Homework 3

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```
library(tidyverse)
```

Tasks that require an answer are bolded (inside ** in the .qmd file). For any task that includes a question (i.e. it ends with "?"), you should also answer the question in sentence form.

Data Manipulation with dplyr

These questions all use the msleep data set that comes with ggplot2. You can view the data by typing its name, or look at the help file to learn more about the variables inside:

```
?msleep
```

Each row of the data characterizes one mammal.

1.

Extract the mammals from the "Vulpes" genus.

```
msleep |>
    filter(genus == "Vulpes")
# A tibble: 2 x 11
          genus vore order conservation sleep_total sleep_rem sleep_cycle awake
          <chr> <chr> <chr> <chr>
                                                <dbl>
                                                          <dbl>
1 Arctic~ Vulp~ carni Carn~ <NA>
                                                12.5
                                                           NΑ
                                                                      NA
                                                                             11.5
2 Red fox Vulp~ carni Carn~ <NA>
                                                            2.4
                                                                      0.35 14.2
                                                  9.8
# i 2 more variables: brainwt <dbl>, bodywt <dbl>
```

Extract the name and vore columns.

```
msleep |>
    select(name, vore)
# A tibble: 83 x 2
  name
                               vore
   <chr>
                               <chr>>
1 Cheetah
                               carni
2 Owl monkey
                               omni
3 Mountain beaver
                               herbi
4 Greater short-tailed shrew omni
5 Cow
                               herbi
6 Three-toed sloth
                               herbi
7 Northern fur seal
                               carni
8 Vesper mouse
                               <NA>
9 Dog
                               carni
10 Roe deer
                               herbi
# i 73 more rows
```

3.

Which mammals sleep less than 3 hours a day?

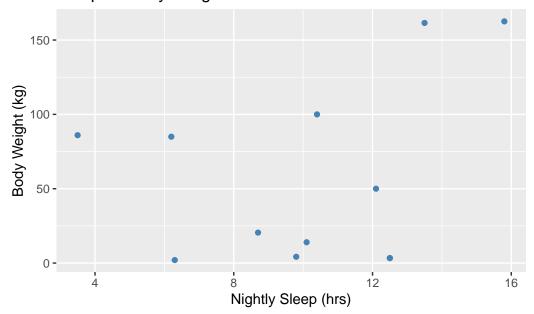
Find the corresponding rows first, then extract the name and vore columns from the result.

The three mammals that sleep less than 3 hours per day are the **horse**, **giraffe**, and **pilot** whale.

Create a scatterplot of sleep_total versus bodywt for mammals in the order "Carnivora". Does there appear to be a relationship between total sleep and body weight for the carnivores in this data?

Find the corresponding rows first, then create the scatterplot with the result.

Sleep vs Body Weight for Order Carnivora



There seems to be a small level of correlation between nightly sleep and body weight for the order Carnivora, but the number of data points makes it difficult to tell if it is just coincidence or not.

Re-write the following code to use the pipe, |>, rather than intermediate variables.

```
msleep |>
    group_by(order) |>
      summarise(
        avg_sleep = mean(sleep_total, na.rm = TRUE)
    filter(avg_sleep > 15)
# A tibble: 4 x 2
 order
                  avg_sleep
  <chr>
                      <dbl>
1 Afrosoricida
                       15.6
2 Chiroptera
                       19.8
3 Cingulata
                       17.8
4 Didelphimorphia
                       18.7
```

6.

Add a column called brain_ratio that contains the ratio of brain weight to body weight.

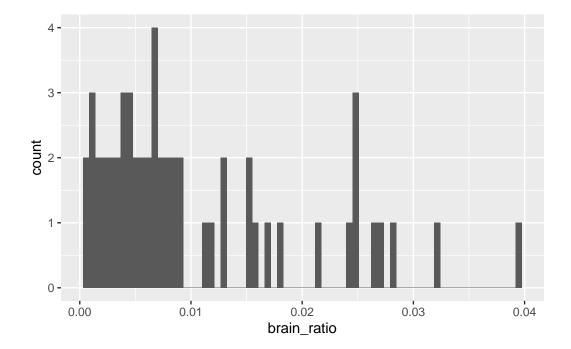
```
msleep |>
    mutate(brain_ratio = brainwt/bodywt) |>
    select(name, brain_ratio)
# A tibble: 83 x 2
                              brain_ratio
  name
  <chr>
                                    <dbl>
1 Cheetah
                                NA
2 Owl monkey
                                 0.0323
3 Mountain beaver
                                NA
4 Greater short-tailed shrew
                                 0.0153
5 Cow
                                 0.000705
6 Three-toed sloth
                                NA
7 Northern fur seal
                                NA
8 Vesper mouse
                                NA
```

```
9 Dog 0.005
10 Roe deer 0.00664
# i 73 more rows
```

Which three animals have the highest brain_ratio?

To answer this question, first make a histogram of brain_ratio:

```
msleep |>
  mutate(brain_ratio = brainwt/bodywt) |>
    ggplot(mapping = aes(x=brain_ratio)) +
    geom_histogram(
    na.rm = TRUE,
    bins = 70)
```



Examine the histogram for a good numeric threshold, then use filter to find brain_ratios above the threshold:

```
msleep |>
  mutate(brain_ratio = brainwt/bodywt) |>
  filter(brain_ratio > 0.0275) |>
  select(name)

# A tibble: 3 x 1
  name
  <chr>
1 Owl monkey
2 Lesser short-tailed shrew
3 Thirteen-lined ground squirrel
```

The three animals with the highest brain ratio are the **owl monkey**, **lesser short-tailed shrew**, and **thirteen-lined ground squirrel**.

8.

Use summarise() to find the mean, smallest and largest values of sleep cycle lengths over all rows in the data.

9.

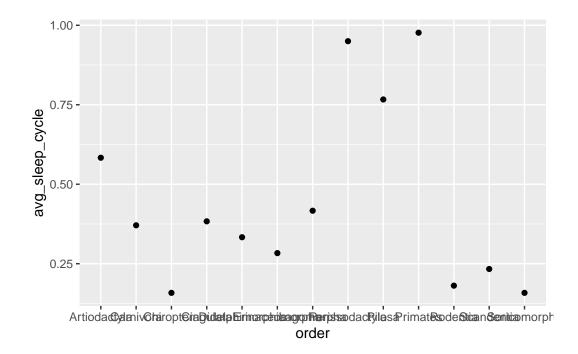
Find the mean, smallest and largest values of sleep cycle lengths for each order. Order here refers to the order column in the data.

```
sleep_by_order <- msleep |>
  group_by(order) |>
```

```
summarise(
   avg_sleep_cycle = mean(sleep_cycle, na.rm = TRUE),
   min_sleep_cycle = min(sleep_cycle, na.rm = TRUE),
   max_sleep_cycle = max(sleep_cycle, na.rm = TRUE)
)
```

Using your result from the previous question, create a scatterplot of the mean sleep cycle length by order.

```
sleep_by_order |>
  filter(!is.nan(avg_sleep_cycle)) |>
  ggplot(mapping = aes(x = order, y = avg_sleep_cycle)) +
  geom_point(na.rm = TRUE)
```



I chose to remove the orders which contained no sleep cycle data, to undo this you would just need to delete the line filter(!is.nan(avg_sleep_cycle)) |>

(Sometimes a scatterplot like this, with a categorical variable on one axis, is called a dot chart).