

# Group Project 1

Biology 368/664 Bucknell University

2 Oct 2024

## Start by loading the data and packages

First, we need to look at our data file and understand what we are dealing with. In our example, the penguin data for three different islands is split up between three sheets in the .xlsx file. In order to read in strictly excel files, you must use the `read_excel` function. It is also important to note that the multiple sheets can cause issues, so you have to read them in sheet by sheet. Binding the data with `rbind` allows us to have each sheet into one data frame in R.

We will need to import the correct library that allows us to read .xlsx files in R. Then, we will need to extract each sheet in the .xlsx file into its own dataframe. It would be helpful for us to use the `as.data.frame()` function to convert the data to dataframes with correct variable types.

```
library(readxl)

torgersenpen <- read_excel("penguins.xlsx", sheet = "Torgersen Island")
bischoopen <- read_excel("penguins.xlsx", sheet = "Biscoe Island")
dreampen <- read_excel("penguins.xlsx", sheet = "Dream Island")

torgbisc <- rbind(torgersenpen, bischoopen)

full <- rbind(torgbisc, dreampen)
fullframe <- as.data.frame(full)
View(fullframe)
```

#load required packages

Packages are required to run certain functions in R, the main ones being used here include 'conflicted', 'tidyverse', 'dplyr', 'ggplot2', and 'cowplot'. These same packages can be found in the "Packages" tab in the lower right panel.

```
if (!require("conflicted")) install.packages("conflicted"); library(conflicted) # For dealing with conf
```

```
## Loading required package: conflicted
```

```
if (!require("tidyverse")) install.packages("tidyverse"); library(tidyverse) # For everything
```

```
## Loading required package: tidyverse
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr    1.5.1
## v ggplot2     3.5.1      v tibble     3.2.1
## v lubridate  1.9.3      v tidyr      1.3.1
## v purrr       1.0.2
```

```

conflict_prefer_all("dplyr", quiet = TRUE)
if (!require("dplyr")) install.packages("dplyr"); library(dplyr)
if (!require("ggplot2")) install.packages("ggplot2"); library(ggplot2)
if (!require("cowplot")) install.packages("cowplot"); library(cowplot)

## Loading required package: cowplot

if (!require("UsingR")) install.packages("UsingR"); library(UsingR) # For the simple.eda function

## Loading required package: UsingR
## Loading required package: MASS
##
## Attaching package: 'MASS'
##
## The following object is masked from 'package:dplyr':
##
##     select
##
## Loading required package: HistData
## Loading required package: Hmisc
##
## Attaching package: 'Hmisc'
##
## The following objects are masked from 'package:dplyr':
##
##     src, summarize
##
## The following objects are masked from 'package:base':
##
##     format.pval, units

```

## Make sure the data is read correctly

Even though you may not be familiar with the data set we are using, we will walk through how to check if your data set was read correctly into R. Checking the rows, columns, and total numbers reassures that no data is missing.

The View() function allows you to see the whole data set completely.

#Check columns and rows

Looking at these makes sure we have loaded in all the data and each variable.

```
nrow(fullframe)
```

```
## [1] 335
```

```
ncol(fullframe)
```

```
## [1] 8
```

```
View(fullframe)
```

```
#Check top and bottom of data
```

The top and the bottom also can show us the kind of data we are looking at, as well as the framework of the set.

```
head(fullframe)
```

```
##   species   island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
## 1  Adelie Torgersen      39.1         18.7           181          3750
## 2  Adelie Torgersen      39.5         17.4           186          3800
## 3  Adelie Torgersen      40.3         18.0           195          3250
## 4  Adelie Torgersen      36.7         19.3           193          3450
## 5  Adelie Torgersen      39.3         20.6           190          3650
## 6  Adelie Torgersen      38.9         17.8           181          3625
##      sex year
## 1   male 2007
## 2 female 2007
## 3 female 2007
## 4 female 2007
## 5   male 2007
## 6 female 2007
```

```
tail(fullframe)
```

```
##      species island bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
## 330 Chinstrap Dream      45.7         17.0           195          3650
## 331 Chinstrap Dream      55.8         19.8           207          4000
## 332 Chinstrap Dream      43.5         18.1           202          3400
## 333 Chinstrap Dream      49.6         18.2           193          3775
## 334 Chinstrap Dream      50.8         19.0           210          4100
## 335 Chinstrap Dream      50.2         18.7           198          3775
##      sex year
## 330 female 2009
## 331   male 2009
## 332 female 2009
## 333   male 2009
## 334   male 2009
## 335 female 2009
```

```
#Run glimpse and catagorize data
```

In the bottom left panel, type “?glimpse” and press enter. What does it show you? Glimpse in the package dplyr allows us to see every column in the data frame. This simply shows you as much data as possible.

Then, we get into the function mutate. This allows us to change the type of variable for our data. R automatically read our data but we need to change the factor variables to factors and the numeric variables to numbers. The as.factor() function is used for the variables sex, island, and species. As you can see, you can also do levels within the factor, as portrayed in the island line of code.

The next code shows the same process but with the as.numeric function for the numerical values of bill length, bill depth, flipper length, and body mass.

Using the summary() function, you can see if the as.factor and as.numeric functions worked.

```
glimpse(fullframe)
```

```
## Rows: 335
## Columns: 8
## $ species      <chr> "Adelie", "Adelie", "Adelie", "Adelie", "Adelie", "A-
## $ island        <chr> "Torgersen", "Torgersen", "Torgersen", "Torgersen", ~
## $ bill_length_mm <dbl> 39.1, 39.5, 40.3, 36.7, 39.3, 38.9, 39.2, 41.1, 38.6~
## $ bill_depth_mm <dbl> 18.7, 17.4, 18.0, 19.3, 20.6, 17.8, 19.6, 17.6, 21.2~
## $ flipper_length_mm <dbl> 181, 186, 195, 193, 190, 181, 195, 182, 191, 198, 18~
## $ body_mass_g    <dbl> 3750, 3800, 3250, 3450, 3650, 3625, 4675, 3200, 3800~
## $ sex            <chr> "male", "female", "female", "female", "male", "femal~
## $ year           <dbl> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007~
```

```
fullframe |>
  mutate(sex = as.factor(sex),
         island = factor(island, levels = c("Dream", "Torgersen", "Biscoe")),
         species = as.factor(species)) -> fullframe
```

```
fullframe |>
  mutate(bill_length_mm = as.numeric(bill_length_mm),
         bill_depth_mm = as.numeric(bill_depth_mm),
         flipper_length_mm = as.numeric(flipper_length_mm),
         body_mass_g = as.numeric(body_mass_g)) -> fullframe
summary(fullframe)
```

```
##      species      island  bill_length_mm  bill_depth_mm
## Adelie   :146   Dream    :123   Min.    :32.10   Min.    :13.10
## Chinstrap: 68   Torgersen: 47   1st Qu.:39.50   1st Qu.:15.55
## Gentoo   :121   Biscoe   :165   Median :44.50   Median :17.30
##                                     Mean    :44.00   Mean    :17.15
##                                     3rd Qu.:48.55   3rd Qu.:18.70
##                                     Max.    :59.60   Max.    :21.50
## flipper_length_mm  body_mass_g      sex      year
## Min.    :172.0    Min.    :2700   female:165   Min.    :2007
## 1st Qu.:190.0    1st Qu.:3550   male  :168   1st Qu.:2007
## Median :197.0    Median :4050   NA    : 2   Median :2008
## Mean    :201.1    Mean    :4208                   Mean    :2008
## 3rd Qu.:213.0    3rd Qu.:4762                   3rd Qu.:2009
## Max.    :231.0    Max.    :6300                   Max.    :2009
```

```
#Check 'n's
```

Again, although you are likely unfamiliar with this data set, the following code allows you to see the total number of observations made in the data set. If this did not match your original data you collected, you would have been made aware that the data didn't read in correctly.

```
str(fullframe)
```

```
## 'data.frame':   335 obs. of  8 variables:
## $ species      : Factor w/ 3 levels "Adelie","Chinstrap",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ island        : Factor w/ 3 levels "Dream","Torgersen",...: 2 2 2 2 2 2 2 2 2 2 ...
```

```
## $ bill_length_mm : num 39.1 39.5 40.3 36.7 39.3 38.9 39.2 41.1 38.6 34.6 ...
## $ bill_depth_mm : num 18.7 17.4 18 19.3 20.6 17.8 19.6 17.6 21.2 21.1 ...
## $ flipper_length_mm: num 181 186 195 193 190 181 195 182 191 198 ...
## $ body_mass_g : num 3750 3800 3250 3450 3650 ...
## $ sex : Factor w/ 3 levels "female","male",...: 2 1 1 1 2 1 2 1 2 2 ...
## $ year : num 2007 2007 2007 2007 2007 ...
```

```
table(fullframe$bill_length_mm)
```

```
##
## 32.1 33.1 33.5 34 34.4 34.5 34.6 35 35.1 35.2 35.3 35.5 35.6 35.7 35.9 36
## 1 1 1 1 1 1 2 2 1 1 1 2 1 3 2 4
## 36.2 36.3 36.4 36.5 36.6 36.7 36.8 36.9 37 37.2 37.3 37.5 37.6 37.7 37.8 37.9
## 3 1 2 2 2 2 1 1 2 2 3 1 3 3 3 2
## 38.1 38.2 38.3 38.5 38.6 38.7 38.8 38.9 39 39.1 39.2 39.3 39.5 39.6 39.7 39.8
## 4 2 1 1 3 1 3 2 3 1 3 1 3 5 4 1
## 40.1 40.2 40.3 40.5 40.6 40.7 40.8 40.9 41 41.1 41.3 41.4 41.5 41.6 41.7 41.8
## 1 3 2 2 4 1 2 4 1 7 2 2 2 1 1 1
## 42 42.1 42.2 42.3 42.4 42.5 42.6 42.7 42.8 42.9 43.1 43.2 43.3 43.4 43.5 43.6
## 2 1 2 1 1 3 1 2 2 2 1 4 2 1 3 1
## 43.8 44 44.1 44.4 44.5 44.9 45 45.1 45.2 45.3 45.4 45.5 45.6 45.7 45.8 45.9
## 1 1 2 1 2 2 1 3 6 2 2 5 2 3 3 1
## 46 46.1 46.2 46.3 46.4 46.5 46.6 46.7 46.8 46.9 47 47.2 47.3 47.4 47.5 47.6
## 2 3 5 1 4 5 2 2 4 2 1 2 1 1 4 2
## 47.7 47.8 48.1 48.2 48.4 48.5 48.6 48.7 48.8 49 49.1 49.2 49.3 49.4 49.5 49.6
## 1 1 2 2 3 3 1 3 1 3 3 2 2 1 3 3
## 49.7 49.8 49.9 50 50.1 50.2 50.3 50.4 50.5 50.6 50.7 50.8 50.9 51 51.1 51.3
## 1 3 1 5 2 3 1 2 5 1 2 4 2 1 2 4
## 51.4 51.5 51.7 51.9 52 52.1 52.2 52.5 52.7 52.8 53.4 53.5 54.2 54.3 55.1 55.8
## 1 2 1 1 3 1 2 1 1 1 1 1 1 1 1 1
## 55.9 58 59.6
## 1 1 1
```

```
table(fullframe$sex)
```

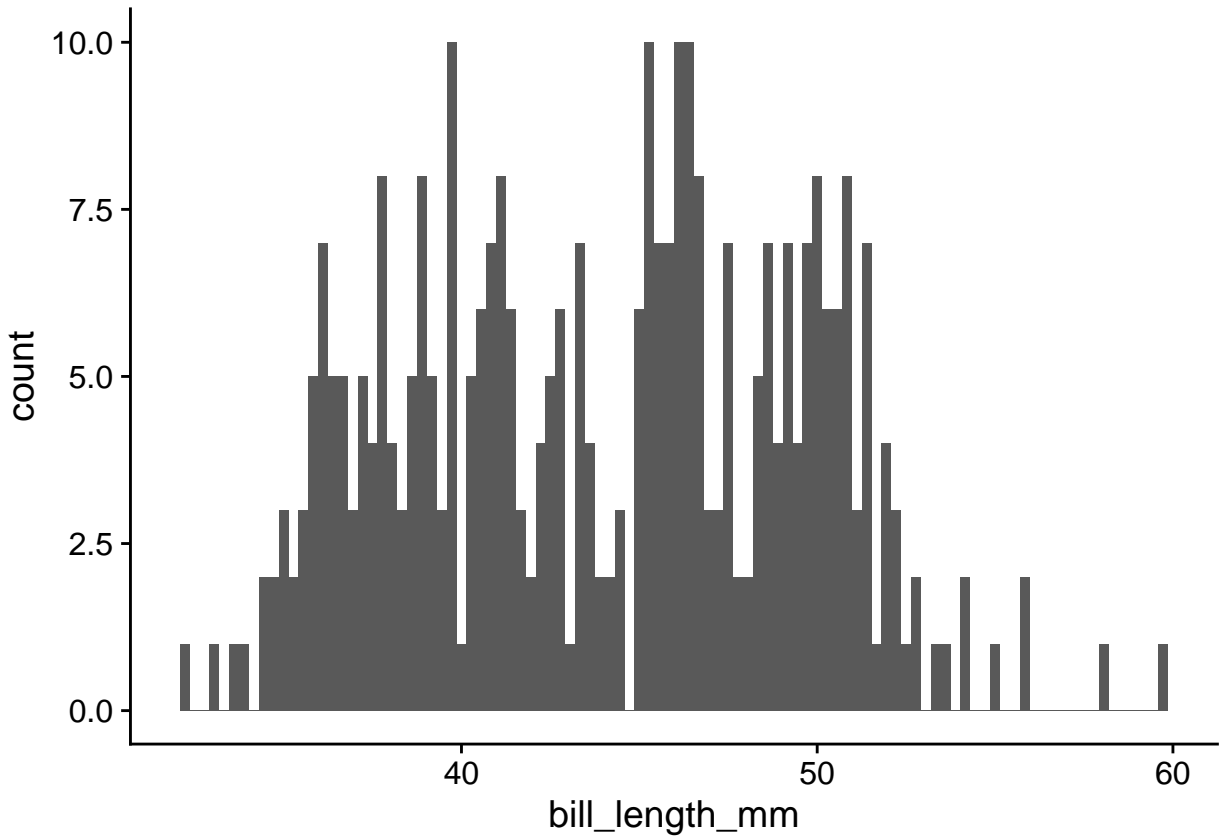
```
##
## female male NA
## 165 168 2
```

