Spatial Simulation of the Spread of a Rapidly Evolving Pathogen

Introduction to Computer Simulations

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1 Introduction

The field of epidemics is one of the most heavily studied fields in science, however, models and simulations are continuously being altered, and changed to make them more and more accurate, and to obtain a more realistic model. In this simulation, we aim to introduce different details that are not usually accounted for in most models, in an attempt to reach a model that represents the spread of a rapidly evolving virus in a small population. Therefore, we cannot model the spread of these diseases merely relying on the SIR model. In this simulation, we take into account the evolutionary nature of these viruses, their latency time, the period when patients are carriers of the disease but could not yet transmit it to other, and the transmission of the virus due to contact between individuals in the space. We aim to provide a more accurate simulation of viruses like HIV, HCV, and SARS, which have proved to be almost impossible to effectively treat. This is due to the fact that they evolve and adapt to different modes of treatment very quickly. As a result, doctors usually administer multiple drugs that attack different virus strains, attempting to restrict the spread of the virus by attacking all possible strains. For the sake of this study, we only allow the virus to evolve into 3 different strains. In this simulation, we study the effect of administering different combinations of treatments and consider the costs that would come with each treatment strategy. For the sake of simplicity, we set the infectivity, virulence, and the cost of treatment for each virus strain to be the same.

2 Equations

This simulation is based on the SEIR model, and adapted the equations below to simulate the spread of the pathogen.

Table 1: List of Variables Used

Variables	Meaning
S	Number of susceptible individuals
E	Number of individuals exposed to virus
I	Number of infected individuals
D	Number of dead individuals
R	Number of recovered individuals who acquired immunity
N	Total population
a	Probability of infection on contact per person
$r_{critical}$	Maximum distance at which transmission between two individuals occurs
$1/b$	Average recovery time per person
τ	Latency time per person
$1/\delta$	Average life span per infected or exposed individual
t'	Time since infection for each individual
m	Mutation Rate per DNA/RNA base per Virus per generation
r	Replication rate of virus
e	Probability of mutation leading to the evolution of a resistant strain
l	Length of DNA/RNA

$$\text{Probability of evolution of a virus} = m \times r \times e \times l. \tag{1}$$

Equation 1 above corresponds to the chance of having a virus evolve into a strain that is resistant to its current mode of treatment. The probability of that occurring is always proportional to its replication rate within a host, r, the product of its mutation rate per DNA\RNA replication process, denoted by m in the equation above, and the length of the DNA \RNA sequence, l, yielding the mutation rate of a single virus molecule per replication process. For the sake of this simulation, we multiply these factors by e, an arbitrary value that we set to appropriately correspond to the probability of the evolution of a resistant virus strain due to the mutations occurring. We need to do this since, most mutations that would take place, would in fact result in non-resistant forms of the virus, and it is only a small fraction that would be beneficial to the virus.

Moving on to the equations pertaining to the spread of the virus, we note that while the equations below were not directly used in the simulation, they describe the framework that was used to implement the spatial simulation. In addition they outline the specifics of the SEIR model followed. For our simulation, each of these equation was adapted for the case by case transmission of the virus, while following the same framework.

$$N = S + E + I + R + D. \tag{2}$$

Equation 2 simply states, that the number of individuals in a population always remains constant, and that it is merely the sum of the different states of the

individuals in a population: individuals susceptible to infection, individuals exposed to infection, individuals infected, recovered individuals and individuals who acquired immunity against the virus strain, and individuals that died due to the infection.

2.1 General Equations for Model

$$\frac{dS}{dt} = -\frac{aSI}{N} \tag{3}$$

$$\frac{dE}{dt} = \frac{aSI}{N} - (\frac{1}{\tau} + b + \delta)E \tag{4}$$

$$\frac{dI}{dt} = (\frac{1}{\tau})E - (b + \delta)I \tag{5}$$

$$\frac{dR}{dt} = b(E + I) \tag{6}$$

$$\frac{dD}{dt} = \delta(E + I). \tag{7}$$

Equation 3 describes the rate of change of the number of susceptible individuals, $\frac{dS}{dt}$, which is proportional to the negative of the fraction of the population that is infected, $\frac{I}{N}$, the number of susceptible individuals, S, and the probability of infection on contact, a.

