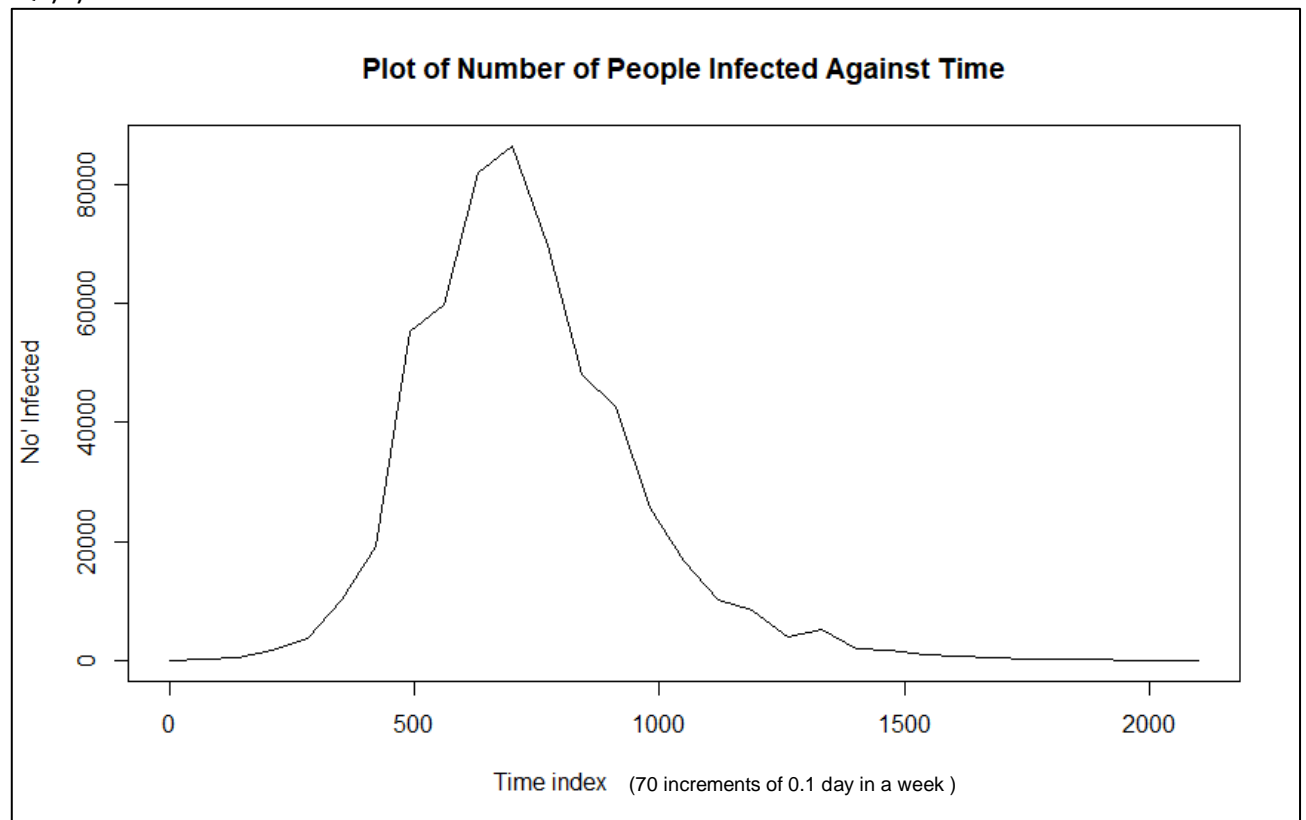


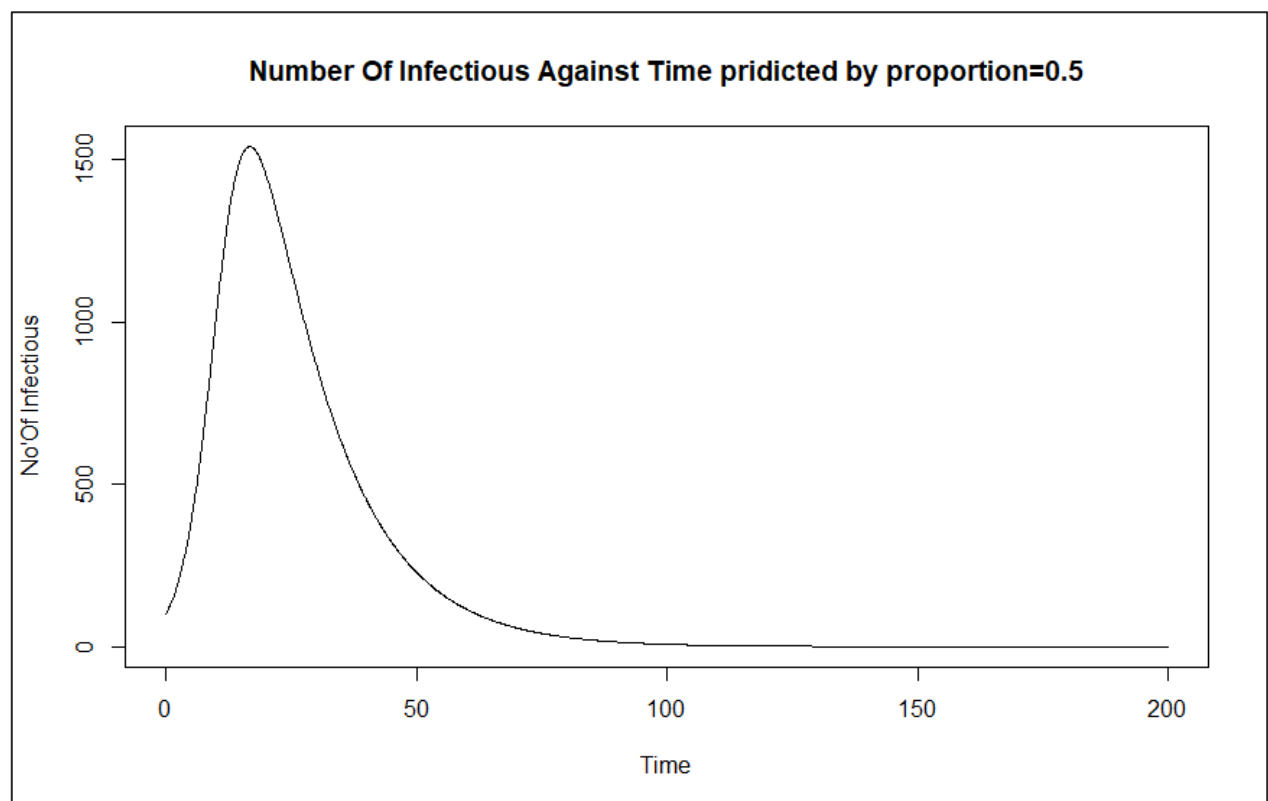
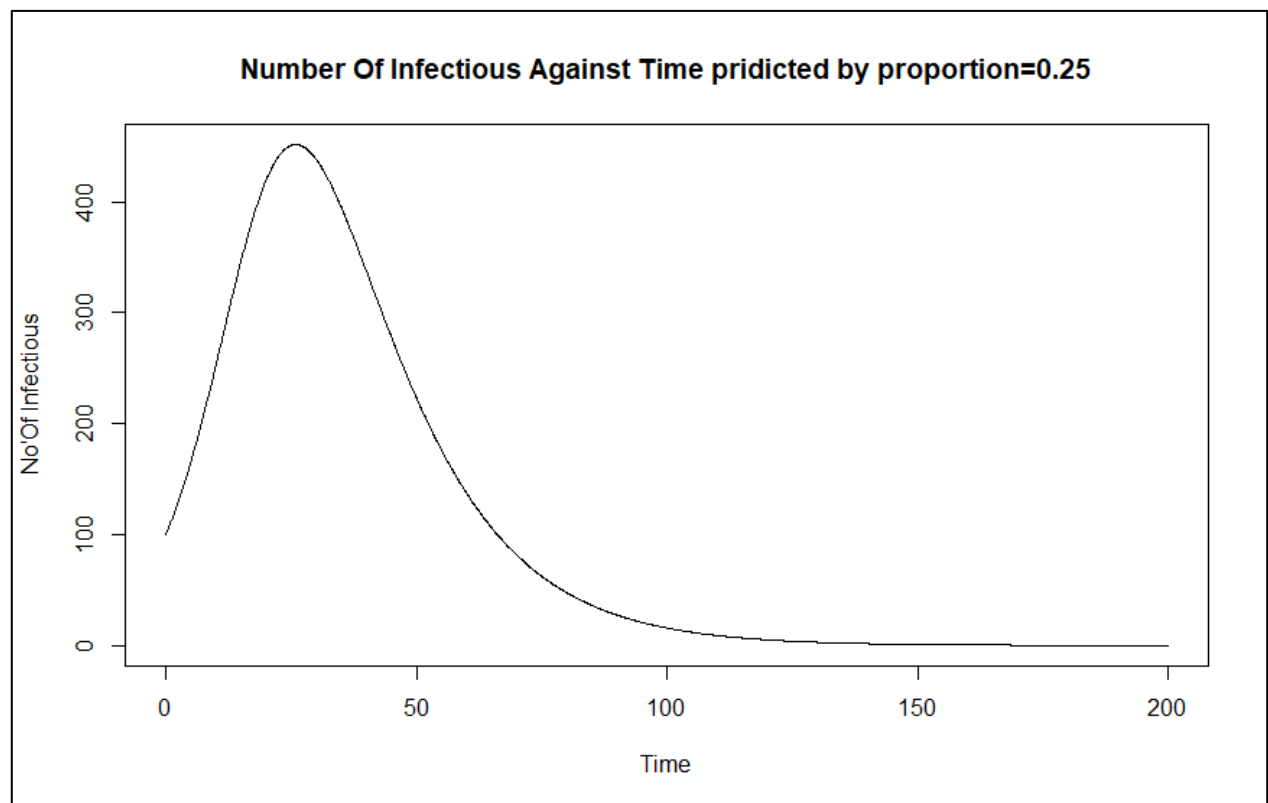
MA35210 Topics In Biological Statistics
Epidemiology Workbook