## Plot the residuals

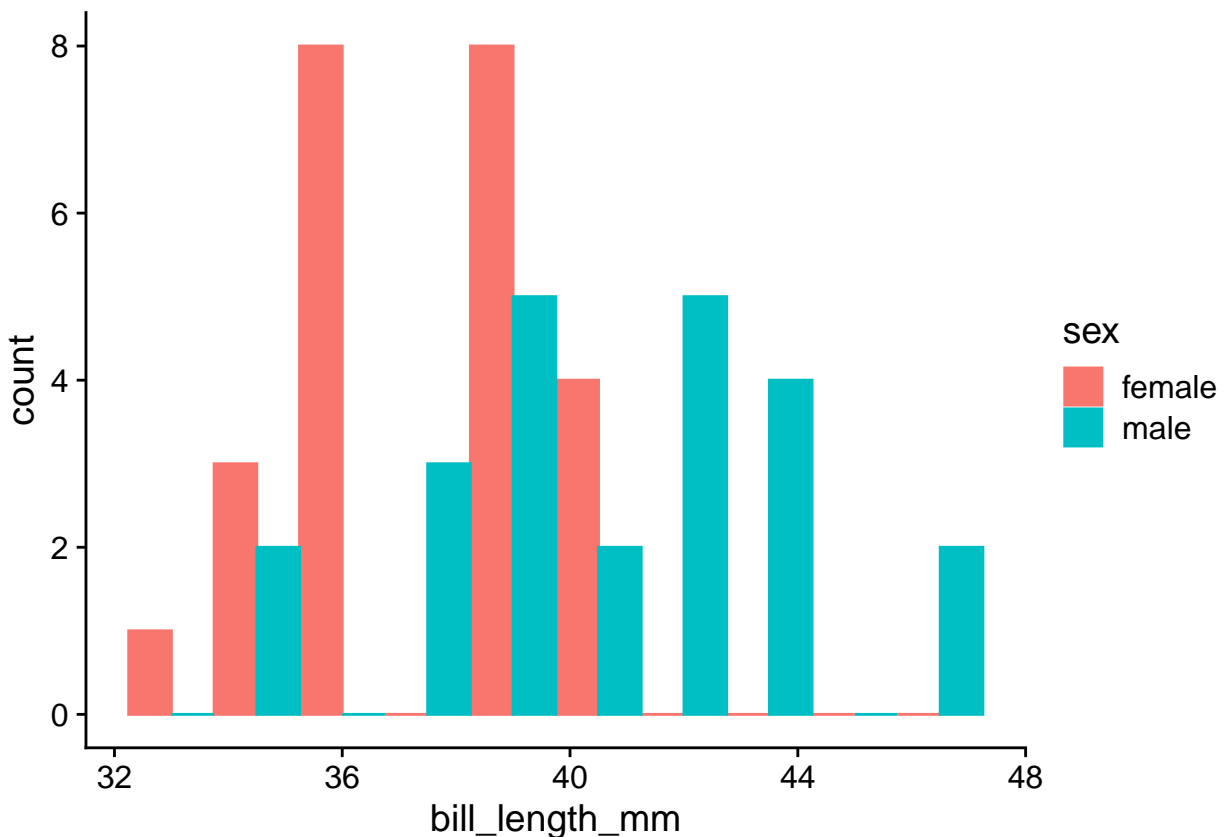
First, let's look at the data. Using the `ggplot()` function, we can create a histogram (`geom_histogram()`) with the bill length (part of our original hypothesis). It is important to note that each time you create a graph, you have to explicitly state where you want the data pulled from. The `theme_cowplot` simply makes the graph pretty.

For the second graph, certain features are added (including changing the data frame) to the aesthetic function (`aes()`) to make the graph specialized. With the `colour()` function, you can group data within a graph. `fill()` simply makes it look better (play around with it and see what happens without the fill option!). The `binwidth` is another way to alter your graph with different widths (play around with this too! Try 0.5, then 3. What looks better?) With the `position()` function, it just indicates where your legend is. You will learn how to better visualize the data later.

```
ggplot(fullframe) +
  aes(x = bill_length_mm) +
  geom_histogram(bins = 100) +
  theme_cowplot()
```



```
ggplot(torgersenpen) +
  aes(x = bill_length_mm, colour = sex, fill = sex) +
  geom_histogram(binwidth = 1.5, position = "dodge") +
  theme_cowplot()
```



Residuals are the difference between an observed data value and a predicted data value. When we plot them, it allows us to see visually whether or not the data is normal or not. Using `lm()`, we can look at the residuals of the linear models we make. So, for our first relationship we want to look at (bill length and species), the code follows this pattern: name of linear model `<- lm(bill length depends on(~) species, from the data frame fullframe)`

We can do a similar thing with our second relationship (bill length and sex). The one thing that needed to be changed was the fact that the data set `torgersenpen` had the specific data we needed, without the clutter of the `fullframe` data set.

`plot()` graphs the linear models that you just made.

```
lmspecieslength <- lm(bill_length_mm ~ species, data = fullframe)
summary(lmspecieslength)
```

```
##
## Call:
## lm(formula = bill_length_mm ~ species, data = fullframe)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.9338 -2.2314  0.0686  2.0674 12.0686
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    38.8240     0.2456  158.06  <2e-16 ***
## speciesChinstrap 10.0099     0.4358   22.97  <2e-16 ***
```

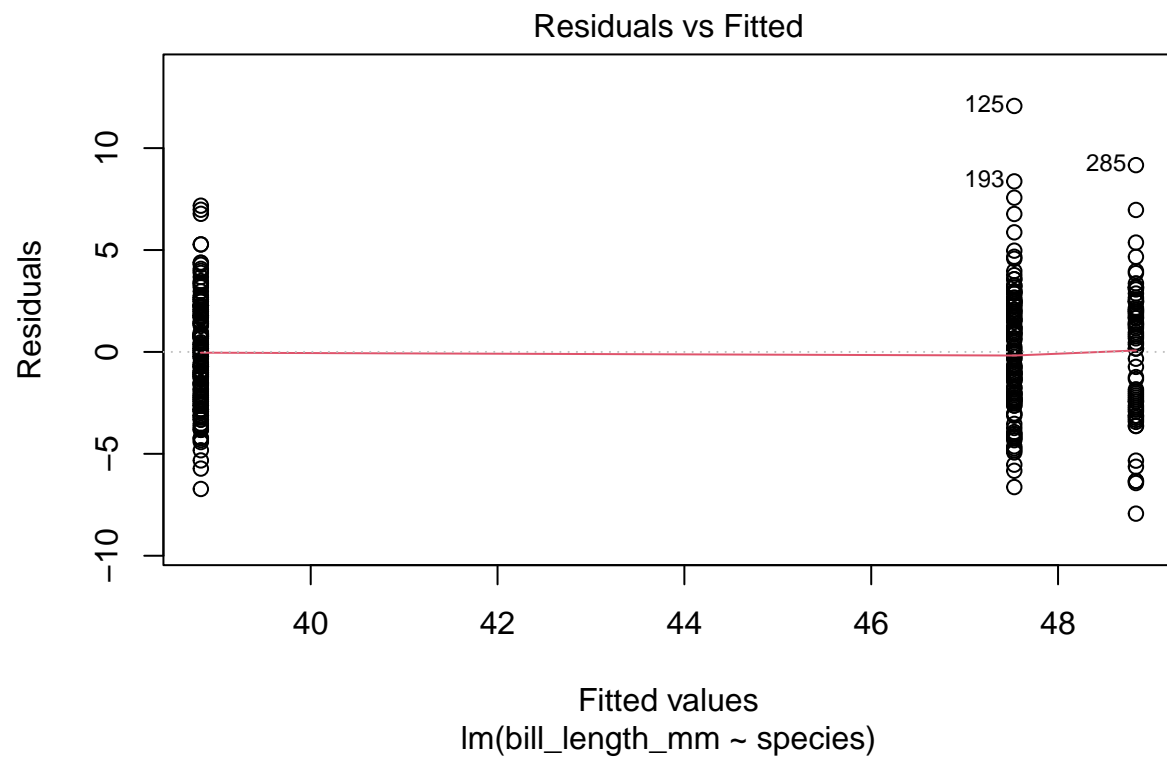
```
## speciesGentoo      8.7074      0.3649    23.86    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.968 on 332 degrees of freedom
## Multiple R-squared:  0.7056, Adjusted R-squared:  0.7038
## F-statistic: 397.8 on 2 and 332 DF,  p-value: < 2.2e-16
```

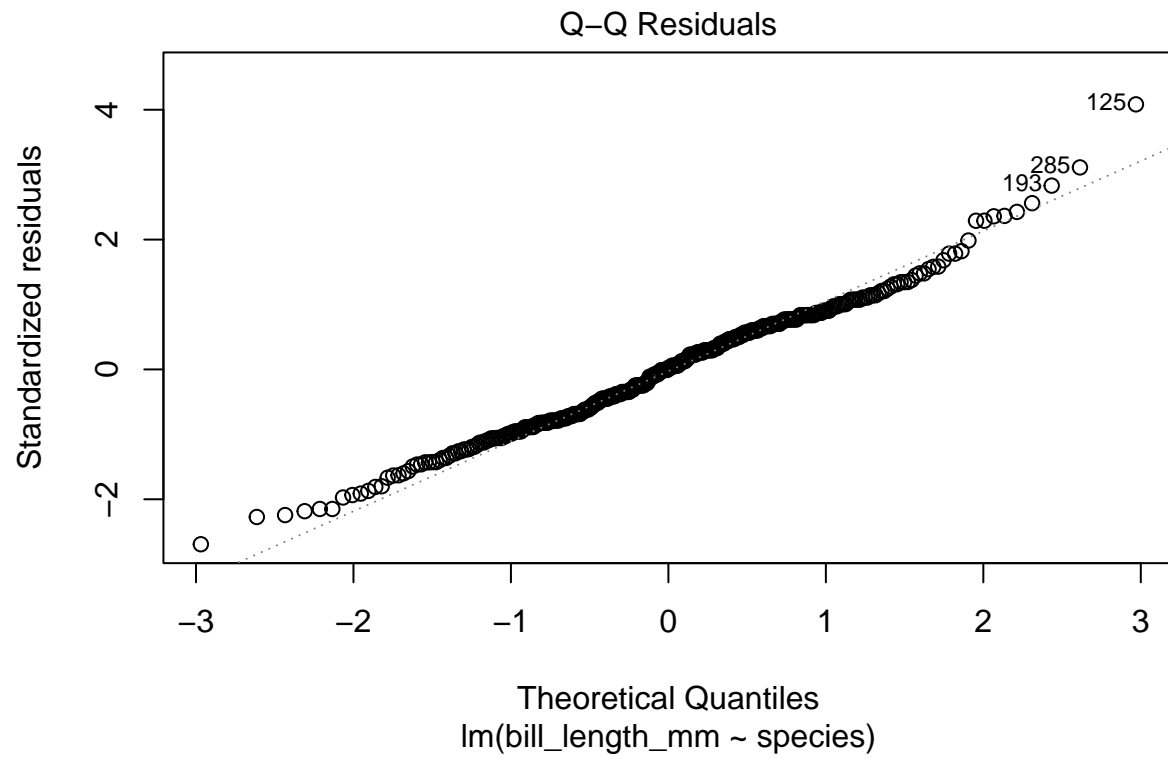
```
lmsexlength <- lm(bill_length_mm ~ sex, data = torgersenpen)
summary(lmsexlength)
```

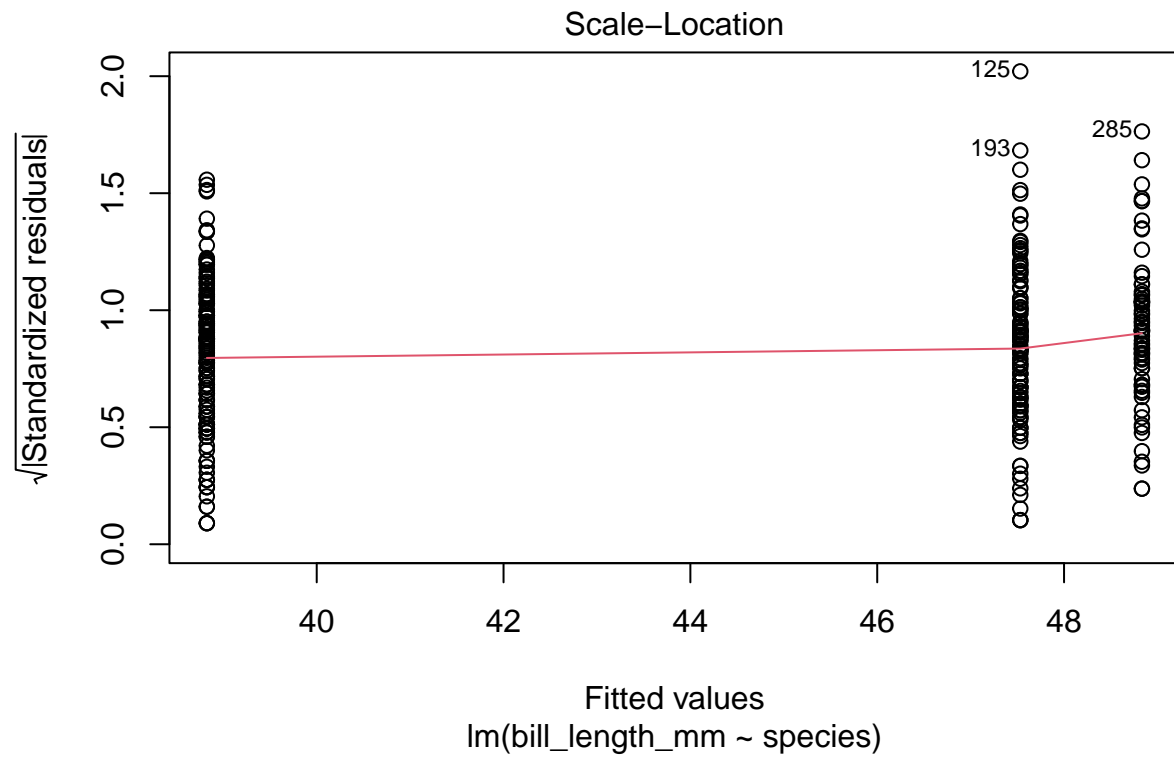
```
##
## Call:
## lm(formula = bill_length_mm ~ sex, data = torgersenpen)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.987 -1.754  0.513  1.929  5.413
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  37.5542     0.5390   69.673 < 2e-16 ***
## sexmale       3.0328     0.7705    3.936 0.000284 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.641 on 45 degrees of freedom
## Multiple R-squared:  0.2561, Adjusted R-squared:  0.2396
## F-statistic: 15.49 on 1 and 45 DF,  p-value: 0.0002844
```

