Transformations

Merlise Clyde

Readings: Gelman & Hill Ch 2-4, ALR 8-9

Assumptions of Linear Regression

$$Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \ldots \beta_p X_{ip} + \epsilon_i$$

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  - constant variance
  - independent Normal errors

Animals

Read in Animal data from MASS. The data set contains measurements on body weight (kg) and brain weight (g) on 28 animals.

Let's try to predict brain weight from body weight.

```r
library(MASS)
data(Animals)
brain.lm = lm(brain ~ body, data=Animals)
```

Diagnostic Plots

```
## Warning in sqrt(crit * p * (1 - hh)/hh): NaNs produced

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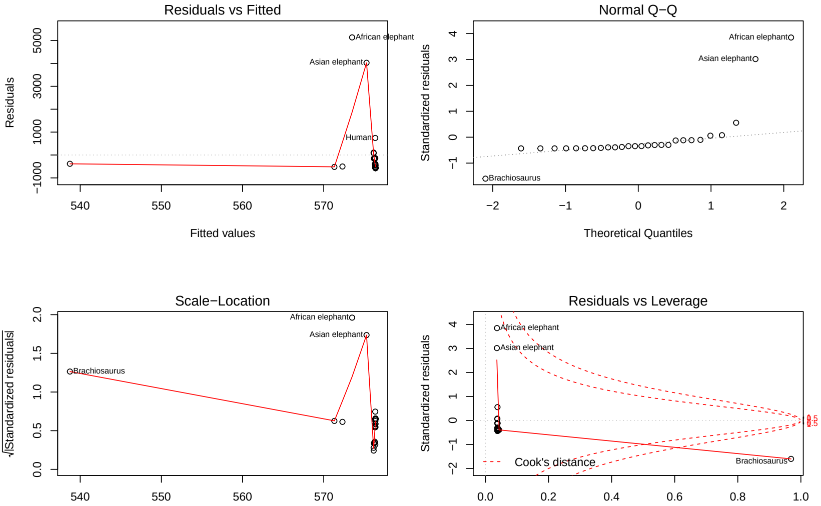

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- Other corrections for False Discoveries possible (STA 532)

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- Link https://en.wikipedia.org/wiki/Bonferroni_correction

Outliers

- Flag outliers after Bonferroni Correction $p_i < \alpha/n$

```
pval = 2*(1 - pt(abs(rstudent(brain.lm)), brain.lm$df -1))
rownames(Animals)[pval <  .05/nrow(Animals)]
```

```
## [1] "Asian elephant"   "African elephant"
```

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after removing the ith case

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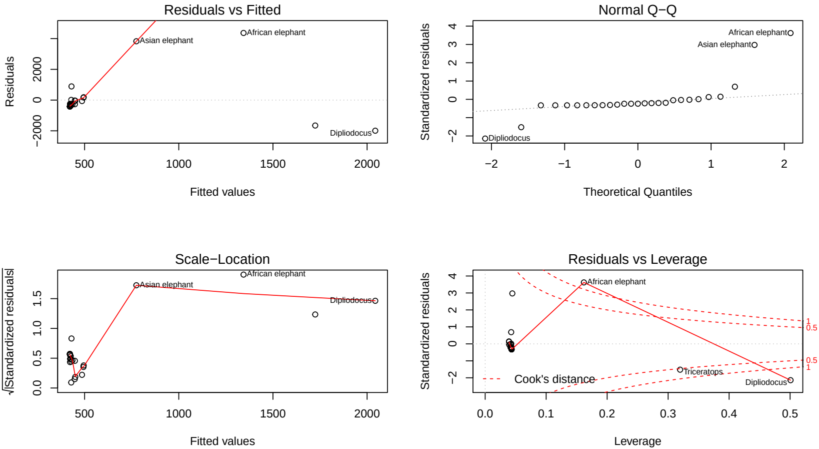
Flag cases where $D_i > 1$ or $D_i > 4/n$