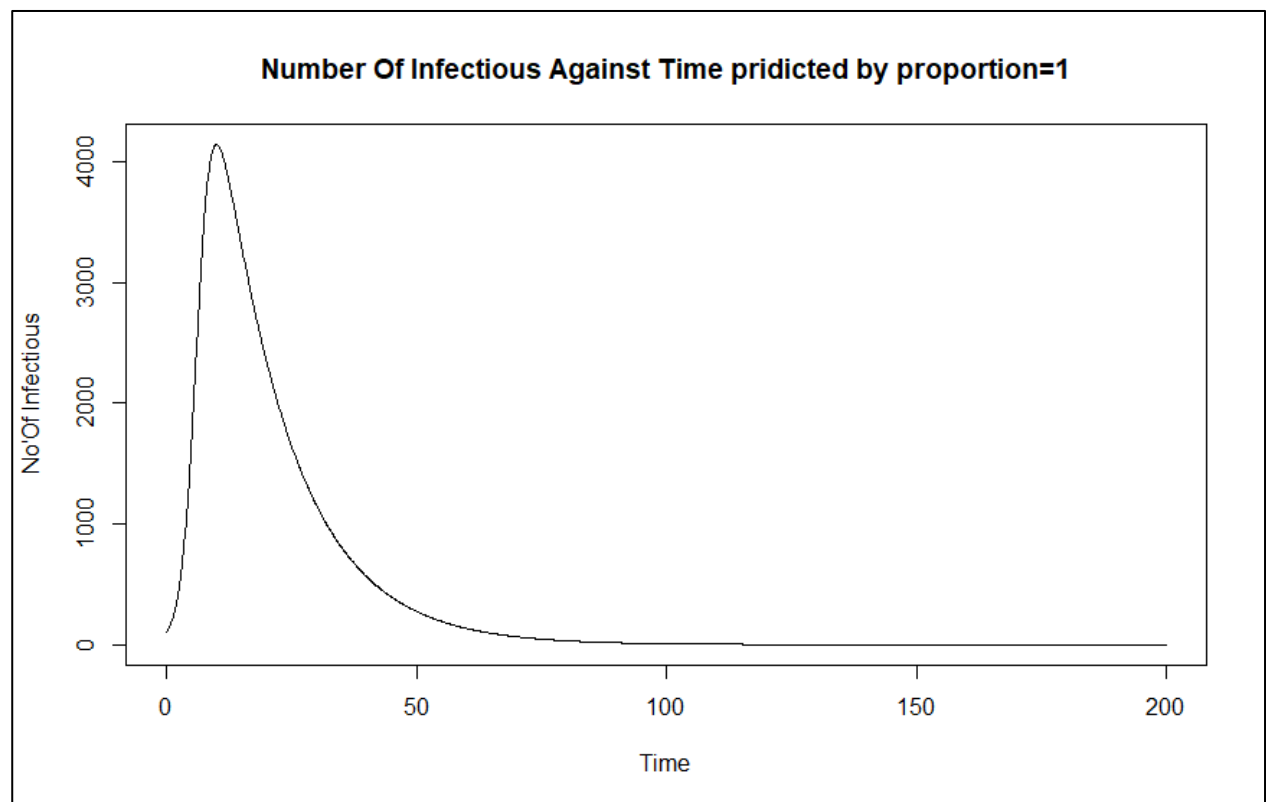
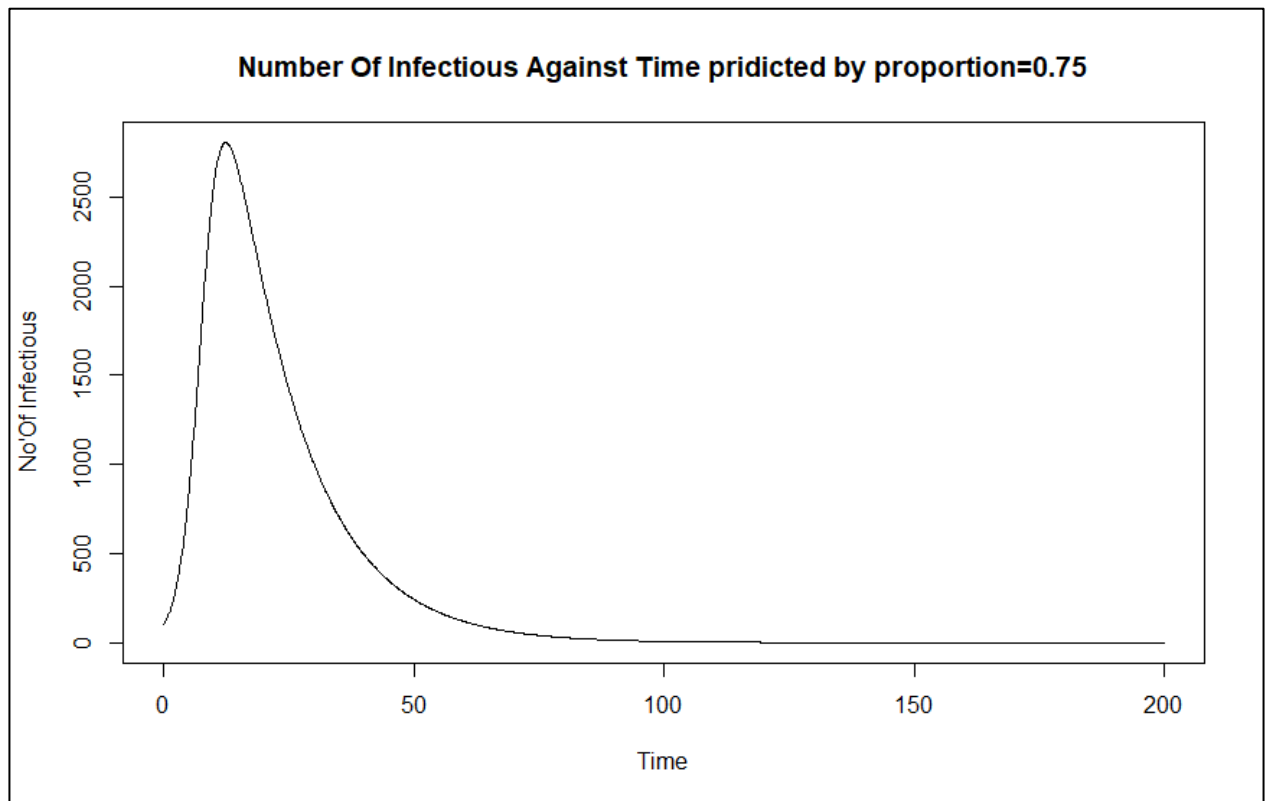
Q2)a)