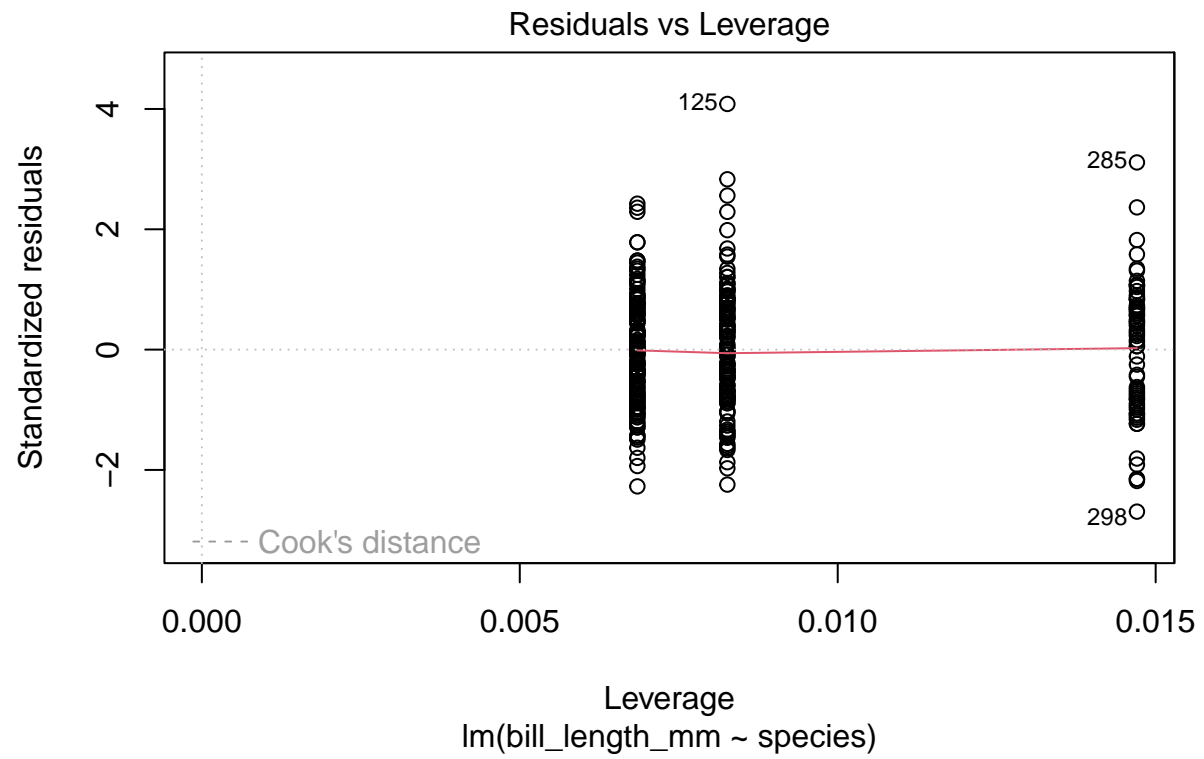
```
plot(lmspecieslength)
```



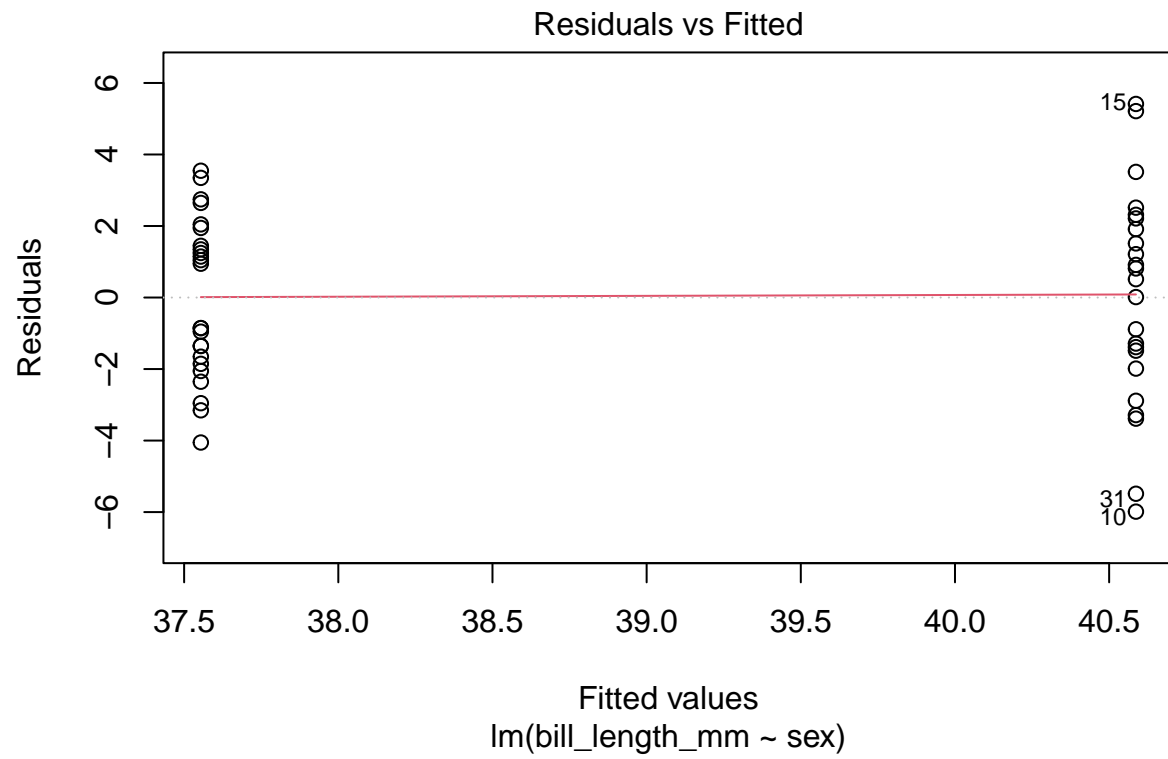


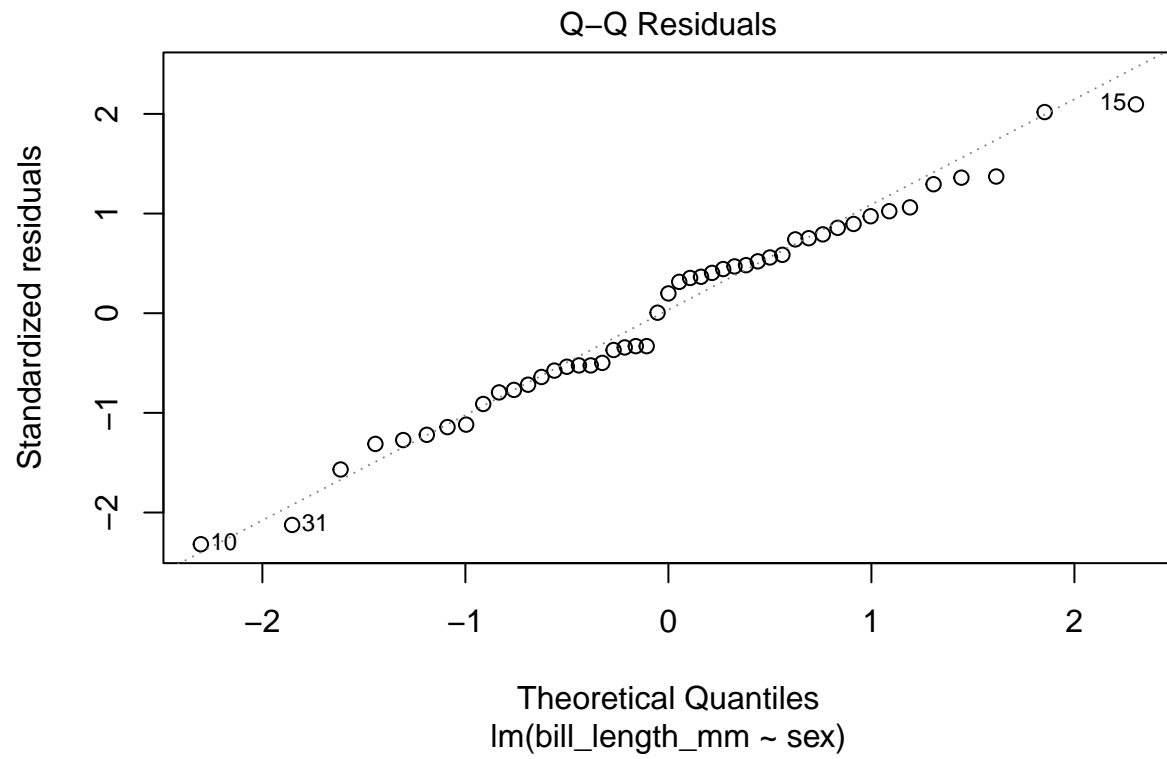


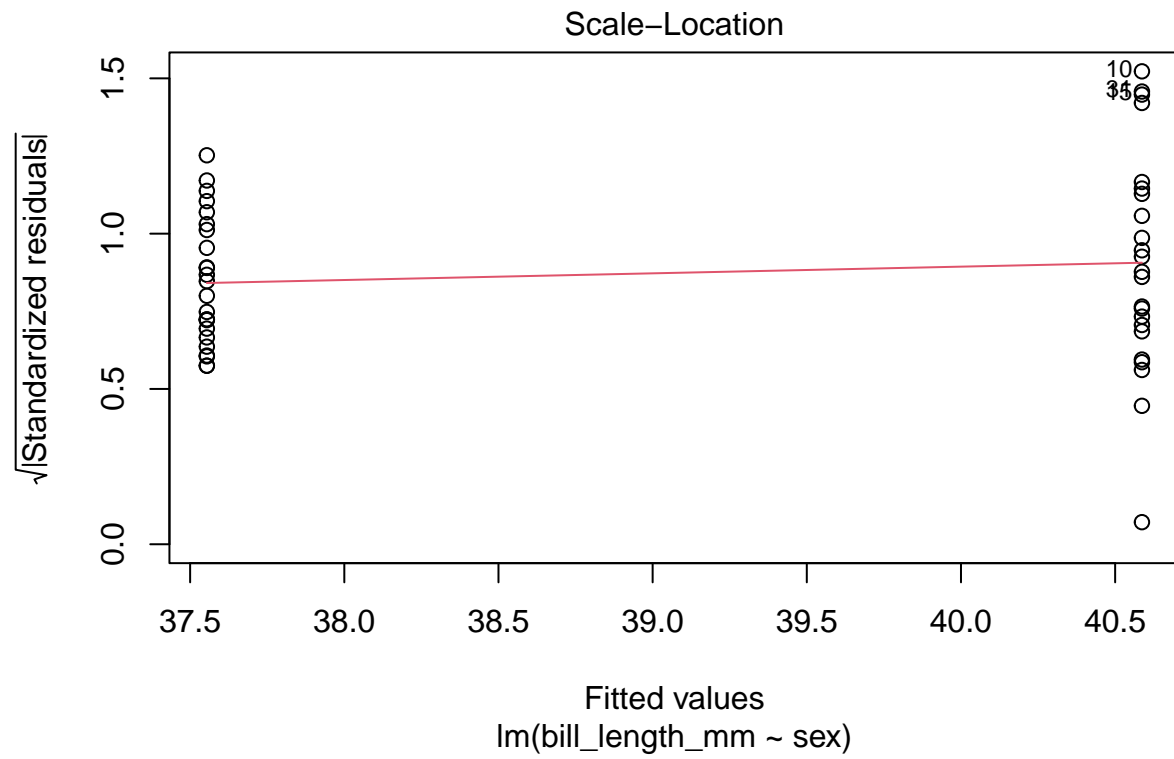


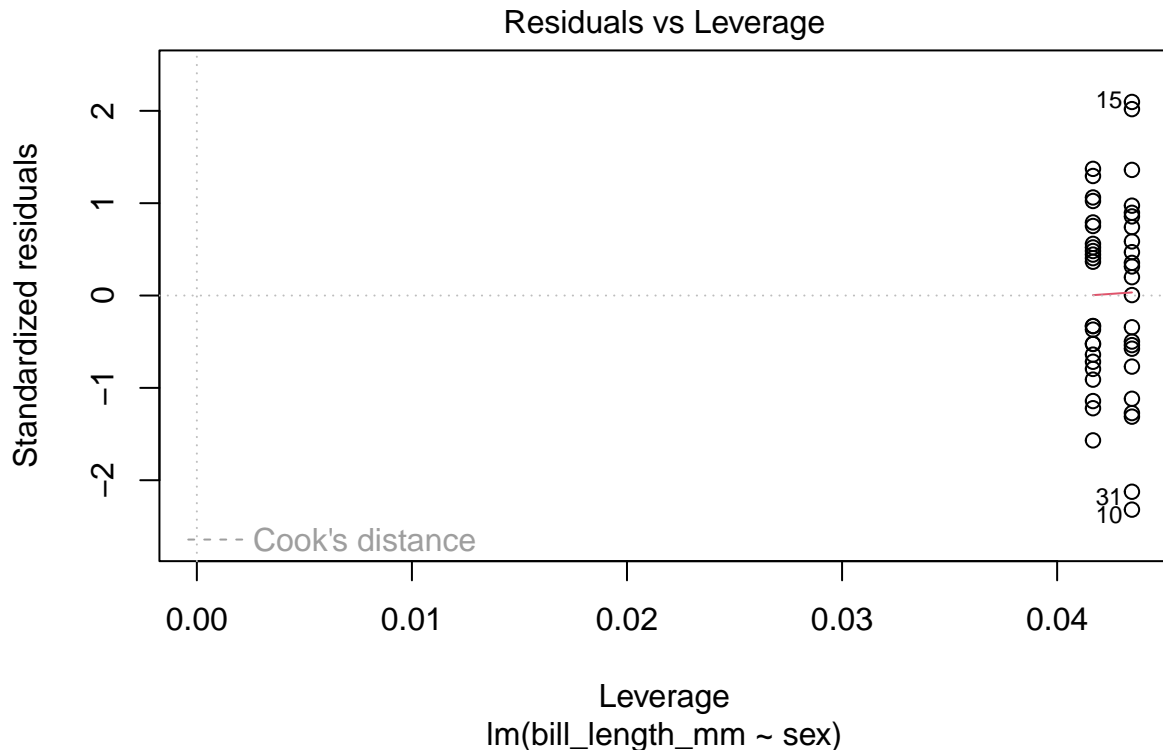


```
plot(lmsexlength)
```









#### 4. Discuss the residuals

Although these graphs are a lot, the main ones we will focus on (to stay within the scope of this tutorial) are the QQ plots. A QQ plot basically shows how well the data matches the theoretical normal distribution. If all of the points are roughly along the dotted line, that means the data is mostly normally distributed. If the data points do not fit along the line at all it means the data is highly skewed.

