

## Modeling Lab 5: Population Models

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### ABSTRACT

Population models are can be described by sets of differential equations. The equations are dependent on several factors including growth (and decay) rate, size constraint and initial conditions.

Growth rate relates to the proportion of births to death, if we are talking about a census model. This value could also describe other relationships between variables, for example, a decay rate is used to describe the relationship between how many rabbits a fox needs to eat to stay alive; this is the similar to a growth rate, but negative. Next, the size constraint is of importance due to its limiting factor. This value is coupled with the traditional exponential growth rate to suppress the population of a certain problem. This constraint accounts for all the resources in an area, including food, land, and allowable density. A decay constraint can be added onto exponential growth in order to simulate an accurate model of population, not one that does not allow for the population to encounter complications in environmental factors and land to spread out into and continues to grow forever. The final variable of note here is the initial conditions. The equations depend directly on these values as they set how the equation begins its trend. If these values are chosen to be higher than the true initial value, then the exponential aspect of the equation spirals quickly out of control. If they are smaller, the decay aspect can have a larger than accurate impact on the final product.

All these variables come into play when plotting the differential equations and can have a significant impact on the final outcome of the population model if they are varied even slightly.

### 1. INTRODUCTION TO THE VERHULST MODEL

Last week, with the Feigenbaum map, we plotted equation [1]. This only accounted for the exponential growth of a population model. The result of this equation was several oscillating values for  $x$ , which ultimately resulted in chaos.

$$x_{n+1} = rx_n(1 - x_n) \tag{1}$$

In order to modify this to model to be used on actual physical population models, we must introduce size constraints. This is done as described in the introduction with the size constraint,  $N$ .  $N$  is set to be the environmental limiting factor for the model, this includes the resources like water, food, shelter and density limit, just to name a few. This does not have to be only the discovered resources. For example, the  $N$  value before and after the westward exploration in the US was the same since the land and resources were available even if the settlers at the time weren't aware of it.

This expression of decay (equation [2]) in addition to exponential growth (equation [3]) results in the Verhulst equation given in equation [4]. Here  $k$  is our growth ratio as described in the introduction.

It represents the fraction of birth to death rate for the population.

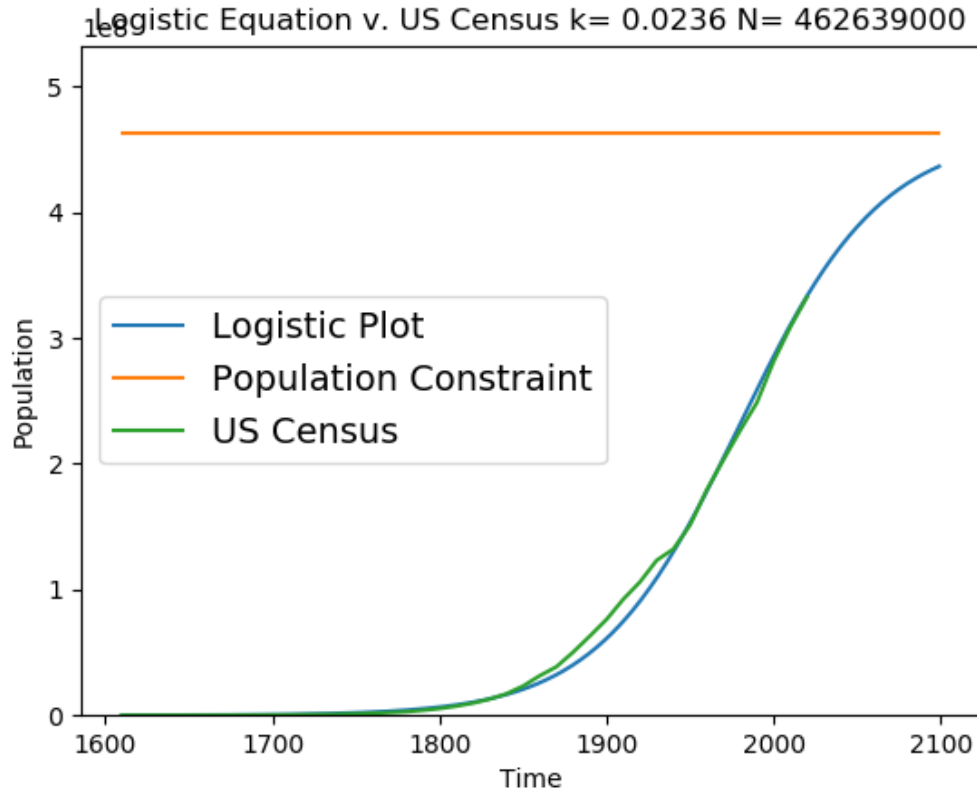
$$N = \frac{1}{\frac{1}{N_0} - kt} \quad (2)$$

$$N = N_0 e^{kt} \quad (3)$$

$$\dot{P} = kP(1 - \frac{P}{N}) \quad (4)$$

### 1.1. Population Model for US from 1610 to 2020

For this section, we were given the population statistics for the US in the past 410 years. This was modeled in a plot after importing the data to the python project. In Figure [1] this is included in green. We can see that for this specific time the growth is still exponential, so the US is not currently running into any issues with resources (enough to limit the population). As an aside, there was a lot of conflicting arguments for the carrying capacity of the US, some as high as 7 billion and some as low as 100 million (which we have already surpassed due to their dismay).



**Figure 1.** Verhulst Model for the US Census from 1610 to 2020.

When plotting the Verhulst Model, there is no precedent for the initial conditions so they must all be inferred or found. For the initial population I used 75,000 people. This is not the initial value on

the census for 1610, but there was a period of massive increases as the census scrambled to include all the people they had missed in the first few years and until about 1650 when it leveled off. This was also the time period where we saw a huge leap in growth rate due to the pilgrims arriving, with  $k$  values up to 500%. Because of this I elected to start the initial value at 75,000 in order to more stabilize the  $k$  value for the rest of the years. I chose 1950- onwards to base my value for  $k$ , because I felt this was the best representation for finding the current growth rate value for the US population and the census overall. This resulted in a  $k$  value ranging from 0.2-0.3. After this  $k$  range was found it was ran with steps of 0.001 each of which was printed to a save file and 0.0236 was resolved as the most accurate  $k$ . The same was run for a range of  $N$  values eventually settling on  $N=432,639,000$ . Attached is the initial and final process of finding these values. (Verhulst\_init.gif and Verhulst\_final.gif).

We can see that when this is plotted there is a non-accurate section from around 1850- 1950. This can be explained as a lag in population growth due to the Civil War in the 1850 time frame, then when the population was trying to rebuild, WW1 happened in 1910, and then this continued the trend until after the Great Depression in 1940 where we see the baby boom in 1950-1960 and the population is back with the current growth value.

We see a leveling off soon as the US faces problems with the limiting factor due to environmental impact on the agriculture, and habitability, this will occur in around 2100. The land filling up is also a large factor in this instance where the farmable land and livable land begin to compete. If the trend of growth rate and environmental impact doesn't change in the next few years then we will have to face the consequences in 2100.

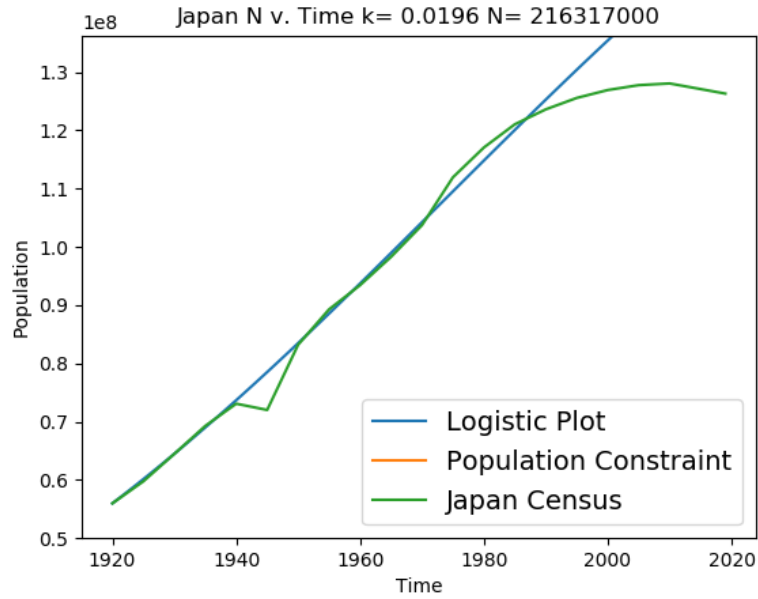
### 1.2. *Population Model for Japan 1920 - 2020*

It is well known to us that there was a significant impact on the population of Japan in the 1950s: WW2 and the atomic bombs. In Figure [2] we can see the census for Japan's population over time. There is the predicted sharp dip in population in 1945, but after that we see Japan recovering. This is not to say that the land recovered though. As we can see the high  $N$  model is not a good fit after around 1970.

