Homework 2

Brian MacCurtin

Table of contents

Link to the Github repository

❗ Due: Tue, Feb 14, 2023 @ 11:59pm

Please read the instructions carefully before submitting your assignment.

1. This assignment requires you to only upload a `PDF` file on Canvas
2. Don't collapse any code cells before submitting.
3. Remember to make sure all your code output is rendered properly before uploading your submission.

Please add your name to the author information in the frontmatter before submitting your assignment

For this assignment, we will be using the Abalone dataset from the UCI Machine Learning Repository. The dataset consists of physical measurements of abalone (a type of marine snail) and includes information on the age, sex, and size of the abalone.

We will be using the following libraries:

```r
rm(list = ls())
library(readr)
library(tidyr)
library(ggplot2)
library(dplyr)
```

```
Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

```r
library(purrr)
library(cowplot)
library(tidyverse)
```

```
-- Attaching packages --------------------------------------- tidyverse 1.3.2 --

v tibble  3.1.8     v forcats 0.5.2
v stringr 1.5.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
```

Question 1

30 points

EDA using `readr`, `tidyr` and `ggplot2`

1.1 (5 points)

Load the "Abalone" dataset as a tibble called `abalone` using the URL provided below. The `abalone_col_names` variable contains a vector of the column names for this dataset (to be consistent with the R naming pattern). Make sure you read the dataset with the provided column names.

```r
library(readr)
url <- "http://archive.ics.uci.edu/ml/machine-learning-databases/abalone/abalone.data"

abalone_col_names <- c(
  "sex",
  "length",
  "diameter",
  "height",
  "whole_weight",
  "shucked_weight",
  "viscera_weight",
  "shell_weight",
  "rings"
)

abalone <- read.csv(url)
colnames(abalone) <- abalone_col_names
head(abalone)
```

```
  sex length diameter height whole_weight shucked_weight viscera_weight
1   M  0.350    0.265  0.090       0.2255         0.0995         0.0485
2   F  0.530    0.420  0.135       0.6770         0.2565         0.1415
3   M  0.440    0.365  0.125       0.5160         0.2155         0.1140
4   I  0.330    0.255  0.080       0.2050         0.0895         0.0395
5   I  0.425    0.300  0.095       0.3515         0.1410         0.0775
6   F  0.530    0.415  0.150       0.7775         0.2370         0.1415
  shell_weight rings
1        0.070     7
2        0.210     9
3        0.155    10
4        0.055     7
5        0.120     8
6        0.330    20
```

1.2 (5 points)

Remove missing values and `NA`s from the dataset and store the cleaned data in a tibble called `df`. How many rows were dropped?

```
#Originally 4176 observations
df <- na.omit(abalone)
head(df)
```

```
  sex length diameter height whole_weight shucked_weight viscera_weight
1   M  0.350    0.265  0.090       0.2255         0.0995         0.0485
2   F  0.530    0.420  0.135       0.6770         0.2565         0.1415
3   M  0.440    0.365  0.125       0.5160         0.2155         0.1140
4   I  0.330    0.255  0.080       0.2050         0.0895         0.0395
5   I  0.425    0.300  0.095       0.3515         0.1410         0.0775
6   F  0.530    0.415  0.150       0.7775         0.2370         0.1415
  shell_weight rings
1        0.070     7
2        0.210     9
3        0.155    10
4        0.055     7
5        0.120     8
6        0.330    20
```

0 rows were dropped. Still have 4176 observations

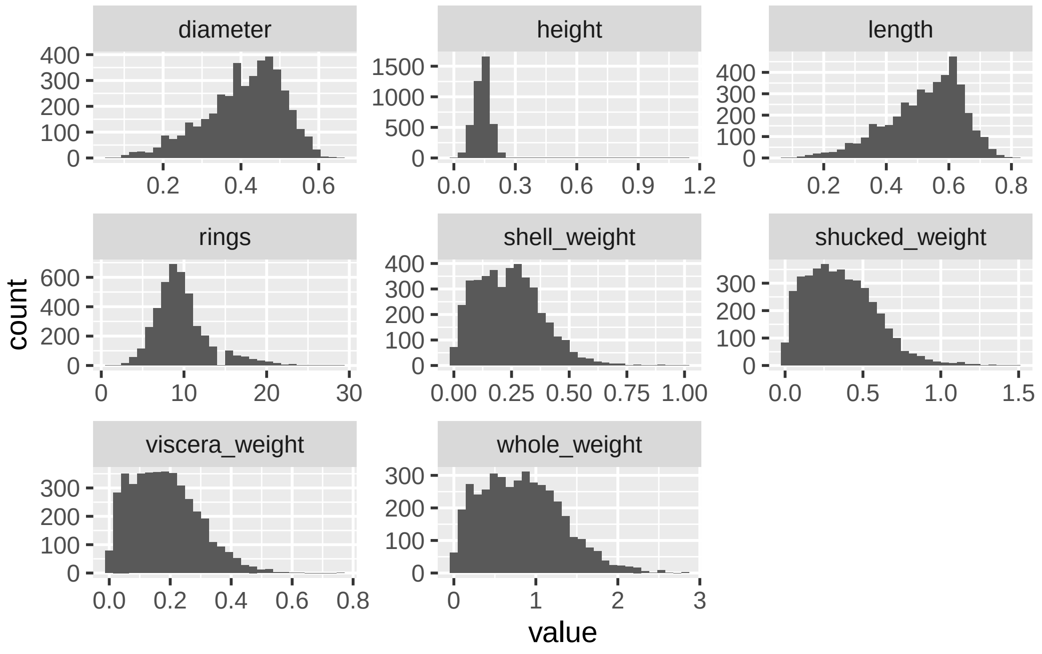
1.3 (5 points)

Plot histograms of all the quantitative variables in a **single plot** [1]

