

## FISH 552 Homework 4

Open a new script in R and put the following information at the top using comments:

```
# Name: First Last
```

```
# Homework 3
```

Complete the tasks below and be sure to label each question with comments as before

```
##Question 1a
```

```
R Code . . .
```

```
##Question 1b
```

```
R Code . . .
```

When your script is complete, save it as `LastName_Homework3.R`, then clear your workspace (Workspace/Clear all) and run through your script again to make sure you don't have any 'object not found' errors. Then go to the drop box at the course website to submit your R script.

### Part 1 – Commit Log

While working on this assignment, please record a commit message at the end of each work session. Here is a reminder of what components to include:

New files created in this work session:

Existing files edited in this work session:

Brief summary of activity/changes completed in this work session ( $\leq 10$  words):

Description of activity/changes completed in this work session (bullet points or 2 sentences):

Note to self for next time (what should you start on the next time you open this assignment?):

### Part 2 – Programming Assignment

#### Question 1: An example of generating "data"

Set a random seed to start the state of R's random number generator

- Generate 1000 random variables from a Cauchy distribution with a location parameter 5 and scale parameter 1. Store these values in `randomCauchy`. What are the minimum and maximum values? What is the mean value?
- Create a sequence of numbers from 0.01 to 0.985 in increments of 0.025. Call this vector `x`.
- For each value in `x`, find the density, assuming a Beta distribution with shape parameters equal to 5 and 2 respectively. Name this vector `betaDensity`.
- Renormalize the vector `betaDensity` by dividing every observation in the vector by the sum of all the observations. Call this new vector `betaDensityNorm`. The sum of all the observations should now be 1. Check this.

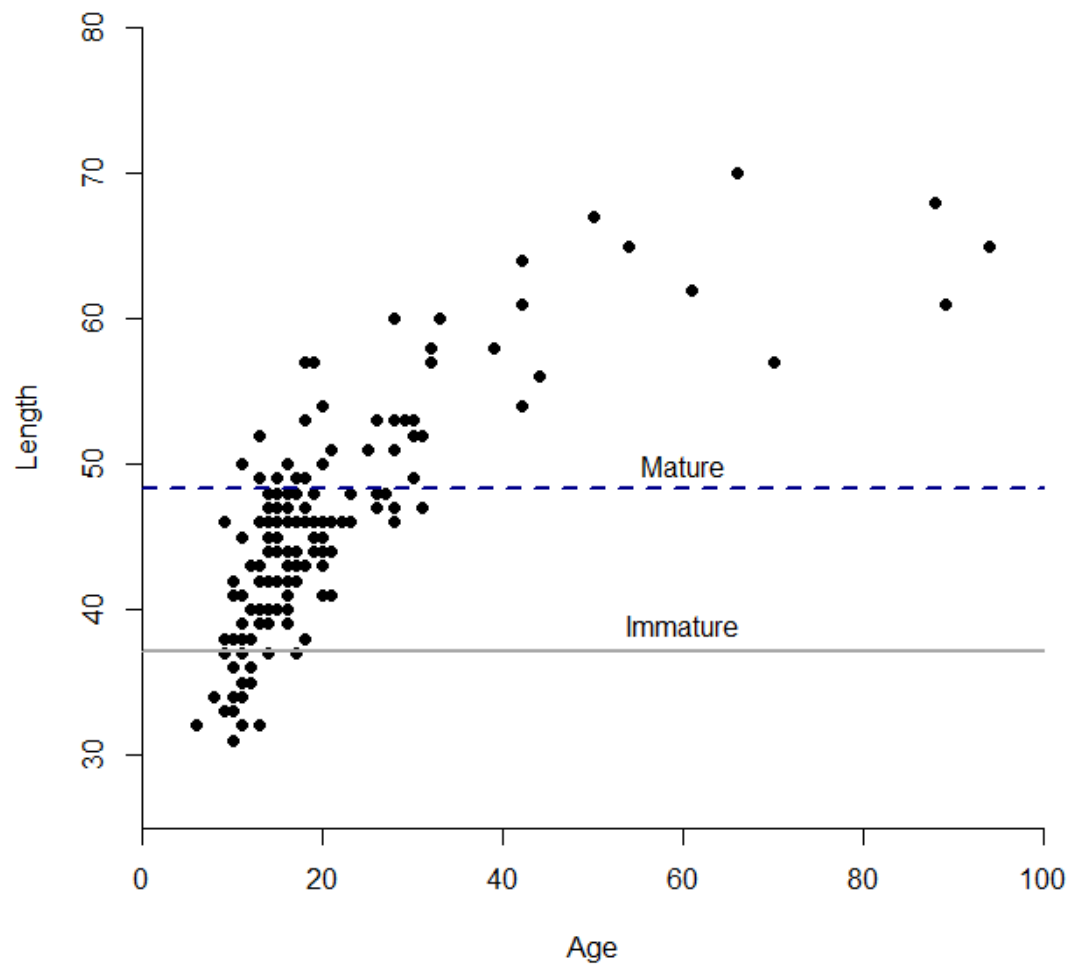
- e) Create a sequence of integers from 12 to 90 in increments of 2. Call this vector `lengths`.
- f) The vectors `betaDensityNorm`, and `lengths` should all be of length 40 (check!). Create a random sample of 1000 lengths from the vector `lengths` with weighted probabilities\* for each length given by the vector `betaDensityNorm`. Call this vector `lengthsSample`. (5 points)
- g) Create a histogram from the vector `lengthsSample`. Add a density curve. Change the default plot to make your histogram “pretty” (*This is subjective so you can add a title, color, . . . or anything that you feel this plot needs*).

Congratulations, you have successfully generated some “data” that can be used to test that your models are working!

## Question 2: Functions & multi-panel plots

For this question we’ll be using the `Cabazon.csv` and `YERockfish.csv` data.

- a) Read in `YERockfish.csv` data and call it `Yelloweye`.
- b) Write a function called `Length.Age.Mat()` that takes three parameters (arguments): `length`, `age`, and `maturity`. The function will plot the length (y-axis) at age (x-axis) data with proper labels. The function will also calculate the mean length and mean age for each stage of maturity (Immature, Mature, and Unknown) and store them as vectors called `Length_Means` and `Age_Means`. Plot the `Length_Means` for Immature and Mature as horizontal lines (e.g., `abline()` function) on the length at age plot. Format the plot to match the plot provided below. Finally, have the function return `Length_Means` and `Age_Means` as a list.



c) Read in `Cabezón.csv` and call it `Cabezón`. Use `Length.Age.Mat()` to create a length at age plot and find the mean lengths and mean ages for Cabezón!

d) Create a multi-panel plot using `Cabezón` and `Yelloweye`'s length at age plots using `layout()` or `par(mfrow)`.