

431 Class 17

thomaseLove.github.io/431

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Today's Agenda

Comparing Population Means with the Analysis of Variance

- Indicator Variable Regression Analysis
 - Interpreting the ANOVA table
 - ANOVA assumptions and the Kruskal-Wallis test
- The Problem of Multiple Comparisons
 - Bonferroni pairwise testing
 - Tukey HSD pairwise comparisons

Today's Setup and Data

```
knitr::opts_chunk$set(comment = NA)
options(dplyr.summarise.inform = FALSE)

library(readxl) # to read in an .xlsx file
library(ggrepel) # to help label residual plots
library(patchwork)
library(knitr)
library(magrittr)
library(janitor)
library(broom)
library(tidyverse)

theme_set(theme_bw())
```

Today's Data (`ohio_2020.xlsx`)

`ohio_2020.xlsx` rows describe one of Ohio's 88 counties in terms of:

- FIPS code (basically an identifier for mapping)
- state and county name
- health outcomes (standardized: more positive means **better** outcomes, because we've taken the negative of the Z score CHR provides)
- health behavior ranking (1-88, we'll divide into 4 groups)
- clinical care ranking (1-88, we'll split into 3 groups)
- proportion of county residents who live in rural areas
- median income, in dollars
- proportion of votes in the 2016 Presidential Election for Pres. Trump

Sources (these bullets are links)

- [County Health Rankings \(2020 Ohio Data\)](#)
- [Wikipedia for 2016 Election Results](#)

Importing the Data / Creating some Factors

```
ohio20 <- read_xlsx("data/ohio_2020.xlsx") %>%  
  mutate(behavior = Hmisc::cut2(rk_behavior, g = 4),  
         clin_care = Hmisc::cut2(rk_clin_care, g = 3)) %>%  
  mutate(behavior = fct_recode(behavior,  
    "Best" = "[ 1,23)", "High" = "[23,45)",  
    "Low" = "[45,67)", "Worst" = "[67,88]")) %>%  
  mutate(clin_care = fct_recode(clin_care,  
    "Strong" = "[ 1,31)", "Middle" = "[31,60)",  
    "Weak" = "[60,88]")) %>%  
  select(FIPS, state, county, outcomes, behavior, clin_care,  
         everything())
```

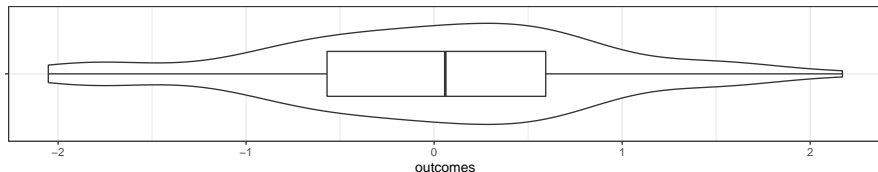
A Quick Look at the Data

```
ohio20 %>% filter(county == "Cuyahoga") %>%  
  select(FIPS, county, outcomes, behavior, clin_care)
```

```
# A tibble: 1 x 5
```

	FIPS	county	outcomes	behavior	clin_care
	<chr>	<chr>	<dbl>	<fct>	<fct>
1	39035	Cuyahoga	-0.807	Worst	Strong

```
ggplot(ohio20, aes(x = "", y = outcomes)) + geom_violin() +  
  geom_boxplot(width = 0.4) + coord_flip() + labs(x = "")
```



Use inspect to inspect the data frame?

```
ohio20 %>% select(outcomes, behavior, clin_care) %>%  
  mosaic::inspect()
```

categorical variables:

	name	class	levels	n	missing
1	behavior	factor	4	88	0
2	clin_care	factor	3	88	0

distribution

1 Best (25%), High (25%) ...

2 Strong (34.1%), Middle (33%) ...

quantitative variables:

	name	class	min	Q1	median
...1	outcomes	numeric	-2.051941	-0.5694916	0.05937935
	Q3	max	mean	sd	n missing
...1	0.5934	2.171502	4.090909e-11	0.8901777	88
					0

