431 Part A: Extra Example

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Sleep and Mammals

This example reviews some of the key work we did in Part A of the course. It uses the `msleep` data set, which is part of the `ggplot2` package. Use the help file for that data set or visit http://ggplot2.tidyverse.org/reference/msleep.html to assist in understanding the data.

1. Identify the number of rows and number of variables in the `msleep` data set.

```
dim(msleep)
```

```
[1] 83 11
```

There are 83 rows and 11 variables.

2. Specify the variable with the largest number of missing values in `msleep`. How many values are missing?

```
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                          
```

`sleep_cycle` is missing for 51 of the 83 mammals.

3. Identify the mammal who remains `awake` the longest, per day. What is the Z score for this mammal?

```
msleep %>% select(name, awake) %>%
  arrange(desc(awake))
```

```
# A tibble: 83 x 2
                name awake
               <chr> <dbl>
 1          Giraffe 22.10
 2      Pilot whale 21.35
 3            Horse 21.10
 4         Roe deer 21.00
 5           Donkey 20.90
 6 African elephant 20.70
 7     Caspian seal 20.50
 8            Sheep 20.20
 9   Asian elephant 20.10
10              Cow 20.00
# ... with 73 more rows
```

It's the giraffe.

4. Display your R code to create a data set (called `sleep2`) from `msleep` which contains the variables `name`, `order`, `vore`, `sleep_cycle` and `sleep_rem` for those animals who have no missing values in any of those four variables, then convert the `vore` information into a factor.

```
sleep2 <- msleep %>%
  select(name, order, vore, sleep_cycle, sleep_rem) %>%
  filter(complete.cases(name, order, vore, sleep_cycle, sleep_rem)) %>%
  mutate(vore = factor(vore))

sleep2
```

```
# A tibble: 31 x 5
                         name           order   vore sleep_cycle sleep_rem
                        <chr>           <chr> <fctr>       <dbl>     <dbl>
 1 Greater short-tailed shrew    Soricomorpha   omni   0.1333333       2.3
 2                          Cow    Artiodactyla  herbi   0.6666667       0.7
 3            Three-toed sloth          Pilosa  herbi   0.7666667       2.2
 4           Northern fur seal       Carnivora  carni   0.3833333       1.4
 5                          Dog       Carnivora  carni   0.3333333       2.9
 6                 Guinea pig        Rodentia  herbi   0.2166667       0.8
 7                 Chinchilla        Rodentia  herbi   0.1166667       1.5
 8  Lesser short-tailed shrew    Soricomorpha   omni   0.1500000       1.4
 9       Long-nosed armadillo       Cingulata  carni   0.3833333       3.1
10     North American Opossum Didelphimorphia   omni   0.3333333       4.9
# ... with 21 more rows
```

