Stat 242 Quiz – Topics Drawn from Chapters 9 through 12

What's Your Name? ________________________________

We have a data set with the following information about different species of mammals:

- `Species`: The species of mammal
- `Body`: Average weight of the body
- `Gestation`: Average length of pregnancy
- `Litter`: Average litter size
- `Brain`: Average weight of the brain

We will use brain size as the response variable and the other variables as explanatory variables. Here is a look at the first few rows of the data, as well as the species in the data set. Note that there appear to be some closely related species in the data set; for example, there are three species of Porcupine, and four species of Deer mouse.

```
head(mammals)
```

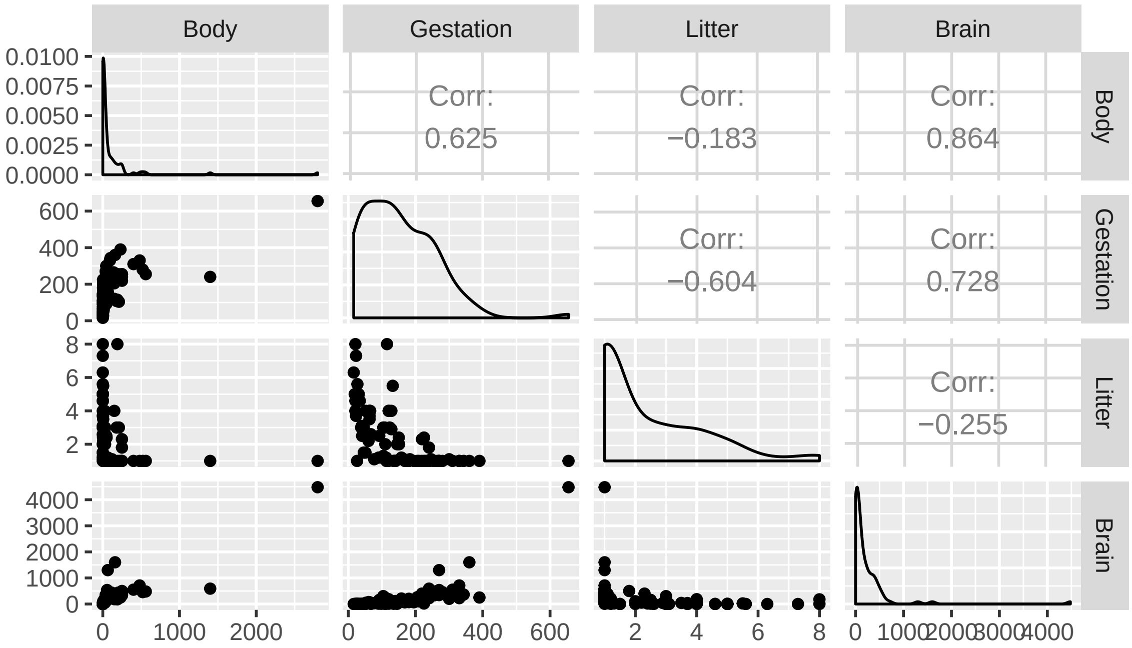
```
##            Species    Body Gestation Litter  Brain
## 1         Aardvark    2.20        31    5.0    9.6
## 2         Acouchis    0.78        98    1.2    9.9
## 3 African elephant 2800.00       655    1.0 4480.0
## 4          Agoutis    2.80       104    1.3   20.3
## 5        Axis deer   89.00       218    1.0  219.0
## 6           Badger    6.00        60    2.2   53.0
```

```
mammals$Species
```

```
##  [1] Aardvark            Acouchis            African elephant   
##  [4] Agoutis             Axis deer           Badger             
##  [7] Barbary sheep       Barking deer        Bat-eared fox      
## [10] Beaked whale        Beaver              Black buck antelope
## [13] Bush baby           Canadian beaver     Capybara           
## [16] Caribou             Cattle              Chimpanzee         
## [19] Chinchilla          Deer mouse I        Deer mouse II      
## [22] Deer mouse III      Deer mouse IV       Dog                
## [25] Dolphin             Domestic cat        Domestic goat      
## [28] Domestic pig        Domestic sheep      Duikers            
## [31] Eland               Elephant shrew I    Elephant shrew II  
## [34] Elk                 Fallow deer         Flying squirrel    
## [37] Fur seal            Gentle lemur        Gorilla            
## [40] Gray fox            Grizzly bear        Guinea pig         
## [43] Hamadryas baboon    Hamster I           Hamster II         
## [46] Harp seal           Hedgehog            Hippopotamus       
## [49] Hopping mouse       Horse               House mouse        
## [52] Howler monkey       Human being         Hyrax              
## [55] Jack rabbit         Kinkajou            Leaf monkey        
## [58] Lemur               Leopard             Lion               
## [61] Llama               Long-nose armadillo Lynx               
## [64] Nutria              Orangutan           Porcupine I        
## [67] Porcupine II        Porcupine III       Porpoise           
## [70] Pygmy gerbil        Pygmy hippopotamus  Quokka             
## [73] Raccoon             Rat I               Rat II             
## [76] Red deer            Red fox             Rhesus monkey I    
## [79] Rhesus monkey II    Ring-tail monkey    Sambar             
## [82] Sea lion            Slow loris          Spider monkey I    
## [85] Spider monkey II    Tapir               Tiger              
## [88] Tree shrew          Tree squirrel       Vervet guenon      
## [91] Vicuna              Weddell seal        Western baboon     
## [94] White-handed gibbon Wild boar           Yak                
## 96 Levels: Aardvark Acouchis African elephant Agoutis Axis deer ... Yak
```

