

Stephen Hanna

What is the doubling time of rabbits without predation?

$$1. N(t, prey) = (N0) * e^{(R0)*t}$$

Assuming an initial population of 1 and $(R0) = .04$

$$2 = e^{.04*t} \quad \ln(2) = .04 * t \quad t = 17.33 \text{ days} = \text{doubling time without predation}$$

(1) What is the death rate of foxes without predation

$$\frac{d(N, predator)}{dt} = -(R0) * N(t)$$

Assuming $(R0) = .2$

The death rate of foxes is .2 times the population at any given moment in time.

The doubling time of rabbits without predation isn't biologically reasonable because rabbits would quickly reach a limiting capacity due to their environment, if not due to predation. The death rate of foxes isn't biologically reasonable because, without prey, they would die off much faster and, with an alternative source of prey, might not die off at all.

(2) Explain the meaning of the terms γ and ϵ and consider their values — do these make sense (consider what conditions will lead to a balance of growth/death in each population)?

3. γ is the predation constant and ϵ describes the relationship between predation rate and predator growth. The given values make sense because the population required for the oscillatory stable point of prey is

$$\frac{R0, predator}{\gamma * \epsilon} = \frac{.2}{.1 * .0005} = 4000$$

The population required for the oscillatory stable point of predator is

$$\frac{\alpha}{\gamma} = \frac{.04}{.0005} = 80$$

So the number of prey for each predator is $\frac{4000}{80} = 50$ which makes sense in my opinion.

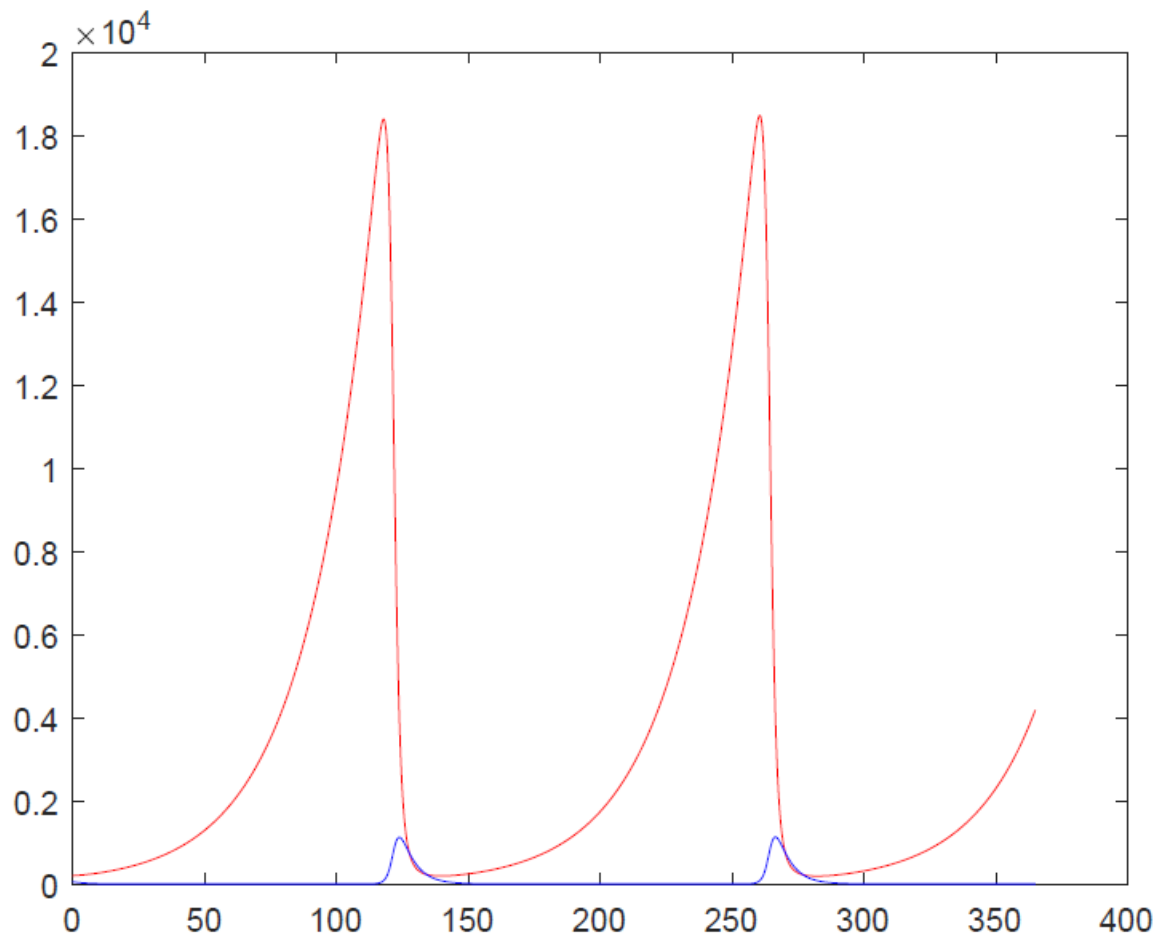
- (3) Using initial populations of 200 rabbits and 50 foxes per km^2 , and a time step of 0.01 days, determine how the rabbit and fox populations will vary over one year. Plot the two populations versus time on the same graph, as well as versus each other (on another graph). Discuss the observed behavior of the populations. What is the range in each population? Do you notice anything odd

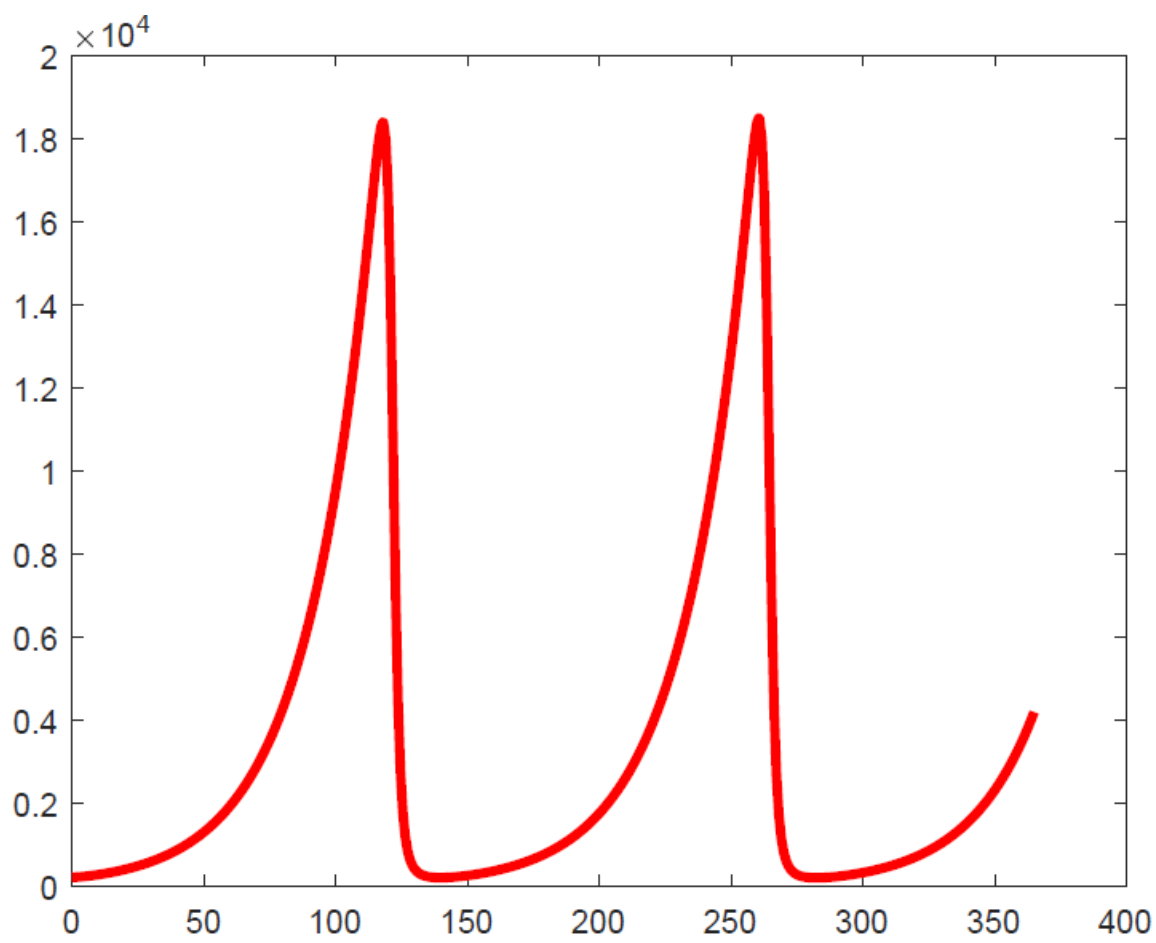
4. Code:

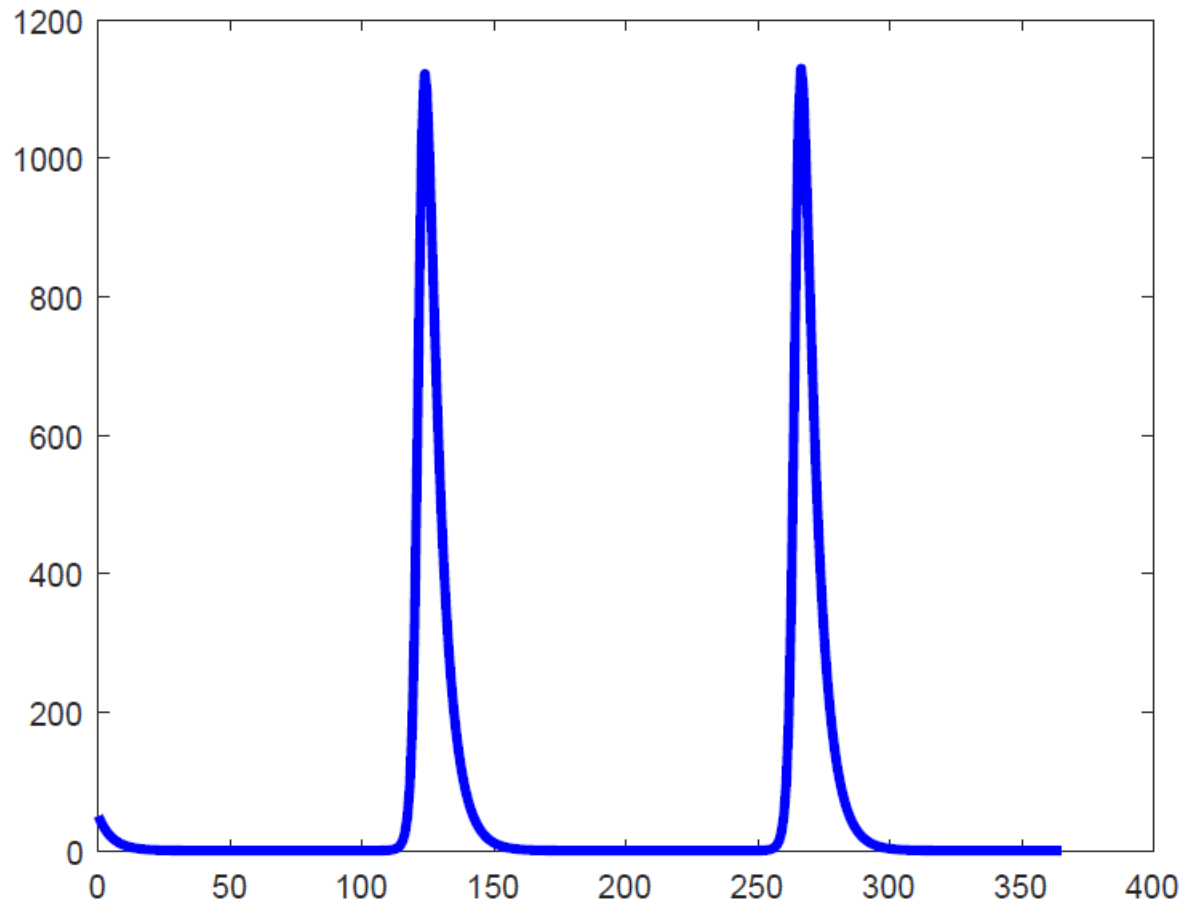
```
%This program uses the forward euler method to create 3
graphs representing the
%predator and prey populations
a = 0:.01:365;
%This creates a vector for the time that has passed
b1 = zeros(1,36501);
b2 = zeros(1,36501);
%This initializes a vector for the population values
b1(1) = 200;
b2(1) = 50;
%This sets the initial population
for i = 2:36501
    x = (.04*(b1(i-1))-.0005*(b1(i-1))*(b2(i-1)))*.01;
    y = (.1*.0005*(b1(i-1))*(b2(i-1))-.2*(b2(i-1)))*.01;
    %This finds the product of the derivative and the
interval of time
    b1(i) = (b1(i-1))+x;
    b2(i) = (b2(i-1))+y;
    %This sums the i-1 value and the derivative times the
interval of time.
end
%This loop inputs values for a vector for the number of
yeast cells after a
%given time interval
fig1 = figure(1);
plot(a,b1,'-r',a,b2,'-b')
fig2 = figure(2);
plot(a,b1,'-r','LineWidth',3.0)
fig3 = figure(3);
plot(a,b2,'-b','LineWidth',3.0)
%This creates all plots with the requested parameters
%and changes the handle of the plotted figures to fig1,2,
and 3
print(fig1,'ForwardEulerPredvsPrey','-dpdf')
```

```
print(fig2,'ForwardEulerPrey','-dpdf')
print(fig3,'ForwardEulerPred','-dpdf')
%This saves the figures as a pdf
```

Execution



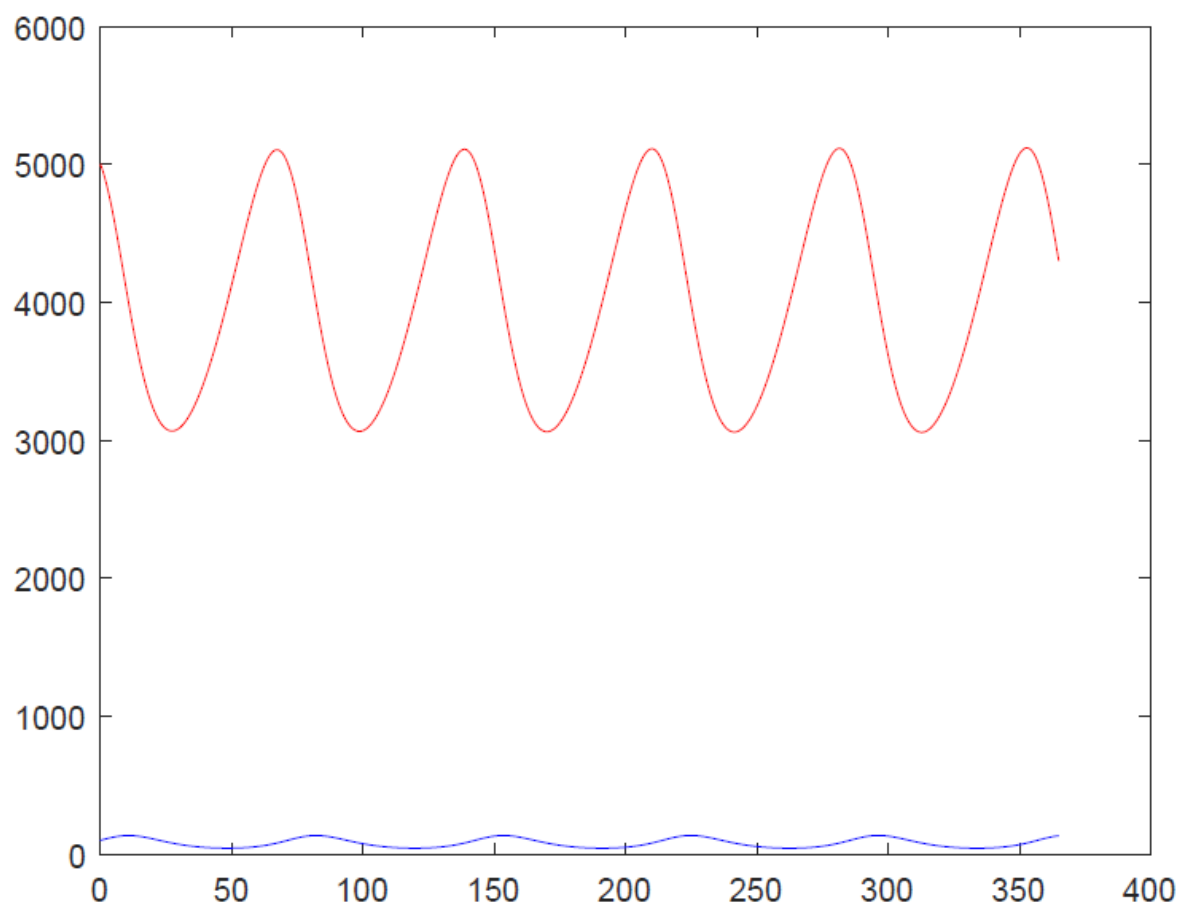


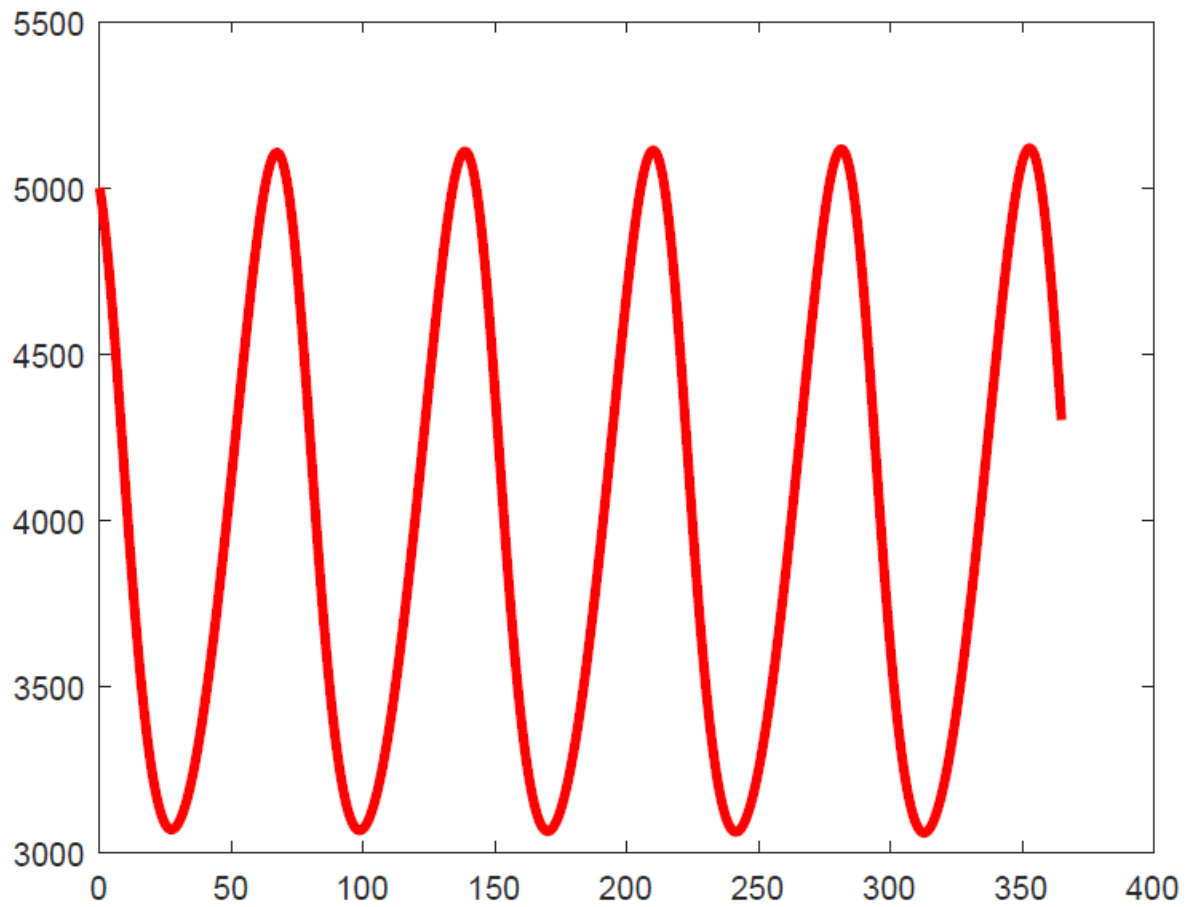


The observed behavior is oscillatory, and matches the behavior around the second stationary point according to the Lotka- Volterra model. The range of the predator population is 1100 and the range of the prey population is approximately $1.8 \cdot 10^4$. Something that seems odd to me is that the populations are both driven to near extinction at different points in time, whilst I imagine both populations would be fairly more resilient and stable. Additionally, the population vary wildly in size, going from an extreme minimum to an extreme maximum.