```r
rownames(Animals)[cooks.distance(brain.lm) > 1]
```

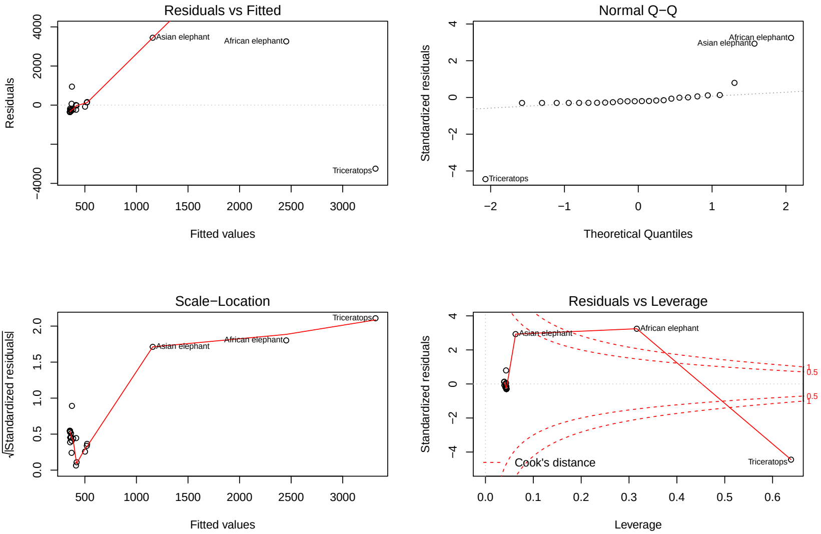
```
## [1] "Brachiosaurus"
```

Remove Influential Point & Refit

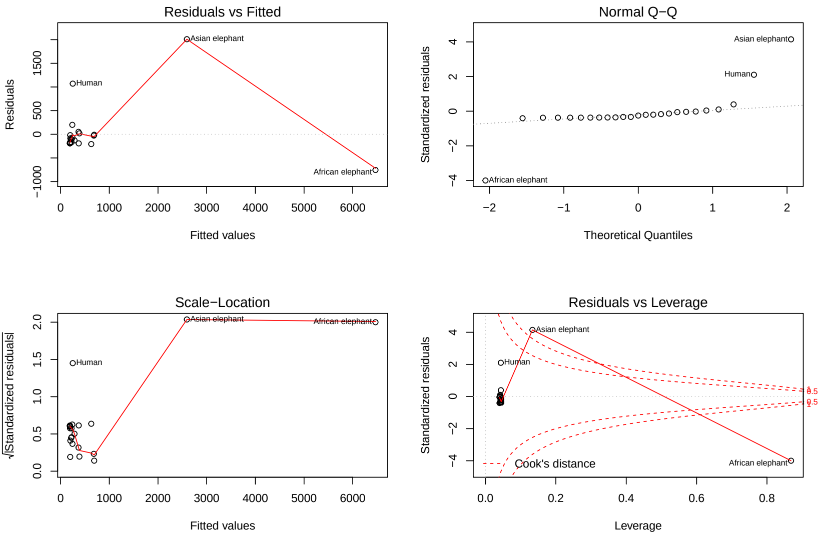
```
brain2.lm = lm(brain ~ body, data=Animals,
                 subset = !cooks.distance(brain.lm)>1)
par(mfrow=c(2,2)); plot(brain2.lm)
```



Keep removing points?



And another one bites the dust



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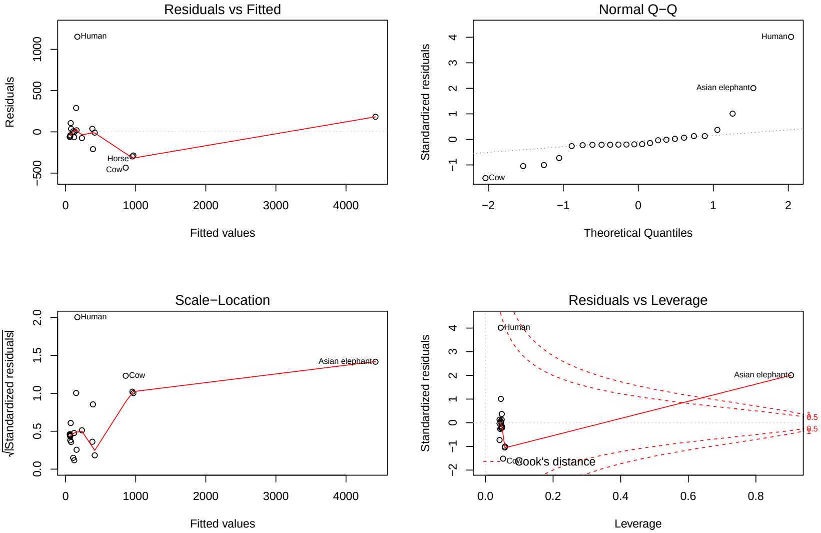
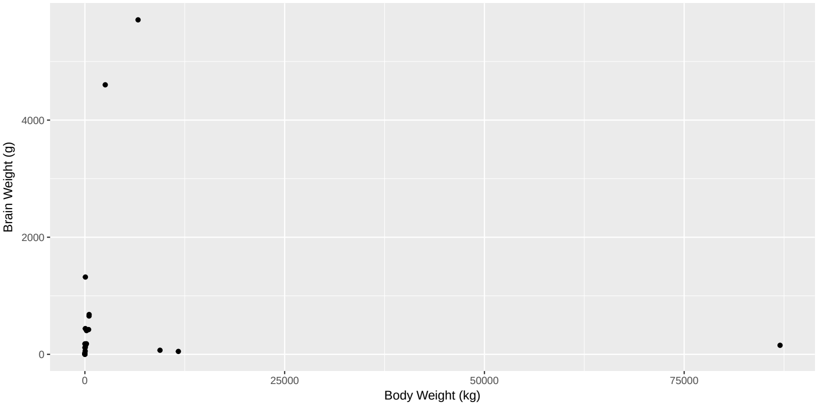


And they just keep coming!

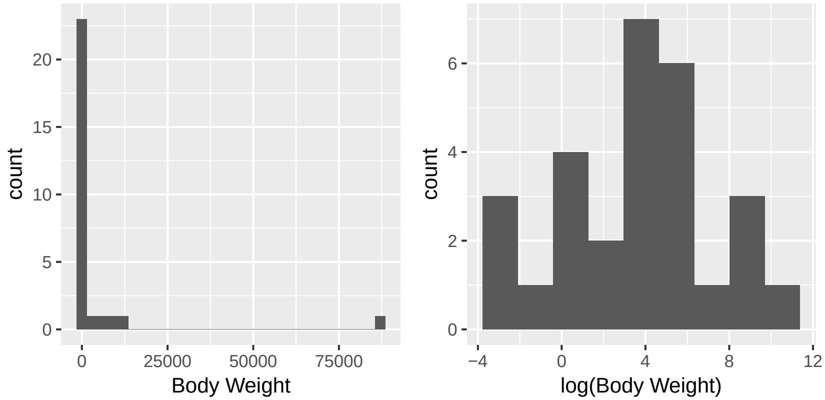
Figure 1: Walt Disney Fantasia

Plot of Original Data (what you should always do first!)