Key Measure Details

- **outcomes** = quantity that describes the county's premature death and quality of life results, weighted equally and standardized (z scores).
 - Higher (more positive) values indicate better outcomes in this county.
- **behavior** = (Best/High/Low/Worst) reflecting adult smoking, obesity, food environment, inactivity, exercise, drinking, alcohol-related driving deaths, sexually transmitted infections and teen births.
 - Counties in the Best group had the best behavior results.
- **clin_care** = (Strong/Middle/Weak) reflects rates of uninsured, care providers, preventable hospital stays, diabetes monitoring and mammography screening.
 - Strong means that clinical care is strong in this county.

Today's Planned Analytic Questions

- 1 How do average health outcomes vary across groups of counties defined by health behavior?
- 2 Do groups of counties defined by clinical care show substantial differences in average health outcomes?

Health Outcomes compared across Health Behavior Groups

Question 1

Do average health outcomes differ by health behavior?

Health Outcomes across Behavior Groups

Ohio's 88 counties, 2020 County Health Rankings



Source: <https://www.countyhealthrankings.org/app/ohio/2020/downloads>

Question 1 Numerical Summaries

How do average health outcomes vary across groups of counties defined by health behavior?

```
mosaic::favstats(outcomes ~ behavior, data = ohio20) %>%  
  rename(na = missing) %>% knitr::kable(digits = 2)
```

behavior	min	Q1	median	Q3	max	mean	sd	n	na
Best	-0.33	0.60	0.86	1.46	2.17	0.96	0.57	22	0
High	-0.35	0.00	0.30	0.55	0.77	0.25	0.35	22	0
Low	-1.15	-0.52	-0.09	0.16	0.73	-0.18	0.47	22	0
Worst	-2.05	-1.75	-0.87	-0.59	-0.08	-1.04	0.63	22	0

Note that there is no missing data here.

Analysis of Variance (ANOVA) testing: Question 1

Does the mean outcomes result differ detectably across the behavior groups?

$H_0 : \mu_{Best} = \mu_{High} = \mu_{Low} = \mu_{Worst}$ vs. H_A : At least one μ is different.

To test this set of hypotheses, we will build a linear model to predict each county's outcome based on what behavior group the county is in.

- We then look at whether the behavior group effect has a statistically detectable impact on the model's predictions of outcomes.

Building the Linear Model: Question 1

Can we detect differences in the population means of outcomes across the four behavior groups, using a 10% significance level?

```
model_one <- lm(outcomes ~ behavior, data = ohio20)
tidy(model_one, conf.int = 0.90) %>%
  select(term, estimate, std.error,
         conf.low, conf.high, p.value) %>% kable(dig = 2)
```

term	estimate	std.error	conf.low	conf.high	p.value
(Intercept)	0.96	0.11	0.75	1.18	0
behaviorHigh	-0.71	0.16	-1.02	-0.40	0
behaviorLow	-1.14	0.16	-1.45	-0.83	0
behaviorWorst	-2.01	0.16	-2.32	-1.70	0

How do we interpret this result?

Interpreting the Indicator Variables

The regression model (model_one) equation is

$$\begin{aligned}\text{outcomes} = & 0.96 - 0.71 \text{ behaviorHigh} \\ & - 1.14 \text{ behaviorLow} \\ & - 2.01 \text{ behaviorWorst}\end{aligned}$$

What do the indicator variables mean?

group	behaviorHigh	behaviorLow	behaviorWorst
Best	0	0	0
High	1	0	0
Low	0	1	0
Worst	0	0	1

- So what is the predicted outcomes score for a county in the High behavior group, according to this model?

