EDA-Challanges

1. Load the dataset data-wrangling and assigning the variable ‘d’

```
library (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   3.4.4     v tibble    3.2.1
v lubridate 1.9.3     v tidyr     1.3.1
v purrr     1.0.2
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becom
```

```
f <- "data-wrangling.csv"
d <- read_csv(f, col_names = TRUE)
```

```
Rows: 213 Columns: 23
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (6): Scientific_Name, Family, Genus, Species, Leaves, Fauna
dbl (17): Brain_Size_Species_Mean, Body_mass_male_mean, Body_mass_female_mea...

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
attach(d)
names(d)
```

```
 [1] "Scientific_Name"         "Family"
 [3] "Genus"                   "Species"
 [5] "Brain_Size_Species_Mean" "Body_mass_male_mean"
 [7] "Body_mass_female_mean"   "MeanGroupSize"
 [9] "AdultMales"              "AdultFemale"
[11] "GR_MidRangeLat_dd"       "Precip_Mean_mm"
[13] "Temp_Mean_degC"          "HomeRange_km2"
[15] "DayLength_km"            "Fruit"
[17] "Leaves"                  "Fauna"
[19] "Canine_Dimorphism"       "Feed"
[21] "Move"                    "Rest"
[23] "Social"
```

2. Create new variable BSD

```
d$BSD <- d$ Body_mass_male_mean/ d$Body_mass_female_mean
print(d)
```

```
# A tibble: 213 x 24
   Scientific_Name             Family       Genus Species Brain_Size_Species_M~1
   <chr>                       <chr>        <chr> <chr>                    <dbl>
 1 Allenopithecus_nigroviridis Cercopithec~ Alle~ nigrov~                   58.0
 2 Allocebus_trichotis         Cercopithec~ Allo~ tricho~                   NA
 3 Alouatta_belzebul           Atelidae     Alou~ belzeb~                   52.8
 4 Alouatta_caraya             Atelidae     Alou~ caraya                    52.6
 5 Alouatta_guariba            Atelidae     Alou~ guariba                   51.7
 6 Alouatta_palliata           Atelidae     Alou~ pallia~                   49.9
 7 Alouatta_pigra              Atelidae     Alou~ pigra                     51.1
 8 Alouatta_seniculus          Atelidae     Alou~ senicu~                   55.2
 9 Aotus_azarai                Cebidae      Aotus azarai                    20.7
10 Aotus_brumbacki             Cebidae      Aotus brumba~                   NA
# i 203 more rows
# i abbreviated name: 1: Brain_Size_Species_Mean
# i 19 more variables: Body_mass_male_mean <dbl>, Body_mass_female_mean <dbl>,
#   MeanGroupSize <dbl>, AdultMales <dbl>, AdultFemale <dbl>,
#   GR_MidRangeLat_dd <dbl>, Precip_Mean_mm <dbl>, Temp_Mean_degC <dbl>,
#   HomeRange_km2 <dbl>, DayLength_km <dbl>, Fruit <dbl>, Leaves <chr>,
#   Fauna <chr>, Canine_Dimorphism <dbl>, Feed <dbl>, Move <dbl>, ...
```

3. Create new variable sex-ratio

```r
d$Sex_ratio <- d$ AdultFemale/ d$ AdultMales
print(d)
```

```
# A tibble: 213 x 25
   Scientific_Name             Family       Genus Species Brain_Size_Species_M~1
   <chr>                       <chr>        <chr> <chr>                    <dbl>
 1 Allenopithecus_nigroviridis Cercopithec~ Alle~ nigrov~                   58.0
 2 Allocebus_trichotis         Cercopithec~ Allo~ tricho~                   NA
 3 Alouatta_belzebul           Atelidae     Alou~ belzeb~                   52.8
 4 Alouatta_caraya             Atelidae     Alou~ caraya                    52.6
 5 Alouatta_guariba            Atelidae     Alou~ guariba                   51.7
 6 Alouatta_palliata           Atelidae     Alou~ pallia~                   49.9
 7 Alouatta_pigra              Atelidae     Alou~ pigra                     51.1
 8 Alouatta_seniculus          Atelidae     Alou~ senicu~                   55.2
 9 Aotus_azarai                Cebidae      Aotus azarai                    20.7
10 Aotus_brumbacki             Cebidae      Aotus brumba~                   NA
# i 203 more rows
# i abbreviated name: 1: Brain_Size_Species_Mean
# i 20 more variables: Body_mass_male_mean <dbl>, Body_mass_female_mean <dbl>,
#   MeanGroupSize <dbl>, AdultMales <dbl>, AdultFemale <dbl>,
#   GR_MidRangeLat_dd <dbl>, Precip_Mean_mm <dbl>, Temp_Mean_degC <dbl>,
#   HomeRange_km2 <dbl>, DayLength_km <dbl>, Fruit <dbl>, Leaves <chr>,
#   Fauna <chr>, Canine_Dimorphism <dbl>, Feed <dbl>, Move <dbl>, ...
```