5. According to the `order` variable, how many Primates (see the `order` variable) exist in your `sleep2` data set?

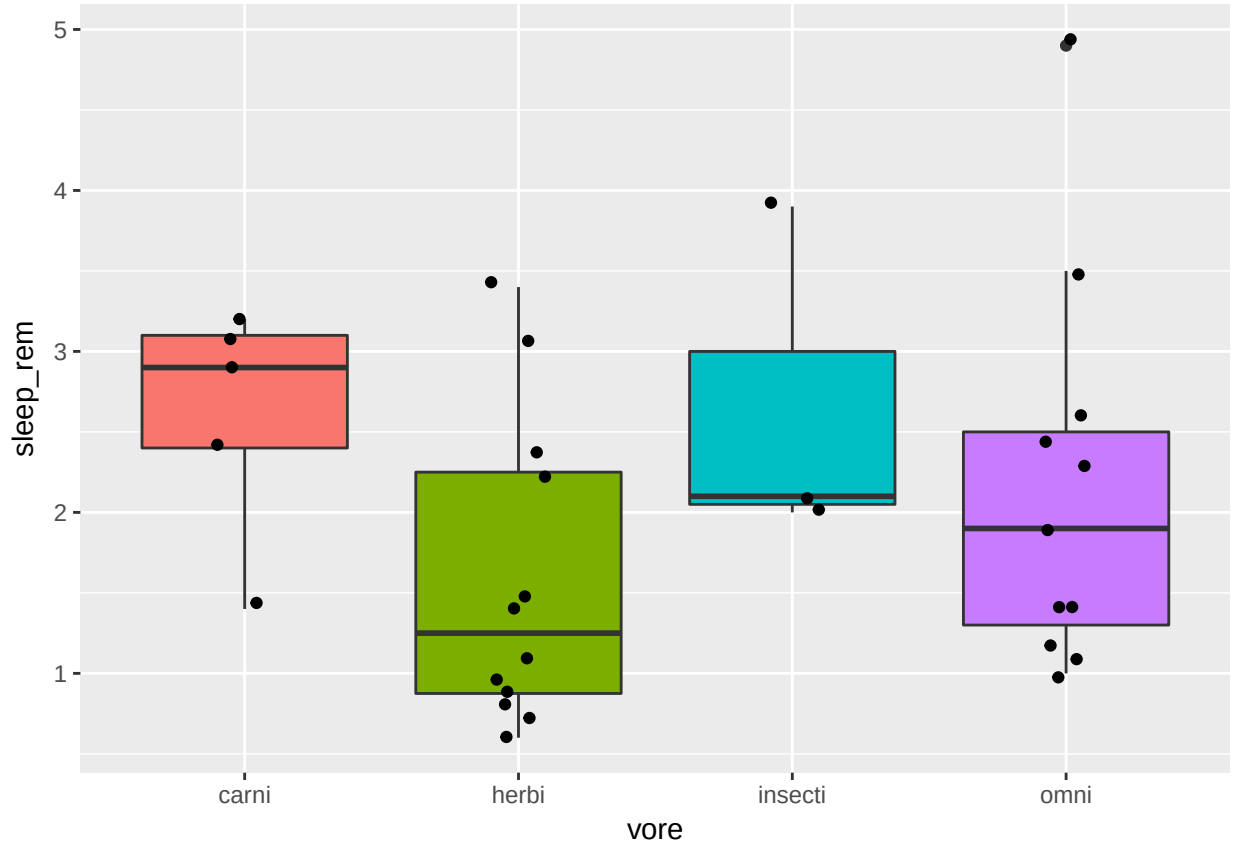
```
sleep2 %>% filter(order == "Primates")
```

```
# A tibble: 5 x 5
        name    order   vore sleep_cycle sleep_rem
       <chr>    <chr> <fctr>       <dbl>     <dbl>
1     Galago Primates   omni   0.5500000       1.1
2      Human Primates   omni   1.5000000       1.9
3    Macaque Primates   omni   0.7500000       1.2
4 Chimpanzee Primates   omni   1.4166667       1.4
5     Baboon Primates   omni   0.6666667       1.0
```

There should be five.

6. Draw a plot to compare the `sleep_rem` levels by `vore` group using your `sleep2` data. What do you conclude?

```
ggplot(sleep2, aes(x = vore, y = sleep_rem, fill = vore)) +
  geom_boxplot() +
  geom_jitter(width = 0.1) +
  guides(fill = FALSE)
```



In general, carnivores have the longest `sleep_rem` while herbivores have the shortest, at least in terms of

medians. There are very few values (looks like just three) in the insectivores, and it looks like just five in the carnivores.

7. Produce R code using the %>% pipe to produce a table which answers these two questions for the sleep2 data: [a] Which vore group has the largest mean sleep_rem level? [b] Which vore group has the largest mean sleep_cycle?

```
sleep2 %>% group_by(vore) %>% summarize(n(), mean(sleep_rem), mean(sleep_cycle))
```

```
# A tibble: 4 x 4
     vore `n()` `mean(sleep_rem)` `mean(sleep_cycle)`
   <fctr> <int>             <dbl>               <dbl>
1   carni     5          2.600000           0.3733333
2   herbi    12          1.591667           0.4180556
3 insecti     3          2.666667           0.1611111
4    omni    11          2.154545           0.5924242
```