Interpreting the Indicator Variables

The regression model (`model_one`) equation is

$$\begin{aligned}\text{outcomes} = & 0.96 - 0.71 \text{ behaviorHigh} \\ & - 1.14 \text{ behaviorLow} \\ & - 2.01 \text{ behaviorWorst}\end{aligned}$$

What predictions does the model make?

group	High	Low	Worst	Prediction
Best	0	0	0	0.96
High	1	0	0	$0.96 - 0.71 = 0.25$
Low	0	1	0	$0.96 - 1.14 = -0.18$
Worst	0	0	1	$0.96 - 2.01 = -1.05$

Do these predictions make sense?

Interpreting the Indicator Variables

The regression model (`model_one`) equation is

$$\begin{aligned}\text{outcomes} = & 0.96 - 0.71 \text{ behaviorHigh} \\ & - 1.14 \text{ behaviorLow} \\ & - 2.01 \text{ behaviorWorst}\end{aligned}$$

Sample means are...

```
ohio20 %>% group_by(behavior) %>%  
  summarize(n = n(), mean = round_half_up(mean(outcomes),2)) %>%
```

behavior	n	mean
Best	22	0.96
High	22	0.25
Low	22	-0.18
Worst	22	-1.04

ANOVA for the Linear Model: Question 1

Are there statistically detectable differences in mean outcome across the behavior group means?

$H_0 : \mu_{Best} = \mu_{High} = \mu_{Low} = \mu_{Worst}$ vs. H_A : At least one μ is different.

```
anova(model_one)
```

Analysis of Variance Table

Response: outcomes

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
behavior	3	46.421	15.4736	57.718	< 2.2e-16 ***
Residuals	84	22.519	0.2681		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

So, what's in the ANOVA table? (df)

The ANOVA table reports here on a single **factor** (behavior group) with 4 levels, and on the residual variation in health **outcomes**.

	Df	Sum Sq	Mean Sq	F value
behavior	3	46.421	15.4736	57.718
Residuals	84	22.519	0.2681	

Degrees of Freedom (df) is an index of sample size. . .

- df for our factor (behavior) is one less than the number of categories. We have four behavior groups, so 3 degrees of freedom.
- Adding $\text{df}(\text{behavior}) + \text{df}(\text{Residuals}) = 3 + 84 = 87 = \text{df}(\text{Total})$, one less than the number of observations (counties) in Ohio.
- n observations and g groups yield $n - g$ residual df in a one-factor ANOVA table.

So, what's in the ANOVA table? (Sum of Squares)

	Df	Sum Sq	Mean Sq	F value
behavior	3	46.421	15.4736	57.718
Residuals	84	22.519	0.2681	

Sum of Squares (Sum Sq, or SS) is an index of variation...

- SS(factor), here SS(behavior) measures the amount of variation accounted for by the behavior groups in our `model_one`.
- The total variation in outcomes to be explained by the model is $SS(\text{factor}) + SS(\text{Residuals}) = SS(\text{Total})$ in a one-factor ANOVA table.
- We describe the proportion of variation explained by a one-factor ANOVA model with η^2 ("eta-squared": same as Multiple R^2)

$$\eta^2 = \frac{SS(\text{behavior})}{SS(\text{Total})} = \frac{46.421}{46.421 + 22.519} = \frac{46.421}{68.94} \approx 0.673$$

So, what's in the ANOVA table? (MS and F)

	Df	Sum Sq	Mean Sq	F value
behavior	3	46.421	15.4736	57.718
Residuals	84	22.519	0.2681	

Mean Square (Mean Sq, or MS) = Sum of Squares / df

$$MS(\text{behavior}) = \frac{SS(\text{behavior})}{df(\text{behavior})} = \frac{46.421}{3} \approx 15.4736$$

- MS(Residuals) estimates the **residual variance**, the square of the residual standard deviation (residual standard error in earlier work).
- The ratio of MS values is the ANOVA **F value**.

$$\text{ANOVA } F = \frac{MS(\text{behavior})}{MS(\text{Residuals})} = \frac{15.4736}{0.2681} \approx 57.718$$

