Disease Spreading Analysis

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Key Words: *spatial analysis, Ebola, Measles, Reproduction Number, M/M queue*

Abstract

A relation is examined in disease spread between Ebola and Measles using basic reproduction numbers. The numerical analysis yielded exponential growth in terms of spreading the disease from one person to another, however the rates of infection and deaths varied. Spatial analysis gave a picture of the concentration of the spread of these diseases. Finally, when taking into account vaccinations, an M/M queueing model found that Measles could be controlled in today's circumstances where an Ebola outbreak could have series consequences.

1.

Parameters and Assumptions. The spread of disease is often quantified by R_0 which is called the birth reproduction rate. Realistically in these terms it is the amount of people that one carrier of the disease can transmit to after one life cycle of the disease. Ebola and the Measles will be examined in this paper, each with $R_0 = 3$ and $R_0 = 12$ respectively.

Ebola and Measles are being studied particularly because of the vast differences in how they are spread as well as their rates.

There will be various assumptions made for these models. Specific assumptions for a particular model will be explained in that section. The general assumptions are as follows. The population spreading this disease is homogenous. Each life cycle or generation happens at regular intervals in a stationary population (no one goes on vacation after catching a disease).

2.

Numerical Analysis of Ebola and Measles. This first model compares the amount infected as well as the deaths caused by Ebola and Measles with each generation. The population is assumed to be boundless in that with each new generation, an individual is guaranteed to transmit to R_0 victims. Also, populations are considered to have no vaccination prerogative in

place. Incubation time and length of the disease is taken at random for each generation to be included in the life cycle time.

```
set.seed(12)
m <- 8                                          #generations
infectcount.eb <- c();deathcount.eb <- numeric(m); t.eb <- numeric(m)
infectcount.eb[1] <- 5                          #initial infected
infect.eb <- 3                                  #R_o
for(i in 2:m){
            incu <- sample(2:21, 1)             #incubation time
            deathtime <- sample(6:16, 1)        #length of disease
            deaths <- sum(sample(c(1, 0), infectcount.eb[i-1], pr=c(0.7,
                        0.3), repl=T))          #proportion of people that live or
                                                #die from the disease

            deathcount.eb[i] <- deaths          #running death total
            infectcount.eb[i] <- infectcount.eb[i-1]*infect.eb - deaths
                                                #infection spreads from those who
                                                #who survive

            t.eb[i] <- incu + deathtime         #time it takes for each life cycle
      }
infectcount.eb
[1]   5   11   23   54  124  284  653 1489 #growth of infected each generation
deathcount.eb
[1]   0   4  10  15  38  88 199 470        #deaths with each generation
```

Note that deaths are only tallied after a life cycle (deaths wait for the disease to spread before occurring). Similar code is used for Measles with a few parameter changes (see Appendix 1a). This is the output for Measles.

```
infectcount.me
[1]         5        59       702      8360     99443   1183320  14081755
[8] 167570067
deathcount.me
[1]       0       1       6      64     877    9996  118085 1410993
```

It is difficult to compare some of these numbers as they are quite large, however the survival rate for each generation can be shown to demonstrate that they are consistent.

```
deathcount.eb/infectcount.eb
[1] 0.0000000 0.3636364 0.4347826 0.2777778 0.3064516 0.3098592 0.3047473
[8] 0.3156481
deathcount.me/infectcount.me
[1] 0.000000000 0.016949153 0.008547009 0.007655502 0.008819123 0.008447419
[7] 0.008385674 0.008420316
```

Each iteration is accurate to a certain degree. Figure 1a shows the time series plot of Ebola infections and deaths. Figure 1b shows the time series plot for Measles infections and deaths. In either case, diseases spread rapidly after picking up momentum, and even low death rates can have catastrophic overall deaths once the disease is more prolific.

