpopulationg ;;number of turtles on patches at-points (1,-1)
  neighborpopulationh ;;number of turtles on patches at-points (-1,1)
  neighborpopulationi ;;number of turtles on patches at-points (-1,-1)
```

psickneighbors	;;the factor used to determine the number of sick per cell
infection-flag	;;colors patch black if any turtle in the cell is sick
immune-flag	;;colors patch white when everyone in the cell is immune
vaccinated-flag	;;colors patch orange when everyone in it is vaccinated
new-sick]	;;set to 0 if patch has not been infected, set to 1 once patch is infected

DEFINITIONS OF TURTLE STATES

```
to get-sick
  set sick? true
  set immune? false
  set susceptible? false
  set vaccinated? false
  set color red
  set sick-count 0
  set immune-count 0
  set susceptible-count 0
end
```

```
to get-immune
  set sick? false
  set sick-count 0
  set immune? true
  set vaccinated? false
  set color green
  set immune-count 0
  set susceptible? false
  set susceptible-count 0
end
```

```
to get-vaccinated
  set sick? false
  set immune? true
  set susceptible? false
  set vaccinated? true
  set color orange
  set sick-count 0
  set immune-count 0
  set susceptible-count 0
end
```

```
to get-susceptible
  set sick? false
  set sick-count 0
  set immune? false
  set vaccinated? false
  set color blue
  set immune-count 0
```

```

    set susceptible? true
    set susceptible-count 0
end

```

DEFINITIONS OF PATCH CALCULATIONS

```

to calculate-patchpopulation
  set patchpopulation (count (turtles-here))
end

```

```

to calculate-immunepopulation
  set immunepopulation (count turtles-here with [immune?])
end

```

```

to calculate-susceptiblepopulation
  set susceptiblepopulation (count turtles-here with [susceptible?])
end

```

```

to calculate-sickpopulation
  set sickpopulation (count (turtles-here with [sick?]))
end

```

```

to calculate-sickpercentage
  set sickpercentage precision (sickpopulation / patchpopulation) 5
end

```

```

to calculate-immunepcentage
  set immunepcentage precision (immunepopulation / patchpopulation) 5
end

```

```

to calculate-susceptiblepercentage
  set susceptiblepercentage precision (susceptiblepopulation / patchpopulation) 5
end

```

```

to calculate-vaccinatedpopulation
  set vaccinatedpopulation (count turtles-here with [vaccinated?])
end

```

```

to calculatenew-sick
  ask patches with [infection-flag] [set new-sick 1]
end

```

SET-UP PROCEDURE

```

to setup
  ca ;;clears all patches
  set-upturtles ;;sub-routine to create turtles
  ask patches [calculateneighborpopulations] ;;computes values for patches
  ask patches [calculate-patchpopulation calculate-immunepopulation
    calculate-susceptiblepopulation calculate-sickpopulation
    calculate-vaccinatedpopulation calculatepsickneighbors initiateflags
    updatecolor calculatenew-sick]
end

```

```

ask patches [calculate-sickpercentage calculate-immunepercentage
              calculate-susceptiblepercentage initiateflags calculatenew-sick ]
do-plot                                           ;;sets up plot to record spread of epidemic
end

to set-up-turtles
ask n-of num-turtles patches [ sprout turtles-percell
[get-susceptible] ]                               ;;puts 20 turtles in every patch and makes
                                                    them all healthy
ask turtles [if xcor = ( 0 ) and ycor = ( 0 ) [die   ;;causes the middle turtle to die
ask patch ((0)) ((0)) [sprout round
              (percent-sick * turtles-percell) [get-sick]   ;;asks percentage of center patch to get sick
sprout round
              (turtles-percell - percent-sick * turtles-percell)
              [get-susceptible]]
ask turtles [set distancetraveled 0]               ;;gives all turtles a distance traveled of 0
ask turtles [set startingpatch patch-here]         ;;labels the starting patch of all turtles
ask patches [initiateflags]                         ;;subroutine to color patches
end

```

USED ONLY WHEN TESTING EFFECT OF VACCINATION

To vaccinate a certain percentage of each patch