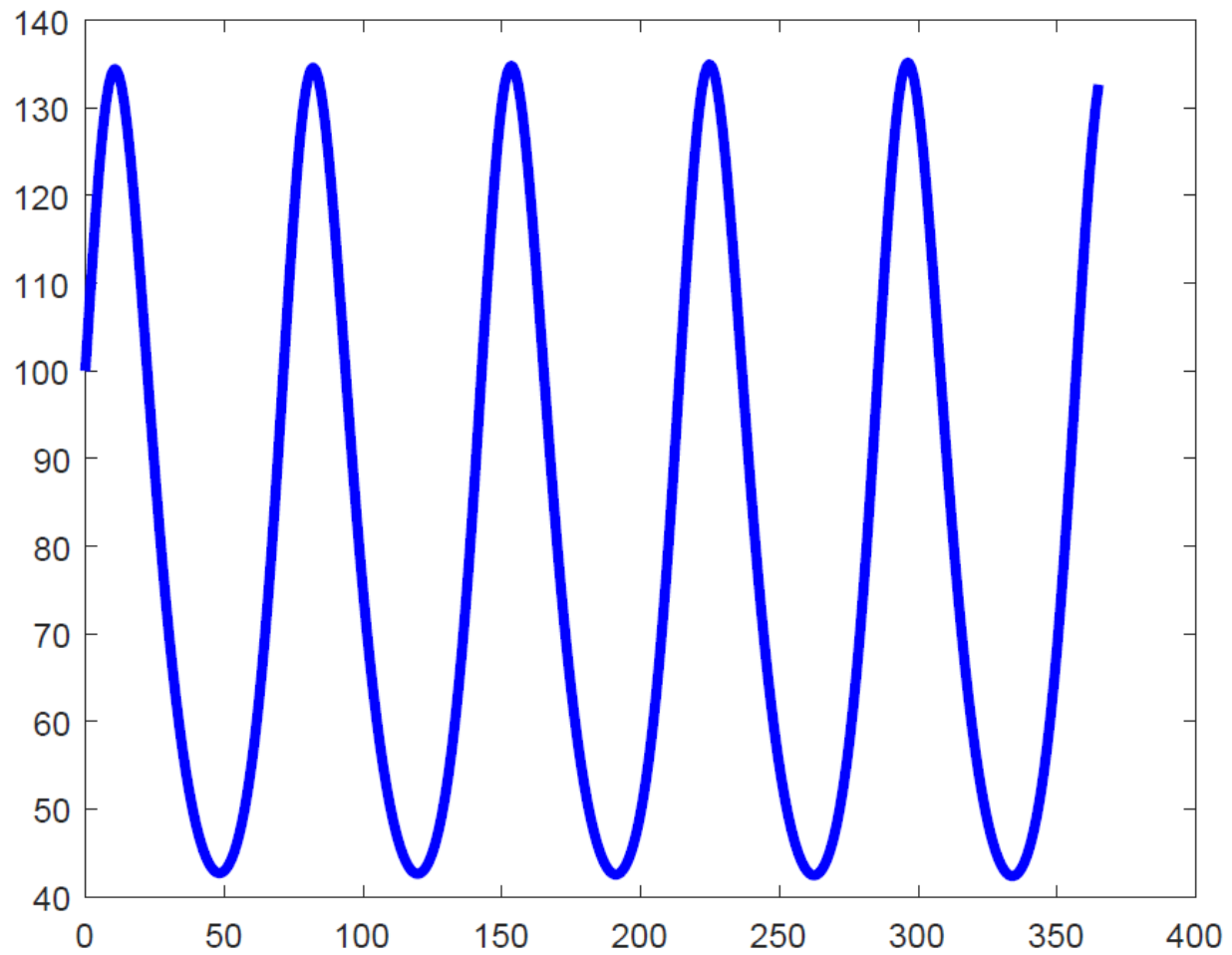
(4) Repeat your calculations with initial populations of 5000 rabbits and 100 foxes per km^2 , and discuss how the behavior of the system changes.

5.





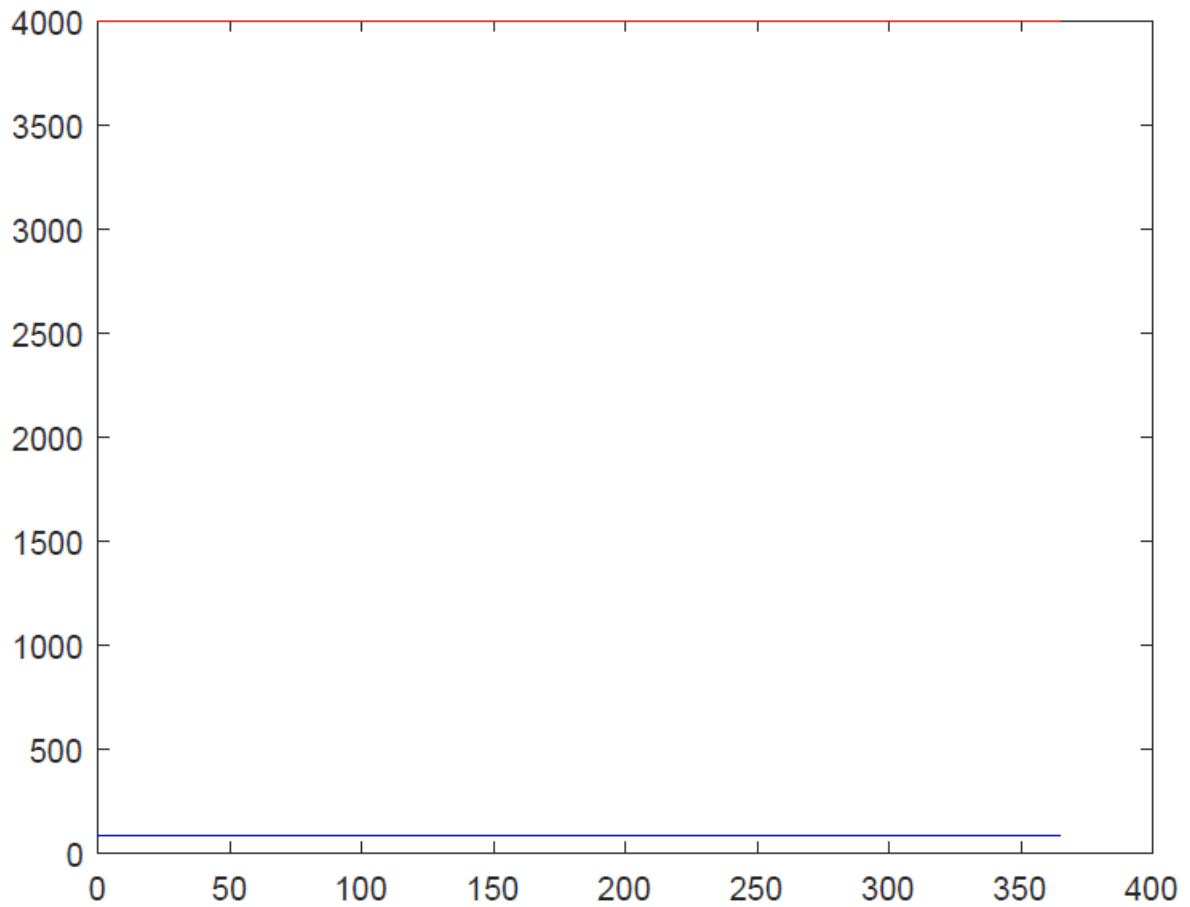
This graph shows the prey population when starting with 5000. The system is more oscillatory, and the rabbits start with a population much closer to their maximum.

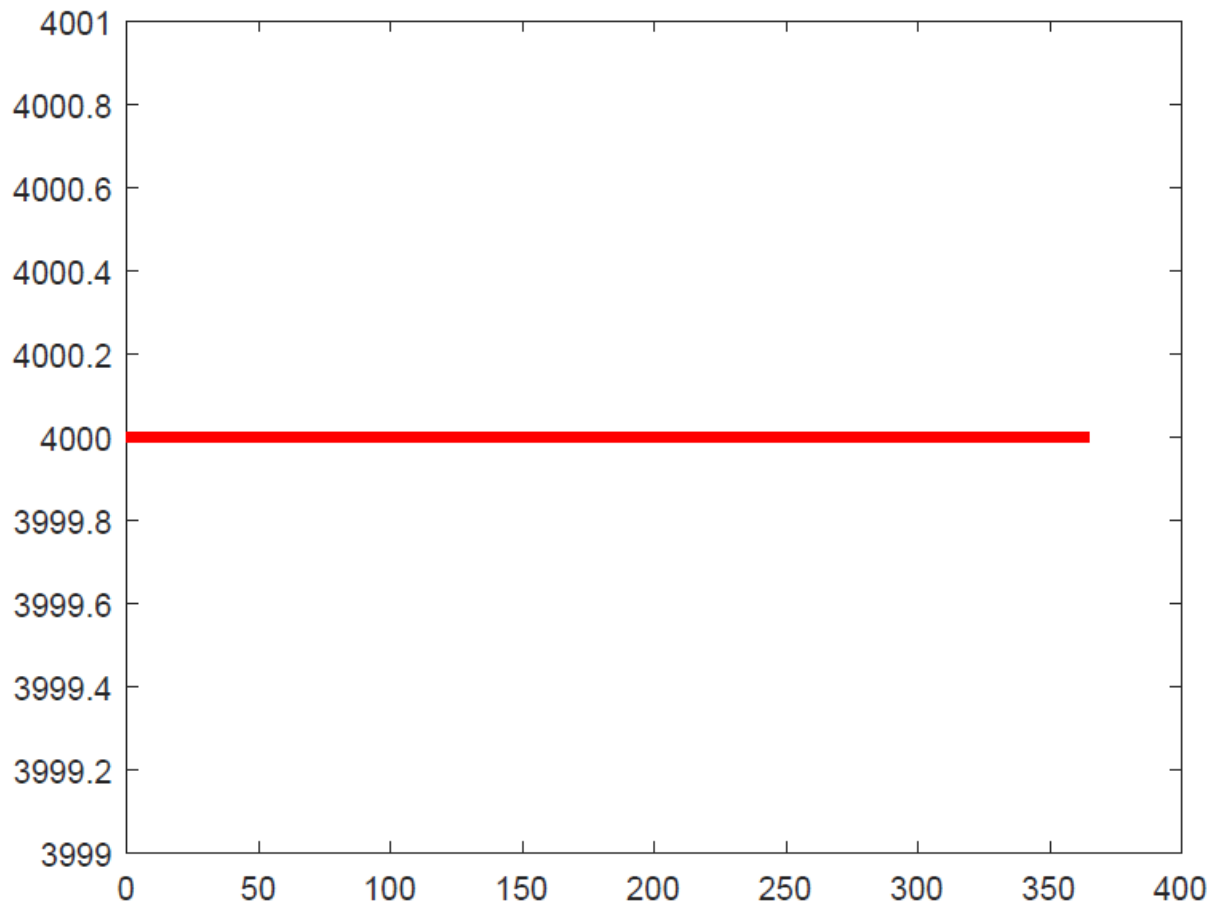


This graph shows the predator population when starting with 100. The system is more oscillatory, and the foxes start with a population much closer to their maximum.

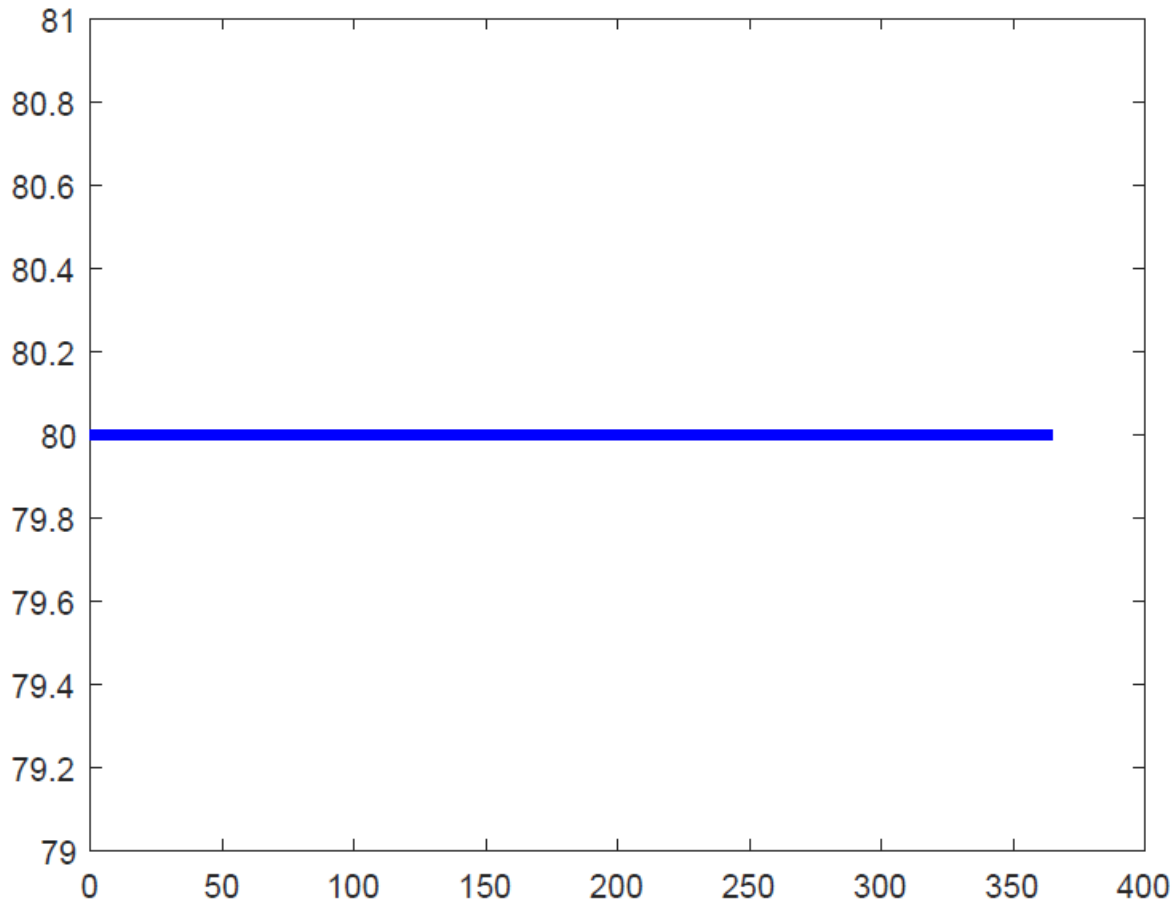
(6) Do the same for 4000 rabbits and 80 foxes per km^2 . What does this result tell you about the system?

6.





This graph shows the prey population when starting with 4000. This system has a birth rate equal to the death rate for the prey, and is thus part of the stationary point for the prey population.



This graph shows the predator population when starting with 80. This system has a birth rate equal to the death rate for the predator, and is thus part of the stationary point for the predator population.

(7) Set $K = 10,000$, $s = \gamma$ and $h = 0.2$. Briefly explain what these values mean, in a biological context.

7. K is the carrying capacity for a population given the finite resources of an environment. s is a proportionality constant. h is the time taken for a predator to kill, eat, and rest.

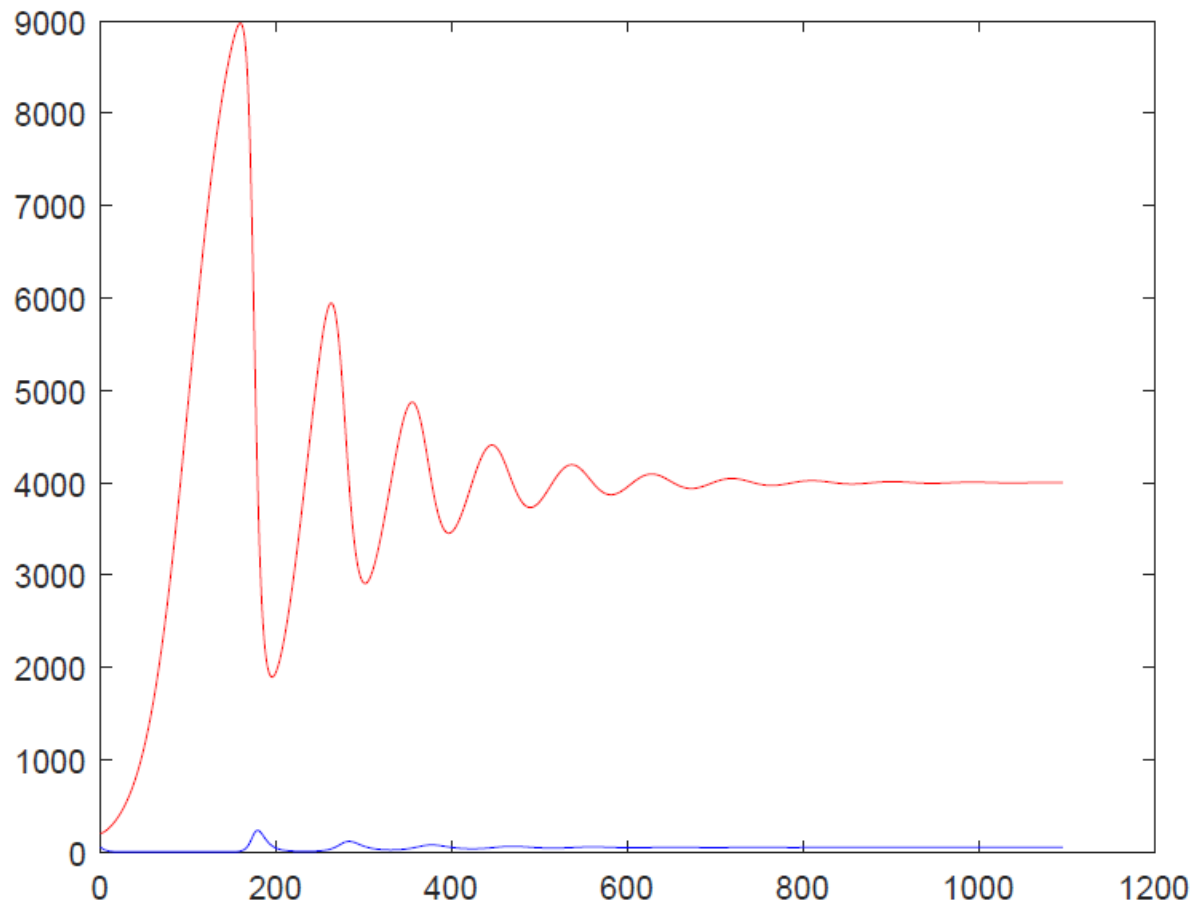
(8) For each case, make a plot of the populations versus time and the populations versus each other, in this case for a time span of at least three years. Describe how each trajectory differs from the original Lotka–Volterra model, and from each other, and give a suggested rationale for why these differences arise.

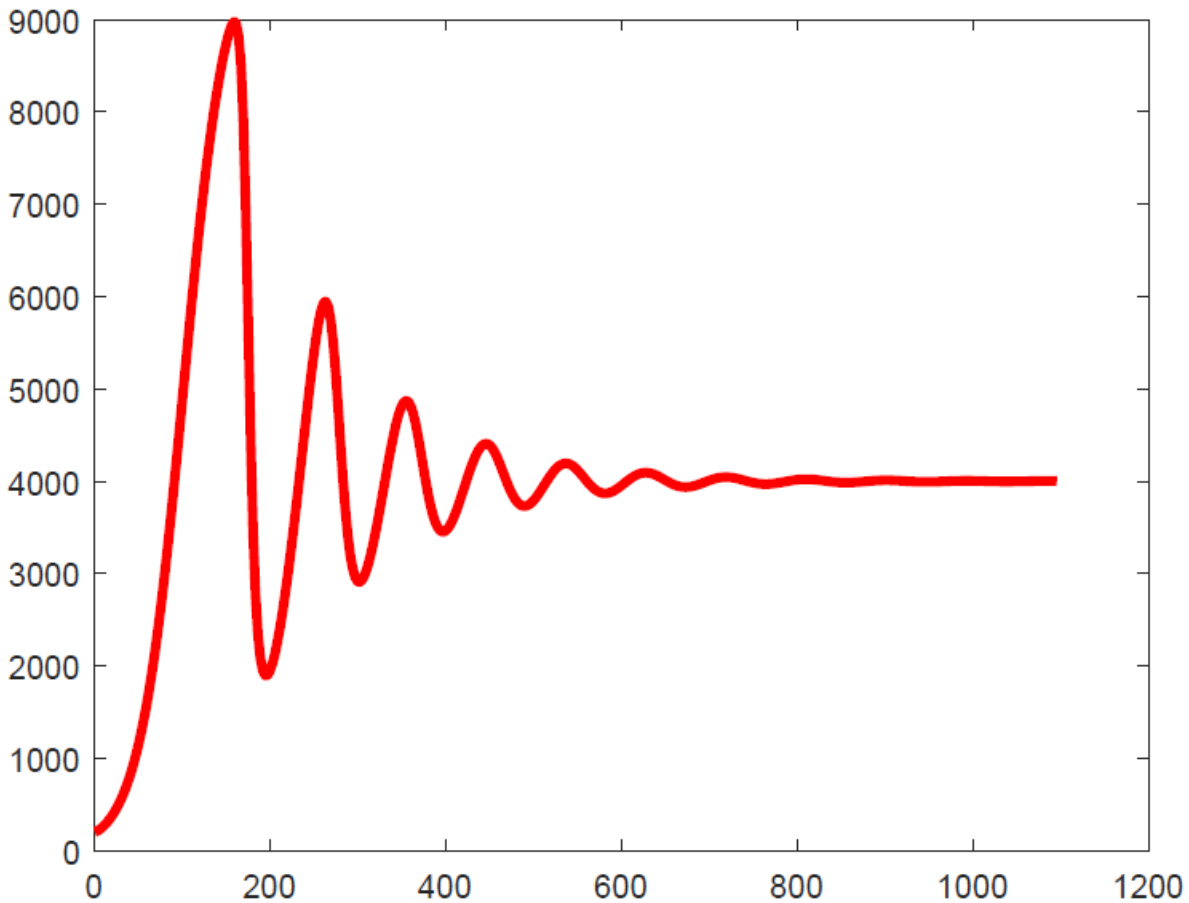
8.