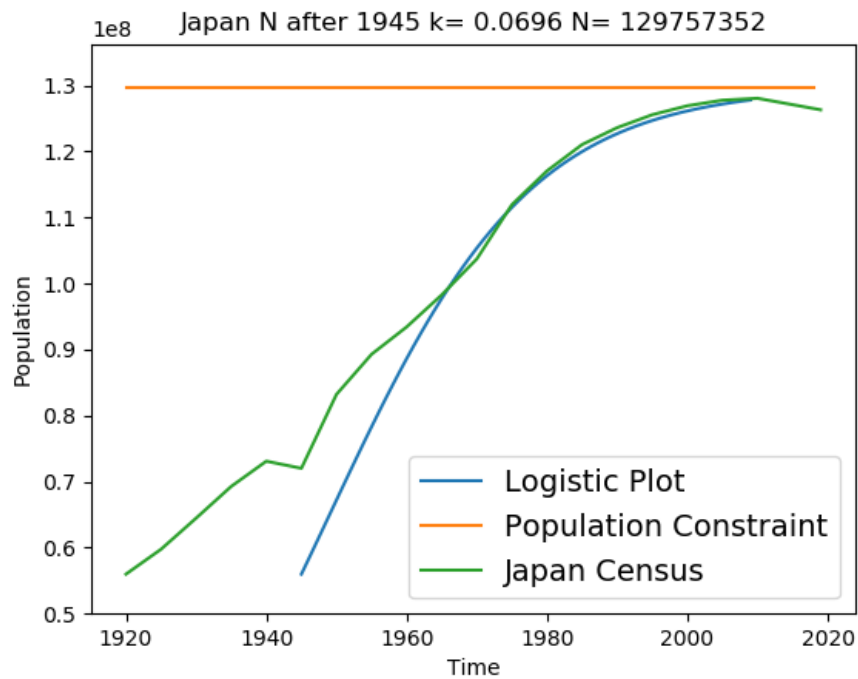
This discrepancy is due to the effect of the atomic bombs on the environment of Japan, not its direct effect on the population. The atomic bombs did not significantly impact the number of people in Japan right after the war, but it did have a large impact on its carrying capacity.

We see in Figure [2] that the carrying capacity before 1970 was 216,317,000 (with a  $k$  value of 0.0196). After 1970 we can see a dampening effect of the population over time. This is because of the atomic bombs which lowered the nation's carrying capacity to only 129,757,352 people just slightly more than their current population, shown in Figure [3]. This is the most accurate model now, but when more data accrues (after 2020) then we can begin to see the effect of reaching the  $N$  has on the nation. It will most likely oscillate around the  $N$  value and then eventually settle onto the  $N$  value and continue on in a straight line. Since this has not happened yet, this is the best approximation of the  $N$  value now.

It is of note that the  $k$  value also increased for this post-war model. This is because there was an economic boom in the 70s for Japan and its manufacturing industry that caused an increase in the economy and thereby the growth rate. This is shown in the change in slope at 1970, this was accounted for in determining the growth rate and  $N$  for post-1945 Japan. This increase could have decreased the time it took Japan to reach the carrying capacity.



**Figure 2.** Verhulst Model for the Japan's Census from 1920 to 2020. Notice that this model is only accurate until 1970.



**Figure 3.** Verhulst Model for the Japan Post WW2 Census from 1945 to 2020. The population was slightly affected in 1945 when the bomb was dropped but quickly recovered. But the bomb's effect still carried substance in the carrying capacity. The environmental impact from the atomic bomb on the population is not seen until 1970.

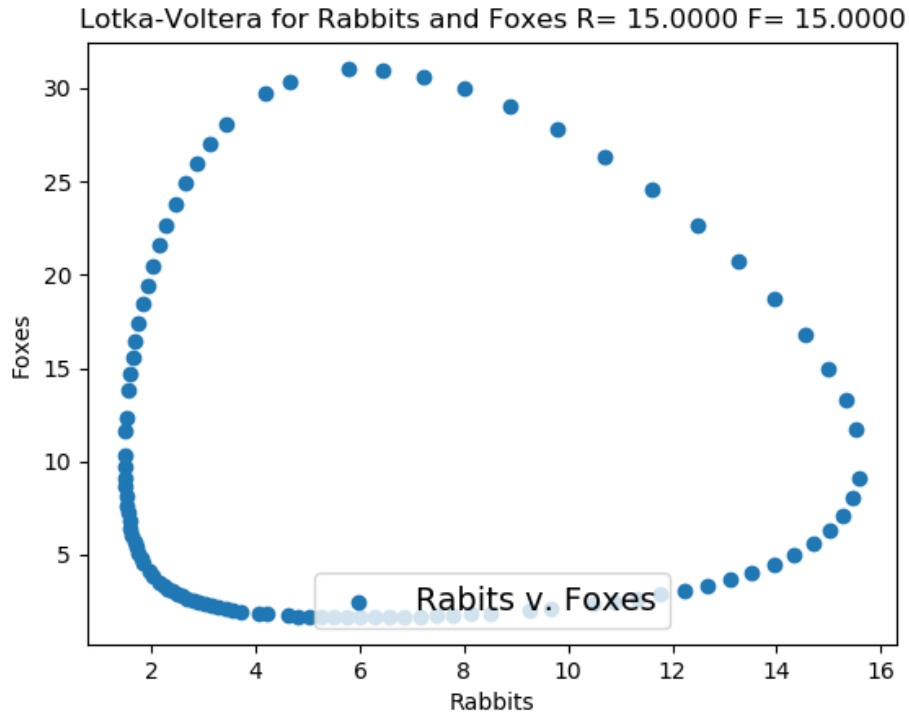
## 2. INTRODUCTION TO LOTKA-VOLTERRA

The Lotka - Volterra model draws upon the Verhulst equation, but under a *slightly* different context. It is still dependent on still growth values but in these differential equations they are several different values, not one for the population growth. This model is describing the interaction between two interactors, predator and prey, where one has unlimited food, but a defined growth rate and the other, the predator, can unlimitedly eat the prey but is limited by the occurrences of meeting. These are modeled through differential equations that change depending on initial conditions, growth rates and the passage of time. They are given in equation [5,6].

$$\dot{R} = \alpha R - \beta RF \quad (5)$$

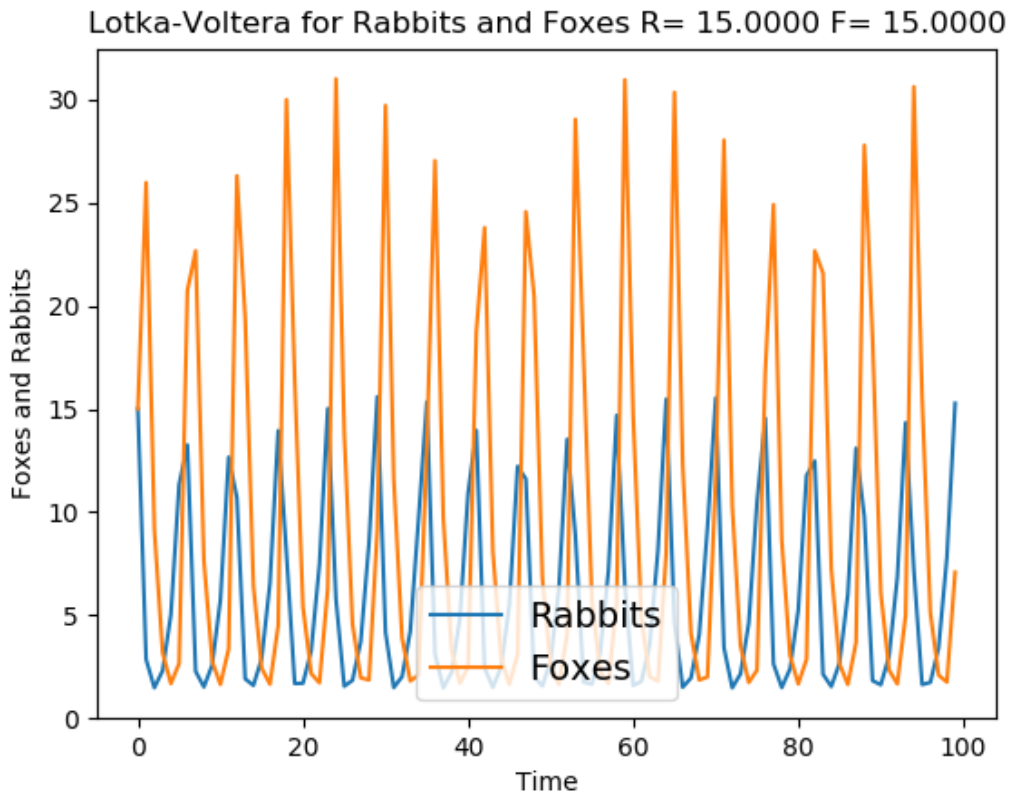
$$\dot{F} = \gamma RF - \delta F \quad (6)$$

The growth values are  $\alpha, \beta, \gamma$ , and  $\delta$ , these are shown in equation [5,6] and they all stand for different growth values. Here we are modeling the interaction between rabbits (prey) and foxes (predators).  $\alpha$  stands for the birth to death rate of the rabbits, so how fast they can grow, I have mine set to 1.0 for the proceeding figures.  $\beta$  is the encounter rate between rabbits and foxes, mine is 0.1.  $\gamma$  is the catch rate of rabbits by foxes, mine is 0.25. Finally,  $\delta$  is a representation of the foxes dying if they do not catch a rabbit, mine is set to 1.5.