So, what's in the ANOVA table? (p value)

```
tidy(anova(model_one)) %>% kable(dig = 3)
```

term	df	sumsq	meansq	statistic	p.value
behavior	3	46.421	15.474	57.718	0
Residuals	84	22.519	0.268	NA	NA

- The p value is derived from the ANOVA F statistic, as compared to the F distribution.
- Which F distribution is specified by the two degrees of freedom values, as the F table is indexed by both a numerator and a denominator df.

```
pf(57.718, df1 = 3, df2 = 84, lower.tail = FALSE)
```

```
[1] 2.377323e-20
```

Alternative ways to show ANOVA results

```
glance(model_one) %>% select(r.squared, statistic, df, df.residual)
```

```
# A tibble: 1 x 5
  r.squared statistic    df df.residual  p.value
  <dbl>      <dbl> <dbl>      <int>      <dbl>
1    0.673      57.7     3         84 2.38e-20
```

```
summary(aov(model_one))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
behavior	3	46.42	15.474	57.72	<2e-16 ***
Residuals	84	22.52	0.268		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

So, what's the conclusion? Is this a surprise?

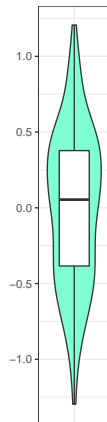
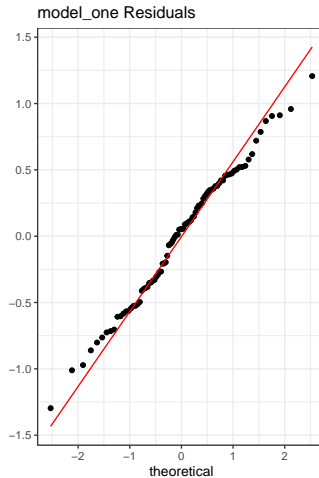
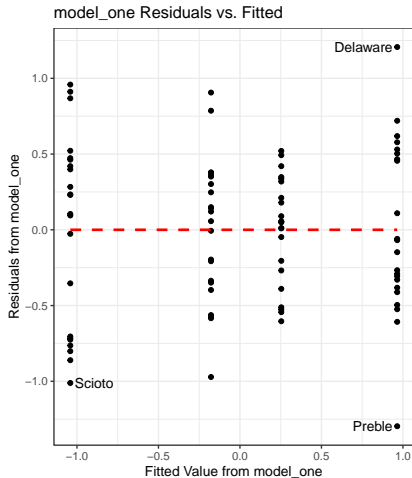
ANOVA Assumptions

The assumptions behind analysis of variance are those behind a linear model. Of specific interest are:

- The samples obtained from each group are independent.
- Ideally, the samples from each group are a random sample from the population described by that group.
- In the population, the variance of the outcome in each group is equal. (This is less of an issue if our study involves a balanced design.)
- In the population, we have Normal distributions of the outcome in each group.

Happily, the ANOVA F test is fairly robust to violations of the Normality assumption.

Residual Plots for model_one



Can we avoid assuming equal population variances?

Yes, but this isn't exciting if we have a balanced design.

```
oneway.test(outcomes ~ behavior, data = ohio20)
```

One-way analysis of means (not assuming equal variances)

data: outcomes and behavior

F = 43.145, num df = 3.000, denom df = 45.494,

p-value = 2.349e-13

- Note that this approach uses a fractional degrees of freedom calculation in the denominator.

The Kruskal-Wallis Test

If you thought the data were severely skewed, you might try:

```
kruskal.test(outcomes ~ behavior, data = ohio20)
```

Kruskal-Wallis rank sum test

data: outcomes by behavior

Kruskal-Wallis chi-squared = 61.596, df = 3,

p-value = 2.681e-13

- H_0 : The four behavior groups have the same center to their outcomes distributions.
- H_A : At least one group has a shifted distribution, with a different center to its outcomes.

What would be the conclusion here?

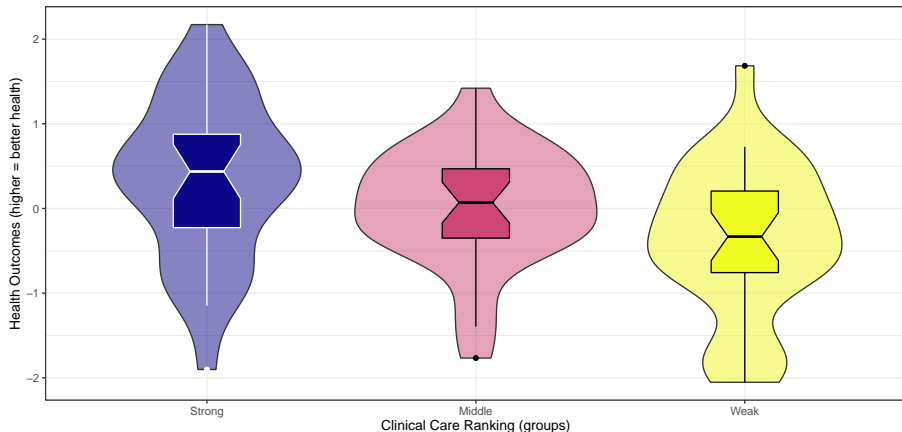
Health Outcomes compared across Clinical Care Groups

Question 2

Do groups of counties defined by clinical care show meaningful differences in average health outcomes?

Health Outcomes across County Clinical Care Ranking

Ohio's 88 counties, 2020 County Health Rankings



Source: <https://www.countyhealthrankings.org/app/ohio/2020/downloads>

Question 2 Numerical Summaries

Do groups of counties defined by clinical care show meaningful differences in average health outcomes?

```
mosaic::favstats(outcomes ~ clin_care, data = ohio20) %>%  
  rename(na = missing) %>% knitr::kable(digits = 2)
```

clin_care	min	Q1	median	Q3	max	mean	sd	n	na
Strong	-1.90	-0.23	0.44	0.88	2.17	0.34	0.94	30	0
Middle	-1.77	-0.35	0.07	0.47	1.42	0.02	0.69	29	0
Weak	-2.05	-0.76	-0.33	0.21	1.68	-0.36	0.90	29	0

Question 2 Analysis of Variance

```
model_two <- lm(outcomes ~ clin_care, data = ohio20)

anova(model_two)
```

Analysis of Variance Table

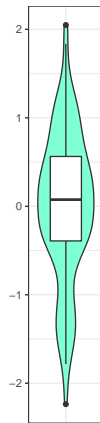
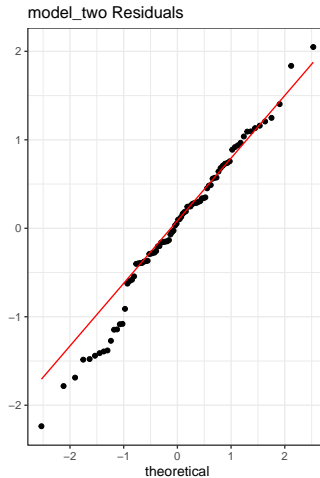
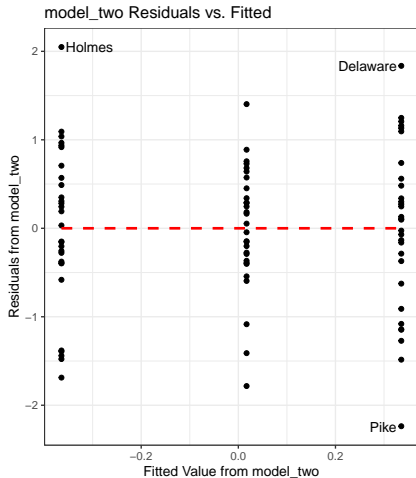
Response: outcomes

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
clin_care	2	7.232	3.6159	4.9807	0.009007 **
Residuals	85	61.708	0.7260		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual Plots for model_two



Question 2 Kruskal-Wallis test