```
ask patches [ask n-of (vaccinated * turtles-percell) turtles-here with [susceptible?] [get-vaccinated]]
```

To create a "ring" of vaccinated patches

```
ask turtles [if distance patch 0 0 = 8 or distance patch 0 0 >= 7 and distance patch 0 0 < 8 [get-vaccinated]]
```

To generate 9 adjacent vaccinated patches

```
ask n-of 1 patches with [distancexy 0 0] < 10][ask turtles-here [get-vaccinated]
ask turtles with [vaccinated?] [ask turtles-on neighbors [get-vaccinated]]
```

SUB-ROUTINE FOR PATCH COLORING

```

to initiateflags
  if sickpercentage > 0 [set immune-flag false set infection-flag true set vaccinated-flag false]
  if sickpercentage = 0 and immunepopulation = patchpopulation [set immune-flag true set infection-
    flag false set vaccinated-flag false]
  if sickpercentage = 0 and immunepopulation < patchpopulation
    [set immune-flag false set infection-flag false set vaccinated-flag false]
  if sickpercentage = 0 and vaccinatedpopulation = patchpopulation [set vaccinated-flag true set
    immune-flag true set infection-flag false]
end

to updatecolor
  if infection-flag [set pcolor black]
  if immune-flag [set pcolor white]
  if vaccinated-flag [set pcolor orange]
  if not infection-flag and not immune-flag and not vaccinated-flag [set pcolor gray]
end

```


GO PROCEDURE

```

to go
  if ticks > tick-count [stop] ;;allows user to determine length of simulation
  ask turtles [set previouspatch patch-here] ;;locates turtles
  ask turtles [if hide-turtles [hide-turtle]] ;;allows user to "hide" turtles
  ask turtles [if not hide-turtles [show-turtle]] ;;allows user to view turtles
  get-older ;;subroutine to age turtles
  recover ;;subroutine to recover and become immune
  becomesusceptible ;;subroutine to lose immunity
  ask patches [calculateneighborpopulations]
  ask patches [calculate-patchpopulation
    calculate-immunepopulation calculate-susceptiblepopulation
    calculate-sickpopulation calculate-vaccinatedpopulation
    calculate-sickpercentage calculate-immunepercentage
    calculate-susceptiblepercentage calculatepsickneighbors
    initiateflags updatecolor]
  ask patches [infect] ;;allows turtles to infect neighboring turtles
  if ticks > 30 [ ask patches [move-turtles]] ;;after thirty time-steps, allows turtles to move
  ask turtles [checkmovement] ;;checks to see if turtles have move too far
  ;;from their starting patch
  do-plot ;;subroutine to record data
  tick ;;one time-step passes
end

```

USED ONLY IN QUARANTINE MODEL

```

ask turtles [checkmovement2] ;;keeps turtles from moving into sick patches
ask turtles [calculatedistancetraveled] ;;calculates distance is from starting patch
ask patches [calculatenew-sick] ;;labels patches that have not been infected
previously

```

SUBROUTINES INCLUDED IN GO PROCEDURE**AGING OF TURTLES**

```

to get-older
  ask turtles [if sick? [set sick-count (sick-count + 1) ]
  if immune? and not vaccinated? [set immune-count (immune-count + 1) ]
  if susceptible? [set susceptible-count (susceptible-count + 1)]]
end

```

RECOVERY FROM ILLNESS AFTER INFECTION TIME HAS PASSED

```

to recover
  ask turtles with [sick?] [if (sick-count) > (infectious-time) [get-immune] ]
end

```

RETURN TO SUSCEPTIBLE STATE AFTER IMMUNE TIME HAS PASSED

```

to becomesusceptible

```

```

    ask turtles with [immune? and not vaccinated?] [if (immune-count) > immune-time [get-
        susceptible]]
end

```

INFECTION OF NEIGHBORING TURTLES

This subroutine uses the fundamentals of equation (1) to determine how many turtles in each patch will get sick

