Lab 2 Homework

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Instructions

Answer the following questions and complete the exercises in RMarkdown. Please embed all of your code and push your final work to our GitHub repository (https://github.com/FRS417-DataScienceBiologists). I will randomly select a few examples of student work at the start of each session to use as examples so be sure that your code is working to the best of your ability.

Load the tidyverse

```r
library("tidyverse")
```

```
## ── Attaching packages ─────────────────────────────────────────
────────── tidyverse 1.2.1 ──
```

```
## ✔ ggplot2 3.1.0      ✔ purrr   0.2.5
## ✔ tibble  2.0.0      ✔ dplyr   0.7.8
## ✔ tidyr   0.8.2      ✔ stringr 1.3.1
## ✔ readr   1.3.1      ✔ forcats 0.3.0
```

```
## ── Conflicts ──────────────────────────────────────────────────
─ tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
```

Mammals Sleep

For this assignment, we are going to use built-in data on mammal sleep patterns.

```r
msleep
```

```
## # A tibble: 83 x 11
##     name   genus vore  order conservation sleep_total sleep_rem sleep_cycle
##     <chr>  <chr> <chr> <chr> <chr>               <dbl>     <dbl>       <dbl>
##  1 Chee… Acin… carni Carn… lc                   12.1       NA         NA
##  2 Owl … Aotus omni  Prim… <NA>                 17          1.8       NA
##  3 Moun… Aplo… herbi Rode… nt                   14.4        2.4       NA
##  4 Grea… Blar… omni  Sori… lc                   14.9        2.3        0.133
##  5 Cow   Bos   herbi Arti… domesticated          4          0.7        0.667
##  6 Thre… Brad… herbi Pilo… <NA>                 14.4        2.2        0.767
##  7 Nort… Call… carni Carn… vu                    8.7        1.4        0.383
##  8 Vesp… Calo… <NA>  Rode… <NA>                  7          NA         NA
##  9 Dog   Canis carni Carn… domesticated         10.1        2.9        0.333
## 10 Roe … Capr… herbi Arti… lc                    3          NA         NA
## # … with 73 more rows, and 3 more variables: awake <dbl>, brainwt <dbl>,
## #   bodywt <dbl>
```

1. From which publication are these data taken from? Don't do an internet search; show the code that you would use to find out in R. To find things on are use ? and type the function/object/data you are looking for

```
?sleep
```

2. Provide some summary information about the data to get you started; feel free to use the functions that you find most helpful.

```
colnames(msleep)
```

```
##  [1] "name"         "genus"        "vore"         "order"
##  [5] "conservation" "sleep_total"  "sleep_rem"    "sleep_cycle"
##  [9] "awake"        "brainwt"      "bodywt"
```

```
summary(msleep)
```

```
##      name                genus               vore
##  Length:83           Length:83           Length:83
##  Class :character    Class :character    Class :character
##  Mode  :character    Mode  :character    Mode  :character
##
##
##
##
##      order              conservation        sleep_total         sleep_rem
##  Length:83           Length:83           Min.   : 1.90      Min.   :0.100
##  Class :character    Class :character    1st Qu.: 7.85      1st Qu.:0.900
##  Mode  :character    Mode  :character    Median :10.10      Median :1.500
##                                          Mean   :10.43      Mean   :1.875
##                                          3rd Qu.:13.75      3rd Qu.:2.400
##                                          Max.   :19.90      Max.   :6.600
##                                                             NA's   :22
##    sleep_cycle           awake              brainwt              bodywt
##  Min.   :0.1167     Min.   : 4.10      Min.   :0.00014    Min.   :    0.005
##  1st Qu.:0.1833     1st Qu.:10.25      1st Qu.:0.00290    1st Qu.:    0.174
##  Median :0.3333     Median :13.90      Median :0.01240    Median :    1.670
##  Mean   :0.4396     Mean   :13.57      Mean   :0.28158    Mean   :  166.136
##  3rd Qu.:0.5792     3rd Qu.:16.15      3rd Qu.:0.12550    3rd Qu.:   41.750
##  Max.   :1.5000     Max.   :22.10      Max.   :5.71200    Max.   :6654.000
##  NA's   :51                            NA's   :27
```