In the SEIR model, when an individual is infected, there is a specific period, the latency time denoted here by the greek symbol τ, where the viral load in their system is still too low for them to transmit the disease to others. They, however, are still carriers of the disease, and once their infection period becomes greater that the latency period, they begin to actively transmit the virus. This is described by the expression in equation 4. To calculate the rate of change of the number of exposed individuals we must add $\frac{aSI}{N}$, which we determined above corresponds to the number of susceptible individuals that are exposed to the disease per unit time. We then, subtract the number of individuals who transition from being merely exposed to the disease, to being able to transmit it to others, by subtracting $\frac{1}{tau}$ which would correspond to the rate at which individuals transition from being exposed to being infective. Further, in this model, exposed individuals can also recover or die from the infection even before being able to transmit, thus, we account for that by subtracting the portion of the exposed individuals that are statistically expected to either recover or die, $(b + \delta)E$.

Equation 5, follows the same logic equation 4 does. To determine the rate of change of infected individuals we add the fraction of individuals exposed to the virus that are statistically expected to transition into the infective phase, and subtract the individuals that are expected to either recover or die from the infection.

To determine the number of individuals that would recover per unit time, we simply need to add the number of exposed and infected individuals that undergo recovery.

Similarly, for equation 7, to determine the rate of death due to infection, we add up the number of individuals that die either due to mere exposure to the virus, and individuals that die during their infective phase.

2.2 Equations for Spatial adaptation of SEIR model

As stated above, equations 3 to 7 were adapted to make a spacial simulation of the SEIR model. The adapted case to case equations are shown below. All the equation below are for calculating the probabilities of transitioning from one phase to another for a single individual in the population.

Table 2: Notation for Equations Below

Variables	Meaning
s'	The probability of being exposed to the disease, S $\rightarrow$ E
e'	The probability of transitioning out of exposed phase, to death, recovery, or infective phase.
i'	The probability of transitioning out of infective phase, to either death or recovery.
r'	The probability of transitioning into the recovered phase.
d'	The probability of transitioning into the death phase.

$$s' = \begin{cases} \text{a} & \text{if } r < r_{critical} \\ 0 & \text{if } r > r_{critical} \end{cases} \tag{8}$$

$$e' = \begin{cases} (b+\delta) & \text{if } t < \tau \\ 1 & \text{if } t > \tau \end{cases} \tag{9}$$

$$i' = \begin{cases} 0 & \text{if } t < \tau \\ (b+\delta) & \text{if } t > \tau \end{cases} \tag{10}$$

If individual is exposed or infected, we proceed to calculate r', d' according to the equations below.

$$r' = b \tag{11}$$

$$d' = \delta \tag{12}$$

The probability of having an individual transition from being susceptible to being exposed, is equal to the infectivity of the virus, denoted by a, if $r > r_{critical}$, where r is the distance between a susceptible individual and an infective one, and $r_{critical}$ is the maximum radius at which transmission could occur. When $r < r_{critical}$, this expression is required to always evaluate to 0 as the $r_{critical}$ is defined. Therefore, in other words, if an individual is within the

radius of infection, the chances of them being exposed to the diseases is equal to a.

Further, in the SEIR model, when an individual is infected, there is a specific period, the latency time denoted here by the greek symbol τ, where the viral load in their system is still too low for them to transmit the disease to others. They, however, are still carriers of the disease, and once their infection period becomes greater that the latency period, they begin to actively transmit the virus. This is described by the expression in equation 9. This expression evaluates to $(b+\delta)$ when the individual is within the latency period, and $1-(b+\delta)$ when the individual surpassed the latency period and can infect others. When $t < \tau$, the individual could either recover, or die, therefore their probability of transitioning out of the exposed phase is equal to the sum of the probability of them recovering, b, or dying, δ. However, if they surpassed the latency period, then as the latency period was defined, their only option is to transition to the infection phase.

Equation 10 follows from equation 9. If the individual is still within their latency period, they cannot transition into or out of the infective phase, therefore their probability remains 0. As they however surpass that period, they could either die or recover, and therefore their probability of transition out of the infective phase is equal to the sum of the probabilities of both these events. Further, for equations 11, 12, we use the definitions of the b, δ defined above where b would correspond to the probability of recovery per person, and δ would correspond to the probability of death per person.

3 Numerical Method

To produce the simulation, the following numerical method was used.