**Figure 4.** Lotka Volterra Model for Rabbits = 15, Foxes=15. This is a stable orbit.

For my first plot, Figure [4], I have set the growth parameters as given above and my initial values for fox and rabbit are both 10 animals. This results in a stable interaction where the foxes eat the

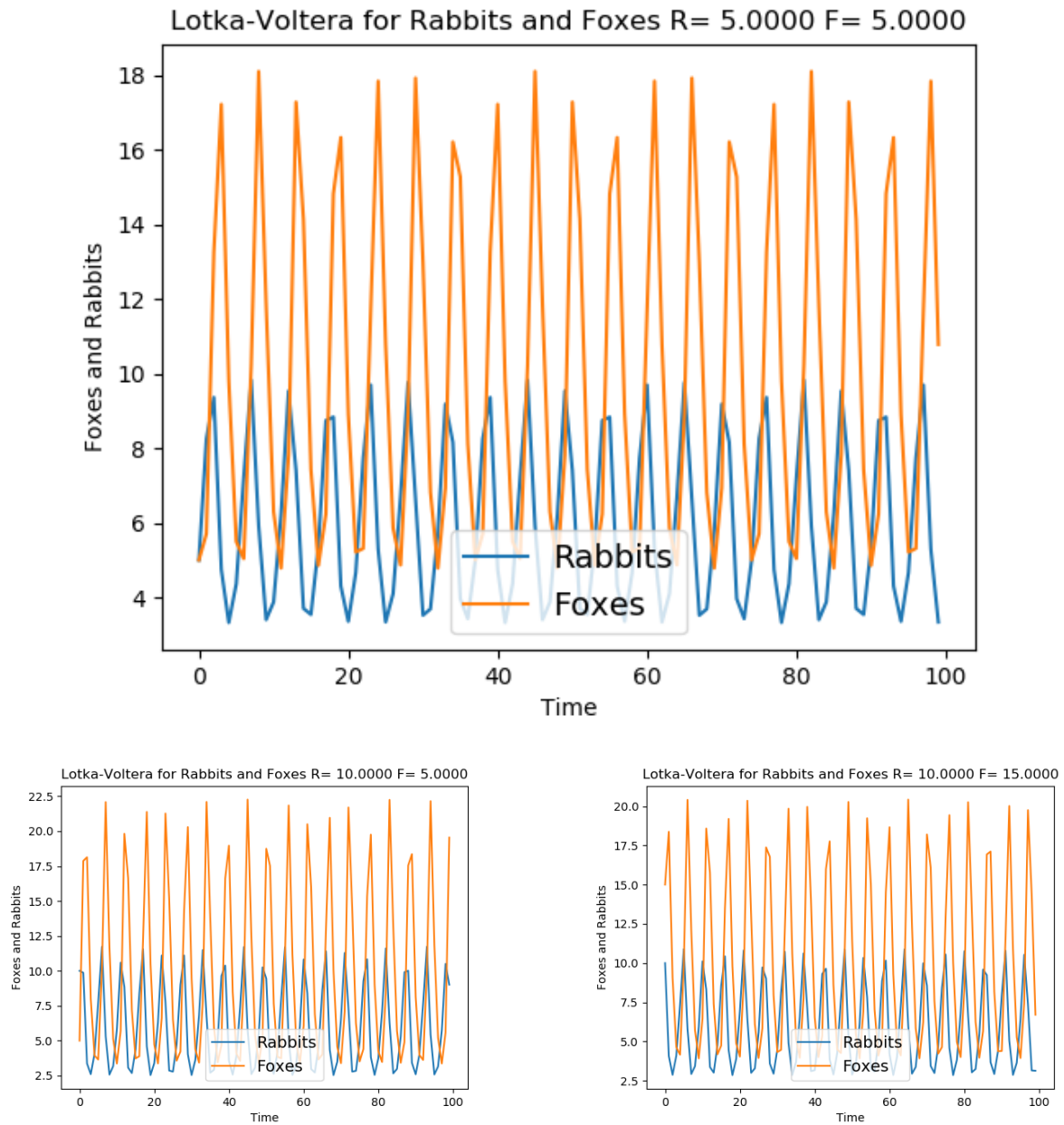


**Figure 5.** Lotka Volterra Model for Rabbits = 15, Foxes=15 with respect to Time. This is a stable orbit. Notice that the foxes are more and less numerous than the rabbits periodically while the rabbits are quite stable around their initial condition.

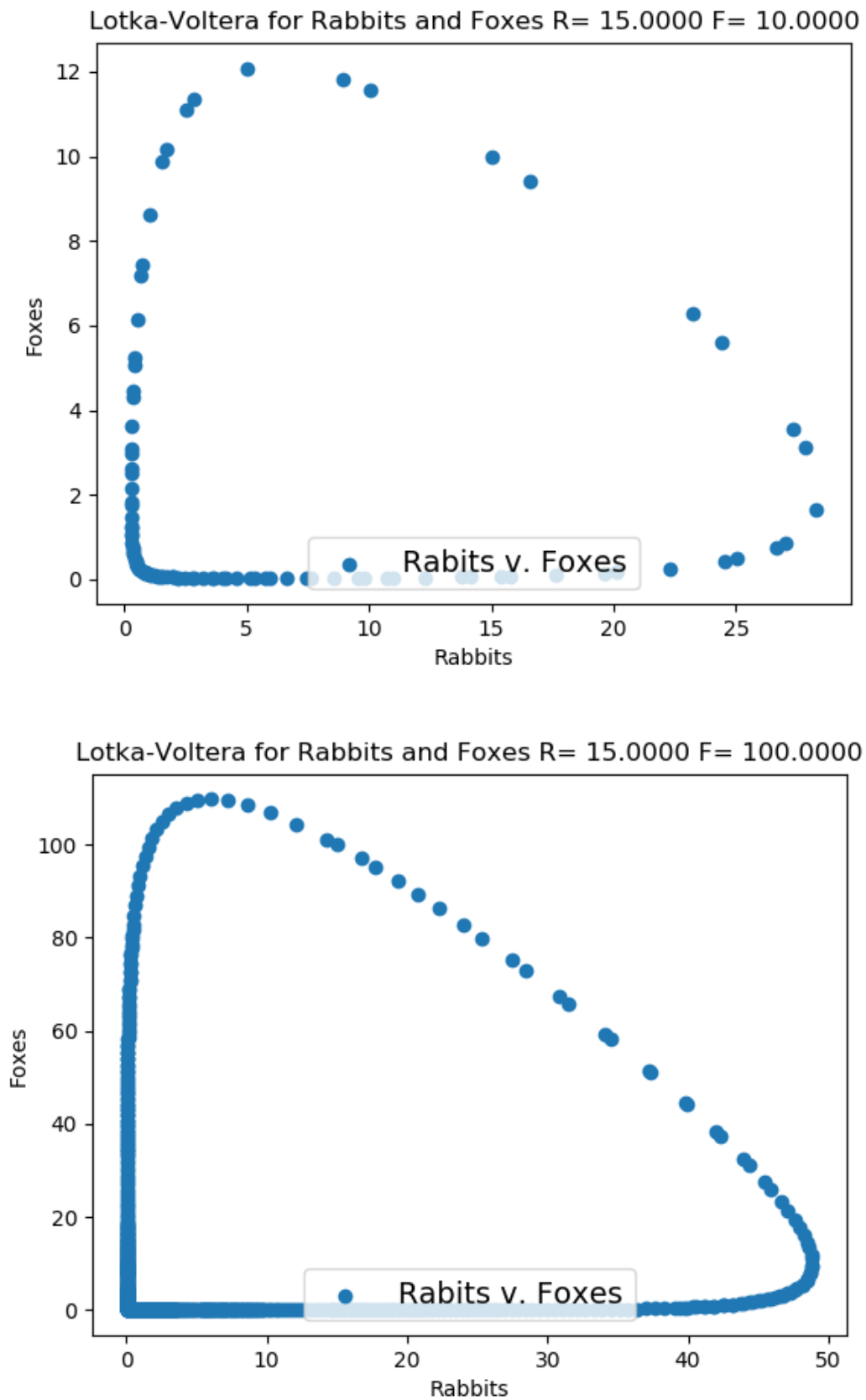
rabbits if they grow too populous and the rabbits have lots of babies if the foxes begin to die off. In Figure [5] this is shown as a function of time. It is clear that fox have larger oscillations than the rabbits. This is due to the initial growth rate conditions. In Figure [6] we see more stable orbits in the time dependent plot form. It should be noted that in all of the pot titles in the project, the *initial values* for each animal are shown.

Next, we have Figure [7a] where Rabbits=15 and Foxes=10. This represent orbits where the fox and rabbit value go down to less than one at several instances. The less than one value is not reached in Figure [7a] so this is still stable, but we can see this (0,0) point beginning to form. This is exaggerated in Figure [7b] where  $R=15$  and  $F=100$ . Here the sharp corner at 0,0 (nearly) represents a flaw in the differential equations where the program accounts for very small values of  $R$  and  $F$  were they are less than one but more than zero so they can become another fox after a while even if there was at one point  $10^{-5}$  of a rabbit which cannot happen in real life. This is also shown in time dependent plots shown in Figure [8].

Trying to set several variables to int in various locations of the program does not work to solve the problem of encountering less than one rabbit or fox either. Figure [9] shows examples of trying to fix this in this manner. There must be new equations developed in order to solve for this shortcoming.

