**Assignment 3**

Write code that performs the following functions or that answers the question. Feel free to do this in R, then copy + paste your code into the assignment turn in space.

1. Download the finch\_beaks\_1975 and finch\_beaks\_2012 dataset from ELMS. These contain data on finches from the Galapagos (think Darwin) to study evolution of beak lengths/depth.

|  |  |  |
| --- | --- | --- |
| **Column name** | **Description** | **Possible values** |
| species | Finch species | fortis, scandens |
| blength | Beak length (mm) | Numeric values |
| bdepth | Beak depth (mm) | Numeric values |

Read both files into R, storing them in variable names of your choice. Missing values are coded as “Missing” in the 1975 dataset and “NA” in the 2012 dataset—make sure to remove these for subsequent analyses.

1. Each file contains data on two finch species. Obtain a summary on the distribution of each species. Store into variable **2a**. Then repeat for the 2012 dataset, storing in **2b**. What’s stored in these variables should look something like this:

fortis scandens  
 316 87

1. What is the difference in mean beak length between 2012 and 1975 for the fortis species? Store this difference in variable **3a**. Repeat for scandens, storing it in **3b**.
2. Finch depth affects if a finch is able to fit its beak into spaces to obtain food. Let’s say for scandens that finches with beak depth between 9 and 10 mm are the most fit. Beaks below that are too narrow, above are too wide. Computer a summary of the three groups in 1975 and store in **q4a**. Repeat for 2012 and store in **q4b**. In other words, what is stored inside the variables should look something like this:

too narrow most fit too wide

43 39 5

References for data:

<https://www.kaggle.com/crbelhekar619/darwins-finches-evolution-dataset>

<https://www.kaggle.com/crbelhekar619/darwins-finches-evolution-dataset?select=finch_beaks_2012.csv>