The Impact of Deforestation on Bobcats

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Chapter 1: Introduction

Wildlife can be unpredictable, which often means human intervention is required to preserve biodiversity. All forms of wildlife, regardless of species, will respond to changes in habitat such as hunting, deforestation, and weather conditions. Changes can be drastic, resulting in extinction of species, loss of food sources, and disturbances in the food chain. These changes can result in low reproduction and survival rates. Frequently, wildlife lose their habitat to human development, resulting in the destruction of their ecosystem. This phenomenon, known as deforestation, forces wildlife to relocate in order to survive.

In this project, our primary focus is to understand how deforestation affects the reproduction rates of bobcat populations. For background information, bobcats are native in North America, ranging from southern Canada to Mexico. Most bobcats prefer to live in forests rather than in urban areas to avoid human interaction.[1,2] Humans are "super predators" to the bobcat population and pose a threat to their survival.[6] Deforestation affects wildlife as trees are being cut down or extinguished.[4] Without forests, there is a loss of biodiversity and wildlife migrate to different areas. Reproduction becomes less frequent since finding a mate becomes more difficult. Additionally, bobcats struggle finding prey in new habitats, leading to suboptimal body conditions necessary for reproduction.[3,6]

We aim to uncover insights into the long-term growth rate and distribution of bobcat populations under varying catastrophe conditions. By understanding the underlying mechanisms driving population dynamics, we can better assess the resilience of bobcat populations to environmental changes and devise effective conservation strategies to ensure their survival.

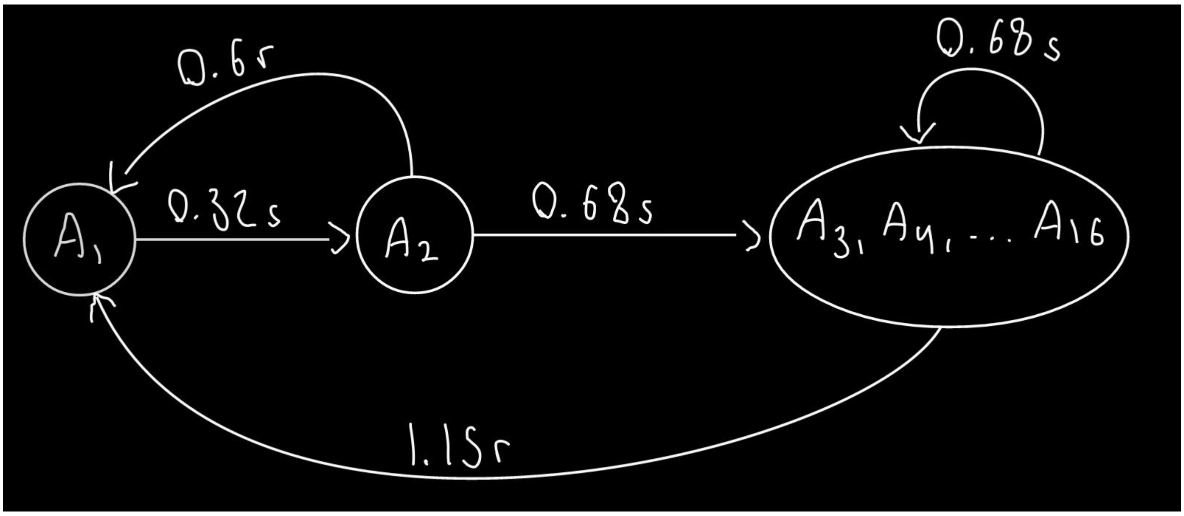
We seek to address the following research questions: How do demographic factors, habitat changes, and catastrophic events (deforestation) influence the dynamics of bobcat populations over time? Furthermore, how can conservation efforts help reduce the effects of habitat loss on bobcat populations in the long term? Our analysis will explore changes in bobcat population dynamics within each age group, comparing scenarios with and without deforestation to assess the impacts on survival and reproduction rates.

Chapter 2: Base Model and Analysis

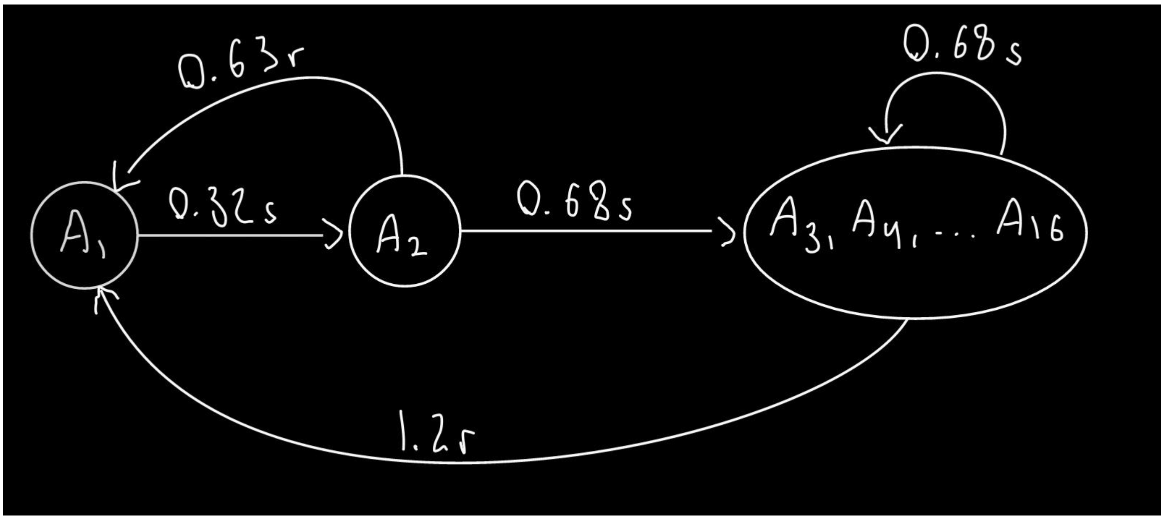
2.1

The model aims to track the population dynamics of bobcats. In our base model, we categorize bobcats into 16 age groups ranging from age 1 to age 16 and assume all bobcats we are tracking can reproduce. We assume that no human intervention such as hunting or deforestation takes place, natural catastrophes are not considered, and no predator/prey relationships are occurring with other species. Furthermore, we are modeling a brand new bobcat population that is introduced to the environment. As part of conservation efforts, we set a certain number of bobcats aged 1 and 2 to be introduced to the population to understand how much they can help sustain the population. The state variable in our model is the bobcat population (popn). Since we are modeling age groups, we decided that it would be best to use a discrete model to showcase each stage of the bobcat population yearly, and each year the population of the age groups would update. The parameters in our model are survival rates (s) and reproduction rates (r). Under these parameters, we assume four scenarios take place, involving the best and worst case reproduction and survival rates for the bobcat population. We can visualize these scenarios with compartmental models.