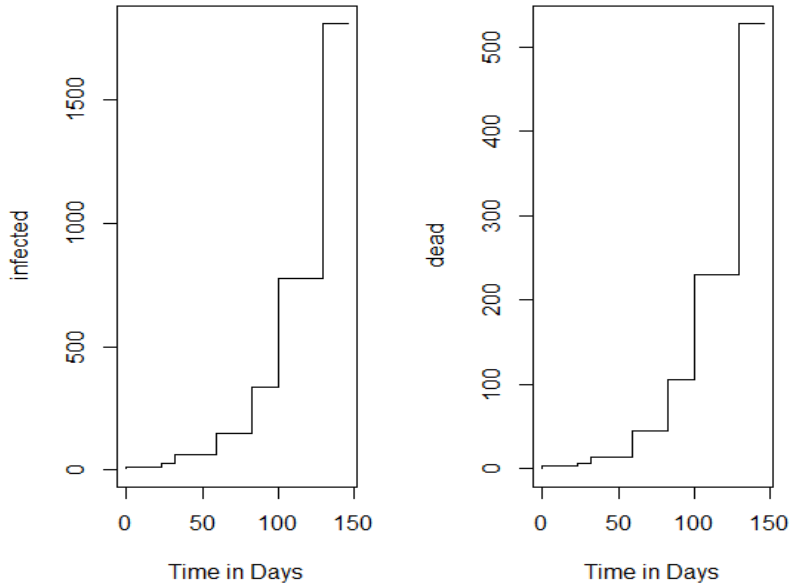

Figure 1a: *The amount infected after a certain amount of days in the case of Ebola. Both deaths and infected people seem to experience exponential growth. For code for this output, see Appendix 1b.*

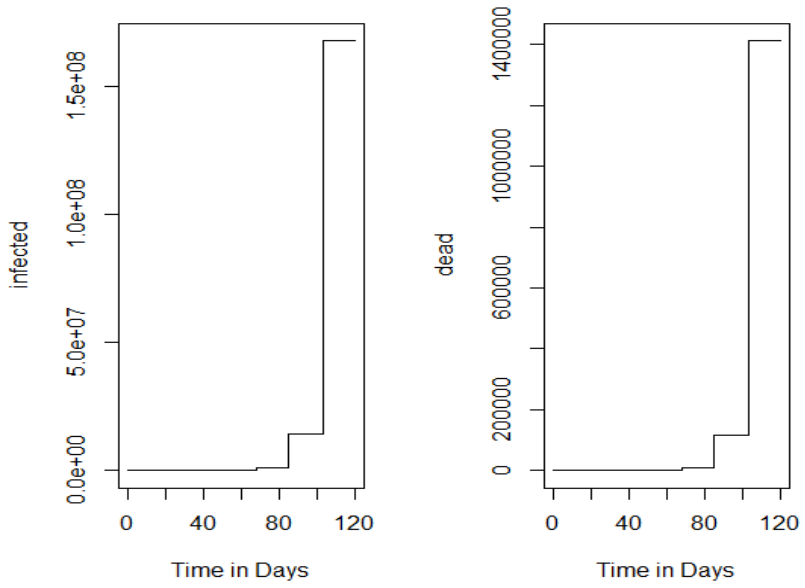

Figure 1b*: The amount of infected after a certain amount of days in the case of Measles. Notice how the exponential growth here is much faster due to its higher* R_0*. For output code, see Appendix 1c.*

3.

Spatial Analysis of Ebola and Measles. While the analysis of a disease from a strictly numerical sense is helpful, it is also useful to look at the spatial pattern of how these diseases spread. With each generation, again Ebola and Measles will infect new people based on their respective R_0 values. Now consider a population where N=5 infected people are dropped in among everyone else and are to spread the disease from their "epicenters." They can be thought of as residing on a specific coordinate of a fixed, two-dimensional space who then infect their neighbors, and in turn they infect their neighbors, and so on. This process of propagation is based on spreading to people on an x-y plane, however the catching of the disease and the direction the disease travels are both random. Therefore polar coordinates are to be used where x = rcos(θ) and y = rsin(θ). In this model, θ indicates the angular spread of the disease, or direction. Since any neighbor is equally likely to catch the disease from someone, this will be drawn at random from uniform. The variable r will indicate the distance, and while disease spreading obeys certain power laws, this model simplifies it down to an exponential distance. Not much is known yet about the intricacies of Ebola, however like the Measles, it is thought to be highly contagious. Therefore EXP(λ), where λ is the rate (in this case, how