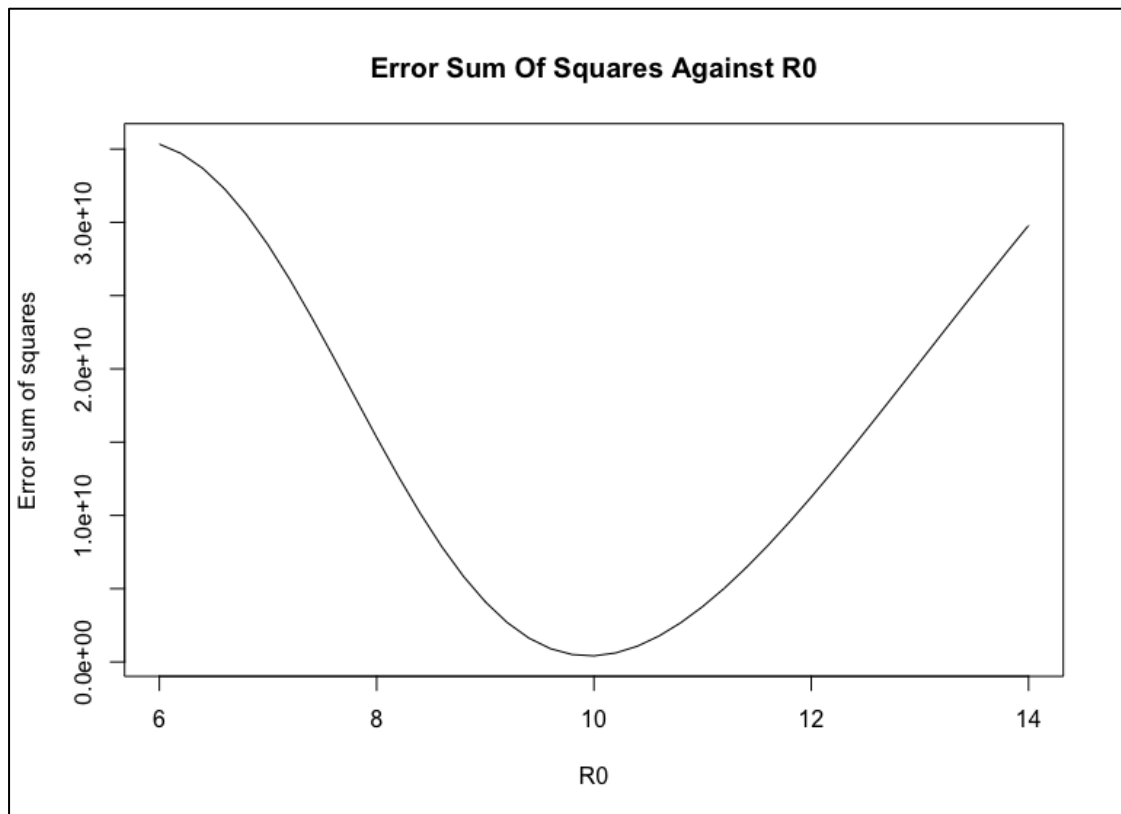
We can see from the graph that there is a very small increase in the number of infected for about 12.5 days. For the next 40 days after the initial infected are introduced into the population there is a gradual climb in the number of infected in the population, to about 1.5% of the entire population. In the proceeding 35 days the number of infected in the population sharply increases by over five times the number of infected from before to the maximum number infected during the 30 week period, 8.5% of the population (roughly 85,000 people). After this there is a slightly less sharp decline in infected numbers for the next 50 resulting in only a small number of the population still being infected. For the final 70 days that can be seen on the graph there is a very gradual decrease in the number of infected until it drops down to a relatively infinitesimal number of infected, indicating the disease has almost died out in the population.

b)





c)

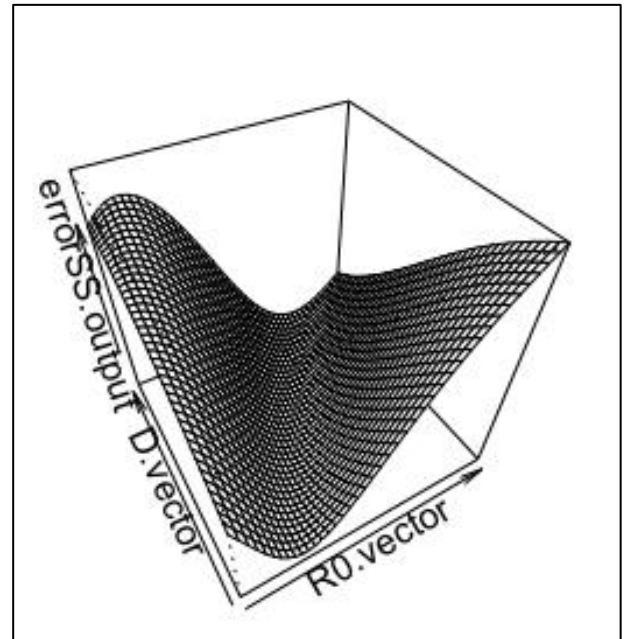


The plot shows that the error sum of squares and R_0 has a non-symmetric quadratic relationship with the Minimum value of R_0 being 10.

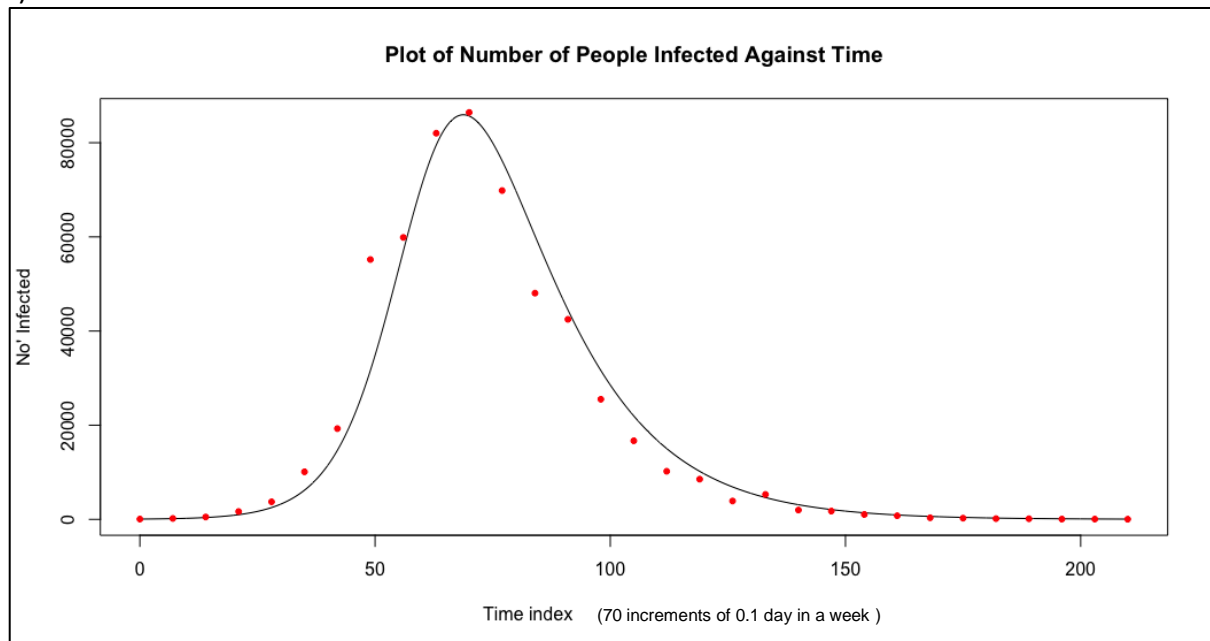
Taking Logarithms is valid in this case as using logarithms on this data helps to get a better regression model allowing us to see the relationship between the variables better.

d) The minimum error sum of squares obtained was 19.7644893 when $R_0 = 9.6$ and $D = 13.8$

e) If we were to break this plot down into comparing individual relationships it is easier to view what is happening. We can start off by observing the relationship between the error sum of squares and the basic reproduction number, which is a non-symmetric quadratic relationship. The relationship between R_0 (the number of cases of one case generates on average over the course of its infectious period) against days is a positive correlation whilst the relationship between the error sum of squares and number of days is a negative correlation.