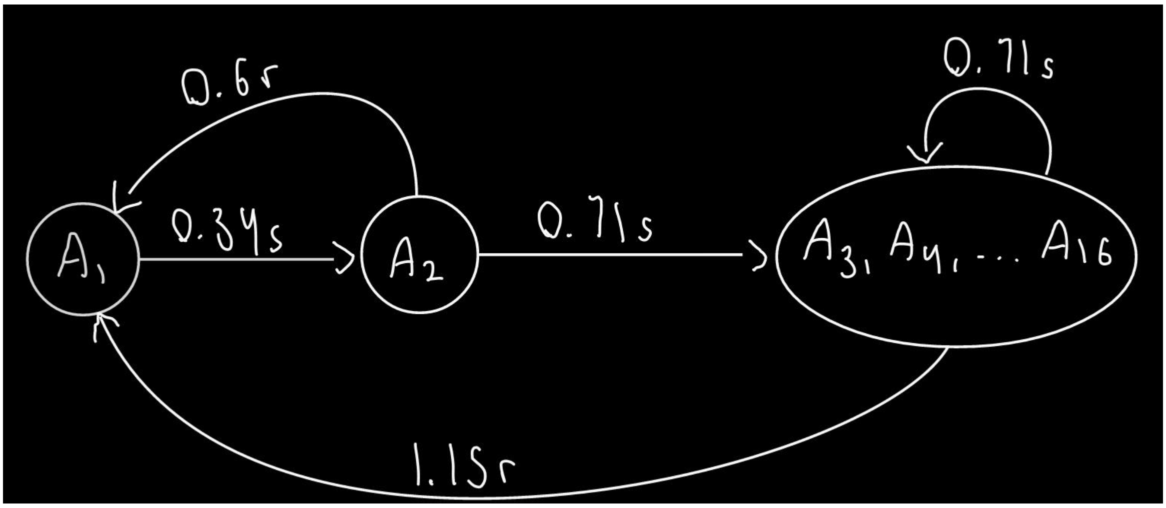
In the first scenario, the bobcat population experiences the worst case survival and reproduction rate:



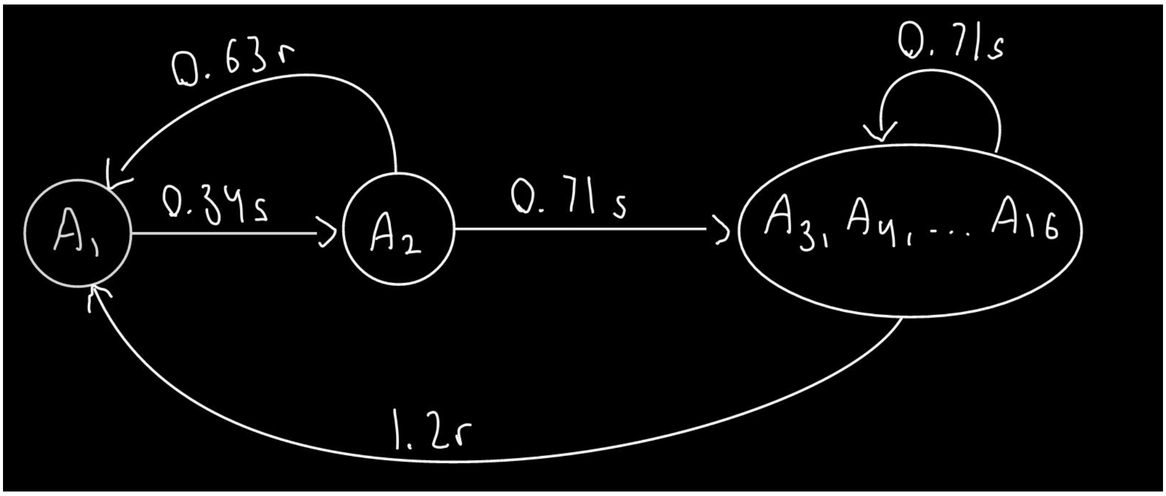
In the 2nd scenario, the population experiences the worst case survival and best case reproduction rate:



In the 3rd scenario, the population experiences the best case survival and worst case reproduction rate:



In the 4th scenario, the population experiences the best case survival and reproduction rate.



2.2

Next, we set up a 16 by 16 null matrix consisting of 16 age classes for bobcats. We then fill the matrix with the known parameters. In the worst case scenario for survival and reproduction rate, our matrix looks like this:

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
[1,]	0.60	0.32	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
[2,]	0.60	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
[3,]	1.15	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
[4,]	1.15	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
[5,]	1.15	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
[6,]	1.15	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
[7,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
[8,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00
[9,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.00
[10,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00	0.00
[11,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00	0.00
[12,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00	0.00
[13,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.00	0.00
[14,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	0.00
[15,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68
[16,]	1.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

The 1st column of the matrix represents the reproduction rates of each bobcat age group, which all go into the age 1 bobcat group. For example, bobcats aged 4 reproduce new bobcats at a rate of 1.15 in 1 year. The rest of the values represent the survival rates of the bobcats to go into next year. For example, in row 2, column 3, bobcats aged 2 survive to age 3 at a rate of 0.68.

After establishing the initial matrix, our team set up a new matrix storing the bobcat population for each year. It contains 16 rows with each row representing different age groups, and the columns represent the bobcat population for each year. We chose to assume that we are modeling an entirely new bobcat population, where we have only 4 age-1 bobcats and no other age groups exist to begin with at year 0:

[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

As time goes on, the population at each timestep is calculated as the product of the bobcat population at the previous timestep by the matrix consisting of the original parameters. We chose to use the round() function in order for each age group's population to be a whole number, as it wouldn't make sense if they were a decimal. As part of conservation efforts, we decided to add 10 young bobcats consisting of 5 age-1 and 5 age-2 bobcats every year starting at year 1, which is reflected in the population growth.

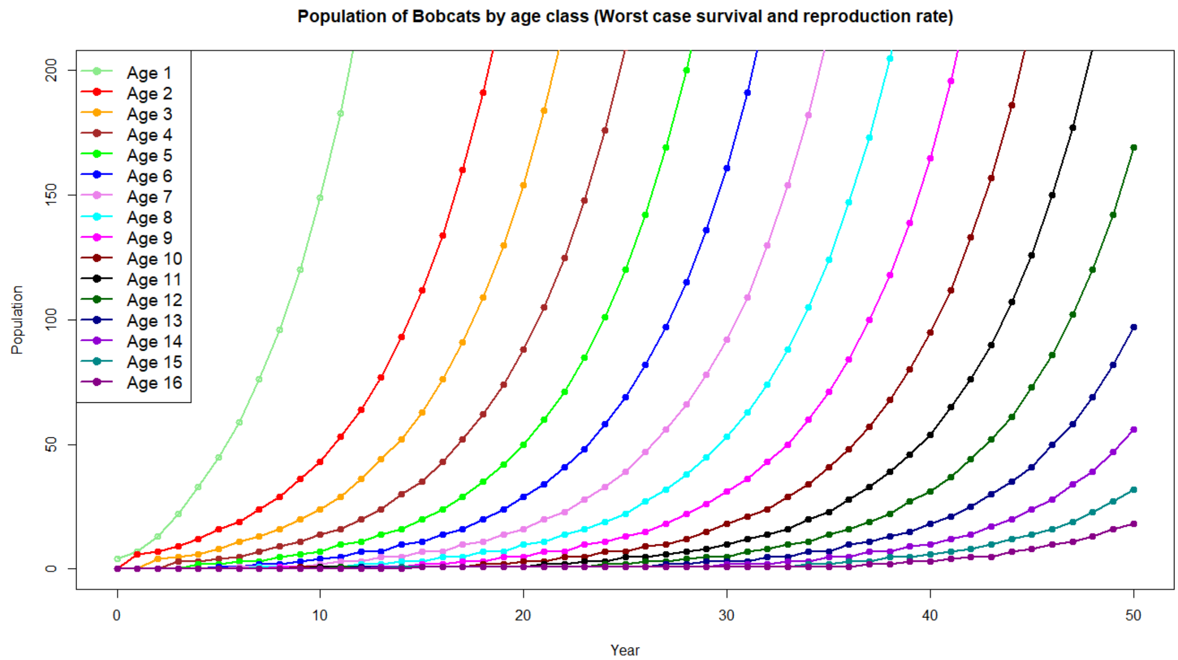
We chose to plot the bobcat population over a span of 50 years. The x-axis represents years, and the y-axis represents the number of bobcats. The graph has 16 coloured lines, each representing a corresponding age group. For all 4 scenarios, we aim to understand which population grows the fastest.

