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 <- "https://raw.githubusercontent.com/difiore/ada-2024-datasets/main/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. Calculate Diameter of the home range for each species

```r
d$home_range_diameter <- 2 * sqrt(d$HomeRange_km2 / pi)
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. Create new variable DI (Defensibility Index)

```
d$DI <- d$DayLength_km / d$home_range_diameter
print(d)
```

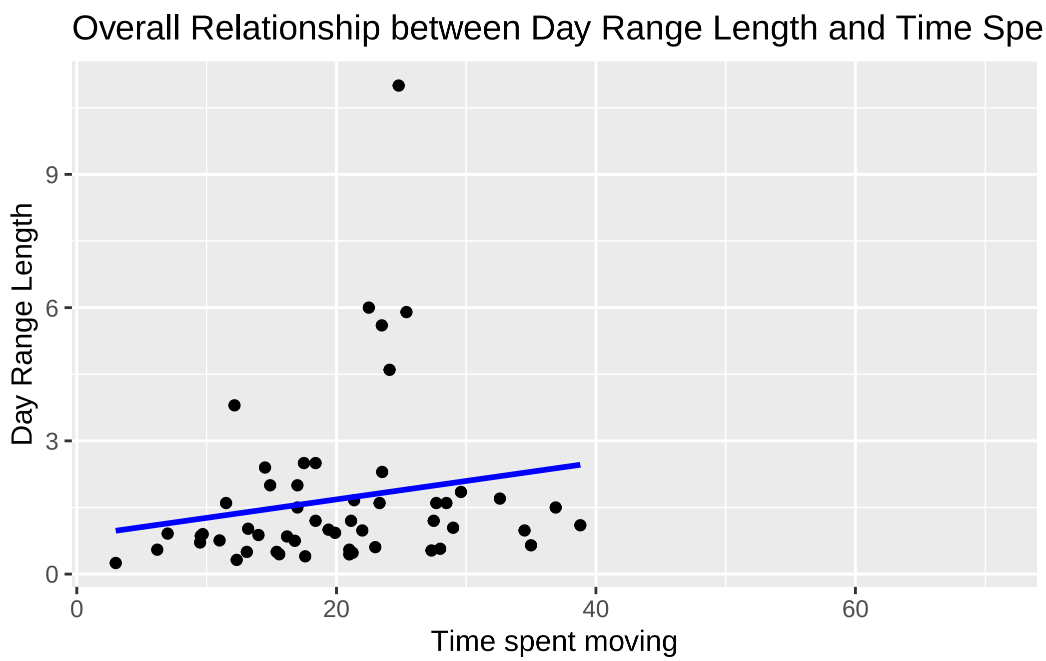
```
# A tibble: 213 x 27
   Scientific_Name              Family       Genus Species Brain_Size_Species_M~1
   <chr>                        <chr>        <chr> <chr>                    <dbl>
 1 Allenopithecus_nigroviridis Cercopithec~ Alle~ nigrov~                   58.0
 2 Allocebus_trichotis          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 22 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

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

```
         y = "Day Range Length")
         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()`).
```