```
kruskal.test(outcomes ~ clin_care, data = ohio20)
```

Kruskal-Wallis rank sum test

data: outcomes by clin_care

Kruskal-Wallis chi-squared = 8.3139, df = 2,

p-value = 0.01566

K-Sample Study Design, Comparing Means

- 1 What is the outcome under study?
- 2 What are the (in this case, $K \geq 2$) treatment/exposure groups?
- 3 Were the data in fact collected using independent samples?
- 4 Are the data random samples from the population(s) of interest? Or is there at least a reasonable argument for generalizing from the samples to the population(s)?
- 5 What is the significance level (or, the confidence level) we require?
- 6 Are we doing one-sided or two-sided testing? (usually 2-sided)
- 7 What does the distribution of each individual sample tell us about which inferential procedure to use?
- 8 Are there statistically meaningful differences between population means?
- 9 If an overall test rejects the null, can we identify pairwise comparisons of means that show detectable differences using an appropriate procedure that protects against Type I error expansion due to multiple comparisons?

Multiple Comparisons

What's Left to do? (Multiple Comparisons)

- 9 If an overall test rejects the null, can we identify pairwise comparisons of means that show detectable differences using an appropriate procedure that protects against Type I error expansion due to multiple comparisons?

Yes. There are two methods we'll study to identify specific pairs of means where we have statistically detectable differences, while dealing with the problem of multiple comparisons.

- Bonferroni pairwise comparisons
- Tukey's HSD (Honestly Significant Differences) approach

Compare behavior group means of outcomes?

ANOVA tells is that there is strong evidence that they aren't all the same. Which ones are different from which?

```
anova(lm(outcomes ~ behavior, data = ohio20))
```

Analysis of Variance Table

Response: outcomes

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
behavior	3	46.421	15.4736	57.718	< 2.2e-16 ***
Residuals	84	22.519	0.2681		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Is, for example, Best detectably different from Worst?

Could we just run a bunch of t tests?

This approach assumes that you need to make no adjustment for the fact that you are doing multiple comparisons, simultaneously.

```
pairwise.t.test(ohio20$outcomes, ohio20$behavior,  
                p.adjust.method = "none")
```

Pairwise comparisons using t tests with pooled SD

data: ohio20\$outcomes and ohio20\$behavior

	Best	High	Low
High	1.8e-05	-	-
Low	1.4e-10	0.007	-
Worst	< 2e-16	1.6e-12	3.6e-07

P value adjustment method: none

The problem of Multiple Comparisons

- The more comparisons you do simultaneously, the more likely you are to make an error.

In the worst case scenario, suppose you do two tests - first A vs. B and then A vs. C, each at the $\alpha = 0.10$ level.

- What is the combined error rate across those two t tests?

The problem of Multiple Comparisons

In the worst case scenario, suppose you do two tests - first A vs. B and then A vs. C, each at the $\alpha = 0.10$ level.

- What is the combined error rate across those two t tests?

Run the first test. Make a Type I error 10% of the time.

A vs B Type I error	Probability
Yes	0.1
No	0.9

Now, run the second test. Assume (perhaps wrongly) that comparing A to C is independent of your A-B test result. What is the error rate now?

The problem of Multiple Comparisons

In the worst case scenario, suppose you do two tests - first A vs. B and then A vs. C, each at the $\alpha = 0.10$ level.

- What is the combined error rate across those two t tests?

Assuming there is a 10% chance of making an error in either test, independently ...

	– Error in A vs. C	No Error	Total
Type I error in A vs. B	0.01	0.09	0.10
No Type I error in A-B	0.09	0.81	0.90
Total	0.10	0.90	1.00

So you will make an error in the A-B or A-C comparison **19%** of the time, rather than the nominal $\alpha = 0.10$ error rate.

But in our case, we're building SIX tests

- 1 Best vs. High
- 2 Best vs. Low
- 3 Best vs. Worst
- 4 High vs. Low
- 5 High vs. Worst
- 6 Low vs. Worst

and if they were independent, and each done at a 5% error rate, we could still wind up with an error rate of

$$.05 + (.95)(.05) + (.95)(.95)(.05) + (.95)^3(.05) + (.95)^4(.05) + (.95)^5(.05) = .265$$

Or worse, if they're not independent.

The Bonferroni Method

If we do 6 tests, we could reduce the necessary α to $0.05 / 6 = 0.0083$ and that maintains an error rate no higher than $\alpha = 0.05$ across the 6 tests.

- Or, R can adjust the p values directly...

