Lab Assignment 6

Loggerhead Sea Turtle Model

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Math 214: Discrete Math Modeling

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We can use matrix algebra to determine index of imprimitivity and the dominant eigenvalue. If the index of imprimitivity is 1 then we can also find the normalized eigenvector representing the equilibrium structure (as we did in Lab 5). In the MATLAB Skills portion of this lab you will learn how to use a combination of built-in MATLAB function to find the index of imprimitivity, and how to use an *if-statement* in MATLAB.

MATLAB Skills

Calculating the Index of Imprimitivity

1. Download the `L06Ex01.m` file from Moodle, and open the file in MATLAB.

L06Ex01.m

```
1  % Lab 6 Example 1 by Prof Bodine
2  clear all
3
4  A = [0 0 0.42; 0.60 0 0; 0 0.75 0.95]; % Leslie matrix for American Bison
5  A = [0 0 1000; 0.02 0 0; 0 0.05 0]; % Leslie matrix for Locust Population
6
7  % Find the dominant eigenvalue
8  [V,D]=eig(A);
9  L = abs(diag(D)) % magintudes of all the eigenvalues
10 imax = find(L==max(L));
11 Lmax = L(imax);
12
13 % Calculate the index of imprimivity
14 tol = 1e-10;   % set the tolerance for what you accept as zero
15 diff = abs(L - max(L)); % calc difference btw each eigenvalue and the dominant eigenvalue
16 d = length(find(diff < tol)) % calc the index of imprimitivity
```

2. Now, let us take a moment to understand everything within this script.
   (a) Lines 1–11 we have essentially seen before in Lab 5.

   Notice that two Leslie matrices are provided: one for the American Bison population and one for the Locust population examples we saw in class. Line 8 will currently execute the `eig` function on the most recently defined version of `A`, thus for the locust population. If we want to make calculations for the bison population, we need only to comment out line 5 by placing a `%` in front of `A`.

   (b) Lines 13–16 are used to determine the index of imprimitivity of the Leslie matrix `A`. Note, if you wish to see what the output for any of these lines of code looks like, remove the semicolon from the end of the lines before running the code.

(i) Recall, the index of imprimitivity is the number of eigenvalues (including the dominant eigenvalue) which have the same absolute magnitude as the dominant eigenvalue. Let λ_1 be the dominant eigenvalue, and λ_i be another eigenvalue such that

$$|\lambda_1| = |\lambda_i|, \quad \text{then} \quad |\lambda_1| - |\lambda_i| = 0.$$

Now, due to the limitations of machine precision (how precise a number is in the memory of a computer), sometimes when you subtract two numbers that are suppose to be equal you end up with a very very small positive or negative number. For example, in the command window if you subtract 0.4 and 0.1 from 0.5, you should end up with zero, but due to limitations of machine precision the calculated value is not zero. It is very close to zero (-2.7756×10^{-17}), but the computer has not calculated it to *be* zero.

Command Window

```
>> 0.5 - 0.4 - 0.1
ans =
       -2.7756e-17
```

To get around this, we calculate the absolute value of the difference between each value in `L` (the eigenvalues calculated in line 9) and the value of `Lmax` (the dominant eigenvalue calculated on line 11), and then check to see if each of those values are less than some small number which we will consider equivalent to zero.

(ii) In line 14 we set `tol` to be a small number which we will consider equivalent to zero. In the example, we have `tol` set to 1×10^{-10}.

(iii) In line 15 we calculate the absolute difference between each eigenvalue and the dominant eigenvalue.

(iv) In line 16 we calculate the index of imprimitivity. The function `find` allows you to search an array (vector or matrix) for values that meet certain criteria (in this case when `diff < tol`). The output of the `find` function are the indices (positions in the array) of the values which do meet the criteria. If you are curious what this output looks like, after you have run the code once, in the command window type

Command Window

```
>> find(diff < tol)
ans =
     1
     2
     3
```

This means that the entries in `diff` that were less than `tol` were in positions 1, 2, and 3 of `diff`. If fewer entries met the criteria we would see fewer entries as the output. Try running `L06Ex01.m` again with line 5 commented out and then typing `find(diff < tol)` into the command window again. You should get only one position listed.