4. Create new variable DI (Defensibility Index)

```r
d$DI <- d$ DayLength_km/ d$ HomeRange_km2
print(d)
```

```
# A tibble: 213 x 26
   Scientific_Name             Family       Genus Species Brain_Size_Species_M~1
   <chr>                       <chr>        <chr> <chr>                    <dbl>
 1 Allenopithecus_nigroviridis Cercopithec~ Alle~ nigrov~                   58.0
 2 Allocebus_trichotis         Cercopithec~ Allo~ tricho~                   NA
 3 Alouatta_belzebul           Atelidae     Alou~ belzeb~                   52.8
 4 Alouatta_caraya             Atelidae     Alou~ caraya                    52.6
 5 Alouatta_guariba            Atelidae     Alou~ guariba                   51.7
 6 Alouatta_palliata           Atelidae     Alou~ pallia~                   49.9
 7 Alouatta_pigra              Atelidae     Alou~ pigra                     51.1
 8 Alouatta_seniculus          Atelidae     Alou~ senicu~                   55.2
 9 Aotus_azarai                Cebidae      Aotus azarai                    20.7
10 Aotus_brumbacki             Cebidae      Aotus brumba~                   NA
```

```
# i 203 more rows
# i abbreviated name: 1: Brain_Size_Species_Mean
# i 21 more variables: Body_mass_male_mean <dbl>, Body_mass_female_mean <dbl>,
#   MeanGroupSize <dbl>, AdultMales <dbl>, AdultFemale <dbl>,
#   GR_MidRangeLat_dd <dbl>, Precip_Mean_mm <dbl>, Temp_Mean_degC <dbl>,
#   HomeRange_km2 <dbl>, DayLength_km <dbl>, Fruit <dbl>, Leaves <chr>,
#   Fauna <chr>, Canine_Dimorphism <dbl>, Feed <dbl>, Move <dbl>, ...
```

5. Calculate Diameter of the home range for each species

```
d$home_range_diameter <- d$HomeRange_km2/ 2
d$home_range_area <- pi * (d$home_range_diameter^2)
d$DI <- d$DayLength_km/ d$HomeRange_km2
print(d)
```

```
# A tibble: 213 x 28
   Scientific_Name             Family       Genus Species Brain_Size_Species_M~1
   <chr>                       <chr>        <chr> <chr>                    <dbl>
 1 Allenopithecus_nigroviridis Cercopithec~ Alle~ nigrov~                   58.0
 2 Allocebus_trichotis         Cercopithec~ Allo~ tricho~                   NA
 3 Alouatta_belzebul           Atelidae     Alou~ belzeb~                   52.8
 4 Alouatta_caraya             Atelidae     Alou~ caraya                    52.6
 5 Alouatta_guariba            Atelidae     Alou~ guariba                   51.7
 6 Alouatta_palliata           Atelidae     Alou~ pallia~                   49.9
 7 Alouatta_pigra              Atelidae     Alou~ pigra                     51.1
 8 Alouatta_seniculus          Atelidae     Alou~ senicu~                   55.2
 9 Aotus_azarai                Cebidae      Aotus azarai                    20.7
10 Aotus_brumbacki             Cebidae      Aotus brumba~                   NA
# i 203 more rows
# i abbreviated name: 1: Brain_Size_Species_Mean
# i 23 more variables: Body_mass_male_mean <dbl>, Body_mass_female_mean <dbl>,
#   MeanGroupSize <dbl>, AdultMales <dbl>, AdultFemale <dbl>,
#   GR_MidRangeLat_dd <dbl>, Precip_Mean_mm <dbl>, Temp_Mean_degC <dbl>,
#   HomeRange_km2 <dbl>, DayLength_km <dbl>, Fruit <dbl>, Leaves <chr>,
#   Fauna <chr>, Canine_Dimorphism <dbl>, Feed <dbl>, Move <dbl>, ...
```

