EDA-challenge

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Explore and Wrangle Data

Load the "data-wrangling.csv" dataset from **this URL** as a tabular data structure named **d** and look at the variables it contains

```r
library(tidyverse)
```

```
Warning: package 'readr' was built under R version 4.2.3
```

```
Warning: package 'dplyr' was built under R version 4.2.3
```

```
Warning: package 'stringr' was built under R version 4.2.3
```

```
-- 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     1.3.0
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
```

```r
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.
```

```r
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"
```

Create new variables - **BSD** (body size dimorphism), the ratio of mean male to female body mass - **sex_ratio**, the ratio of the number of adult females to adult males in a typical group - **DI** (for "defensibility index"), the ratio of day range length to the diameter of the home range

```r
d <- d %>%
  mutate(BSD = Body_mass_male_mean/Body_mass_female_mean,
         sex_ratio = AdultFemale/AdultMales,
         DI = DayLength_km/(sqrt(HomeRange_km2/pi)*2)) # sqrt(Area/pi)*2 = d
```

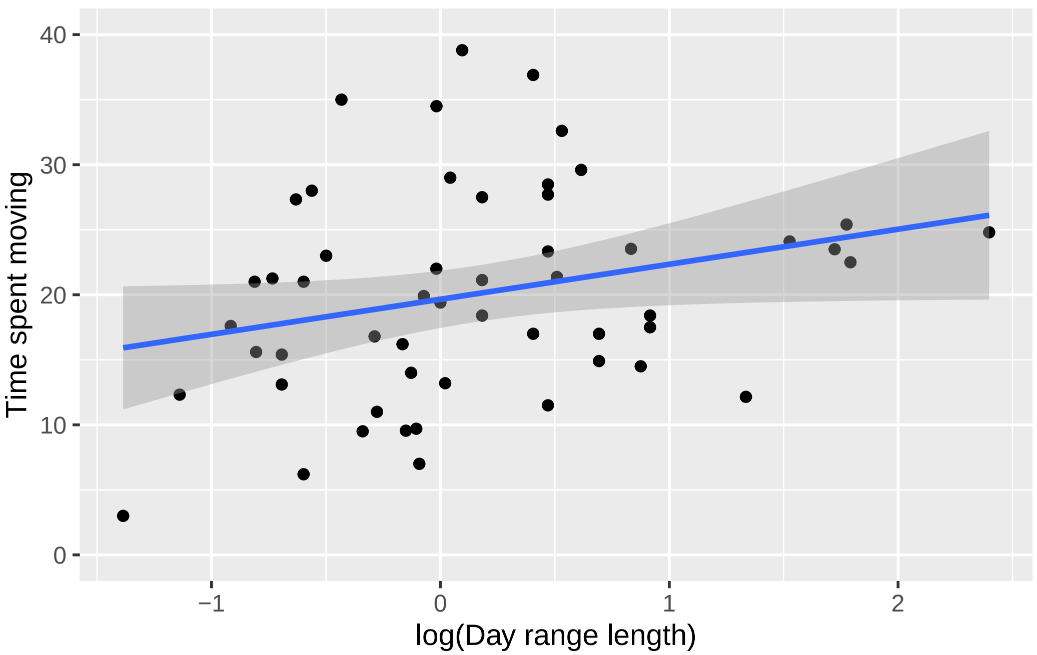
Plot the relationship between **day range length** and **time spent moving**, for these primate species overall and by family. - Do species that spend more time moving travel farther overall? *A: Yes, based on regression line* - How about within any particular primate family? *A: Yes for Atelidae, Hylobatidae, Cebidae* - Should you transform either of these variables? *A: log transformed day range length*

```
library(ggplot2)
library(cowplot) # to show graphs side by side
```

```
Warning: package 'cowplot' was built under R version 4.2.3


Attaching package: 'cowplot'

The following object is masked from 'package:lubridate':

    stamp
```

```
plot1 <- ggplot(data = d,
            aes(x = log(DayLength_km),
                y = Move)) +  # build a plot object
  xlab("log(Day range length)") + ylab("Time spent moving") + # modify the axis labels
  geom_point(na.rm = TRUE) + # make a scatterplot
  geom_smooth(method = "lm", na.rm = TRUE) + # add a regression line
  ylim(0, 40) + # set y-axis range
  theme(legend.title = element_blank()) # modify the legend
plot1 # plot the object
```