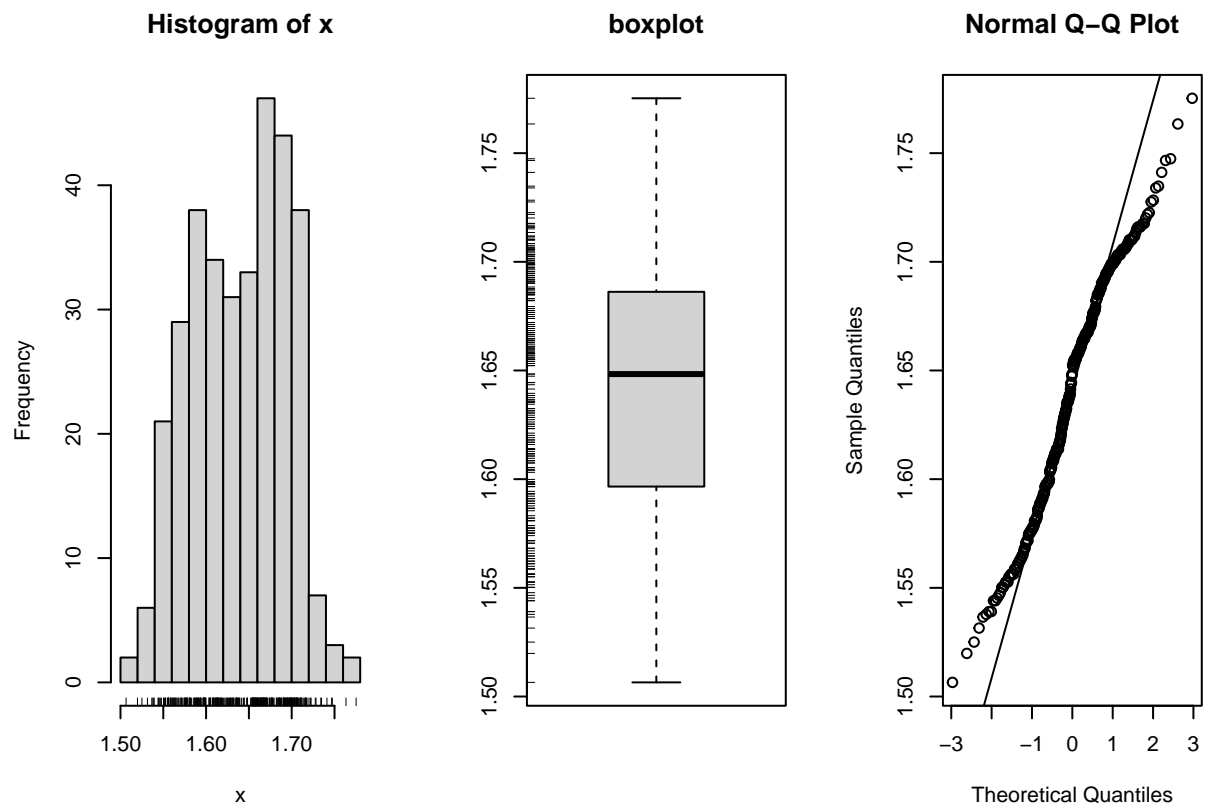
For these, it looks like the data is fairly normalized. The data on both the bill length ~ species and the bill length ~ sex look normal with closely fit data on the line. Normally, this would be it for making sure our data is normalized since it already looks normal, but the following code gives some tips on how to normalize a skewed set.

#### 5. Figure out how to normalize the data and plot residuals

Using this following code, this allows us to take log10 of the bill length. Although our data looks fairly normalized, what would happen if you took the log10 of it?

```
fullframe$log10bill_length <- log10(fullframe$bill_length_mm)
simple.eda(fullframe$log10bill_length)
```





As you can see, it doesn't make it that much better, it even makes the QQ plot look worse. Since we are lucky with a normal data set, we don't need to use any normalizing functions.

### ## Visualization of Your Data

The Hypothesis that we are testing are: -Is Bill Length in Penguins from Torgersen's Island is Sex Dependent  
-Is Bill Length is different between the 3 species

We will be visualizing "Is Bill Length in Penguins from Torgersen's Island is Sex Dependent."

First view your data and get familiar with your variables. In this tutorial we will be testing if the Bill Length is different between the 3 species, and if Bill length in Penguins from Torgersen's Island is Sex Dependent.

There are two simple ways to get a basic view of your data. You can simply type the name of your dataset to view the full data. You can also use `summary(YourDataSet)` to view the dataset with some summary statistics. Try both bellow!

### ## View Data

```
summary(torgersenpen)
```

```
##   species      island  bill_length_mm  bill_depth_mm
## Length:47    Length:47      Min.   :33.50      Min.   :15.90
## Class :character Class :character 1st Qu.:36.65      1st Qu.:17.45
## Mode  :character Mode  :character Median :39.00      Median :18.40
##                                     Mean  :39.04      Mean  :18.45
##                                     3rd Qu.:41.10      3rd Qu.:19.25
##                                     Max.   :46.00      Max.   :21.50
## flipper_length_mm  body_mass_g    sex      year
```

```
## Min.      :176.0      Min.      :2900      Length:47      Min.      :2007
## 1st Qu.:187.5      1st Qu.:3338      Class :character 1st Qu.:2007
## Median :191.0      Median :3700      Mode  :character Median :2008
## Mean    :191.5      Mean    :3709                      Mean    :2008
## 3rd Qu.:195.5      3rd Qu.:4000                      3rd Qu.:2009
## Max.    :210.0      Max.    :4700                      Max.    :2009
```

We created a dataset for Penguins in Torgersen's Island called "torgersenpenguins". Simply type in the dataset's name to view the data. Try below.

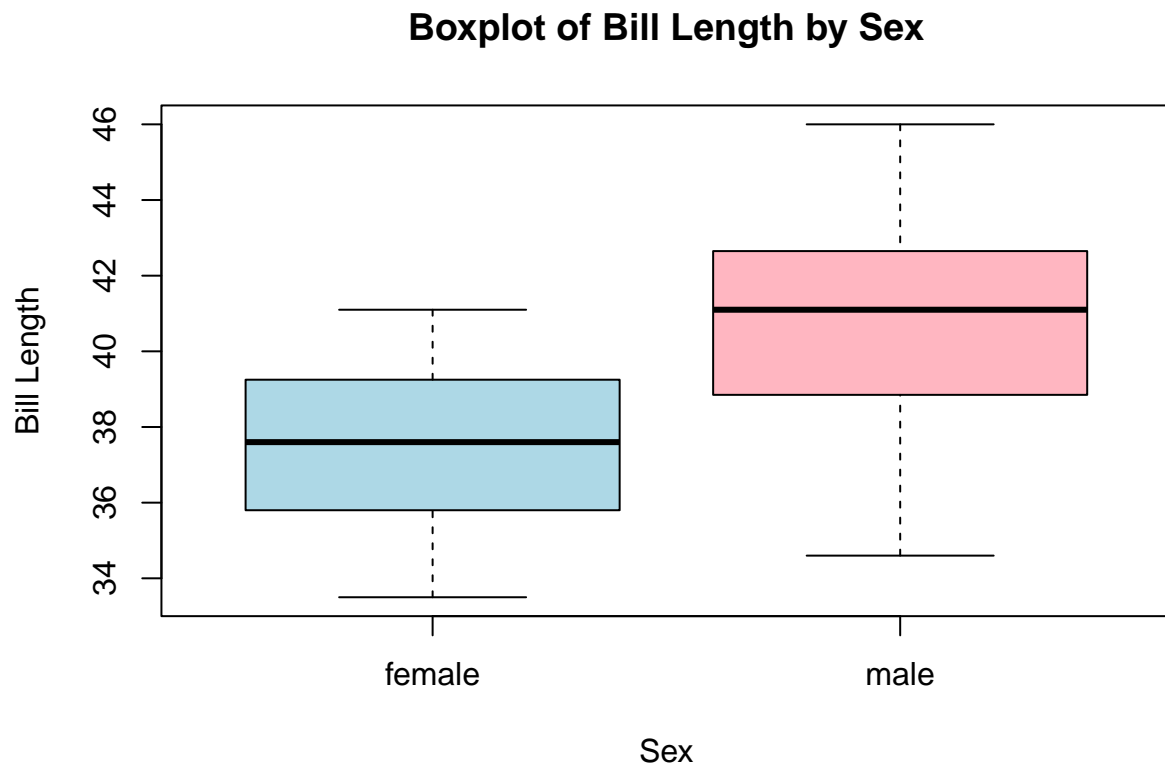
```
torgersenpen
```

```
## # A tibble: 47 x 8
##   species island   bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
##   <chr>   <chr>         <dbl>         <dbl>         <dbl>         <dbl>
## 1 Adelie Torgersen      39.1           18.7           181           3750
## 2 Adelie Torgersen      39.5           17.4           186           3800
## 3 Adelie Torgersen      40.3            18           195           3250
## 4 Adelie Torgersen      36.7           19.3           193           3450
## 5 Adelie Torgersen      39.3           20.6           190           3650
## 6 Adelie Torgersen      38.9           17.8           181           3625
## 7 Adelie Torgersen      39.2           19.6           195           4675
## 8 Adelie Torgersen      41.1           17.6           182           3200
## 9 Adelie Torgersen      38.6           21.2           191           3800
## 10 Adelie Torgersen      34.6           21.1           198           4400
## # i 37 more rows
## # i 2 more variables: sex <chr>, year <dbl>
```

Next we will visualize the data comparing Bill Length by Sex to visualize if there is a significant difference in Bill Length, depending on Sex.

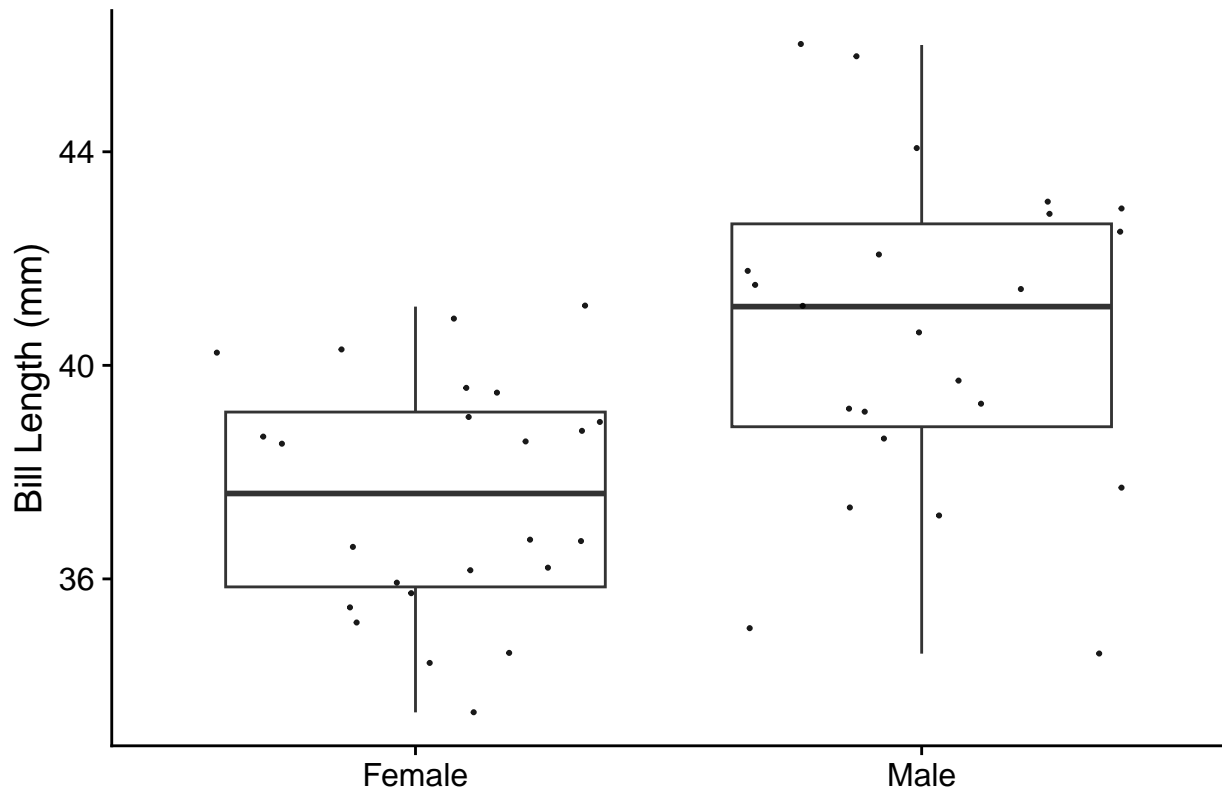
## Basic boxplot

```
boxplot(bill_length_mm ~ sex, data = torgersenpen,
        xlab = "Sex",
        ylab = "Bill Length",
        main = "Boxplot of Bill Length by Sex",
        col = c("lightblue", "lightpink"))
```



Now we will add jitter to our boxplot :

```
ggplot(torgersenpen) +  
  aes(x = factor(sex), y = bill_length_mm) +  
  geom_boxplot() +  
  geom_jitter(color="black", size=0.4, alpha=0.9) +  
  theme_cowplot() +  
  ylab("Bill Length (mm)") +  
  xlab(c(" ")) +  
  scale_x_discrete(labels=c("Female", "Male"))
```



##Analyze Graph Now you want to analyze your results and look for any differences in the data for our boxplots :

In both of boxplot we can see a significant difference between the Bill Length. It seems that males on average have a higher bill length than female penguins from Torgersen's island. Of course we will have to use a statistical test to check if this correlation is actually significant.