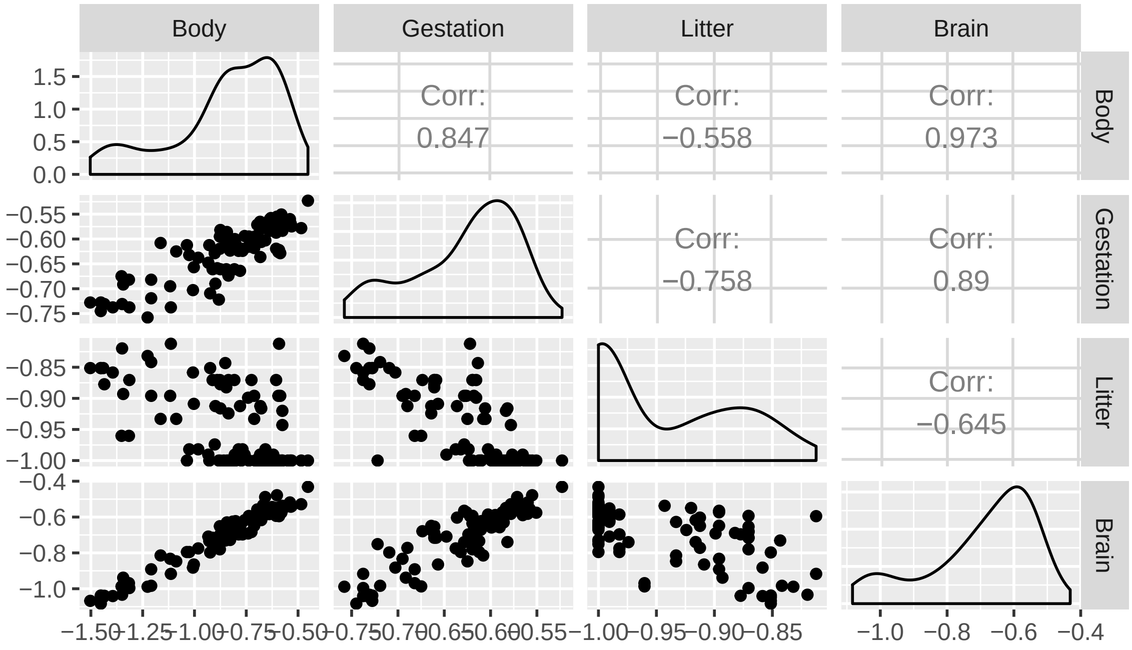
Initial Set Up

```
ggpairs(mammals %>% select(-Species))
```



```
mammals_transformed <- mammals %>%
  mutate(
    Body = -1/(Body^0.1),
    Gestation = -1/(Gestation^0.1),
    Litter = -1/(Litter^0.1),
    Brain = -1/(Brain^0.1)
  )

ggpairs(mammals_transformed %>% select(-Species))
```