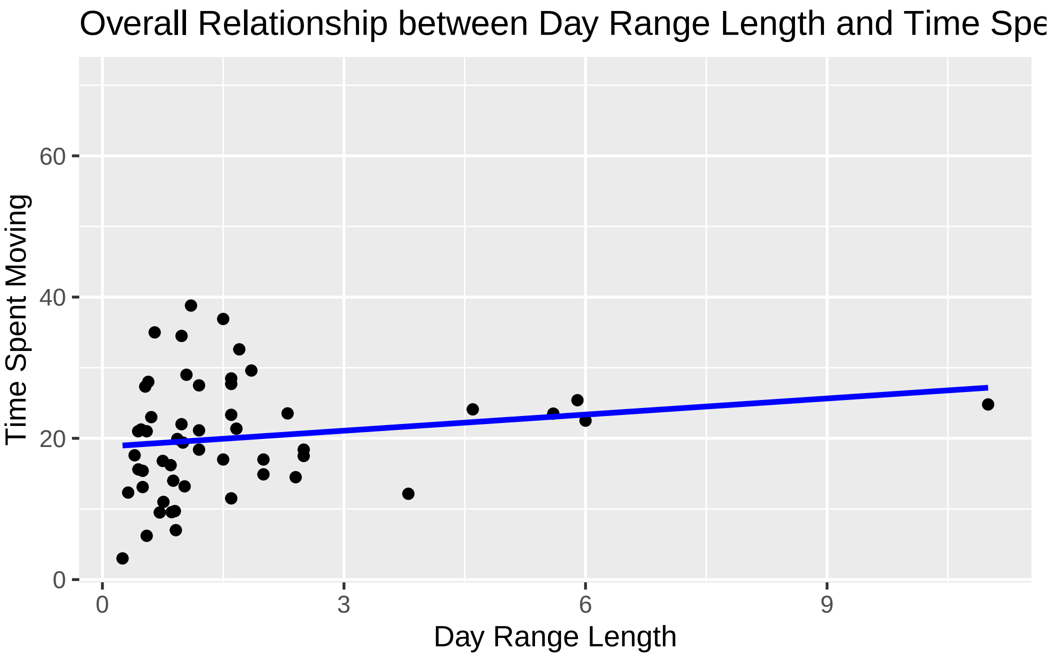
6. Create the plot for showing overall relationship between day range length and time spent moving

```
library(ggplot2)
overall_plot <- ggplot(d, aes(x = DayLength_km, y = Move)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "blue") +
  labs(title = "Overall Relationship between Day Range Length and Time Spent Moving",
       x = "Day Range Length",
       y = "Time Spent Moving")
       print(overall_plot)
```

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

Warning: Removed 160 rows containing non-finite values (`stat_smooth()`).

Warning: Removed 160 rows containing missing values (`geom_point()`).
```



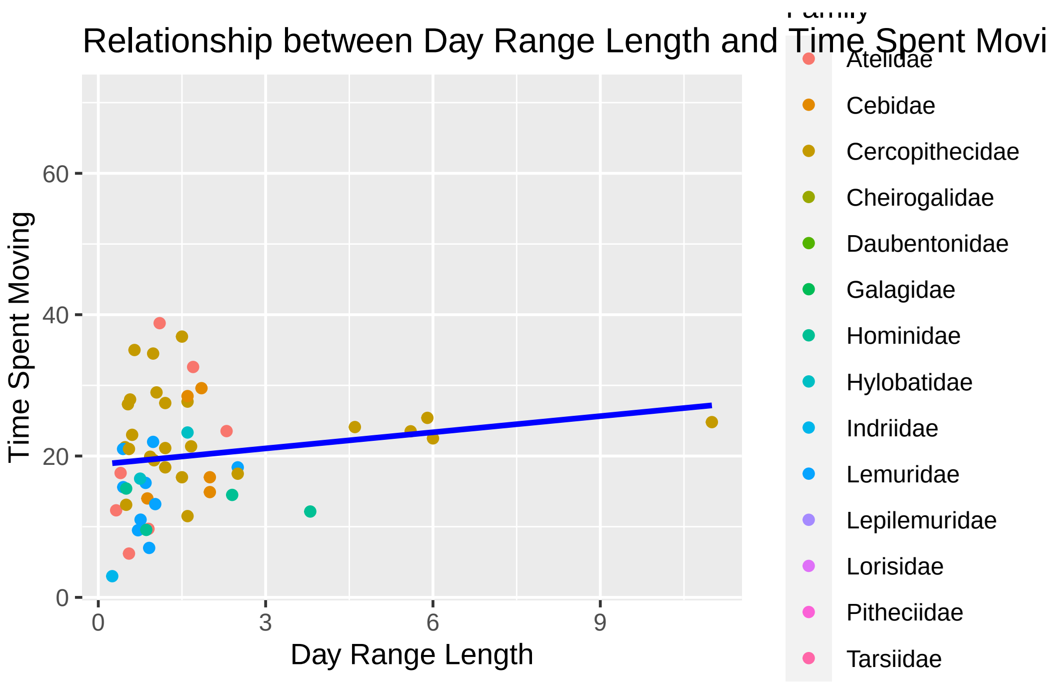
7. Create the plot by family