3.1 Moving the Individuals in the Space

To move the individuals on the spatial grid, a vector field function f was defined for each point on the grid, and the individuals velocities, v_x, v_y were determined accordingly.

$$\frac{x(t+\Delta t)-x(t)}{\Delta t} = v_x(t+\Delta t) \tag{13}$$

$$\frac{y(t+\Delta t)-y(t)}{\Delta t} = v_y(t+\Delta t) \tag{14}$$

$$v_x(t+\Delta t) = v_{max} \times f_x(x(t), y(t)) \tag{15}$$

$$v_y(t+\Delta t) = v_{max} \times f_y(x(t), y(t)) \tag{16}$$

$$x(t+\Delta t) = x(t) + v_x(t+\Delta t) \times \Delta t \tag{17}$$

$$y(t + \Delta t) = y(t) + v_y(t + \Delta t) \times \Delta t \tag{18}$$

3.2 Tracking the Spread of Virus

To track the spread of the disease, the equation in section 2.2 were used to calculate the probabilities of the transitions in between the possible states that an individual could occupy. Further, to keep track of these states, several $N \times 3$ matrices that correspond to the following states were created as follows. Exposed to matrix, **E**, to track the different strains that each individual in the population has been exposed to, a viral load matrix, **V** to track the time since each individual was exposed to each strain, and an immunity matrix, **I** to track the strains to which individuals developed immunity towards. There was no need to create a matrix to correspond to deaths, as individuals were no longer interacting with the rest of the population, and were no longer taken into account. t in V_{ij}, denotes time since exposure to virus.

$$E_{ij} = \begin{cases} 0 & \text{if individual } i \text{ was exposed to virus strain } j \\ 1 & \text{if individual } i \text{ was not exposed to virus strain } j \end{cases} \tag{19}$$

$$V_{ij} = \begin{cases} 0 & \text{if } E_{ij} = 0 \\ \text{t} & \text{if } E_{ij} = 1 \end{cases} \tag{20}$$

$$I_{ij} = \begin{cases} 0 & \text{if individual } i \text{ developed immunity to virus strain } j \\ 1 & \text{if individual } i \text{ did not develop immunity to virus strain } j \end{cases} \tag{21}$$