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

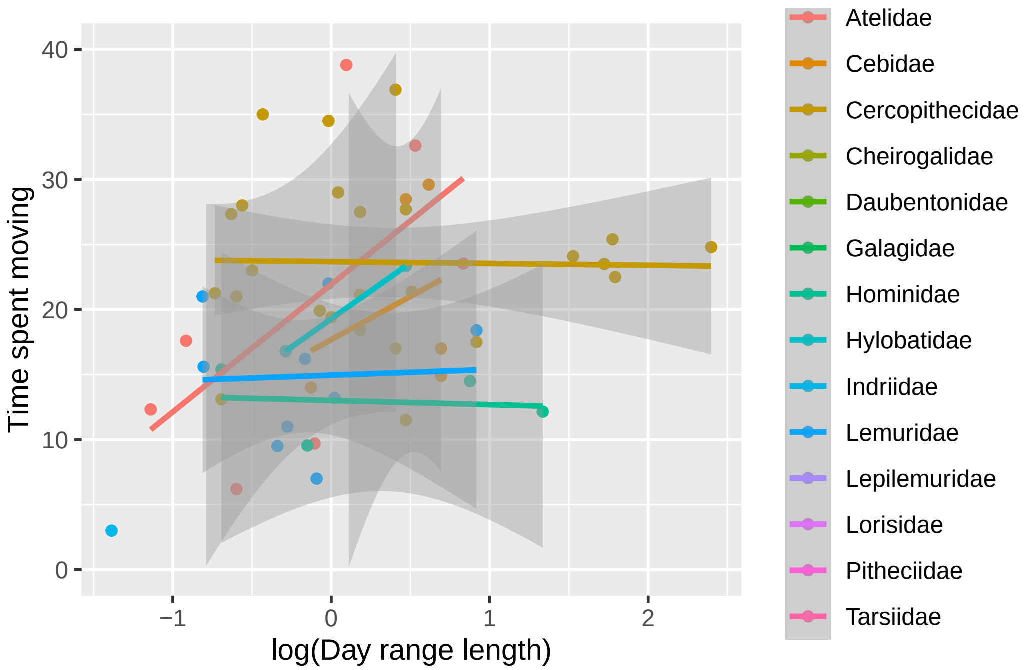


```r
plot2 <- ggplot(data = d,
            aes(x = log(DayLength_km),
                y = Move,
                color = factor(Family))) +  # build a plot object and color points by Family
  xlab("log(Day range length)") + ylab("Time spent moving") + # modify the axis labels
  geom_point(na.rm = TRUE) + # make a scatterplot
  geom_smooth(method = "lm", na.rm = TRUE) + # add a regression line
  ylim(0, 40) + # set y-axis range
  theme(legend.title = element_blank()) # modify the legend
plot2 # plot the object
```

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

```
Warning in qt((1 - level)/2, df): NaNs produced
```

```
Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning
-Inf
```



```r
plot_grid(plot1, plot2, rel_widths = c(1, 1.5), labels = "AUTO")
```