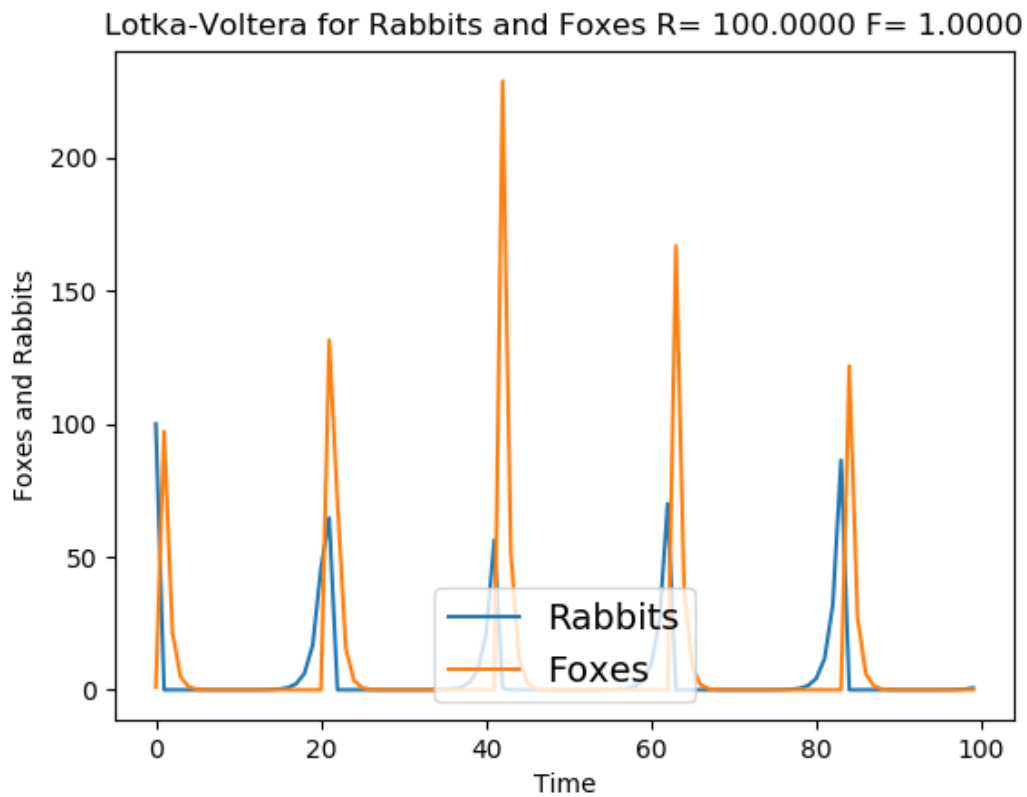
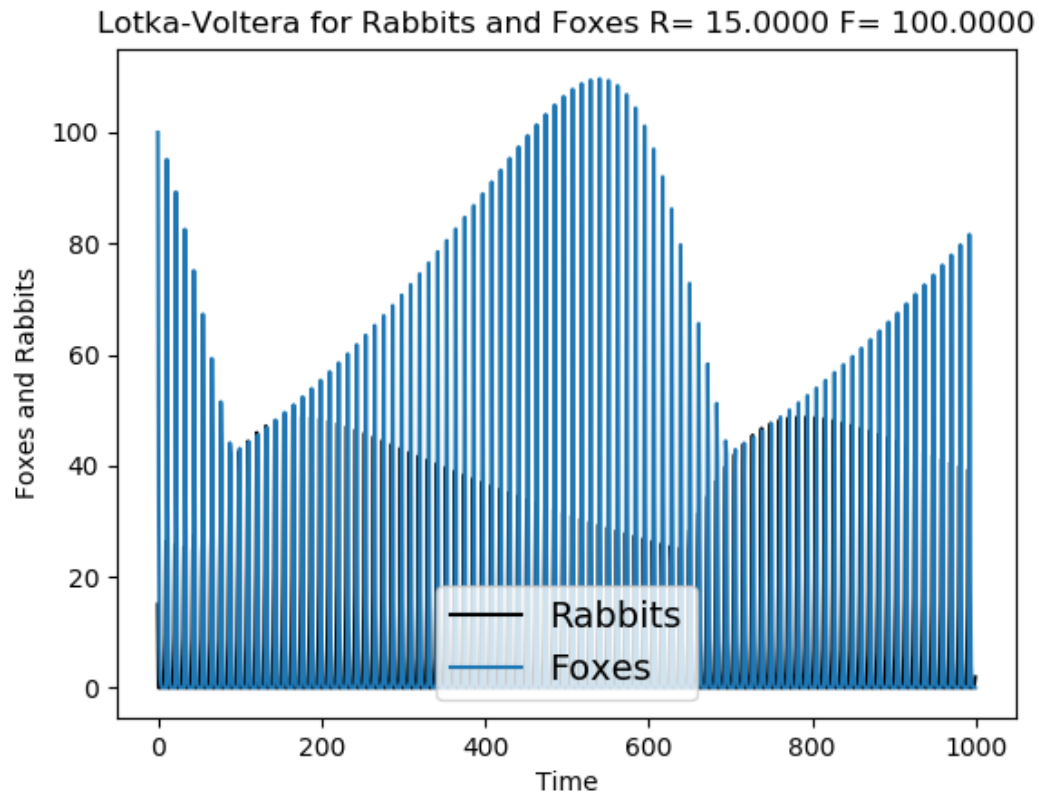


**Figure 6.** Lotka Volterra Models showing stable orbits in the time dependent plots.

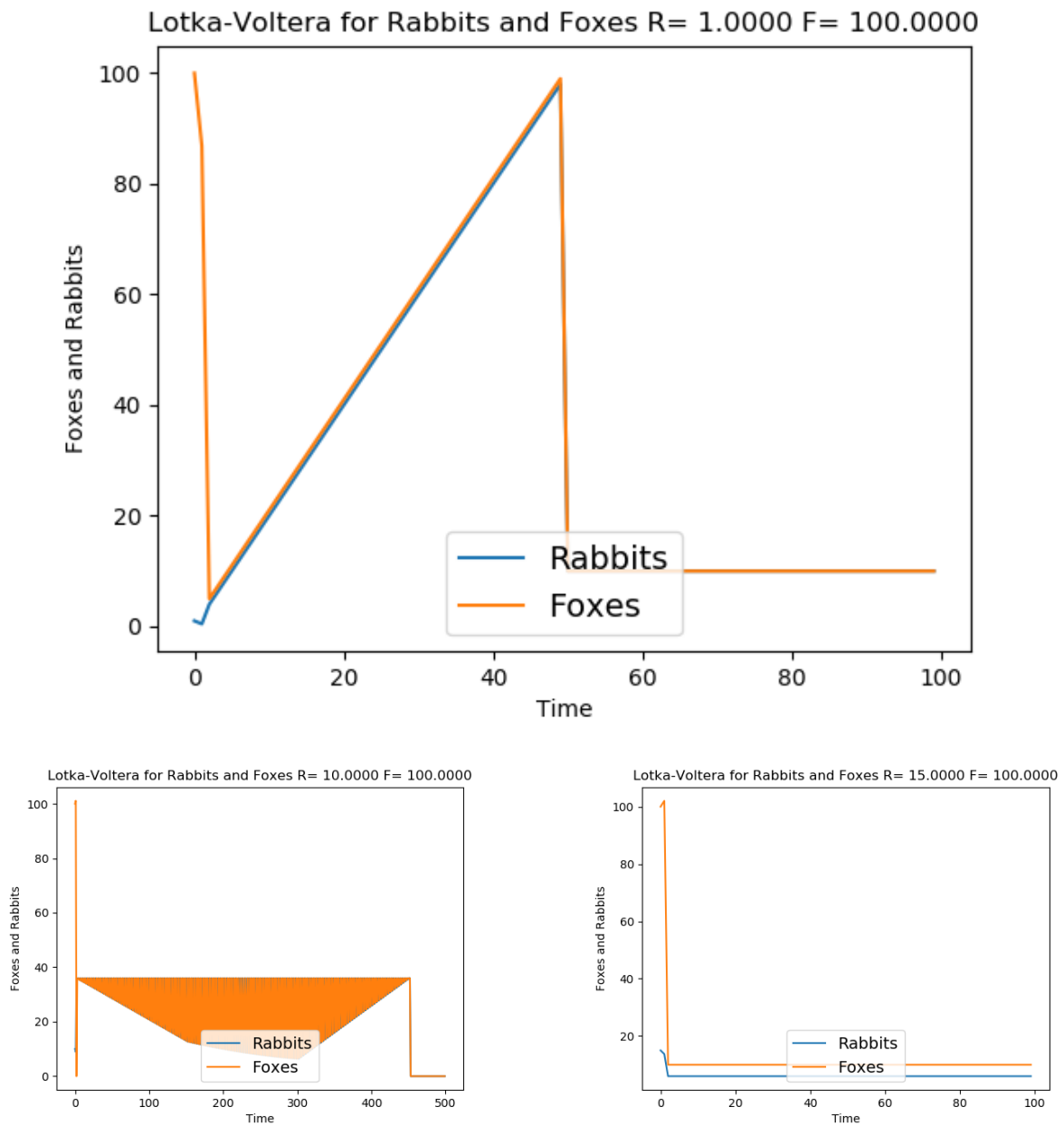


**Figure 7.** Lotka Volterra Models showing that the program accounts for less than one rabbit for fox and can continue the model after that





**Figure 8.** Lotka Volterra Models showing that the program accounts for less than one rabbit for fox in time dependent plots. We see that in both plots the fox and rabbit value go to less than one in both cases.



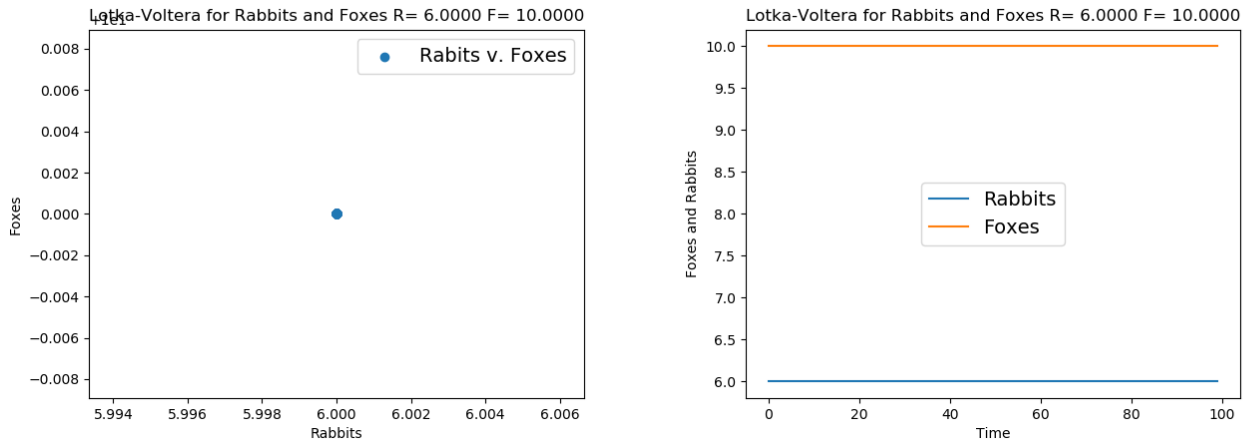
**Figure 9.** Lotka Volterra Models showing failure to set values to int to account for less than one rabbit for fox in time dependent plots.