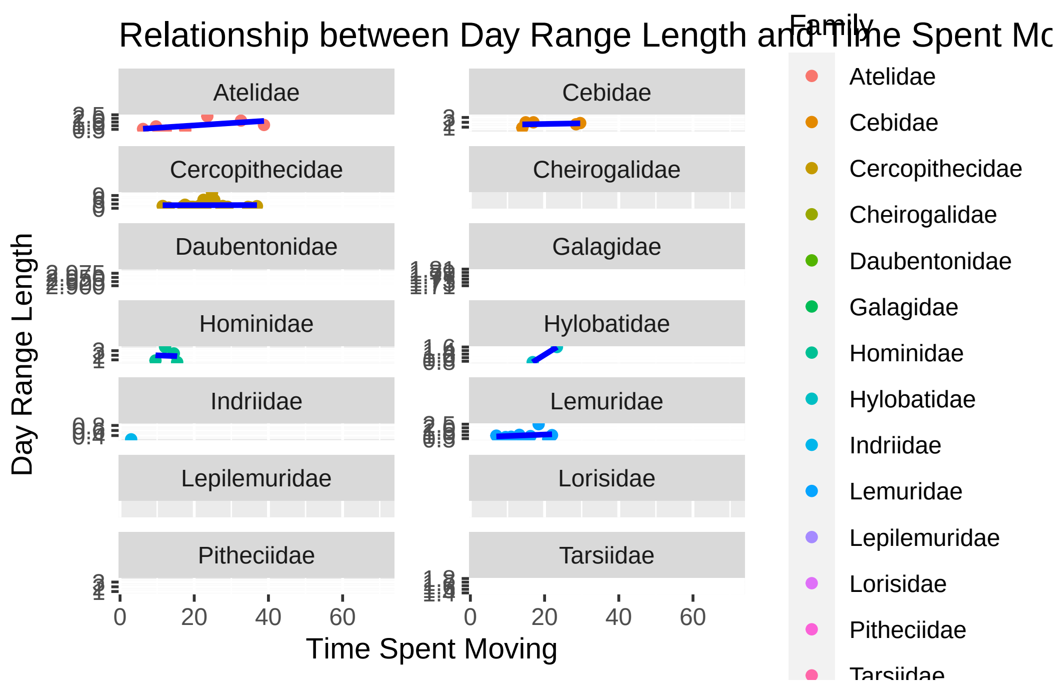
7. Create the plot by family

```
family_plot <- ggplot(d, aes(x = Move, y = DayLength_km, color = Family)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "blue") +
  facet_wrap(~Family, scales = "free_y", ncol = 2) +
  labs(title = "Relationship between Day Range Length and Time Spent Moving by Primat
       x = "Time Spent Moving",
       y = "Day Range Length")

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, overall .However, when we see the relationship by family, Atelidae, cebidae, and Hylobatidae family shows some degree of linear relationship. Yes, I think we should transform the either of the variables (logarithmic transformation may improve the linearity).

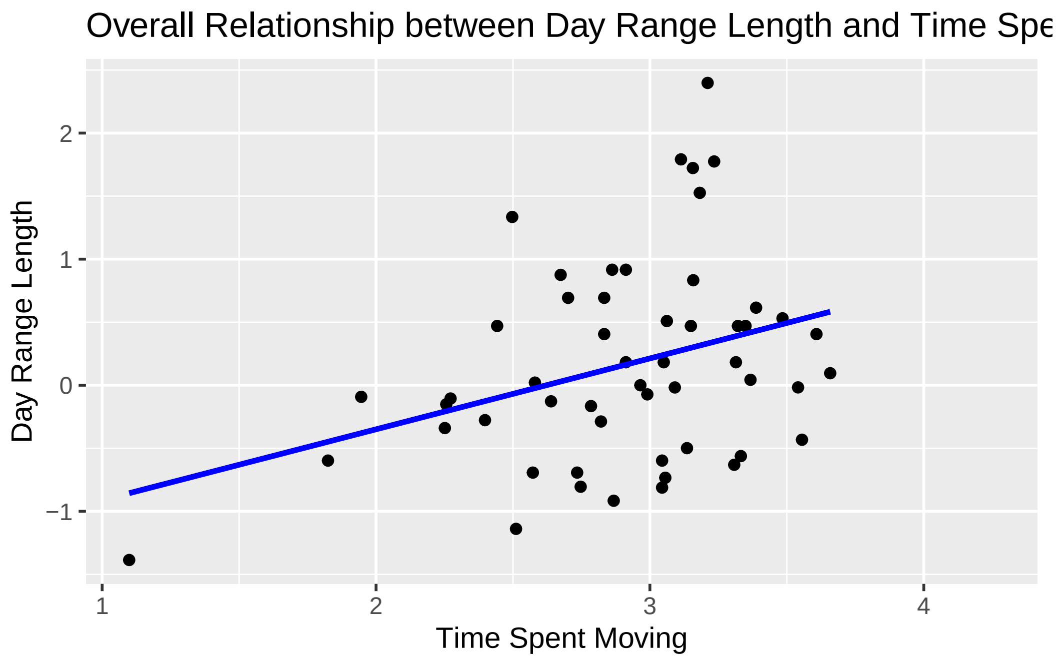
8. Applying logarithmic transformation to both variable

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



The logarithmic scale improved the linearity

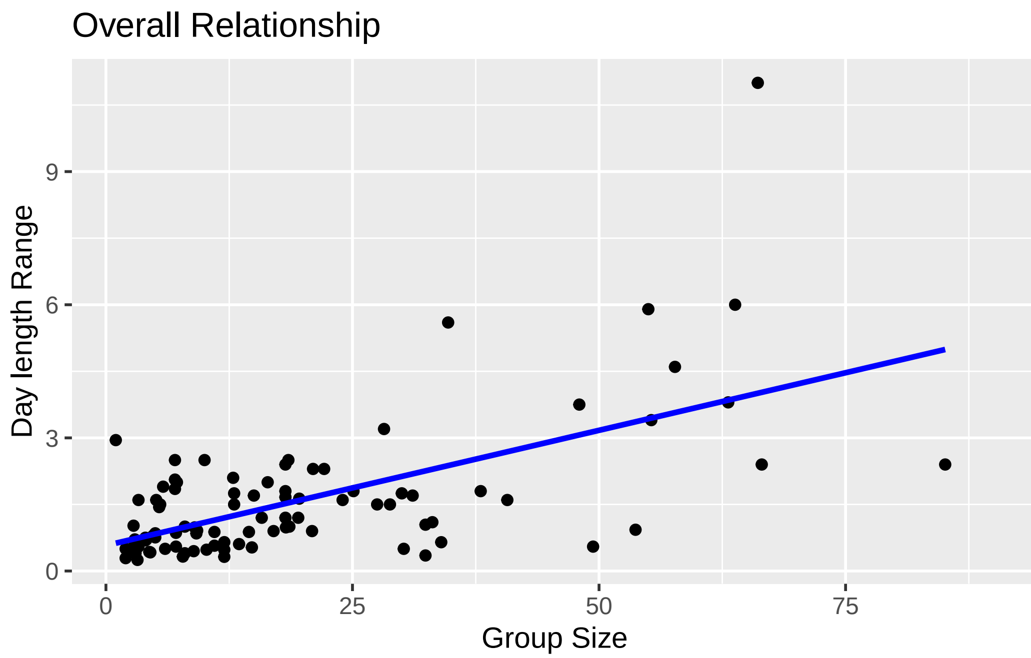
```
9.  Create the plot to show relationship between day range length and time group size overal
```

