BE7023_Homework_2

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```r
setwd("C:/Users/lapt3u/Box/UC/Fall_2018/BE7023_Adv_Biostats/adv_biostats/hw_2")
library(MASS)
dat <- Animals
```

1. What is the dimension of the data.

```r
dim(dat)
```

```
## [1] 28  2
```

```r
# The data has 28 rows/observations and 2 columns/variables
```

2. Describe the data.

```r
# The animals dataset contains the average brain and body weights for
# 28 species of land animals.  The body variable represents body weight in kg,
# and the brain variable represents the brain weight in g.
# We can also look at the summary statistics for the data to see what's going on. Also,
# we can look at the first 6 rows to get a good view of how the data is organized.
summary(dat)
```

```
##       body              brain
##  Min.   :    0.02   Min.   :   0.40
##  1st Qu.:    3.10   1st Qu.:  22.23
##  Median :   53.83   Median : 137.00
##  Mean   : 4278.44   Mean   : 574.52
##  3rd Qu.:  479.00   3rd Qu.: 420.00
##  Max.   :87000.00   Max.   :5712.00
```

```r
# It looks like our lightest animal weighs in at only 0.02 kg, while our biggest
# weighs 87,000 kg!  Likewise, the lightest brain weighs 0.4 g, whereas the
# largest brain is 5712 g.
head(dat)
```

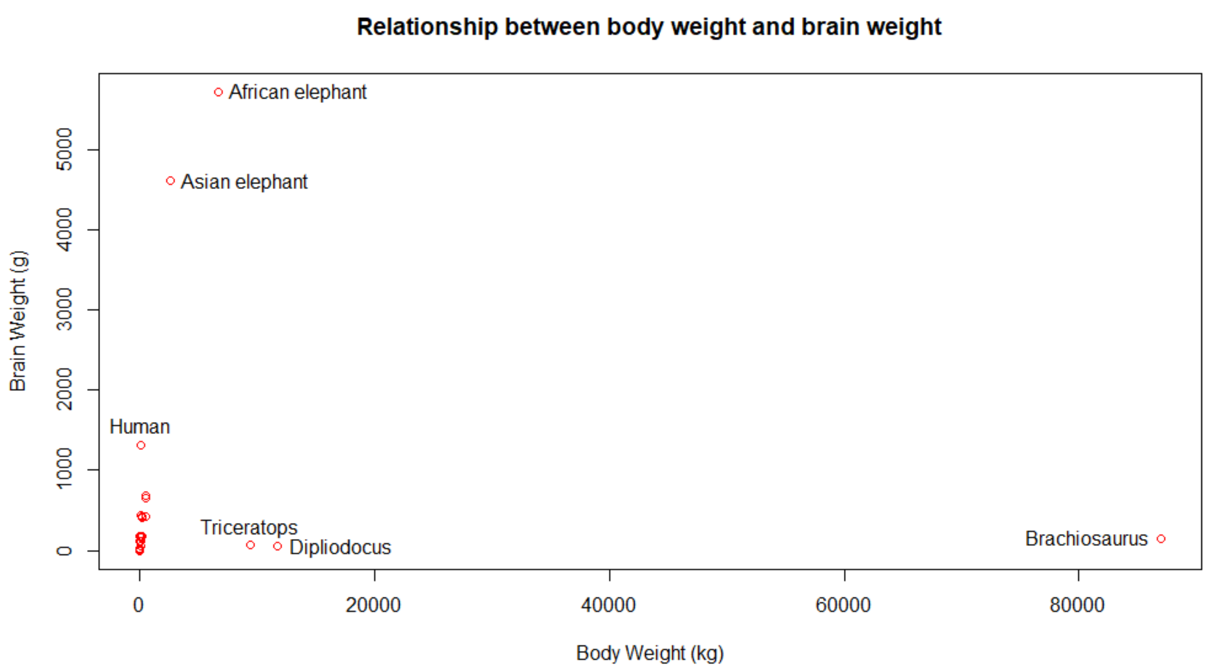
```
##                      body brain
## Mountain beaver      1.35   8.1
## Cow                465.00 423.0
## Grey wolf           36.33 119.5
## Goat                27.66 115.0
## Guinea pig           1.04   5.5
## Dipliodocus      11700.00  50.0
```

3. Scatter plot of the data with x-axis ‘body’ and y-axis ‘brain.’ Identify as many data points as you can. Comment on the plot.