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

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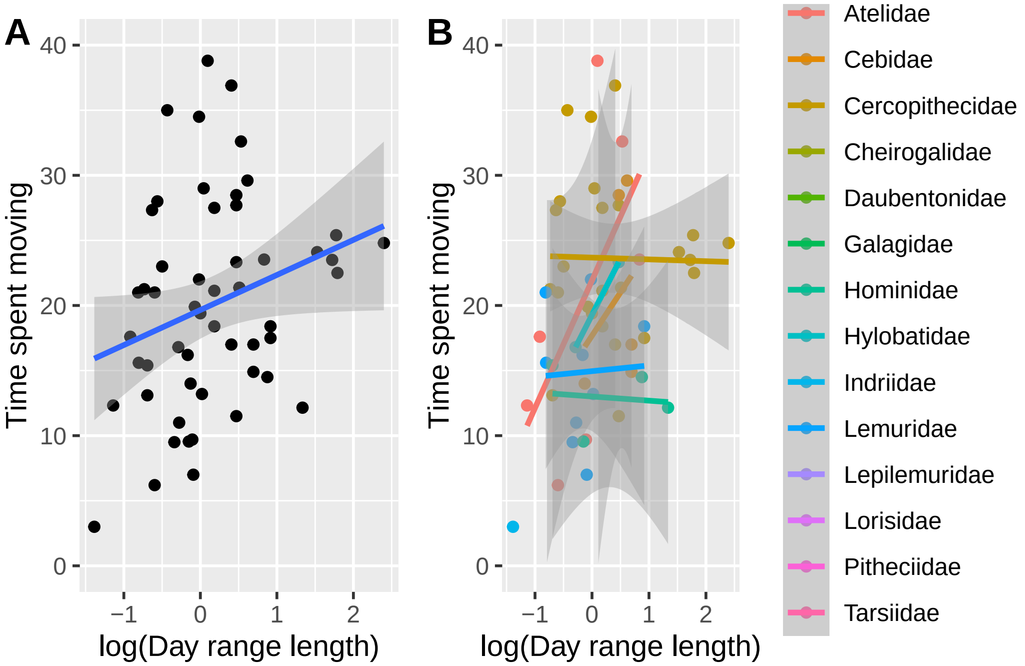
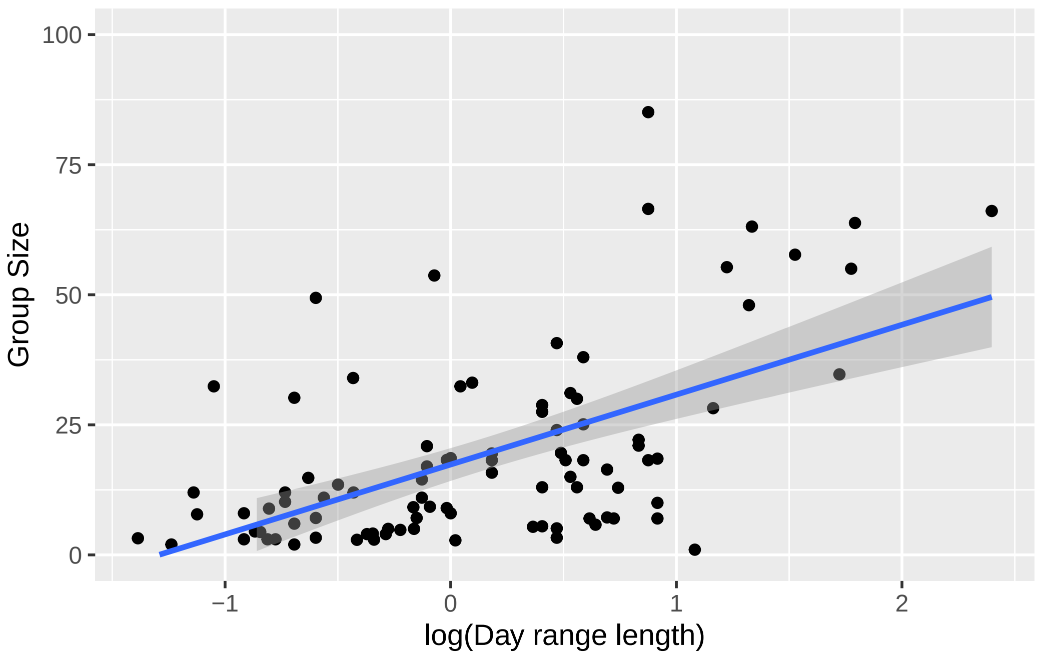