Note, that the number of elements in the output of `find(diff < tol)` represents the number of eigenvalues of `L` which have the same absolute magnitude as the dominant eigenvalue. Thus, we take the length of the array output by `find(diff < tol)` to determine index of imprimitivity.

(v) Take another moment to review `L06Ex01.m`. **Do you understand what each line of code is doing?** If not, now is the time to stop and ask.

(c) Run the script again. Notice since lines 9 and 16 have no semicolons at the end, the results of these lines of code should appear in the command window. If lines 5 is not commented out, you should get $\lambda_1 = 1$ and $d = 3$; if line 5 is commented out, you should get $\lambda_1 = 1.1$ and $d = 1$.

If-Statements

The idea of an *if-statement* is that you can check to see *if* some condition is true. If it is, then you will execute one set of commands, but if it is not then you will execute another set of commands.

1. From Moodle, download the script `L06Ex02.m`.

L06Ex02.m

```
% Lab 6 Example 2 by Prof Bodine
clear all

A = [0 0 0.42; 0.60 0 0; 0 0.75 0.95]; % Leslie matrix for American Bison
A = [0 0 1000; 0.02 0 0; 0 0.05 0]; % Leslie matrix for Locust Population

% Find the dominant eigenvalue
[V,D]=eig(A);
L = abs(diag(D)); % magintudes of all the eigenvalues
imax = find(L==max(L));
Lmax = L(imax);

% Calculate the index of imprimivity
tol = 1e-10;   % set the tolerance for what you accept as zero
diff = abs(L - max(L)); % calc difference btw each eigenvalue and the dominant eigenvalue
d = length(find(diff < tol)); % calc the index of imprimitivity

% Print out results
if d > 1
  fprintf('Oscillates with a period of %d\n',d)
  fprintf('Dominant eigenvalue is %.3f\n',Lmax)
else
  Vmax = V(:,imax);
  normVmax = Vmax/sum(Vmax);
  fprintf('Dominant eigenvalue is %.3f\n',Lmax)
  fprintf('Population structure is \n')
  fprintf('  %4.3f\n',normVmax)
```

```
28 end
```

2. Now, let us take a moment to understand everything within this script.
   (a) First, note that lines 1–16 are copied from the script file `L06Ex01.m`. Note also that a semicolon has been added to the end of lines 9 and 16.

   (b) Lines 19–28 contains an if-statement. The condition of the if-statement (`d > 1`) is given in line 19. If the index of imprimitivity is greater than 1, then the script will execute lines 20–21 and print out the period of the oscillations along with the dominant eigenvalue. If, on the other hand, the index of imprimitivity is not greater than 1 (which would mean it is 1), then lines 23–27 will execute and print out the dominant eigenvalue and the normalized eigenvector corresponding to the dominant eigenvalue. Lines 23 – 24, which calculate the normalized eigenvector corresponding to the dominant eigenvalue, have been used before in code presented in Lab 5.

   Note that the command `else` on line 22 indicates the end of the commands to be executed if the condition is true, and the beginning of the commands to be executed if the condition is false.

   Lastly, like with a for-loop, we end an if-statement with the `end` command (see line 28).

3. Run the script file. If line 5 is not commented out, you should see the following in the command window

   Command Window

   ```
   >> L06Ex02
   Oscillates with a period of 3
   Dominant eigenvalue is 1.000
   ```

   If line 5 is commented out, you should see the following in the command window

   Command Window

   ```
   >> L06Ex02
   Dominant eigenvalue is 1.105
   Population structure is
   0.240
   0.130
   0.630
   ```

Lab Group Discussion

Week 1:

1. In `L06Ex01.m`, the `find` function is used twice: once in line 10, and again in line 16. Describe the condition checked for each use of the `find` function and how they differ.
2. Instead of lines 14 – 16 in `L06Ex01.m`, why can we not just use `d = length(find(L==max(L)))`? *You may want to try typing this into the command window after you have run `L06Ex01.m` once to see what happens?*

3. Why do we need to create the `tol` variable?
4. Why is it important to test the `L06Ex01.m` and `L06Ex02.m` codes on two different matrices?
5. Enter a third matrix into `L06Ex02.m`. Use the Leslie matrix for killer whales (from class and given below). Interpret the output from the code in biological terms.