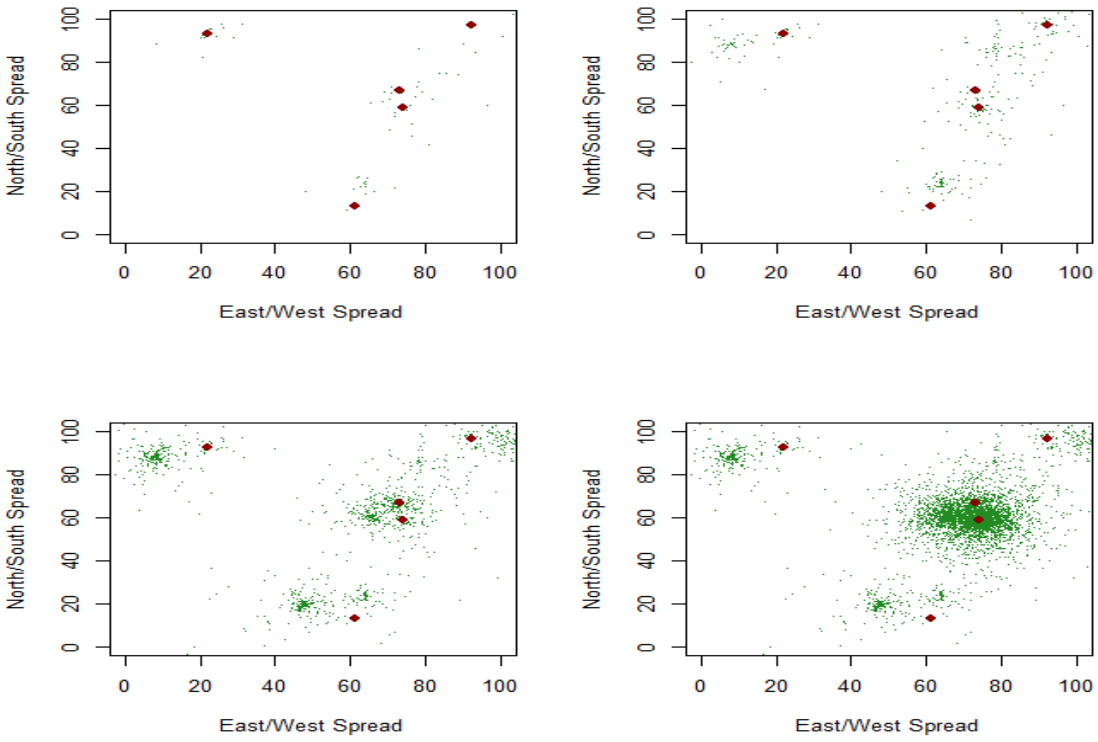

***Figure 2a**: Spatial spread of Ebola from generation 2 through generation 5 (top left to bottom right). Each plot is an iteration of the loop. Red points are the initial infected and green represents the concentration of infected individuals.*