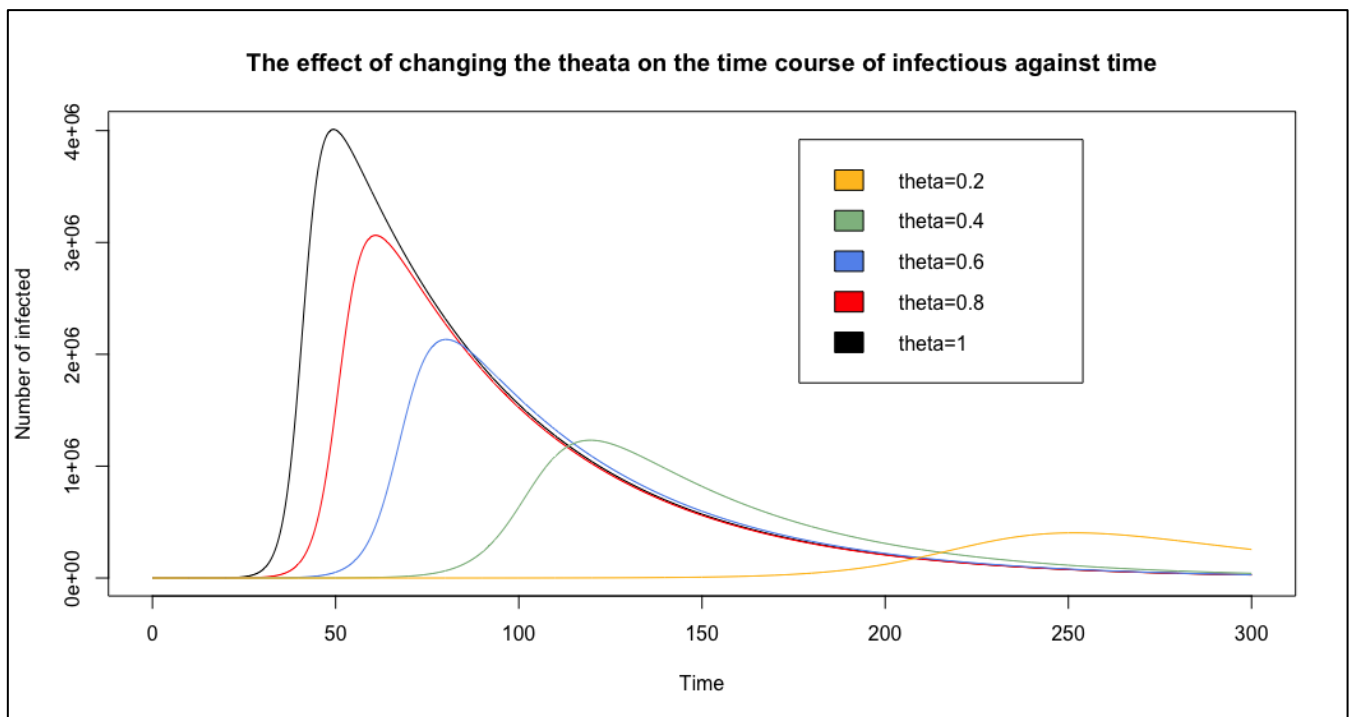
f)



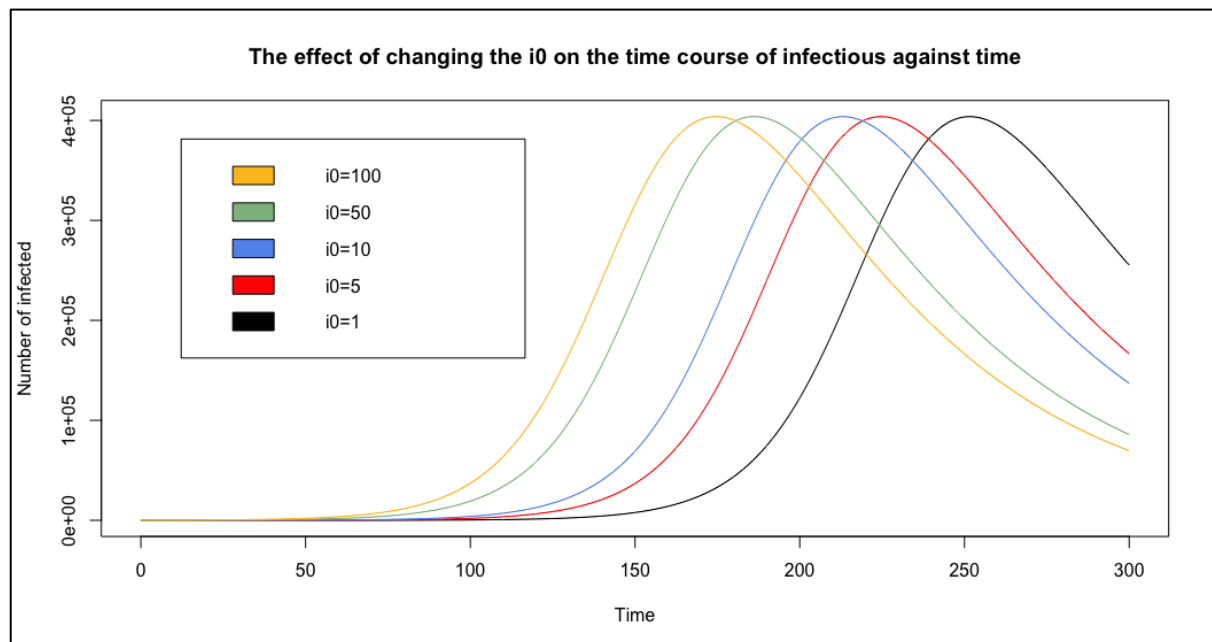
This graph shows the change of infection over 30 weeks, it shows a negative quadratic relationship between the number of infectious and time. There is a steep growth in the number of infected over the first 10 weeks until the infected numbers stop rising and start falling once reaching the maximum infected at 82,500 individuals. Then there is a more gradual decline in the number of infected till the infection dies out significantly. From week six to seven there is such a steep increase in the number infected that the seventh data point becomes an outlier from the curve.

Q3)a) $\beta = 0.0000004$ as $\beta = \mu N$

b)



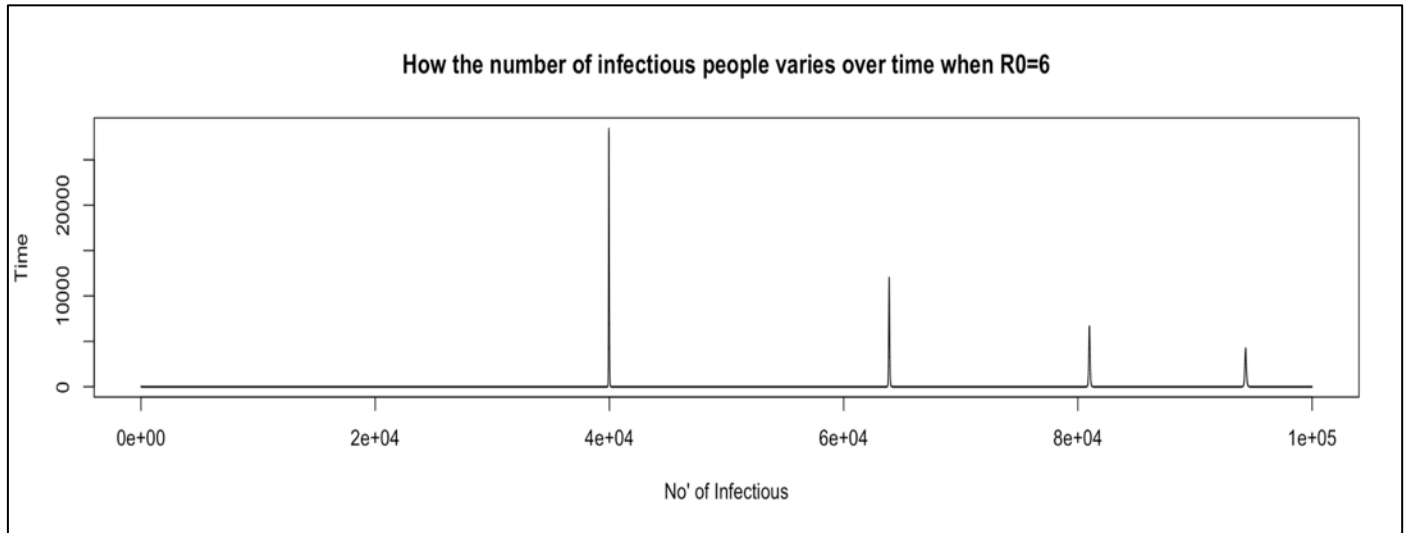
We can observe from the above plot that as the theta value decrease the maximum number of infected during the given time also decreases in value. We also can observe that the time taken to reach the maximum number of infected increases as the theta decreases in value.



We can observe from the above plot that as the i0 value decreases the time taken to reach the maximum number of infected increases however the i0 value has no effect on the maximum value of infected that is reached.