   The killer whale Lefkovitch matrix model is given by

$$\begin{bmatrix} y(t+1) \\ j(t+1) \\ m(t+1) \\ p(t+1) \end{bmatrix} = \begin{bmatrix} 0 & 0.0043 & 0.1132 & 0 \\ 0.9775 & 0.9111 & 0 & 0 \\ 0 & 0.0736 & 0.9534 & 0 \\ 0 & 0 & 0.0452 & 0.9804 \end{bmatrix} \begin{bmatrix} y(t) \\ j(t) \\ m(t) \\ p(t) \end{bmatrix},$$

   where $y(t)$, $j(t)$, $m(t)$, and $p(t)$ are the numbers of yearlings, juveniles, mature adults, and post-reproductive adults at time t, respectively.
6. Suppose the condition for the if-statement on line 19 of `L06Ex02.m` were `d == 1`. How would the construction of lines 19 – 28 need to change so that the code still functioned properly?

Week 2: Read the following information about calculating population proportional increases, and then answer the weekly discussion questions.

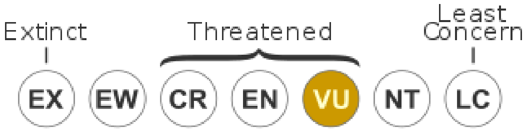


Figure 1: Global Loggerhead Sea Turtle IUCN Listing

The International Union for the Conservation of Nature (IUCN) maintains the Red List, the most comprehensive list of the global conservation status of species. The IUCN currently lists the loggerhead sea turtle globally as vulnerable. However, there are 10 distinct subpopulations and the IUCN states, "the global listing is not an appropriate representation of the conservation status of the biologically relevant subpopulations that make up the global Loggerhead Turtle population." Figure 2 show the global distributions of the 10 subpopulations and Table 1 shows the conservation status and abundance of each subpopulation. The abundance is measured as the number of nests counted per year. Though the abundance is not a measure of the total population size, the change in abundance over time is used to approximate how the population is changing over time. The generational change is abundance is calculated as

$$\frac{\text{current abundance} - \text{past abundance}}{\text{past abundance}} \tag{1}$$

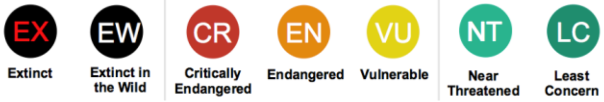
and represents the proportional increase (if positive) or decrease (if negative) over the amount of time between abundance measures. The abundance change shown in Table 1 is over three generations (approximately 135 years; 45 years between generations). Thus, for example, the Northwest Atlantic population increased by 2% over three generations. How does this translate into a yearly increase?

Recall the exponential growth difference equation, $x_{n+1} = ax_n$, where a represents the proportional increase per time step. Further recall that the closed form solution of the exponential growth model is $x_n = a^n x_0$ where x_0 is the population size or density at time step $n = 0$. Now, suppose that the proportional increase after n years is s, that is,

$$\frac{x_n - x_0}{x_0} = s. \tag{2}$$

Table 1: IUNC listings and abundance counts of the 10 loggerhead sea turtle subpopulations. Abundance is measured as the number of counted nests per year. Current abundance measured in 2013, past abundance measured 3 generations prior to 2013 (generational time is approximately 45 years), and the 3-generation changes is measured as (current–past)/past. Details of the IUNC listing for *Caretta caretta* can be found at http://www.iucnredlist.org/details/3897/0.

Subpopulation	**Status**	**Past Abundance**	**Current Abundance**	**3-Generation Change**
NW Atlantic	LC	82 342	83 717	0.02
NE Atlantic	EN	—	15 000	—
SW Atlantic	LC	4519	7696	0.70
Mediterranean	LC	6723	7200	0.07
NW Indian	CR	243 040	70 000	−0.71
NE Indian	CR	—	25	—
SW Indian	NT	1097	4600	3.19
SE Indian	NT	—	2955	—
N Pacific	LC	3368	9053	1.69
S Pacific	CR	—	—	—