Plot the relationship between **day range length** and **mean group size**, overall and by family. - Do species that live in larger groups travel farther overall? *A: Yes, based on regression line* - How about within any particular primate family? *A: Yes for Cercopithecidae, Hominidae, Tarsiidae, Cebidae* - Should you transform either of these variables? *A: log transformed day range length*

```
plot1 <- ggplot(data = d,
            aes(x = log(DayLength_km),
                y = MeanGroupSize)) +  # build a plot object
  xlab("log(Day range length)") + ylab("Group Size") + # modify the axis labels
  geom_point(na.rm = TRUE) + # make a scatterplot
  geom_smooth(method = "lm", na.rm = TRUE) + # add a regression line
  ylim(0, 100) + # set y-axis range
  theme(legend.title = element_blank()) # modify the legend
plot1 # plot the object
```

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



```
plot2 <- ggplot(data = d,
            aes(x = log(DayLength_km),
                y = MeanGroupSize,
                color = factor(Family))) +  # build a plot object and color points by Family
  xlab("log(Day range length)") + ylab("Group Size") + # modify the axis labels
  geom_point(na.rm = TRUE) + # make a scatterplot
  geom_smooth(method = "lm", na.rm = TRUE) + # add a regression line
  ylim(0, 100) + # set y-axis range
  theme(legend.title = element_blank()) # modify the legend
plot2 # plot the object
```

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

Warning in qt((1 - level)/2, df): NaNs produced

Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning
-Inf

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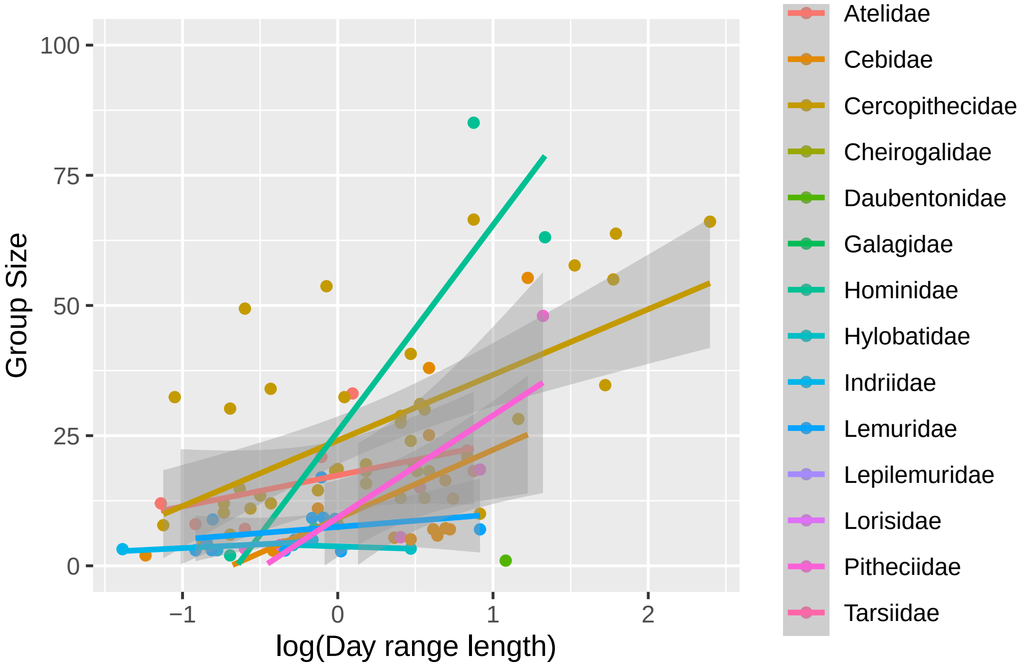

```
plot_grid(plot1, plot2, rel_widths = c(1, 1.5), labels = "AUTO")
```