Model 1: All Observations

```r
lm_fit <- lm(Brain ~ Body + Gestation + Litter, data = mammals_transformed)
summary(lm_fit)
```

```
##
## Call:
## lm(formula = Brain ~ Body + Gestation + Litter, data = mammals_transformed)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.069831 -0.020271 -0.002648  0.024110  0.080942
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.22674    0.13609  -1.666  0.09909 .
## Body         0.49035    0.02303  21.295  < 2e-16 ***
## Gestation    0.42641    0.13799   3.090  0.00265 **
## Litter      -0.22420    0.07939  -2.824  0.00581 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03037 on 92 degrees of freedom
## Multiple R-squared:  0.9654, Adjusted R-squared:  0.9643
## F-statistic: 856.5 on 3 and 92 DF,  p-value: < 2.2e-16
```

```r
confint(lm_fit)
```

```
##                  2.5 %      97.5 %
## (Intercept) -0.4970256  0.04354491
## Body         0.4446130  0.53607702
## Gestation    0.1523581  0.70046413
## Litter      -0.3818769 -0.06653050
```

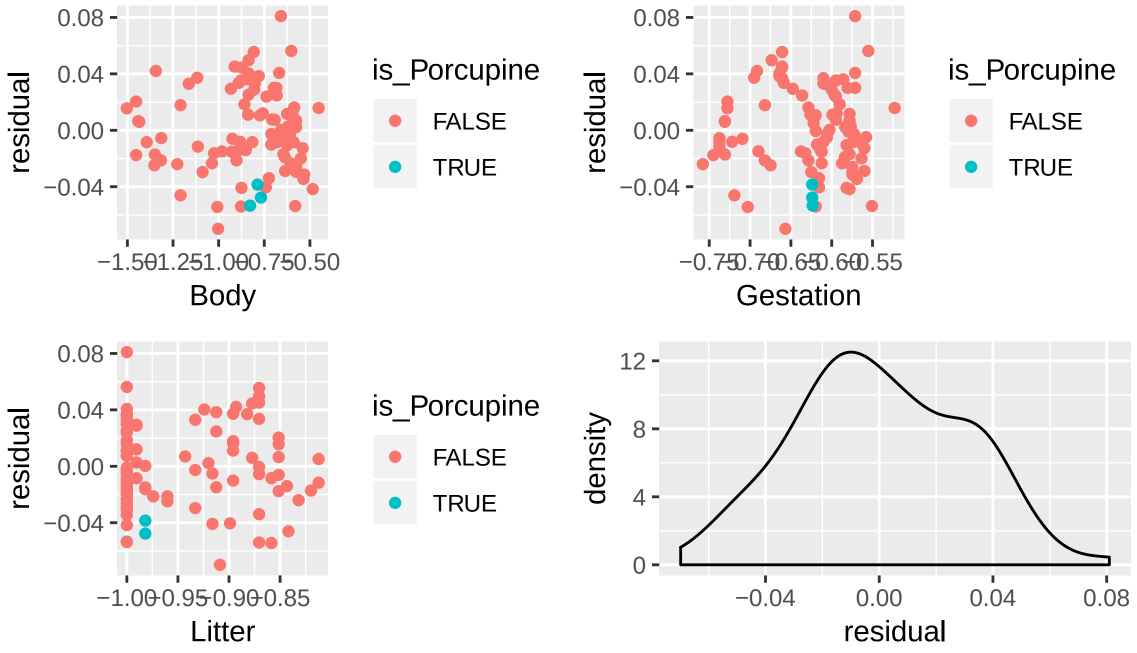
Examining Residuals

Let's look at the residuals plots. Recalling that there were three species of Porcupines in the data set, I have used a different color for the residuals for those species.

```r
mammals_transformed <- mammals_transformed %>%
  mutate(
    is_Porcupine = Species %in% c("Porcupine I", "Porcupine II", "Porcupine III"),
    residual = residuals(lm_fit)
  )

p1 <- ggplot(data = mammals_transformed, mapping = aes(x = Body, y = residual, color = is_Porcupine)) +
  geom_point()
p2 <- ggplot(data = mammals_transformed, mapping = aes(x = Gestation, y = residual, color = is_Porcupine)) +
  geom_point()
p3 <- ggplot(data = mammals_transformed, mapping = aes(x = Litter, y = residual, color = is_Porcupine)) +
  geom_point()
p4 <- ggplot(data = mammals_transformed, mapping = aes(x = residual)) +
  geom_density()

grid.arrange(p1, p2, p3, p4, nrow = 2, ncol = 2)
```