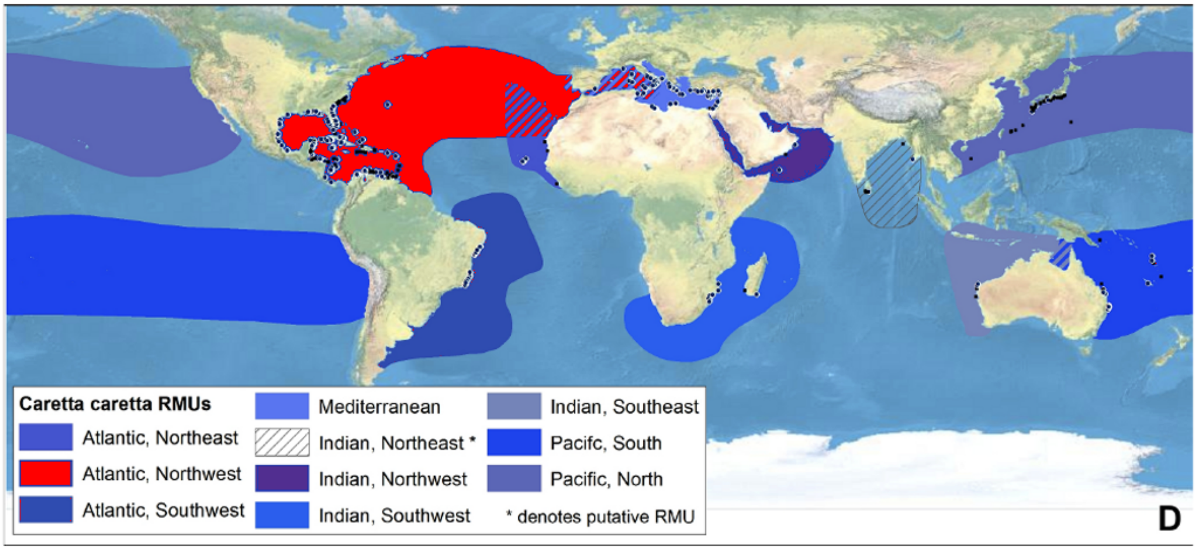


Figure 2: Global distribution of the 10 *Caretta caretta* subpopulations.

Notice that Equation (2) is the same as Equation (1) where x_0 represents past abundance and x_n represents current abundance, and thus $n = 135$. Using the closed form solution of the exponential difference equation, we can solve Equation (2) for a to find

$$a = (1+s)^{1/n}.$$

Thus, in the example of the Northwest Atlantic population, $s = 0.02$ and $n = 135$, and therefore $a = (1+0.02)^{1/135} \approx 1.000147$. This means that the population was increasing by 0.0147% per year. In our notation for matrix models, the value of a corresponds to the dominant eigenvalue of the Leslie matrix.

1. Show how to use the closed form solution $x_n = a^n x_0$ and Equation (2) to get $a = (1+s)^{1/n}$.
2. Calculate the value of a for each of the six loggerhead sea turtle subpopulations which list both a current and past abundance.
3. The matrix **A** given in the Lab Assignment also models a loggerhead sea turtle population. In `L06Ex02.m`, replace `A` with the matrix given the Lab Assignment.
    (a) Does the population oscillate? If so, what is the period of oscillation? If not, what is the structural equilibrium?
    (b) What is the dominant eigenvalue?
    (c) Is the population growing or declining?
    (d) Given the six values of a calculated above, which loggerhead sea turtle subpopulation has a yearly population growth rate similar to that of the population modeled by **A**?

Checkpoint Exercise

In an attempt to save the endangered northern spotted owl (*Strix occidentalis caurina*), in the 1989 the U.S. Fish and Wildlife Service imposed strict guidelines for the use of 12 million acres of Pacific Northwest forest. This decision led to a national debate between the logging industry and environmentalists. Mathematical ecologists have created a mathematical model to analyze the population dynamics of the north spotted owl by dividing the female owl population into three categories: juvenile (up to 1 year old), subadult (1 to 2 years old), and adult (over 2 years old). the female owl population can be modeled by the Leslie matrix model

$$\begin{bmatrix} j(t+1) \\ s(t+1) \\ a(t+1) \end{bmatrix} = \begin{bmatrix} 0 & 0 & 0.33 \\ 0.18 & 0 & 0 \\ 0 & 0.71 & 0.94 \end{bmatrix} \begin{bmatrix} j(t) \\ s(t) \\ a(t) \end{bmatrix}.$$

1. Write a MATLAB script similar to `L06Ex02.m` which calculates the dominant eigenvalue for the spotted owl Leslie matrix model given above, and reports the index of imprimitivity if it is greater than 1, but otherwise reports the structural equilibrium of the population.
2. Modify you MATLAB script which generates solutions for the above Leslie matrix model over 100 years. Start

with a population of 4000 female northern spotted owls made up of 900 juveniles, 500 subadults, and 2600 adults. In the for-loop use to generate the solution over time, if the total female population falls below 800, print the year and the population size in the command window.

