

# Homework 1: R Introduction

*Your\_Name\_Here*

*Adapted from University of Tennessee Biometry course by Dr. Jim Fordyce*

Turn in via Canvas on the due date by the end of the day. It should be a PDF file generated from knitting an RMarkdown document. Please see me well in advance if you have problems knitting. Knit as you go along to make sure it's working periodically. Do not wait until the end to knit the first time because it will be much more difficult to track down any problems.

1. Assign to a vector called X the values 1,3,5,6,7, and 9. Assign to a vector called Y the values 2,7,4,5,2 and 12.
2. Combine the two vectors together as one large vector called Z.
3. Create a new vector that includes all the values in Z that are less than 6.
4. Using R functions, calculate the mean of Z.
5. Create an matrix where the columns are X and Y. Assign this matrix to an object called mat1.
6. Using the R function rowSums, calculate the sum of each row. You may have to look up how to use this function.
7. Calculate the mean of the rows of mat1 and add this as a third column. You can use the rowMeans function.
8. Extract the value of mat1 at the second row and first column.
9. Write mat1 to a .csv file.
10. Read the .csv file and assign it to an object called mat\_new.
- 11 Show that the third number in the first column of mat\_new is equal to the fourth number in the second column.
- 12 Make 'mat1' a data frame.
- 13 Using R functions, calculate the length of X.
- 14 Assign the name "mean" to the third column of mat1.
- 15 Create a sequence of numbers from -10 to 10 with intervals of 0.5 using R functions. Assign it to an object and calculate the sum of the values.
16. Using the iris data, make a new dataframe called iris\_petal with just the petal length and width columns.

```
str(iris)

## 'data.frame':   150 obs. of  5 variables:
## $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
## $ Species      : Factor w/ 3 levels "setosa","versicolor",...: 1 1 1 1 1 1 1 1 1 1 ...
```

Based on the structure of iris I see that there are 150 observations of 5 variables.

17. Now add a new column to `iris_petal` called `Random` filled with normally distributed random numbers.
18. Display the first 15 rows of the `iris_petal` dataframe.
19. Print a summary of the `iris_petal` dataframe.
20. Read the `mallard_counts.csv` file into R and assign the dataframe as an object call `ducks`. Be sure to use `stringsAsFactors = FALSE`.
21. Print at the structure of `ducks`. How many rows and columns does it have?
22. Plot the elevation vs. counts and include a linear regression line using `ggplot`.
23. Read in the salamander demographic csv file and then select just the columns `sex`, `mass`, `svl`, `tl`, and `recap`. DO NOT print all the results.
24. Filter the salamander data to just males (“Y”) and individuals where recapture equals “N”. DO NOT print the entire results. Either the first 10 rows or just the structure of the resulting object.
25. Make a scatterplot of `svl` (x-axis) vs. `mass` (y-axis) and add a linear regression line through the data points.