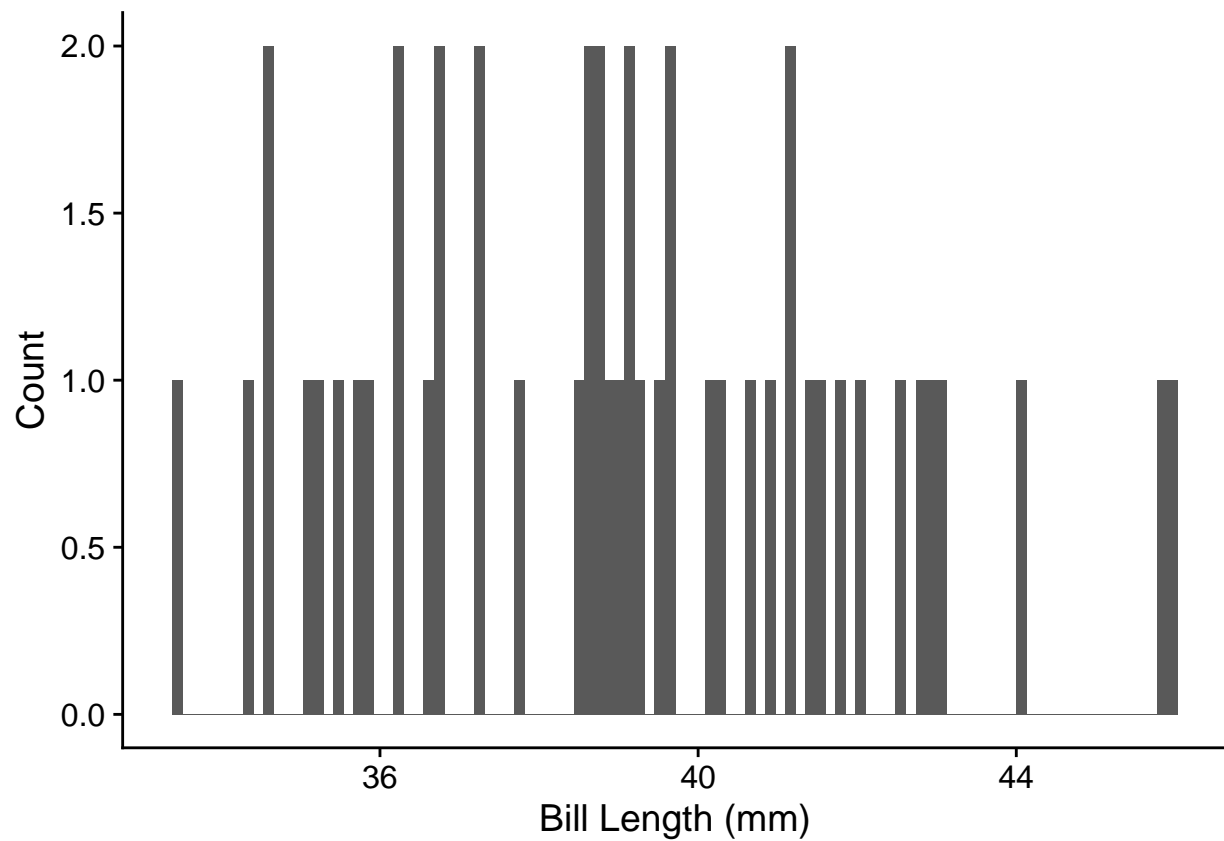
#Histogram

Next we will create a Histogram to visualize the same thing in the data.

In our histogram we want to display the Bill Length on the x-axis and separate these values by female and male.

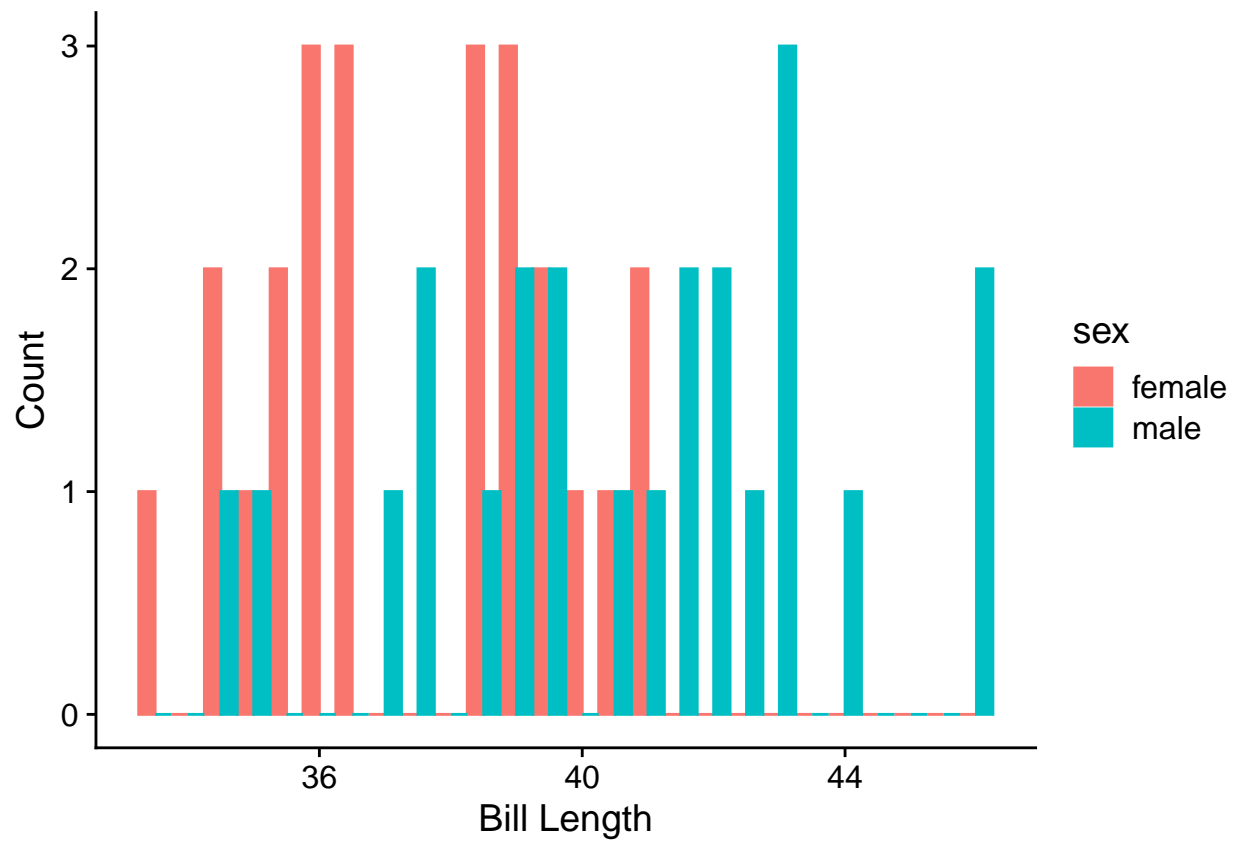
First lets create a histogram that includes just the Bill Length.

```
ggplot(torgersenpen) +
  aes(x = bill_length_mm) +
  geom_histogram(bins=100) +
  theme_cowplot()+
  xlab("Bill Length (mm)") +
  ylab("Count")
```



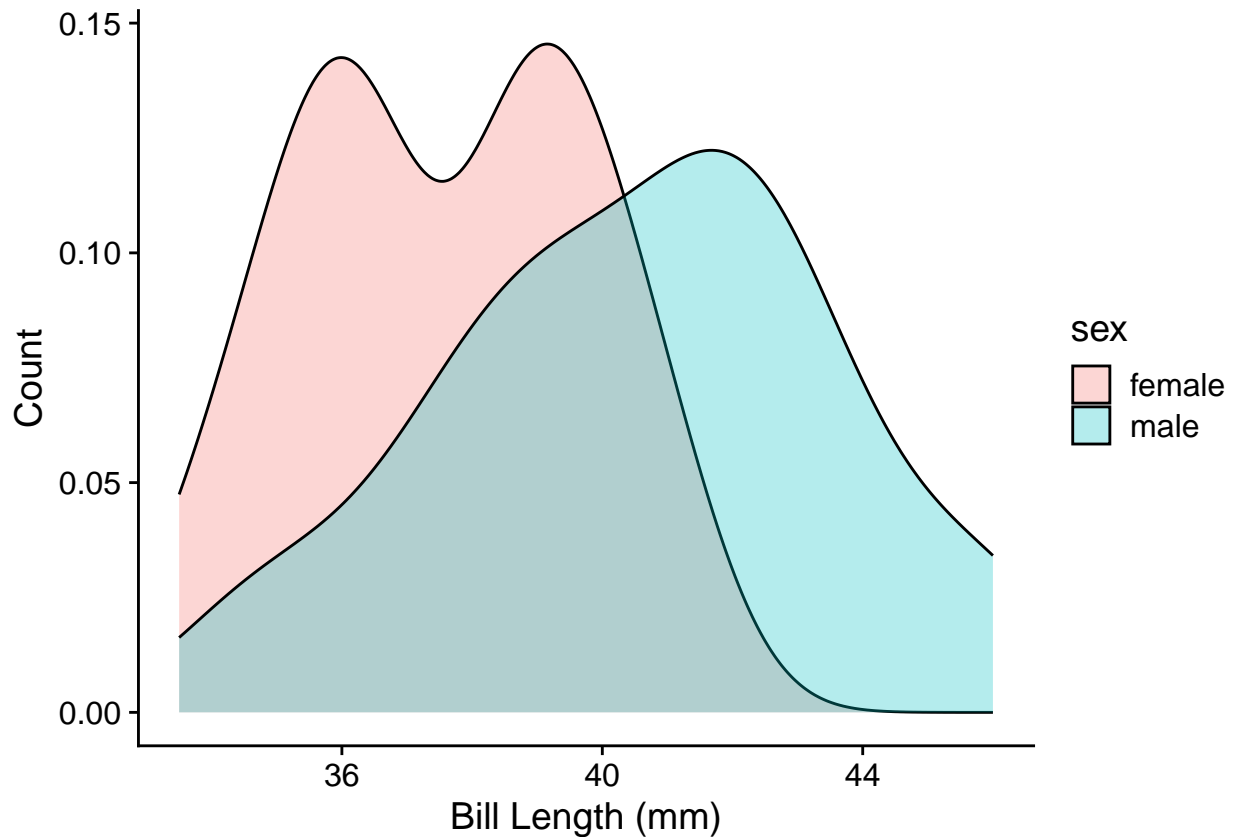
Next lets separate these results by sex :

```
ggplot(torgersenpen) +
  aes(x = bill_length_mm, color = sex, fill = sex) +
  geom_histogram(binwidth = 0.5, position = "dodge") +
  theme_cowplot() +
  xlab("Bill Length") +
  ylab("Count")
```



Finally, lets make these results look better in our graph :

```
ggplot(torgersenpen) +
  aes(x = bill_length_mm, fill = sex) +
  geom_density(alpha=.3) +
  theme_cowplot() +
  xlab("Bill Length (mm)") +
  ylab("Count")
```



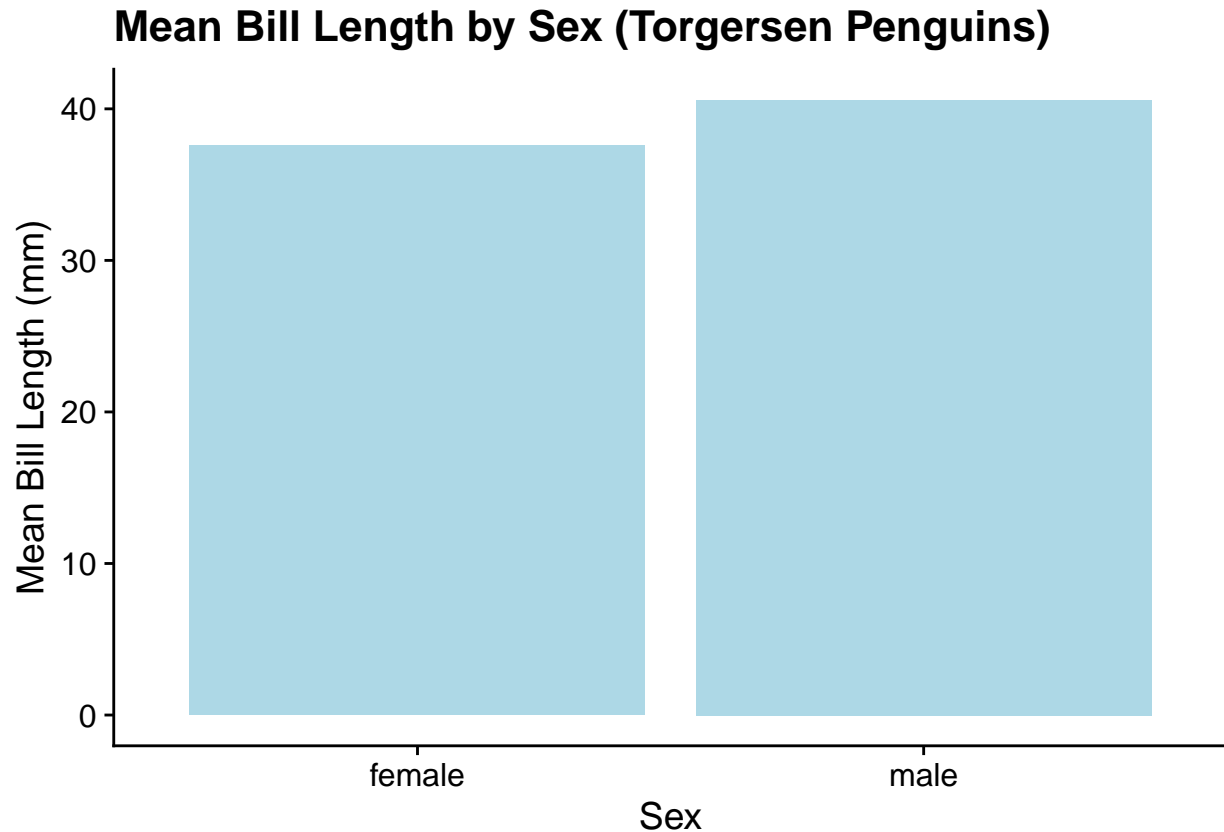
##Analyze Graph Now you want to analyze your results and look for any differences in the data for our Histogram :

Our Histogram displays similar results to our boxplot, in which we can see a significant difference between the Bill Length separated by sex. It seems that males on average have a higher bill length than female penguins from Torgersen's island. Of course we will have to use a statistical test to check if this correlation is actually significant.