4 The program

The program was written and run in MATLAB with the following code.

```
%Epidemic Simulation -- Project 2
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% total number of individuals
N=100;
% infectivity
a=0.9;
% recovery rate
b=[0.1/10 0.1/10 0.1/10];
%death rate
d = [0.1/2 0.1/2 0.1/2];

replication_rate = 10e10;
```

```
length =9600;
mutation_rate = 10e-4;
chance_of_resitance = 1e-12;
viral_load = zeros(N, 3);
critical = [7 7 7];
critical1 = [7 0 0];
critical2= [7 7 0];
alpha = zeros(N, 1);

dt=0.1;
tmax=10000;
clockmax=ceil(tmax/dt);

color = zeros(N, 3);

%black
dead = [0 0 1];

%turquoise
immune = [0 1 1];
% color when individual develops immunity to 1 or 2 strains, but not all
% pink
immune2 = [1 0 1];

%white
alive = [1 1 1];

%red
all_strains = [1 0 0];

%yellow
one_strain  = [1 1 0];

%orange
two_strains = [255 153 51]/255;

%for loop for setting the initial colors to white
for i= 1:N
color(i,:) = alive;
end

population = zeros(N,3);
immunity = zeros(N, 3);
initial_infected = 2;

% initial conditions
```

```
for i= 1:initial_infected
population(i ,1) = 1;
color(i ,:) = one_strain;
end

%counts
dead_count =0;
healthy_count =N-initial_infected;
infected_count=initial_infected;
immune_count =0;
partial_immune =0;
cost = 0;
number_of_treatments_per_time = 3;
%average cost per 0.1 of a day for HCV treatment
cost_per_treatment =number_of_treatments_per_time* 50;

%x, y positions of each individual
x=zeros(1,N);
y=zeros(1,N);

%velocities at which each individual will move
u = zeros(1,N);
v = zeros(1,N);

%the space at which individuals begin moving
space = 100;

% fasted allocated speed for each individual
maxspeed = 5;

%limits where individuals are allowed to be
min= -100;
maximum = 100;

% initializiations for positions and velocities
for i=1:N
x(i) = - space+ rand*2*space;
y(i) = - space+ rand*2*space;
u(i) = - maxspeed+ rand*2*maxspeed;
v(i) = - maxspeed+ rand*2*maxspeed;
end

%intitializing the vector field for movement of individuals
rand_value = randn;
[xx,yy] = meshgrid(min:10:maximum,min:10:maximum);
f = sin(2*xx/100 + 2*yy/100)+ rand_value;
```

```
x_fac = sin(f);
y_fac = cos(f);
uu = x_fac;
vv = y_fac;

%spread of disease
for clock = 1: clockmax
dead_count =0;
healthy_count = 0;
immune_count =0;
partial_immune =0;
for i = 1:N
%first check that they are alive, if not skip them
if color(i,:) == dead
continue
else
%updating positions
ff = sin(2*x(i)/100 + 2*y(i)/100)+ rand_value;
x_fac = sin(ff);
y_fac = cos(ff);
x(i)= x(i) + u(i);
y(i)= y(i) + v(i);

%making sure individuals dont exit space // they bounce off edges
if x(i)> maximum || x(i)<min
      if x(i)> maximum
          x(i) = x(i) -5;
     elseif x(i)<min
          x(i) = x(i) + 5;
      end
     v(i)= v(i)*-1;
     u(i)= u(i)*-1;
end
if y(i)> maximum || y(i)<min
     if y(i)> maximum
          y(i) = y(i) -5;
     elseif y(i)<min
          y(i) = y(i) + 5;
     end
          u(i) = u(i)*-1;
          v(i)= v(i)*-1;
end
%mutation
%skip healthy and fully immune individuals
if immunity(i,:) == [1 1 1]
     continue
```

```
elseif population(i,:) == [0 0 0]
    continue
else
    if rand<0.1*replication_rate *length* mutation_rate* chance_of_resitance
        population(i,2) = 1;
        if population(i,:) == [1 1 0]
            color(i,:) = two_strains;
        else if population(i,:) == [0 1 0]
            color(i,:) = one_strain;
        end
    end
    if rand<0.1*replication_rate *length* mutation_rate* chance_of_resitance
        population(i,3) = 1;
    end
end
alpha = max(viral_load,[],N);
% recovery
    %cure for strain a
if population(i,:) == [1 0 0]
    viral_load(i,1) = viral_load(i,1)+1;
    cost= cost+(cost_per_treatment);
    if rand< b(1)
        immunity(i,:) = [1 0 0];
        population(i,:) = [0 0 0];
        %individual has recovered
        color(i,:) = immune2;
        viral_load(i,:) = [0 0 0];
    end
%                 %cure for strain b
elseif population(i,:) == [0 1 0]
     viral_load(i,2) = viral_load(i,2)+1;
     cost= cost+(1*cost_per_treatment);
     if rand< b(2)
        %individual has recovered
        immunity(i,:) = [0 1 0]
        population(i,:) = [0 0 0];
        color(i,:) = immune2;
        viral_load(i,:) = [0 0 0];
     end
 %cure for strain c
elseif population(i,:) == [0 0 1]
     viral_load(i,3) = viral_load(i,3)+1;
     cost= cost+(1*cost_per_treatment);
     if rand< b(3)
        %individual has recovered
        immunity(i,:) = population(i,:);
```

```
        population(i,:) = [0 0 0];
        color(i,:) = immune2;
        viral_load(i,:) = [0 0 0];
      end
 %cure for strain ab
elseif logical(population(i,:)) == logical([1 1 0])
     viral_load(i,1:2) = viral_load(i,1:2)+1;
     cost= cost+(1*cost_per_treatment);
     p = rand;
     if p< (b(1)) && p< (b(2))
        %individual has recovered
        immunity(i,:) = population(i,:);
        population(i,:) = [0 0 0];
        color(i,:) = immune2;
        viral_load(i,:) = [0 0 0];
     end
 %cure for strain ac
elseif logical(population(i,:)) ==logical([1 0 1])
     viral_load(i,1) = viral_load(i,1)+1;
     viral_load(i,3) = viral_load(i,3)+1;
     cost= cost+(1*cost_per_treatment);
     p = rand;
     if p< (b(1)) && p< (b(3))
        %individual has recovered
        immunity(i,:) = [1 0 1];
        population(i,:) = [0 0 0];
        color(i,:) = immune2;
        viral_load(i,:) = [0 0 0];
     end
%%              %cure for strain bc
elseif logical(population(i,:)) == logical([0 1 1])
    viral_load(i,2:3) = viral_load(i,2:3)+1;
    cost= cost+(1*cost_per_treatment);
    p = rand;
      if p< (b(2)) && p< (b(3))
        %individual has recovered
        immunity(i,:) = population(i,:);
        population(i,:) = [0 0 0];
        color(i,:) = immune2;
        viral_load(i,:) = [0 0 0];
     end
%cure for strain abc
elseif logical(population(i,:)) == logical([1 1 1])
     viral_load(i,1:3) = viral_load(i,1:3)+1;
     cost= cost+(1*cost_per_treatment);
     p = rand;
```

```
      if p< (b(1)) && p< (b(2)) && p< (b(3))
         %individual has recovered
         immunity(i,:) = population(i,:);
         population(i,:) = [0 0 0];
         color(i,:) = immune;