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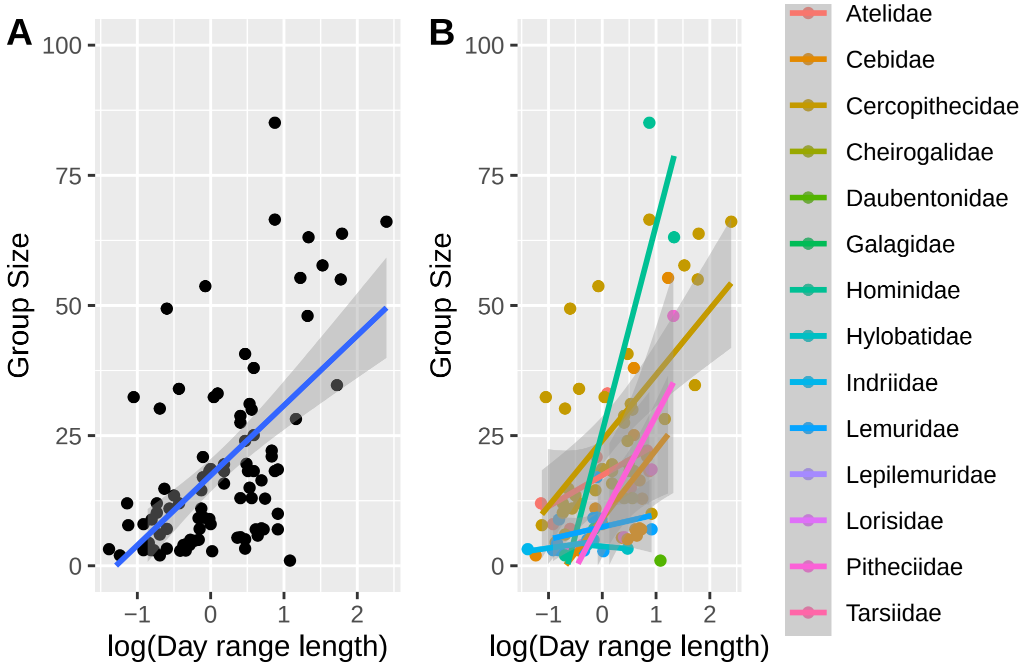
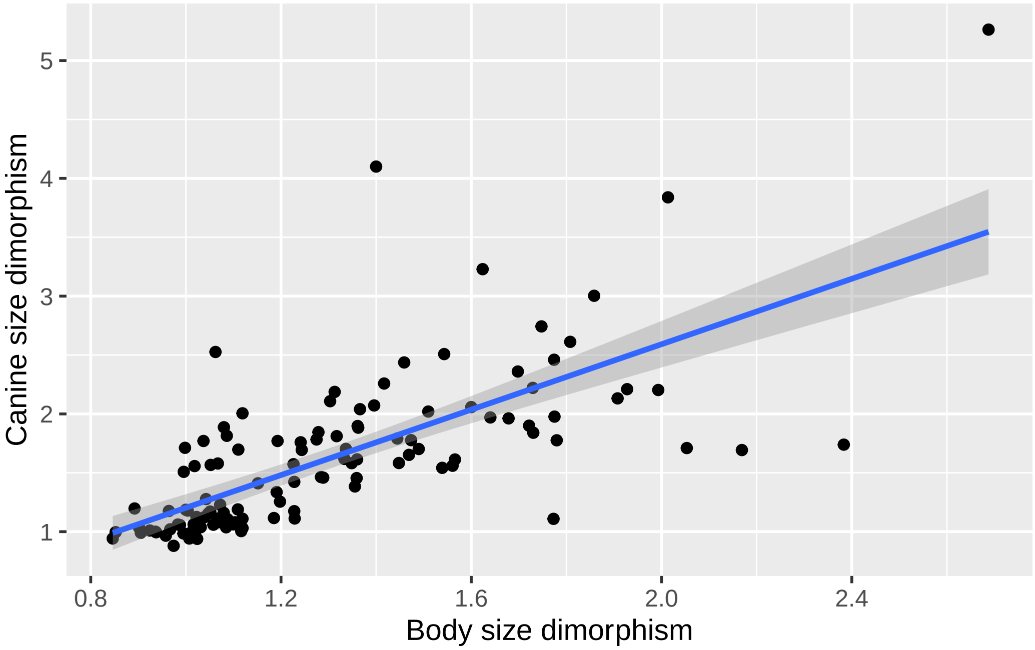


