0-

alcohol

## Agenda

- 1. Type I and Type II error
- 2. ANOVA and Multiple Testing
- 3. Intro to the Bootstrap

**ANOVA** We just developed a way to compare differences in means between *two* groups. But what if we have more than two groups? Analysis of Variance (ANOVA) provides a mechanism for simultaneously assessing the differences between multiple groups.

The HELP study was a clinical trial for adult inpatients recruited from a detoxification unit. Patients with no primary care physician were randomized to receive a multidisciplinary assessment and a brief motivational intervention or usual care, with the goal of linking them to primary medical care. We'll consider two variables:

- cesd: Center for Epidemiologic Studies Depression measure at baseline (high scores indicate more depressive symptoms)
- substance: primary substance of abuse: alcohol, cocaine, or heroin

Are there important differences in the depression scores among patients depending on their drug of abuse?

```
library(mosaic)
favstats(cesd ~ substance, data = HELPrct)
##
     substance min Q1 median Q3 max
                                          mean
                                                      sd
                                                           n missing
## 1
       alcohol
                  4 26
                           36 42 58 34.37288 12.05041 177
                                                                    0
                           30 39 60 29.42105 13.39740 152
                                                                    0
## 2
       cocaine
                  1 19
                           35 43 56 34.87097 11.19812 124
## 3
        heroin
                  4 28
                                                                    \cap
grand_mean <- mean(~cesd, data = HELPrct)</pre>
ggplot(data = HELPrct, aes(y = cesd, x = substance)) +
  geom_boxplot() +
  geom_jitter(height = 0, width = 0.03, alpha = 0.4, aes(color = substance)) +
 geom_hline(vintercept = grand_mean, col = "blue", size = 1.5)
      60 -
                                                                                substance
      40
                                                                                   alcohol
   cesd
                                                                                   cocaine
                                                                                   heroin
      20
```

cocaine

substance

heroin

```
anova(lm(cesd ~ substance, data = HELPrct))
## Analysis of Variance Table
##
## Response: cesd
## Df Sum Sq Mean Sq F value Pr(>F)
## substance 2 2704 1352.1 8.9363 0.0001563 ***
## Residuals 450 68084 151.3
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

1. Write down the null and alternative hypotheses

2. Check the conditions for ANOVA: is independence reasonable? Is normality reasonable? What about equal variance?

3. Find the value of the test statistic (F) in the ANOVA table. Can you derive it from the other numbers in the table?

4. Draw a picture of the sampling distribution of F. How many degrees of freedom do we have?

5. Find the p-value. [You will need the function pf().]

6. What do you conclude? Write a sentence summarizing your findings.

Multiple Testing Why is the comic on our home page funny?: http://www.science.smith.edu/~rgarcia/sds201-S17/index.html

The simplest (and most conservative) way to correct for multiple testing is to use Bonferroni's correction: simply divide the  $\alpha$ -level by the number of comparisons that you are making.

**The Bootstrap** The bootstrap is a powerful computational technique for estimating all kinds of things. It is particularly useful when our actual data sample is non-normal.

- The bootstrap works in three steps:
  - Construct a sample of n items from your original data set, sampling with replacement (resample())
  - 2. Compute the statistic of interest on this sample (in our case, the mean (mean()))
  - 3. Repeat this process many, many times and collect the results (do())
- This bootstrap distribution is an approximation of the sampling distribution of your statistic
- Big Idea: The middle P% of the bootstrap distribution makes a P% confidence interval for the statistic in question, without making many assumptions about the distribution of X!

**Example** Consider the following sample of 534 hourly wages from the Current Population Survey (of 1985):

```
favstats(~wage, data = CPS85)
## min Q1 median Q3 max mean sd n missing
## 1 5.25 7.78 11.25 44.5 9.024064 5.139097 534 0
```

1. Construct a 95% confidence interval for the mean wage in the 1985 CPS, based on this sample. Assume that 5.139 is the true population standard deviation, and thus, we can use the z-distribution for the critical value. 2. Now using the t-statistic below, construct a 95% confidence interval for the mean wage that makes no assumption about the population standard deviation, but assumes that wages are normally distributed.

qt(c(0.025, 0.975), df = nrow(CPS85) - 1)

- 3. Examine the distribution of wage. Is it normally distributed?
- 4. Using the bootstrap, construct a 95% confidence interval for the mean wage that does not assume that wages are normally distributed.

```
bstrap <- do(10000) * mean(~wage, data = resample(CPS85))
qdata(~mean, p = c(0.025, 0.975), data = bstrap)
## quantile p
## 2.5% 8.593360 0.025
## 97.5% 9.463228 0.975</pre>
```

5. Compare the three confidence intervals you constructed. Do you see any important differences?