contagious it is), will be the same for both diseases. As in the last model, vaccinations will not be considered in the spatial spread. Individuals are to spread according to their R_0 rate, and no vaccinations or death rates are considered.

```
set.seed(110)
gen <- 5                                    #generations
n <- 5                                      #initial infected
infect <- 3                                 #R_o
lam <- 0.15                                 #disease rate
loc <- matrix(round(runif(2*n, min=0, max=100),0),
              nrow=n, ncol=2)               #coordinates of initial infected

par(mfrow=c(2, 2))
ngrow <- n                                  #vector to store additional infected
for(i in 1:gen){

      ycoord <- loc[i*1:n, 2]               #north/south positions of infected
      xcoord <- loc[i*1:n, 1]               #east/west position of infected
      direction <- runif(infect*ngrow, -pi, pi)  #uniformly sampling θ
      spreaddistance <- rexp(infect*ngrow, lam)  #exponentially sampling r
      #new infected east/west position
      newinfectx <- xcoord + spreaddistance*cos(direction)
      #new infected north/south position
      newinfecty <- ycoord + spreaddistance*sin(direction)
      newcoord <- cbind(newinfectx, newinfecty)  #new coordinate of infected
      loc <- rbind(loc, newcoord)
    #for each generation a new plot is made
    if(i > 1){plot(loc, xlim=c(0, 100), ylim=c(0, 100),
                   xlab="East/West  Spread",
                   ylab="North/South Spread",
                   col="green", pch=".")
                   points(loc[1:n,1], loc[1:n,2],
                   col="darkred", pch=16)}
      #these plots are on a 100 by 100 grid and boundaries are taken care of
      #by restricting which points can actually be seen, therefore it is
      #possible for points to be generated off of the boundary

      ngrow <- length(loc[,1])              #the total infected to be
                                            #considered for the next
                                            #generation
      }
```

The important output generated from this model are the spatial plots for Ebola (Figure 2a) and the spatial plots for Measles (Figure 2b). The code for Measles is exactly the same, save for a few parameters changed to accommodate the disease type (see Appendix 2).

This really puts the numbers into visualized form. However, now with the density of the points, the critical zones of the disease can be realized. For this particular generated data, two initial infected people are quite close together, so the critical zone is even more magnified by how heavily dispersed the disease is. Also, with each generation it can be readily seen how quickly an epidemic needs to be controlled before it gets out of hand.