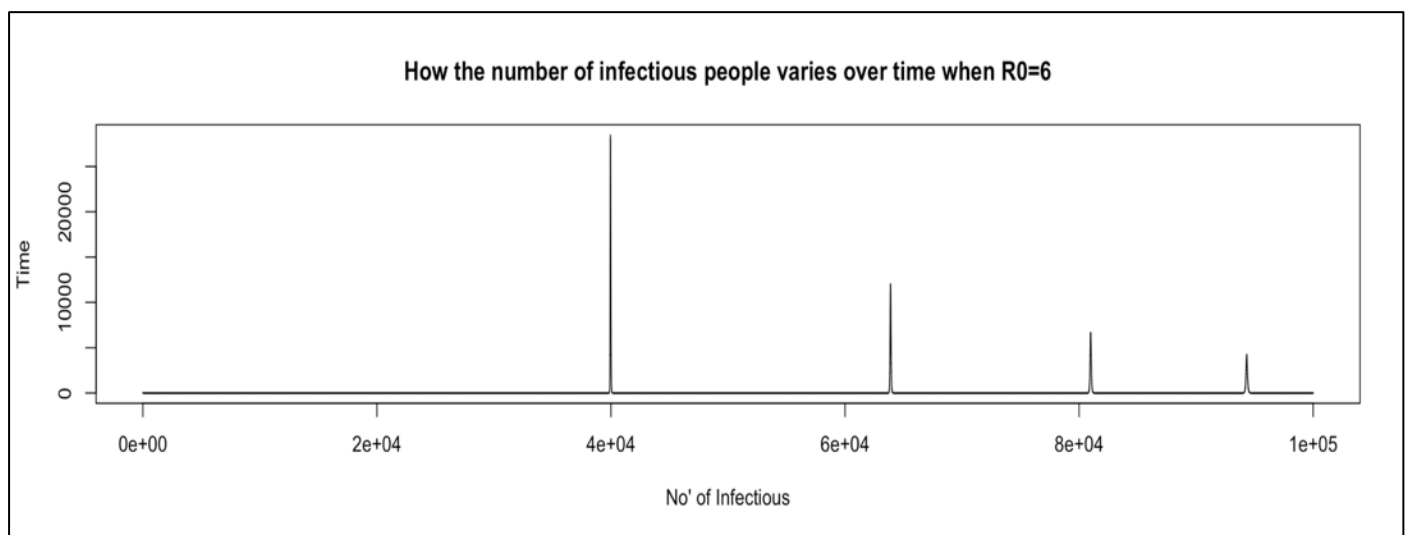
Q4) a) B =Births per unit time, βSI = Number of encounters resulting in infection, μS = Number of encounters resulting in Death

b)

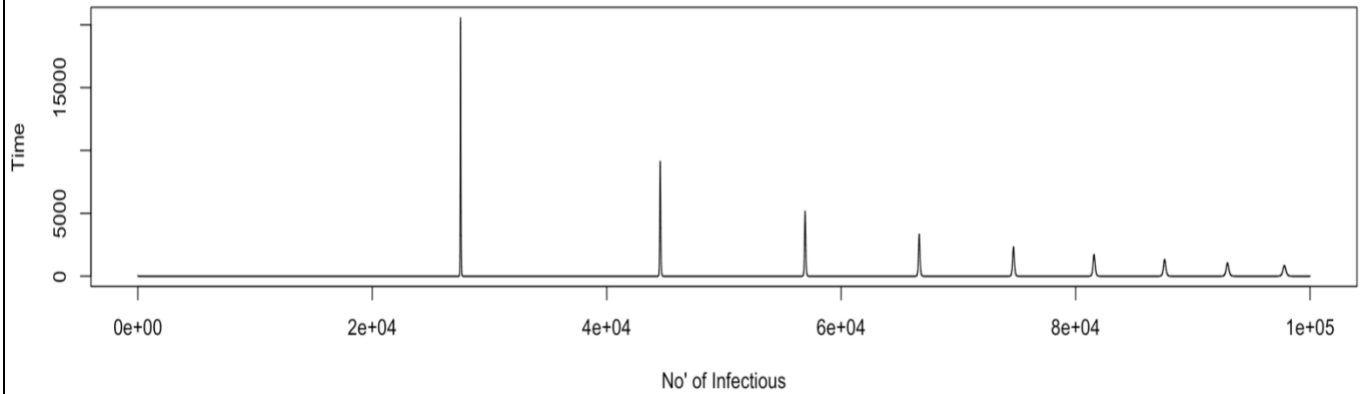


This graph shows that as the maximum value of infected decreases in value the time taken to reach the diseases maximum value increases. We can also observe that the difference in maximum value of infected increases as time decreases.

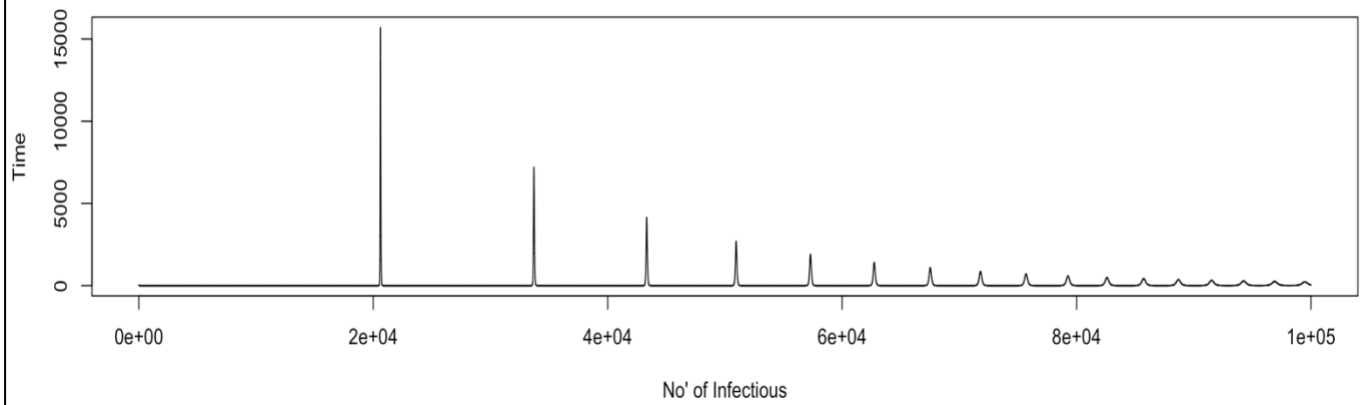
c)



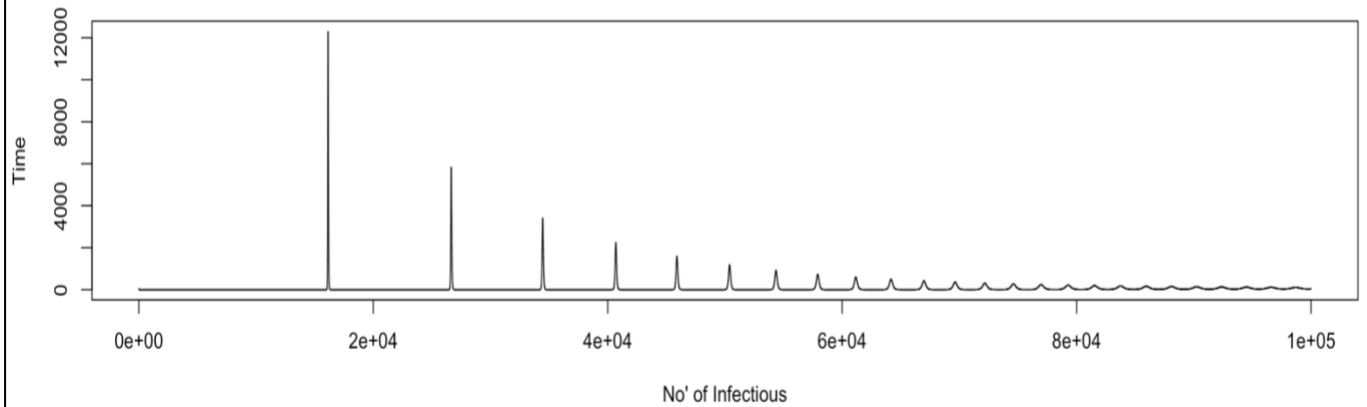
How the number of infectious people varies over time when $R_0=8$