Given the computational complexity associated with manually calculating the eigenvalues of the matrix by hand, we used the "eigen()" function in R to perform the computation, revealing a total of 16 eigenvalues. Notably, for all 4 scenarios, almost all the eigenvalues from the eigen function return as real numbers augmented by the imaginary unit (x+iy), with the exception of the 1st and last eigenvalue. For all 4 cases, the 1st eigenvalue also happened to be the largest eigenvalue in absolute value. So, this eigenvalue dictates the long term behaviour of our model. Furthermore, the results are amplified since conservation efforts are adding new bobcats aged 1 and 2 to our population.

In case 1, with the worst survival and reproduction rate, our eigenvalues are:

```
> eigen(bobcat_population, only.values = TRUE)
$values
 [1]  1.1828518+0.0000000i  0.6117292+0.2789076i  0.6117292-0.2789076i  0.4480233+0.4905486i
 [5]  0.4480233-0.4905486i  0.2296965+0.6184589i  0.2296965-0.6184589i -0.0120604+0.6517932i
 [9] -0.0120604-0.6517932i -0.2464271+0.5899047i -0.2464271-0.5899047i -0.4421333+0.4450492i
[13] -0.4421333-0.4450492i -0.5717348+0.2388734i -0.5717348-0.2388734i -0.6170387+0.0000000i
```

Since the largest eigenvalue has a value of 1.1828518, which is positive and greater than 1, we predict that in the long run, the model will grow without bound, and will grow monotonically. Our simulation proves that this appears to be the case:



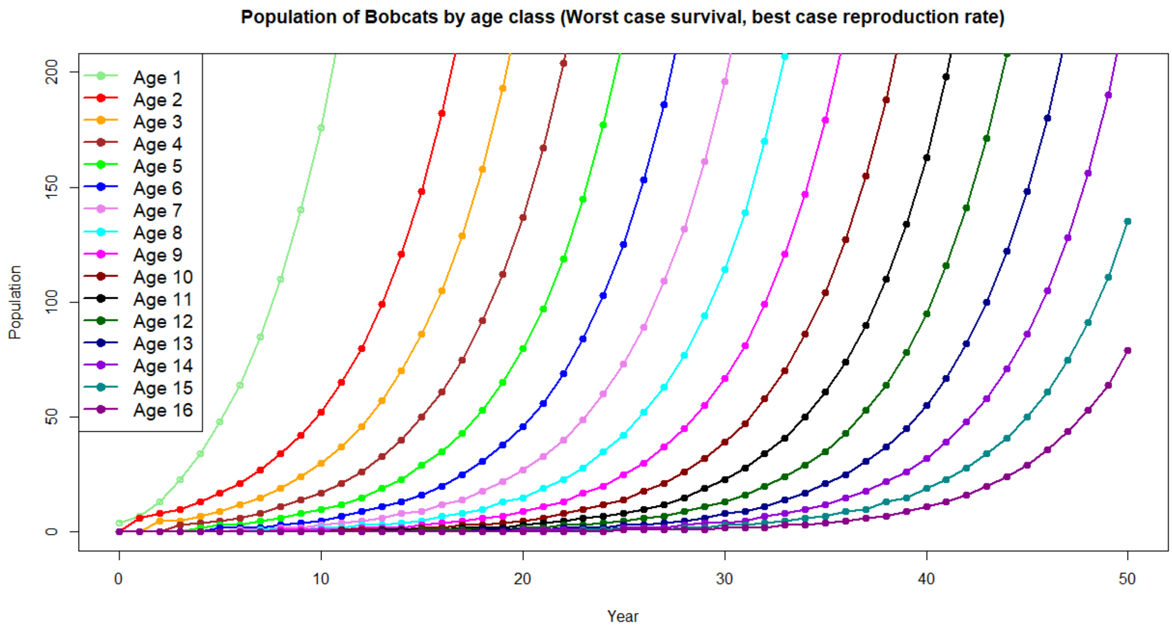
The final population after 50 years for each age group is:

```
  [,1]   [,2]   [,3]   [,4]  [,5]  [,6]  [,7]  [,8]  [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
158104 42775 24590 14136 8126 4672 2685 1544  887   510   293   169    97    56    32    18
```

In case 2, with the worst survival and best reproduction rate, our eigenvalues are:

```
> eigen(bobcat_population, only.values = TRUE)
$values
 [1]  1.2071778+0.0000000i  0.6126134+0.2785287i  0.6126134-0.2785287i  0.4493013+0.4909239i
 [5]  0.4493013-0.4909239i  0.2308210+0.6194213i  0.2308210-0.6194213i -0.0113380+0.6529685i
 [9] -0.0113380-0.6529685i -0.2462425+0.5910071i -0.2462425-0.5910071i -0.4424499+0.4459002i
[13] -0.4424499-0.4459002i -0.5723889+0.2393380i -0.5723889-0.2393380i -0.6178106+0.0000000i
```

Since the largest eigenvalue has a value of 1.2071778, which is positive and greater than 1, we predict that in the long run, the model will grow without bound, and will grow monotonically. Our simulation proves that this appears to be the case:



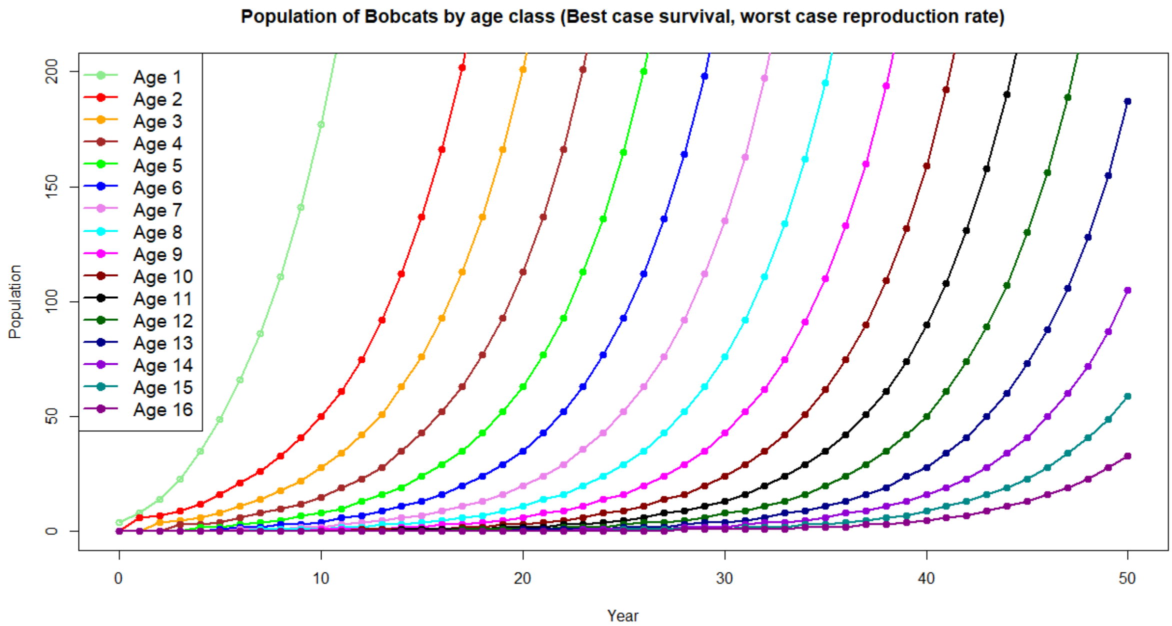
The final population after 50 years for each age group is:

```
  [,1]   [,2]   [,3]   [,4]   [,5]   [,6]   [,7]  [,8]  [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
532143 148655 86716 50584 29508 17213 10041 5857 3417  1993  1163   678   396   231   135    79
```