```
df %>%
  select(length, diameter, height, whole_weight, shucked_weight, viscera_weight, shell_wei
  gather() %>%
  ggplot(aes(value)) +
  facet_wrap(~ key, scales = "free") +
  geom_histogram()
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

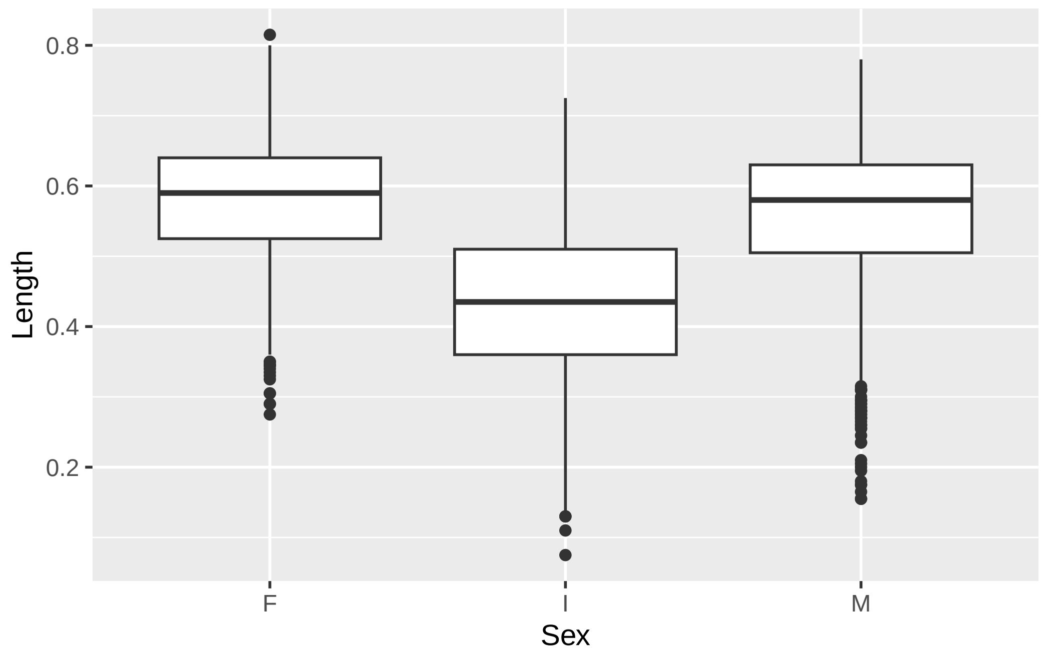
[1]You can use the `facet_wrap()` function for this. Have a look at its documentation using the help console in R



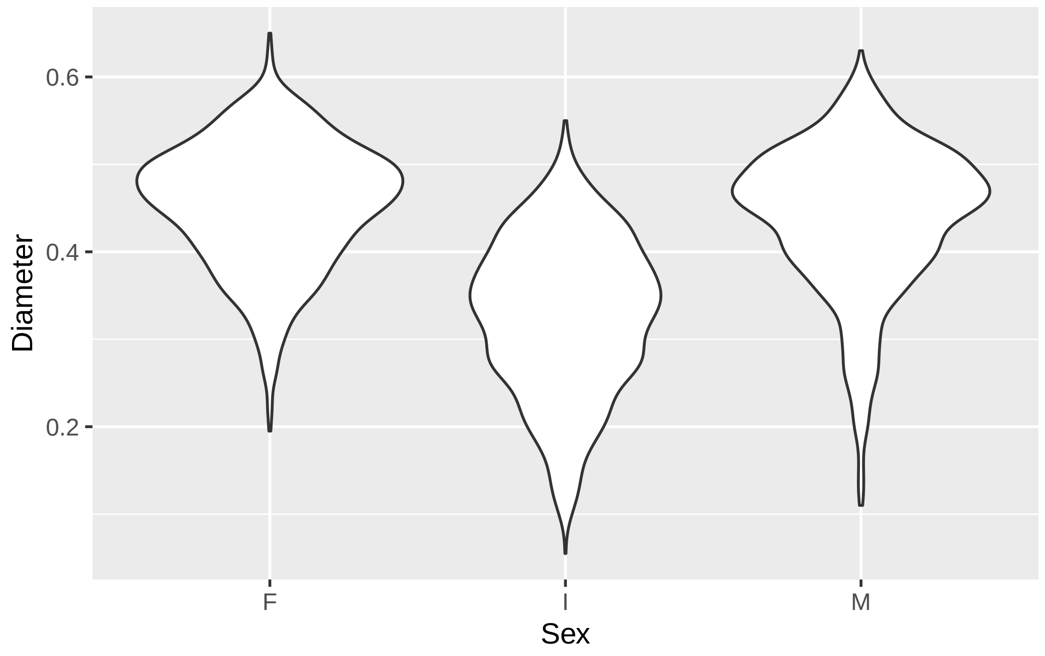
1.4 (5 points)