How the number of infectious people varies over time when $R_0=10$

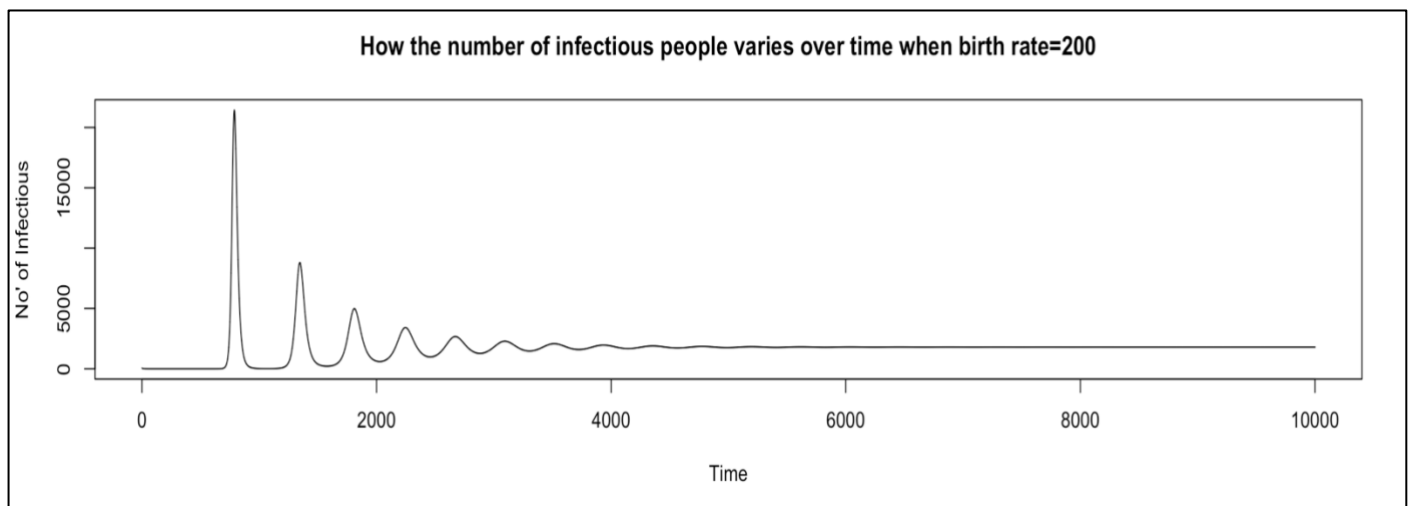
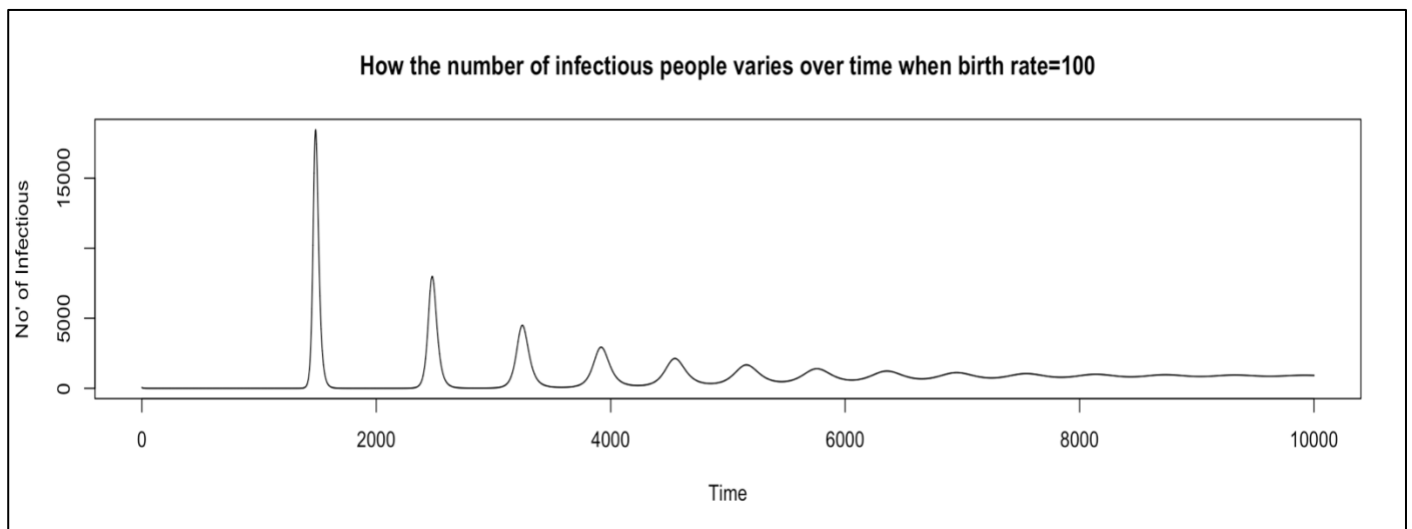


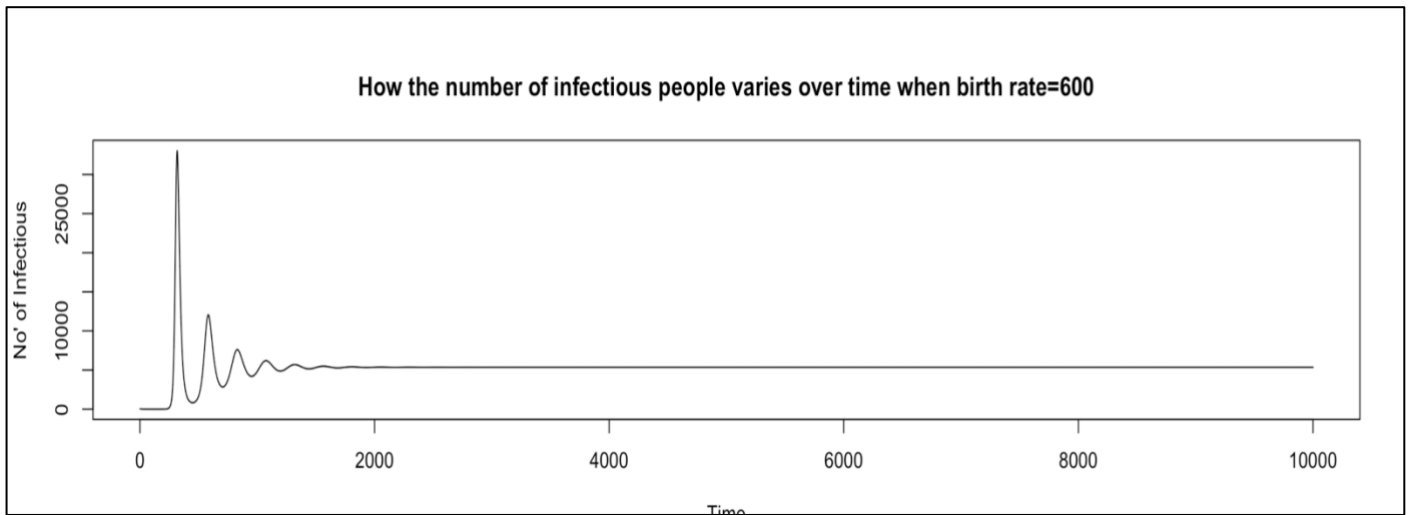
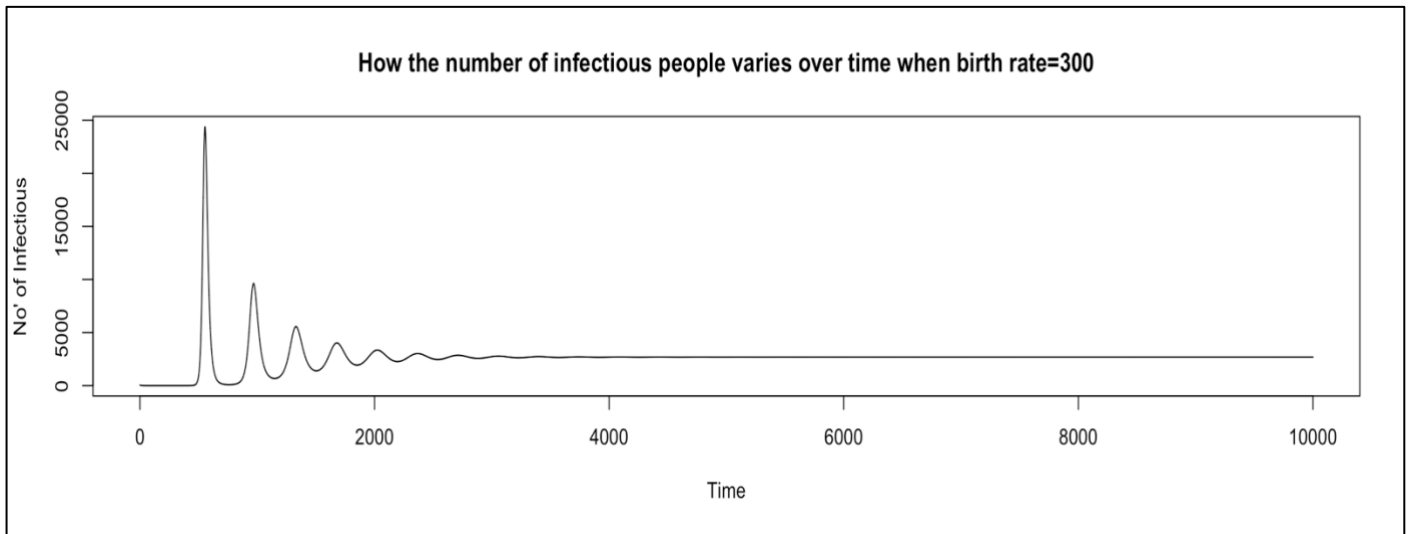
How the number of infectious people varies over time when $R_0=12$



As the R_0 value, the basic reproduction number, increases the peaks in the graphs shift to the left, meaning there is a smaller maximum number of infected each time the population becomes infected with this disease. The space between the peaks also decreases as the basic reproduction number increases, meaning the change in the value of the maximum number of infected during an infection period becomes less each time the population becomes infected. Finally the heights of the peaks decrease as the basic reproduction number increases, meaning the time period before reaching the maximum number of infected becomes smaller.