Another thing that is interesting to note is where neither of the animals have any impact on each other, or when change for both is zero. The definition for a differential equation is that it is the change of a value over time. So if there is no change over time then the differential equation = 0. Here we use equations [5,6] and set  $\dot{R}$  and  $\dot{F}$  to zero. This is where equations [7,8] come into play:

$$\dot{R} = 0 = \alpha R - \beta RF \rightarrow \alpha R = \beta RF \rightarrow \alpha = \beta F \rightarrow F = \frac{\alpha}{\beta} \quad (7)$$

$$\dot{F} = 0 = \gamma RF - \delta F \rightarrow \gamma RF = \delta F \rightarrow \gamma R = \delta \rightarrow R = \frac{\delta}{\gamma} \quad (8)$$

When R and F initial values are set to these variables, then we get the plots in Figure [10]. Here we see that the change in R and F is constant and results in a dot, not a circle in the phase plot, and in the time dependent plot we see two lines that do not cross or interact.



**Figure 10.** Lotka Volterra Models showing when the differential equations = 0

### 2.1. Modeling Lotka-Volterra for Three Animals (Peas, Deer, Bears)

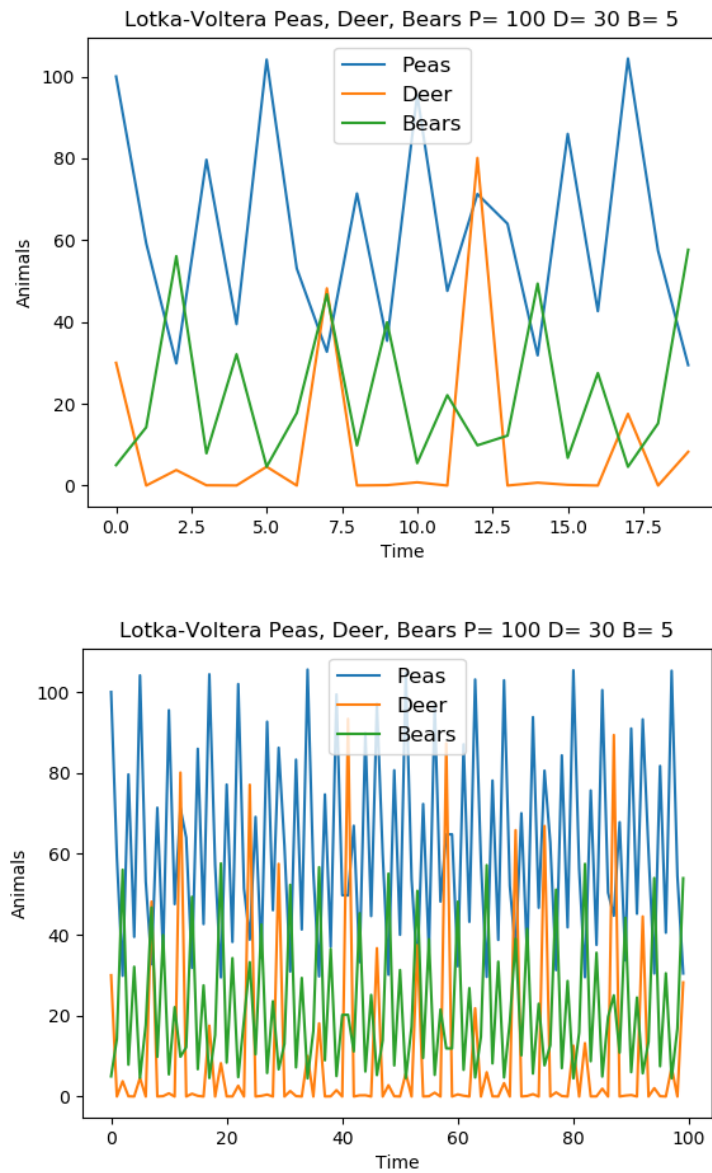
Here another animal was introduced. In this instance, the animals on the food chain had no interactions other than the one that was directly below them. For example, I chose an instance I am familiar with, deer eating peas. (And bears who eat deer but, don't eat peas.) I have a garden every summer and a lot of my peas are sacrificed to the bellies of deer. This is modeled in the same way that the rabbit-fox model was based. In this instance, our first differential equation, now  $\dot{P}$  for peas, is the exact same as equation [5]. For our  $\dot{D}$ , we can use the same equation as equation [6], but we have to account for them also being eaten so another term must be added.  $\dot{B}$  is not present at all in the previous equations, but it can be set up to allow for decay variables if they don't eat enough deer as the deer will die if they don't eat enough peas, and then growth variables for when they encounter deer and get vengeance for my sweet peas. These are given in equations [9,10,11]:

$$\dot{P} = \alpha P - \beta PD \quad (9)$$

$$\dot{D} = -\gamma D + \delta PD - \epsilon DB \quad (10)$$

$$\dot{B} = -\lambda B + \omega DB \quad (11)$$

Attention should be paid to the signs in these equations because they denote if an animal is benefiting or not benefiting from the interaction between the others. It also should be noted that only the animal that has unlimited resources has a positive 'self' value, the rest will have negative ones because if they don't eat enough then they die. For example, the peas  $\alpha$  value is positive since they have unlimited sun and water from my expert gardening, but the deer do not so their  $\gamma$  is negative because I am doing my very best to starve them. These equations are then modeled in Figure [11].



**Figure 11.** Lotka Volterra Models showing the same graphs for PDB with one zoomed with respect to time.

We can see here that due to the initial conditions. Peas and Bears and Deer interact periodically. Again, we see that Deer are going down to less than 1. While I wish they would disappear after this, they do not due to the constraints of the int and floats in the equations. So, we have to continue to deal with them...

## 2.2. Modeling Lotka-Volterra for Three Animals (Fly, Spider, Old Lady)

In this section, three 'animals' are again modeled, but this time they all can interact. While the bear didn't eat peas, the 'bear' in this model would. Here, there is an old lady, she swallowed a fly, but I don't know why she swallowed the fly. And then, I modeled an old lady who swallow a spider (It wiggled and jiggled and tickled inside her). She swallowed a spider to catch the fly, but I don't know why she swallowed the fly.

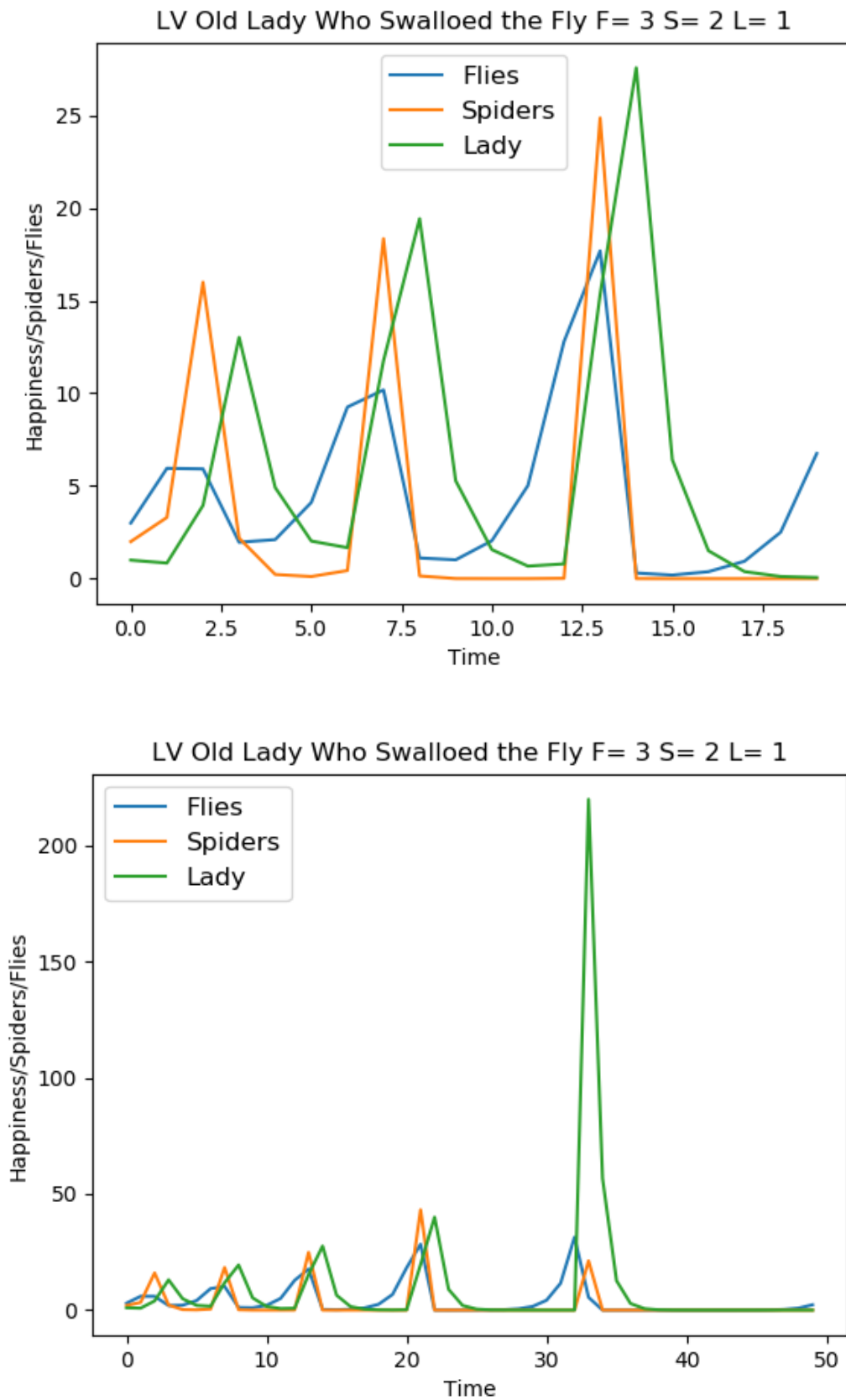
We can see that the old lady swallows both the spider and the fly, and then the spider swallows the fly... I don't know why. This means we have to include an eating variable to our first differential equation, the second stays the same, and the third has to have a new variable to account for eating the fly. These additions are given below in equations [12,13,14] (also all growth variables are given as Latin letters because I don't know that many Greek letters):