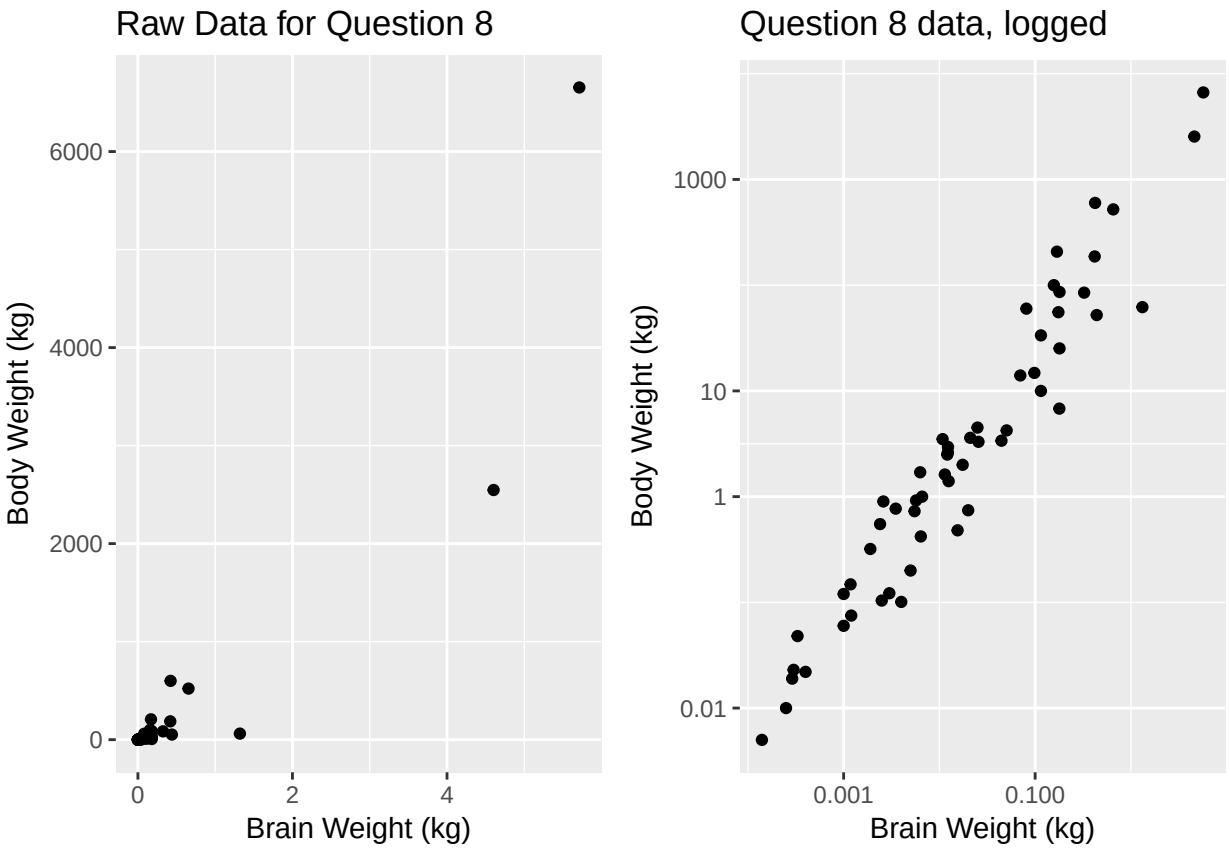
8. Now, return to the original msleep data for questions 8-10. Build a scatterplot of brainwt and bodywt, first using the raw data and then using a logarithmic scale for each variable.

```
sleep1 <- msleep %>%
  filter(complete.cases(brainwt, bodywt))

p1 <- ggplot(sleep1, aes(x = brainwt, y = bodywt)) +
  geom_point() +
  labs(title = "Raw Data for Question 8",
       x = "Brain Weight (kg)",
       y = "Body Weight (kg)")

p2 <- ggplot(sleep1, aes(x = brainwt, y = bodywt)) +
  geom_point() +
  scale_y_log10(breaks = c(0.01, 1, 10, 1000), labels = c(0.01, 1, 10, 1000)) +
  scale_x_log10() +
  labs(title = "Question 8 data, logged",
       x = "Brain Weight (kg)",
       y = "Body Weight (kg)")

gridExtra::grid.arrange(p1, p2, nrow = 1)
```



9. Fit a linear model to the scatterplot you drew in part 8 for which a linear model seems more appropriate, and specify and describe (in a sentence of two) both the fitted least squares equation *and* the Pearson correlation coefficient.

Clearly the log-log model is the better choice. I'll revert to a natural logarithm for the plot below, and the model.

```
model9 <- lm(log(bodywt) ~ log(brainwt), data = sleep1)

summary(model9)
```