Plot the relationship between **body size dimorphism** and **canine size dimorphism** overall and by family.

Do taxa with greater size dimorphism also show greater canine dimorphism? *A: Yes, overall and in Carcopithecidae, Hominidae, Cebidae, Tarsiidae, and Lorisidae families*

```
plot1 <- ggplot(data = d,
            aes(x = BSD,
                y = Canine_Dimorphism)) +  # build a plot object
  xlab("Body size dimorphism") + ylab("Canine size dimorphism") + # modify the axis labels
  geom_point(na.rm = TRUE) + # make a scatterplot
  geom_smooth(method = "lm", na.rm = TRUE) + # add a regression line
  # ylim(0, 100) + # set y-axis range
  theme(legend.title = element_blank()) # modify the legend
plot1 # plot the object
```

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

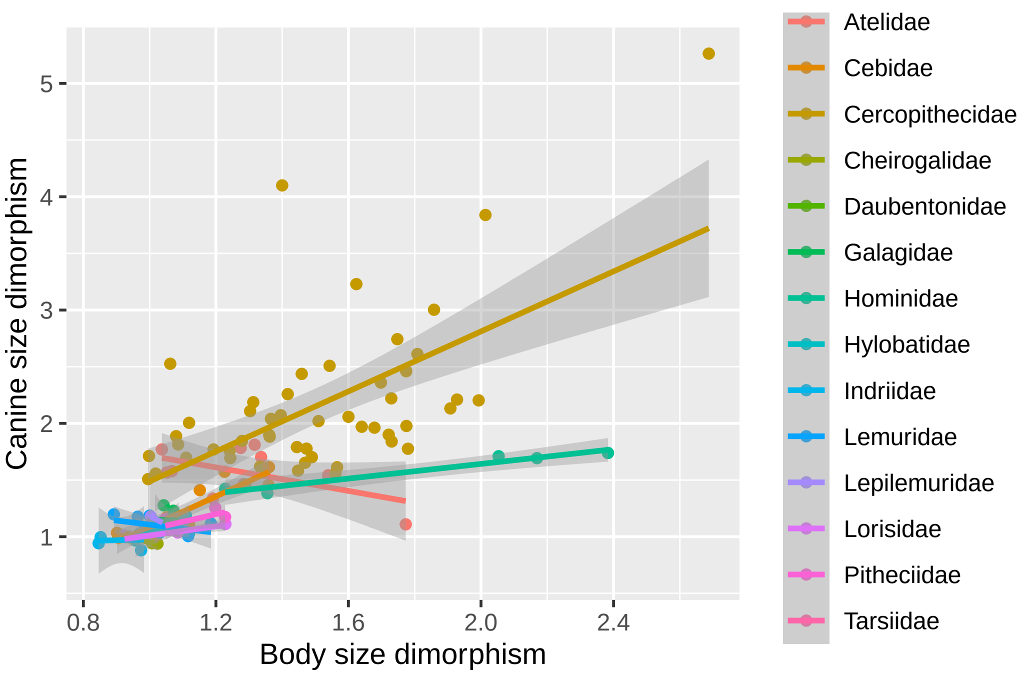


```r
plot2 <- ggplot(data = d,
             aes(x = BSD,
                 y = Canine_Dimorphism,
                 color = factor(Family))) +  # build a plot object and color points by Family
  xlab("Body size dimorphism") + ylab("Canine size dimorphism") + # modify the axis labels
  geom_point(na.rm = TRUE) + # make a scatterplot
  geom_smooth(method = "lm", na.rm = TRUE) + # add a regression line
  # ylim(0, 100) + # set y-axis range
  theme(legend.title = element_blank()) # modify the legend
plot2 # plot the object
```