```
overall_plot <- ggplot(d, aes(x =MeanGroupSize , y = DayLength_km)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "blue") +
  labs(title = "Overall Relationship",
       x = "Group Size",
       y = "Day length Range")
print(overall_plot)
```

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

```
Warning: Removed 120 rows containing non-finite values (`stat_smooth()`).
```

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



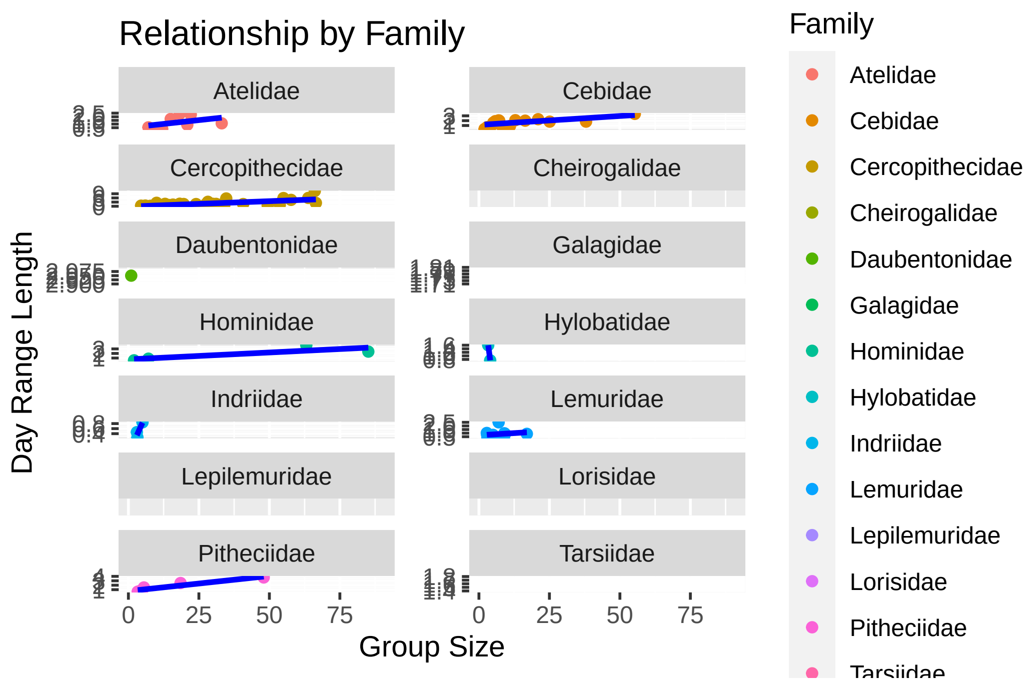
9. Create the plot by family