Create a boxplot of `length` for each `sex` and create a violin-plot of of `diameter` for each `sex`. Are there any notable differences in the physical appearences of abalones based on your analysis here?

```r
ggplot(data = df, mapping = aes(x=sex, y=length)) +
  geom_boxplot() +
  labs(x = "Sex", y = "Length")
```



```
ggplot(data = df, mapping = aes(x=sex, y=diameter)) +
  geom_violin() +
  labs(x = "Sex", y = "Diameter")
```



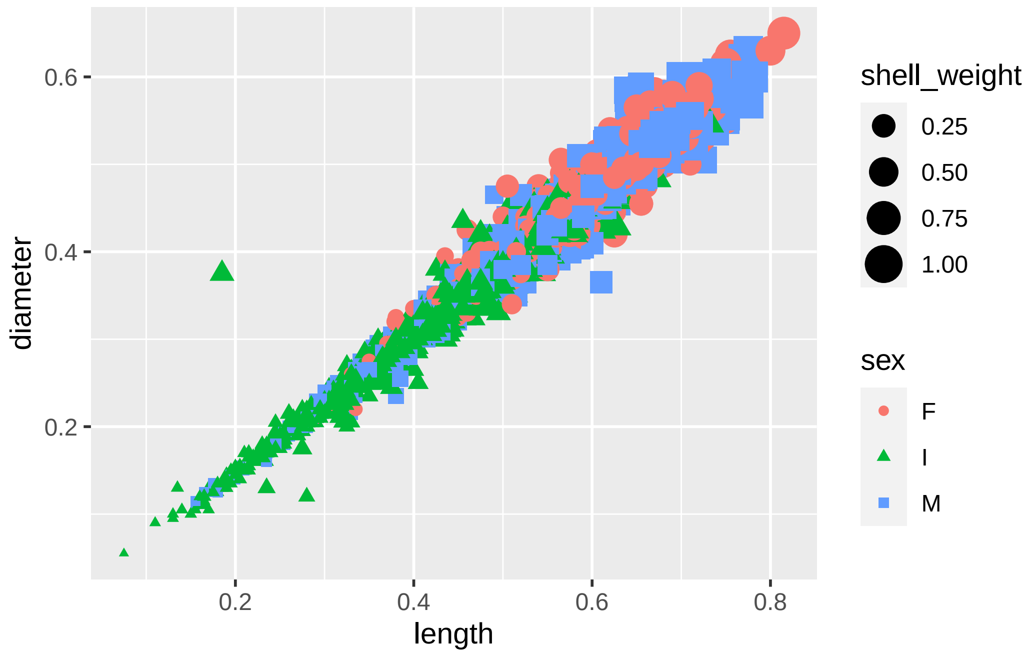
We can clearly see that the lengths and diameters of infants are less than non infants. However, between males and females, there is no obvious differences in the lengths and diameters of the abalone. They have similar means and similar spreads

---

1.5 (5 points)

Create a scatter plot of `length` and `diameter`, and modify the shape and color of the points based on the `sex` variable. Change the size of each point based on the `shell_wight` value for each observation. Are there any notable anomalies in the dataset?

```
ggplot(data = df, mapping = aes(x=length, y=diameter, color = sex, shape= sex, size = shel
  geom_point()
```