```
#plot(dat$body, dat$brain, xlab = "Body Weight (kg)", ylab = "Brain Weight (g)",
#     main = "Relationship between body weight and brain weight",
#     col = "red")

# ID points we want to label:
#identify(dat$body, dat$brain, labels = rownames(dat))

# Plots were generated using commands above and saved, then inserted into this document.
```



This plot is definitely interesting. It looks like these 3 dinosaurs, Triceratops, Diplodocus, and Brachiosaurus, have very different brain to body ratios than the rest of the animals. We should do a log transform to see if that gives us a linear relationship, but even then it’s possible we might need to remove the dinosaurs from the data to get a good linear relationship between the brain weight and the body weight.

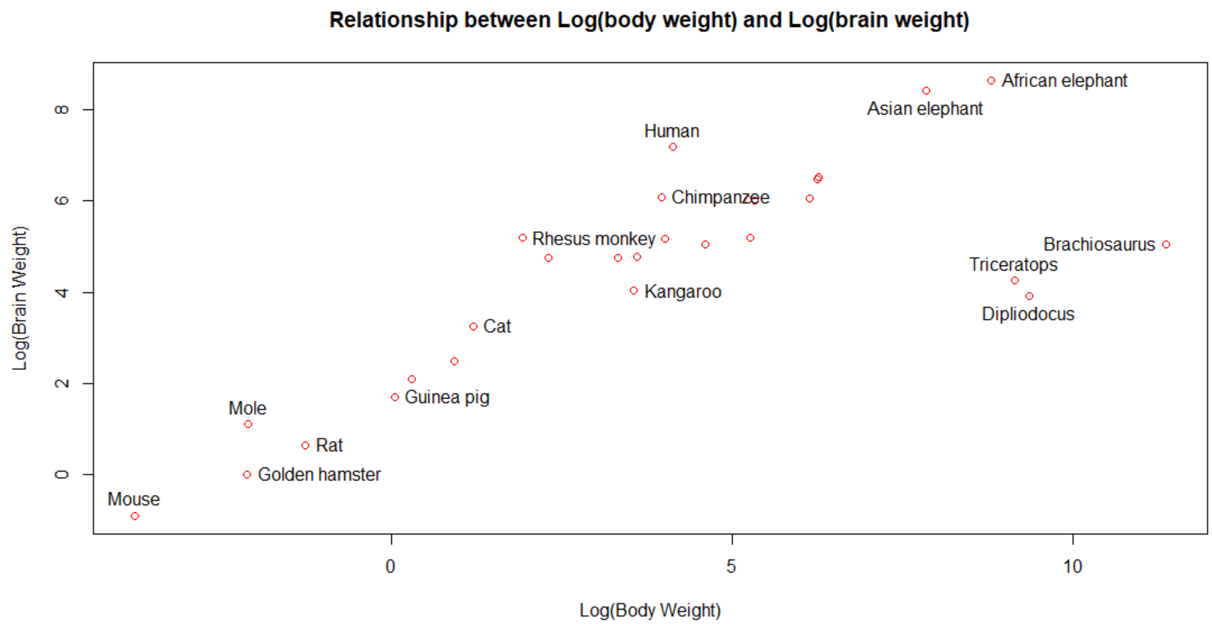
4. Show the scatter plot of the data after the logarithmic transformation. Identify as many points as you can. Comment on the plot. Obtain the simple linear regression model. Draw the line on the scatter plot. Make the graph as informative as possible.

```
l_dat <- log(dat[,1:2])


#plot(l_dat$body, l_dat$brain, xlab = "Log(Body Weight)", ylab = "Log(Brain Weight)",
#     main = "Relationship between Log(body weight) and Log(brain #weight)",
#     col = "red")
```

```r
# ID points we want to label:
#identify(l_dat$body, l_dat$brain, labels = rownames(l_dat))

