Homework 4 Instructions

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Part 1 - Programming Assignment

Open a new script in RStudio and create an assignment header using comments.

```
# Name: First Last
# Homework 4
```

Complete the tasks below. Please label each question and task with comments.

```
#==Question 1a ####
# Your R code here
#==Question 1b ####
# Your R code here
```

When your script is complete, save it as LastName_Homework4.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 course website to submit your R script.

Question 1: An example of generating simulated "data"

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

- a) 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?
- b) Create a sequence of numbers from 0.01 to 0.985 in increments of 0.025. Call this vector x.
- c) 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.
- d) 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.

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*).

Question 2: Functions & multi-panel plots

For this question we'll be using the Cabezon.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 at least (i.e, you may add more for plotting) three parameters (arguments): length, age, and maturity. The function will:
- plot the length (y-axis) at age (x-axis) data with proper labels
- HINT!: In part c) you will reuse this function for a different species that has a different range of length and ages. This will cause issues with your xlim and ylim specifications. Think of a way to make setting the limits of your plot generalizable.
- 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 horizonal lines (e.g., abline() function) on the length at age plot. Format the plot to match the plot provided below.
- return Length Means and Age Means as a list.
- c) Read in Cabezon.csv and call it Cabezon. Use Length.Age.Mat() to create a length at age plot and find the mean lengths and mean ages for Cabezon!
- d) Create a multi-panel plot using Cabezon and Yelloweye's length at age plots using layout() or par(mfrow).

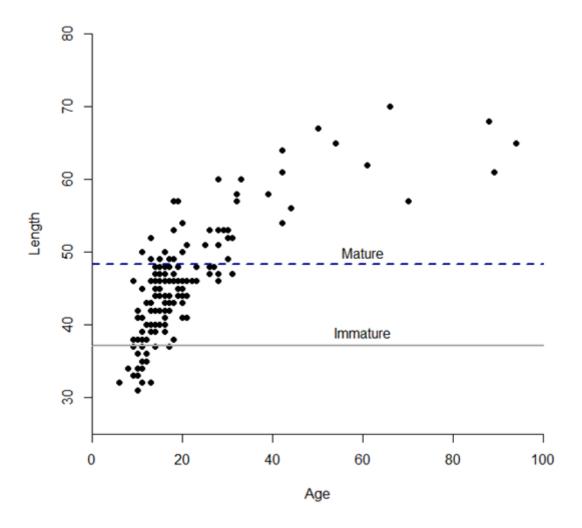


Figure 1: Figure to recreate for part b)