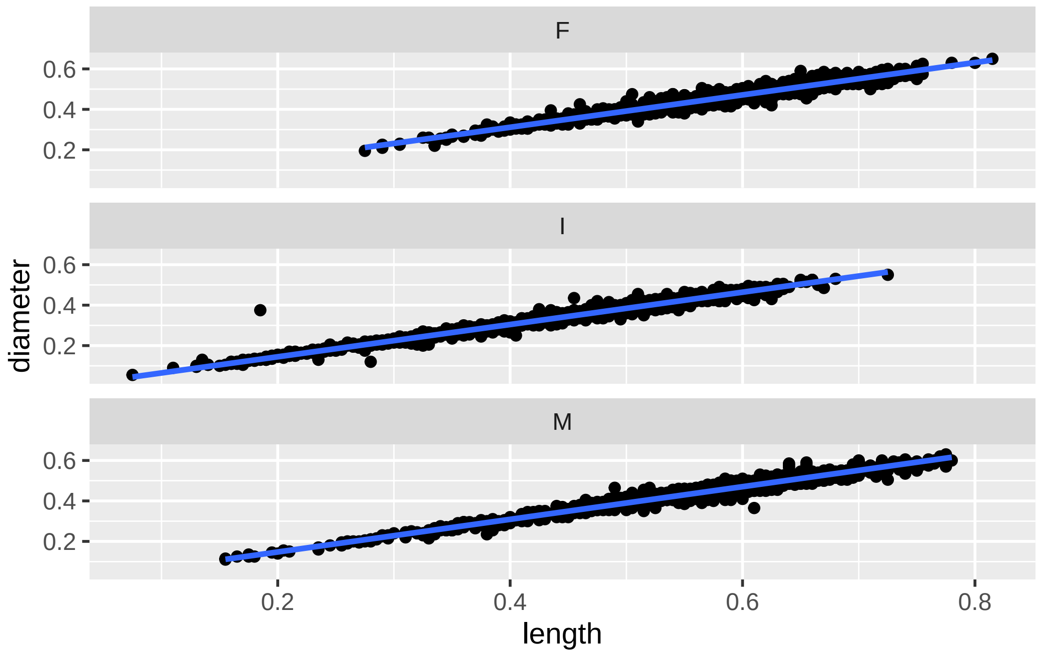
There is one infant who has about double the diameter of other abalones at the same length. Because of this, it also has a much bigger shell weight than other infant abalones at the same length. Otherwise, we can see that as the length of the abalone grows, the diameter and shell weight grow as well.

1.6 (5 points)

For each **sex**, create separate scatter plots of `length` and `diameter`. For each plot, also add a **linear** trendline to illustrate the relationship between the variables. Use the `facet_wrap()` function in R for this, and ensure that the plots are vertically stacked **not** horizontally. You should end up with a plot that looks like this: [2]

```r
ggplot(data = df, mapping = aes(x=length, y=diameter)) +
  geom_point() +
  geom_smooth(method = lm) +
  facet_wrap(~sex, dir = "v")
```

```
`geom_smooth()` using formula = 'y ~ x'
```



[2]Plot example for 1.6

Question 2

40 points

More advanced analyses using `dplyr`, `purrrr` and `ggplot2`

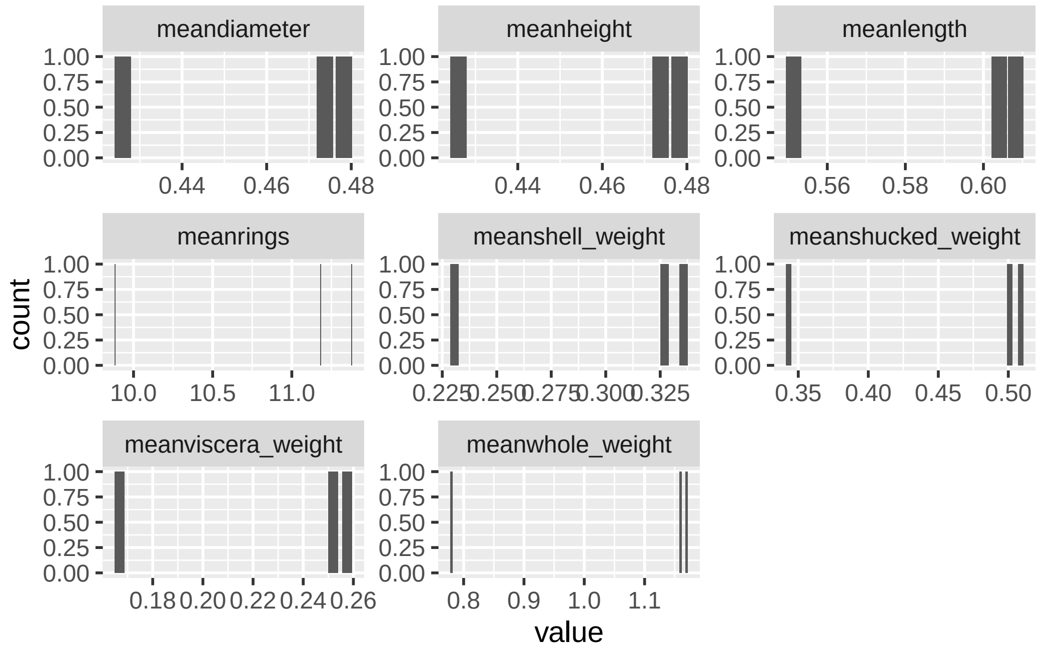
2.1 (10 points)