Code:

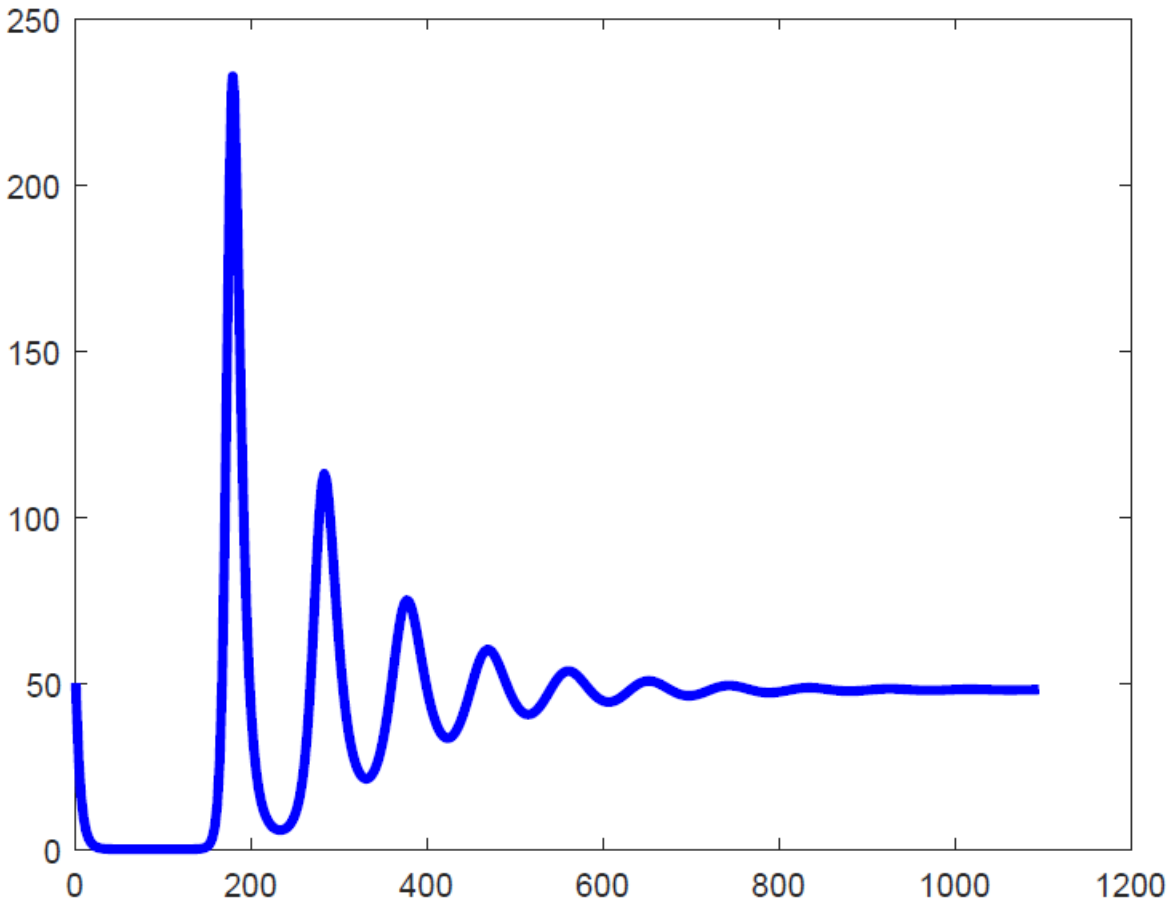
```
%This program uses the forward euler method to create 3
graphs representing the
%predator and prey populations
a = 0:.01:1095;
%This creates a vector for the time that has passed
b1 = zeros(1,109501);
b2 = zeros(1,109501);
%This initializes a vector for the population values
b1(1) = 200;
b2(1) = 50;
%This sets the initial population
for i = 2:109501
    x = (.04*(1-(b1(i-1))/10000)*(b1(i-1))-.0005*(b1(i-
1))*(b2(i-1)))*.01;
    y = (.1*.0005*(b1(i-1))*(b2(i-1))-.2*(b2(i-1)))*.01;
    %This finds the product of the derivative and the
interval of time
    b1(i) = (b1(i-1))+x;
    b2(i) = (b2(i-1))+y;
    %This sums the i-1 value and the derivative times the
interval of time.
end
%This loop inputs values for a vector for the number of
yeast cells after a
%given time interval
fig1 = figure(1);
plot(a,b1,'-r',a,b2,'-b')
fig2 = figure(2);
plot(a,b1,'-r','LineWidth',3.0)
fig3 = figure(3);
plot(a,b2,'-b','LineWidth',3.0)
%This creates all plots with the requested parameters
%and changes the handle of the plotted figures to fig1,2,
and 3
print(fig1,'ForwardEulerPredvsPreyRestrictedGrowth','-
dpdf')
print(fig2,'ForwardEulerPreyRestrictedGrowth','-dpdf')
print(fig3,'ForwardEulerPredRestrictedGrowth','-dpdf')
%This saves the figures as a pdf
```

Execution:





This graph shows the prey population with restricted prey growth. It differs from the Lotka- Volterra model in that the population reaches a maximum, and achieves the population required for the stable stationary point, much faster. It likely has a much lower population maximum because the prey cannot reach the immense maximal population they reached in the Lotka- Volterra model without restricted prey growth.



This graph shows the predator population with restricted prey growth. It differs from the Lotka- Volterra model in that the population reaches a maximum, and achieves the population required for the stable stationary point, much faster. It likely has a much lower population maximum because the prey cannot reach the immense maximal population they reached in the Lotka- Volterra model without restricted prey growth.

Code:

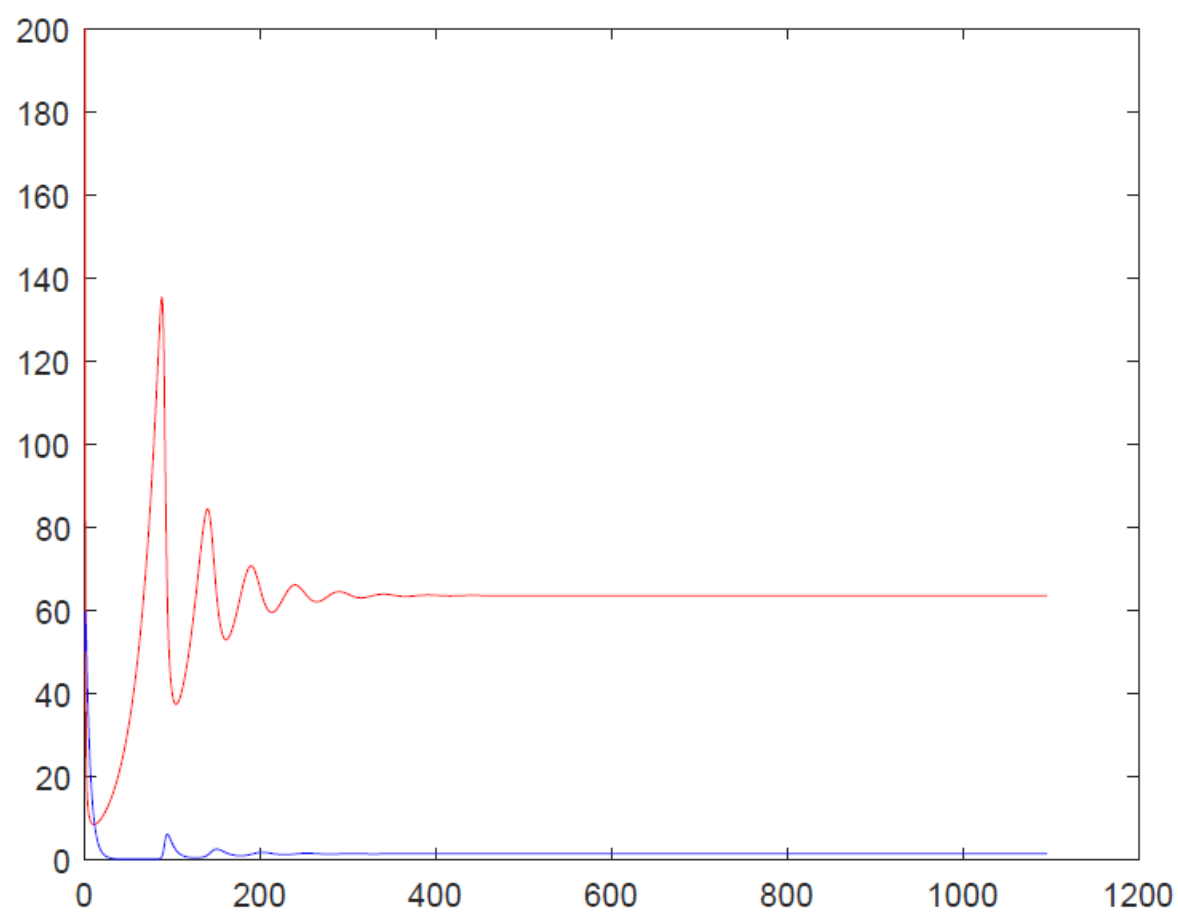
```
%This program uses the forward euler method to create 3
graphs representing the
%predator and prey populations
a = 0:.01:1095;
%This creates a vector for the time that has passed
b1 = zeros(1,109501);
b2 = zeros(1,109501);
%This initializes a vector for the population values
b1(1) = 200;
b2(1) = 50;
```

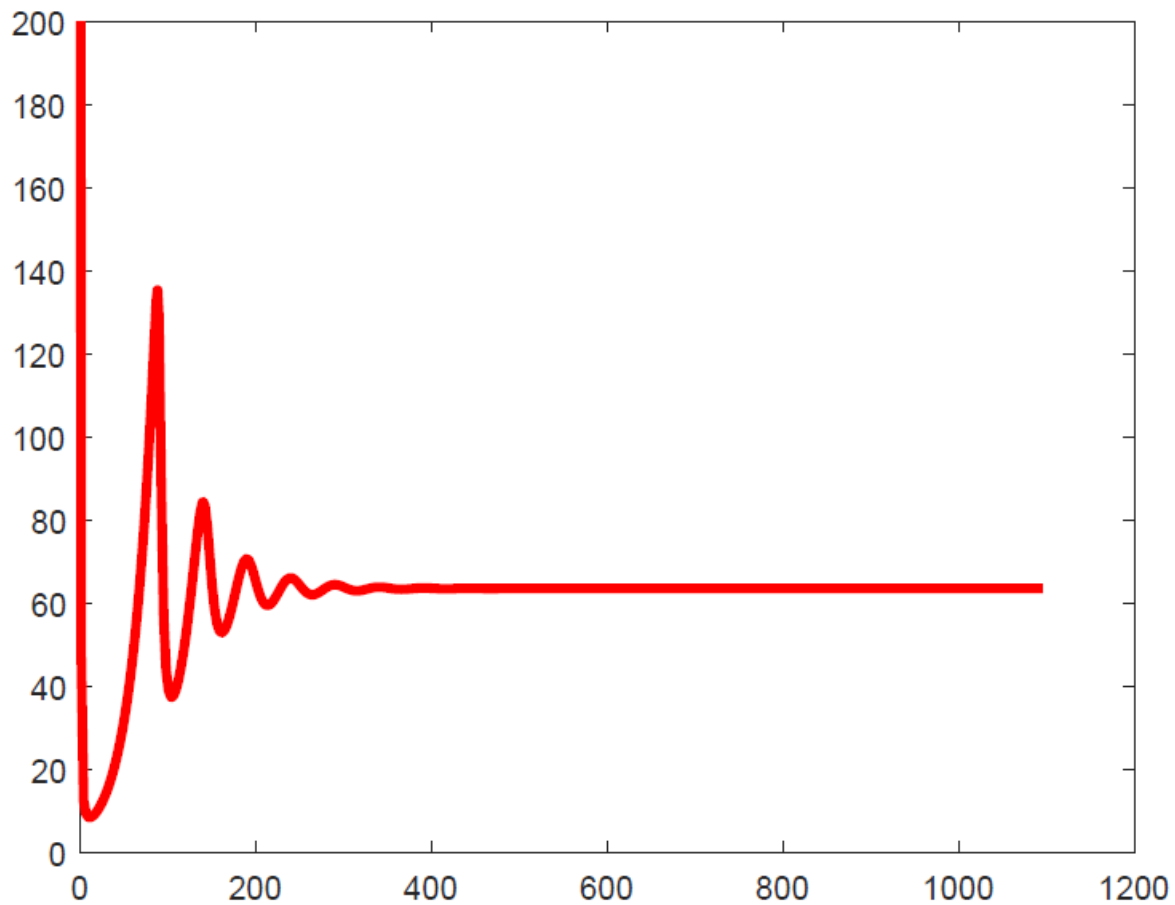
```

%This sets the initial population
for i = 2:109501
    x = (.04*(1-(b1(i-1))/10000)*(b1(i-1))-(.0005*(b1(i-1)))/(1+.0005*.2*(b1(i-1)))*(b1(i-1))*(b2(i-1)))*.01;
    y = (.1*(.0005*(b1(i-1)))/(1+.0005*.2*(b1(i-1)))*(b1(i-1))*(b2(i-1))-.2*(b2(i-1)))*.01;
    %This finds the product of the derivative and the
    interval of time
    b1(i) = (b1(i-1))+x;
    b2(i) = (b2(i-1))+y;
    %This sums the i-1 value and the derivative times the
    interval of time.
end
%This loop inputs values for a vector for the number of
yeast cells after a
%given time interval
fig1 = figure(1);
plot(a,b1,'-r',a,b2,'-b')
fig2 = figure(2);
plot(a,b1,'-r','LineWidth',3.0)
fig3 = figure(3);
plot(a,b2,'-b','LineWidth',3.0)
%This creates all plots with the requested parameters
%and changes the handle of the plotted figures to fig1,2,
and 3
print(fig1,'PredvsPreyRestrictedGrowthAndPredSaturation','-dpdf')
print(fig2,'PreyRestrictedGrowthAndPredSaturation','-dpdf')
print(fig3,'PredRestrictedGrowthAndPredSaturation','-dpdf')
%This saves the figures as a pdf

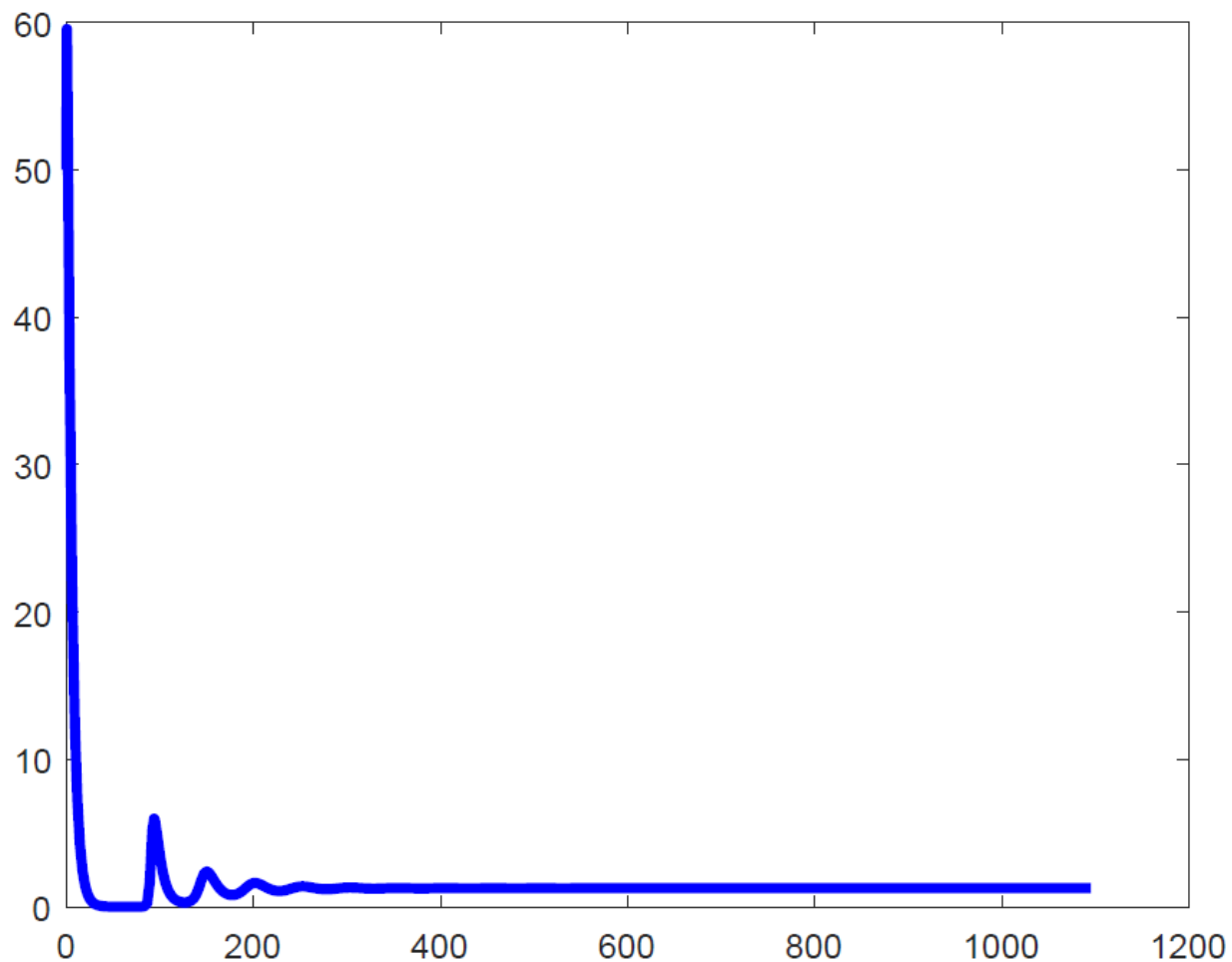
```

Execution:





This graph shows the prey population with restricted prey growth and a saturated predator response. It differs from the Lotka- Volterra model in that the population reaches a maximum, and achieves the population required for the stable stationary point, much faster. The stationary point is when the prey population is 60 and the predator population is 1.2. It differs from only having restricted prey growth in that the stationary point has much lower population values. It likely has a much lower population value at all times, as compared to only the restricted growth model, because the predators now have a consumption limit, whereas before they reproduced at unreasonably high rates because they consumed unreasonably large amounts.



This graph shows the predator population with restricted prey growth and a saturated predator response. It differs from the Lotka- Volterra model in that the population reaches a maximum, and achieves the population required for the stable stationary point, much faster. The stationary point is when the prey population is 60 and the predator population is 1.2. It differs from only having restricted prey growth in that the stationary point has much lower population values. It likely has a much lower population value at all times, as compared to only the restricted growth model, because the predators now have a consumption limit, whereas before they reproduced at unreasonably high rates because they consumed unreasonably large amounts.

(8) What are the units of β ? Does this number seem reasonable?

8. The unit of β is the number of times a person will contact another individual and effectively transmit the disease per unit of time. $5 \cdot 10^{-7}$ seems low, but given the great variety of transmittable diseases, means of infection, different units of time,

and different values of infected population and susceptible population in different circumstances lends credibility to a great range of different β values for varying circumstances.

(9) Implement a model of an SIR disease (use the same approach as for the Lotka–Volterra model, but with the appropriate evolution rules). Consider an initial population of one million individuals, with 10 of them infected. Use a time step of 0.001 days, and model the system for one year (365 days).

9.

