

5-Homework Using `dplyr` and `ggplot2`

BIOL 5000

You will need these libraries:

```
library(ggplot2)
library(dplyr)
library(tidyr)
```

You will need this data:

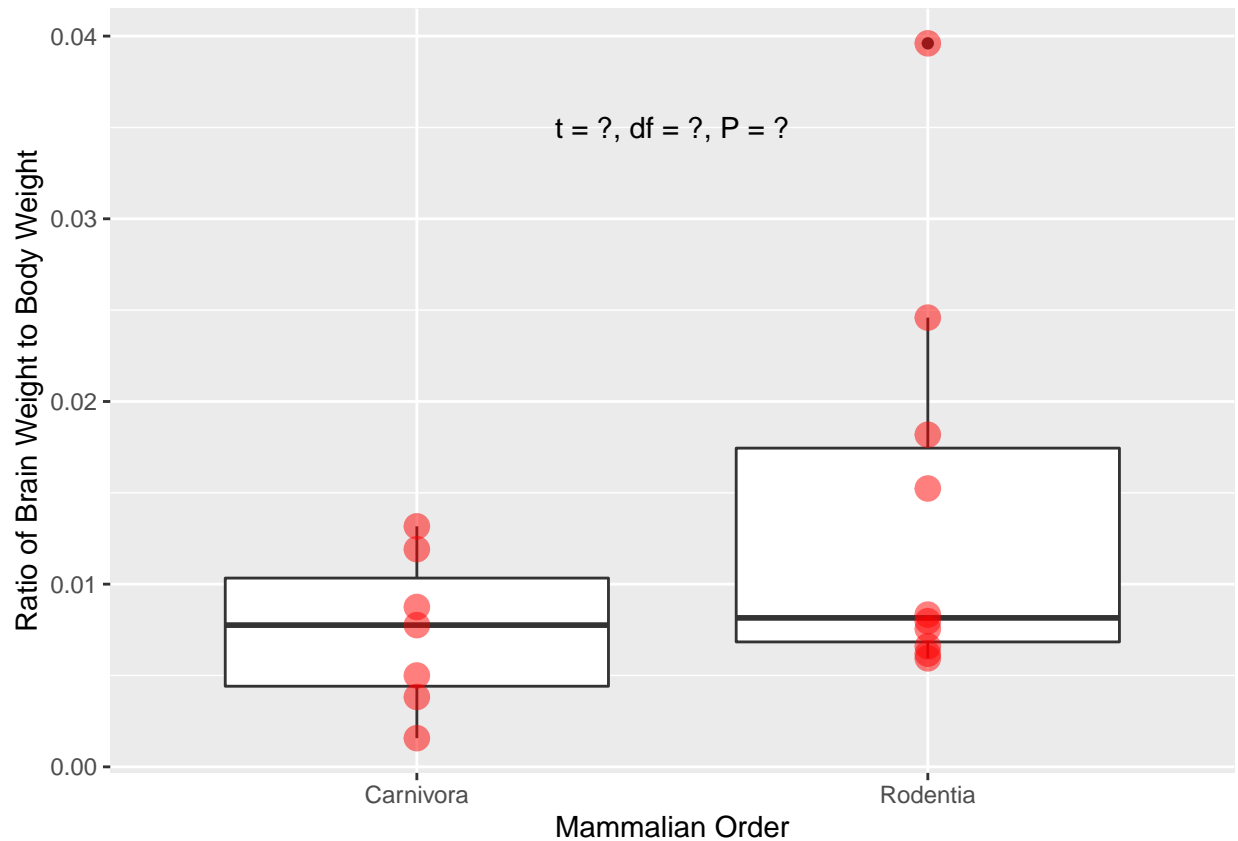
```
data(msleep)
```

Question 1. Use `dplyr` to recreate the summary table below using the `msleep` dataset (built into `ggplot`). You will need to use several of the `dplyr` verbs (functions) we have learned in class. Your full table should have 17 rows (although fewer rows may be displayed by default).

```
## # A tibble: 17 x 5
##   name                order  brainwt bodywt  ratio
##   <chr>              <chr>    <dbl>   <dbl>  <dbl>
## 1 Jaguar            Carnivora 0.157   100    0.00157
## 2 Gray seal         Carnivora 0.325    85    0.00382
## 3 Dog               Carnivora 0.07     14    0.005
## 4 Red fox           Carnivora 0.0504   4.23  0.0119
## 5 Arctic fox        Carnivora 0.0445   3.38  0.0132
## 6 Domestic cat      Carnivora 0.0256   3.3   0.00776
## 7 Genet             Carnivora 0.0175    2    0.00875
## 8 African giant pouched rat Rodentia 0.0066    1    0.0066
## 9 Arctic ground squirrel Rodentia 0.0057   0.92  0.00620
## 10 Guinea pig       Rodentia 0.0055   0.728 0.00755
## 11 Chinchilla       Rodentia 0.0064   0.42  0.0152
## 12 Laboratory rat   Rodentia 0.0019   0.32  0.00594
## 13 Cotton rat       Rodentia 0.00118  0.148 0.00797
## 14 Mole rat         Rodentia 0.003    0.122 0.0246
## 15 Golden hamster   Rodentia 0.001    0.12  0.00833
## 16 Thirteen-lined ground squirrel Rodentia 0.004    0.101 0.0396
## 17 House mouse      Rodentia 0.0004   0.022 0.0182
```

Question 2. Use a t-test to compare the two mammal orders, Rodentia and Carnivora, in their ratio of brain weight to body weight. Format your answer as you would see in the results section of a scientific journal article.

Question 3. Using `ggplot2`, replicate the following figure. Fill in the values from your t-test (Question 2).



Question 4. Save the plot to your Rproject folder for this exercise as a 6" X 6" .jpg file.

Homework (folder containing .rproj file and all associated input/output files) is due to the D2L Assignments dropbox **before class one week from today**. As before, make each of your 'answers' an object. (e.g.) `Answer_3 <- ggplot(data_summary, aes(x =))` and 'print' the name of the object below the specified code (e.g. `Answer_3`). Each object is then displayed automatically in the console (if a model or table) or plot viewer (if its a graph) without having to click on anything.