```
family_plot <- ggplot(d, aes(x =MeanGroupSize , y = DayLength_km, color = Family)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "blue") +
   facet_wrap(~Family, scales = "free_y", ncol = 2) +
  labs(title = "Relationship by Family",
       x = "Group Size",
       y = "Day Range Length")
print(family_plot)
```

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

```
Warning: Removed 120 rows containing non-finite values (`stat_smooth()`).
```

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

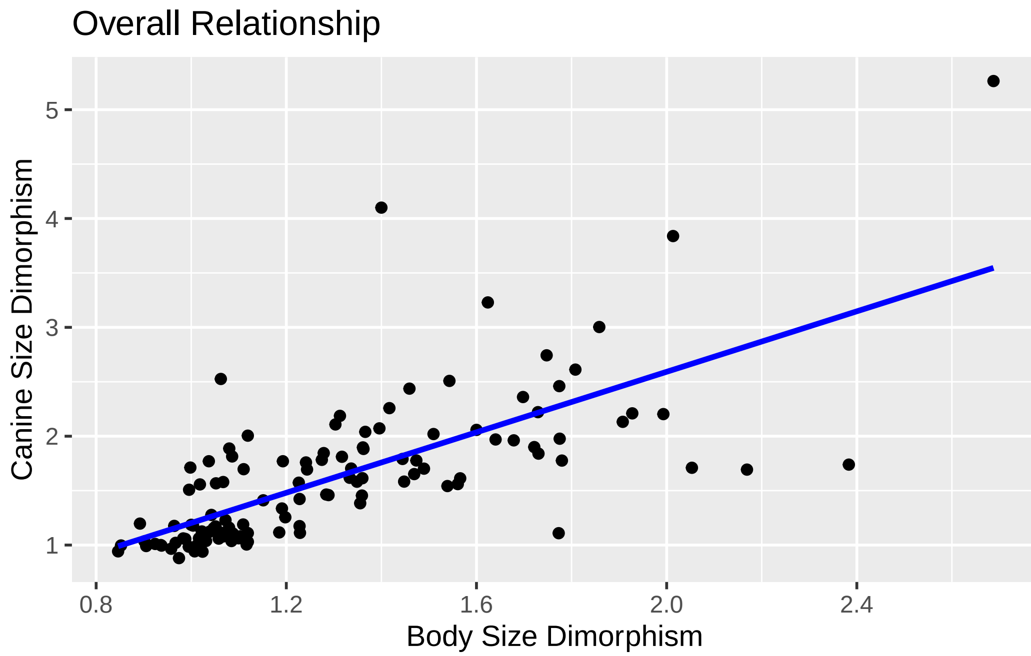


There is some degree of positive linear relationship between Day range length and time group size overall. In this plot, when relationship is analyzed by family, positive linear relationship is seen among Atelidae, Cebidae, cercopithecidae, hominidae, Indriidae. and Pithecidae, and negative relationship is seen in Hylobatidae family. In my opinion, transformation off data is not required.

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