```

to infect
  if (patchpopulation) < (psickneighbors * patchpopulation)
    [ask turtles-here [if susceptible? [get-sick]]]
  if (patchpopulation) > (psickneighbors * patchpopulation)
    [ask n-of (psickneighbors * patchpopulation) turtles-here [if susceptible? [get-sick]]]
end

```

COUNTS TURTLES ON NEIGHBORING PATCHES

```

to calculateneighborpopulations
  set neighborpopulationa ((count ((turtles-on patches at-points [[0 1]])))
  set neighborpopulationb ((count ((turtles-on patches at-points [[0 -1]])))
  set neighborpopulationc ((count ((turtles-on patches at-points [[1 0]])))
  set neighborpopulationd ((count ((turtles-on patches at-points [[-1 0]])))
  set neighborpopulationf ((count ((turtles-on patches at-points [[1 1]])))
  set neighborpopulationg ((count ((turtles-on patches at-points [[1 -1]])))
  set neighborpopulationh ((count ((turtles-on patches at-points [[-1 1]])))
  set neighborpopulationi ((count ((turtles-on patches at-points [[-1 -1]])))
end

```

CALCULATES NUMBER OF TURTLES THAT WILL BE INFECTED IN "INFECT" SUBROUTINE

```

to calculatepsickneighbors
  set psickneighbors (sickpopulation / patchpopulation +
    adjacent * ((count ((turtles-on patches at-points [[0 1]] with [sick?])) /
    neighborpopulationa + (count ((turtles-on patches at-points [[0 -1]] with [sick?])) /
    neighborpopulationb + (count ((turtles-on patches at-points [[1 0]] with [sick?])) /
    neighborpopulationc + (count ((turtles-on patches at-points [[-1 0]] with [sick?])) /
    neighborpopulationd) + 0.04 * ((count ((turtles-on patches at-points [[1 1]] with [sick?]))
    / neighborpopulationf + (count ((turtles-on patches at-points [[1 -1]] with [sick?])) /
    neighborpopulationg + (count ((turtles-on patches at-points [[-1 1]] with [sick?])) /
    neighborpopulationh + (count ((turtles-on patches at-points [[-1 -1]] with [sick?])) /
    neighborpopulationi))
end

```

ALLOWS TURTLES TO MOVE IN A RANDOM DIRECTION AND A RANDOM DISTANCE *THE not sick? CONDITION IS REMOVED WHEN NOT UNDER QUARANTINE*

```

to move-turtles
  ask n-of round (percent-move * patchpopulation) turtles-here
  [if not sick? [let movement (random max-distance) right random 360 forward (movement)]]
end

```

CHECKS TO MAKE SURE TURTLES HAVE NOT TRAVELED FARTHER THAN MAXIMUM ALLOWED DISTANCE IF THEY HAVE TRAVELED TOO FAR, THEY RETURN TO THEIR PREVIOUS LOCATION

```
to checkmovement
  set currentpatch patch-here
  let trial (distance startingpatch)
  if trial > max-distance [move-to previouspatch]
end
```

CALCULATES DISTANCE TURTLES HAVE TRAVELED FROM STARTING PATCH

```
to calculatedistancetraveled
  set distancetraveled (distance startingpatch)
end
```

CREATES PLOT AND RECORDS DATA FOR THE SPREAD OF THE EPIDEMIC

```
to do-plot
  set-current-plot "Sick Patches"
  set-current-plot-pen "area covered"
  plot (count patches with [new-sick = 1])
end
```

USED ONLY IN QUARANTINE MODEL

PREVENTS TURTLES FROM MOVING INTO A PATCH WITH SICK TURTLES

```
to checkmovement2
  let sickhere (count ((turtles-here with [sick?])))
  if sickhere > 0 [ask turtles-here [move-to previouspatch]]
end
```

VITA

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Ashley pursued her undergraduate degree in mathematics and chemistry at Bridgewater College where she was a Presidential Scholar. Ashley graduated summa cum laude in 2001. She also received a teaching certificate and taught for four years in Chesterfield County Public Schools before returning to graduate school.