```
library(ggplot2)
ggplot(Animals, aes(x=body, y=brain)) +
  geom_point() +
  xlab("Body Weight (kg)") + ylab("Brain Weight (g)")
```

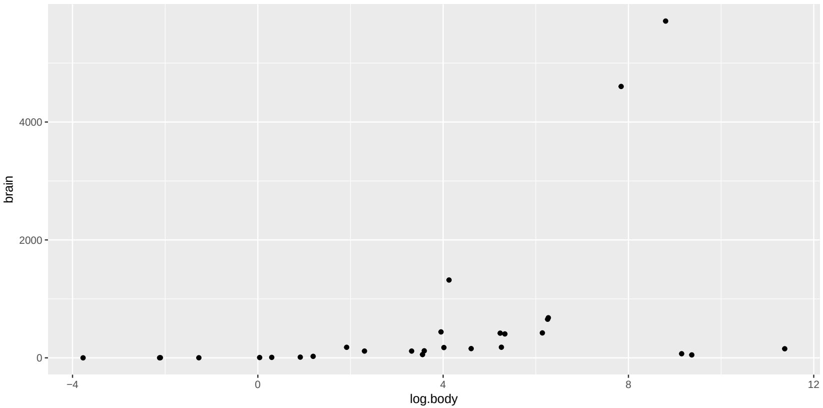


Log Transform



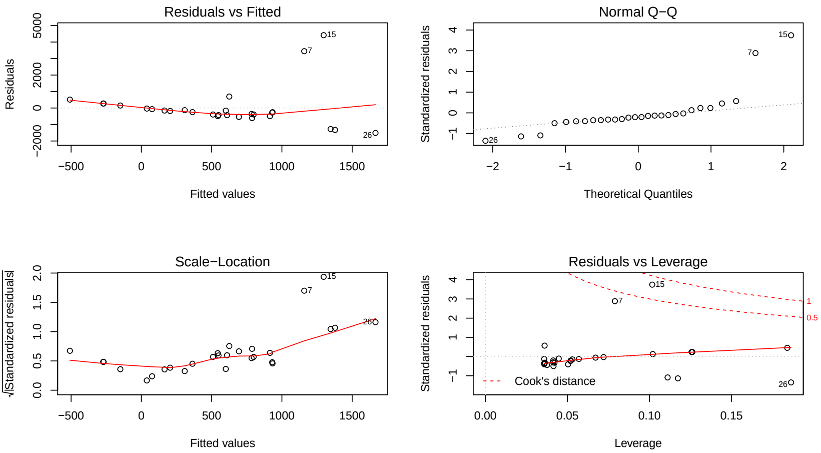
Plot of Transformed Data