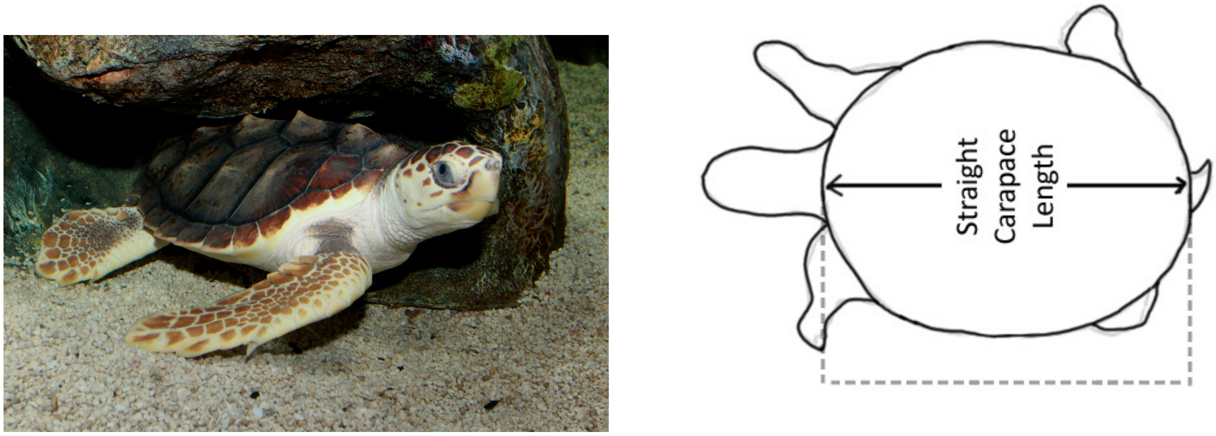
3. CHECKPOINT: Verify that your code is running correctly by executing your script file for the lab tutor.

Lab Assignment

In 1987, Crouse, Crowder, & Caswell proposed a matrix model to simulate the population dynamics of loggerhead sea turtles (*Caretta caretta*).[1] The model is similar to a Leslie matrix model, but the individuals in each stage do not necessarily age into the next stage at each time step if they do not die. Instead, some proportion can stay in each stage at every time step. This is because the time step is one year, but each stage represents multiple years (see Table 2).

Table 2: Stage-based life table for loggerhead sea turtles from [1].

Stage Number	Class Description	Straight Carapace Length (cm)	Approximate Age (yrs)	Annual Survivorship	Fecundity (# eggs/yr)
1	eggs, hatchlings	< 10	< 1	0.6747	0
2	small juveniles	10.1–58.0	1–7	0.7857	0
3	large juveniles	58.1–80.0	8–15	0.6758	0
4	subadults	80.1–87.0	16–21	0.7425	0
5	novice breeders	> 87.0	22	0.8091	127
6	1st-yr remigrants	> 87.0	23	0.8091	4
7	mature breeders	> 87.0	24–54	0.8089	80



(a) A loggerhead sea turtle. **(b)** Diagram of straight carapace length measurement.

Figure 3: Loggerhead sea turtle (*Caretta caretta*).