Filter the data to only include abalone with a length of at least 0.5 meters. Group the data by `sex` and calculate the mean of each variable for each group. Create a bar plot to visualize the mean values for each variable by `sex`.

```
df2 <-
  df %>%
  filter(length >= .5) %>%
  group_by(sex) %>%
  summarize(meanlength = mean(length),
            meandiameter = mean(diameter),
            meanheight = mean(diameter),
            meanwhole_weight = mean(whole_weight),
            meanshucked_weight = mean(shucked_weight),
            meanviscera_weight = mean(viscera_weight),
            meanshell_weight = mean(shell_weight),
            meanrings = mean(rings))

df2
```

```
# A tibble: 3 x 9
  sex   meanlength meandiameter meanhe~1 meanw~2 means~3 meanv~4 means~5 meanr~6
  <chr>      <dbl>        <dbl>    <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
1 F          0.608        0.478    0.478   1.17    0.501   0.258   0.336   11.4
2 I          0.551        0.426    0.426   0.780   0.343   0.167   0.231    9.88
3 M          0.604        0.474    0.474   1.16    0.509   0.252   0.327   11.2
# ... with abbreviated variable names 1: meanheight, 2: meanwhole_weight,
#   3: meanshucked_weight, 4: meanviscera_weight, 5: meanshell_weight,
#   6: meanrings
```

```
df2 %>%
  select(meanlength, meandiameter, meanheight, meanwhole_weight, meanshucked_weight, meanv
  gather() %>%
  ggplot(aes(x=value)) +
  facet_wrap(~key, scales = "free") +
  geom_bar()
```



DO THIS UGTNEJWKTHT2EGJLW KH2BTJLWK

2.2 (15 points)

Implement the following in a **single command**:

1. Temporarily create a new variable called `num_rings` which takes a value of:

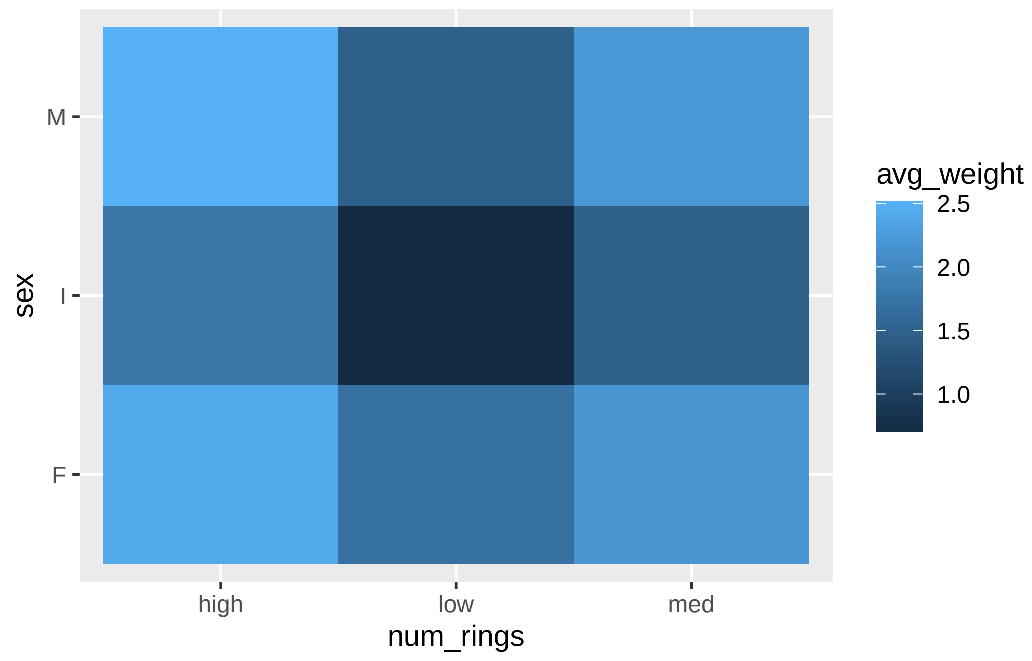
- `"low"` if `rings < 10`
- `"high"` if `rings > 20`, and
- `"med"` otherwise

2. Group `df` by this new variable and `sex` and compute `avg_weight` as the average of the `whole_weight + shucked_weight + viscera_weight + shell_weight` for each combination of `num_rings` and `sex`.

3. Use the `geom_tile()` function to create a tile plot of `num_rings` vs `sex` with the color indicating of each tile indicating the `avg_weight` value.

```r
df %>%
  mutate(num_rings = ifelse(rings < 10, "low",
                            ifelse(rings > 20, "high", "med"))) %>%
  group_by(sex, num_rings) %>%
  summarize(avg_weight = mean(whole_weight + shucked_weight + viscera_weight + shell_weigh
  ggplot(aes(x=num_rings, y=sex, fill=avg_weight)) +
  geom_tile()
```

```
`summarise()` has grouped output by 'sex'. You can override using the `.groups`
argument.
```



2.3 (5 points)

Make a table of the pairwise correlations between all the numeric variables rounded to 2 decimal points. Your final answer should look like this [3]