```
family_plot <- ggplot(d, aes(x = DayLength_km, y = Move, color = Family)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "blue") +
  labs(title = "Relationship between Day Range Length and Time Spent Moving by Primat
       x = "Day Range Length",
       y = "Time Spent Moving")
print(family_plot)
```

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

Warning: Removed 160 rows containing non-finite values (`stat_smooth()`).

Warning: Removed 160 rows containing missing values (`geom_point()`).
```

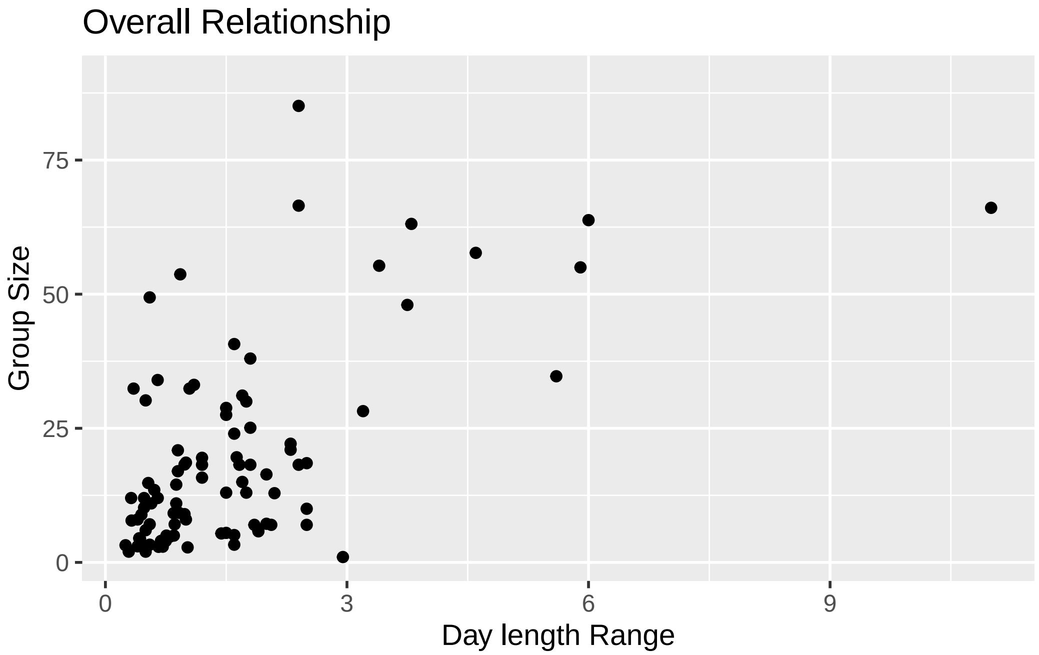


No , the species that spend more time moving does not travel farther overall.There is no linear relationship between time spent moving and the day range length, neither overall nor by family species. Yes, I think we should transform the either of the variables (logarithmic transformation may improve the linearity).

8. Create the plot to show relationship between day range length and time group size overall

```r
overall_plot <- ggplot(d, aes(x = DayLength_km, y = MeanGroupSize)) +
  geom_point() +
  labs(title = "Overall Relationship",
       x = "Day length Range",
       y = "Group Size")
print(overall_plot)
```