Code:

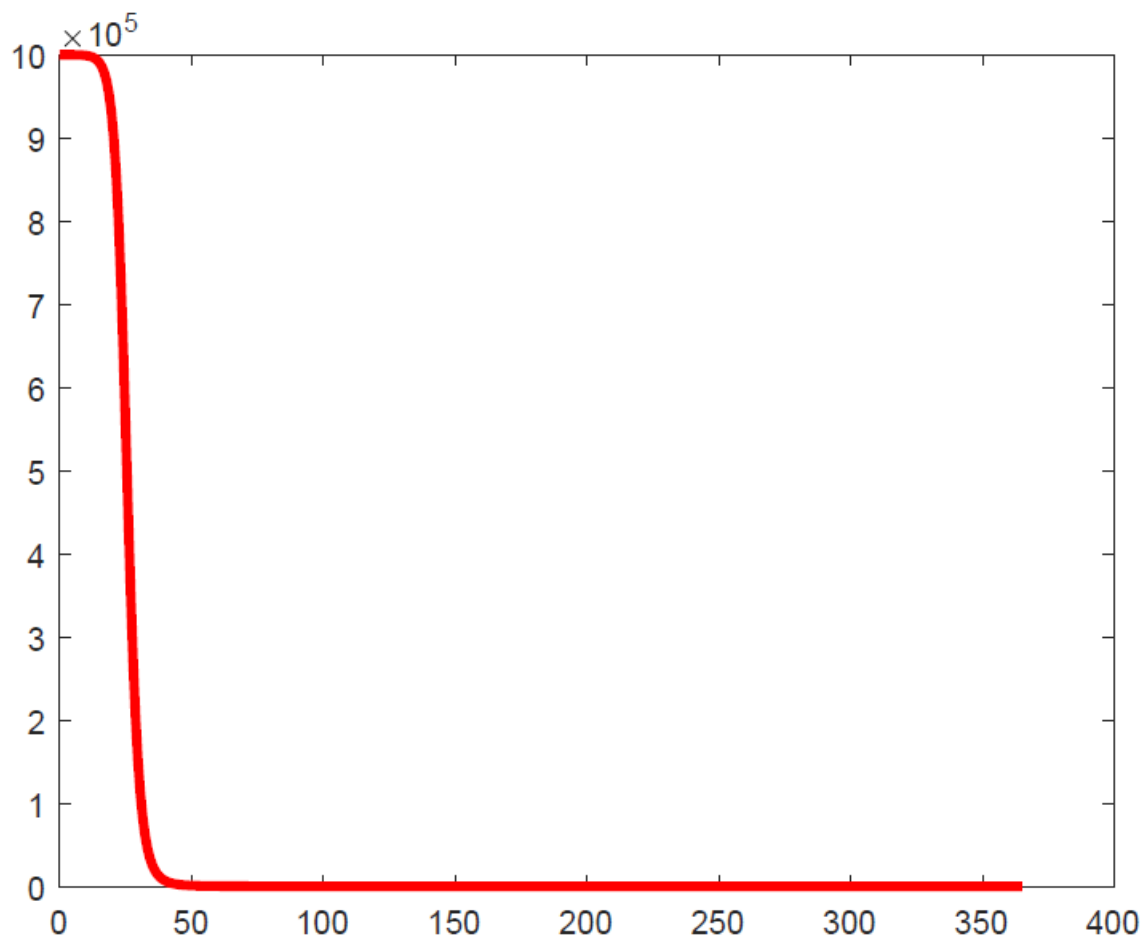
```
%This program uses the forward euler method to create
graphs representing
%susceptible, infected, and recovered populations
a = 0:.001:365;
%This creates a vector for the time that has passed
b1 = zeros(1,365001);
b2 = zeros(1,365001);
b3 = zeros(1,365001);
%This initializes a vector for the population values
b1(1) = 999990;
b2(1) = 10;
b3(1) = 0;
%This sets the initial population
for i = 2:365001
    x = -5*(10^-7)*(b2(i-1))*(b1(i-1)).*0.001;
    y = (5*(10^-7)*(b2(i-1))*(b1(i-1))-.05*(b2(i-1))).*0.001;
    z = .05*(b2(i-1)).*0.001;
    %This finds the product of the derivative and the
interval of time
    b1(i) = (b1(i-1))+x;
    b2(i) = (b2(i-1))+y;
    b3(i) = (b3(i-1))+z;
    %This sums the i-1 value and the derivative times the
interval of time.
end
%This loop inputs values for a vector for the number of
yeast cells after a
%given time interval
%,a,b2,a,b3,a,b4)
fig1 = figure(1);
plot(a,b1,'-r','LineWidth',3.0)
```

```

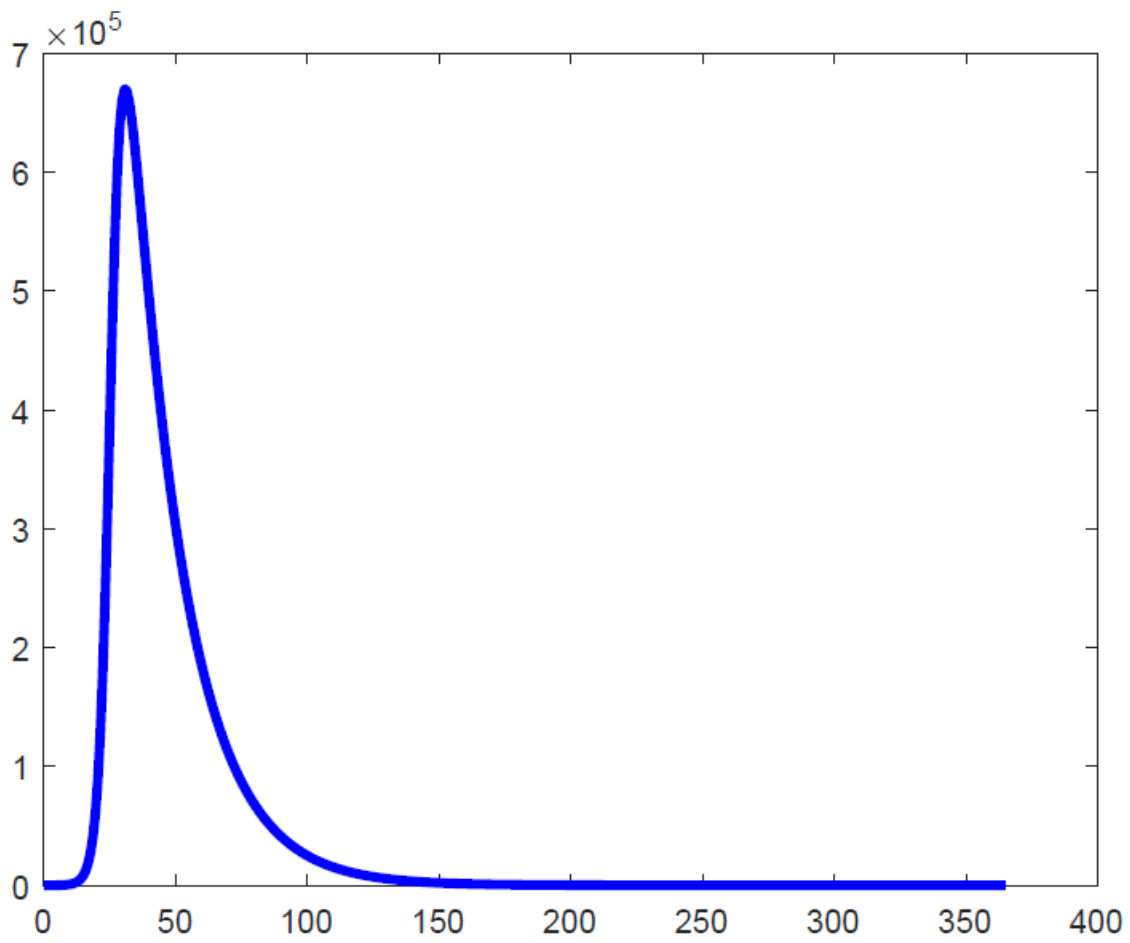
fig2 = figure(2);
plot(a,b2,'-b','LineWidth',3.0)
fig3 = figure(3);
plot(a,b3,'-g','LineWidth',3.0)
fig4 = figure(4);
plot(a,b1,'-r',a,b2,'-b',a,b3,'-g')
%This creates all plots with the requested parameters
%and changes the handle of the plotted figures to fig1,2,
and 3
print(fig1,'SIRModelSusceptible1','-dpdf')
print(fig2,'SIRModelInfected1','-dpdf')
print(fig3,'SIRModelRecovered1','-dpdf')
print(fig4,'SIRModelAll1','-dpdf')
%This saves the figures as a pdf

```

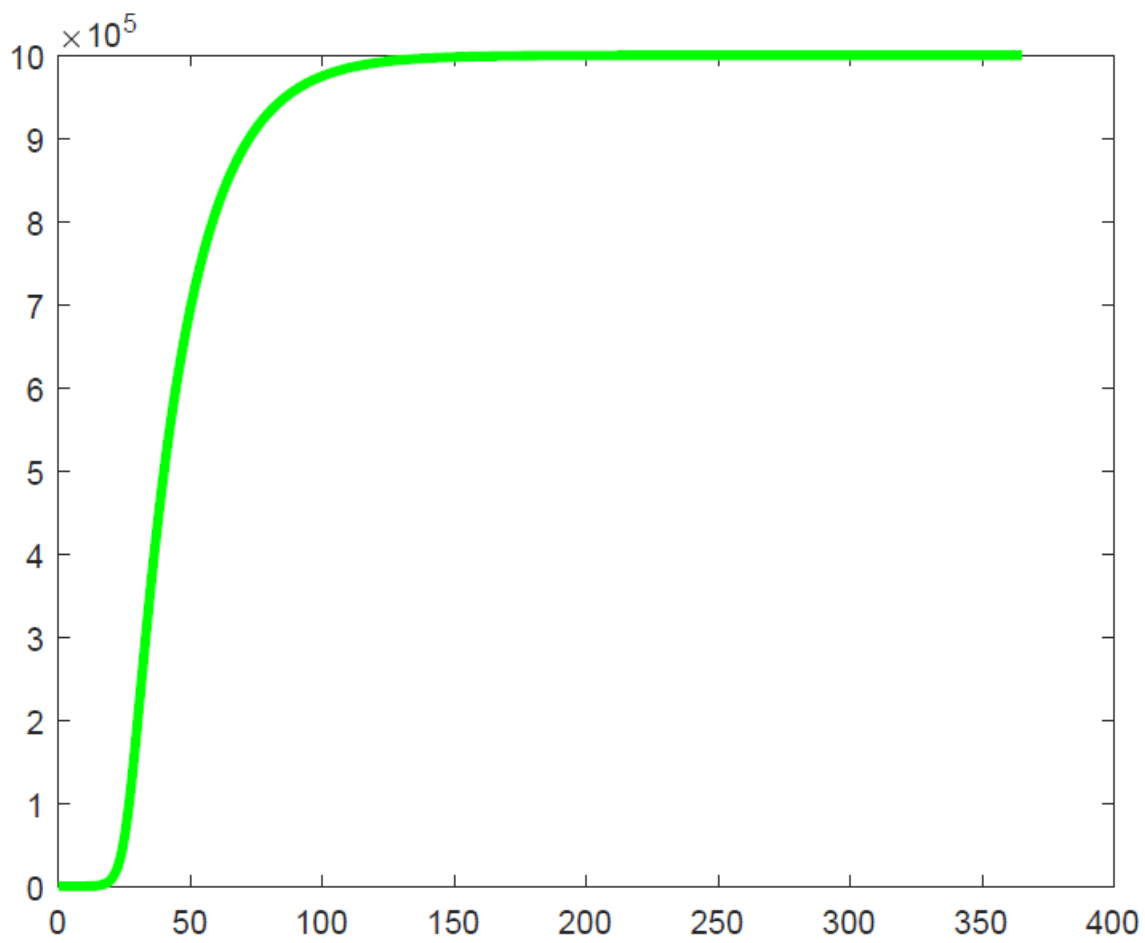
Execution:



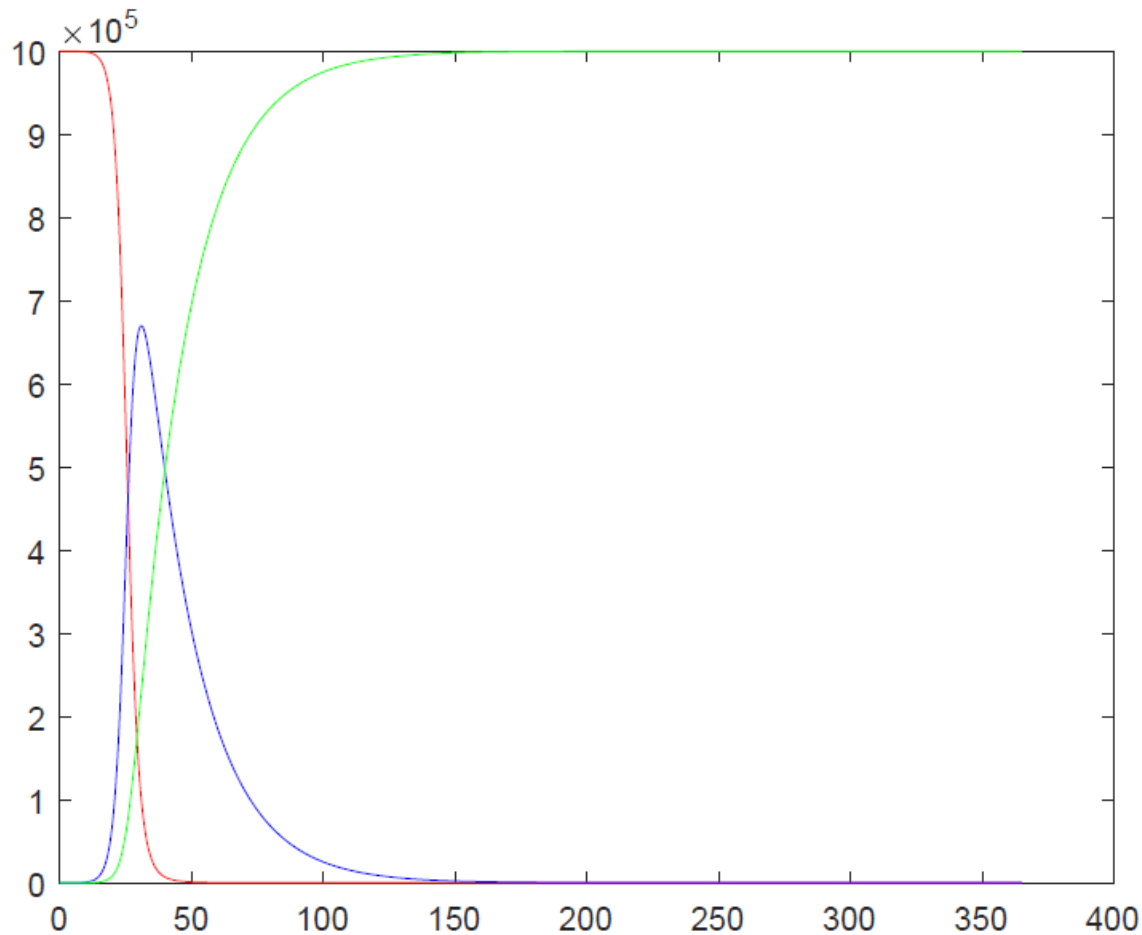
This graph shows the susceptible population over time



This graph shows the infected population over time



This graph shows the recovered population over time

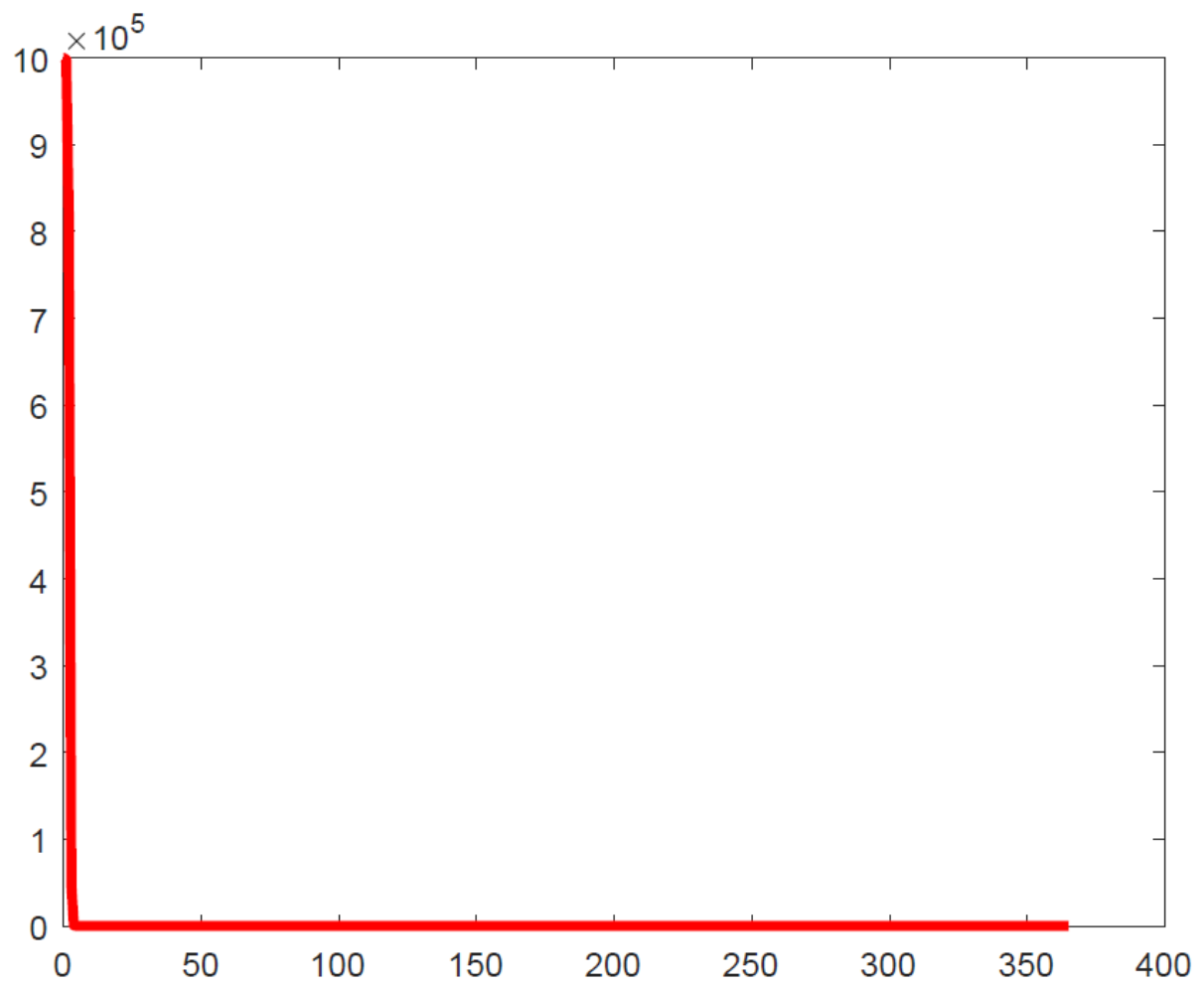


(10) Describe the dynamics of the resulting epidemic. Approximately when does the epidemic begin, and how long does it last? By the end of the epidemic, how many individuals have been infected, and how many avoided the disease? With a 5% mortality rate, how many individuals would die?

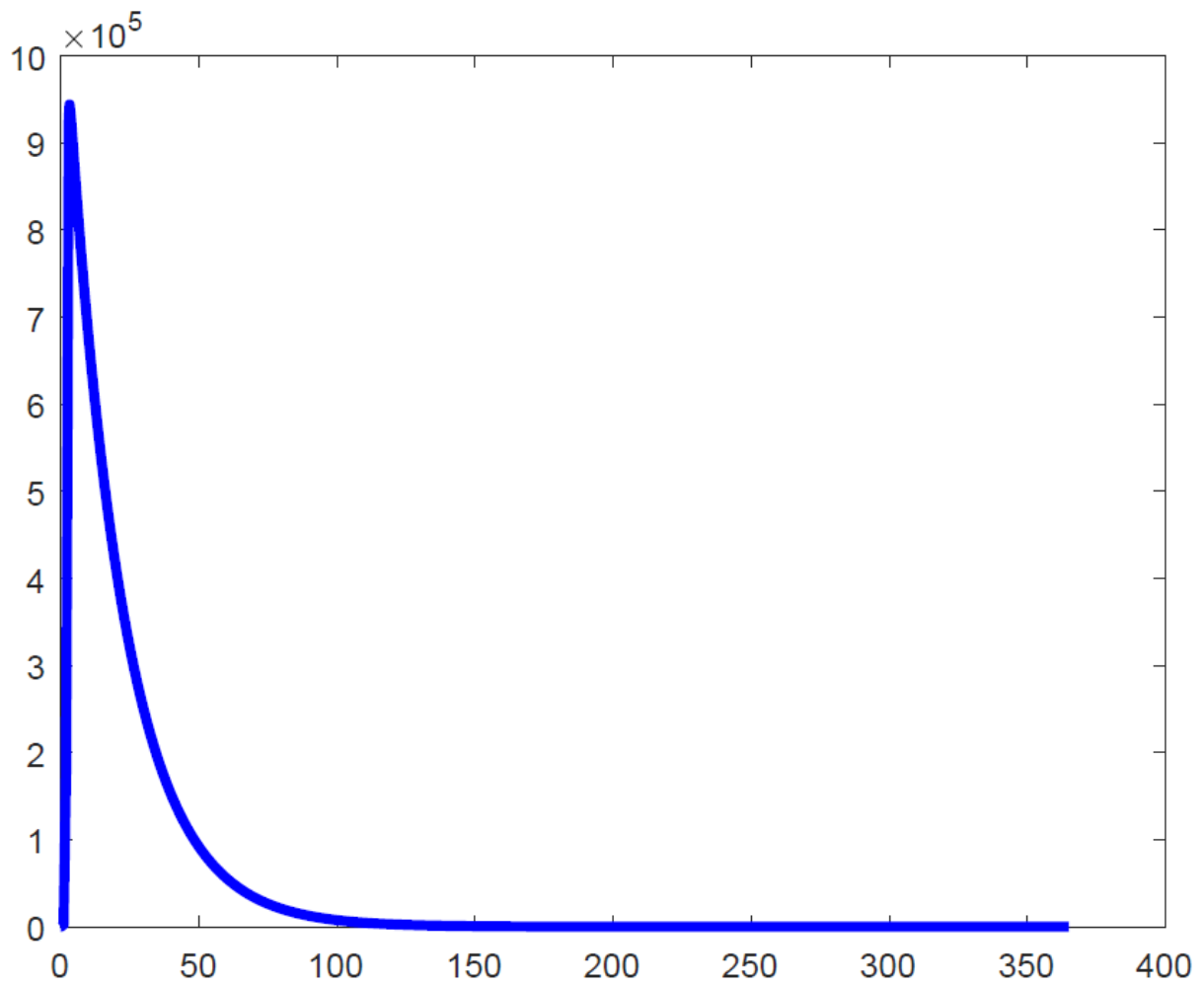
10. The epidemic begins at approximately 15-20 days. By the end of the epidemic, the entire population has been infected and 0 avoided the disease. Given a 5% mortality rate, 5% of the population would die, or 50000 people.

(11) Increase β by a factor of 10, and discuss the differences in dynamics (e.g. when does the epidemic begin and how long does it last).