$$\dot{F} = aF - bFS - cFL \quad (12)$$

$$\dot{S} = -dS + eFS - fSL \quad (13)$$

$$\dot{L} = -gL + hFL + iSL \quad (14)$$

These equations are represented in Figure [12]. Again, we see that the spiders should technically go to less than one and disappear. This is not the same case, so the function is periodic. Here the old lady's happiness is modeled as a function of how many flies and spiders she eats. We can see that due to the initial growth rates in this example that she begins to become inexplicably happy after only around 5 meals. We can also see nicely that when the flies increase, we see spikes in the spiders quickly after because they have more food to eat so they reproduce quicker. Then right after spikes in the spiders we see spikes in the lady's happiness as they wiggle and jiggle and tickle inside her.



**Figure 12.** Lotka Volterra Models showing the same graphs for FSL with one zoomed with respect to time.

### 2.3. Competing Equations in the Lotka Voltera Model

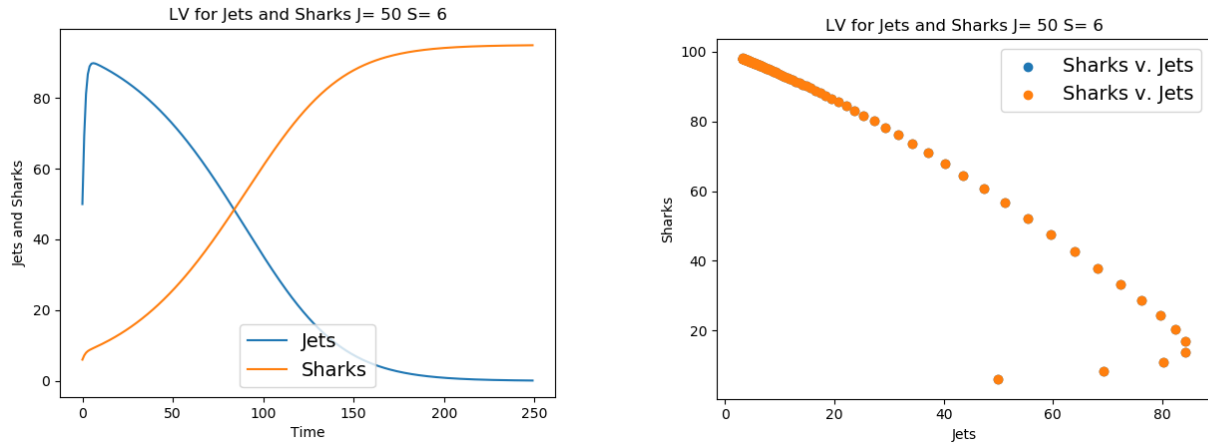
This model was to show an example of two 'animals', like the fox and the rabbit, except this time they could both 'eat' each other. For this model, we go back to the population model given in equation [4]. To modify it we use two differential equations modified to include the competition of the rival animal, here rival gang, as the form of a growth parameter and the size of the other gang. These are given in equations [15,16]. Here  $k$  is the growth rate,  $N$  is the population constraint,  $S$  and  $J$  are initial gang sizes and  $\alpha$  and  $\beta$  are the lethality of each gang.

$$\dot{S} = k_1 S \left(1 - \frac{S + \alpha J}{N_1}\right) \quad (15)$$

$$\dot{J} = k_2 J \left(1 - \frac{J + \alpha S}{N_2}\right) \quad (16)$$

Here the decay is adapted to add the  $\alpha$  and  $\beta$  in order to show the impact of the rival gang and growth is modeled by the rest of the equation outside of the fraction.

This model shows the interaction of the Jets and the Sharks from West Side Story. Here the Sharks begin as smaller but mightier and the Jets are larger (they have more members) but they are not as passionate, so their lethality is lower. We can see these interactions in Figure [13].



**Figure 13.** Lotka Voltera Models of competing gangs where one quickly exterminates the other.

We see in Figure [13a] that even though the Jets were bigger to begin with even a small difference in their growth rate and their lethality will cause a large impact on the opposing gang. The values that were used are  $k_J=1, k_S=0.5, a=1.1, b=0.9, J=50, S=6$ . I set both  $N$  values equal to 100 because the city of NYC sets a limit (I made this up) on the size of gangs at 100 members and the gangs are very afraid to break this law. The growth rate of the Jets was larger as well as having a larger initial value for gang members. But the Sharks had a higher lethality rate (lower means less effect from the Jets on their members), so even though they were not bigger, they still won out over the Jets since they were stronger. We see that there happening around 75 in the x-axis. Here the Sharks exceed the Jets in number of members and the Jets cannot come back from that and we see them go extinct. We also have the time dependent plot here at Figure [13b] we see that this is not a stable

circle, but it does show curved tendencies. We see it break off at the top because this is where the domination of the Sharks is represented.

### 3. INTRODUCTION TO EPIDEMIC MODELS

Here we are modeling an epidemic. This is set up almost the same as the Pea-Deer-Bear model, but we can neglect certain variables. First, we must understand what we are modeling. For this step we want to have three types of people, healthy, sick and immune. All people are healthy in the beginning except one. This one person is sick; they can then spread the disease to healthy people making them sick. When the person is sick, they are either spreading the disease or becoming healthy. There is a period of time where the person has to wait to become healthy and when they wait that time then they can become immune. This means that even if they come in contact with a sick person, they will not get sick again.

There is something important to keep track of, there is no one leaving the system. This is a system set to equal 1 if a person gets healthy sick or immune they are still a part of that system, so at the end when everyone is immune, they may have changed categories, but everyone must be present and the whole group must be equal to one or in other words  $H+S+I=1$  no matter what the time period is. As stated before, we can adapt the PDB equations. Here there are no new healthy people being born so we only need the ones being taken to become sick, then the sick can gain from healthy people becoming sick and lose from a time period to people becoming immune (similar to the deer dying over time due to no food), then the immune are adapted to only one variable to gather all the people who have become immune over time. These equations are given in equations [17,18,19]:

$$\dot{H} = -\alpha HS \quad (17)$$

$$\dot{S} = \alpha HS - \beta S \quad (18)$$

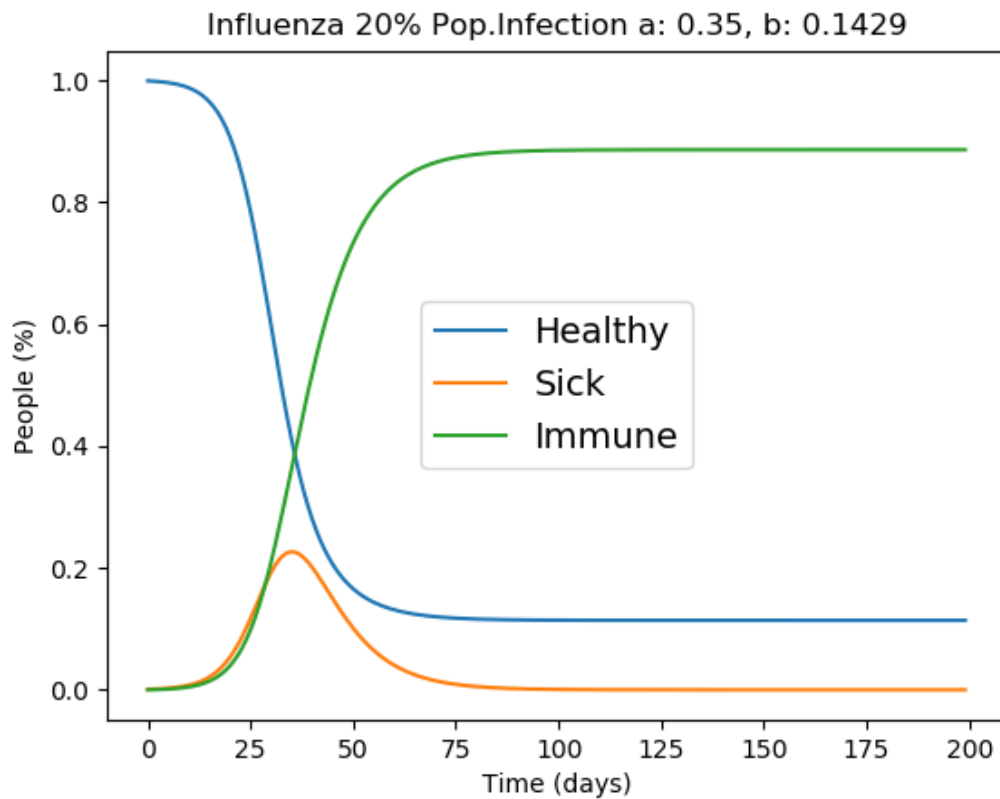
$$\dot{I} = \beta S \quad (19)$$

Here we should also note the signs, where H loses HS, S gains HS but loses immune people, and I gains immune people. Also, of note is there are only two variables. This is because  $\alpha$  is the rate that people become sick and can be used twice and  $\beta$  is the rate where people become immune so again this can be used in S and I.