#Bar Chart

```
# Calculate means for bill length by sex
summary_data <- torgersenpen %>%
  group_by(sex) %>%
  summarize(mean_bill_length = mean(bill_length_mm, na.rm = TRUE))

# Create bar plot without error bars
ggplot(summary_data, aes(x = sex, y = mean_bill_length)) +
  geom_bar(stat = "identity", fill = "lightblue") +
  labs(title = "Mean Bill Length by Sex (Torgersen Penguins)",
       x = "Sex",
       y = "Mean Bill Length (mm)") +
  theme_cowplot()
```



This will create a very basic Bar Chart to visualize our Data.

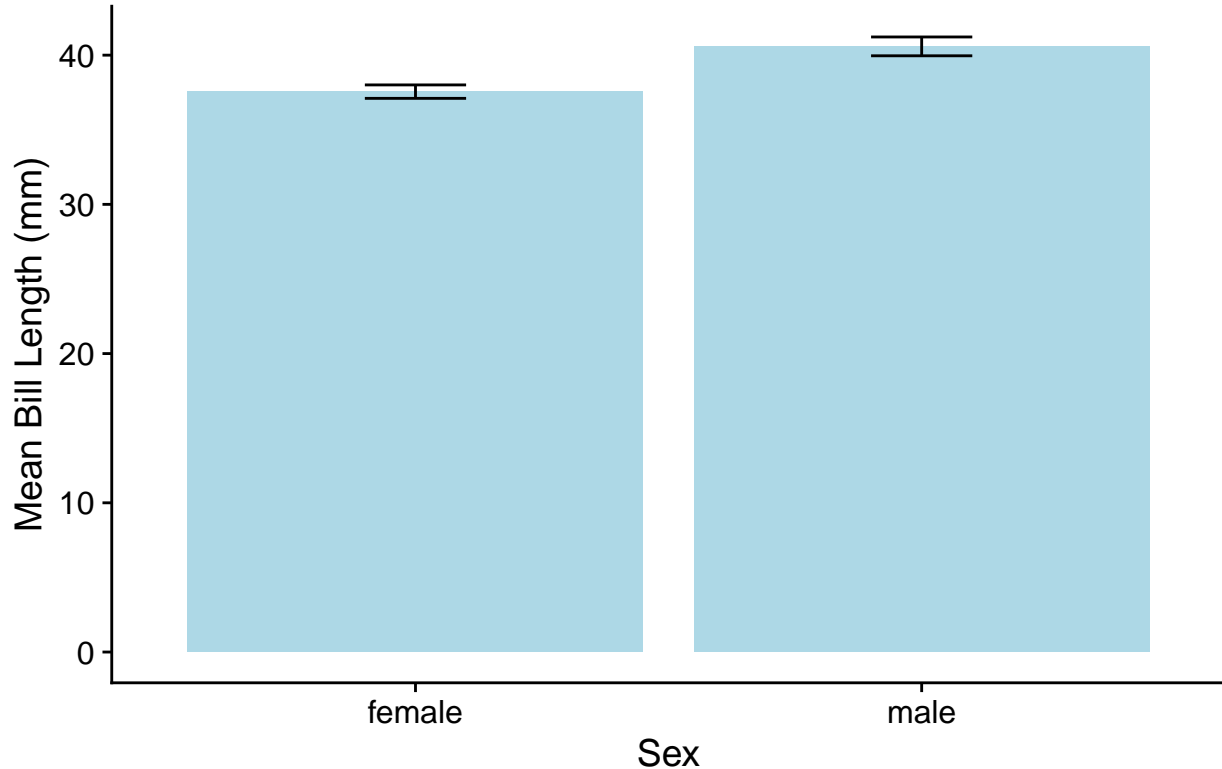
Next we will add error lines to this barchart:

```
# Calculate means and standard errors for bill length by sex
summary_data <- torgersenpen %>%
  group_by(sex) %>%
  summarize(mean_bill_length = mean(bill_length_mm, na.rm = TRUE),
            se_bill_length = sd(bill_length_mm, na.rm = TRUE) / sqrt(n()))

# Create bar plot with error bars
ggplot(summary_data, aes(x = sex, y = mean_bill_length)) +
  geom_bar(stat = "identity", fill = "lightblue") +
  geom_errorbar(aes(ymin = mean_bill_length - se_bill_length,
                    ymax = mean_bill_length + se_bill_length,
                    width = 0.2)) +
  labs(title = "Bill Length by Sex (Torgersen Penguins)",
       x = "Sex",
       y = "Mean Bill Length (mm)") +
  theme_cowplot()
```



## Bill Length by Sex (Torgersen Penguins)



### ##Analyze Bar Charts

As you can see, our graphs are all consistent in that Males appear to have a higher average Bill Length than Female penguins on Torgersen's island. We must test this with statistical models to verify if the correlation is actually there.

### ##Analyzing Data using t-test, and Anova Now you will learn how to analyze data using T-tests and Anova.

First, Which type of analysis to use / using t-test, anova...

- Recognize the differences between one-way, two-way, mixed, or ANCOVA anova test, execute the test and interpret the results
  - Determine if the explanatory variable(s) is continuous, discrete, or mixed
  - Understand the meaning of p-values and how it relates to a normal distribution
- Understand the differences between one-sample t test, two-sample t test, or paired t test, execute the test and interpret the results
  - Learn how to assess an experimental design in order to choose the appropriate t-test
  - Understand probability distributions and how it relates to t-tests

### #Checking dataframe structure using str()

```
str(torgersenpen)
```

```
## tibble [47 x 8] (S3: tbl_df/tbl/data.frame)
## $ species      : chr [1:47] "Adelie" "Adelie" "Adelie" "Adelie" ...
## $ island       : chr [1:47] "Torgersen" "Torgersen" "Torgersen" "Torgersen" ...
```

```
## $ bill_length_mm : num [1:47] 39.1 39.5 40.3 36.7 39.3 38.9 39.2 41.1 38.6 34.6 ...
## $ bill_depth_mm : num [1:47] 18.7 17.4 18 19.3 20.6 17.8 19.6 17.6 21.2 21.1 ...
## $ flipper_length_mm: num [1:47] 181 186 195 193 190 181 195 182 191 198 ...
## $ body_mass_g : num [1:47] 3750 3800 3250 3450 3650 ...
## $ sex : chr [1:47] "male" "female" "female" "female" ...
## $ year : num [1:47] 2007 2007 2007 2007 2007 ...
```

```
str(biscoepen)
```

```
## tibble [165 x 8] (S3: tbl_df/tbl/data.frame)
## $ species : chr [1:165] "Adelie" "Adelie" "Adelie" "Adelie" ...
## $ island : chr [1:165] "Biscoe" "Biscoe" "Biscoe" "Biscoe" ...
## $ bill_length_mm : num [1:165] 37.8 37.7 35.9 38.2 38.8 35.3 40.6 40.5 37.9 40.5 ...
## $ bill_depth_mm : num [1:165] 18.3 18.7 19.2 18.1 17.2 18.9 18.6 17.9 18.6 18.9 ...
## $ flipper_length_mm: num [1:165] 174 180 189 185 180 187 183 187 172 180 ...
## $ body_mass_g : num [1:165] 3400 3600 3800 3950 3800 3800 3550 3200 3150 3950 ...
## $ sex : chr [1:165] "female" "male" "female" "male" ...
## $ year : num [1:165] 2007 2007 2007 2007 2007 ...
```

```
str(dreampen)
```

```
## tibble [123 x 8] (S3: tbl_df/tbl/data.frame)
## $ species : chr [1:123] "Adelie" "Adelie" "Adelie" "Adelie" ...
## $ island : chr [1:123] "Dream" "Dream" "Dream" "Dream" ...
## $ bill_length_mm : num [1:123] 39.5 37.2 39.5 40.9 36.4 39.2 38.8 42.2 37.6 39.8 ...
## $ bill_depth_mm : num [1:123] 16.7 18.1 17.8 18.9 17 21.1 20 18.5 19.3 19.1 ...
## $ flipper_length_mm: num [1:123] 178 178 188 184 195 196 190 180 181 184 ...
## $ body_mass_g : num [1:123] 3250 3900 3300 3900 3325 ...
## $ sex : chr [1:123] "female" "male" "female" "male" ...
## $ year : num [1:123] 2007 2007 2007 2007 2007 ...
```

For the sake of our data exploration, we should have a dataframe which includes all of the data from each separate island. Using the `rbind()` function, we are able to first bind the Torgersen data with the Biscoe data. Then, we can put it all together using `rbind()` on the `torgersen+biscoe` frame with the Dream frame. For safe measure, we will use `as.data.frame()` on the full set.

```
torgbisc <- rbind(torgersenpen, biscoepen)
```

```
full <- rbind(torgbisc, dreampen)
```

```
fullframe <- as.data.frame(full)
```

```
fullframe
```

```
##      species      island bill_length_mm bill_depth_mm flipper_length_mm
## 1    Adelie Torgersen      39.1          18.7           181
## 2    Adelie Torgersen      39.5          17.4           186
## 3    Adelie Torgersen      40.3          18.0           195
## 4    Adelie Torgersen      36.7          19.3           193
## 5    Adelie Torgersen      39.3          20.6           190
## 6    Adelie Torgersen      38.9          17.8           181
## 7    Adelie Torgersen      39.2          19.6           195
## 8    Adelie Torgersen      41.1          17.6           182
## 9    Adelie Torgersen      38.6          21.2           191
```

## 10	Adelie Torgersen	34.6	21.1	198
## 11	Adelie Torgersen	36.6	17.8	185
## 12	Adelie Torgersen	38.7	19.0	195
## 13	Adelie Torgersen	42.5	20.7	197
## 14	Adelie Torgersen	34.4	18.4	184
## 15	Adelie Torgersen	46.0	21.5	194
## 16	Adelie Torgersen	35.9	16.6	190
## 17	Adelie Torgersen	41.8	19.4	198
## 18	Adelie Torgersen	33.5	19.0	190
## 19	Adelie Torgersen	39.7	18.4	190
## 20	Adelie Torgersen	39.6	17.2	196
## 21	Adelie Torgersen	45.8	18.9	197
## 22	Adelie Torgersen	35.5	17.5	190
## 23	Adelie Torgersen	42.8	18.5	195
## 24	Adelie Torgersen	40.9	16.8	191
## 25	Adelie Torgersen	37.2	19.4	184
## 26	Adelie Torgersen	36.2	16.1	187
## 27	Adelie Torgersen	42.1	19.1	195
## 28	Adelie Torgersen	34.6	17.2	189
## 29	Adelie Torgersen	42.9	17.6	196
## 30	Adelie Torgersen	36.7	18.8	187
## 31	Adelie Torgersen	35.1	19.4	193
## 32	Adelie Torgersen	38.6	17.0	188
## 33	Adelie Torgersen	37.3	20.5	199
## 34	Adelie Torgersen	35.7	17.0	189
## 35	Adelie Torgersen	41.1	18.6	189
## 36	Adelie Torgersen	36.2	17.2	187
## 37	Adelie Torgersen	37.7	19.8	198
## 38	Adelie Torgersen	40.2	17.0	176
## 39	Adelie Torgersen	41.4	18.5	202
## 40	Adelie Torgersen	35.2	15.9	186
## 41	Adelie Torgersen	40.6	19.0	199
## 42	Adelie Torgersen	38.8	17.6	191
## 43	Adelie Torgersen	41.5	18.3	195
## 44	Adelie Torgersen	39.0	17.1	191
## 45	Adelie Torgersen	44.1	18.0	210
## 46	Adelie Torgersen	38.5	17.9	190
## 47	Adelie Torgersen	43.1	19.2	197
## 48	Adelie Biscoe	37.8	18.3	174
## 49	Adelie Biscoe	37.7	18.7	180
## 50	Adelie Biscoe	35.9	19.2	189
## 51	Adelie Biscoe	38.2	18.1	185
## 52	Adelie Biscoe	38.8	17.2	180
## 53	Adelie Biscoe	35.3	18.9	187
## 54	Adelie Biscoe	40.6	18.6	183
## 55	Adelie Biscoe	40.5	17.9	187
## 56	Adelie Biscoe	37.9	18.6	172
## 57	Adelie Biscoe	40.5	18.9	180
## 58	Adelie Biscoe	39.6	17.7	186
## 59	Adelie Biscoe	40.1	18.9	188
## 60	Adelie Biscoe	35.0	17.9	190
## 61	Adelie Biscoe	42.0	19.5	200
## 62	Adelie Biscoe	34.5	18.1	187
## 63	Adelie Biscoe	41.4	18.6	191

