#### **Announcements**

- Homework
  - Homework 7 and Lab due on Monday
- Test a week from today!
  - Over Chapters 2,3,4
  - I'm trying to get study materials posted today or tomorrow
  - I'm also trying hard to have grading done by that point
- Final Project Info sent out today!
  - I'm getting potential datasets uploaded over the weekend.
  - You are always free to find your own as well. Just make sure they have enough variables to give your options for multiple regression.
- Polling: rembold-class.ddns.net

#### **ANOVA in R**

Run the ANOVA test on a linear fit to the data:

anova(lm(aldrin\$aldrin ~ aldrin\$depth))

```
Response: aldrin$aldrin

Df Sum Sq Mean Sq F value Pr(>F)

aldrin$depth 2 16.961 8.4803 6.1338 0.006367 **

Residuals 27 37.329 1.3826

---

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

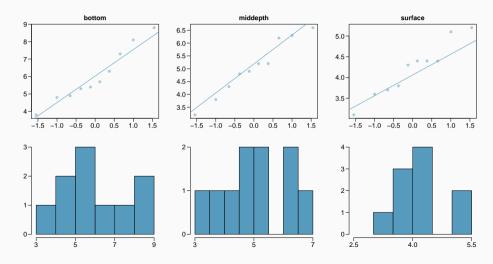
## Checking Conditions: (1) independence

Does this condition appear to be satisfied?

In this study the we have no reason to believe that the aldrin concentration won't be independent of each other.

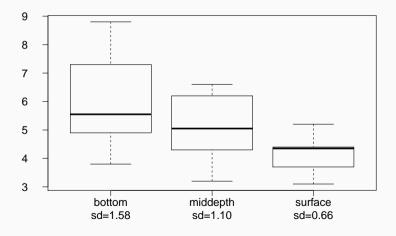
# **Checking Conditions: (2) approximately normal**

### Does this condition appear to be satisfied?



# **Checking Conditions: (3) constant variance**

Does this condition appear to be satisfied?



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#### Can you see any pitfalls with this approach?

- When we run too many tests, the Type 1 Error rate increases.
- This issue is resolved by using a modified significance level.

### **Multiple comparisons**

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where K is the number of comparisons being considered.

• If there are k groups, then usually all possible pairs are compared and  $K = \frac{k(k-1)}{2}$ .

## **Understanding Check!**

In the aldrin data set depth has 3 levels: bottom, mid-depth, and surface. If  $\alpha = 0.05$ , what should be the modified significance level for two sample t tests for determining which pairs of groups have significantly different means?

A) 
$$\alpha^* = 0.05$$

B) 
$$\alpha^* = 0.05/2 = 0.025$$

C) 
$$\alpha^* = 0.05/3 = 0.0167$$

D) 
$$\alpha^* = 0.05/6 = 0.0083$$

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If the ANOVA assumption of equal variability across groups is satisfied, we can use the data from all groups to estimate variability:

- Estimate any within-group standard deviation with  $\sqrt{MSE}$ , which is  $s_{pooled}$
- Use the error degrees of freedom, n k, for t-distributions

#### Difference in two means: after ANOVA

$$SE = \sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}} \approx \sqrt{\frac{MSE}{n_1} + \frac{MSE}{n_2}}$$

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	n	mean	sd
bottom	10	6.04	1.58
middepth	10	5.05	1.10
surface	10	4.2	0.66
overall	30	5.1	1.37

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
depth	2	16.96	8.48	6.13	0.0063
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$$T_{df_{E}} = \frac{(\bar{x}_{bottom} - \bar{x}_{middepth})}{\sqrt{\frac{MSE}{n_{bottom}} + \frac{MSE}{n_{middepth}}}}$$

$$T_{27} = \frac{(6.04 - 5.05)}{\sqrt{\frac{1.38}{10} + \frac{1.38}{10}}} = \frac{0.99}{0.53} = 1.87$$

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$$0.05 < p-value < 0.10$$
 (two-sided) 
$$\alpha^{\star} = 0.05/3 = 0.0167$$

Is there a difference between the average aldrin concentration at the bottom and at mid depth?

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 $0.05 (two-sided)
 $\alpha^* = 0.05/3 = 0.0167$$ 

Fail to reject  $H_0$ , the data do not provide convincing evidence of a difference between the average aldrin concentrations at bottom and mid depth.

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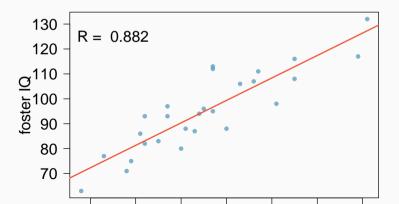
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Reject  $H_0$ , the data provide convincing evidence of a difference between the average aldrin concentrations at bottom and surface.

# Back to Linear Regression!

#### Nature or nurture?

In 1966 Cyril Burt published a paper called "The genetic determination of differences in intelligence: A study of monozygotic twins reared apart?" The data consist of IQ scores for [an assumed random sample of] 27 identical twins, one raised by foster parents, the other by the biological parents.



## Testing for the slope

Assuming that these 27 twins comprise a representative sample of all twins separated at birth, we would like to test if these data provide convincing evidence that the IQ of the biological twin is a significant predictor of IQ of the foster twin. What are the appropriate hypotheses?

- (a)  $H_0: b_0 = 0; H_A: b_0 \neq 0$
- (b)  $H_0: \beta_0 = 0; H_A: \beta_0 \neq 0$
- (c)  $H_0: b_1 = 0; H_A: b_1 \neq 0$
- (d)  $H_0: \beta_1 = 0; H_A: \beta_1 \neq 0$

Remember: We use  $\beta_0$  and  $\beta_1$  for the population intercept and slope and  $b_0$  and  $b_1$  for our samples intercept and slope.

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	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	9.2076	9.2999	0.99	0.3316
bioIQ	0.9014	0.0963	9.36	0.0000

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Remember: We lose 1 degree of freedom for each parameter we estimate, and in simple linear regression we estimate 2 parameters,  $\beta_0$  and  $\beta_1$ .

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$$T = \frac{0.9014 - 0}{0.0963} = 9.36$$
  
 $df = 27 - 2 = 25$   
 $p - value = P(|T| > 9.36) < 0.01$ 

## Confidence interval for the slope

Remember that a confidence interval is calculated as *point estimate*  $\pm$  *ME* and the degrees of freedom associated with the slope in a simple linear regression is n-2. Which of the below is the correct 95% confidence interval for the slope parameter? Note that the model is based on observations from 27 twins.

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- (a)  $9.2076 \pm 1.65 \times 9.2999$
- (b)  $0.9014 \pm 2.06 \times 0.0963$
- (c)  $0.9014 \pm 1.96 \times 0.0963$
- (d)  $9.2076 \pm 1.96 \times 0.0963$

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- (c)  $0.9014 \pm 1.96 \times 0.0963$
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- The regression output gives  $b_1$ ,  $SE_{b_1}$ , and **two-tailed** p-value for the *t*-test for the slope where the null value is 0.
- We rarely do inference on the intercept, so we'll be focusing on the estimates and inference for the slope.

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- Statistical inference, and the resulting p-values, are meaningless when you already have population data.
- If you have a sample that is non-random (biased), inference on the results will be unreliable.
- The ultimate goal is to have independent observations.