Here are the residuals for the three species of porcupines in the data set:

```
mammals_transformed %>%
  filter(is_Porcupine) %>%
  pull(residual)
```

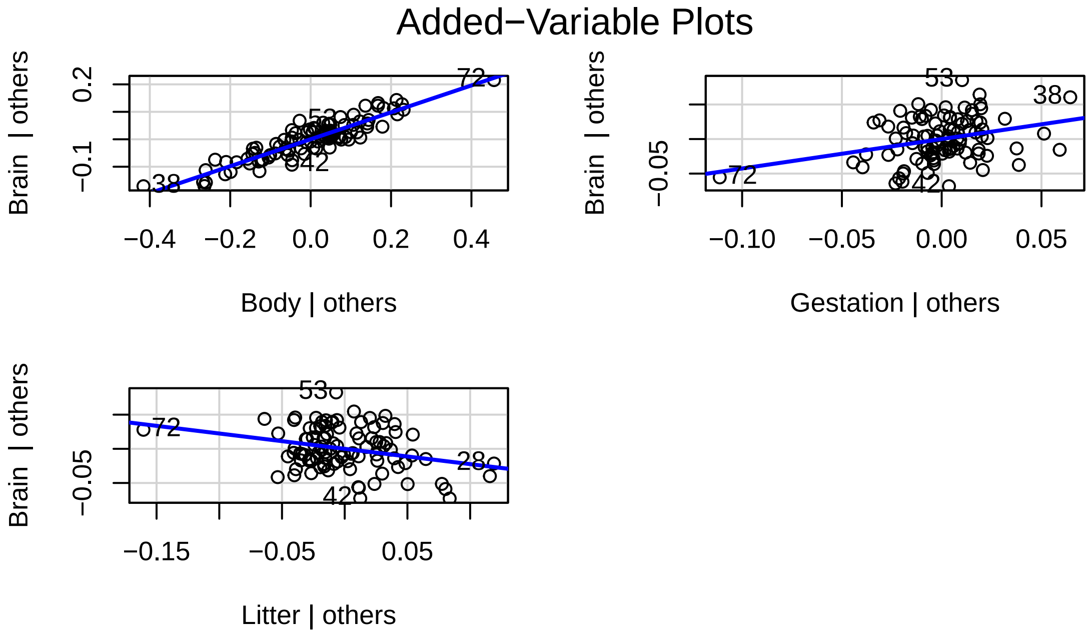
```
## [1] -0.03851209 -0.04770483 -0.05340879
```

Variance Inflation Factor and added variable plot

```
vif(lm_fit)
```

```
##      Body Gestation    Litter
##  3.754219  6.072703  2.494167
```

```
avPlots(lm_fit)
```