[3] Table for 2.3

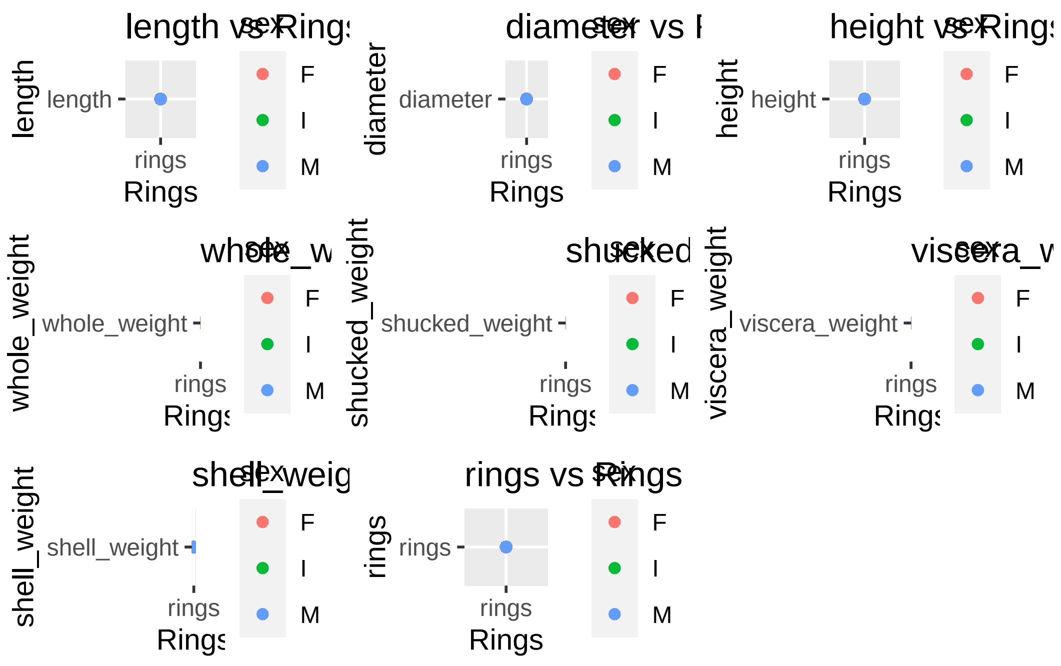
```
df3 <-
  df %>%
  select(length, diameter, height, whole_weight, shucked_weight, viscera_weight, shell_wei


table <- round(cor(df3), 2)
table
```

```
               length diameter height whole_weight shucked_weight
length           1.00     0.99   0.83         0.93           0.90
diameter         0.99     1.00   0.83         0.93           0.89
height           0.83     0.83   1.00         0.82           0.77
whole_weight     0.93     0.93   0.82         1.00           0.97
shucked_weight   0.90     0.89   0.77         0.97           1.00
viscera_weight   0.90     0.90   0.80         0.97           0.93
shell_weight     0.90     0.91   0.82         0.96           0.88
rings            0.56     0.58   0.56         0.54           0.42
               viscera_weight shell_weight rings
length                   0.90         0.90  0.56
diameter                 0.90         0.91  0.58
height                   0.80         0.82  0.56
whole_weight             0.97         0.96  0.54
shucked_weight           0.93         0.88  0.42
viscera_weight           1.00         0.91  0.50
shell_weight             0.91         1.00  0.63
rings                    0.50         0.63  1.00
```

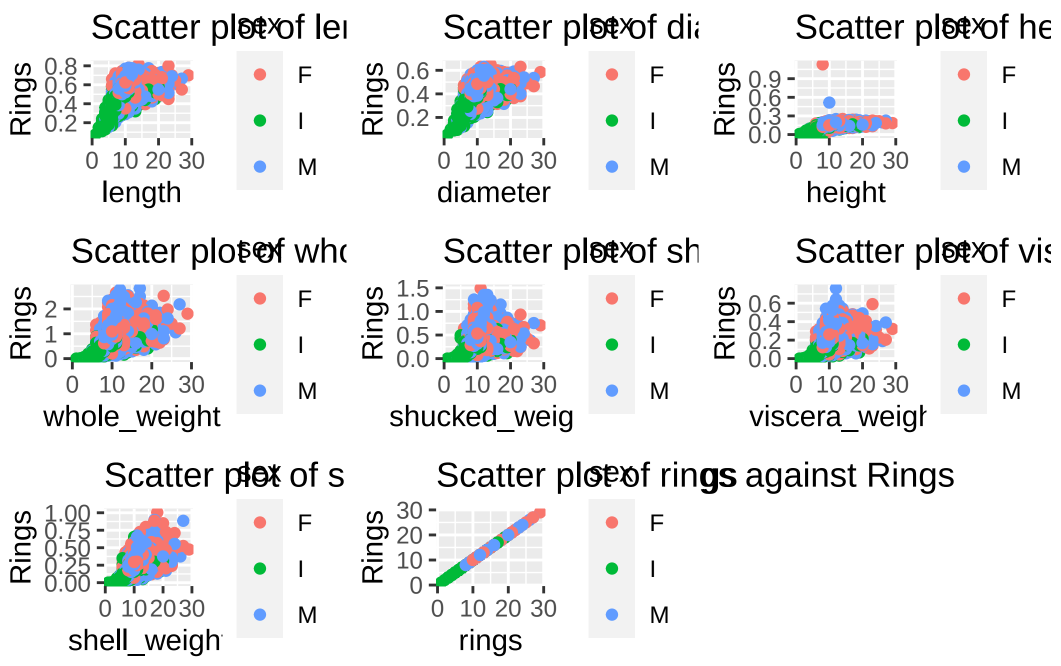
2.4 (10 points)