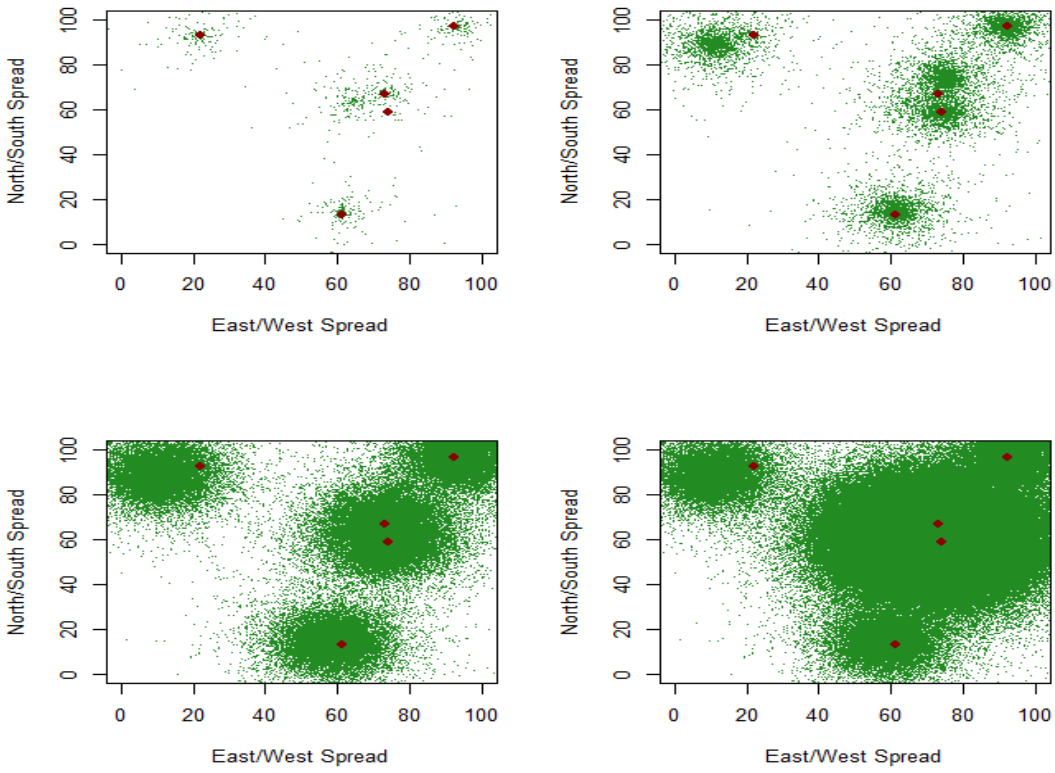

Figure 2b: Spatial spread of Measles. Red is the initial infected and green is the concentration of infected people. From the top left to bottom right: generation 2, 3, 4, 5. Areas are much more dense than Ebola.

Disease with Vaccination

In order to control these two diseases, now consider there is a state-of-the-art hospital that develops a vaccine to administer to carriers of Ebola or Measles. This will follow an M/M queue with infinite many states, S = {0, 1, 2, 3…} and will not produce negative states. There are two rates to be considered, the rate by which the disease is spread, λ_i (which in this case is the same

as R_0), and the rate of vaccination, μ_i. Both are greater than 0, describe the instantaneous change in state, and are proportional to the population of the i^{th} state (see Appendix 3a). The [i+1] state corresponds to a newly infected person while the [i-1] state will be someone who gets vaccinated. The time in each state will be distributed as EXP($\lambda_i + \mu_i$). In the case of Ebola the hospital has limited supply of vaccines for patients per day, thereby making $\lambda_i > \mu_i$. As such, this infinite capacity system will not actually have a steady-state. Realistically there is a finite population to the entire world, but the time frame is limited so only the short-term consequences will be examined.

```
lam <- 3/2                  #3 infections every 2 days, worst case scenario
mu <- 5/7                   #5 vaccinations per week
m <- 5000; x <- numeric(m); t <- numeric(m)
x[1] <- 5                   #initial infected
for(i in 2:m){
            tau <- x[i-1]*(lam + mu)
            #proportions of vaccine/infections in terms of population
            pr <- c(x[i-1]*mu, x[i-1]*lam)/tau
            #either jumping up or down a sate
            x[i] <- x[i-1] + sample(c(-1, 1), 1, prob=pr)
            #time elapsed
            t[i-1] <- rexp(1, tau)
      }
plot(c(0, cumsum(t)[1:100]), c(x[1], x[1:100]), xlab="Elapsed time",
      ylab="Infection Size", type="S")
mx <- max(x)
t.avg <- numeric(mx+1)
n <- 1:(mx+1)
for(j in n){
            #computing average time of being in each state
            t.avg[j] <- sum(t[x==(j-1)])/sum(t)
      }
L.sim <- sum((0:mx)*t.avg)
L.sim
[1] 355.6195            #average size of infected people
mx
[1] 1769                #maximum infected people
sum(t)
[1] 8.602051            #time elapsed
```

For the case of Measles, the code is very similar with a few changes to the parameters (see Appendix 3b). One major difference in the model are the rates, in that $\lambda_i < \mu_i$. By current day standards, vaccines for the Measles are much more available than that for Ebola, so the hospital can keep on top of the incoming patients. A new parameter is introduced, δ, which indicates that the hospital will take the overflow from other hospitals so that they still have patients to treat should they run out.

