STA 371H Scribes Notes

Prediction Intervals

- Initially, we tried to figure out how much a value deviated from the least squares line.
- With an interval we determined accuracy by seeing how many 'cases' fall within it.

Odometer vs. Mileage graph:

- Standard deviation: how much a data point deviates from the line.
- How spread out is the data?
 - We look at the shaded area (1 standard deviation)
 - How accurate is this shaded area?
 - Figure out by counting how many cases are in the area
 - 1 standard deviation= 65%-75%
 - 2 standard deviation = 95%

Brain vs. Body graph:

- Transform the graph to a log scale to get linear data
- Dashed lines: confidence interval borders
 - This is prediction of confidence interval on log scale
 - On the original scale, the confidence intervals (dashed lines) would be curved.
- In the past, we used the equation:

$$y_i = \hat{B}_o + \hat{B}_i x_i + e_i$$

- When estimating the value of y* for a new x*:

$$\hat{q}^* = \hat{B}_0 + \hat{B}_1 X^*$$

$$q^* = \hat{q}^* \pm ?$$

$$\pm 1\hat{O}_e$$

$$\pm 2\hat{O}_e$$
- likely size of error

- The predicted y could be +/- 1 standard deviation or 2 standard deviations
- So the equation to find the upper and lower bound 1 standard deviation away would be:
 - O Upper:

- After converting to the log scale:

o Upper:

$$\frac{\log y^* = \hat{B}_0 + \hat{B}_1 \log x_* + \hat{\sigma}_{\varepsilon}}{e^{\log y^*} = e^{\hat{B}_0} + \hat{B}_1 \log x_* + \hat{\sigma}_{\varepsilon}}$$

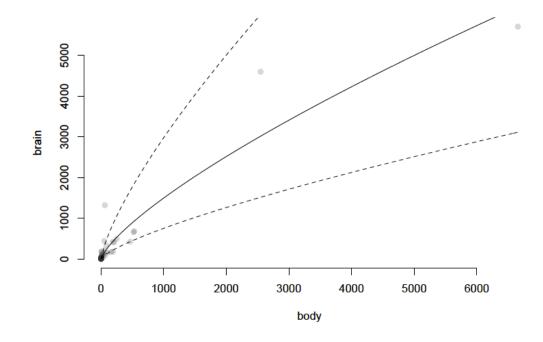
$$y^* = e^{\hat{B}_0} \times_*^{\hat{B}_1} e^{\hat{\sigma}_{\varepsilon}}$$

o Lower:

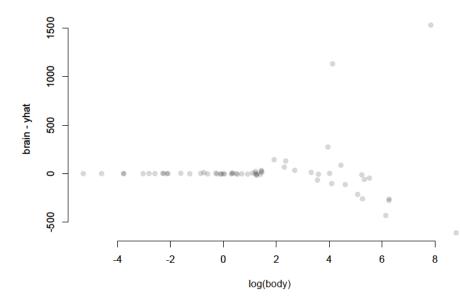
$$|094* = \hat{B}_0 + \hat{B}_1 |09x_* - \hat{\sigma}_{\epsilon}$$

$$4* = e^{\hat{B}_0} x_*^{\hat{B}_1} e^{-\hat{\sigma}_{\epsilon}}$$

- From the graph, you can see that when the confidence intervals are plotted, they "fan out":



- o Bigger errors as you move to the right.
- When you graph the residuals, you can see there are more errors with a larger body size:



Transformation:

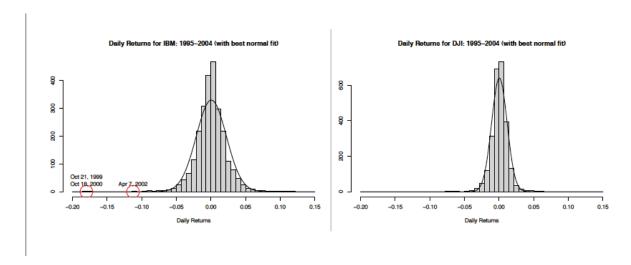
- 1. Estimate everything from model on log scale
- 2. Transform last

Regression:

- Sampling distribution: distribution of samples fit in linear line
- Confidence in your estimates → stability of those estimates under influence of chance
- Bootstrapping: Think of sample as the population, and then resample from sample with **replacement**.
 - o Two criteria:
 - Sample needs to be of the same size as the original sample
 - Sample with replacement or else you will have no variability
 - The goal of bootstrapping is to replicate the variability of the original population
- Residuals also follow normal distribution
 - Put in: (Pg. 111; equations 4.6 & 4.7)

$$\begin{split} \widehat{\beta}_0 &\sim & \text{N}\left(\beta_0, \sigma_0^2\right) \\ \widehat{\beta}_1 &\sim & \text{N}\left(\beta_1, \sigma_1^2\right) \,. \end{split}$$

- Get out: errors bars (sampling distribution from B₀ & B₁)
- Residuals are an aggregate of nudges ("stuff" left out of the model) that you cannot forecast using variable x.
 - Mad libs example
 - Aggregate of positive and negative words to move the data point away from the line
 - Coin flip to decide whether to use a positive or negative word = binomial distribution
 - Good, we moved up one, bad we moved down one
 - We discovered the actual finished point did not deviate too much from the line.
- Conclusion: Cumulative effect of residuals is an aggregate of nudges that are described using a binomial distribution (if there are enough "nudges," a normal distribution will form)
 - o Ex: NASDAQ vs. IBM
 - NASDAQ is a better representation of the trend of the economy because it is an aggregate of different company's stocks put together.
 - IBM is just one "nudge," so it will not fit the normal distribution
 - As we add more nudges the distribution of residuals becomes more normal and less variable



- o Ex: School of fish vs. shark
 - School of fish is an aggregate of individual fish acting together, which will create a normal distribution
 - Shark is just the movement of one fish

Creatine R. & Creatine csv.

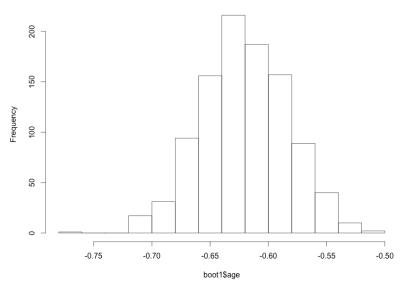
- This data set shows the effectiveness of the kidney by measuring creatine difference between the kidney and urine.
- "summary(lm1)"

 Makes assumption of normal distribution of residuals and gives you standard errors:

Coefficients:

- "boot1 = do(1000)*Im(creatclear~age, data=resample(creatinine))"
 - Perform bootstrapping 1000 times
 - Standard error of histogram:

Histogram of boot1\$age



hist(boot1\$age) \rightarrow [1] 0.03702145

o Check that standard error and standard deviation are similar

Bootlegging vs. Naïve Prediction Intervals

- Naïve prediction intervals:
 - Ignore uncertainty about parameters
 - Should be wider by the value of standard error to take into account the systematic components that have error

Takeaway Lesson

- Using bootlegging incorporates residual uncertainty as well as uncertainty about predictors (b₀ and b₁)
- The goal of bootstrapping is to replicate the variability of the original population
- As you use bootlegging, you should assume that your residuals follow a normal distribution