Model 2: Setting aside some observations

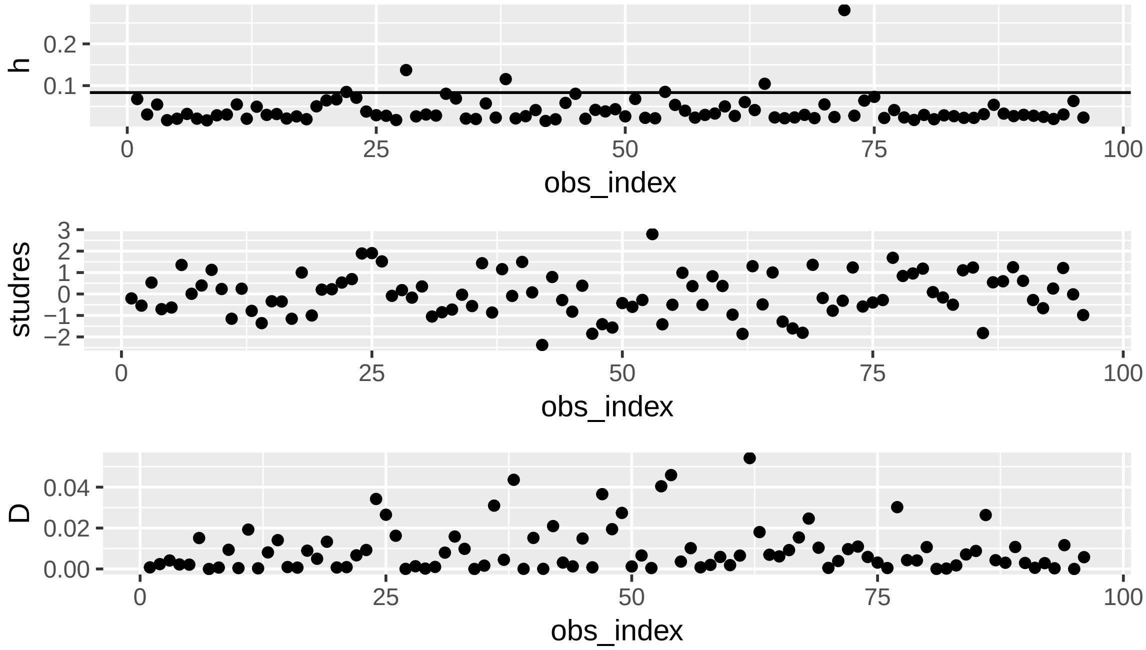
```
mammals_transformed <- mammals_transformed %>%
  mutate(
    obs_index = row_number(),
    h = hatvalues(lm_fit),
    studres = rstudent(lm_fit),
    D = cooks.distance(lm_fit)
  )

p1 <- ggplot(data = mammals_transformed, mapping = aes(x = obs_index, y = h)) +
  geom_hline(yintercept = 2*4/nrow(mammals_transformed))+
  geom_point()

p2 <- ggplot(data = mammals_transformed, mapping = aes(x = obs_index, y = studres)) +
  geom_point()

p3 <- ggplot(data = mammals_transformed, mapping = aes(x = obs_index, y = D)) +
  geom_point()

grid.arrange(p1, p2, p3, ncol = 1)
```



```
obs_to_investigate <- c(28, 38, 53, 64, 72)

mammals_transformed <- mammals_transformed %>%
  mutate(
    suspicious = row_number() %in% obs_to_investigate
  )
mammals_no_suspicious <- mammals_transformed %>% filter(!suspicious)
```

```r
lm_fit_no_suspicious <- lm(Brain ~ Body + Gestation + Litter, data = mammals_no_suspicious)
summary(lm_fit_no_suspicious)
```

```
##
## Call:
## lm(formula = Brain ~ Body + Gestation + Litter, data = mammals_no_suspicious)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.068596 -0.019677 -0.000896  0.022801  0.059827
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.31302    0.17954  -1.743   0.0848 .
## Body         0.50516    0.02647  19.082   <2e-16 ***
## Gestation    0.31709    0.17734   1.788   0.0773 .
## Litter      -0.25513    0.10075  -2.532   0.0131 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02963 on 87 degrees of freedom
## Multiple R-squared:  0.9679, Adjusted R-squared:  0.9668
## F-statistic: 875.2 on 3 and 87 DF,  p-value: < 2.2e-16
```

Problems

(a) Explain why a transformation was necessary.

(b) Check all model conditions based on the model fit using the transformed data. For any conditions that are not met, suggest a step to take to address the problem.

(c) Summarize the findings from this analysis about the strength of evidence of an association between body size, gestation length, litter size, and brain weight.

(d) What is the interpretation of the coefficient estimate for the Body variable in the model fit including all observations (Model 1)?

(e) What is the interpretation of the confidence interval for the coefficient of the Body variable in the model fit including all observations (Model 1)? Include a description of the meaning of the phrase "95% confident".

(f) The variance inflation factor for Body is 3.75. Rounding up to 4 for convenience, what does this value say about the width of a confidence interval for the coefficient of Body in the linear model?

(g) In the added variable plot for the Body variable, what is on the horizontal and vertical axes of the plot? How does the slope of the line in that plot relate to the coefficient estimate in the linear model?

(h) What is a high leverage observation? Why can high leverage observations be problematic?

(You should be able to draw a picture of a simple linear regression setting illustrating why this is a problem.)

(i) What does Cook's distance measure, at an intuitive level?

(j) Define multicollinearity in a sentence or two. Why can multicollinearity be problematic?