Use the `map2()` function from the `purrr` package to create a scatter plot for each *quantitative* variable against the number of `rings` variable. Color the points based on the `sex` of each abalone. You can use the `cowplot::plot_grid()` function to finally make the following grid of plots.

```
variables <- c("length", "diameter", "height", "whole_weight", "shucked_weight", "viscera_

plots <- map2(.x = "rings", .y = variables,
              .f = ~ ggplot(data = df, aes(x = .x, y = .y, color = sex)) +
                geom_point() +
                ggtitle(paste0(.y, " vs Rings")) +
                    xlab("Rings") +
                    ylab(.y))


# Create the plot grid
cowplot::plot_grid(plotlist = plots, ncol = 3)
```



```
plots <- abalone %>%
  select_if(is.numeric) %>%
  map2(., names(.), ~ ggplot(abalone, aes(x = rings, y = .x, color = sex)) +
          geom_point() +
          ggtitle(paste0("Scatter plot of ", .y, " against Rings")) +
          xlab(.y) +
          ylab("Rings"))

# Plot the grid of plots using cowplot
cowplot::plot_grid(plotlist = plots, ncol = 3)
```



DO THIS THWUIGKRQBIAJKLSHIOGRW;l

Question 3

30 points

Linear regression using `lm`

3.1 (10 points)

Perform a simple linear regression with `diameter` as the covariate and `height` as the response. Interpret the model coefficients and their significance values.

```r
model <- lm(height ~ diameter, data = df)
summary(model)
```

```
Call:
lm(formula = height ~ diameter, data = df)

Residuals:
     Min       1Q   Median       3Q      Max 
-0.15513 -0.01044 -0.00148  0.00852  1.00906 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) -0.003784   0.001512  -2.502   0.0124 *  
diameter     0.351346   0.003602  97.540   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.0231 on 4174 degrees of freedom
Multiple R-squared:  0.6951,	Adjusted R-squared:  0.695 
F-statistic:  9514 on 1 and 4174 DF,  p-value: < 2.2e-16
```

The y-intercept, β_0 - The mean height of a hypothetical abalone is -.0037 mm when the diameter is 0 mm

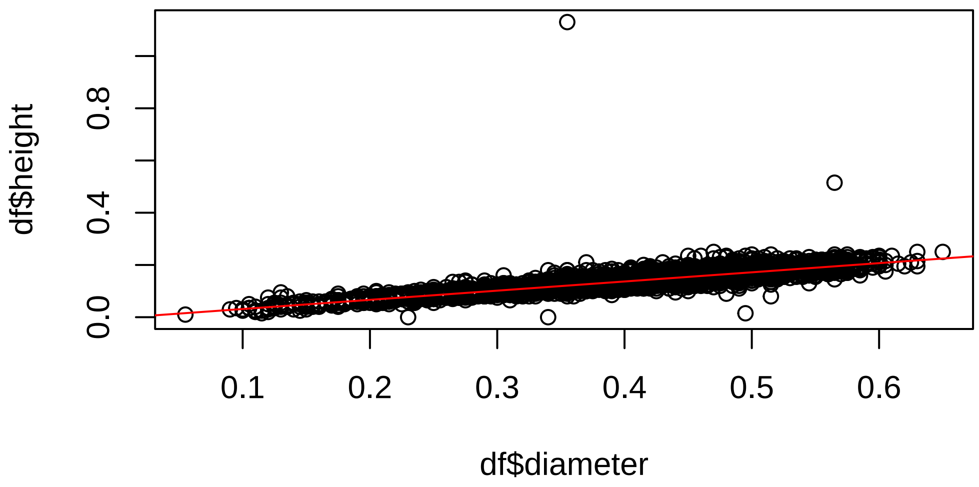
The slope, β_1 - For each additional mm in diameter, we expect the height of an abalone to increase by .3513 mm

Since REGYHAKJSB,M DO THIS HUGWIRLQJD,M

3.2 (10 points)

Make a scatterplot of `height` vs `diameter` and plot the regression line in `color="red"`. You can use the base `plot()` function in R for this. Is the linear model an appropriate fit for this relationship? Explain.

```r
plot(df$diameter, df$height)
abline(model, col="red")
```



Yes a linear model seems appropriate. The regression line follows the trend of the data really well and there is no curvature to the points in the plot

