Exercise: **Data Frames**

Day 1, Part C

For this exercise, we will use the `msleep` data frame from the `ggplot2` library. This can be loaded using the following code:

```r
library(ggplot2)
data("msleep")
msleep <- data.frame(msleep)
```

Some information about the data set is available in the help file for `msleep`.

1. Check that `msleep` is a data frame.

2. Use each of the following functions to explore the data frame: `head()`, `tail()`, `summary()`, and `View()`.

3. How many rows and columns does this data frame have?

4. What are the names of the columns? What data type is each column?

5. Select the `name` column three different ways.

6. Select just rows where the `order` column is "Carnivora."

7. Select just rows for animals with body weight > 200kg.

8. Create a new variable for the total amount of sleep in minutes (`sleep_total_min`).

    a. What is the longest time any animal sleeps (in minutes)?

    b. Which animal sleeps this long?

9. Create a new variable for the proportion of total sleep spent in REM (`prop_rem`).

    a. What is the minimum proportion? (hint, look at the argument options in the help file for `min()`)

    b. How long is REM sleep for the animal with the smallest proportion REM? (hint, this requires two conditions be met: `prop_rem` is NOT missing, and `prop_rem` is the minimum value)

10. Create a new variable for the ratio of body weight to brain weight (`bdy_brn_ratio`).

    a. What is the median body-to-brain weight ratio?

    b. What is the variance of the body-to-brain weight ratio?

11. Drop the `conservation`, `sleep_cycle`, and `bodywt` variables from the `msleep` object.

12. Create a new object (`msleep_carni`) that contains just the data for carnivores and only the `name`, `genus`, `order`, `sleep_total`, and `brainwt` variables.