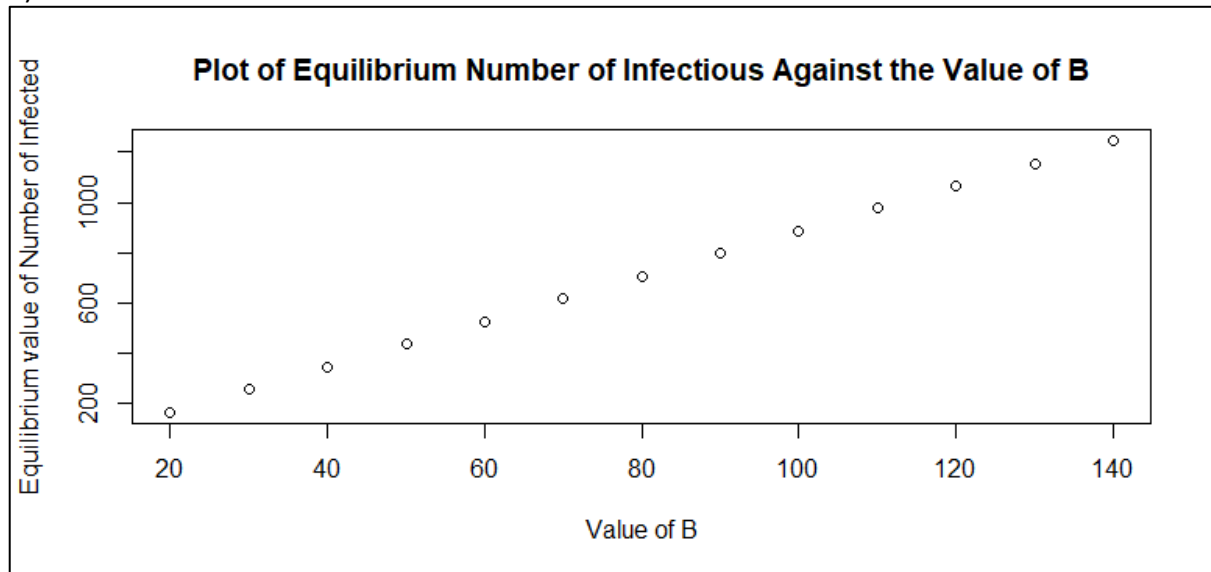
d)





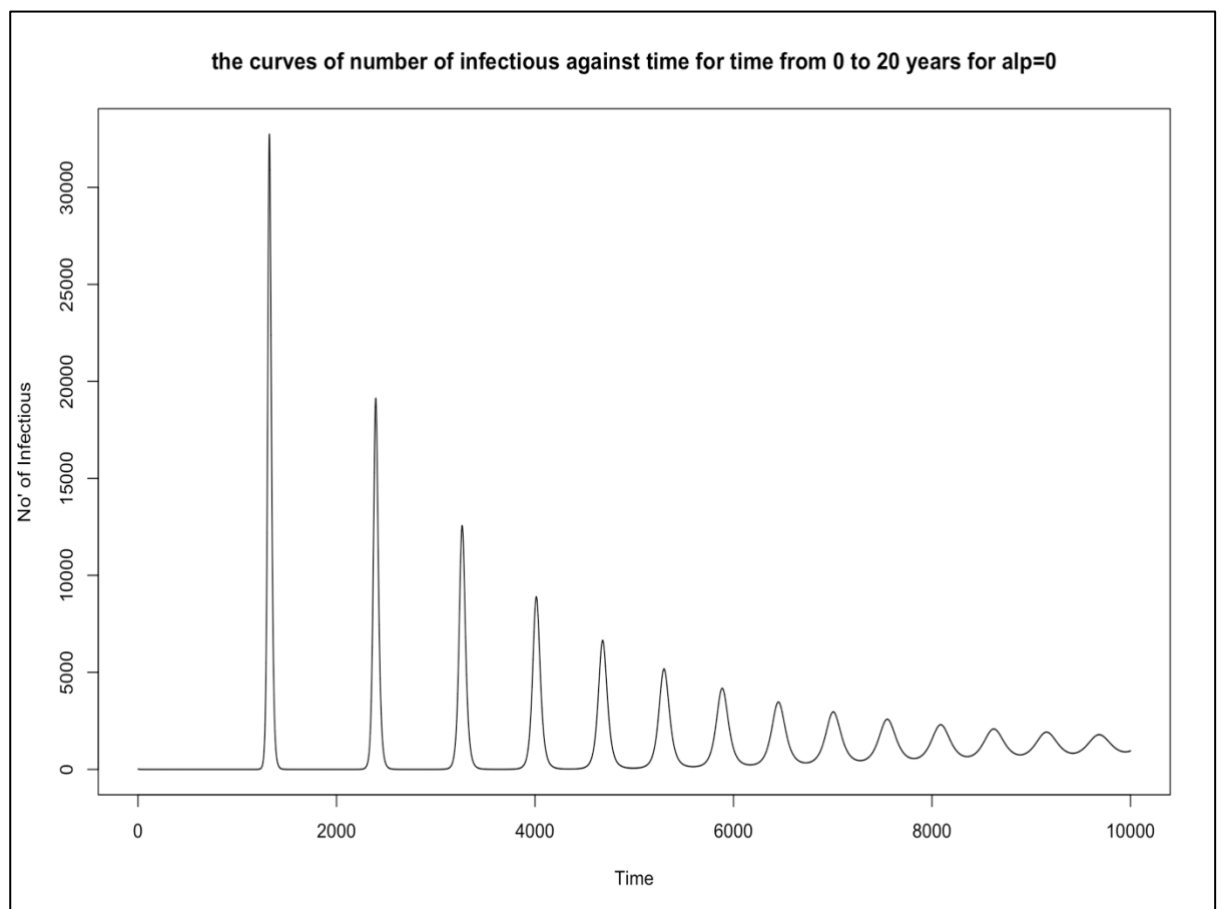
Four observations can be made from comparing these graphs, first is that the outbreaks occur and die out over shorter periods of time as the birth rates increase. We can also observe that the outbreak cycles happen more rapidly (shorter time between each epidemic) as the birth rate increases. As the birth-rate increases the number of major outbreaks decreases as the graph plateaus with fewer peaks. As the birth rate increases the maximum values of the number of infectious increases.

e)

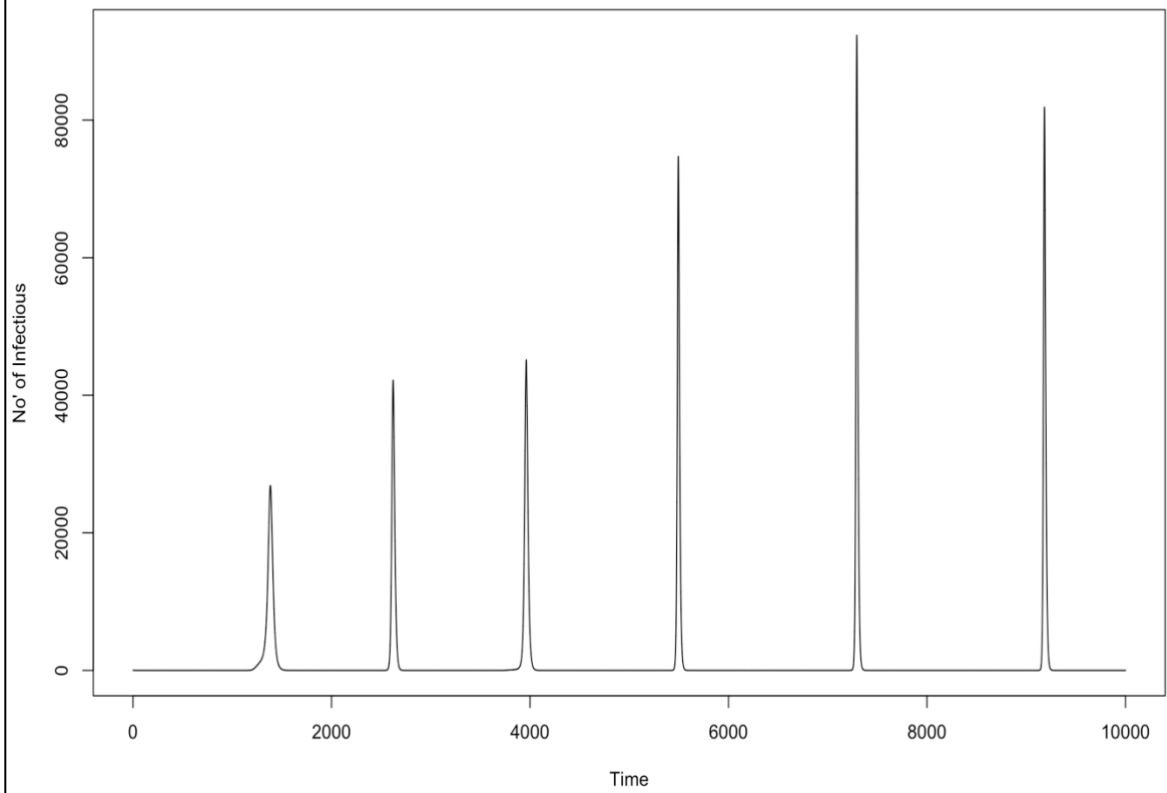


From this graph we can see there is a positive correlation between the equilibrium value of number of infected and the birth rate.