In case 3, with the best survival and worst reproduction rate, our eigenvalues are:

```
> eigen(bobcat_population, only.values = TRUE)
$values
 [1]  1.2171290+0.0000000i  0.6379729+0.2915750i  0.6379729-0.2915750i  0.4666642+0.5120190i
 [5]  0.4666642-0.5120190i  0.2387182+0.6451918i  0.2387182-0.6451918i -0.0134708+0.6799064i
 [9] -0.0134708-0.6799064i -0.2577926+0.6153538i -0.2577926-0.6153538i -0.4617696+0.4642396i
[13] -0.4617696-0.4642396i -0.5968509+0.2491669i -0.5968509-0.2491669i -0.6440717+0.0000000i
```

Since the largest eigenvalue has a value of 1.2171290, which is positive and greater than 1, we predict that in the long run, the model will grow without bound, and will grow monotonically. Our simulation proves that this appears to be the case:



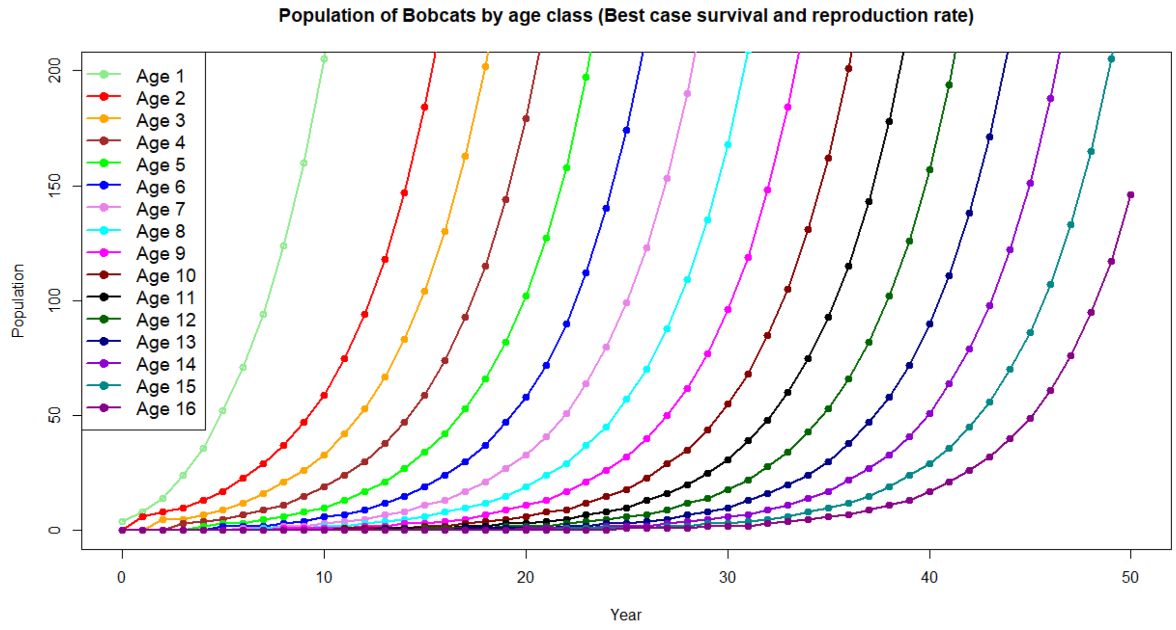
The final population after 50 years for each age group is:

```
  [,1]    [,2]   [,3]   [,4]   [,5]   [,6]  [,7]  [,8]  [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
389716 103309 58193 32780 18464 10401 5859 3300 1859  1047   590   332   187   105    59    33
```

In case 4, with the best reproduction and survival rate, our eigenvalues are:

```
> eigen(bobcat_population, only.values = TRUE)
$values
 [1]  1.2414402+0.0000000i  0.6389141+0.2911959i  0.6389141-0.2911959i  0.4679897+0.5124445i
 [5]  0.4679897-0.5124445i  0.2398663+0.6462321i  0.2398663-0.6462321i -0.0127441+0.6811687i
 [9] -0.0127441-0.6811687i -0.2576225+0.6165321i -0.2576225-0.6165321i -0.4621207+0.4651450i
[13] -0.4621207-0.4651450i -0.5975540+0.2496598i -0.5975540-0.2496598i -0.6448978+0.0000000i
```

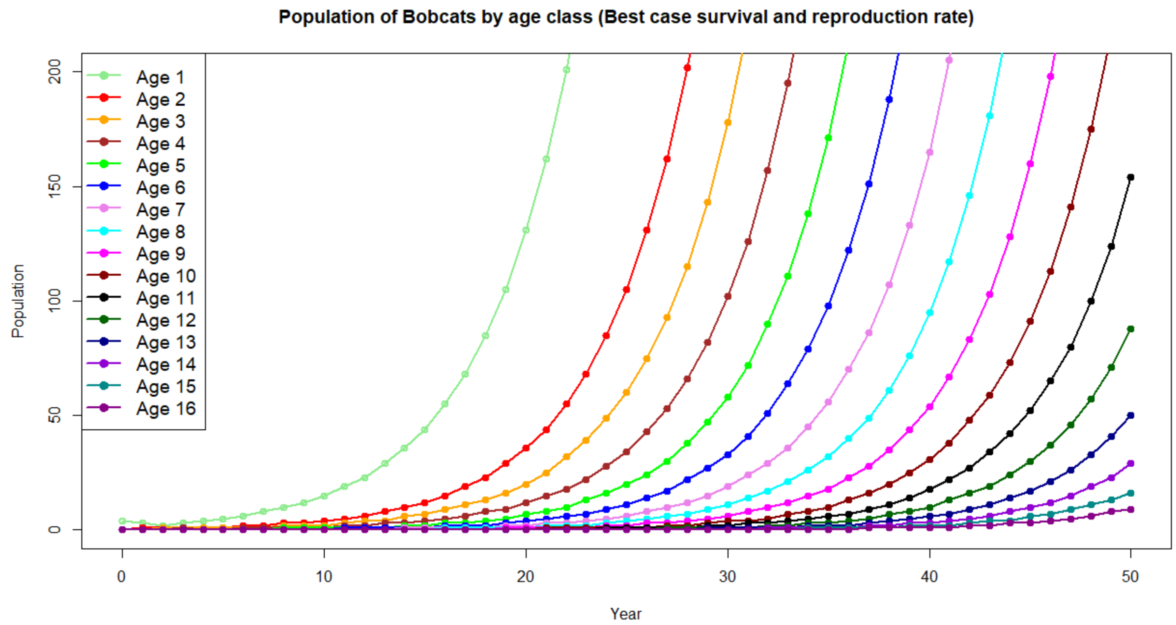
Since the largest eigenvalue has a value of 1.2414402, which is positive and greater than 1, we predict that in the long run, the model will grow without bound, and will grow monotonically. Our simulation proves that this appears to be the case:



The final population after 50 years for each age group is:

[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
1328975	363977	208164	119052	68087	38940	22270	12737	7284	4166	2383	1363	779	446	255	146

Now, to illustrate the impact that conservation efforts have on our model, we chose to model the best reproduction and survival rate scenario with no bobcats added each year to ages 1 and 2 to understand how much conservation efforts help. The plot and final population after 50 years for each age group are:



[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
85810	23501	13441	7687	4396	2514	1438	822	470	269	154	88	50	29	16	9

Clearly, compared to the chart above, the bobcat population for each age group is significantly less compared to the age group which had conservation efforts added. Even with only 5 bobcats aged 1 and 2 being added to the population each year, the long term impact on the bobcat population results in significantly more bobcats.

Comparing the four cases of survival and reproduction rates, the model predicts that after 50 years the group with the best survival and reproduction rate will end up with the highest number of population, while the lowest survival and reproduction rate will result in the lowest total population.

Without any predators, diseases, or catastrophes to impact the bobcat population, there is nothing to stop them from growing indefinitely. In the next section, we will see how catastrophes can impact and keep the bobcat population in check.