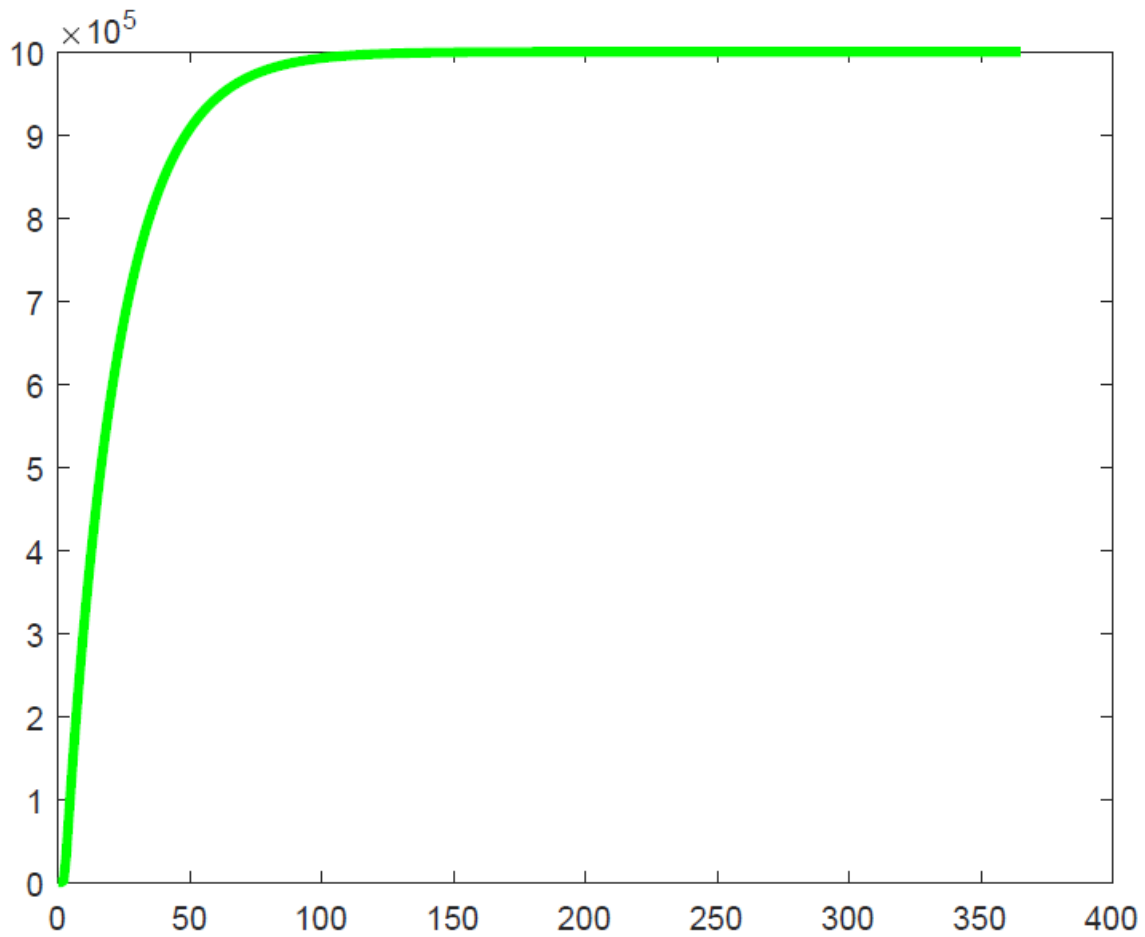
11.



This graph shows the susceptible population over time. The population is infected much faster.

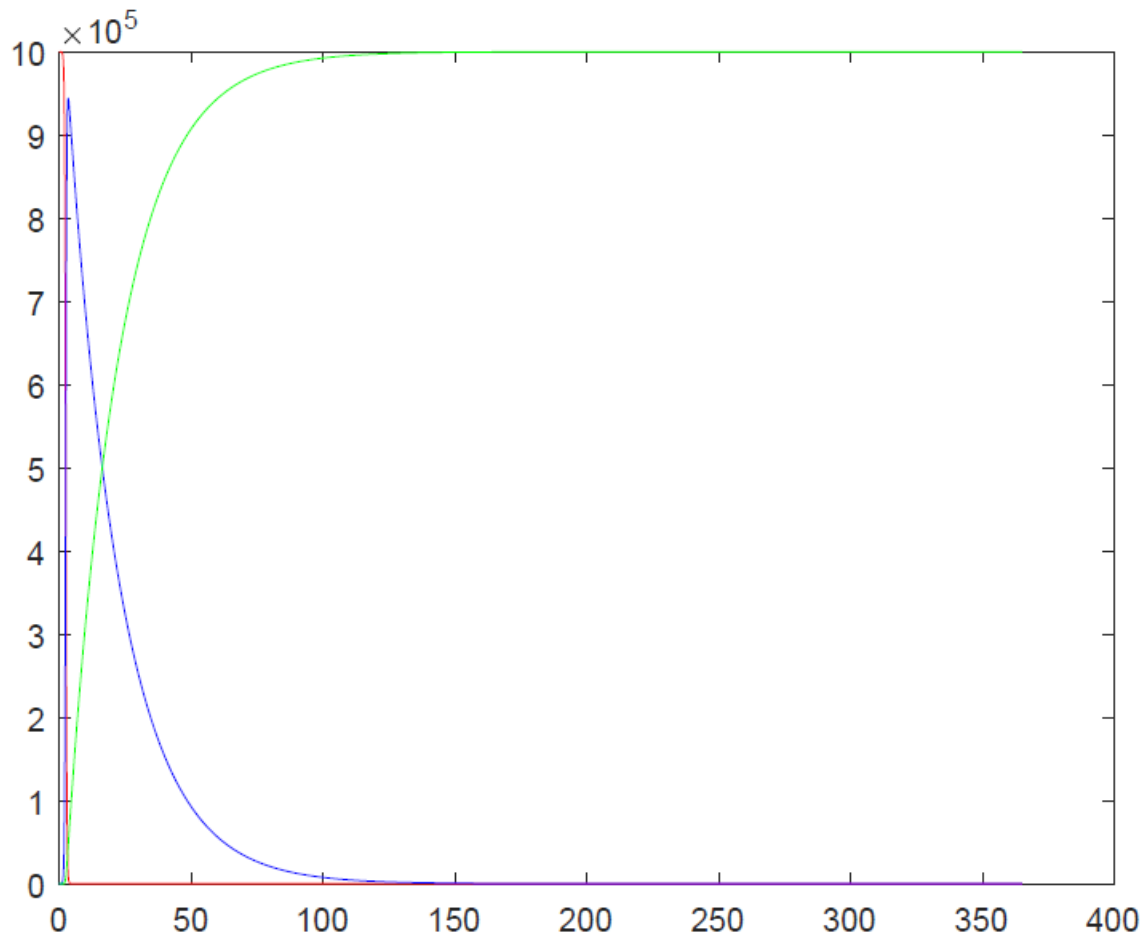


This graph shows the infected population over time. The population becomes infected much earlier.



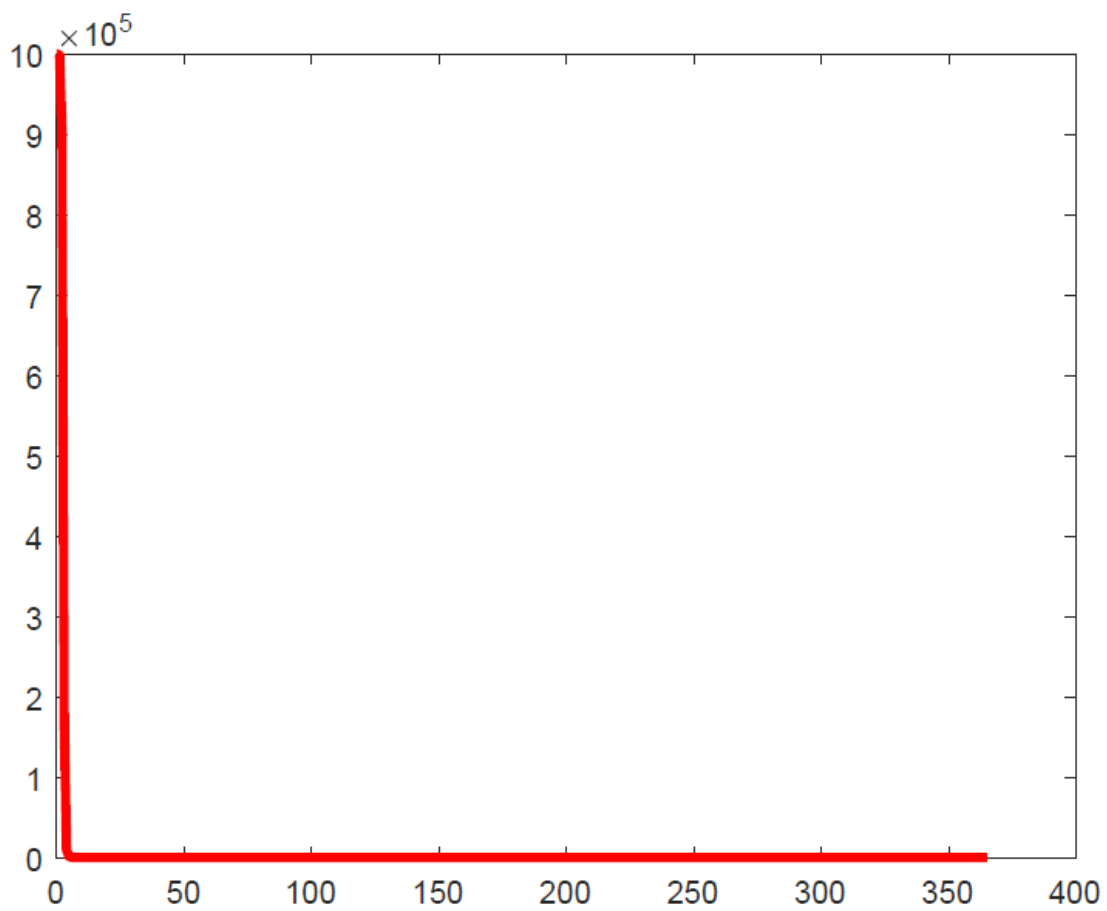
This graph shows the recovered population over time. The population recovers much earlier.

The epidemic begins approximately 5-10 days in and finishes after about 75 days

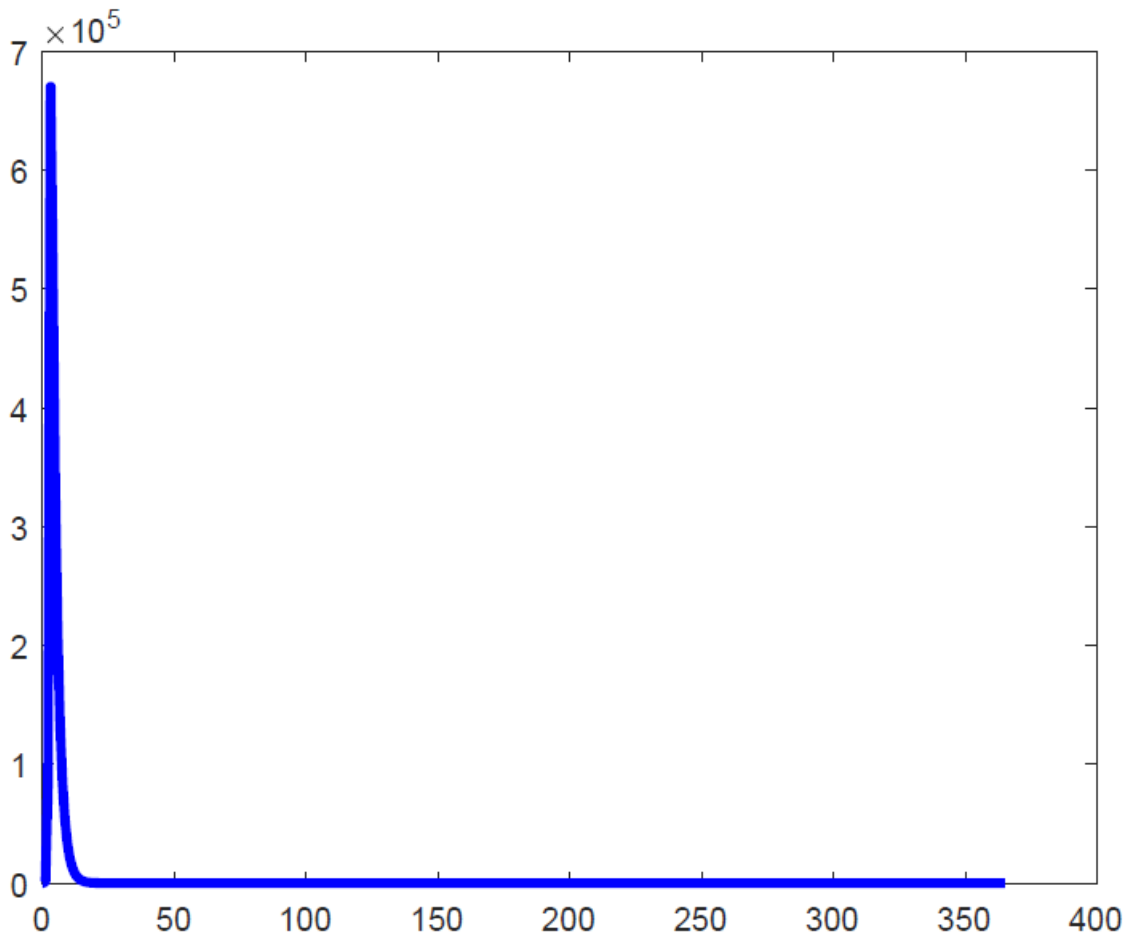


(12) Now also increase γ by a factor of 10 and do the same. Comment on your observations, and how they can be interpreted biologically.

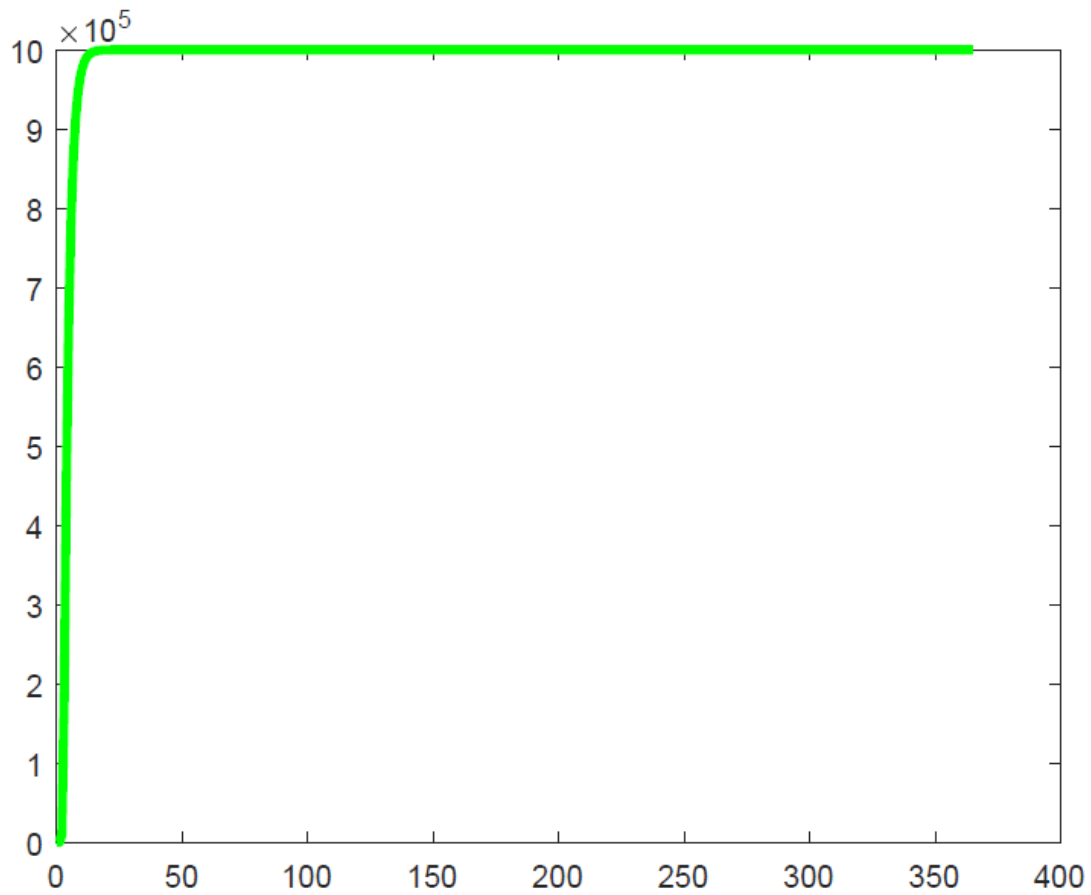
12.



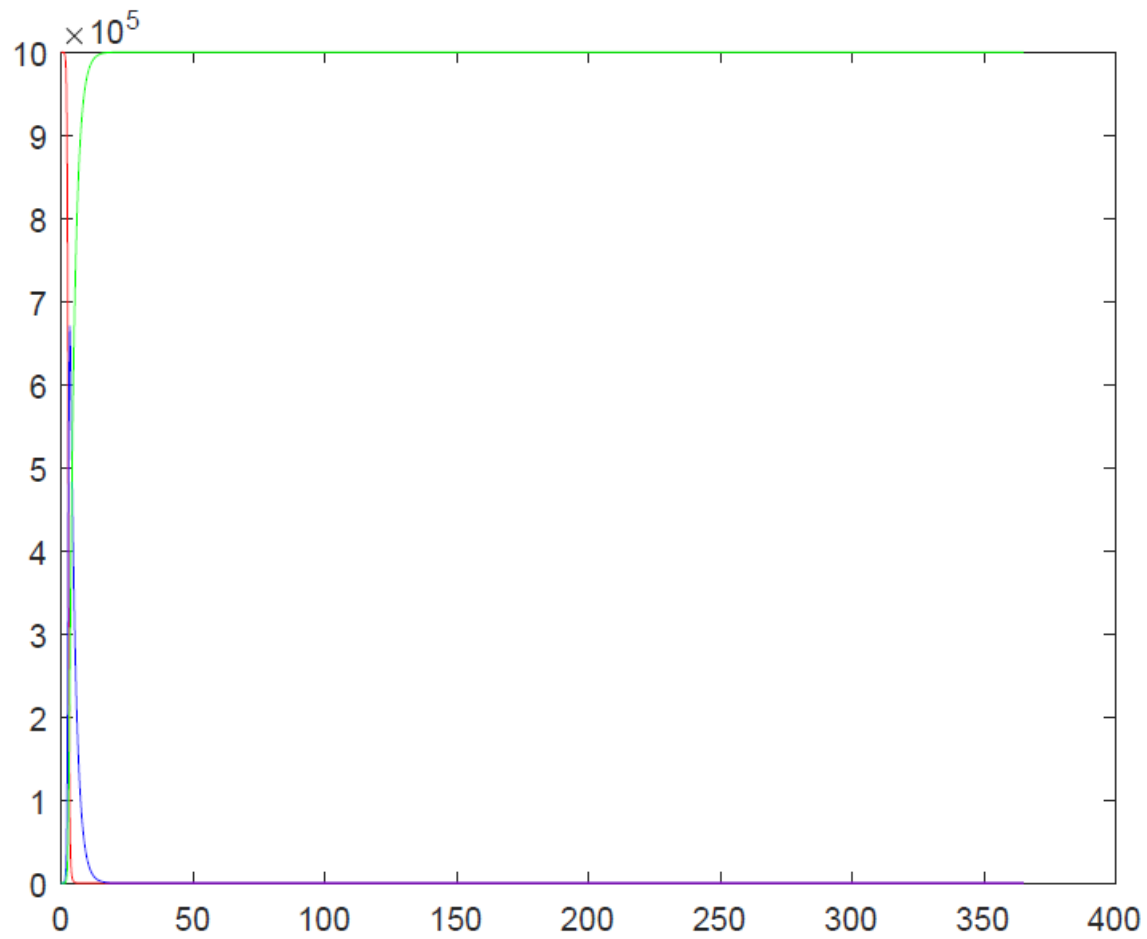
This graph shows the susceptible population over time. Its about the same as the last population graph.



This graph shows the infected population over time. The population recovers at a much higher rate.

