FISH 552
Homework 4

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

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

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

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 drop box at the course website to submit your R script.

Question 1
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? (5 points)

b) Create a sequence of numbers from 0.01 to 0.985 in increments of 0.025. Call this vector `x`. (5 points)

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`. (5 points)

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. (5 points)

e) Create a sequence of integers from 12 to 90 in increments of 2. Call this vector `lengths`. (5 points)

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*). (10 points)

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

Question 2
For this question we'll be using the `iris` data in R.

a) Compute a test to see whether *versicolor* and *virginica* irises have equal or unequal variances in sepal widths. (10 points)

b) Compute a t-test using the results from (a) to decide if *versicolor* and *virginica* irises have equal or unequal mean sepal widths. Decide if the observations should be paired and the variances treated as equal. (10 points)

c) Check the normality assumption of the test in a). Add comments in your code with your analysis about whether you think the assumptions have been met. (10 points)

d) Repeat the comparison of means, but this time without assuming normality. (10 points)

e) Create a plot of the `iris` data that color codes by species and includes multiple plots, using `layout` or `par(mfrow)`. Which plots to combine are up to you. (20 points)