2.3

To continue our research, we chose to extend our model by adding a catastrophe scenario to the base model. The catastrophe taken into consideration is deforestation (includes fragmentation, agriculture and urbanization). The extension model will specifically focus on how the catastrophes affect the reproduction rate and ultimately the population size of the species. This catastrophe will occur periodically and lowers the reproduction rate of all age groups by the same proportion p. To limit other changes that can also affect the population, we assume survival rates remain unchanged, hunting is prohibited, and no natural disaster affects the population (i.e erosion and weather deaths). Reproduction rate (r) and survival rate (s) are the state variables, and the parameters are frequency of catastrophe in years (n), where n is greater than 1, and proportional change to reproduction rate caused by the catastrophe in percentage (p), which is between 0 and 1.

We will continue to use the four scenarios for survival and reproduction rates described in the base model section. For all four scenarios of reproduction and survival, since each scenario results in similar plots, we chose to set different n and p values in our model for each scenario to learn and discover different patterns in our plot. For all scenarios, the formula to decrease the population is:

```
if (t %% n == 0 && t >= 15) {
  # Reduce reproduction rates in the first column by proportion p
  bobcat_population[, 1] <- bobcat_population[, 1] * (1 - p)
}
```

We also chose to assume that the first of these deforestation events occurs first at 15 years, as this allows the total bobcat population to be rather large before a disaster occurs. The equation used in the model is the same as the basic model, and the same parameters were used to model the best and worst case scenario for survival and reproduction. The initial matrix setup also remains the same and we still assume 5 bobcats are added to the population each year.

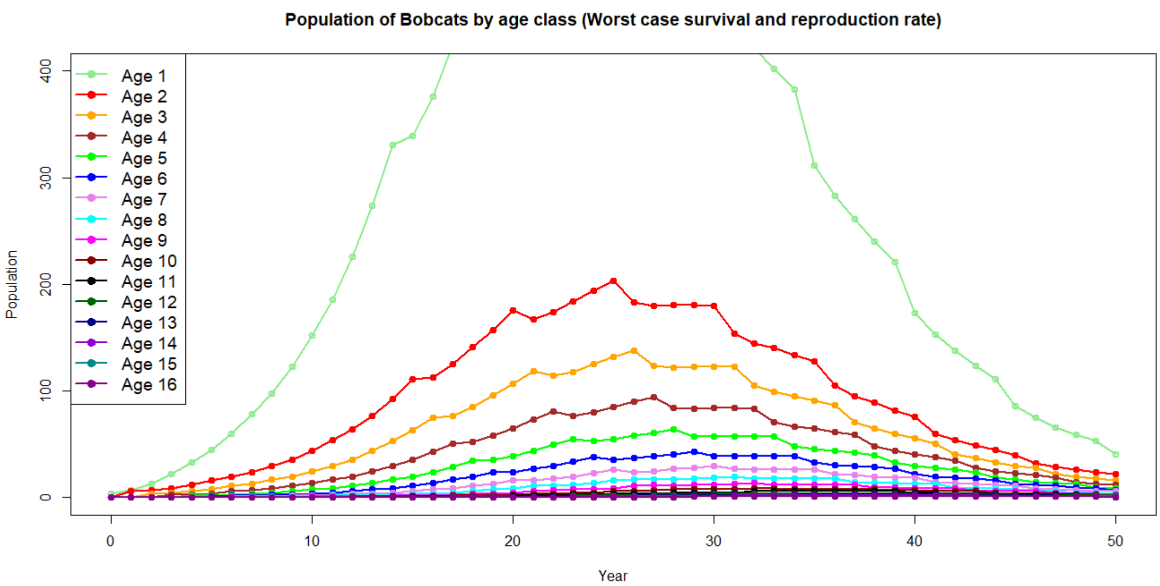
Chapter 3: Analysis of Extended Model and Results

Since a deforestation event changes the parameters of our original matrix, it is clear that it is going to change how our model appears. In our base model, we learned that for all scenarios, the population of the bobcats will grow without bound. In our extension, we are now interested in learning for all 4 scenarios how many deforestation events can affect the bobcat population to the point where they are threatened by extinction. The way to test this is to see by what percentage p of the reproduction rates can be changed until the dominant eigenvalue of the matrix is less than 1. Through rigorous testing, we were able to find p values for all 4 scenarios which would eventually result in extinction. Our results will showcase these p values, and also plot the impact of deforestation events on each scenario. We will also plot each scenario with different n and p values to discover interesting patterns.

In the 1st scenario, with the worst survival and reproduction rate, if we set p around 0.36, then a deforestation event will decrease the reproduction rate by 36%. Our eigenvalues for the matrix now look like:

```
> eigen(bobcat_population, only.values = TRUE)
$values
 [1]  1.0016258+0.0000000i  0.6018994+0.2808682i  0.6018994-0.2808682i  0.4362705+0.4837600i
 [5]  0.4362705-0.4837600i  0.2205950+0.6055283i  0.2205950-0.6055283i -0.0170286+0.6366803i
 [9] -0.0170286-0.6366803i -0.2463346+0.5760928i -0.2463346-0.5760928i -0.4371496+0.4346899i
[13] -0.4371496-0.4346899i -0.5633440+0.2333259i -0.5633440-0.2333259i -0.6074422+0.0000000i
```

Now, the largest eigenvalue has a value of 1.0016258, which is positive and very close to 1. This means that at this rate, the bobcat population will stay relatively stable, and any more decrease in the reproduction rate will result in the largest eigenvalue being less than 1, which will eventually result in extinction for the bobcat population. For this scenario, we chose to set a deforestation event occurring every 5 years, with a p value of 0.15, meaning the population decreases by 15% every time an event occurs.



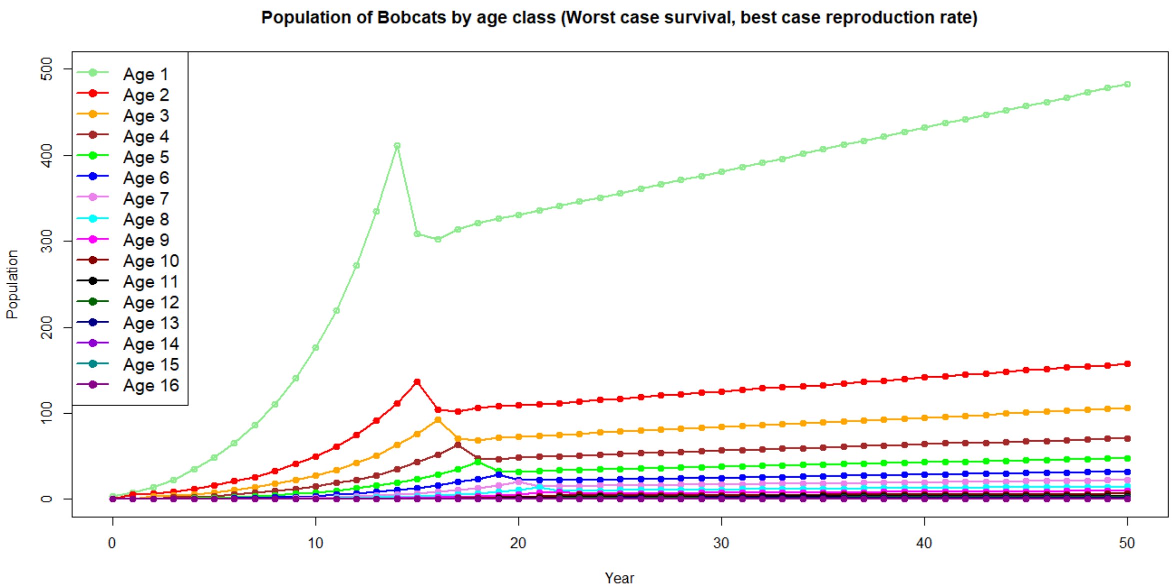
```
[,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
  41   22   16   12    9    7    6    4    3     2     2     2     1     1     1     0
```

Over a long period, the population clearly struggles and by 50 years it appears that the bobcat population is close to going extinct. The deforestation event has a 'chain reaction' throughout the population. For example, for age group 1, we see the population stagnate for a year at year 15 coinciding with the first deforestation event. At age 2, we see the population stagnate for a year at year 16, and so on for the rest of the age groups. This pattern repeats itself for all deforestation events.