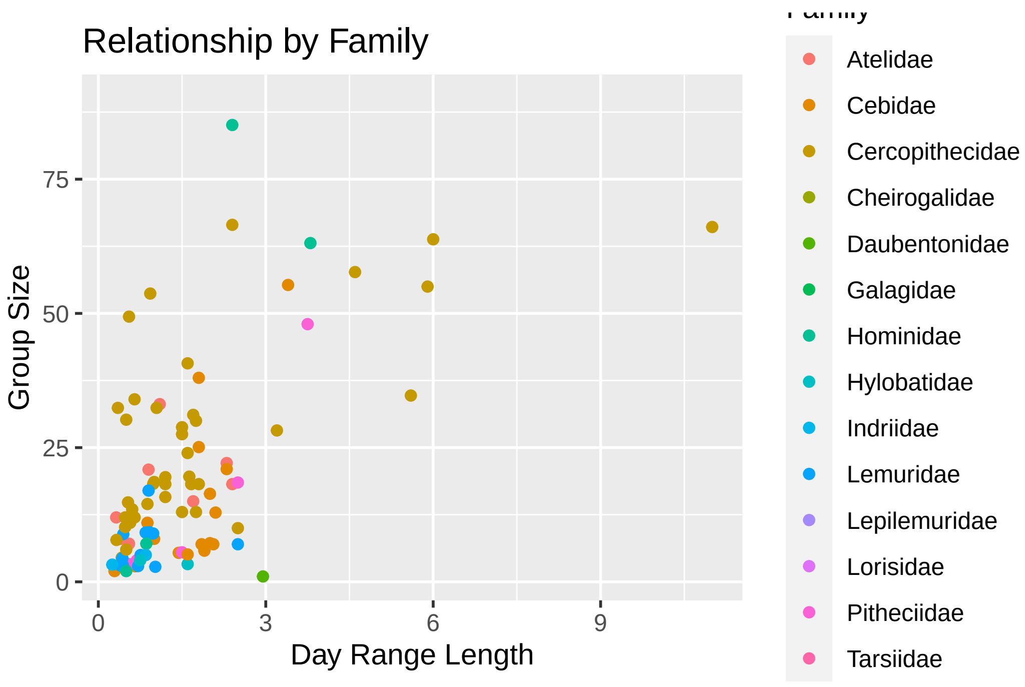
```
Warning: Removed 120 rows containing missing values (`geom_point()`).
```



9. Create the plot by family

```
family_plot <- ggplot(d, aes(x = DayLength_km, y = MeanGroupSize, color = Family)) +
  geom_point() +
  labs(title = "Relationship by Family",
       x = "Day Range Length",
       y = "Group Size")
print(family_plot)
```

```
Warning: Removed 120 rows containing missing values (`geom_point()`).
```

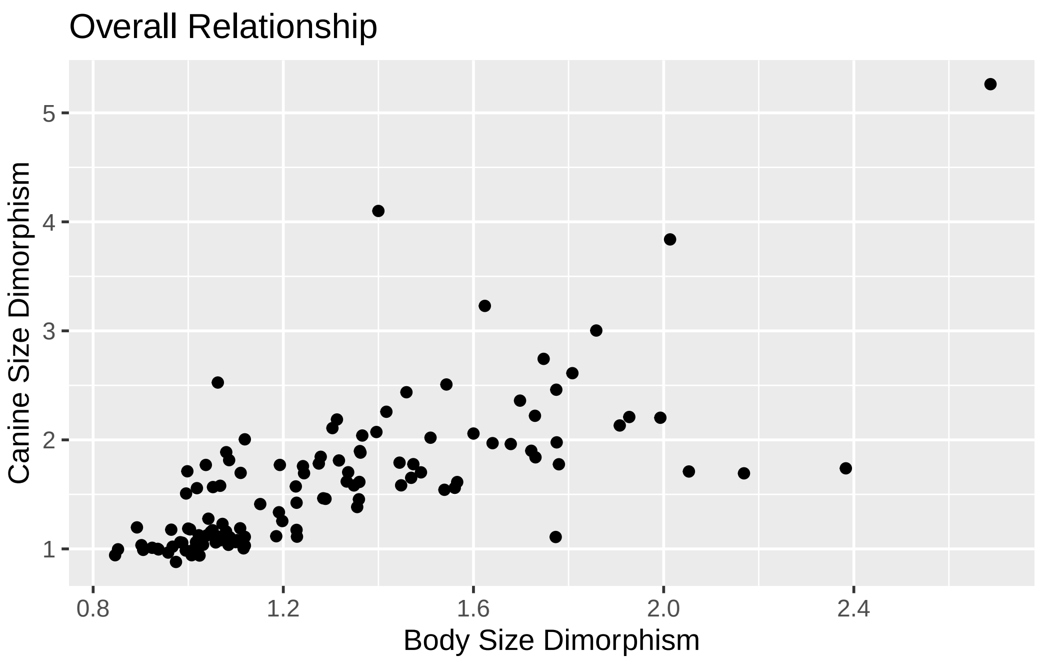


There is no linear relationship between Day range length and time group size neither overall, nor by family. In this plot also, transformation of either or both variable can help linearize relationships and improve the interpretability of the data.