# Plots were generated using commands above and saved, then inserted into this document.
```



Do the linear regression and plot again…

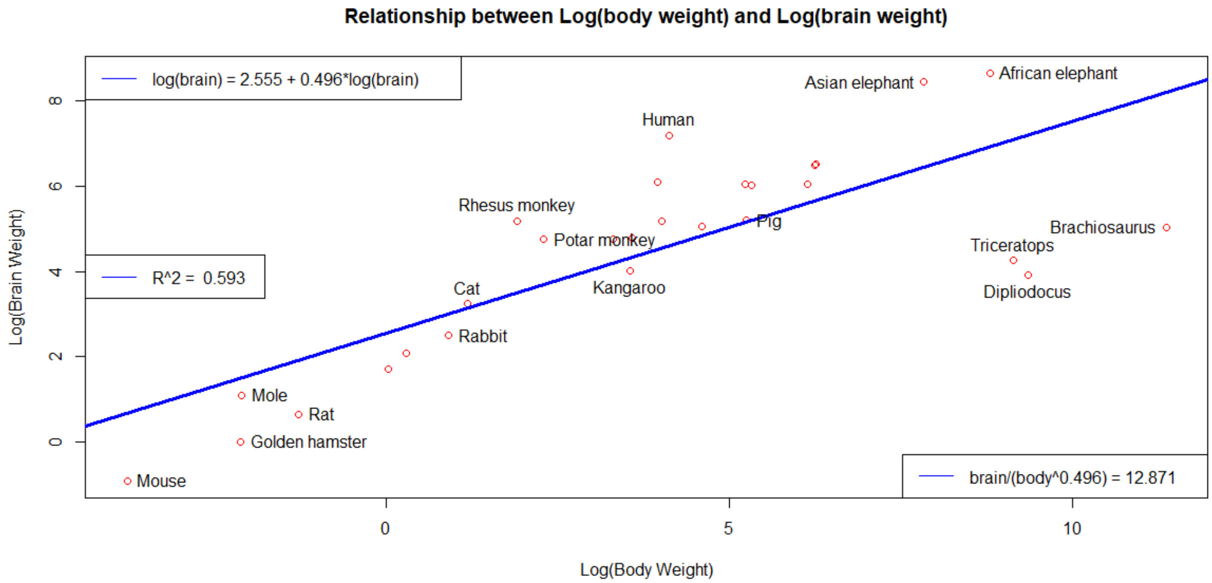
```r
mod <- lm(brain ~ body, l_dat)

#plot(l_dat$body, l_dat$brain, xlab = "Log(Body Weight)", ylab = "Log(Brain Weight)",
#     main = "Relationship between Log(body weight) and Log(brain weight)",col = "red")

#identify(l_dat$body, l_dat$brain, labels = rownames(l_dat))


# Now lets add the linear regression to the plot.
#abline(mod, col = "blue", lwd = 3, lty = 1)
#legend("topleft", legend = "log(brain) = 2.555 + 0.496*log(brain) ", lty = 1, col = "blue")
#legend("bottomright", legend = "brain/(body^0.496) = 12.871", lty = 1, col = "blue")
#legend("left", legend = paste("R^2 = ", round(summary(mod)$adj.r.squared,3)), lty = 1, col = "blue")

# Plots were generated using commands above and saved, then inserted into this document.
```



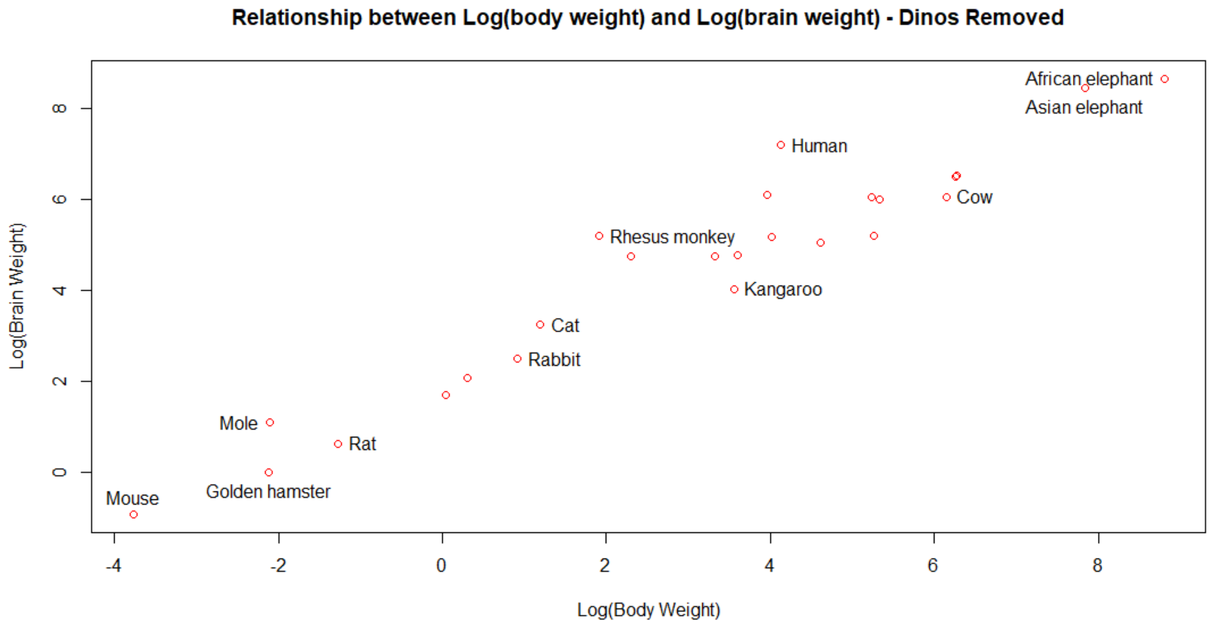
The Log of brain weight and log of body weight seem to have a much more linear relationship than the non-log forms of each value. However when we do the actual linear fit, we get a low R^2 value of 0.592, indicating the fit isn't very good, further we can see the dinosaurs are still very far from the rest of the animals so it might be good to think about removing those from the data and trying the linear fit again.

5. Remove the dinosaurs. Show the scatter plot of the resultant data after the logarithmic transformation. Identify as many points as you can. Comment on the plot. Obtain the simple linear regression model. Draw the line on the scatter plot. Make the graph as informative as possible.