In the 2nd scenario, with the worst survival and best reproduction rate, if we set p around 0.39, then a deforestation event will decrease the reproduction rate by 39%. Our eigenvalues for the matrix now look like:

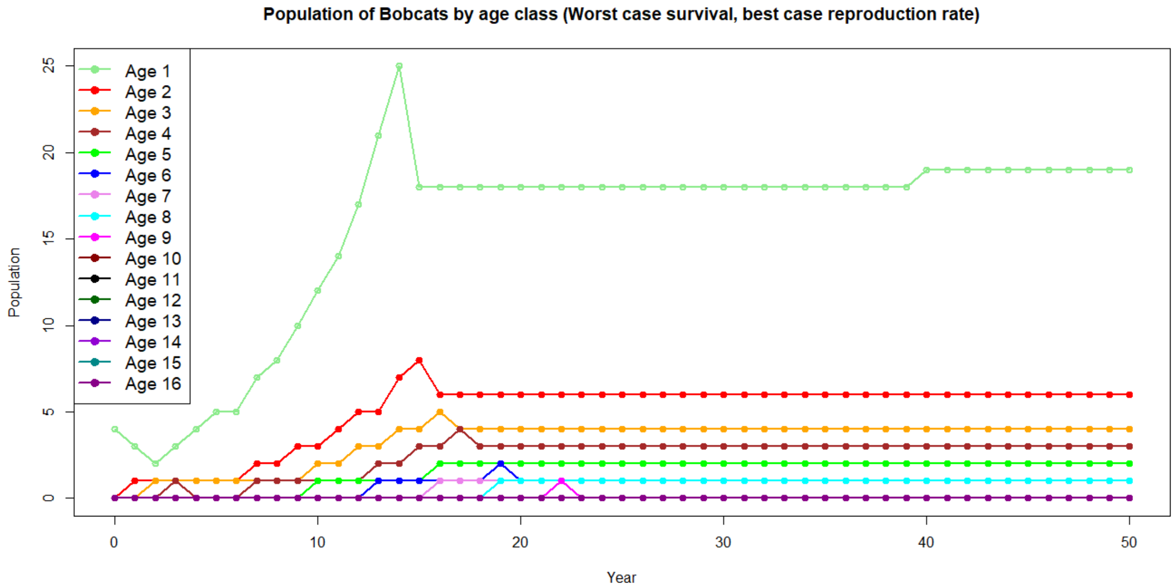
```
> eigen(bobcat_population, only.values = TRUE)
$values
 [1]  1.0008903+0.0000000i  0.6018655+0.2807989i  0.6018655-0.2807989i  0.4362669+0.4835835i
 [5]  0.4362669-0.4835835i  0.2206327+0.6052677i  0.2206327-0.6052677i -0.0169660+0.6363857i
 [9] -0.0169660-0.6363857i -0.2462468+0.5758310i -0.2462468-0.5758310i -0.4370247+0.4345022i
[13] -0.4370247-0.4345022i -0.5631866+0.2332289i -0.5631866-0.2332289i -0.6072722+0.0000000i
```

Now, the largest eigenvalue has a value of 1.0008903, which is positive and very close to 1. This means that at this rate, the bobcat population will stay relatively stable, and any more decrease in the reproduction rate will result in the largest eigenvalue being less than 1, which will eventually result in extinction for the bobcat population. For this scenario, we decided to model assuming only 1 deforestation ever took place at year 15, but it would decrease the birth rates by 39% (p = 0.39), which should result in a stable population.




```
[,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
 483  158  106   71   48   32   22   15   10     7     4     3     2     1     1     1
```

In fact, we see that even after the deforestation event, the bobcat population actually continues to increase slightly for some of the younger age groups. The reason this occurs is due to the fact that 5 bobcats aged 1 and 2 are added each year to the population. Comparing this to a model with no conservation efforts:



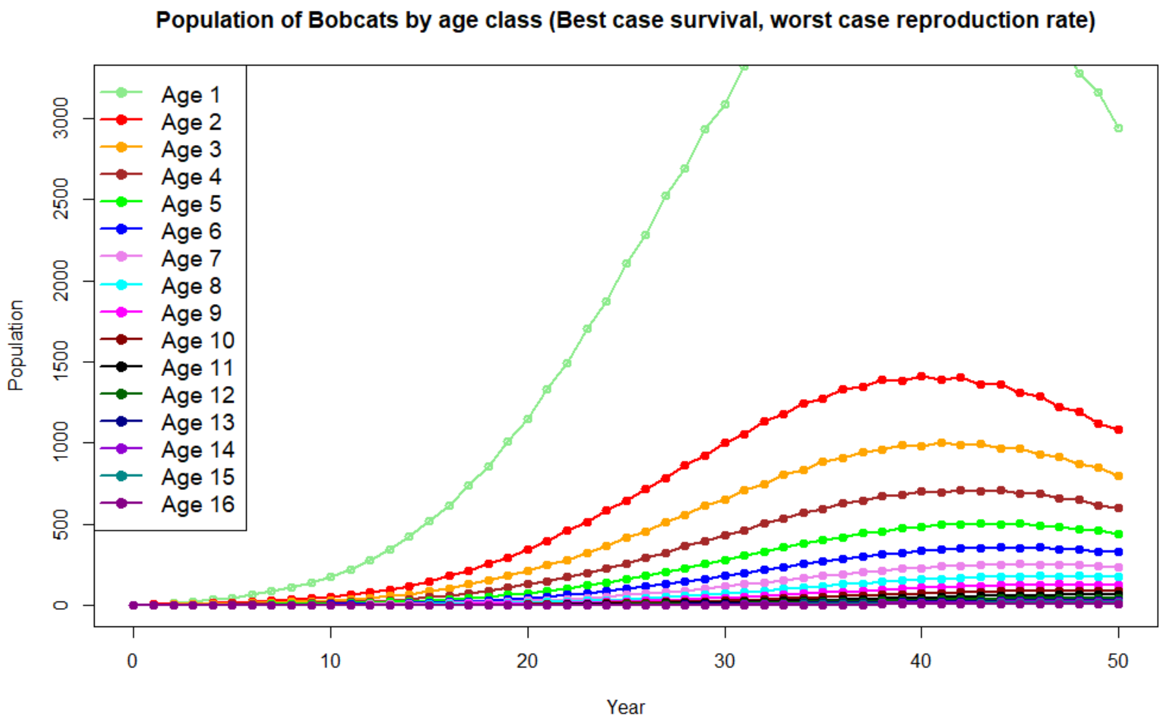

```
 [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
   19    6    4    3    2    1    1    1    0     0     0     0     0     0     0     0
```

The final population does stabilize but the population remains very low for all age groups after 50 years, which clearly shows the impact of conservation efforts.

In the 3rd scenario, with the best survival and worst reproduction rate, if we set p around 0.43, then a deforestation event will decrease the reproduction rate by 43%. Our eigenvalues for the matrix now look like:

```
> eigen(bobcat_population, only.values = TRUE)
$values
 [1]  1.0048936+0.0000000i  0.6248784+0.2935995i  0.6248784-0.2935995i  0.4517896+0.5027718i
 [5]  0.4517896-0.5027718i  0.2275808+0.6282636i  0.2275808-0.6282636i -0.0192035+0.6602461i
 [9] -0.0192035-0.6602461i -0.2571213+0.5973993i -0.2571213-0.5973993i -0.4549410+0.4507965i
[13] -0.4549410-0.4507965i -0.5857212+0.2419802i -0.5857212-0.2419802i -0.6314173+0.0000000i
```

Now, the largest eigenvalue has a value of 0.9998306, which is positive and very close to 1. This means that at this rate, the bobcat population will stay relatively stable, and any more decrease in the reproduction rate will result in the largest eigenvalue being less than 1, which will eventually result in extinction for the bobcat population. For this scenario, we chose to model a deforestation event occurring every 2 years, but will only decrease the birth rates by 4% (p = 0.04).