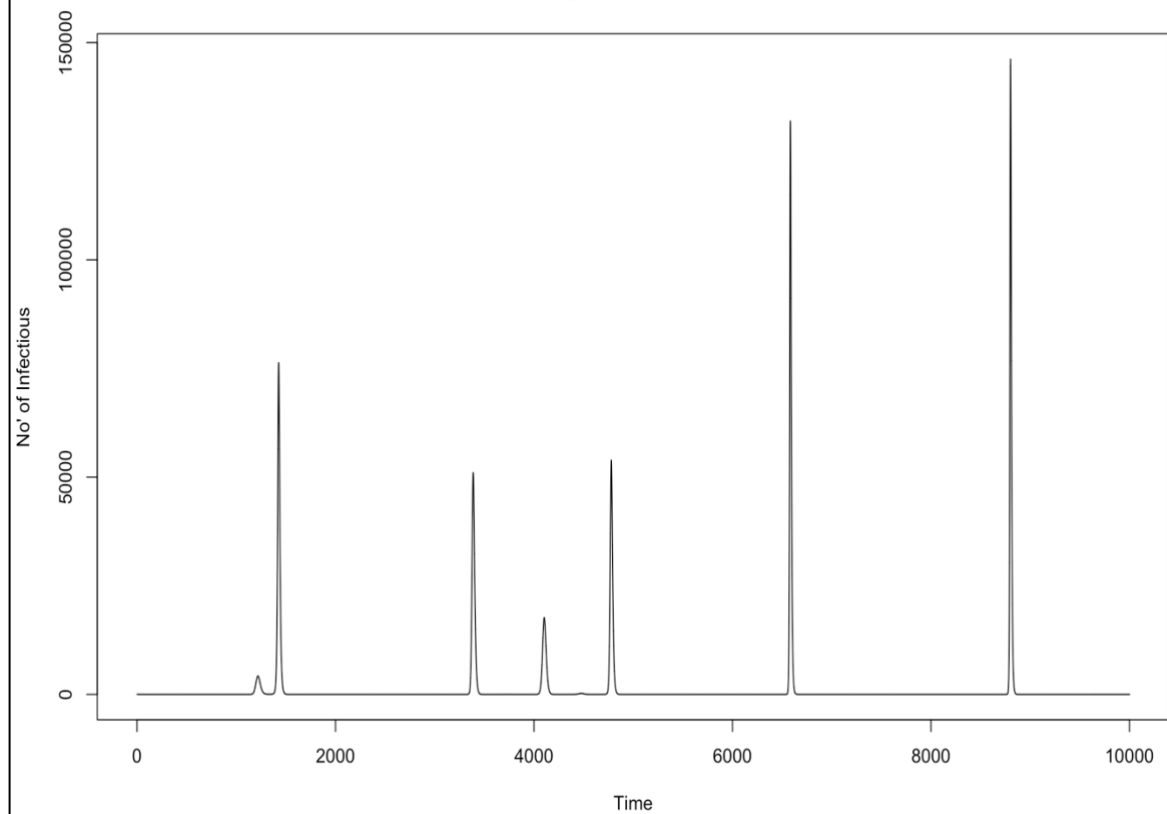
Q5)

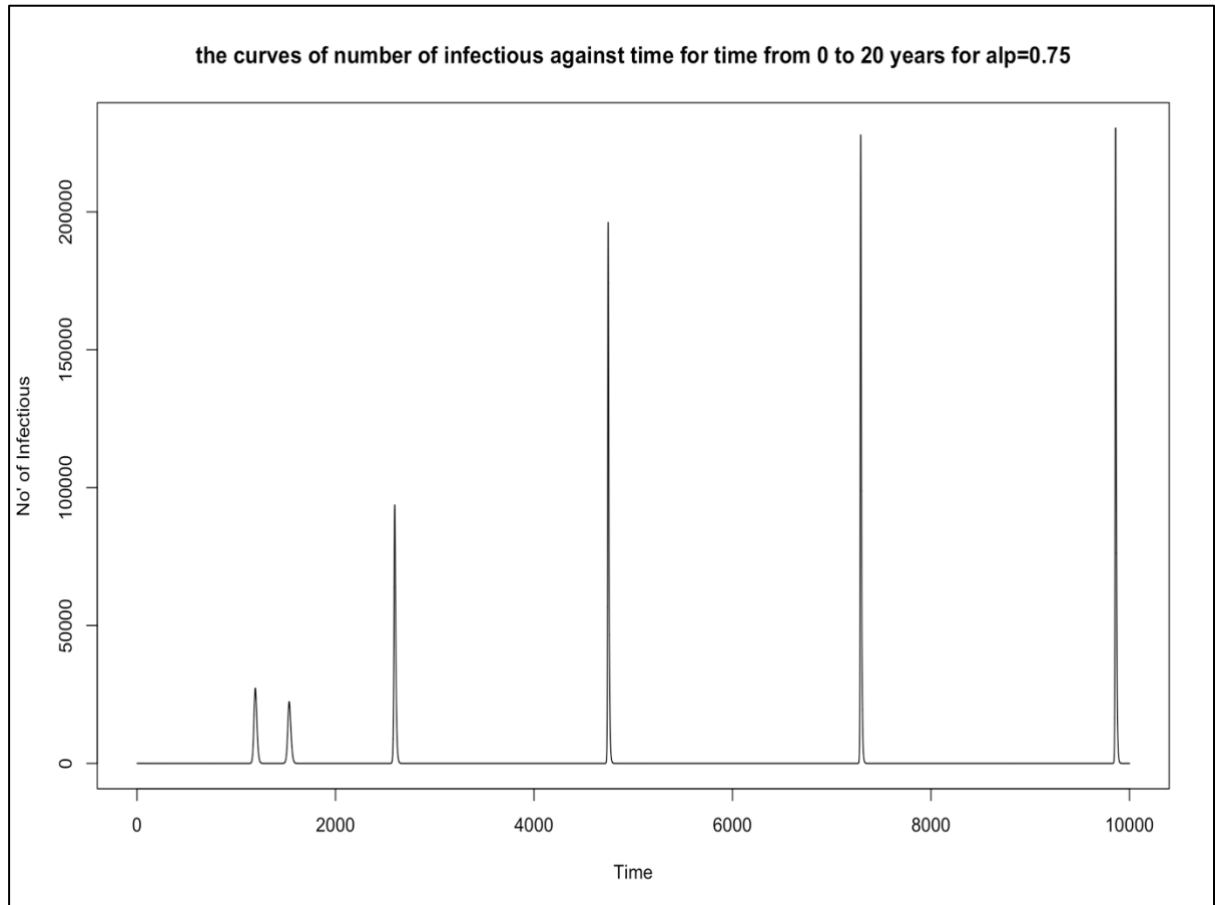


the curves of number of infectious against time for time from 0 to 20 years for $\alpha p=0.25$



the curves of number of infectious against time for time from 0 to 20 years for $\alpha p=0.5$





```

1  #Q5)
2  N.time.steps<-3000
3  ~ generate.S.I.by.time.vital.dynamics.seasonal.forcing<- function(N.time.steps,delta.t=0.1,S0=200000,I0=50/3,R0=14,gamma=0.2,mu=1/18250,N=500000,alpha=0){
4  S<-numeric(N.time.steps+1)
5  I<-numeric(N.time.steps+1)
6  S[1]<-S0
7  I[1]<-I0
8  beta0<-R0*gamma/N
9  alp<-0.75
10 ~ for (i in 1:(N.time.steps)){
11   betat<-beta0*(1+alp*cos(2*pi*(i/(365*10))))
12   S[i+1]<-S[i]+mu*N*delta.t-betat*S[i]*I[i]*delta.t- mu*S[i]*delta.t
13   I[i+1]<-I[i]+betat*S[i]*I[i]*delta.t-gamma*I[i]*delta.t- mu*I[i]*delta.t
14 }
15 time.vector<-seq(0,N.time.steps*delta.t,by=delta.t)
16 out<-list(S=S,I=I,time.vector=time.vector)
17 return(out)
18 }
19
20 #plot(time.vector,I,type="l",xlab="Time",ylab="No' of Infectious", main = "How the number of infectious people varies over time")
21
22 temp1<-generate.S.I.by.time.vital.dynamics.seasonal.forcing(100000)
23 plot(temp1$time.vector,temp1$I,type="l",xlab="Time",ylab="No' of Infectious", main = "the curves of number of infectious against time for time from 0 to 20 years for a
24
25

```

Megan Thompson