10. Plot the relationship between body size dimorphism and canine dimorphism

```
overall_plot <- ggplot(d, aes(x = BSD, y = Canine_Dimorphism)) +
  geom_point() +
  labs(title = "Overall Relationship",
       x = "Body Size Dimorphism",
       y = "Canine Size Dimorphism")
print(overall_plot)
```

```
Warning: Removed 94 rows containing missing values (`geom_point()`).
```

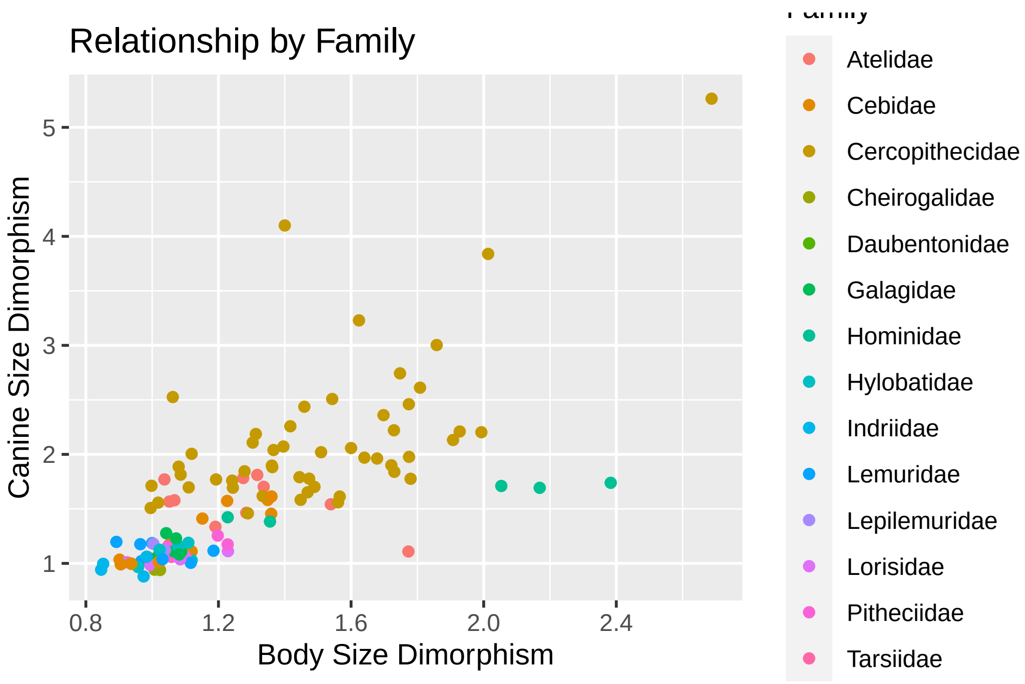


Yes, the taxa with greater size dimorphism also show greater canine dimorphism. There is a linear relationship between body size dimorphism and canine size dimorphism

11.Plot the relationship between body size dimorphism and canine dimorphism by family

```
family_plot <- ggplot(d, aes(x = BSD, y = Canine_Dimorphism, color = Family)) +
  geom_point() +
  labs(title = "Relationship by Family",
       x = "Body Size Dimorphism",
       y = "Canine Size Dimorphism")
print(family_plot)
```

```
Warning: Removed 94 rows containing missing values (`geom_point()`).
```



Linear relationship between Body size Dimorphism and canine size Dimorphism is observed greatly among Cercopithecidae family.