3. Make a new data frame focused on body weight, but be sure to indicate the common name and genus of each mammal. Sort the data in descending order by body weight.

```
New_data <- select(msleep, genus, name, bodywt) %>%
  arrange(desc(bodywt))
New_data
```

```
## # A tibble: 83 x 3
##    genus          name                 bodywt
##    <chr>          <chr>                 <dbl>
##  1 Loxodonta      African elephant       6654
##  2 Elephas        Asian elephant         2547
##  3 Giraffa        Giraffe                 900.
##  4 Globicephalus  Pilot whale             800
##  5 Bos            Cow                     600
##  6 Equus          Horse                   521
##  7 Tapirus        Brazilian tapir         208.
##  8 Equus          Donkey                  187
##  9 Tursiops       Bottle-nosed dolphin    173.
## 10 Panthera       Tiger                   163.
## # … with 73 more rows
```

4. We are interested in two groups; small and large mammals. Let's define small as less than or equal

to 1kg body weight and large as greater than or equal to 200kg body weight. For our study, we are interested in body weight and sleep total Make two new dataframes (large and small) based on these parameters. Sort the data in descending order by body weight.

```
Small_mammals <- select( msleep, genus, name, bodywt, sleep_total) %>%
   filter(bodywt<=1) %>%
   arrange(desc(bodywt))
Small_mammals
```

```
## # A tibble: 36 x 4
##     genus        name                        bodywt sleep_total
##     <chr>        <chr>                        <dbl>       <dbl>
##  1 Cricetomys   African giant pouched rat   1            8.3
##  2 Spermophilus Arctic ground squirrel       0.92        16.6
##  3 Tenrec       Tenrec                       0.9         15.6
##  4 Erinaceus    European hedgehog            0.77        10.1
##  5 Saimiri      Squirrel monkey              0.743        9.6
##  6 Cavis        Guinea pig                   0.728        9.4
##  7 Paraechinus  Desert hedgehog              0.55        10.3
##  8 Aotus        Owl monkey                   0.48        17
##  9 Chinchilla   Chinchilla                   0.42        12.5
## 10 Lutreolina   Thick-tailed opposum         0.37        19.4
## # ... with 26 more rows
```

```
Large_mammals <- select(msleep, genus, name, bodywt, sleep_total) %>%
   filter(bodywt>=200) %>%
   arrange(desc(bodywt))
Large_mammals
```

```
## # A tibble: 7 x 4
##    genus        name              bodywt sleep_total
##    <chr>        <chr>              <dbl>       <dbl>
## 1 Loxodonta    African elephant  6654          3.3
## 2 Elephas      Asian elephant    2547          3.9
## 3 Giraffa      Giraffe            900.          1.9
## 4 Globicephalus Pilot whale       800           2.7
## 5 Bos          Cow                600           4
## 6 Equus        Horse              521           2.9
## 7 Tapirus      Brazilian tapir    208.          4.4
```

5. Let's try to figure out if large mammals sleep, on average, longer than small mammals. What is the average sleep duration for large mammals as we have defined them?

```
mean(Large_mammals$sleep_total)
```

```
## [1] 3.3
```

6. What is the average sleep duration for small mammals as we have defined them?

```
mean(Small_mammals$sleep_total)
```

```
## [1] 12.65833
```

7. Which animals sleep at least 18 hours per day? Be sure to show the name, genus, order, and sleep total. Sort by order and sleep total.

```
Animal_Sleep <- select(msleep, name, genus, order, sleep_total) %>%
  filter(sleep_total>=18) %>%
  arrange(order, sleep_total)
Animal_Sleep
```

```
## # A tibble: 5 x 4
##   name                    genus      order             sleep_total
##   <chr>                   <chr>      <chr>                   <dbl>
## 1 Big brown bat           Eptesicus  Chiroptera               19.7
## 2 Little brown bat        Myotis     Chiroptera               19.9
## 3 Giant armadillo         Priodontes Cingulata                18.1
## 4 North American Opossum  Didelphis  Didelphimorphia          18
## 5 Thick-tailed opposum    Lutreolina Didelphimorphia          19.4
```

Push your final code to GitHub (https://github.com/FRS417-DataScienceBiologists)