         viral_load(i,:) = [0 0 0];
      end
end

%death
if logical(population(i,:)) == logical([1 0 0])
    if rand< d(1)
         population(i,:) = [0 0 0];
         color(i,:) = dead;
    end
%death for strain b
elseif logical(population(i,:)) == logical([0 1 0])
     if rand< d(2)
         color(i,:) = dead;
     end
%death for strain c
elseif logical(population(i,:)) == logical([0 0 1])
     if rand< d(3)
         population(i,:) = [0 0 0];
         color(i,:) = dead;
     end
%death for strain ab
elseif logical(population(i,:)) == logical([1 1 0])
     if rand< (d(2))
         population(i,:) = [0 0 0];
         color(i,:) = dead;
     end
%death for strain ac
elseif logical(population(i,:)) == logical([1 0 1])
     if rand< (d(3))
         population(i,:) = [0 0 0];
         color(i,:) = dead;
     end
%death for strain bc
elseif logical(population(i,:)) == logical([0 1 1])
     if rand< (d(3))
         population(i,:) = [0 0 0];
         color(i,:) = dead;
     end
%death for strain abc
elseif logical(population(i,:) == [1 1 1])
```

```
      if rand< (d(3))
         population(i,:) = [0 0 0];
         color(i,:) = dead;
      end
end
for j= 1:N
if color(j,:) == dead
    continue
end
if immunity(j,:) == [1 1 1]
    continue
else
    dx = x(i) - x(j);
    dy = y(i) - y(j);
    rsquared = dx^2+ dy^2;

    % spreading the infection
    if rsquared<100
        if immunity(i,:) == [1 1 1]
            continue
        elseif abs(population(j,:) + immunity(j,:) - population(i,:)) == [0 0 0]
            continue
        %check if they actually transmit if probability is
        %greater than infectivity
        %the condition is set so that they have an
        %"a"(variable above) chance to transmit any strain
        else if (rand<a)
                if max(viral_load(i,:))> 7
                    if abs(logical(population(j,:) +immunity(j,:)- population(i,
                        %uninfected person came into contact with
                        %a completely resitant strain
                        population(i,:) = [1 1 1];
                        population(j,:) = [1 1 1];
                        color(i,:) = all_strains;
                        color(j,:) = all_strains;

                    elseif abs((population(j,:)+immunity(j,:) - population(i,:))
                        % person not infected with strain a came into contact
                        % with someone who has strain a
                        population(i,1) = 1;
                        population(j,1) = 1;
                        color(i,:) = one_strain;
                        color(j,:) = one_strain;
                    elseif abs((population(j,:) +immunity(j,:) - population(i,:)
                        % person not infected with strain b came into contact
                        % with someone who has strain b
```

```
                    population(i,2) = 1;
                    population(j,2) = 1;
                    color(i,:) = one_strain;
                    color(j,:) = one_strain;
                elseif abs((population(j,:)+immunity(j,:) - population(i,:))
                    % person not infected with strain c came into contact
                    % with someone who has strain c
                    population(i,3) = 1;
                    population(j,3) = 1;
                    color(i,:) = one_strain;
                    color(j,:) = one_strain;
                elseif abs((population(j,:) +immunity(j,:)- population(i,:))
                    % person not infected with strain ab came into contact
                    % with someone who has strain ab
                    population(i,1) = 1;
                    population(j,1) = 1;
                    population(i,2) = 1;
                    population(j,2) = 1;
                    color(i,:) = two_strains;
                    color(j,:) = two_strains;
                elseif abs((population(j,:) +immunity(j,:)- population(i,:))
                    % person not infected with strain ac came into contact
                    % with someone who has strain ac
                    population(i,1) = 1;
                    population(j,1) = 1;
                    population(i,3) = 1;
                    population(j,3) = 1;
                    color(i,:) = two_strains;
                    color(j,:) = two_strains;
                elseif abs((population(j,:) +immunity(j,:)- population(i,:))
                    % person not infected with strain abc came into contact
                    % with someone who has strain bc
                    population(i,2) = 1;
                    population(j,2) = 1;
                    population(i,3) = 1;
                    population(j,3) = 1;
                    color(i,:) = two_strains;
                    color(j,:) = two_strains;
                end
            end
        end
    end
end
end
end
```

```
end
end
%plotting
%plotting the vector field
quiver(xx,yy,uu,vv, 'FaceColor', 'b')
hold on

%plotting the individuals
scatter(x,y, 30, color, 'filled')
%plotting the radius of infectivity
for i= 1:N
if color(i,:) == dead
    dead_count = dead_count+1;
    continue
elseif immunity(i,:) == [1 1 1]
    immune_count = immune_count +1;
    continue
elseif (immunity(i,1) >0) ||(immunity(i,2) >0) || (immunity(i,3) >0)
    partial_immune = partial_immune+1;
elseif population(i,:) == [0 0 0]
    healthy_count = healthy_count+1;
    continue;
end
t = 0 : 0.5 : 2 * pi;
r = 10;
x_circ = x(i)+(r*cos(t));
y_circ = y(i)+(r*sin(t));
if alpha(i)>=7
    alpha(i) = 6;
end
patch( x_circ,y_circ,color(i,:),'FaceAlpha',alpha(i)/7,'EdgeColor', 'none');
end
hold off
infected_count = N-(healthy_count+ dead_count + immune_count+partial_immune);
whitebg(1,'k')
set(gca,'color','black')
set(gcf,'color','black')
axis equal
%displaying counts
title({['Susceptible Count: ' ,num2str(healthy_count)];...
['Partially Immune Count: ' , num2str(partial_immune)];...
['Fully Immune Count: ' , num2str(immune_count)];...
['Infected Count : ', num2str(infected_count)];...
['Death Count: ', num2str(dead_count)];...
['Cost of Treatment: ', num2str(cost)]});
axis([min-40, maximum+40, min-40, maximum+40])
```

```
drawnow
axis manual

end
```