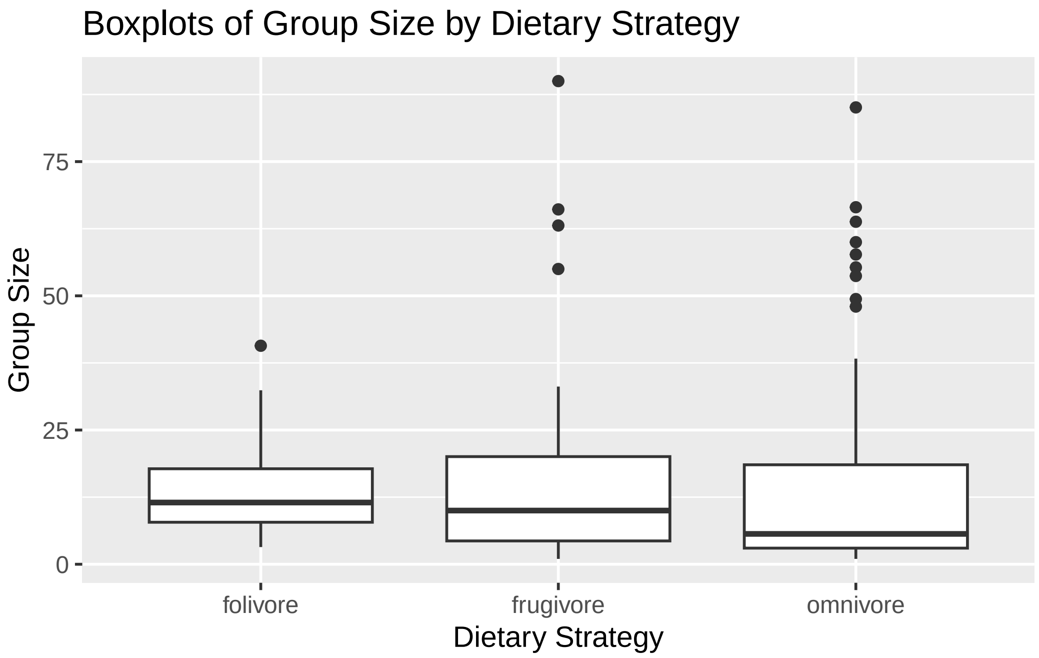
12.Creating a new variable named **diet_strategy** and the box-plots

```
d <- d%>%
  mutate(diet_strategy = case_when(
    Fruit > 50 ~ "frugivore",
    Leaves > 50 ~ "folivore",
    TRUE ~ "omnivore"
  ))
print(d)
```

```
# A tibble: 213 x 29
   Scientific_Name             Family       Genus Species Brain_Size_Species_M~1
   <chr>                       <chr>        <chr> <chr>                    <dbl>
 1 Allenopithecus_nigroviridis Cercopithec~ Alle~ nigrov~                   58.0
 2 Allocebus_trichotis         Cercopithec~ Allo~ tricho~                   NA
 3 Alouatta_belzebul           Atelidae     Alou~ belzeb~                   52.8
 4 Alouatta_caraya             Atelidae     Alou~ caraya                    52.6
 5 Alouatta_guariba            Atelidae     Alou~ guariba                   51.7
 6 Alouatta_palliata           Atelidae     Alou~ pallia~                   49.9
 7 Alouatta_pigra             Atelidae     Alou~ pigra                   51.1
 8 Alouatta_seniculus         Atelidae     Alou~ senicu~                 55.2
 9 Aotus_azarai               Cebidae      Aotus azarai                  20.7
10 Aotus_brumbacki            Cebidae      Aotus brumba~                 NA
# i 203 more rows
# i abbreviated name: 1: Brain_Size_Species_Mean
# i 24 more variables: Body_mass_male_mean <dbl>, Body_mass_female_mean <dbl>,
#   MeanGroupSize <dbl>, AdultMales <dbl>, AdultFemale <dbl>,
#   GR_MidRangeLat_dd <dbl>, Precip_Mean_mm <dbl>, Temp_Mean_degC <dbl>,
#   HomeRange_km2 <dbl>, DayLength_km <dbl>, Fruit <dbl>, Leaves <chr>,
#   Fauna <chr>, Canine_Dimorphism <dbl>, Feed <dbl>, Move <dbl>, ...
```

```
boxplot_plot <- ggplot(d, aes(x = diet_strategy, y = MeanGroupSize)) +
  geom_boxplot() +
  labs(title = "Boxplots of Group Size by Dietary Strategy",
       x = "Dietary Strategy",
       y = "Group Size")
print(boxplot_plot)
```

```
Warning: Removed 60 rows containing non-finite values (`stat_boxplot()`).
```