```
Animals= mutate(Animals, log.body = log(body))
ggplot(Animals, aes(log.body, brain)) + geom_point()
```



```
#plot(brain ~ body, Animals, log="x")
```

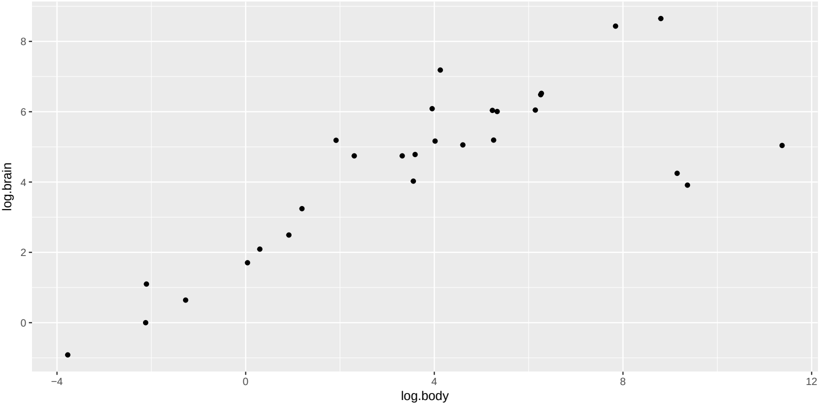
Diagnostics with log(body)



Variance increasing with mean

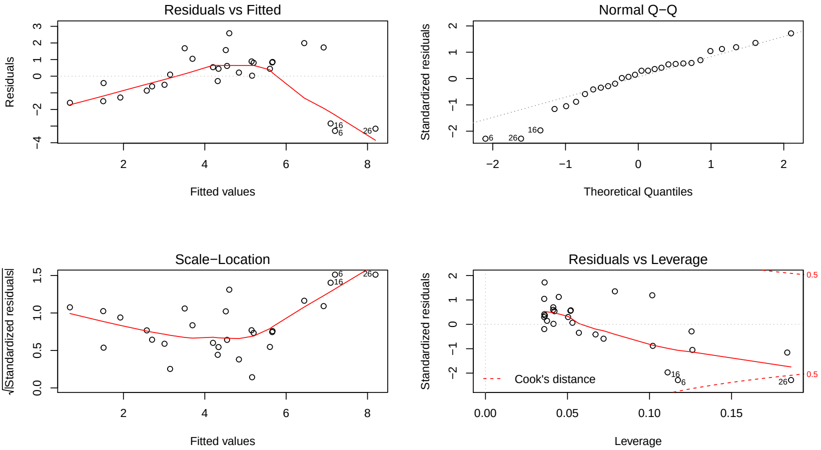
Try Log-Log