```
dinos <- c("Dipliodocus", "Brachiosaurus", "Triceratops")
dat_dino <- dat[!rownames(dat) %in% dinos,]
l_dat_dino <- l_dat[!rownames(l_dat) %in% dinos,]

#plot(l_dat_dino$body, l_dat_dino$brain, xlab = "Log(Body Weight)", ylab = "Log(Brain Weight)",
#     main = "Relationship between Log(body weight) and Log(brain weight) - Dinos Removed",
#     col = "red")

# ID points we want to label:
#identify(l_dat_dino$body, l_dat_dino$brain, labels = rownames(l_dat_dino))
# Plots were generated using commands above and saved, then inserted into this document.
```



The relationship between the log of the body weight and the log of the brain weight after removing the dinosaurs looks much more linear, which makes sense as the dinosaurs definitely appeared to be outliers.

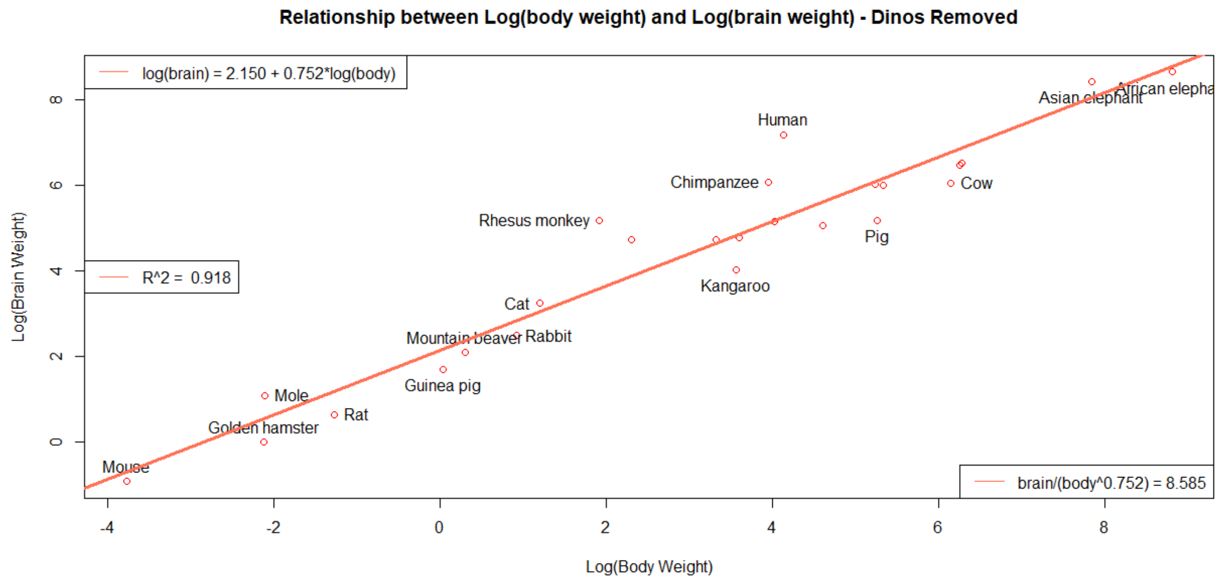
Do the linear regression and plot again…