13. Loading my own dataset “Boxplot.csv” and calculating the summary statistics

```r
library (tidyverse)
f <- "Boxplot.csv"
d <- read_csv(f, col_names = TRUE)
```

```
Rows: 120 Columns: 4
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (1): Group
dbl (3): Frequency, Delay, Absorbance

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
attach(d)
names(d)
```

```
[1] "Frequency"  "Group"      "Delay"      "Absorbance"
```

```r
nrow(d)
```

```
[1] 120
```

```r
ncol(d)
```

```
[1] 4
```

```r
variable_names <- names(d)
print(variable_names)
```

```
[1] "Frequency"  "Group"      "Delay"      "Absorbance"
```

```r
numeric_variables <- names(d)[sapply(d, is.numeric)]
summary_list <- list()
for (variable in numeric_variables) {
  num_obs <- sum(!is.na(d[[variable]]))
  mean_val <- mean(d[[variable]], na.rm = TRUE)
  sd_val <- sd(d[[variable]], na.rm = TRUE)
  five_num_summary <- summary(d[[variable]], na.rm = TRUE)
```

```
    summary_list[[variable]] <- list(
      variable = variable,
      num_obs = num_obs,
      mean_val = mean_val,
      sd_val = sd_val,
      five_num_summary = five_num_summary
    )
  }
  for (variable_summary in summary_list) {
    print(paste("Variable:", variable_summary$variable))
    print(paste("Number of observations:", variable_summary$num_obs))
    print(paste("Mean:", variable_summary$mean_val))
    print(paste("Standard Deviation:", variable_summary$sd_val))
    print("Five-Number Summary:")
    print(variable_summary$five_num_summary)
  }
```

```
[1] "Variable: Frequency"
[1] "Number of observations: 120"
[1] "Mean: 1810.5"
[1] "Standard Deviation: 689.416816025318"
[1] "Five-Number Summary:"
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   1000    1310    1707    1810    2207    2828 
[1] "Variable: Delay"
[1] "Number of observations: 97"
[1] "Mean: 126.638350515464"
[1] "Standard Deviation: 62.0801261254426"
[1] "Five-Number Summary:"
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
  12.25   83.71  120.71  126.64  175.58  283.58      23 
[1] "Variable: Absorbance"
[1] "Number of observations: 108"
[1] "Mean: 0.541361111111111"
[1] "Standard Deviation: 0.164624322156487"
[1] "Five-Number Summary:"
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.    NA's 
 0.1790  0.4255  0.5435  0.5414  0.6615  0.8820      12 
```

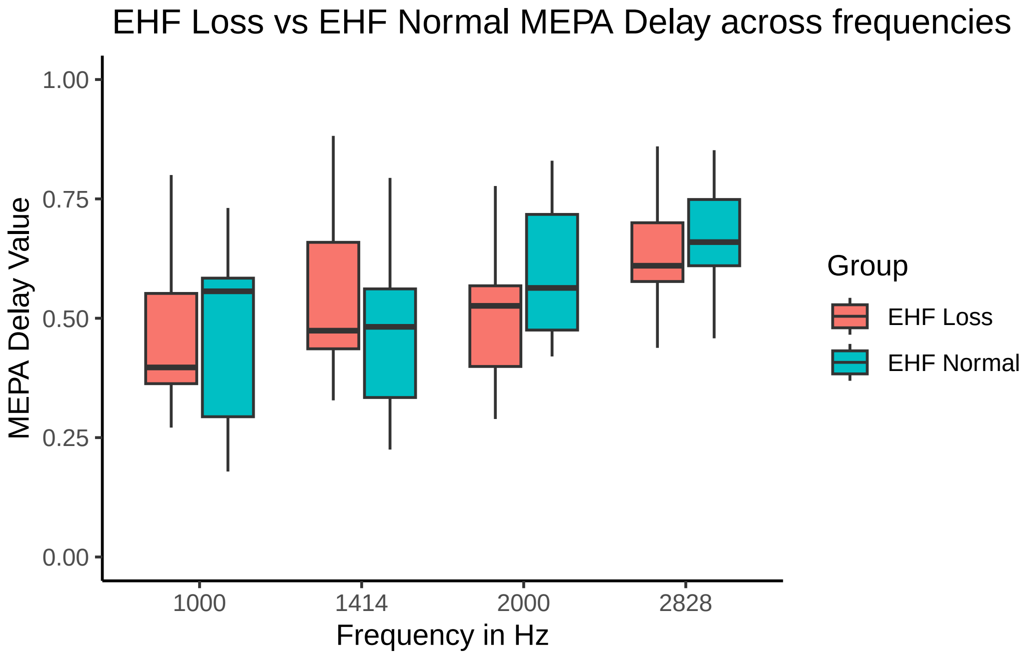
14. Ploting box-plot for my own dataset “Boxplot.csv”

```r
library(tidyverse)
f <- "Boxplot.csv"
d <- read_csv(f, col_names = TRUE)
```

```
Rows: 120 Columns: 4
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (1): Group
dbl (3): Frequency, Delay, Absorbance

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
ggplot(d, aes(x = as.factor(Frequency), y = Absorbance, fill = Group)) +
  geom_boxplot(width = 0.7, outlier.shape = NA, na.rm = TRUE) +
  labs(x = "Frequency in Hz", y = "MEPA Delay Value",
       title = " EHF Loss vs EHF Normal MEPA Delay across frequencies") +
  theme_classic() +
  ylim(0, 1) +
  theme(strip.text = element_blank())
```


EHF Loss vs EHF Normal MEPA Delay across frequencies
MEPA Delay Value
Frequency in Hz
Group
EHF Loss
EHF Normal