## 64	Adelie	Biscoe	39.0	17.5	186
## 65	Adelie	Biscoe	40.6	18.8	193
## 66	Adelie	Biscoe	36.5	16.6	181
## 67	Adelie	Biscoe	37.6	19.1	194
## 68	Adelie	Biscoe	35.7	16.9	185
## 69	Adelie	Biscoe	41.3	21.1	195
## 70	Adelie	Biscoe	37.6	17.0	185
## 71	Adelie	Biscoe	41.1	18.2	192
## 72	Adelie	Biscoe	36.4	17.1	184
## 73	Adelie	Biscoe	41.6	18.0	192
## 74	Adelie	Biscoe	35.5	16.2	195
## 75	Adelie	Biscoe	41.1	19.1	188
## 76	Adelie	Biscoe	35.0	17.9	192
## 77	Adelie	Biscoe	41.0	20.0	203
## 78	Adelie	Biscoe	37.7	16.0	183
## 79	Adelie	Biscoe	37.8	20.0	190
## 80	Adelie	Biscoe	37.9	18.6	193
## 81	Adelie	Biscoe	39.7	18.9	184
## 82	Adelie	Biscoe	38.6	17.2	199
## 83	Adelie	Biscoe	38.2	20.0	190
## 84	Adelie	Biscoe	38.1	17.0	181
## 85	Adelie	Biscoe	43.2	19.0	197
## 86	Adelie	Biscoe	38.1	16.5	198
## 87	Adelie	Biscoe	45.6	20.3	191
## 88	Adelie	Biscoe	39.7	17.7	193
## 89	Adelie	Biscoe	42.2	19.5	197
## 90	Adelie	Biscoe	39.6	20.7	191
## 91	Adelie	Biscoe	42.7	18.3	196
## 92	Gentoo	Biscoe	46.1	13.2	211
## 93	Gentoo	Biscoe	50.0	16.3	230
## 94	Gentoo	Biscoe	48.7	14.1	210
## 95	Gentoo	Biscoe	50.0	15.2	218
## 96	Gentoo	Biscoe	47.6	14.5	215
## 97	Gentoo	Biscoe	46.5	13.5	210
## 98	Gentoo	Biscoe	45.4	14.6	211
## 99	Gentoo	Biscoe	46.7	15.3	219
## 100	Gentoo	Biscoe	43.3	13.4	209
## 101	Gentoo	Biscoe	46.8	15.4	215
## 102	Gentoo	Biscoe	40.9	13.7	214
## 103	Gentoo	Biscoe	49.0	16.1	216
## 104	Gentoo	Biscoe	45.5	13.7	214
## 105	Gentoo	Biscoe	48.4	14.6	213
## 106	Gentoo	Biscoe	45.8	14.6	210
## 107	Gentoo	Biscoe	49.3	15.7	217
## 108	Gentoo	Biscoe	42.0	13.5	210
## 109	Gentoo	Biscoe	49.2	15.2	221
## 110	Gentoo	Biscoe	46.2	14.5	209
## 111	Gentoo	Biscoe	48.7	15.1	222
## 112	Gentoo	Biscoe	50.2	14.3	218
## 113	Gentoo	Biscoe	45.1	14.5	215
## 114	Gentoo	Biscoe	46.5	14.5	213
## 115	Gentoo	Biscoe	46.3	15.8	215
## 116	Gentoo	Biscoe	42.9	13.1	215
## 117	Gentoo	Biscoe	46.1	15.1	215

## 118	Gentoo	Biscoe	44.5	14.3	216
## 119	Gentoo	Biscoe	47.8	15.0	215
## 120	Gentoo	Biscoe	48.2	14.3	210
## 121	Gentoo	Biscoe	50.0	15.3	220
## 122	Gentoo	Biscoe	47.3	15.3	222
## 123	Gentoo	Biscoe	42.8	14.2	209
## 124	Gentoo	Biscoe	45.1	14.5	207
## 125	Gentoo	Biscoe	59.6	17.0	230
## 126	Gentoo	Biscoe	49.1	14.8	220
## 127	Gentoo	Biscoe	48.4	16.3	220
## 128	Gentoo	Biscoe	42.6	13.7	213
## 129	Gentoo	Biscoe	44.4	17.3	219
## 130	Gentoo	Biscoe	44.0	13.6	208
## 131	Gentoo	Biscoe	48.7	15.7	208
## 132	Gentoo	Biscoe	42.7	13.7	208
## 133	Gentoo	Biscoe	49.6	16.0	225
## 134	Gentoo	Biscoe	45.3	13.7	210
## 135	Gentoo	Biscoe	49.6	15.0	216
## 136	Gentoo	Biscoe	50.5	15.9	222
## 137	Gentoo	Biscoe	43.6	13.9	217
## 138	Gentoo	Biscoe	45.5	13.9	210
## 139	Gentoo	Biscoe	50.5	15.9	225
## 140	Gentoo	Biscoe	44.9	13.3	213
## 141	Gentoo	Biscoe	45.2	15.8	215
## 142	Gentoo	Biscoe	46.6	14.2	210
## 143	Gentoo	Biscoe	48.5	14.1	220
## 144	Gentoo	Biscoe	45.1	14.4	210
## 145	Gentoo	Biscoe	50.1	15.0	225
## 146	Gentoo	Biscoe	46.5	14.4	217
## 147	Gentoo	Biscoe	45.0	15.4	220
## 148	Gentoo	Biscoe	43.8	13.9	208
## 149	Gentoo	Biscoe	45.5	15.0	220
## 150	Gentoo	Biscoe	43.2	14.5	208
## 151	Gentoo	Biscoe	50.4	15.3	224
## 152	Gentoo	Biscoe	45.3	13.8	208
## 153	Gentoo	Biscoe	46.2	14.9	221
## 154	Gentoo	Biscoe	45.7	13.9	214
## 155	Gentoo	Biscoe	54.3	15.7	231
## 156	Gentoo	Biscoe	45.8	14.2	219
## 157	Gentoo	Biscoe	49.8	16.8	230
## 158	Gentoo	Biscoe	46.2	14.4	214
## 159	Gentoo	Biscoe	49.5	16.2	229
## 160	Gentoo	Biscoe	43.5	14.2	220
## 161	Gentoo	Biscoe	50.7	15.0	223
## 162	Gentoo	Biscoe	47.7	15.0	216
## 163	Gentoo	Biscoe	46.4	15.6	221
## 164	Gentoo	Biscoe	48.2	15.6	221
## 165	Gentoo	Biscoe	46.5	14.8	217
## 166	Gentoo	Biscoe	46.4	15.0	216
## 167	Gentoo	Biscoe	48.6	16.0	230
## 168	Gentoo	Biscoe	47.5	14.2	209
## 169	Gentoo	Biscoe	51.1	16.3	220
## 170	Gentoo	Biscoe	45.2	13.8	215
## 171	Gentoo	Biscoe	45.2	16.4	223

## 172	Gentoo	Biscoe	49.1	14.5	212
## 173	Gentoo	Biscoe	52.5	15.6	221
## 174	Gentoo	Biscoe	47.4	14.6	212
## 175	Gentoo	Biscoe	50.0	15.9	224
## 176	Gentoo	Biscoe	44.9	13.8	212
## 177	Gentoo	Biscoe	50.8	17.3	228
## 178	Gentoo	Biscoe	43.4	14.4	218
## 179	Gentoo	Biscoe	51.3	14.2	218
## 180	Gentoo	Biscoe	47.5	14.0	212
## 181	Gentoo	Biscoe	52.1	17.0	230
## 182	Gentoo	Biscoe	47.5	15.0	218
## 183	Gentoo	Biscoe	52.2	17.1	228
## 184	Gentoo	Biscoe	45.5	14.5	212
## 185	Gentoo	Biscoe	49.5	16.1	224
## 186	Gentoo	Biscoe	44.5	14.7	214
## 187	Gentoo	Biscoe	50.8	15.7	226
## 188	Gentoo	Biscoe	49.4	15.8	216
## 189	Gentoo	Biscoe	46.9	14.6	222
## 190	Gentoo	Biscoe	48.4	14.4	203
## 191	Gentoo	Biscoe	51.1	16.5	225
## 192	Gentoo	Biscoe	48.5	15.0	219
## 193	Gentoo	Biscoe	55.9	17.0	228
## 194	Gentoo	Biscoe	47.2	15.5	215
## 195	Gentoo	Biscoe	49.1	15.0	228
## 196	Gentoo	Biscoe	46.8	16.1	215
## 197	Gentoo	Biscoe	41.7	14.7	210
## 198	Gentoo	Biscoe	53.4	15.8	219
## 199	Gentoo	Biscoe	43.3	14.0	208
## 200	Gentoo	Biscoe	48.1	15.1	209
## 201	Gentoo	Biscoe	50.5	15.2	216
## 202	Gentoo	Biscoe	49.8	15.9	229
## 203	Gentoo	Biscoe	43.5	15.2	213
## 204	Gentoo	Biscoe	51.5	16.3	230
## 205	Gentoo	Biscoe	46.2	14.1	217
## 206	Gentoo	Biscoe	55.1	16.0	230
## 207	Gentoo	Biscoe	48.8	16.2	222
## 208	Gentoo	Biscoe	47.2	13.7	214
## 209	Gentoo	Biscoe	46.8	14.3	215
## 210	Gentoo	Biscoe	50.4	15.7	222
## 211	Gentoo	Biscoe	45.2	14.8	212
## 212	Gentoo	Biscoe	49.9	16.1	213
## 213	Adelie	Dream	39.5	16.7	178
## 214	Adelie	Dream	37.2	18.1	178
## 215	Adelie	Dream	39.5	17.8	188
## 216	Adelie	Dream	40.9	18.9	184
## 217	Adelie	Dream	36.4	17.0	195
## 218	Adelie	Dream	39.2	21.1	196
## 219	Adelie	Dream	38.8	20.0	190
## 220	Adelie	Dream	42.2	18.5	180
## 221	Adelie	Dream	37.6	19.3	181
## 222	Adelie	Dream	39.8	19.1	184
## 223	Adelie	Dream	36.5	18.0	182
## 224	Adelie	Dream	40.8	18.4	195
## 225	Adelie	Dream	36.0	18.5	186

## 226	Adelie	Dream	44.1	19.7	196
## 227	Adelie	Dream	37.0	16.9	185
## 228	Adelie	Dream	39.6	18.8	190
## 229	Adelie	Dream	41.1	19.0	182
## 230	Adelie	Dream	36.0	17.9	190
## 231	Adelie	Dream	42.3	21.2	191
## 232	Adelie	Dream	37.3	17.8	191
## 233	Adelie	Dream	41.3	20.3	194
## 234	Adelie	Dream	36.3	19.5	190
## 235	Adelie	Dream	36.9	18.6	189
## 236	Adelie	Dream	38.3	19.2	189
## 237	Adelie	Dream	38.9	18.8	190
## 238	Adelie	Dream	35.7	18.0	202
## 239	Adelie	Dream	41.1	18.1	205
## 240	Adelie	Dream	34.0	17.1	185
## 241	Adelie	Dream	39.6	18.1	186
## 242	Adelie	Dream	36.2	17.3	187
## 243	Adelie	Dream	40.8	18.9	208
## 244	Adelie	Dream	38.1	18.6	190
## 245	Adelie	Dream	40.3	18.5	196
## 246	Adelie	Dream	33.1	16.1	178
## 247	Adelie	Dream	43.2	18.5	192
## 248	Adelie	Dream	36.8	18.5	193
## 249	Adelie	Dream	37.5	18.5	199
## 250	Adelie	Dream	38.1	17.6	187
## 251	Adelie	Dream	41.1	17.5	190
## 252	Adelie	Dream	35.6	17.5	191
## 253	Adelie	Dream	40.2	20.1	200
## 254	Adelie	Dream	37.0	16.5	185
## 255	Adelie	Dream	39.7	17.9	193
## 256	Adelie	Dream	40.2	17.1	193
## 257	Adelie	Dream	40.6	17.2	187
## 258	Adelie	Dream	32.1	15.5	188
## 259	Adelie	Dream	40.7	17.0	190
## 260	Adelie	Dream	37.3	16.8	192
## 261	Adelie	Dream	39.0	18.7	185
## 262	Adelie	Dream	39.2	18.6	190
## 263	Adelie	Dream	36.6	18.4	184
## 264	Adelie	Dream	36.0	17.8	195
## 265	Adelie	Dream	37.8	18.1	193
## 266	Adelie	Dream	36.0	17.1	187
## 267	Adelie	Dream	41.5	18.5	201
## 268	Chinstrap	Dream	46.5	17.9	192
## 269	Chinstrap	Dream	50.0	19.5	196
## 270	Chinstrap	Dream	51.3	19.2	193
## 271	Chinstrap	Dream	45.4	18.7	188
## 272	Chinstrap	Dream	52.7	19.8	197
## 273	Chinstrap	Dream	45.2	17.8	198
## 274	Chinstrap	Dream	46.1	18.2	178
## 275	Chinstrap	Dream	51.3	18.2	197
## 276	Chinstrap	Dream	46.0	18.9	195
## 277	Chinstrap	Dream	51.3	19.9	198
## 278	Chinstrap	Dream	46.6	17.8	193
## 279	Chinstrap	Dream	51.7	20.3	194