```
overall_plot <- ggplot(d, aes(x = BSD, y = Canine_Dimorphism)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "blue") +
  labs(title = "Overall Relationship",
       x = "Body Size Dimorphism",
       y = "Canine Size Dimorphism")
print(overall_plot)
```

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

Warning: Removed 94 rows containing non-finite values (`stat_smooth()`).

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

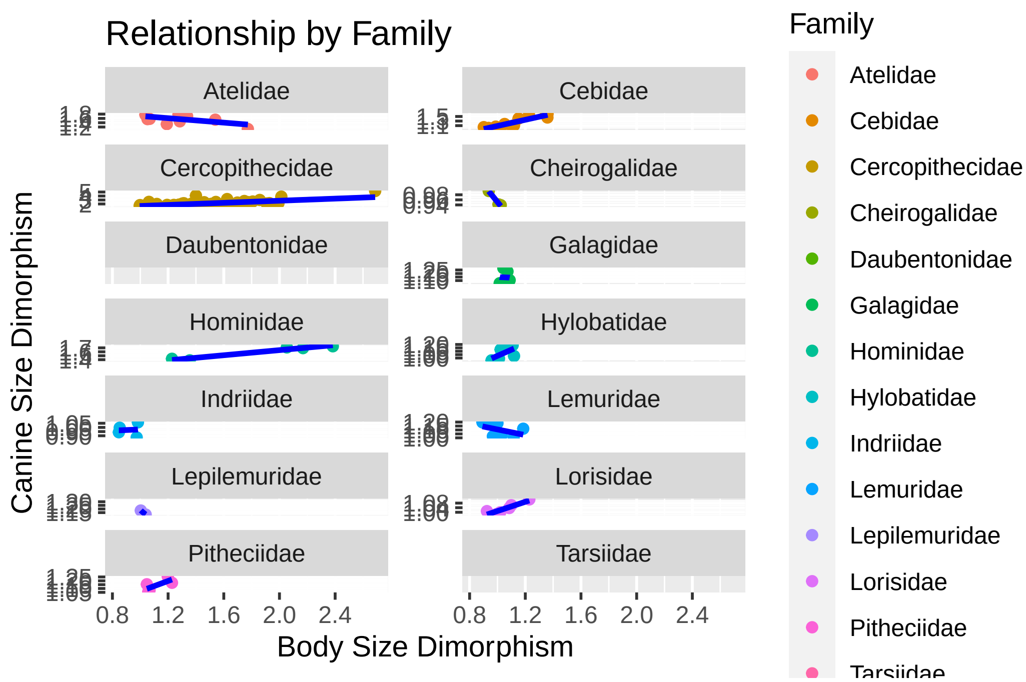
11.Plot the relationship between body size dimorphism and canine dimorphism by family

```
family_plot <- ggplot(d, aes(x = BSD, y = Canine_Dimorphism, color = Family)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, color = "blue") +
  facet_wrap(~Family, scales = "free_y", ncol = 2) +
  labs(title = "Relationship by Family",
       x = "Body Size Dimorphism",
       y = "Canine Size Dimorphism")
print(family_plot)
```

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