5 Results

To study the spread of such a rapidly evolving pathogen, the mode of treatment was systematically varied, and the results were observed and recorded.

5.1 Mode of Treatment

To observe the effect of the mode of treatment on the nature of spread of the virus, the following permutations were studied.

- Treatment administered for 1 strain only.
- Treatment administered for 2 strains simultaneously.
- Treatment administered for all 3 strains simultaneously.

To obtain the results below, the number of the population was set to 100, and the values for rates of recovery were kept the same if the corresponding strain was being treated, or set to zero, if no treatment for the specific strain was being administered. Each simulation was run for the same amount of time, several times, and average values were calculated.

Table 3: Treatment for 1 Strain at a Time

Run Number	t_1	t_2	t_3	t_4	t_5	$t_{average}$
Susceptible	4	9	6	13	8	8
Infected	12	16	15	11	6	12
Partially Immune	0	0	1	0	0	0
Fully Immune	0	0	0	0	0	0
Dead	84	75	78	76	80	98
Cost	91600	101600	88700	89500	100550	94390

Table 4: Treatment for 2 Strains at a Time

Run Number	t_1	t_2	t_3	t_4	t_5	$t_{average}$
Susceptible	6	0	11	5	14	7
Infected	16	13	11	19	15	15
Partially Immune	2	0	1	1	0	1
Fully Immune	0	0	0	0	0	0
Dead	76	87	77	75	71	77
Cost	215100	164500	190500	219900	184899	194960

Table 5: Treatment for 3 Strains at a Time

Run Number	t_1	t_2	t_3	t_4	t_5	$t_{average}$
Susceptible	14	15	10	8	13	12
Infected	7	20	14	5	17	13
Partially Immune	7	6	10	0	2	5
Fully Immune	9	12	6	11	13	10
Dead	63	47	60	76	55	60
Cost	213150	200250	240450	246900	213900	222930