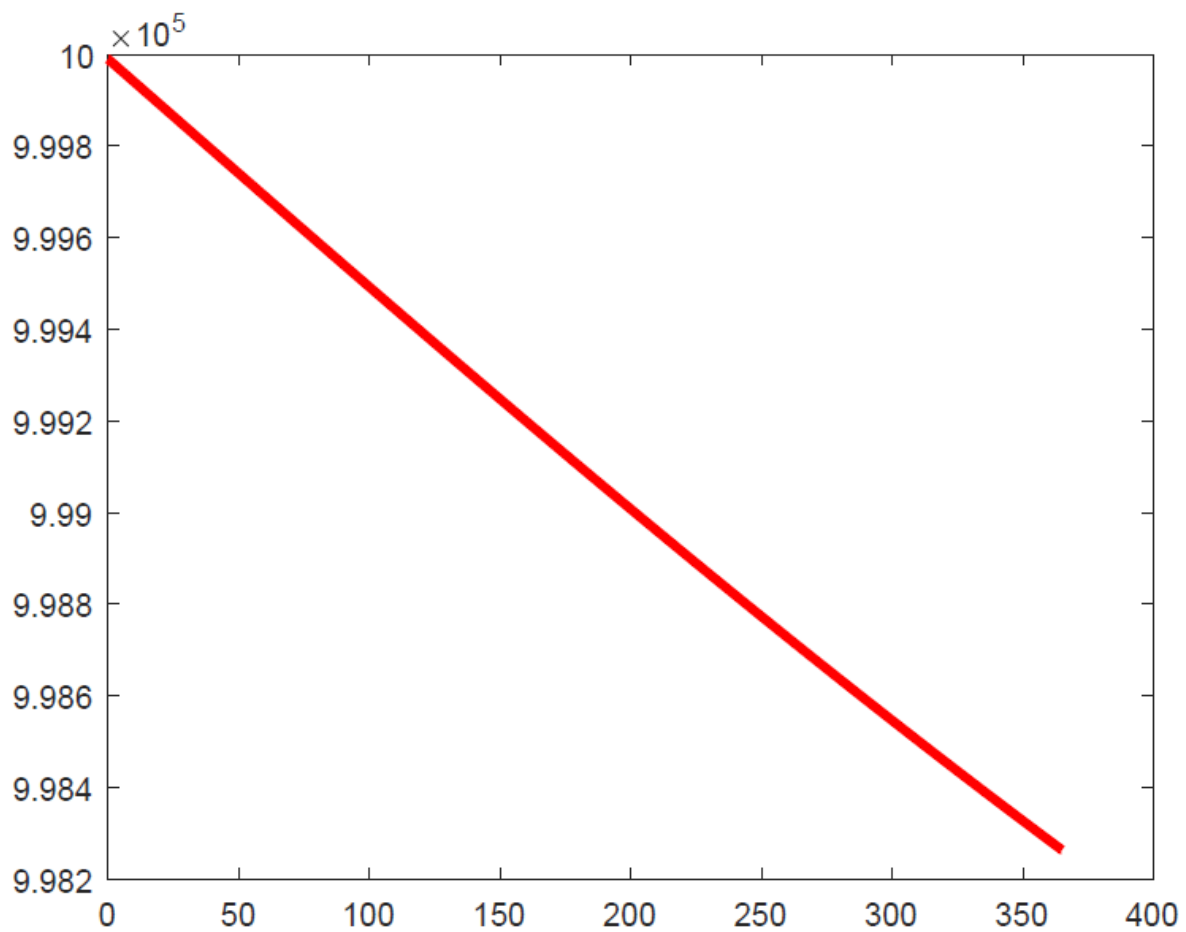


This graph shows the recovered population over time. The population recovers at a much higher rate, leading to the entire population being recovered much earlier.

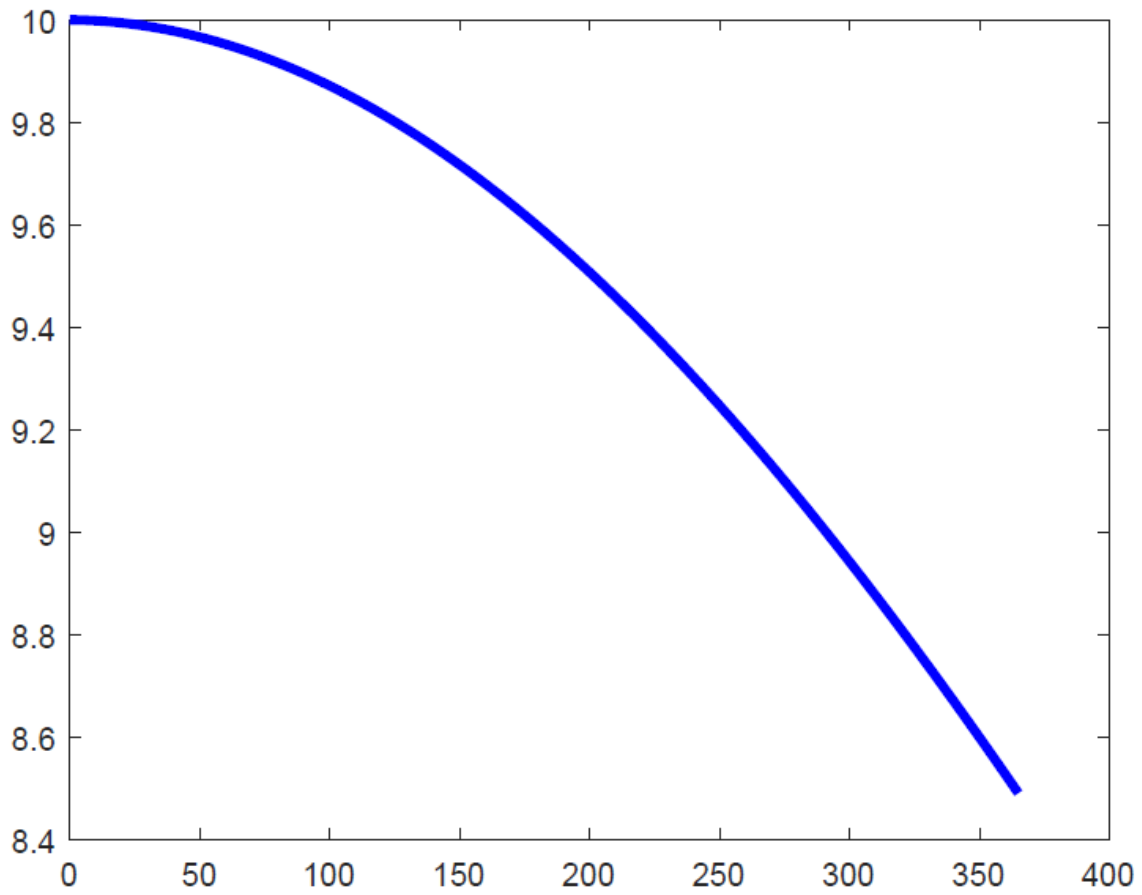


(13) Now decrease β by a factor of 10 keeping γ unchanged. What is different? How many individuals are infected at the end of 1 year, and how many have recovered?

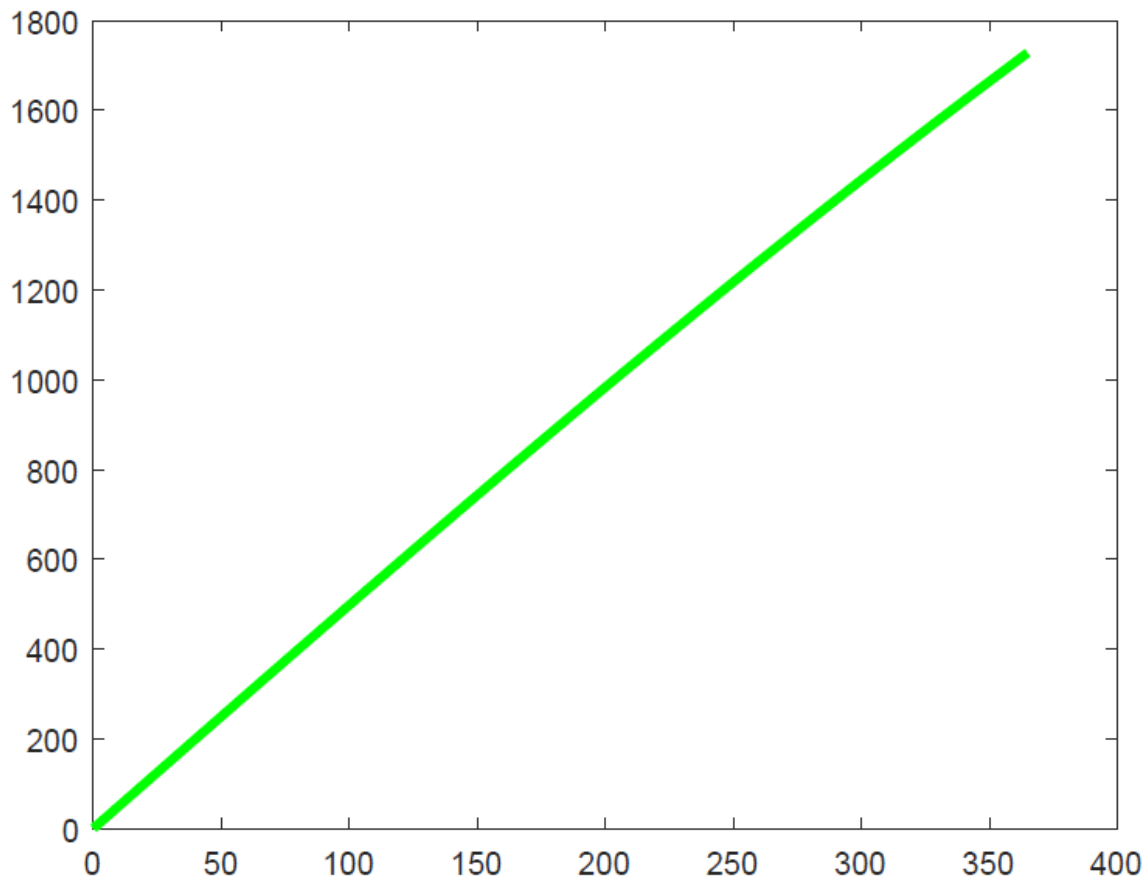
13.



This graph shows the susceptible population over time. The susceptible population barely changes over time, meaning relatively few people become infected. Additionally, the graph is now linear.

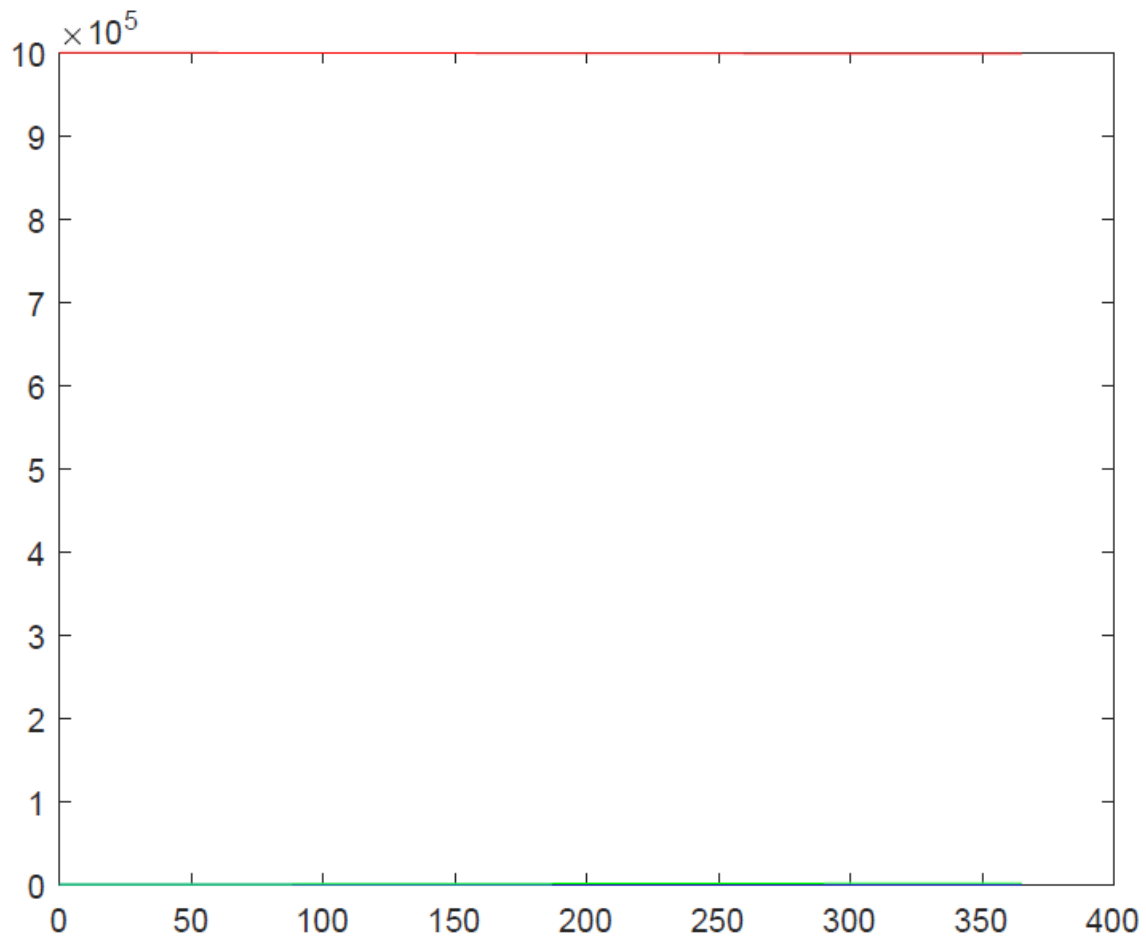


The graph shows the infected population over time. Relatively few are infected over time. Additionally, the graph is now parabolic.



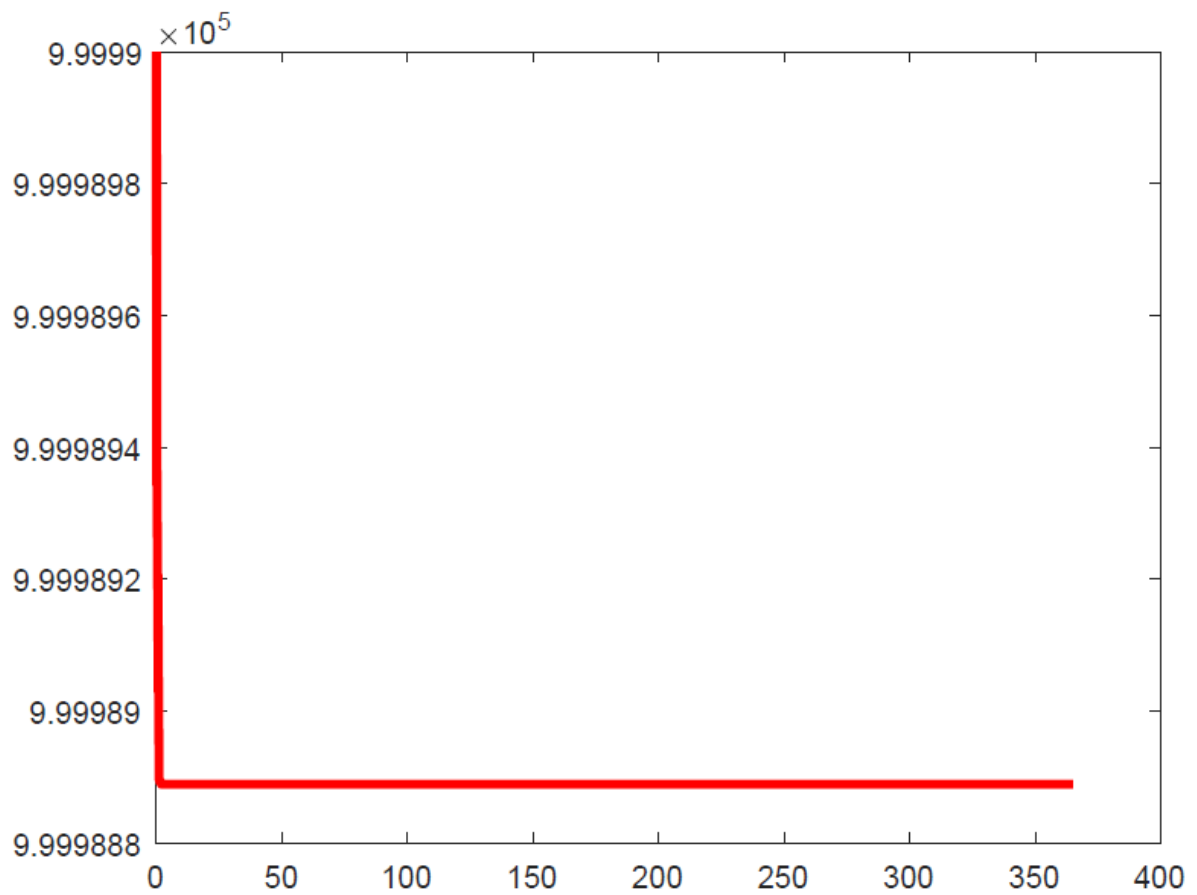
The graph shows the recovered population over time. Relatively few are infected over time, so relatively few recover. Additionally, the graph is now linear.

Approximately 8.5 individuals are infected at the end of 1 year. Approximately 1700 individuals have recovered.

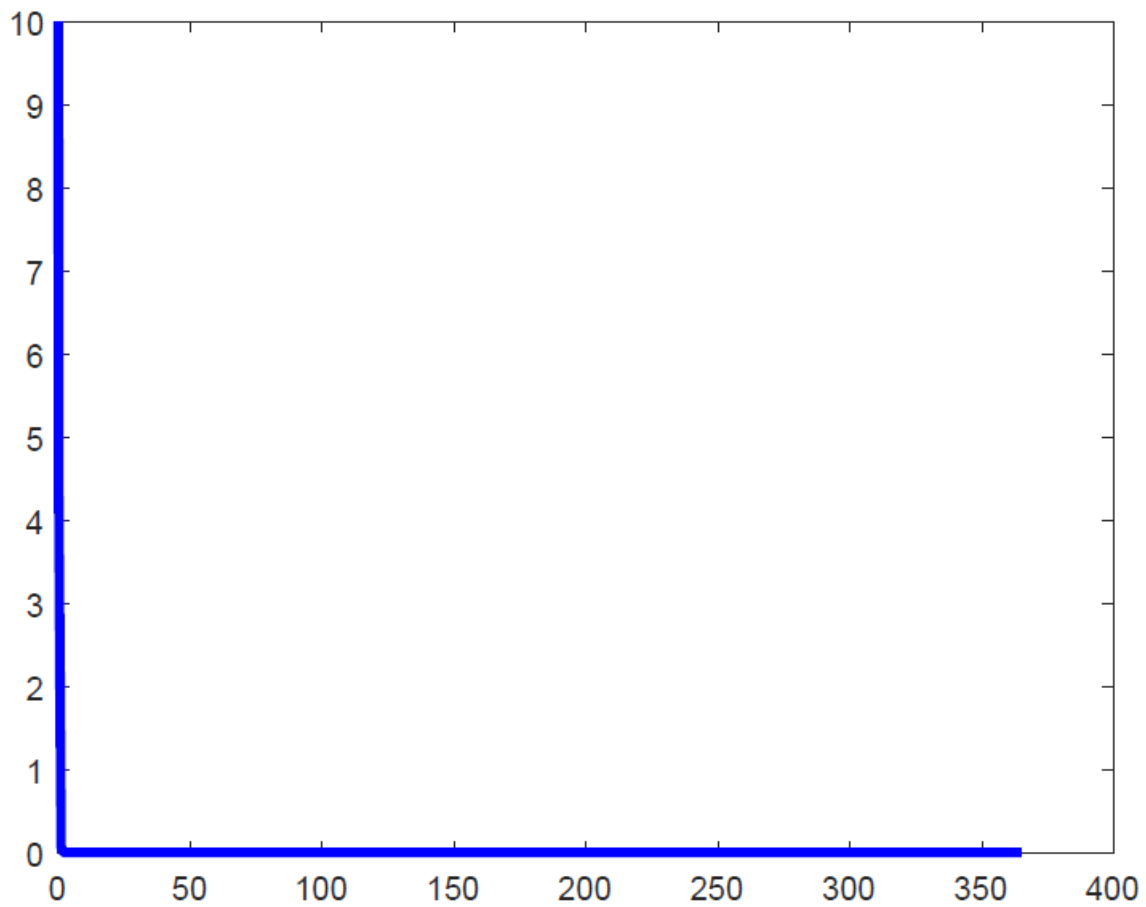


(14) Next increase γ by a factor of 10 (returning β to the first value. Again, how many individuals are infected at the end of 1 year, and how many have recovered?

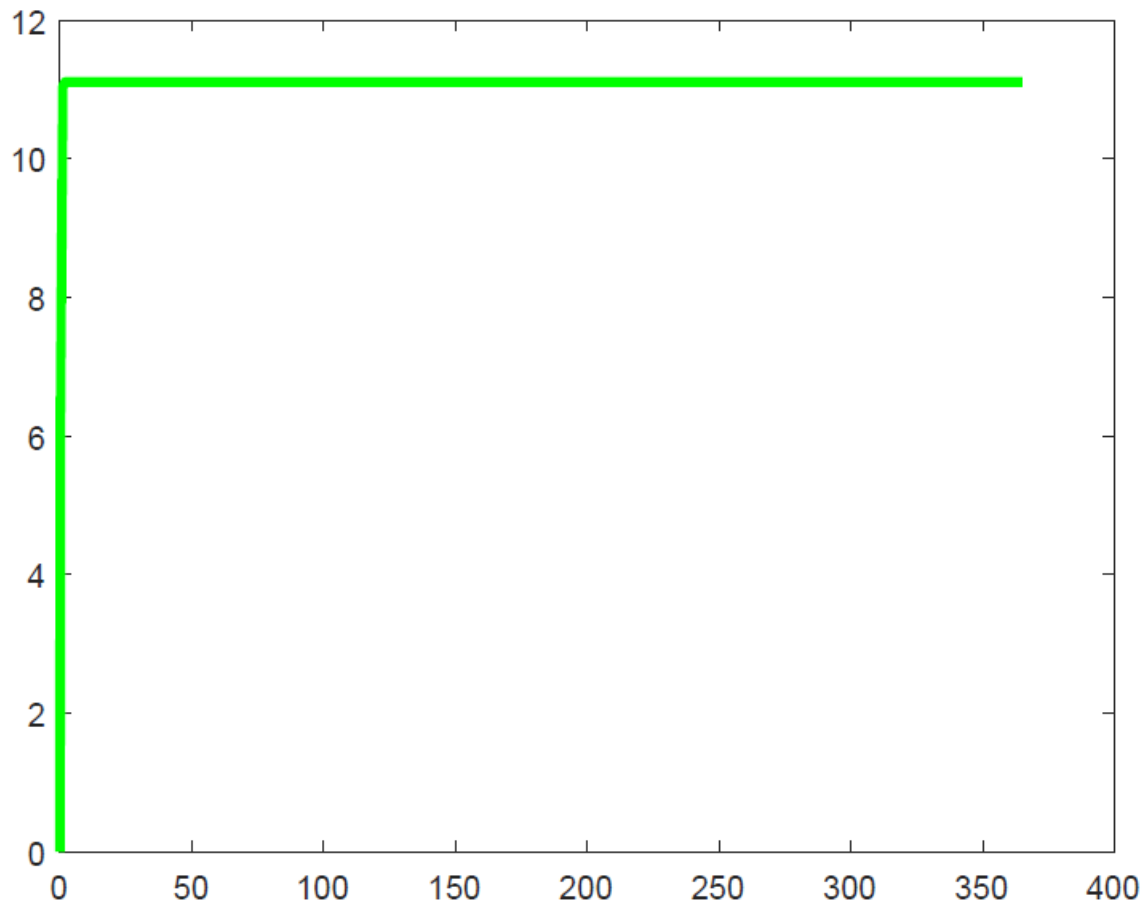
14.