## 280	Chinstrap	Dream	47.0	17.3	185
## 281	Chinstrap	Dream	52.0	18.1	201
## 282	Chinstrap	Dream	45.9	17.1	190
## 283	Chinstrap	Dream	50.5	19.6	201
## 284	Chinstrap	Dream	50.3	20.0	197
## 285	Chinstrap	Dream	58.0	17.8	181
## 286	Chinstrap	Dream	46.4	18.6	190
## 287	Chinstrap	Dream	49.2	18.2	195
## 288	Chinstrap	Dream	42.4	17.3	181
## 289	Chinstrap	Dream	48.5	17.5	191
## 290	Chinstrap	Dream	43.2	16.6	187
## 291	Chinstrap	Dream	50.6	19.4	193
## 292	Chinstrap	Dream	46.7	17.9	195
## 293	Chinstrap	Dream	52.0	19.0	197
## 294	Chinstrap	Dream	50.5	18.4	200
## 295	Chinstrap	Dream	49.5	19.0	200
## 296	Chinstrap	Dream	46.4	17.8	191
## 297	Chinstrap	Dream	52.8	20.0	205
## 298	Chinstrap	Dream	40.9	16.6	187
## 299	Chinstrap	Dream	54.2	20.8	201
## 300	Chinstrap	Dream	42.5	16.7	187
## 301	Chinstrap	Dream	51.0	18.8	203
## 302	Chinstrap	Dream	49.7	18.6	195
## 303	Chinstrap	Dream	47.5	16.8	199
## 304	Chinstrap	Dream	47.6	18.3	195
## 305	Chinstrap	Dream	52.0	20.7	210
## 306	Chinstrap	Dream	46.9	16.6	192
## 307	Chinstrap	Dream	53.5	19.9	205
## 308	Chinstrap	Dream	49.0	19.5	210
## 309	Chinstrap	Dream	46.2	17.5	187
## 310	Chinstrap	Dream	50.9	19.1	196
## 311	Chinstrap	Dream	45.5	17.0	196
## 312	Chinstrap	Dream	50.9	17.9	196
## 313	Chinstrap	Dream	50.8	18.5	201
## 314	Chinstrap	Dream	50.1	17.9	190
## 315	Chinstrap	Dream	49.0	19.6	212
## 316	Chinstrap	Dream	51.5	18.7	187
## 317	Chinstrap	Dream	49.8	17.3	198
## 318	Chinstrap	Dream	48.1	16.4	199
## 319	Chinstrap	Dream	51.4	19.0	201
## 320	Chinstrap	Dream	45.7	17.3	193
## 321	Chinstrap	Dream	50.7	19.7	203
## 322	Chinstrap	Dream	42.5	17.3	187
## 323	Chinstrap	Dream	52.2	18.8	197
## 324	Chinstrap	Dream	45.2	16.6	191
## 325	Chinstrap	Dream	49.3	19.9	203
## 326	Chinstrap	Dream	50.2	18.8	202
## 327	Chinstrap	Dream	45.6	19.4	194
## 328	Chinstrap	Dream	51.9	19.5	206
## 329	Chinstrap	Dream	46.8	16.5	189
## 330	Chinstrap	Dream	45.7	17.0	195
## 331	Chinstrap	Dream	55.8	19.8	207
## 332	Chinstrap	Dream	43.5	18.1	202
## 333	Chinstrap	Dream	49.6	18.2	193



## 334	Chinstrap	Dream	50.8	19.0	210
## 335	Chinstrap	Dream	50.2	18.7	198
##	body_mass_g	sex year			
## 1	3750	male 2007			
## 2	3800	female 2007			
## 3	3250	female 2007			
## 4	3450	female 2007			
## 5	3650	male 2007			
## 6	3625	female 2007			
## 7	4675	male 2007			
## 8	3200	female 2007			
## 9	3800	male 2007			
## 10	4400	male 2007			
## 11	3700	female 2007			
## 12	3450	female 2007			
## 13	4500	male 2007			
## 14	3325	female 2007			
## 15	4200	male 2007			
## 16	3050	female 2008			
## 17	4450	male 2008			
## 18	3600	female 2008			
## 19	3900	male 2008			
## 20	3550	female 2008			
## 21	4150	male 2008			
## 22	3700	female 2008			
## 23	4250	male 2008			
## 24	3700	female 2008			
## 25	3900	male 2008			
## 26	3550	female 2008			
## 27	4000	male 2008			
## 28	3200	female 2008			
## 29	4700	male 2008			
## 30	3800	female 2008			
## 31	4200	male 2008			
## 32	2900	female 2009			
## 33	3775	male 2009			
## 34	3350	female 2009			
## 35	3325	male 2009			
## 36	3150	female 2009			
## 37	3500	male 2009			
## 38	3450	female 2009			
## 39	3875	male 2009			
## 40	3050	female 2009			
## 41	4000	male 2009			
## 42	3275	female 2009			
## 43	4300	male 2009			
## 44	3050	female 2009			
## 45	4000	male 2009			
## 46	3325	female 2009			
## 47	3500	male 2009			
## 48	3400	female 2007			
## 49	3600	male 2007			
## 50	3800	female 2007			
## 51	3950	male 2007			

## 52	3800	male	2007
## 53	3800	female	2007
## 54	3550	male	2007
## 55	3200	female	2007
## 56	3150	female	2007
## 57	3950	male	2007
## 58	3500	female	2008
## 59	4300	male	2008
## 60	3450	female	2008
## 61	4050	male	2008
## 62	2900	female	2008
## 63	3700	male	2008
## 64	3550	female	2008
## 65	3800	male	2008
## 66	2850	female	2008
## 67	3750	male	2008
## 68	3150	female	2008
## 69	4400	male	2008
## 70	3600	female	2008
## 71	4050	male	2008
## 72	2850	female	2008
## 73	3950	male	2008
## 74	3350	female	2008
## 75	4100	male	2008
## 76	3725	female	2009
## 77	4725	male	2009
## 78	3075	female	2009
## 79	4250	male	2009
## 80	2925	female	2009
## 81	3550	male	2009
## 82	3750	female	2009
## 83	3900	male	2009
## 84	3175	female	2009
## 85	4775	male	2009
## 86	3825	female	2009
## 87	4600	male	2009
## 88	3200	female	2009
## 89	4275	male	2009
## 90	3900	female	2009
## 91	4075	male	2009
## 92	4500	female	2007
## 93	5700	male	2007
## 94	4450	female	2007
## 95	5700	male	2007
## 96	5400	male	2007
## 97	4550	female	2007
## 98	4800	female	2007
## 99	5200	male	2007
## 100	4400	female	2007
## 101	5150	male	2007
## 102	4650	female	2007
## 103	5550	male	2007
## 104	4650	female	2007
## 105	5850	male	2007

## 106	4200	female	2007
## 107	5850	male	2007
## 108	4150	female	2007
## 109	6300	male	2007
## 110	4800	female	2007
## 111	5350	male	2007
## 112	5700	male	2007
## 113	5000	female	2007
## 114	4400	female	2007
## 115	5050	male	2007
## 116	5000	female	2007
## 117	5100	male	2007
## 118	4100	NA	2007
## 119	5650	male	2007
## 120	4600	female	2007
## 121	5550	male	2007
## 122	5250	male	2007
## 123	4700	female	2007
## 124	5050	female	2007
## 125	6050	male	2007
## 126	5150	female	2008
## 127	5400	male	2008
## 128	4950	female	2008
## 129	5250	male	2008
## 130	4350	female	2008
## 131	5350	male	2008
## 132	3950	female	2008
## 133	5700	male	2008
## 134	4300	female	2008
## 135	4750	male	2008
## 136	5550	male	2008
## 137	4900	female	2008
## 138	4200	female	2008
## 139	5400	male	2008
## 140	5100	female	2008
## 141	5300	male	2008
## 142	4850	female	2008
## 143	5300	male	2008
## 144	4400	female	2008
## 145	5000	male	2008
## 146	4900	female	2008
## 147	5050	male	2008
## 148	4300	female	2008
## 149	5000	male	2008
## 150	4450	female	2008
## 151	5550	male	2008
## 152	4200	female	2008
## 153	5300	male	2008
## 154	4400	female	2008
## 155	5650	male	2008
## 156	4700	female	2008
## 157	5700	male	2008
## 158	4650	NA	2008
## 159	5800	male	2008

## 160	4700	female	2008
## 161	5550	male	2008
## 162	4750	female	2008
## 163	5000	male	2008
## 164	5100	male	2008
## 165	5200	female	2008
## 166	4700	female	2008
## 167	5800	male	2008
## 168	4600	female	2008
## 169	6000	male	2008
## 170	4750	female	2008
## 171	5950	male	2008
## 172	4625	female	2009
## 173	5450	male	2009
## 174	4725	female	2009
## 175	5350	male	2009
## 176	4750	female	2009
## 177	5600	male	2009
## 178	4600	female	2009
## 179	5300	male	2009
## 180	4875	female	2009
## 181	5550	male	2009
## 182	4950	female	2009
## 183	5400	male	2009
## 184	4750	female	2009
## 185	5650	male	2009
## 186	4850	female	2009
## 187	5200	male	2009
## 188	4925	male	2009
## 189	4875	female	2009
## 190	4625	female	2009
## 191	5250	male	2009
## 192	4850	female	2009
## 193	5600	male	2009
## 194	4975	female	2009
## 195	5500	male	2009
## 196	5500	male	2009
## 197	4700	female	2009
## 198	5500	male	2009
## 199	4575	female	2009
## 200	5500	male	2009
## 201	5000	female	2009
## 202	5950	male	2009
## 203	4650	female	2009
## 204	5500	male	2009
## 205	4375	female	2009
## 206	5850	male	2009
## 207	6000	male	2009
## 208	4925	female	2009
## 209	4850	female	2009
## 210	5750	male	2009
## 211	5200	female	2009
## 212	5400	male	2009
## 213	3250	female	2007

## 214	3900	male	2007
## 215	3300	female	2007
## 216	3900	male	2007
## 217	3325	female	2007
## 218	4150	male	2007
## 219	3950	male	2007
## 220	3550	female	2007
## 221	3300	female	2007
## 222	4650	male	2007
## 223	3150	female	2007
## 224	3900	male	2007
## 225	3100	female	2007
## 226	4400	male	2007
## 227	3000	female	2007
## 228	4600	male	2007
## 229	3425	male	2007
## 230	3450	female	2007
## 231	4150	male	2007
## 232	3350	female	2008
## 233	3550	male	2008
## 234	3800	male	2008
## 235	3500	female	2008
## 236	3950	male	2008
## 237	3600	female	2008
## 238	3550	female	2008
## 239	4300	male	2008
## 240	3400	female	2008
## 241	4450	male	2008
## 242	3300	female	2008
## 243	4300	male	2008
## 244	3700	female	2008
## 245	4350	male	2008
## 246	2900	female	2008
## 247	4100	male	2008
## 248	3500	female	2009
## 249	4475	male	2009
## 250	3425	female	2009
## 251	3900	male	2009
## 252	3175	female	2009
## 253	3975	male	2009
## 254	3400	female	2009
## 255	4250	male	2009
## 256	3400	female	2009
## 257	3475	male	2009
## 258	3050	female	2009
## 259	3725	male	2009
## 260	3000	female	2009
## 261	3650	male	2009
## 262	4250	male	2009
## 263	3475	female	2009
## 264	3450	female	2009
## 265	3750	male	2009
## 266	3700	female	2009
## 267	4000	male	2009

## 268	3500	female	2007
## 269	3900	male	2007
## 270	3650	male	2007
## 271	3525	female	2007
## 272	3725	male	2007
## 273	3950	female	2007
## 274	3250	female	2007
## 275	3750	male	2007
## 276	4150	female	2007
## 277	3700	male	2007
## 278	3800	female	2007
## 279	3775	male	2007
## 280	3700	female	2007
## 281	4050	male	2007
## 282	3575	female	2007
## 283	4050	male	2007
## 284	3300	male	2007
## 285	3700	female	2007
## 286	3450	female	2007
## 287	4400	male	2007
## 288	3600	female	2007
## 289	3400	male	2007
## 290	2900	female	2007
## 291	3800	male	2007
## 292	3300	female	2007
## 293	4150	male	2007
## 294	3400	female	2008
## 295	3800	male	2008
## 296	3700	female	2008
## 297	4550	male	2008
## 298	3200	female	2008
## 299	4300	male	2008
## 300	3350	female	2008
## 301	4100	male	2008
## 302	3600	male	2008
## 303	3900	female	2008
## 304	3850	female	2008
## 305	4800	male	2008
## 306	2700	female	2008
## 307	4500	male	2008
## 308	3950	male	2008
## 309	3650	female	2008
## 310	3550	male	2008
## 311	3500	female	2008
## 312	3675	female	2009
## 313	4450	male	2009
## 314	3400	female	2009
## 315	4300	male	2009
## 316	3250	male	2009
## 317	3675	female	2009
## 318	3325	female	2009
## 319	3950	male	2009
## 320	3600	female	2009
## 321	4050	male	2009

```
## 322      3350 female 2009
## 323      3450  male 2009
## 324      3250 female 2009
## 325      4050  male 2009
## 326      3800  male 2009
## 327      3525 female 2009
## 328      3950  male 2009
## 329      3650 female 2009
## 330      3650 female 2009
## 331      4000  male 2009
## 332      3400 female 2009
## 333      3775  male 2009
## 334      4100  male 2009
## 335      3775 female 2009
```

Now that our full dataframe is established, we can begin exploring the data. We will first assess whether the bill length is different between the three species. To do this, we will conduct an anova. - What type of variable is our explanatory variable? Response variable?

```
fullframe$species <- as.factor(fullframe$species)
billLaov <- aov(bill_length_mm ~ species, data = fullframe)
summary(billLaov)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## species        2    7009     3505   397.8 <2e-16 ***
## Residuals     332    2925         9
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

What type of ANOVA did our code conduct? Why was this type of ANOVA conducted? What do the results of our ANOVA tell us?

Next, we will test whether or not the bill length in penguins for Torsøen's Island is sex-dependent. To do this, we will conduct yet another anova to determine the significance (if any) in this relationship.

```
billLaov2 <- aov(bill_length_mm ~ sex, data = torsersenpen)
summary(billLaov2)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## sex           1  108.0   108.03    15.49 0.000284 ***
## Residuals    45  313.8     6.97
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

What type of ANOVA did our code conduct? Why was this type of ANOVA conducted? What do the results of our ANOVA tell us?

I want you to think about the other available statistical tests which are available to us in R, and which would be more appropriate for completing the task of comparing bill lengths between sexes on Torsøen Island. What would this look like as code?

```
t.test(bill_length_mm ~ sex, data = torgersenpen)
```

```
##  
## Welch Two Sample t-test  
##  
## data: bill_length_mm by sex  
## t = -3.91, df = 40.162, p-value = 0.0003468  
## alternative hypothesis: true difference in means between group female and group male is not equal to  
## 95 percent confidence interval:  
## -4.600230 -1.465349  
## sample estimates:  
## mean in group female mean in group male  
## 37.55417 40.58696
```

Why would we want to use this type of statistical test as opposed to an anova? What are the advantages and/or disadvantages? What type of t-test is R studio running for this comparison? How would the results of our analyses be different if the data was non-normal? Normalized?