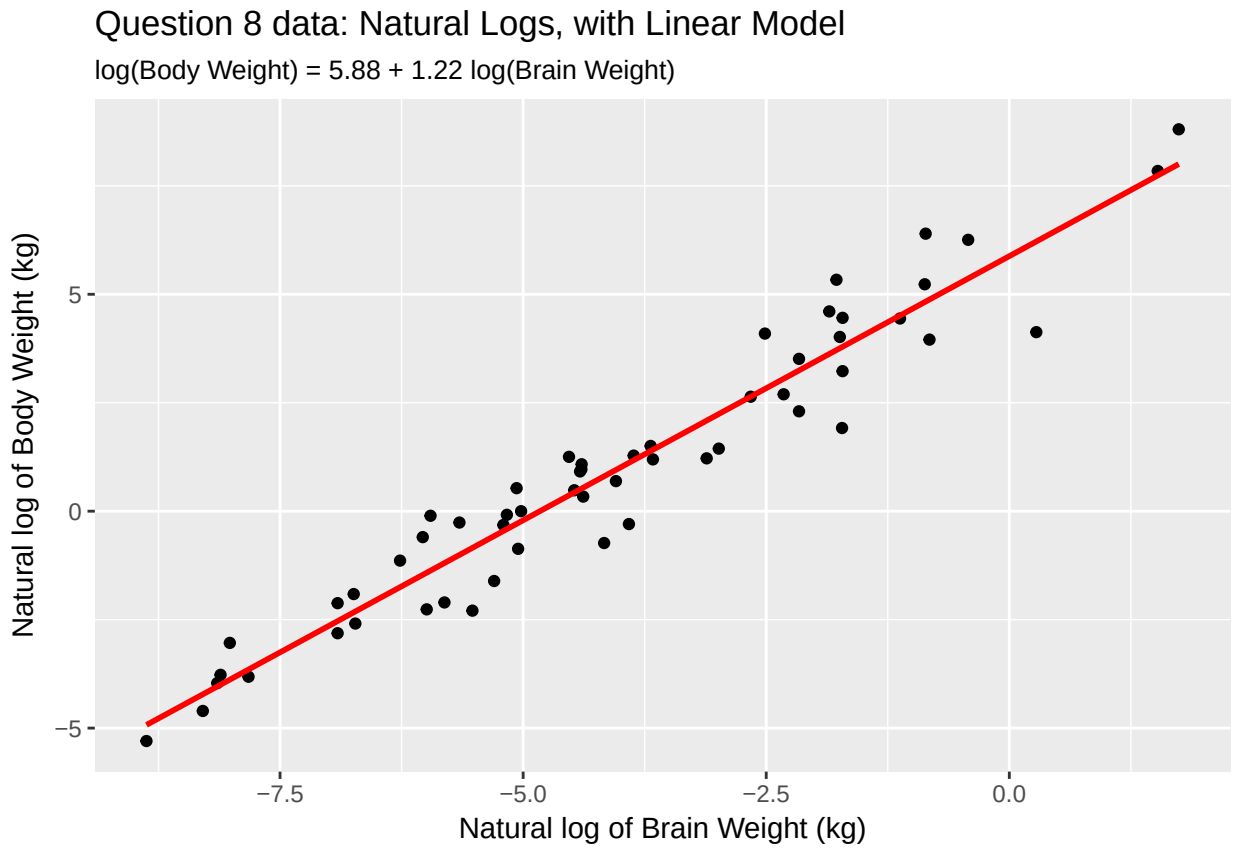
```
Call:
lm(formula = log(bodywt) ~ log(brainwt), data = sleep1)

Residuals:
    Min      1Q  Median      3Q     Max
-2.0902 -0.4282  0.1054  0.5723  1.6211

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)   5.87919    0.21393   27.48   <2e-16 ***
log(brainwt)  1.21785    0.04482   27.17   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 0.8403 on 54 degrees of freedom
Multiple R-squared:  0.9319,    Adjusted R-squared:  0.9306
F-statistic: 738.4 on 1 and 54 DF,  p-value: < 2.2e-16
```

```
ggplot(sleep1, aes(x = log(brainwt), y = log(bodywt))) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE, col = "red") +
  labs(title = "Question 8 data: Natural Logs, with Linear Model",
       subtitle = "log(Body Weight) = 5.88 + 1.22 log(Brain Weight)",
       x = "Natural log of Brain Weight (kg)",
       y = "Natural log of Body Weight (kg)")
```



10. Identify the mammal in your model (in part 9) with the largest (in absolute value) regression residual.

```
sleep1$abs_res <- abs(model9$residuals)

sleep1 %>% select(name, abs_res) %>% arrange(desc(abs_res))
```

```
# A tibble: 56 x 2
                          name  abs_res
                         <chr>    <dbl>
 1                       Human 2.090169
 2                    Macaque 1.867117
```

```
 3                Brazilian tapir 1.621108
 4                           Cow 1.565557
 5                    Owl monkey 1.538485
 6 Thirteen-lined ground squirrel 1.447518
 7                Squirrel monkey 1.411995
 8                Giant armadillo 1.275983
 9                         Tenrec 1.264385
10                         Galago 1.036076
# ... with 46 more rows
```

The answer is Human.