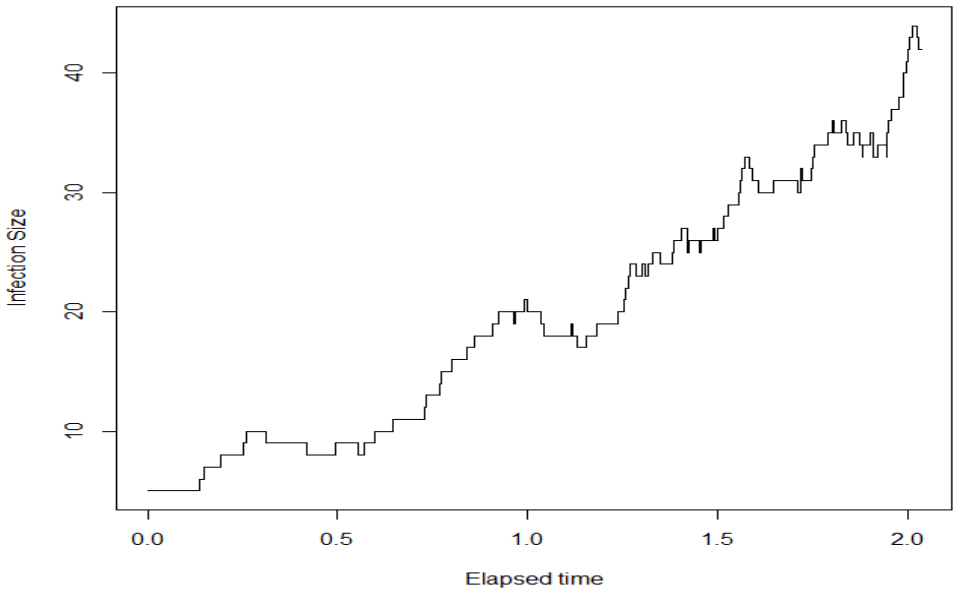

***Figure 3a**: Ebola's infection size against elapsed time. The ever-rising slope indicates that the while the vaccinations may try to keep up, if the disease is consistently spread then a true epidemic will happen.*

```
L.sim
[1] 1.415137            #average size of infected people
mx
[1] 16                  #maximum infected people
sum(t)
[1] 169.9036            #time elapsed
```

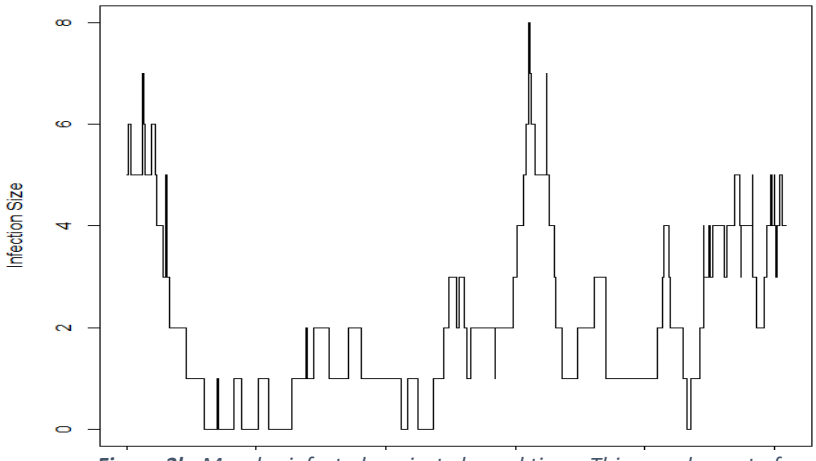

***Figure 3b**: Measles infected against elapsed time. This spends most of it's time well below the rate of infection, 12 people every 4 days. The disease does not appear to get out of hand.*

The two results differ vastly. In the case of Ebola, the vaccines cannot keep up with those infected. This is due to the expensive costs for making the vaccine even by today's current standards. This is virtually why there will always be a growing number of cases as seen in the time series plot (Figure 3a). However in Figure 3b, it would seem that Measles is easily contained with the steady vaccination

supply, and even with the constant flow of patients from other hospitals. In fact, with 16 patients as the maximum amount of infected patients at one time, 62.5% of them come from the overflow. With the average size of infected people being under 2, it's obvious that this hospital can keep the disease well under control. With Ebola, the results speak a much different story.

4.