---

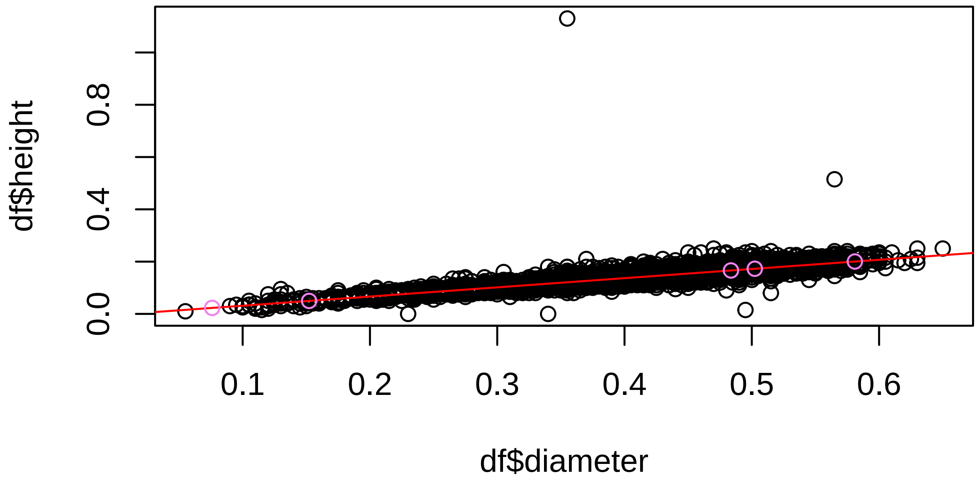
3.3 (10 points)

Suppose we have collected observations for "new" abalones with `new_diameter` values given below. What is the expected value of their `height` based on your model above? Plot these new observations along with your predictions in your plot from earlier using `color="violet"`

```
new_diameters <- c(
  0.15218946,
  0.48361548,
  0.58095513,
  0.07603687,
  0.50234599,
  0.83462092,
  0.95681938,
  0.92906875,
  0.94245437,
  0.01209518
)


predicted_height <- predict(model, data.frame(diameter = new_diameters))
predicted_height
```

```
           1            2            3            4            5            6 
0.0496872736 0.1661323358 0.2003321901 0.0229313989 0.1727132174 0.2894565404 
           7            8            9           10 
0.3323904273 0.3226403666 0.3273433448 0.0004657697 
```

```r
plot(df$diameter, df$height)
abline(model, col="red")
points(new_diameters, predicted_height, col = "violet")
```



Appendix

Session Information

Print your `R` session information using the following command

```
sessionInfo()
```

```
R version 4.2.1 (2022-06-23)
Platform: x86_64-apple-darwin17.0 (64-bit)
Running under: macOS Big Sur ... 10.16

Matrix products: default
BLAS:   /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRblas.0.dylib
LAPACK: /Library/Frameworks/R.framework/Versions/4.2/Resources/lib/libRlapack.dylib

locale:
[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats     graphics  grDevices datasets  utils     methods   base

other attached packages:
 [1] forcats_0.5.2   stringr_1.5.0   tibble_3.1.8    tidyverse_1.3.2
 [5] cowplot_1.1.1   purrr_1.0.1     dplyr_1.0.10    ggplot2_3.4.0
 [9] tidyr_1.2.1     readr_2.1.3

loaded via a namespace (and not attached):
 [1] lattice_0.20-45     lubridate_1.9.0     assertthat_0.2.1
 [4] digest_0.6.31       utf8_1.2.2          R6_2.5.1
 [7] cellranger_1.1.0    backports_1.4.1     reprex_2.0.2
[10] evaluate_0.20       httr_1.4.4          pillar_1.8.1
[13] rlang_1.0.6         googlesheets4_1.0.1 readxl_1.4.1
[16] rstudioapi_0.14     Matrix_1.5-1        rmarkdown_2.20
[19] labeling_0.4.2      splines_4.2.1       googledrive_2.0.0
[22] munsell_0.5.0       broom_1.0.2         compiler_4.2.1
[25] modelr_0.1.10       xfun_0.36           pkgconfig_2.0.3
[28] mgcv_1.8-41         htmltools_0.5.4     tidyselect_1.2.0
```

```
[31] fansi_1.0.3         crayon_1.5.2        tzdb_0.3.0
[34] dbplyr_2.2.1        withr_2.5.0         grid_4.2.1
[37] nlme_3.1-160        jsonlite_1.8.4      gtable_0.3.1
[40] lifecycle_1.0.3     DBI_1.1.3           magrittr_2.0.3
[43] scales_1.2.1        cli_3.6.0           stringi_1.7.12
[46] farver_2.1.1        renv_0.16.0-53      fs_1.5.2
[49] xml2_1.3.3          ellipsis_0.3.2      generics_0.1.3
[52] vctrs_0.5.1         tools_4.2.1         glue_1.6.2
[55] hms_1.1.2           fastmap_1.1.0       yaml_2.3.6
[58] timechange_0.2.0    colorspace_2.0-3    gargle_1.2.1
[61] rvest_1.0.3         knitr_1.41          haven_2.5.1
```