```
mod_dino <- lm(brain ~ body, l_dat_dino)
# Now lets add the linear regression to the plot.
#plot(l_dat_dino$body, l_dat_dino$brain, xlab = "Log(Body Weight)", ylab = "Log(Brain Weight)",
#     main = "Relationship between Log(body weight) and Log(brain weight) - Dinos Removed",
#     col = "red")

# ID points we want to label:
#identify(l_dat_dino$body, l_dat_dino$brain, labels = rownames(l_dat_dino))

#abline(mod_dino, col = "coral1", lwd = 3, lty = 1)
#legend("topleft", legend = "log(brain) = 2.150 + 0.752*log(body) ", lty = 1, col = "coral1")
#legend("bottomright", legend = "brain/(body^0.752) = 8.585", lty = 1, col = "coral1")
#legend("left", legend = paste("R^2 = ", round(summary(mod_dino)$adj.r.squared,3)), lty = 1, col = "cor

# Plots were generated using commands above and saved, then inserted into this document.
```



6. Write the prediction model coming from Question 5 directly in terms of the original variables.
   $\text{log(brain)} = 2.150 + 0.752 log(body)$
   $log(brain) = log(8.585) + 0.752\text{log(body)}$
   $\text{log(brain)} = \text{log(8.585)} + 0.752 log(body)$
   $log(brain) = log(8.585\ \ \text{body}\hat{}0.752)$
   brain/(body^0.752) = 8.585

7. Calculate the ratio of the model from Question 6 for all animals in the data. Arrange the ratios in increasing order of magnitude. Comment on the output.

```r
# Starting with the original animals data that still includes dinosaurs.
dat$ratio <- dat$brain/(dat$body^0.752)
dat <- dat[order(dat$ratio),]
dat
```

```
##                      body  brain      ratio
## Brachiosaurus   87000.000  154.5 0.02981330
## Dipliodocus     11700.000   50.0 0.04362086
## Triceratops      9400.000   70.0 0.07199559
## Pig               192.000  180.0 3.45326559
## Kangaroo           35.000   56.0 3.86410445
## Cow               465.000  423.0 4.17268640
## Jaguar            100.000  157.0 4.91925859
## Golden hamster      0.120    1.0 4.92556101
## Rat                 0.280    1.9 4.94869584
## Guinea pig          1.040    5.5 5.34015199
## Horse             521.000  655.0 5.93170210
## Rabbit              2.500   12.1 6.07483496
## Giraffe           529.000  680.0 6.08793837
```

```
## Mountain beaver      1.350    8.1  6.46359334
## Mouse                0.023    0.4  6.82402578
## Gorilla            207.000  406.0  7.36065282
## African elephant  6654.000 5712.0  7.61780648
## Grey wolf           36.330  119.5  8.01767275
## Donkey             187.100  419.0  8.19623751
## Sheep               55.500  175.0  8.53748051
## Goat                27.660  115.0  9.47163610
## Cat                  3.300   25.6 10.43079674
## Asian elephant    2547.000 4603.0 12.63883978
## Mole                 0.122    3.0 14.59414517
## Potar monkey        10.000  115.0 20.35625302
## Chimpanzee          52.160  440.0 22.49131325
## Rhesus monkey        6.800  179.0 42.34540868
## Human               62.000 1320.0 59.25095855
```

```r
library(car)
```

```
## Loading required package: carData
```

```r
outlierTest(mod)
```

```
## No Studentized residuals with Bonferonni p < 0.05
## Largest |rstudent|:
##              rstudent unadjusted p-value Bonferonni p
## Dipliodocus -2.507366           0.019026      0.53272
```

```r
# This data shows that humans have the greatest brain to body ratio of the 28
# animals included in this study.  Our evolutionary neighbors, monkeys and chimps
# also have higher than the average brain to body ratios as well.
#Using the outlierTest function we can see that none of the brain to body
#ratios are outliers using the Bonferonni adjusted p-value.
```

8. Comment on the graphs in Questions 5 and 6.(Assuming 4 and 5 were meant)

While both plots to the eye look decently linear, although when the dinosaurs are removed it does look more linear, the true test of the linear relationship between the log of the brain weight and the log of the body weight is to complete a linear fit and examine the R2 value to see how well the fit, fits on the data. The original data has an R2 of 0.593 while the data when leaving out the dinosaurs has an R2 of 0.918, indicating that the relationship is much more linear having removed the dinosaurs from the data. However using the outlierTest method in the car package none of the dinosaurs or any other animals for that fact are outliers when using the Bonferonni adjusted p-value.