Concluding Remarks. Between Ebola and the Measles, there are many things to consider. Their rate of spreading from person to person, how deadly they are, and how easily they can be contained. While Measles spreads more rapidly (do to its Airborne means of transmitting), the trade-off is that a smaller proportion of the population is expected to die from the disease, whereas Ebola is just the opposite. However, with current practices (in America), Measles can be contained. Ebola, unless quarantined or infected patients are cured almost immediately, can take off in just a few generations of the disease bringing a severe death toll with it. The gravity of this matter speaks for why quick action is needed if someone has the disease. Hopefully these simulations can shed some light on why epidemics can be a serious problem should they be left unchecked.

Bibliography

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Appendix

1.

a.

```
infectcount.me <- c()
t.me <- numeric(m)
infectcount.me[1] <- 5
infect.me <- 12              #same functionality, changes are in red
deathcount.me <- numeric(m)

for(i in 2:m){
         incu <- sample(10:12, 1) #incubation
         deathtime <- sample(4:7, 1) #someone dies 70% chance
                                     #this happens
         deaths <- sum(sample(c(1, 0), infectcount.me[i-1],
                   pr=c(0.1, 0.9), repl=T))
         deathcount.me[i] <- deaths
         infectcount.me[i] <- infectcount.me[i-1]*infect.me - deaths
         t.me[i] <- incu + deathtime
   }
```

b.

```
plot(cumsum(t.eb), infectcount.eb, xlab="Time in Days",
ylab="infected", type="S")
plot(cumsum(t.eb), deathcount.eb, xlab="Time in Days", ylab="dead",
type="S")
#plots for Ebola
```

c.

```
plot(cumsum(t.me), infectcount.me, xlab="Time in Days",
ylab="infected", type="S")
plot(cumsum(t.me), deathcount.me, xlab="Time in Days", ylab="dead",
type="S")
#plots for Measles
```

2.

```
set.seed(110)
gen <- 5
n <- 5
infect <- 12            #same functionality, changes are in red
lam <- 0.15
loc <- matrix(round(runif(2*n, min=0, max=100),0), nrow=n, ncol=2)
par(mfrow=c(2, 2))

ngrow <- n
for(i in 1:gen){

         ycoord <- loc[i*1:n, 2]
         xcoord <- loc[i*1:n, 1]
         direction <- runif(infect*ngrow, -pi, pi)
         spreaddistance <- rexp(infect*ngrow, lam)
```

```
            newinfectx <- xcoord + spreaddistance*cos(direction)
            newinfecty <- ycoord + spreaddistance*sin(direction)
            newcoord <- cbind(newinfectx, newinfecty)
            loc <- rbind(loc, newcoord)
      if(i > 1){plot(loc, xlim=c(0, 100), ylim=c(0, 100),
                     xlab="East/West Spread",
                     ylab="North/South Spread", col="forestgreen",
                     pch=".")
                     points(loc[1:n,1], loc[1:n,2], col="darkred",
                     pch=16)}

      ngrow <- length(loc[,1])
      }
```

3.

a. **Probability for Infection:** $\frac{\lambda_i}{(\lambda_i + \mu_i)}$ **Probability for Vaccination:** $\frac{\mu_i}{(\lambda_i + \mu_i)}$

b.
```
lam <- 12/4                  #same functionality, changes are in red
mu <- 10
dlt <- 10
m <- 5000
x <- numeric(m)
t <- numeric(m)
x[1] <- 5
for(i in 2:m){
         if(x[i-1]==0) {tau <- dlt
                        x[i] <- 1}
         if(x[i-1]>=1) {tau <- dlt + x[i-1]*(lam + mu)
                        pr <- c(x[i-1]*mu, dlt + x[i-1]*lam)/tau
                        x[i] <- x[i-1] + sample(c(-1, 1), 1,
prob=pr)}
         t[i-1] <- rexp(1, tau)
   }
plot(c(0, cumsum(t)[1:100]), c(x[1], x[1:100]), xlab="Elapsed time",
   ylab="Infection Size", type="S")
mx <- max(x)
t.avg <- numeric(mx+1)
n <- 1:(mx+1)
for(j in n){
         t.avg[j] <- sum(t[x==(j-1)])/sum(t)
   }
L.sim <- sum((0:mx)*t.avg)
```