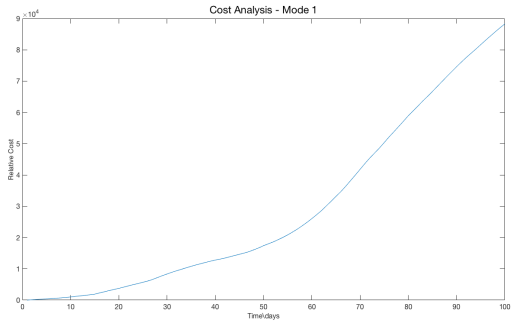


Figure 1: Graph of Relative Cost/Time of Mode 1

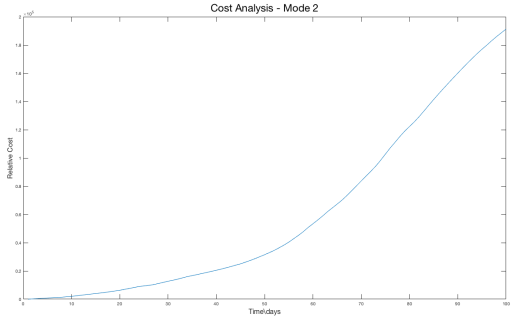


Figure 2: Graph of Relative Cost/Time of Mode 2

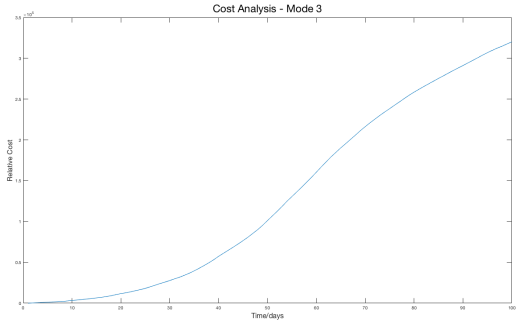


Figure 3: Graph of Relative Cost/Time of Mode 3

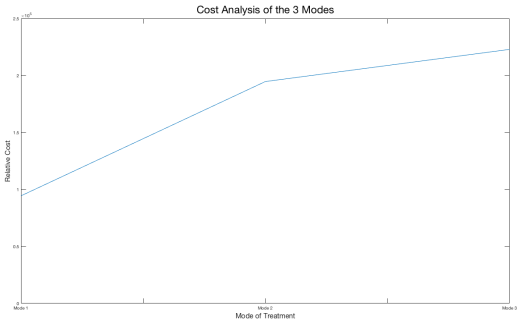
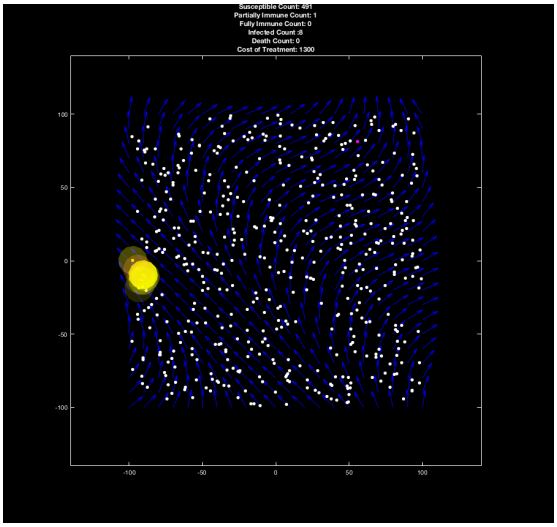
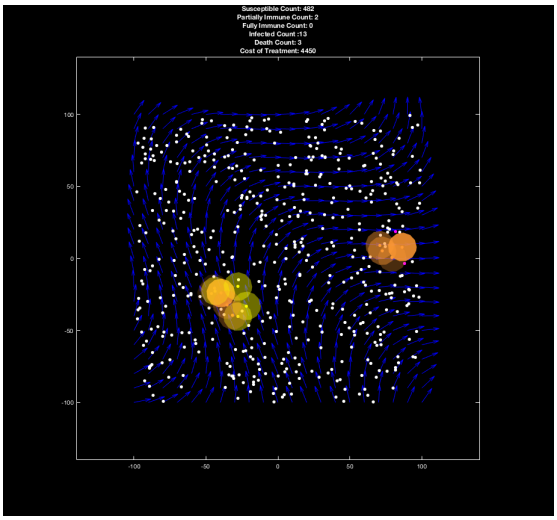
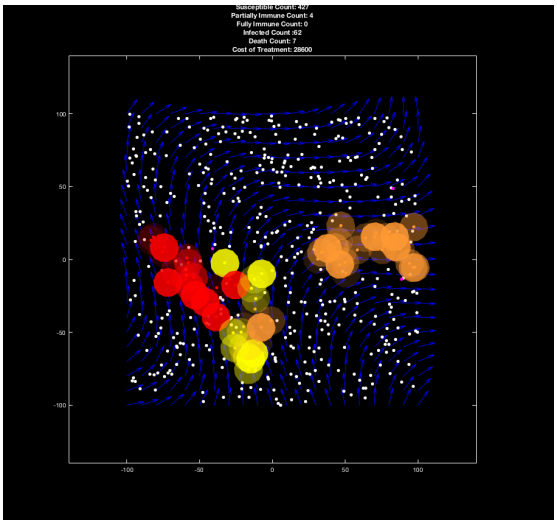