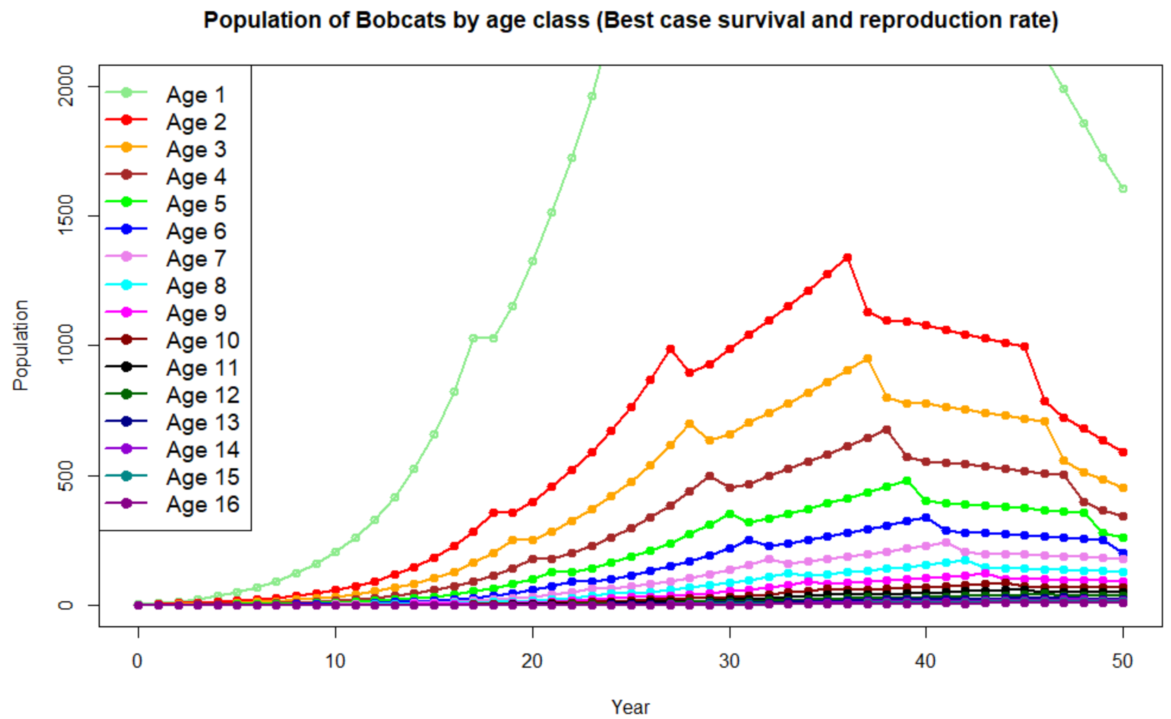

```
[,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
2939 1080  795  601  438  327  236  174  124    91    64    46    32    23    16    11
```

At this stage, the eigenvalue is 0.9537801, which suggests the bobcat population is now on course to become extinct. However, we can see that even if a deforestation event occurs often but doesn't affect the reproduction rates by too much such as in this case, the bobcat population does alright in the short term.

In the 4th scenario, with the best survival and reproduction rate, if we set p around 0.45, then a deforestation event will decrease the reproduction rate by 45%. Our eigenvalues for the matrix now look like:

```
> eigen(bobcat_population, only.values = TRUE)
$values
 [1]  1.0026499+0.0000000i  0.6246892+0.2935356i  0.6246892-0.2935356i  0.4516348+0.5024907i
 [5]  0.4516348-0.5024907i  0.2275162+0.6278336i  0.2275162-0.6278336i -0.0191805+0.6597594i
 [9] -0.0191805-0.6597594i -0.2570075+0.5969598i -0.2570075-0.5969598i -0.4547322+0.4504744i
[13] -0.4547322-0.4504744i -0.5854401+0.2418111i -0.5854401-0.2418111i -0.6311096+0.0000000i
```

Now, the largest eigenvalue has a value of 1.0026499, which is positive and very close to 1. This means that at this rate, the bobcat population will stay relatively stable, and any more decrease in the reproduction rate will result in the largest eigenvalue being less than 1, which will eventually result in extinction for the bobcat population. For this scenario, we chose to set a deforestation event occurring every 9 years, (so the first starts at 18 years), but with the birth rates being decreased by 20% each time (p = 0.2).




```
[,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16]
1605  592  451  344  259  200  180  130   94    67    49    35    25    18    13    11
```

Once again, we see the impact of deforestation on the bobcat population, with all age groups decreasing in population at year 50. Each deforestation event has a big impact on each age group.

From all 4 scenarios, it is clear that the bobcat population is resilient to deforestation up to a certain point. However, once the birth rates decrease to a certain point, there is nothing to be done to sustain the bobcat population and it is clear in the long term that the population will go extinct.

With the help of conservation efforts, it is possible that the bobcat population can continue to grow even if the largest eigenvalue of the matrix suggests the population should go extinct. However, this only helps in the short term against deforestation. It is clear that deforestation is a big issue that needs to be addressed and stopped in order to sustain the bobcat population.

Chapter 4: Discussion: Summary, Limitations, and Possible Future Research

The implication of our results shows that deforestation has a big impact on the bobcat population, but conservation efforts can greatly help. In the worst-case scenarios, where both survival and reproduction rates are at their lowest, the bobcat population remains stable if birth rates are reduced by 37% of the original parameters. Even in scenarios with the worst-case survival and the best-case reproduction rates for bobcats, the population stays stable if bobcat birth rates are reduced by around 39% of the original parameters. Similarly, under the best-case survival and worst-case reproduction rates, a reduction of about 43% in birth rates keeps the population stable. In scenarios with the best-case survival and reproduction rates, the population remains stable with a reduction of roughly 45% in birth rates. However, with conservation efforts, we've seen through analysis that even if the model predicts the population to go extinct, adding a set number of bobcats each year to the population for the younger bobcats helps the bobcats to continue to grow and stabilize.

Overall, we see that for each age group, the trend for all scenarios is that bobcats aged 1 have the highest population, and all bobcats at higher ages decrease in the number of bobcats. The results from our extended model suggest that bobcats are only resilient to deforestation up to a certain point, and that it is important that deforestation stops or slows down.

Now, while our team's model tries to capture all the critical elements of the bobcat population dynamics, we still left out some aspects that might limit the usefulness of the model. The model categorises bobcats into 16 age groups while assuming any individual would be deceased after age 16, which leads to the limitation that the model is unable to track outliers. Elder bobcats who can live beyond 16 are omitted. The model assumes all bobcats start at age 1 including newborns, which affects the accuracy of the results since new additions to the population should start at age 0. Furthermore, it only tracks the population that can reproduce, ignoring the fact that certain bobcats might not be able to reproduce.

As deforestation is the sole factor implemented in our model, the model has difficulty presenting more accurate population dynamics such as hunting, other catastrophes, and predator/prey relations. The model assumes that deforestation has the same effect on all bobcats, while corresponding survival rates remain unchanged. It is likely that deforestation should also be able to impact survival rates. For example, a reduction of trees would lead to bobcats being more open in the wild and exposed to predators.

We were given parameters for the general bobcat population, future research could look at the population dynamics in different regions of North America. For example, bobcats living in the lush forests of the eastern United States are likely to have higher rates of survival and reproduction compared to bobcats living in the deserts of southern United States and Mexico. The different parameters should result in different long term population dynamics. Shifts in phenology and vegetation dynamics could impact prey availability, potentially affecting bobcat reproduction and survival rates.[8]

As the bobcat population increases, their need for habitat space will grow as well, potentially leading them to inhabit human residential areas. Additionally, the expanding bobcat population could disrupt local animal food chains by intensifying predation on species such as squirrels, deer, and chickens, which may result in the localized extinction of these animals.