```
Animals= mutate(Animals, log.brain= log(brain))
ggplot(Animals, aes(log.body, log.brain)) + geom_point()
```



```
#plot(brain ~ body, Animals, log="xy")
```

Diagnostics with log(body) & log(brain)



Optimal Transformation for Normality

The BoxCox procedure can be used to find "best" power transformation λ of Y (for positive Y) for a given set of transformed predictors.

$$\Psi(\mathbf{Y}, \lambda) = \begin{cases} \frac{\mathbf{Y}^{\lambda} - 1}{\lambda} & \text{if } \lambda \neq 0 \\ \log(\mathbf{Y}) & \text{if } \lambda = 0 \end{cases}$$

Find value of λ that maximizes the likelihood derived from $\Psi(\mathbf{Y}, \lambda) \sim \mathrm{N}(\mathbf{X}\beta_{\lambda}, \sigma^2_{\lambda})$ (need to obtain distribution of **Y** first)

Find λ to minimize

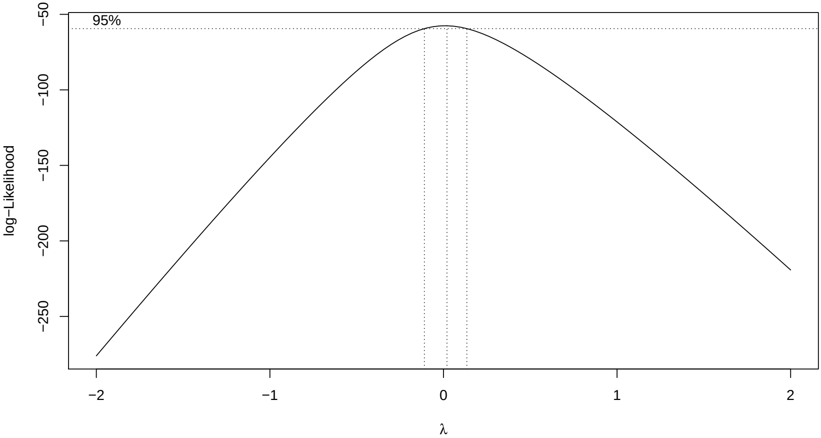
$$\mathrm{RSS}(\lambda) = \|\Psi_M(\mathbf{Y}, \lambda) - \mathbf{X}\hat{\beta}_{\lambda}\|^2$$

$$\Psi_M(\mathbf{Y}, \lambda) = \begin{cases} (\mathrm{GM}(\mathbf{Y})^{1-\lambda}(\mathbf{Y}^{\lambda} - 1)/\lambda & \text{if } \lambda \neq 0 \\ \mathrm{GM}(\mathbf{Y}) \log(\mathbf{Y}) & \text{if } \lambda = 0 \end{cases}$$

where $\mathrm{GM}(\mathbf{Y}) = \exp(\sum \log(Y_i)/n)$ (Geometric mean)

boxcox in R: Profile likelihood

```r
library(MASS)
boxcox(braintransX.lm)
```



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- Reproducibility - describe steps and decisions

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- should you test each one individually or as a group; if as a group how do you think you would you do this using lm?
- do you think your final model is adequate? What else might you change?

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After you determine whether dinos can stay or go and refine your model, what about prediction?

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- Can you find any data on Rose-Breasted Cockatoo brain sizes? Are the values in the prediction interval?