The stage-structured model proposed by Crouse, et al. used the seven age classes given in Table 2, however, since each class could represent more than one year, not only does the model have parameters for the fecundity of the i^{th}

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[1] To read a copy of the original paper, visit `http://www.d.umn.edu/~thrabik/Crouse%20et%20al.%201987.pdf`.

stage (F_i), and the probability of surviving and growing to the next stage (G_i), but it also includes the probability of surviving and remaining in the same stage (P_i). The Leslie-like matrix for the model is

$$\mathbf{A} = \begin{bmatrix} P_1 & F_2 & F_3 & F_4 & F_5 & F_6 & F_7 \\ G_1 & P_2 & 0 & 0 & 0 & 0 & 0 \\ 0 & G_2 & P_3 & 0 & 0 & 0 & 0 \\ 0 & 0 & G_3 & P_4 & 0 & 0 & 0 \\ 0 & 0 & 0 & G_4 & P_5 & 0 & 0 \\ 0 & 0 & 0 & 0 & G_5 & P_6 & 0 \\ 0 & 0 & 0 & 0 & 0 & G_6 & P_7 \end{bmatrix} = \begin{bmatrix} 0 & 0 & 0 & 0 & 127 & 4 & 80 \\ 0.6747 & 0.7371 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.0486 & 0.6611 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.0147 & 0.6907 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.0518 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.8091 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0.8091 & 0.8089 \end{bmatrix}.$$

Notice that for each stage $G_i + P_i$ is equal to the annual survivorship of that class (shown in Table 2). The matrix model is then given by $\mathbf{x}(t+1) = \mathbf{A}\mathbf{x}(t)$.

1. Construct a script file in MATLAB, saved as `Lab06_YourLastName.m`, which accomplishes the following tasks in the order given:
   (a) Erase the values of all variables and parameters stored in the workspace.
   (b) Create the matrix $\mathbf{A}$ (as given above).
   (c) Generate a plot of the number of female turtles in each age class over 100 years if you start with only 200 notice breeders (half of which are female). Note, to do this you will have to generate solutions first.
   (d) Determine if the population is oscillating by finding the index of imprimitivity. Use an if-statement to print out the results as in `L06Ex02.m`. If the index of imprimitivity is greater than 1 print out the period of the oscillations and the value of the dominant eigenvalue. If the index of imprimitivity is not greater than 1, then print out the value of the dominant eigenvalue and the population structure at the structural equilibrium.
2. CHECKPOINT: Run your script file to show that the long term trajectory of the loggerhead sea turtle population is extinction.

Figure 4: Loggerhead sea turtles escapes from a net through the turtle excluder device (TED).

There have been conservation efforts to protect loggerhead sea turtle populations (and globally the species) for several decades. The data collected for the Crouse, et al. paper was for the Northwest Atlantic population with data collected in Florida locations. One focus of conservation in Florida has been to protect nesting site to ensure hatchling survival. Another form of conservation has worked with shrimp trawling industry to add turtle excluder devices (TEDs) to shrimp trawling nets to provide a means of escape for even the largest sea turtles. TEDs are now mandatory in the shrimp trawling industry. Typically, with the implementation of conservation measures, resources are limited and choices must be made as to how those resources are allocated. The next two steps are designed to help you evaluate the efficacy of each of these two conservation measures.

3. Using your script file, increase the hatchling survival rate (G_1) to 1, and calculate the dominant eigenvalue and either the stable stage structure or the period of oscillation. Determine the total population size after 5 and 10 decades if the population started with 100 female novice breeders.

   Run your script file. Save the graph produced as `Lab06_YourLastNameA.jpg`.

4. Suppose the TEDs increase the annual survivorship of all age classes (except the hatchlings) by 1%. Thus, for example, the small juveniles annual survivorship would increase from 0.7857 to $1.01 \times 0.7857 = 0.7936$. Moreover, the P_2 and G_2 increase equally and thus also each increase by 1%. Thus, P_2 increases to 0.7445, and G_2 increases to 0.0491.

   Using your script file, increase the annual survivorship of all age classes (except the hatchlings) by 7% be increasing the P_i and G_i values by 7%. Then run the script to calculate the dominant eigenvalue and either the stable stage structure or the period of oscillation. Determine the total population size after 5 and 10 decades if the population started with 100 female novice breeders.

   Run your script file. Save the graph produced as `Lab06_YourLastNameB.jpg`.

Submit:

- 1 script files (`Lab07_YourLastName.m`)
- 1 Word document (`Lab07_YourLastName.docx`)

References

[1] D.T. Crouse, L.B. Crowder, and H. Caswell. 1987. A Stage-Based Population Model for Loggerhead Sea Turtles and Implications for Conservation. *Ecology*, 68(5): 1412–1423.