```
Warning: Removed 94 rows containing non-finite values (`stat_smooth()`).
```

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



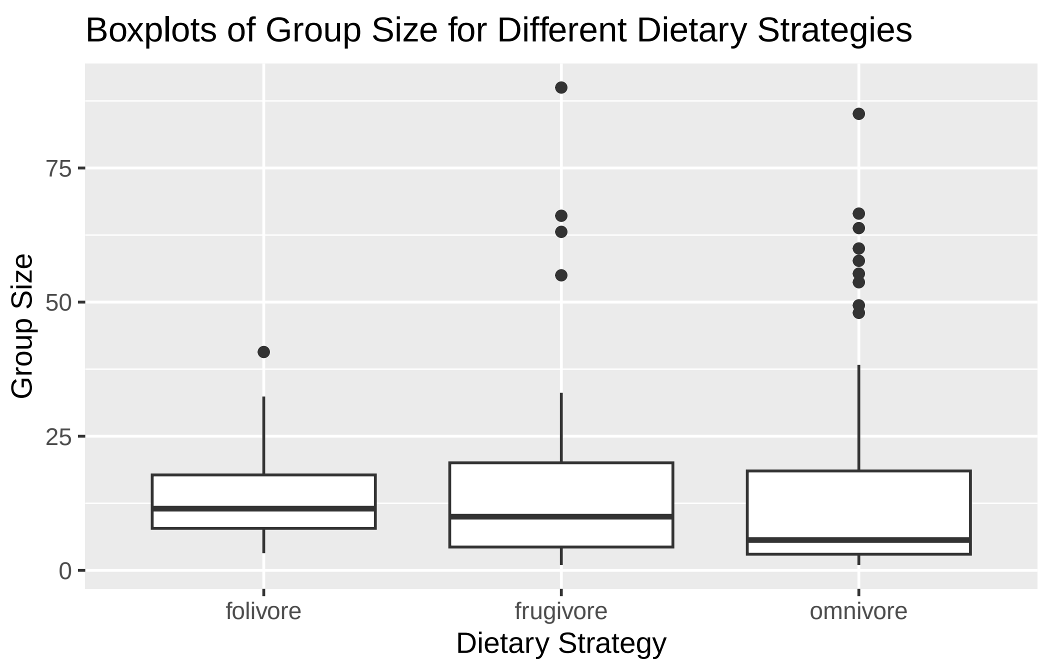
Positive Linear relationship between Body size Dimorphism and canine size Dimorphism is observed among Cebidae, Cercopithecidae, Hominidae,Hylobatidae, Pitheciidae, and Lorisidae family. However, negative linear relationship is observed among Atelidae, Lemuridae, and cheirogalidae family.

12.Create a new variable named **diet_strategy** that is "frugivore" if fruits make up >50% of the diet, "folivore" if leaves make up >50% of the diet, and "omnivore" if neither of these is true.

```
library(dplyr)
library(ggplot2)


# Creating the new variable diet_strategy
d <- d %>%
  mutate(diet_strategy = case_when(
    Fruit > 50 ~ "frugivore",
    Leaves > 50 ~ "folivore",
    TRUE ~ "omnivore"
  ))

# Updating omnivore category to exclude species where both Fruit and Leaves > 50%
```

```r
d <- d %>%
  mutate(diet_strategy = case_when(
    diet_strategy == "omnivore" & (is.na(Fruit) | Fruit <= 50) & (is.na(Leaves) | Leaves <
    TRUE ~ diet_strategy
  ))

# Create boxplots
boxplot_plot <- ggplot(d, aes(x = diet_strategy, y = MeanGroupSize)) +
  geom_boxplot() +
  labs(title = "Boxplots of Group Size for Different Dietary Strategies",
       x = "Dietary Strategy",
       y = "Group Size")
print(boxplot_plot)
```

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



13. In one line of code, using {dplyr} verbs and the forward pipe (`%>%` or `|>`) operator, do the following:

```r
library(dplyr)
library(readr)
```

```r
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.
```

```r
D <- d %>%
  mutate(Binomial = paste(Genus, Species, sep = " ")) %>%
  select(Binomial, Family, Brain_Size_Species_Mean, Body_mass_male_mean) %>%
  group_by(Family) %>%
  summarize(
    Avg_Brain_size_species_mean = mean(Brain_Size_Species_Mean, na.rm = TRUE),
    Avg_Body_mass_male_mean = mean(Body_mass_male_mean, na.rm = TRUE)
  ) %>%
  arrange(Avg_Brain_size_species_mean)
D
```

```
# A tibble: 14 x 3
   Family          Avg_Brain_size_species_mean Avg_Body_mass_male_mean
   <chr>                                 <dbl>                   <dbl>
 1 Tarsiidae                              3.26                     131
 2 Cheirogalidae                          4.04                     193.
 3 Galagidae                              5.96                     395.
 4 Lepilemuridae                          7.27                     792
 5 Lorisidae                              8.67                     512.
 6 Lemuridae                             23.1                     2077.
 7 Cebidae                               23.9                     1012.
 8 Indriidae                             27.3                     3638.
 9 Daubentonidae                         44.8                     2620
10 Pitheciidae                           56.3                     1955.
11 Atelidae                              80.6                     7895.
12 Cercopithecidae                       85.4                     9543.
13 Hylobatidae                          101.                      6926.
14 Hominidae                            410.                     98681.
```

14. 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 
```

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

```
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)
```