Consequently, as prey populations decline, bobcats themselves may face starvation.[3,6] This can be modelled in future research.

Future studies should work on improving existing models by fixing their limitations and including more detailed environmental factors. This will help us better understand how different factors affect bobcat populations, so we can create stronger plans to protect them from environmental threats.

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Appendix: R Code

Base Model

```
bobcat_population <- matrix(0, nrow = 16, ncol = 16)

# Reproduction rate
bobcat_population[1:2, 1] <- 0.63
bobcat_population[3:16, 1] <- 1.2

# Survival rate
bobcat_population[1, 2] <- 0.34
for (i in 2:15) {
  bobcat_population[i, i+1] <- 0.71
}

t_vals <- seq(1, 51, by = 1)
popn <- matrix(rep(NA, times = 2*length(t_vals)), nrow = 16, ncol = length(t_vals))

# Initialize population for all age groups at year 0
popn[,1] <- c(4,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)

for (t in 2:length(t_vals)) {
  for (i in 1:16) {
    # Calculate population for each age group at time step t
    popn[i, t] <- sum(bobcat_population[, i] * popn[, t-1])
  }
  popn[1, t] <- popn[1, t] + 5  # Add 5 new bobcats to age 1
  popn[2, t] <- popn[2, t] + 5  # Add 5 new bobcats to age 2
}

popn <- round(popn)
t(popn)

plot(t_vals - 1, popn[1,], type = "o", col = "lightgreen", ylim = c(0,200), xlab = "Year",
     ylab = "Population", main = "Population of Bobcats by age class (Best case survival and
reproduction rate)", lwd = 2)

points(t_vals - 1, popn[2,], type = "o", col = "red", pch = 19, lwd = 2)
points(t_vals - 1, popn[3,], type = "o", col = "orange", pch = 19, lwd = 2)
points(t_vals - 1, popn[4,], type = "o", col = "brown", pch = 19, lwd = 2)
points(t_vals - 1, popn[5,], type = "o", col = "green", pch = 19, lwd = 2)
```

```
points(t_vals - 1, popn[6,], type = "o", col = "blue", pch = 19, lwd = 2)
points(t_vals - 1, popn[7,], type = "o", col = "violet", pch = 19, lwd = 2)
points(t_vals - 1, popn[8,], type = "o", col = "cyan", pch = 19, lwd = 2)
points(t_vals - 1, popn[9,], type = "o", col = "magenta", pch = 19, lwd = 2)
points(t_vals - 1, popn[10,], type = "o", col = "darkred", pch = 19, lwd = 2)
points(t_vals - 1, popn[11,], type = "o", col = "black", pch = 19, lwd = 2)
points(t_vals - 1, popn[12,], type = "o", col = "darkgreen", pch = 19, lwd = 2)
points(t_vals - 1, popn[13,], type = "o", col = "darkblue", pch = 19, lwd = 2)
points(t_vals - 1, popn[14,], type = "o", col = "darkviolet", pch = 19, lwd = 2)
points(t_vals - 1, popn[15,], type = "o", col = "darkcyan", pch = 19, lwd = 2)
points(t_vals - 1, popn[16,], type = "o", col = "darkmagenta", pch = 19, lwd = 2)

legend("topleft", legend = c(paste("Age", 1:16)), col = c("lightgreen", "red", "orange",
"brown", "green",
                           "blue", "violet", "cyan", "magenta", "darkred",
                           "black", "darkgreen", "darkblue", "darkviolet",
                           "darkcyan", "darkmagenta"), lty = 1, pch = 19, cex = 1.2,
lwd = 2)
```

Extended Model

```
bobcat_population <- matrix(0, nrow = 16, ncol = 16)

# Reproduction rate
bobcat_population[1:2, 1] <- 0.6
bobcat_population[3:16, 1] <- 1.15

# Survival rate
bobcat_population[1, 2] <- 0.32
for (i in 2:15) {
  bobcat_population[i, i+1] <- 0.68
}

t_vals <- seq(1, 51, by = 1)
popn <- matrix(rep(NA, times = 2*length(t_vals)), nrow = 16, ncol = length(t_vals))

# Initialize population for all age groups at year 0
popn[,1] <- c(4,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)

n <- 5   # Frequency of catastrophes (in years)
p <- 0.15  # Proportion by which reproduction rates are lowered
```

```
for (t in 2:length(t_vals)) {
  for (i in 1:16) {
    # Calculate population for each age group at time step t
    popn[i, t] <- sum(bobcat_population[, i] * popn[, t-1])
  }
  popn[1, t] <- popn[1, t] + 5  # Add 5 new bobcats to age 1
  popn[2, t] <- popn[2, t] + 5  # Add 5 new bobcats to age 2

  if (t %% n == 0 && t >= 15) {
    # Reduce reproduction rates in the first column by proportion p
    bobcat_population[, 1] <- bobcat_population[, 1] * (1 - p)
  }
}

popn <- round(popn)

plot(t_vals - 1, popn[1,], type = "o", col = "lightgreen", ylim = c(0,400), xlab = "Year",
     ylab = "Population", main = "Population of Bobcats by age class (Best case survival, worst
case reproduction rate)", lwd = 2)

points(t_vals - 1, popn[2,], type = "o", col = "red", pch = 19, lwd = 2)
points(t_vals - 1, popn[3,], type = "o", col = "orange", pch = 19, lwd = 2)
points(t_vals - 1, popn[4,], type = "o", col = "brown", pch = 19, lwd = 2)
points(t_vals - 1, popn[5,], type = "o", col = "green", pch = 19, lwd = 2)
points(t_vals - 1, popn[6,], type = "o", col = "blue", pch = 19, lwd = 2)
points(t_vals - 1, popn[7,], type = "o", col = "violet", pch = 19, lwd = 2)
points(t_vals - 1, popn[8,], type = "o", col = "cyan", pch = 19, lwd = 2)
points(t_vals - 1, popn[9,], type = "o", col = "magenta", pch = 19, lwd = 2)
points(t_vals - 1, popn[10,], type = "o", col = "darkred", pch = 19, lwd = 2)
points(t_vals - 1, popn[11,], type = "o", col = "black", pch = 19, lwd = 2)
points(t_vals - 1, popn[12,], type = "o", col = "darkgreen", pch = 19, lwd = 2)
points(t_vals - 1, popn[13,], type = "o", col = "darkblue", pch = 19, lwd = 2)
points(t_vals - 1, popn[14,], type = "o", col = "darkviolet", pch = 19, lwd = 2)
points(t_vals - 1, popn[15,], type = "o", col = "darkcyan", pch = 19, lwd = 2)
points(t_vals - 1, popn[16,], type = "o", col = "darkmagenta", pch = 19, lwd = 2)

legend("topleft", legend = c(paste("Age", 1:16)), col = c("lightgreen", "red", "orange",
"brown", "green",
                                "blue", "violet", "cyan", "magenta", "darkred",
                                "black", "darkgreen", "darkblue", "darkviolet",
                                "darkcyan", "darkmagenta"), lty = 1, pch = 19, cex = 1.2,
lwd = 2)
```

Appendix: Individual Contributions

Nicholas Hobinca: Base Model Code, Extended Model Code, Results, Discussion: Summary, Presentation Slide

Sheri Kabashi: Introduction, Extended Model Code, Results, Presentation Script, Final Edits

Gabriel Pangan: Introduction, Presentation Script, Presentation Slide

James Xu: Base Model Analysis, Discussion: Limitations, Presentation Script

Torres Zheng: Base Model Analysis, Discussion: Future Research

Kelly Zhu: Results