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

```
Warning in qt((1 - level)/2, df): NaNs produced
```

```
Warning in max(ids, na.rm = TRUE): no non-missing arguments to max; returning
-Inf
```

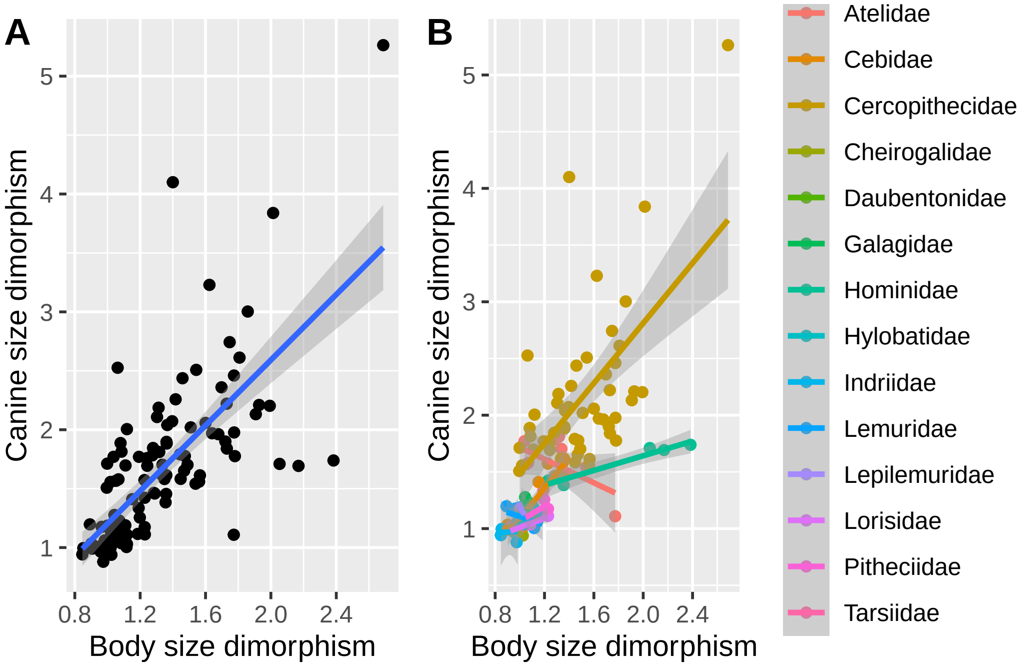


```
plot_grid(plot1, plot2, rel_widths = c(1, 1.5), labels = "AUTO")
```