#### 3.1. Modeling the Yearly Influenza Virus

In order to apply this, the yearly Influenza outbreak was chosen because the author has already gotten it **twice** this season. As background, Influenza (the flu) is an outbreak that occurs from January to March every year, effecting 20% of the US population. This can be greatly reduced with the use of vaccines, but first we will model the infection without any intervention from science.  $\beta$  was chosen to be this value because the flu is generally healed over one week, so the value to heal is  $1/7$ . Here there are 99.9% healthy people and only 0.1% sick people. This is modeled through the differential equations above to produce what we see in Figure [14]. We see the number of healthy people drastically drop to at the same time the virus starts to infect a significant amount of people. This is because they must always  $=1$  so if someone is not healthy, they must be either sick or immune.

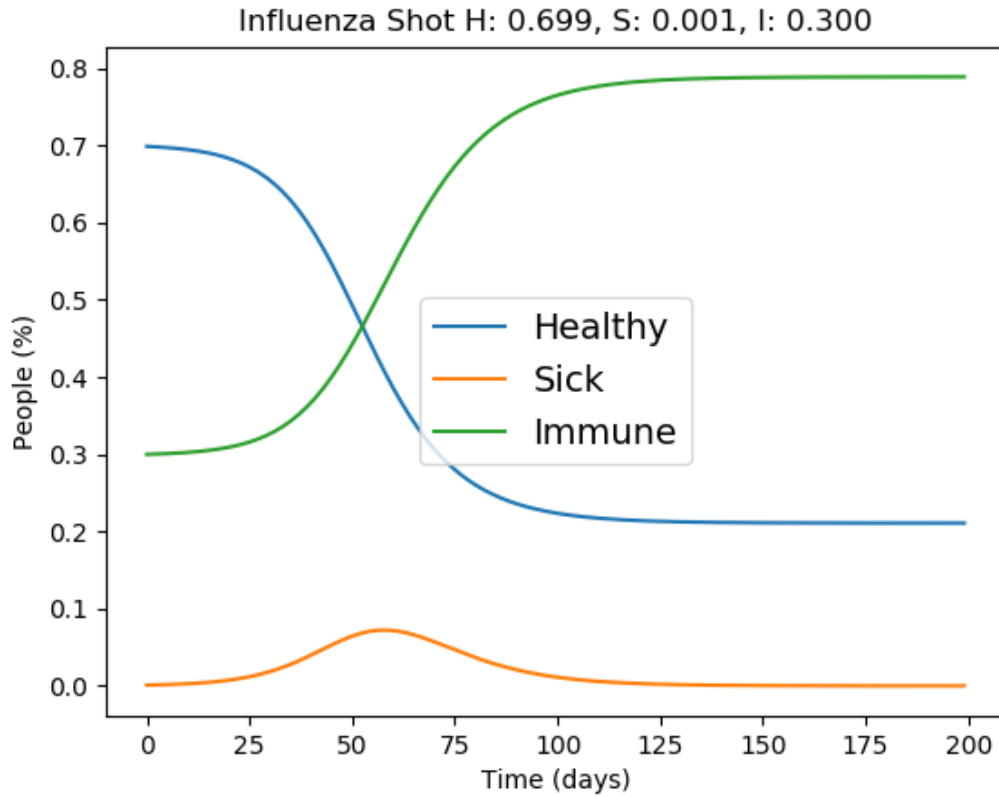




**Figure 14.** Model for the Influenza Yearly Outbreak without Immunization Shots.

We see that immunity begins to take over around 30 days.  $\alpha$  was chosen to be what it is because we know from the previous section that 20% of the population is affected by the flu, so  $\alpha$  was adjusted until we saw that value for the number of the sick on the plot. We can also see that it takes about 100 days for the trend to even out to all being immune and none sick. This is around 3 months which is the average period of the flu. We can see that around 15% of the healthy people are unaffected due to the immunization killing out the virus. With all this in mind we can be assured that Figure [14] is an accurate model for the yearly flu.

Next, we can see the fit if the populous got their shots. Here we assume that 1/3 of the population got their shots so 33% of the population begins as immune and 69.9% is healthy, and again 0.1% is sick. In Figure [15] we see that this greatly reduces the drop in healthy people. Where nearly 25% of the population is affected by the flu with only a 1/3 turnout for the shots. We also can see that the outbreak of the flu only effected less than 10% of the population, cutting those infected in half, whether or not they got the flu shot that year. If only that would happen on campus...



**Figure 15.** Model for the Influenza Yearly Outbreak WITH Immunization Shots.

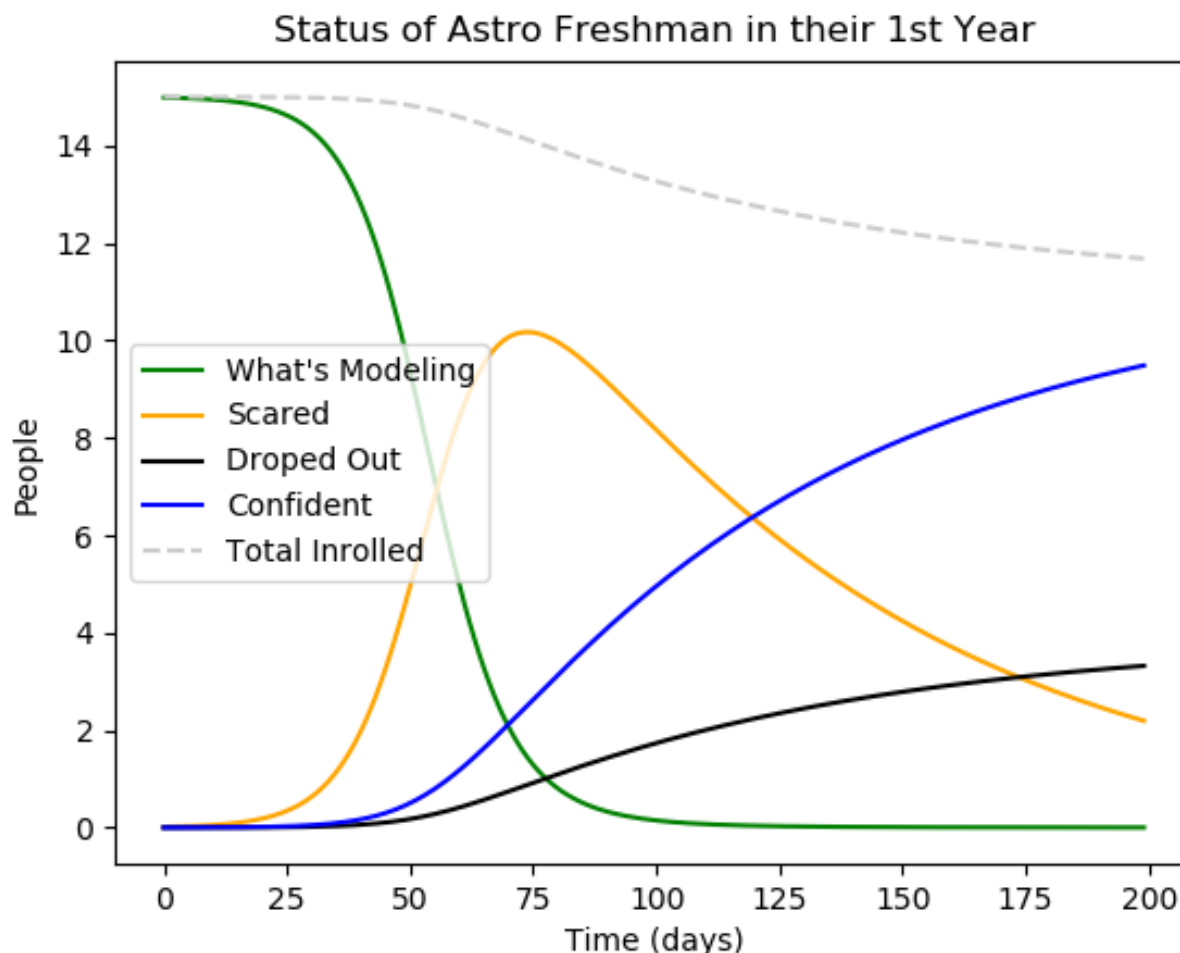
### 3.2. Modeling non-Closed Outbreaks

The next step in this project is to model an outbreak that is not a closed system. That means that while  $H+S+I=1$  no matter what, we can introduce another factor that goes outside the bounds of that one and causes the population total to drop: ... death. If we include death but don't account for it as a differential equation, then we will see a real-life trend of the population dropping off due to the loss of life for a certain epidemic. Here we introduce  $\gamma$  or the lethality of a certain outbreak this effects only the sick and is given as such in equation [20]:

$$\dot{S} = \alpha HS - (\beta + \gamma)S \quad (20)$$

With this introduced we can model sick people increasing by infecting healthy people, then them becoming immune over time as well as the chance that they will die depending on the value of  $\gamma$ . For this model the freshman class in the Villanova Astronomy major is chosen. This is any class so please don't worry about bullying. In this situation the freshman who recently arrive are 'healthy', or, they haven't heard of Modeling yet. One person is told by one of the upper-classmen on Candidate's Day so there is again a 99.9% Unaware population and a 0.1% population that is now scared. This person can tell one person they meet on the first day and then the other person has a 2/15 chance of telling one of the other freshman in class since the class size is given as 15 for that year. The freshman has a period of one semester (100 days) after which they forget about what they had heard about modeling and become immune to the terrors. If they do not become confident then they have a 0.35% chance

of dropping out and becoming a Philosophy major. This plot tells us the outcome of the class size after one full year.