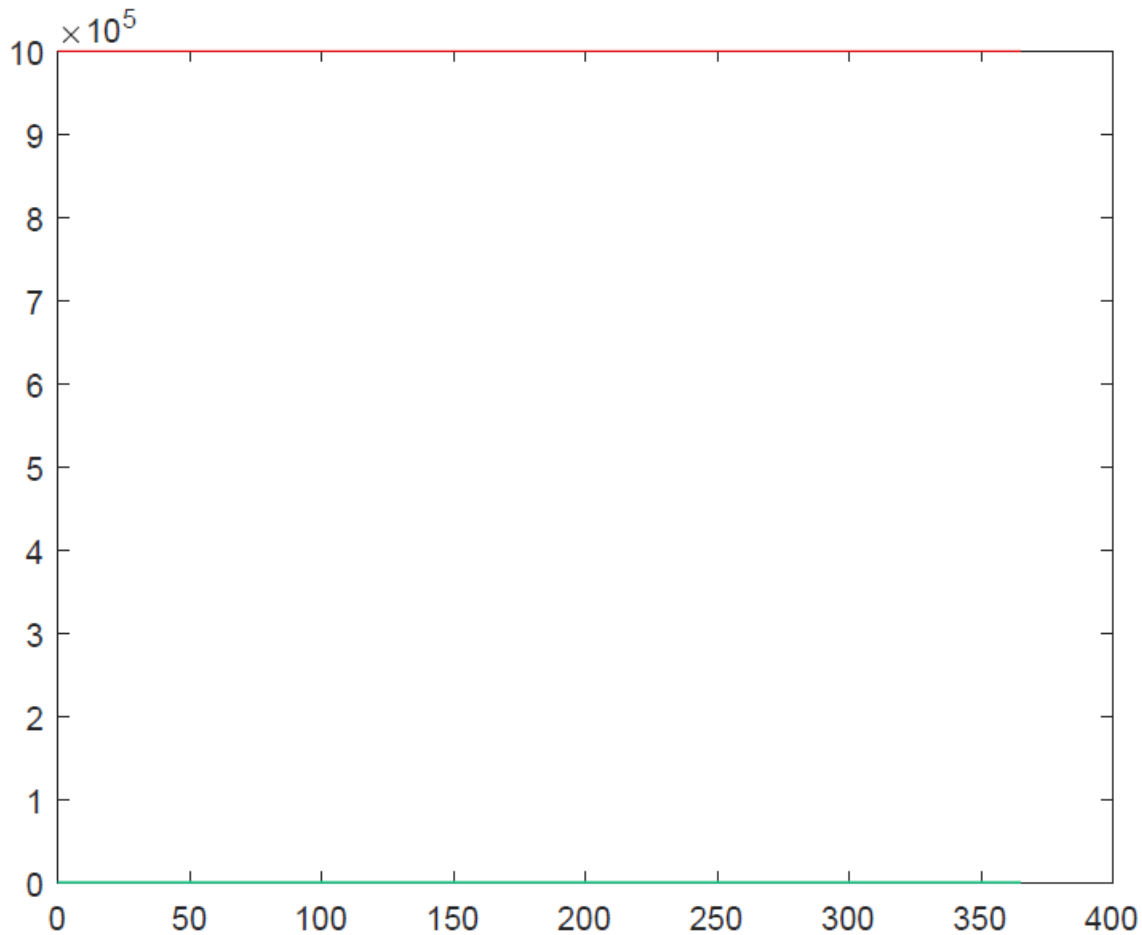
This graph shows the susceptible population over time. Almost no one was infected, leaving almost the entire population susceptible.



This graph shows the infected population over time. Almost no one was infected and the infection died out nearly immediately.



This graph shows the recovered population over time. Only 11 people were infected in total.



At the end of the year, 0 individuals are infected and all 11 infected individuals recovered.

(15) Discuss the biological implications of your results; make sure you discuss how the results may relate to simple public health programs to prevent disease.

15. The implications effectively show that the faster you eliminate infection in individuals, the faster the infection will be eliminated as a whole. Eliminating an infection early on is immensely faster and easier than eliminating it otherwise, and health programs would greatly benefit from enacting serious precautions early on to ensure the infection has no time or ability to spread.

(16) Discuss how you might add this feature into your model; include a schematic diagram to demonstrate your new model. Your model should include a parameter that describes the effectiveness of the quarantine response. Explain how your model can be used to predict how many people will die from the epidemic. Be detailed in your answer.

16. I have included a new proportionality constant in the model that is multiplied by the infection rate. The constant is between 0 and 1 and the smaller the constant, the more effective the methods of quarantine are. A value of 0 would mean the initial infected population are quarantined immediately and so the infection has no chance to spread. A value of 1 would mean the quarantine methods are either completely ineffective or were not used at all. The model predicts how many die from the epidemic by multiplying the mortality rate by the total number of people “recovered” (as in they either died or recovered from the disease). I have included my code using a quarantine constant of .5, which means the infection rate was effectively cut in half. The difference the quarantine makes can be seen in the graphs when compared to the initial problem where the infection rate and recovery rate were unchanged.

Code:

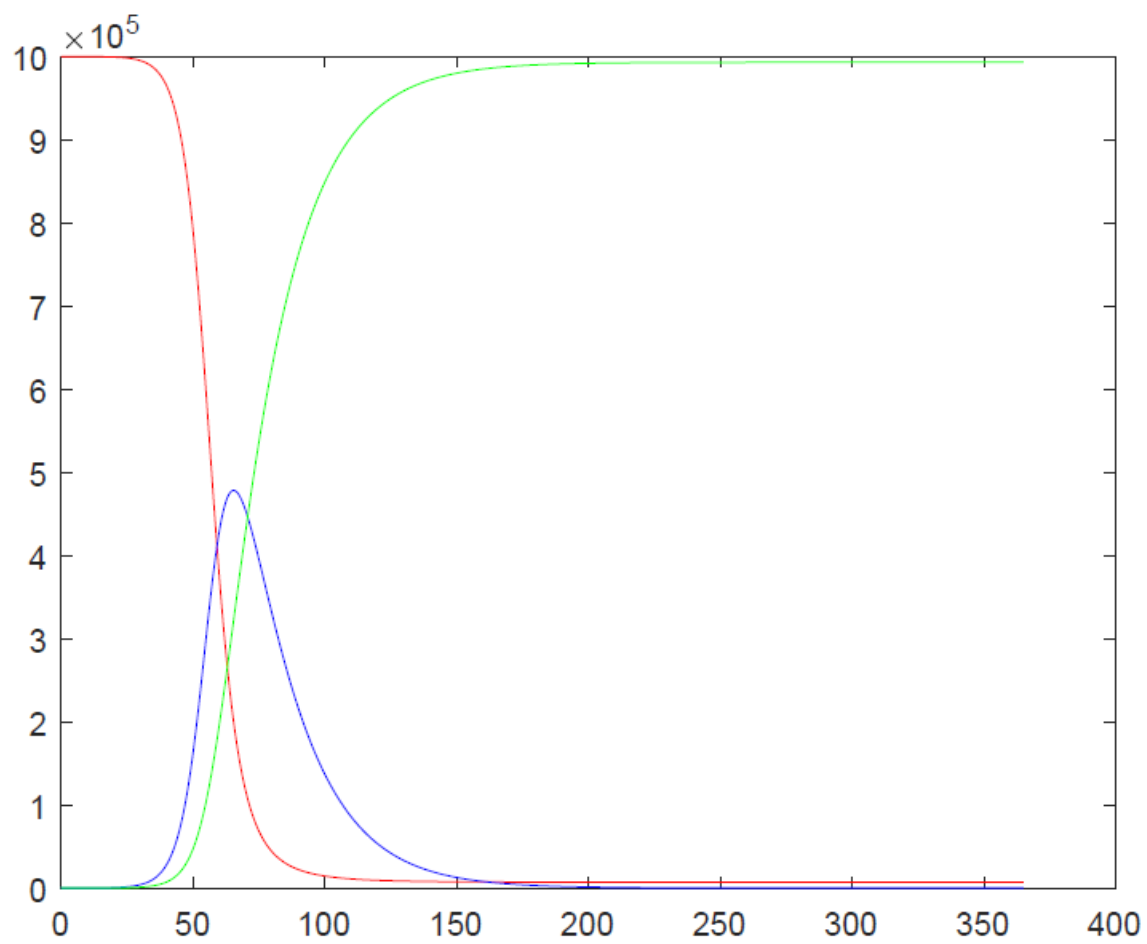
```
%This program uses the forward euler method to create
graphs representing
%susceptible, infected, and recovered populations
a = 0:.001:365;
%This creates a vector for the time that has passed
b1 = zeros(1,365001);
b2 = zeros(1,365001);
b3 = zeros(1,365001);
%This initializes a vector for the population values
b1(1) = 999990;
b2(1) = 10;
b3(1) = 0;
%This sets the initial population
for i = 2:365001
    x = -5*(10^-7)*.5*(b2(i-1))*(b1(i-1)).001;
    y = (5*(10^-7)*.5*(b2(i-1))*(b1(i-1))-.05*(b2(i-
1)))*.001;
    z = .05*(b2(i-1)).001;
    %This finds the product of the derivative and the
interval of time
    b1(i) = (b1(i-1))+x;
    b2(i) = (b2(i-1))+y;
    b3(i) = (b3(i-1))+z;
    %This sums the i-1 value and the derivative times the
interval of time.
end
```

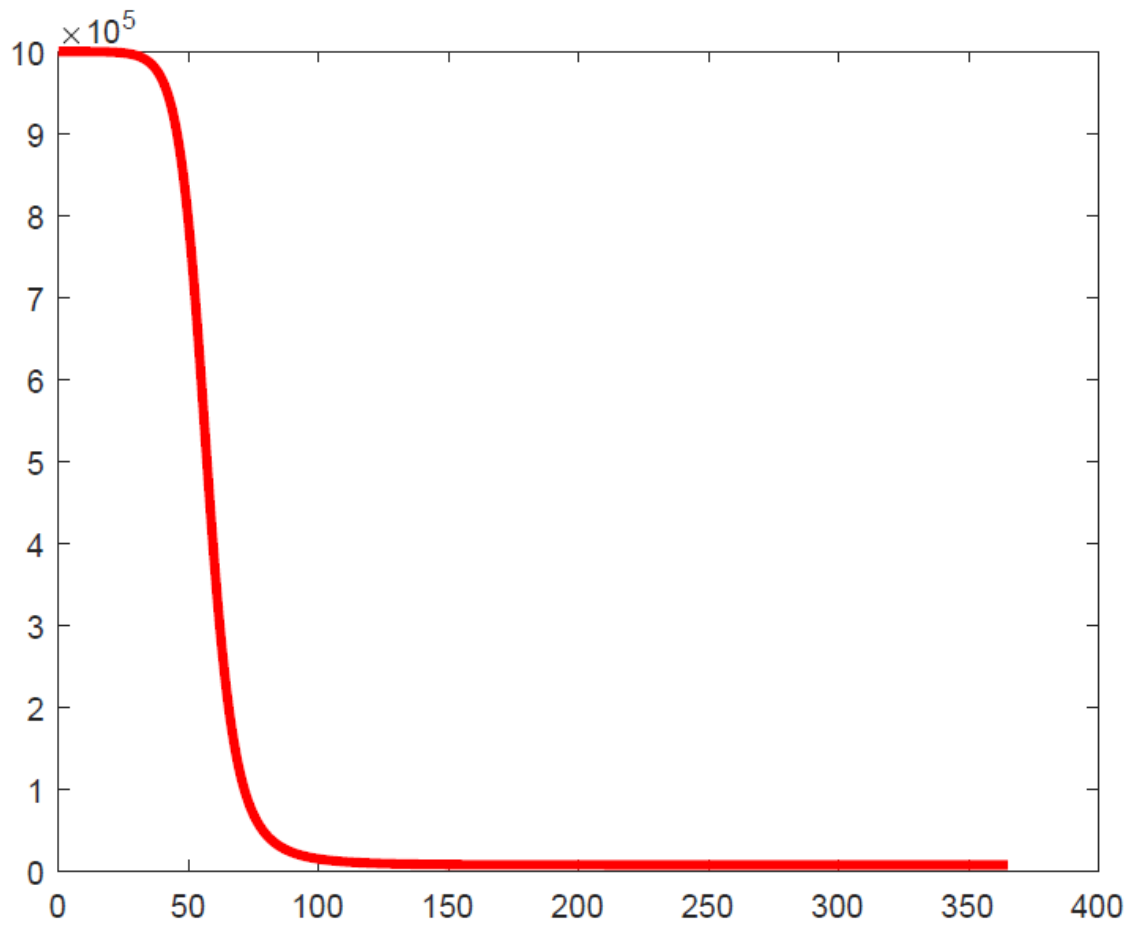
```

%This loop inputs values for a vector for the number of
yeast cells after a
%given time interval
fig1 = figure(1);
plot(a,b1,'-r',a,b2,'-b',a,b3,'-g')
fig2 = figure(2);
plot(a,b1,'-r','LineWidth',3.0)
fig3 = figure(3);
plot(a,b2,'-b','LineWidth',3.0)
fig4 = figure(4);
plot(a,b3,'-g','LineWidth',3.0)
%This creates all plots with the requested parameters
%and changes the handle of the plotted figures to fig1,2,
and 3
print(fig1,'SIRModelAll2','-dpdf')
print(fig2,'SIRModelSusceptible2','-dpdf')
print(fig3,'SIRModelInfected2','-dpdf')
print(fig4,'SIRModelRecovered2','-dpdf')
%This saves the figures as a pdf

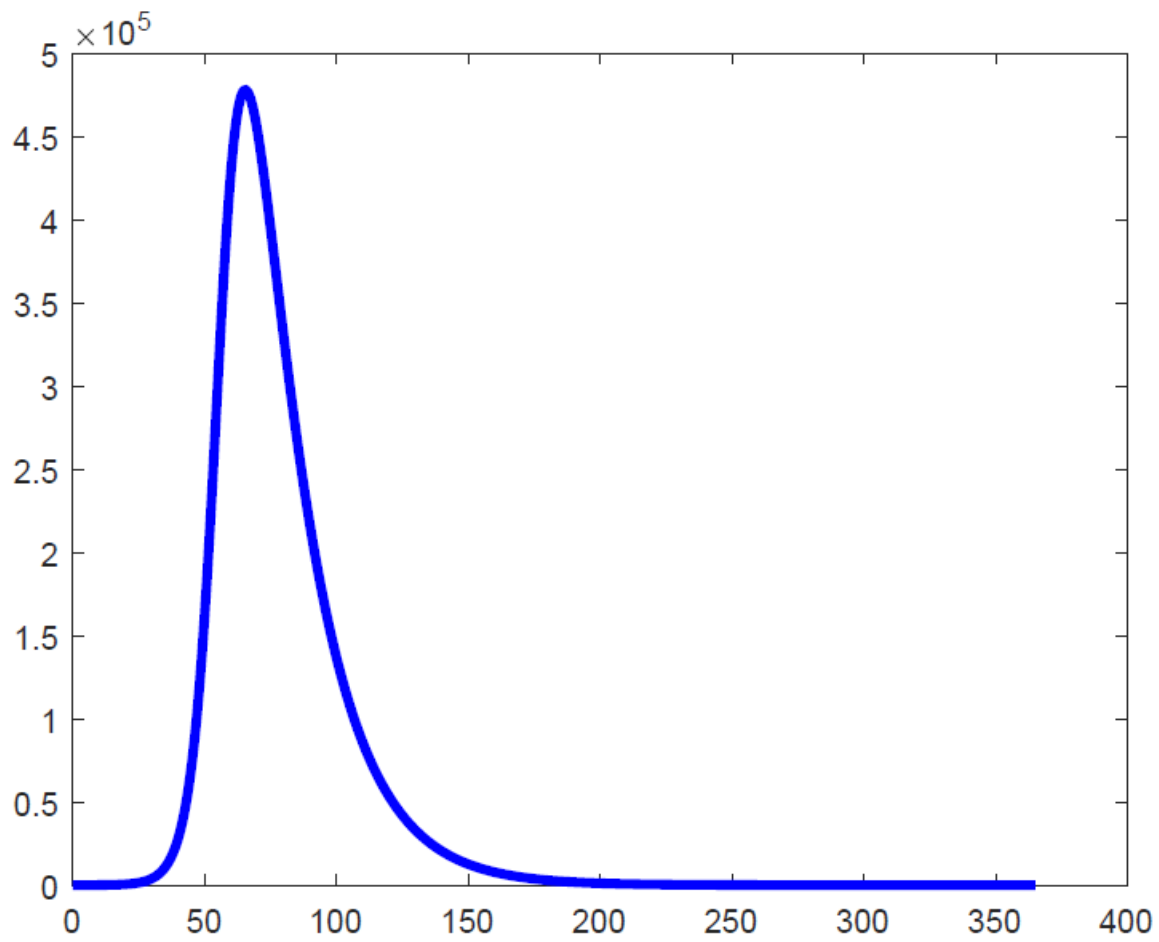
```

Execution:

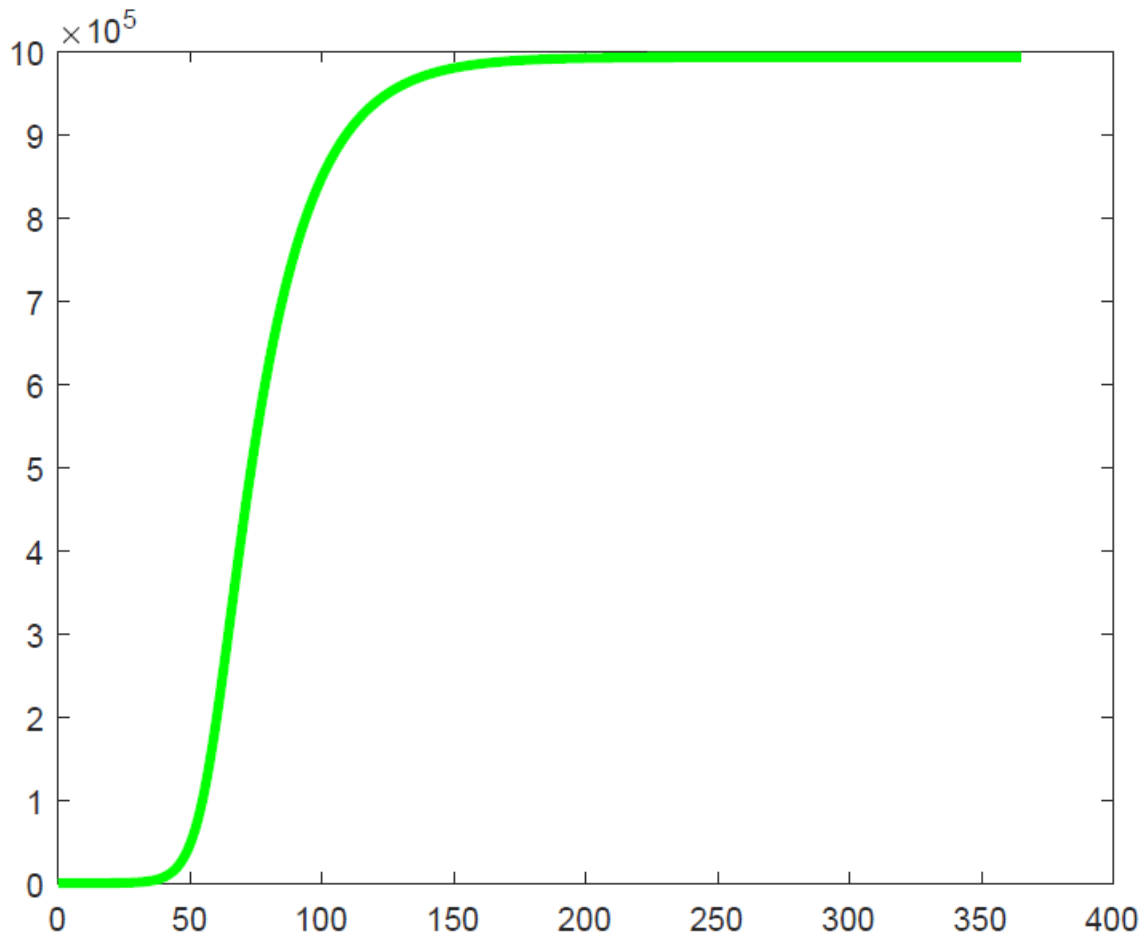




This graph shows the susceptible population over time



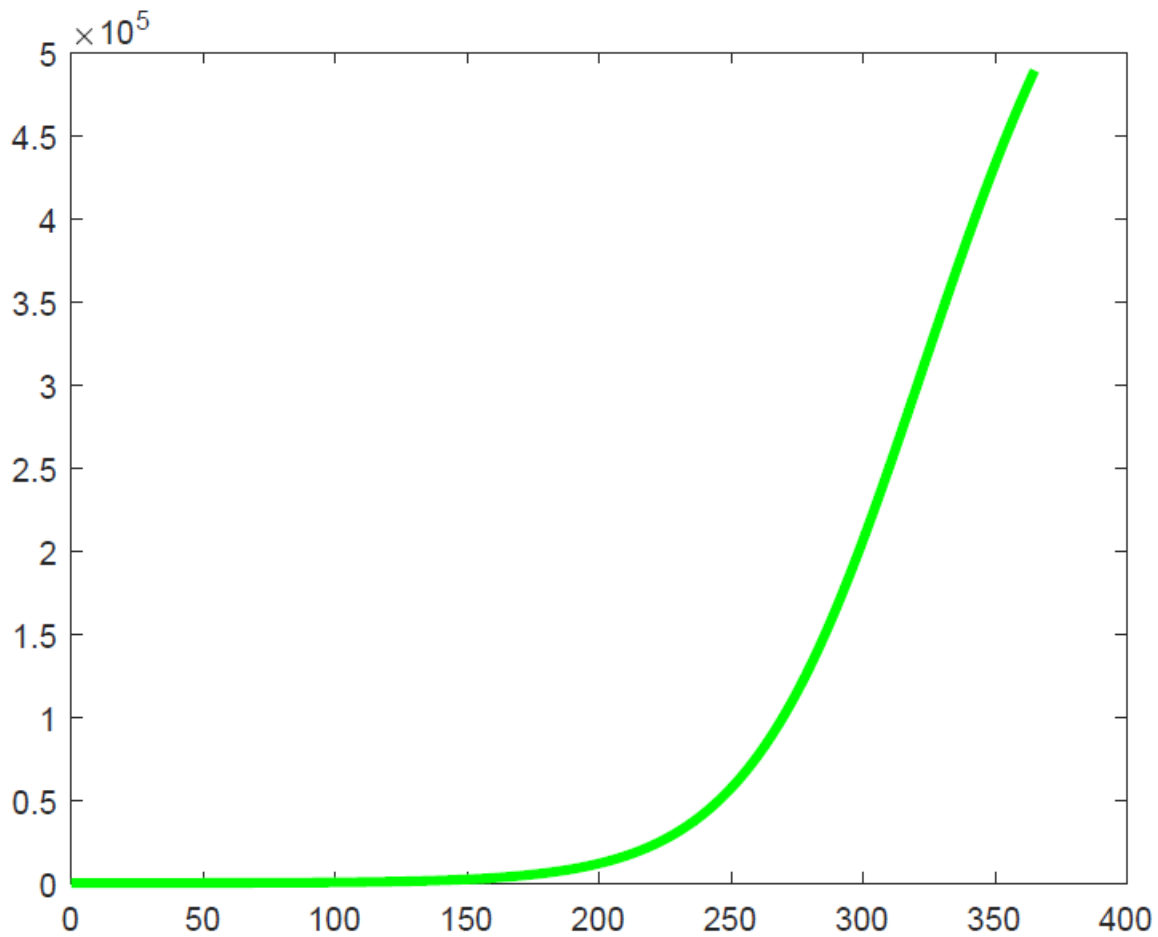
This graph shows the infected population over time.