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

Warning in qt((1 - level)/2, df): NaNs produced

Warning in qt((1 - level)/2, df): no non-missing arguments to max; returning
-Inf
```



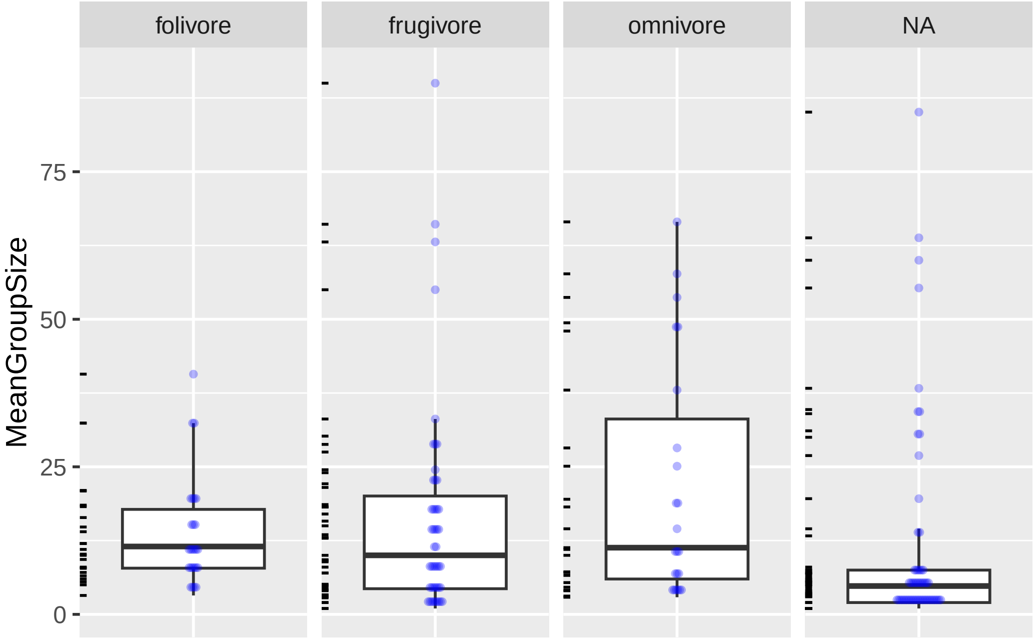
Create a new variable named diet_strategy that is "frugivore" if fruits make up >50% of the diet, "folivore" if leaves make up >50% of the diet, and "omnnivore" if neither of these is true. Then, do boxplots of group size for species with different dietary strategies.

Do frugivores live in larger groups than folivores? *A: No, overlap in IQR (frugivore has more outliers)*

```
d <- d %>%
  mutate(diet_strategy = case_when(Fruit > 50 ~ "frugivore",
                                   Leaves > 50 ~ "folivore",
                                   Fruit < 50 & Leaves < 50 ~ "omnivore")) # specify to avoi
```

```
p <- ggplot(data = d,
           aes(x = factor(0), y = MeanGroupSize)) +
  geom_boxplot(na.rm = TRUE, outlier.shape = NA) +
  theme(axis.title.x = element_blank(),
        axis.text.x = element_blank(),
        axis.ticks.x = element_blank()) +
  geom_dotplot(binaxis = "y", stackdir = "center",
              stackratio = 0.2, alpha = 0.3, dotsize = 0.5, color = NA,
              fill = "blue", na.rm = TRUE) +
  facet_grid(. ~ diet_strategy) + geom_rug(sides = "l")
p
```

```
Bin width defaults to 1/30 of the range of the data. Pick better value with
`binwidth`.
```



In one line of code, using {dplyr} verbs and the forward pipe (`%>%` or `|>`) operator, do the following: - Add a variable, **Binomial** to the data frame **d**, which is a concatenation of the **Genus** and **Species**… - Trim the data frame to only include the variables **Binomial**, **Family**, **Brain_size_species_mean**, and **Body_mass_male_mean**… - Group these variables by **Family**… - Calculate the average value for **Brain_size_species_mean** and **Body_mass_male_mean** per **Family** (remember, you may need to specify na.rm = TRUE)… - And arrange by increasing **average brain size**

```r
d <- d %>%
  mutate(Binomial = str_c(Genus, " ", Species)) %>%
  select(Binomial, Family, Brain_Size_Species_Mean, Body_mass_male_mean) %>%
  group_by(Family) %>%
  summarize(avg_brain_size = mean(Brain_Size_Species_Mean),
            avg_male_body_mass = mean(Body_mass_male_mean)) %>%
  arrange(avg_brain_size)
```