**Figure 16.** Model for the Freshman Class in Villanova Astronomy, accounting for dropouts.

From Figure [16] we see that there is a sharp drop in clueless people, and this is quickly replaced by scared students. Then around 50 days or half a semester we see an increase of either confident students who are just going to try to get through Ob Lab first or we see a few students tuck tail and drop out. After the first year, we see a few students still afraid, consistent to real life, no clueless students, 3 students dropped out and one 90% out the door (drop rate of 3.8 makes three people and one about to leave), and we see almost 10 students confident and ready to take on the class. This gives a class size of 12 with 3 dropping out after the first year, which has generally been consistent with the freshman drop ratio in our department.

It is of note to see the total enrolled dashed line. This is an indicator of all the people in the class. If this was the situation in the last section this line would be flat, but it is not since  $H+S+I$  does not equal one in this instance because some students have dropped out and left the closed loop.

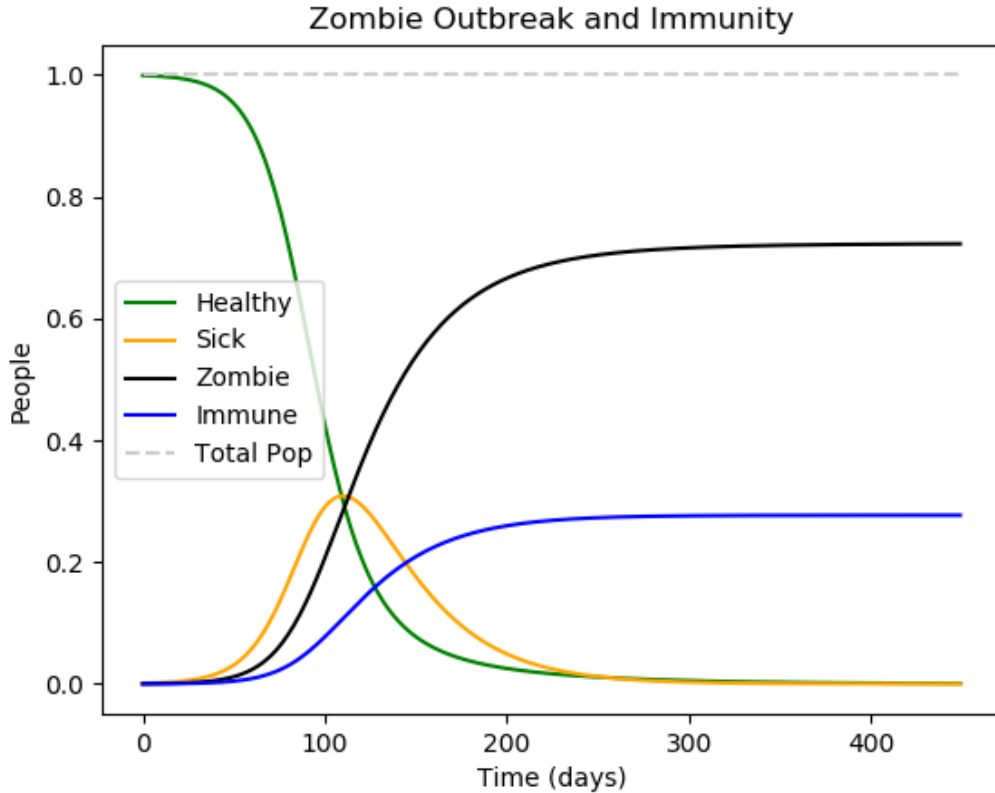
### 3.3. ZOMBIES!

After the death simulation, the next logical projection is to reanimate them. This is done by modifying the previous equation to allow for the death to be present in the closed loop and having the dead have an effect on the healthy. Here the dead don't interact with the immune or the sick because that would do nothing for them and they would probably taste bad, instead they focus only on the healthy and can infect healthier through their dead bodies. Here we are modifying the equations for the freshman dropout to include the zombies infecting people who are healthy and causing them to become zombies themselves.  $S$  and  $I$  stay the same. So, here are the adapted and introduced Healthy and Zombie differential equations in equation [21,22]:

$$\dot{H} = -\alpha HS - \gamma HZ \quad (21)$$

$$\dot{Z} = \gamma S + \gamma HZ \quad (22)$$

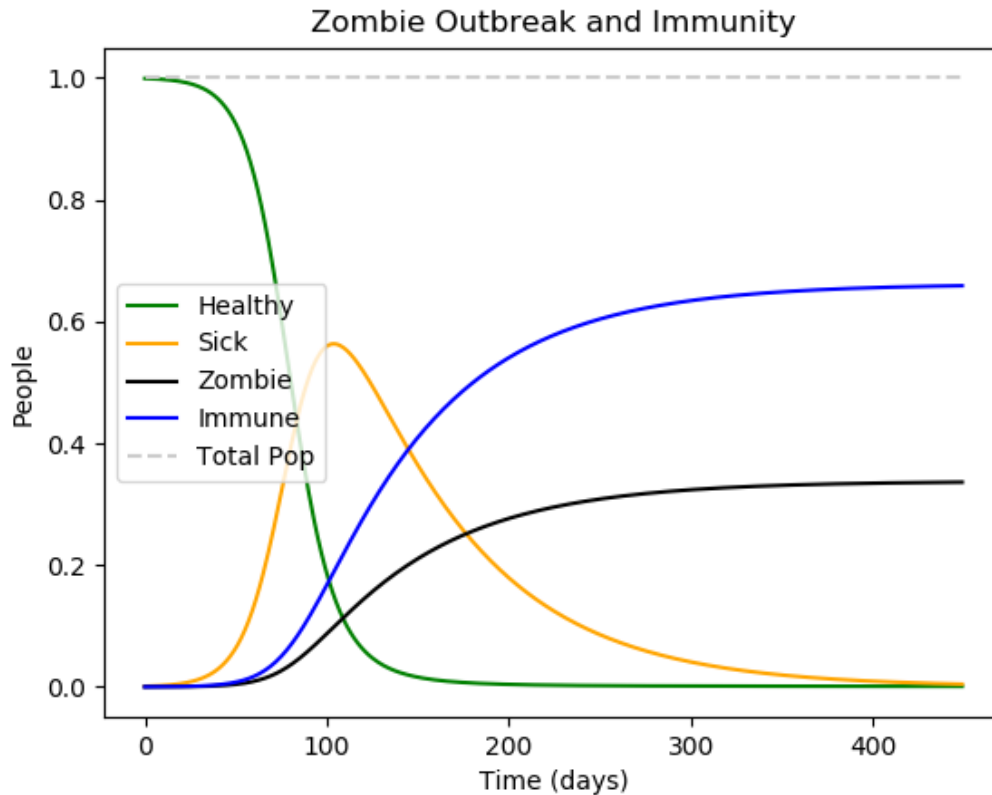
Here there is a 0.1 chance of getting the infection, a 100-day recovery period and a 2% chance of becoming a zombie while infected. This is shown in Figure [17].



**Figure 17.** Model for the Zombie Epidemic.

This figure shows how the healthy people quickly drop off, the majority of the people then become zombies and at the same time a few people become immune. We see no people being sick after 300 day because if they were then they would either have to become a zombie or become immune over that amount of time. The we see no healthy people either as they would have to become zombies as well or become infected. In this model the zombies win out and produce a hell-scape for the 20% of the population that was left immune. It should be noted that the total population dashed line is constant this time because the dead were accounted for and became zombies that had an impact on the closed system, meaning  $H+S+I+Z=1$  no matter the time frame. This is because when healthy people leave healthy, they either go into zombies or sick then the sick catch the infected healthy then either go into zombie or immune and the immune catch the sick and the zombies catch the unlucky healthy and the zombified sick. Thus, a closed loop.

Next is the instance if the zombies weren't as lethal, so the healthy didn't have as high of a chance to become bitten and jump straight to zombie. Here the  $\gamma$  is 0.5% and shown in Figure [18]. This shows still a closed loop but since the healthy have a better chance to become sick and then immune now there is an uptick in the immune and they win out over the zombies. This could allow them to clear out the zombies later (open loop) and begin to rebuild the world.



**Figure 18.** Model for the Zombie Epidemic with Weaker Zombies.

#### 4. CONCLUSION

In this project, we see there are a lot of applications for the population models. These models can be adapted to fit a multitude of different constraints and model various instances of interactions by simply adding or subtracting different variables from the original equations. The main downfall of the Lotka-Volterra model is that it still accounts for animals if they are less than one, where they would go extinct at this time in real life. The population model provided accurate values for the census they were compared to and gave insight into the conditions that could have changed the  $k$  or  $N$  values over time in certain nations. Finally, the epidemic model was possibly the most accurate model for this project. It was able to successfully model the flu outbreak every year, the freshman drop rate as well as provide necessary information in case there is a zombie outbreak. While these equations had a few downfalls. Overall, they were able to model the situation they attempted to solve, thereby they were successful for this project.

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