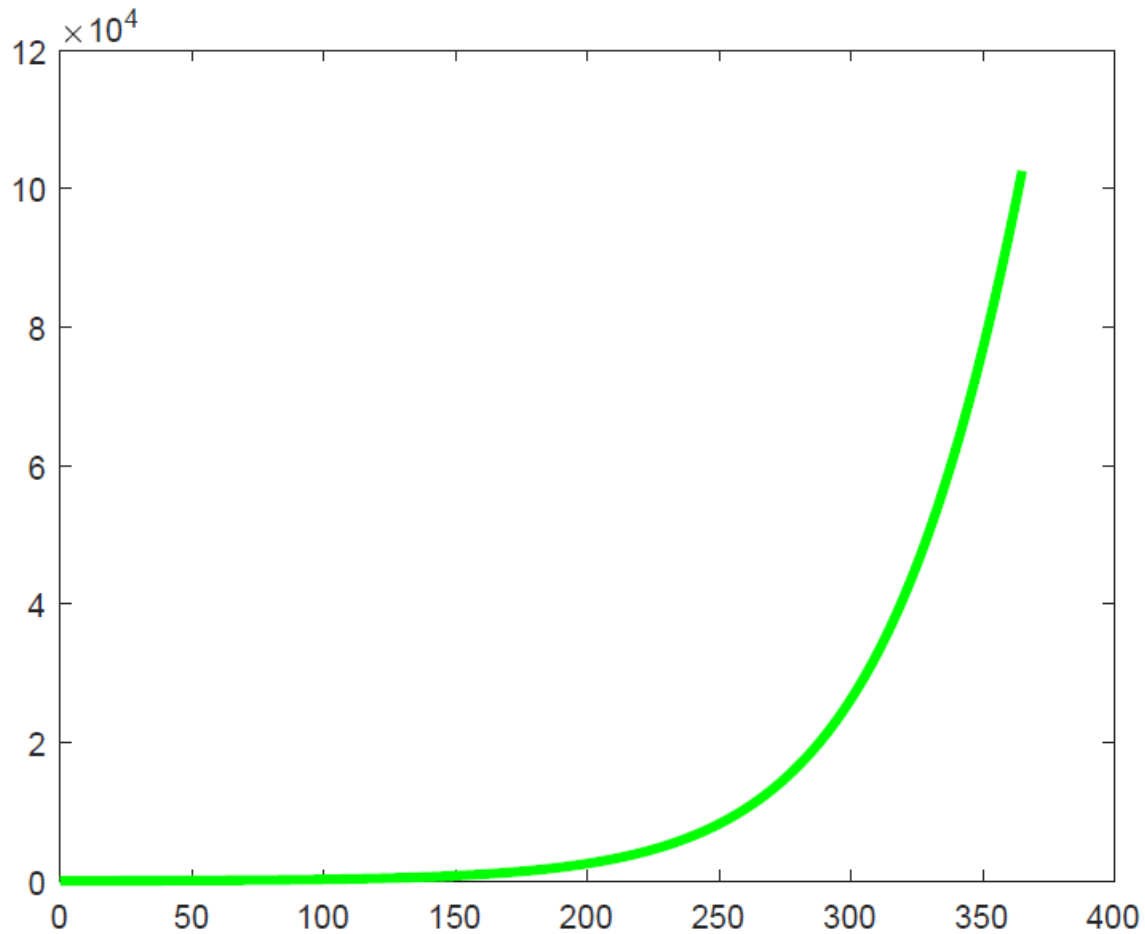
This graph shows the recovered population over time.

(17) Implement the addition to the model that you suggested in (1), and explore how the epidemic changes with different levels of effectiveness. How effective does the quarantine need to be to reduce total deaths by 50%? What about to reduce deaths by 90%, or 99%? Comment on whether this would be a feasible solution.

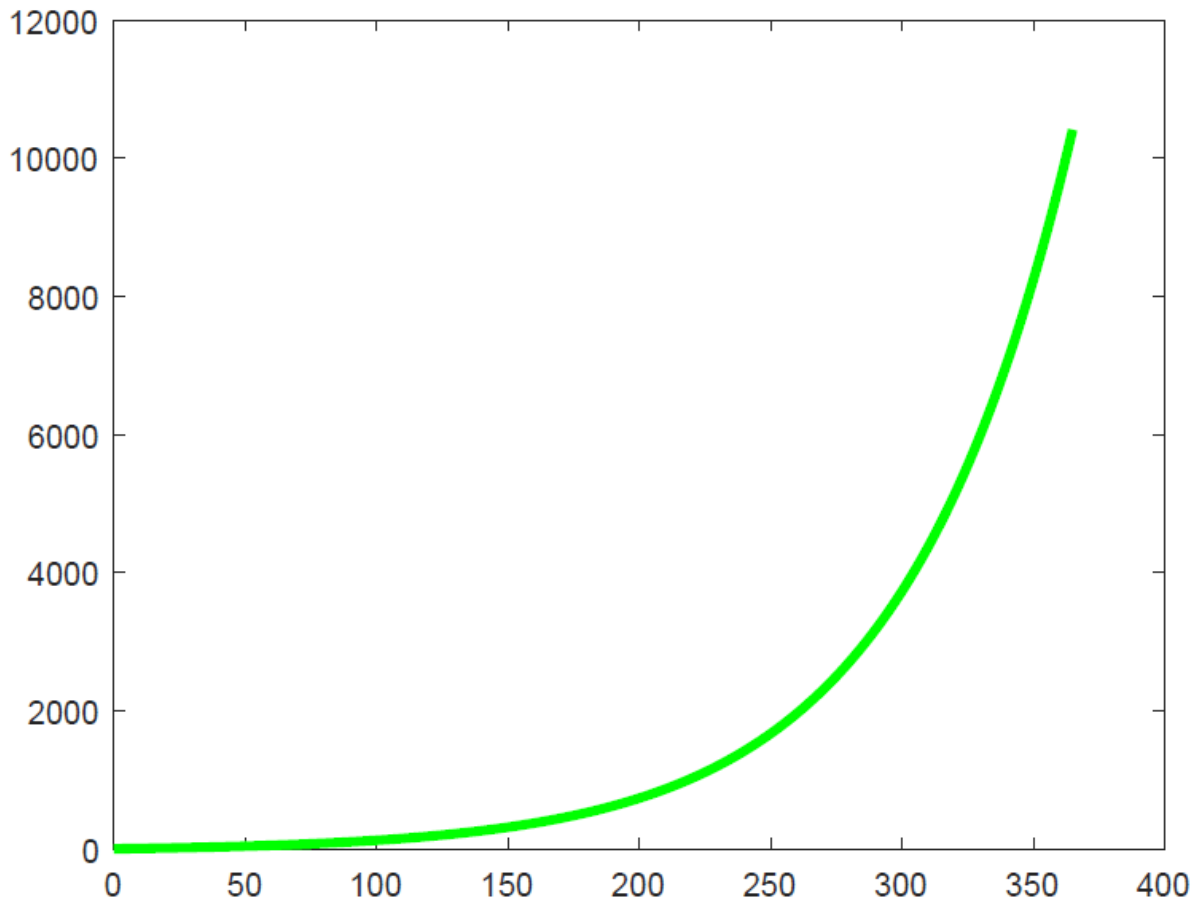
To reduce the total deaths by 50%, the number of recovered individuals must be reduced by 50%. This is achieved when the proportionality constant is approximately .167, and is demonstrated by the graph below. This would mean 83.3% of the infected individuals would need to be quarantined, and whether or not it is feasible depends on a country's resources and number of infections.



To reduce the total deaths by 90%, the number of recovered individuals must be reduced by 90%. This is achieved when the proportionality constant is approximately .148, and is demonstrated by the graph below. This would mean 85.2% of the infected individuals would need to be quarantined, and whether or not it is feasible depends on a country's resources and number of infections.



To reduce the total deaths by 99%, the number of recovered individuals must be reduced by 99%. This is achieved when the proportionality constant is approximately .132, and is demonstrated by the graph below. This would mean 86.8% of the infected individuals would need to be quarantined, and whether or not it is feasible depends on a country's resources and number of infections.



(18) Using your first model as a base, explain how you might add vaccination, and implement this. Again, determine how effective a vaccination program would have to be to reduce the total number of deaths by 50%, 90% or 99%, and comment on the feasibility of this solution.

18. I have cut the initial susceptible population by some percentage to represent the percent of the population that has not yet been vaccinated. Additionally, I have left the quarantine constant at .5 to give the idea that only 50% of the infected population can be quarantined at any point in time. My example code has the susceptible population cut by 20%, which is to say 20% of the initial susceptible population was vaccinated and no longer susceptible. The model predicts how many die from the epidemic by multiplying the mortality rate by the total number of people “recovered” (as in they either died or recovered from the disease). I have included my code using a quarantine constant of .5, which means the infection rate was effectively cut in half. The difference the quarantine, with the addition of vaccinations, makes can be seen in the graphs when compared to the initial problem where the infection rate and recovery rate were unchanged.

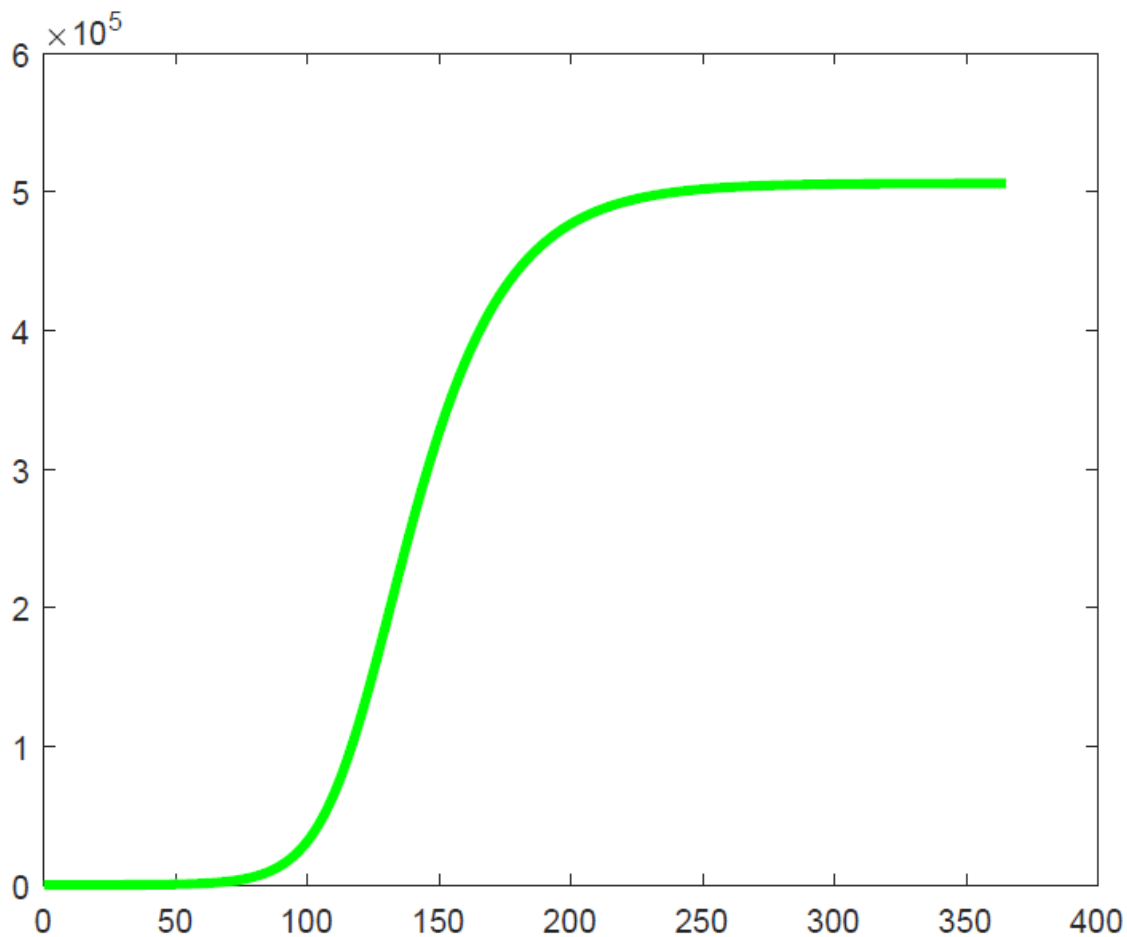
Code:

```
%This program uses the forward euler method to create
graphs representing
%susceptible, infected, and recovered populations
a = 0:.001:365;
%This creates a vector for the time that has passed
b1 = zeros(1,365001);
b2 = zeros(1,365001);
b3 = zeros(1,365001);
%This initializes a vector for the population values
b1(1) = 999990*.8;
b2(1) = 10;
b3(1) = 0;
%This sets the initial population
for i = 2:365001
    x = -5*(10^-7)*.5*(b2(i-1))*(b1(i-1)).*0.001;
    y = (5*(10^-7)*.5*(b2(i-1))*(b1(i-1))-.05*(b2(i-
1))).*0.001;
    z = .05*(b2(i-1)).*0.001;
    %This finds the product of the derivative and the
interval of time
    b1(i) = (b1(i-1))+x;
    b2(i) = (b2(i-1))+y;
    b3(i) = (b3(i-1))+z;
    %This sums the i-1 value and the derivative times the
interval of time.
end
%This loop inputs values for a vector for the number of
yeast cells after a
%given time interval
fig1 = figure(1);
plot(a,b1,'-r',a,b2,'-b',a,b3,'-g')
fig2 = figure(2);
plot(a,b1,'-r','LineWidth',3.0)
fig3 = figure(3);
plot(a,b2,'-b','LineWidth',3.0)
fig4 = figure(4);
plot(a,b3,'-g','LineWidth',3.0)
%This creates all plots with the requested parameters
%and changes the handle of the plotted figures to fig1,2,
and 3
print(fig1,'SIRModelAll2','-dpdf')
print(fig2,'SIRModelSusceptible2','-dpdf')
```

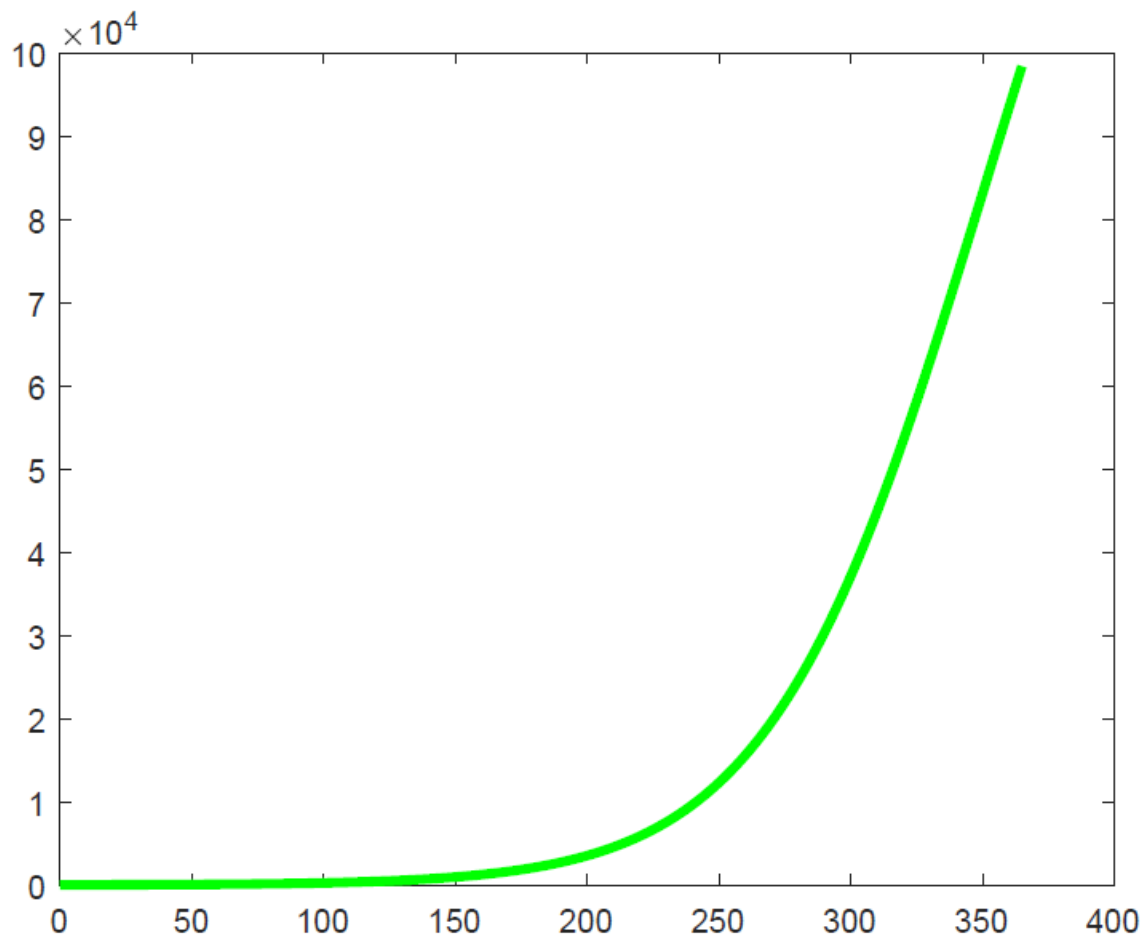
```
print(fig3, 'SIRModelInfected2', '-dpdf')
print(fig4, 'SIRModelRecovered2', '-dpdf')
%This saves the figures as a pdf
```

Execution:

To reduce the total deaths by 50%, the number of recovered individuals must be reduced by 50%. This is achieved when the quarantine constant is approximately .5, and the percentage of the population vaccinated is approximately 45% and is demonstrated by the graph below. This would mean 50% of the infected individuals would need to be quarantined, and 45% would have to be vaccinated prior to outbreak of the infection, and whether or not it is feasible depends on a country's resources and number of infections.



To reduce the total deaths by 90%, the number of recovered individuals must be reduced by 90%. This is achieved when the quarantine constant is approximately .5, and the percentage of the population vaccinated is approximately 69.5% and is demonstrated by the graph below. This would mean 50% of the infected individuals would need to be quarantined, and 69.5% would have to be vaccinated prior to outbreak of the infection, and whether or not it is feasible depends on a country's resources and number of infections.



To reduce the total deaths by 90%, the number of recovered individuals must be reduced by 90%. This is achieved when the quarantine constant is approximately .5, and the percentage of the population vaccinated is approximately 73.5% and is demonstrated by the graph below. This would mean 50% of the infected individuals would need to be quarantined, and 73.5% would have to be vaccinated prior to outbreak of the infection, and whether or not it is feasible depends on a country's resources and number of infections.