Figure 4: Graph Comparing Relative Cost of all Modes

5.2 The Simulation







As shown above in the table, it is rather difficult to find a consistent result pattern due to the random nature of the simulation. Therefore, we cannot come to any definitive conclusions. However, from tables 3 and 5above, we could note that the number of susceptible or healthy individuals at the end of the time period, is not significant, the average difference is only 1. However, it is important to note that there is much more variation in the number of susceptible individuals at the end of each run, when two modes of treatment are administered at a time. Further, the number of individuals that remained infected at the end of both runs is greater when 2 drugs are administered at a time. While this might seem counter-intuitive at first, we notice that the death count is significantly decreased in the second mode of treatment, this is shown in figure 4. Therefore, it is possible that while more people remain infected at the end of the run, less patients die from infected, and they have a higher chance of recovery, when 2 drugs are being administered. Additionally, individuals are more likely to develop partial immunity, immunity towards 1, 2 but not all strains of the virus, when exposed to the second mode of treatment. As expected, no individuals acquired full immunity at either runs, and the cost of treatment in the second mode is significantly much more expensive than the first mode of treatment.

However, we notice the most significant difference when we look at table 5. We note that there is a higher number of individuals that did not acquire the disease at the end of the run. The number of infected individuals at the number stayed within the same range as the two previous runs, however, we notice that there are significantly more individuals that acquired both partial, and full immunity. Further, the death count dropped further from the second mode of treatment. This is due to the fact that when 3 drugs are administered at a time, and all virus strains are curable, the spread of the virus is much more controlled and is less likely to result in the death of patients. Additionally, it

is critical to note that while the cost of treatment increased greatly from the first mode of treatment to the second mode, the increase was much less between the second mode and third mode. This is a result of the fact noted above. As the disease is more controlled, and as the chances of recovery are greater as all strains are curable, individuals remain sick and in need of treatment for much shorter periods of time. Even though the number of infected individuals remains about the same across all three modes, there are less infected individuals at any given point in time during the run, in the third mode.

The difference in the rate of change of cost could be easily observed in figures 1,2,3, and 4 above. One can see that that for both figures 1 and 2, the rate of change of the cost is either constant, the gradient of the curve is the same, or is increasing. This is consistent with our observations above, that in modes 1 and 2, the rate of increase of the cost of treatment increases as the infection gets more difficult to manage and control due to the new incurable strains. If we look at figure 1, we notice two major increases in the rate of change of cost. These are the moments in the simulation, where the virus strain evolves, and the epidemic begins to spread at a faster rate. Similarly, we notice the same thing in figure 1, however, it has only one major increase in the rate, as the infection only gets out of control when the third incurable strain has evolved. The introduction of the second strain does not affect the curve as significantly as in figure 1, as strain 2 is curable in the second mode. However, what is most interesting is the curve shown in figure 3 corresponding to the third mode of treatment. We notice that while the cost is increasing at the beginning of the simulation, the rate of increase of cost begins to slow down, and the curve appears to level off. The virus initially spreads, however, as time passes, it is kept under control, and the costs do not keep increasing.

Nonetheless, further investigation is required to obtain more conclusive results. This could be done by running the simulation for longer time intervals, larger populations, and for more times to obtain average results that are more accurate.