

## 5-Homework Using `dplyr` and `ggplot2`

BIOL 5000

You will need these libraries:

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

You will need this data:

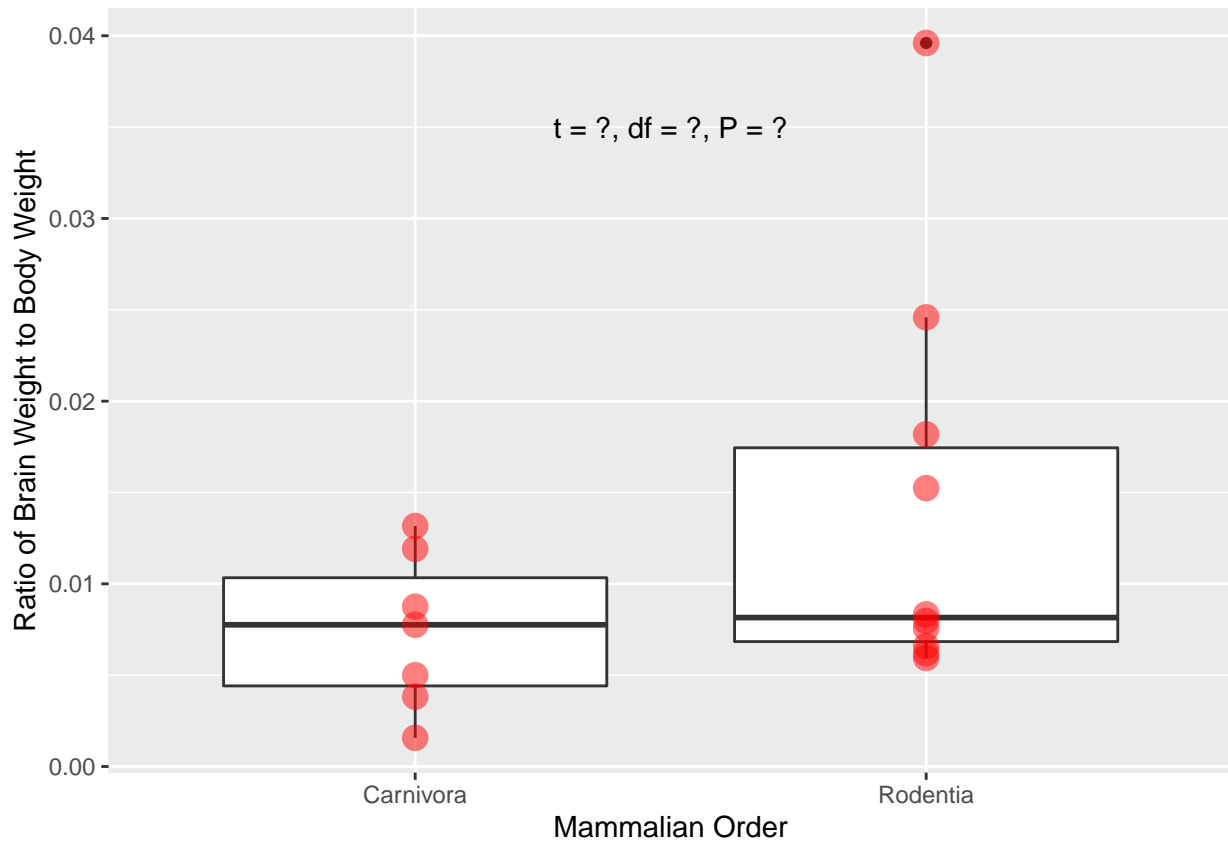
```
data(msleep)
```

**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.

```
## # 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.

**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 on November 4th**. 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 then shows up automatically in the console (if a model or table) or plot viewer (if its a graph) without having to click on anything.