```
pairwise.t.test(ohio20$outcomes, ohio20$behavior,  
                p.adjust.method = "bonferroni")
```

Pairwise comparisons using t tests with pooled SD

data: ohio20\$outcomes and ohio20\$behavior

	Best	High	Low
High	0.00011	-	-
Low	8.3e-10	0.04224	-
Worst	< 2e-16	9.4e-12	2.1e-06

Tukey Honestly Significant Differences (HSD)

Tukey's HSD approach is a better choice for pre-planned comparisons with a balanced (or nearly balanced) design. It provides confidence intervals and an adjusted p value for each comparison.

- Let's run some confidence intervals to yield an overall 99% confidence level, even with 6 tests...

```
TukeyHSD(aov(lm(outcomes ~ behavior, data = ohio20)),  
          conf.level = 0.99, ordered = TRUE)
```

Output on the next slide...

Tukey HSD Output

Tukey multiple comparisons of means
99% family-wise confidence level
factor levels have been ordered

Fit: aov(formula = lm(outcomes ~ behavior, data = ohio20))

\$behavior

	diff	lwr	upr	p adj
Low-Worst	0.8632211	0.36223069	1.3642115	0.0000021
High-Worst	1.2945256	0.79353515	1.7955159	0.0000000
Best-Worst	2.0056105	1.50462011	2.5066009	0.0000000
High-Low	0.4313045	-0.06968593	0.9322949	0.0348350
Best-Low	1.1423894	0.64139903	1.6433798	0.0000000
Best-High	0.7110850	0.21009456	1.2120753	0.0001023

Tidying the Tukey HSD confidence intervals

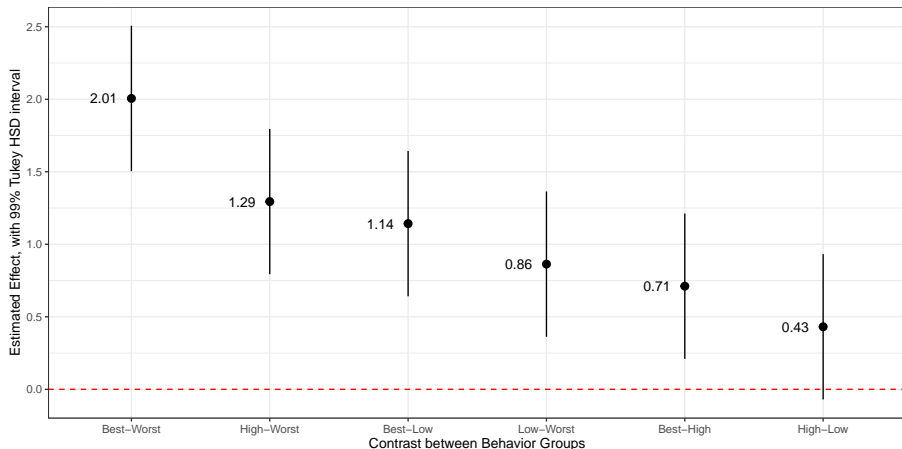
```
model_one <- lm(outcomes ~ behavior, data = ohio20)
tukey_one <- tidy(TukeyHSD(aov(model_one),
                           ordered = TRUE,
                           conf.level = 0.99))
tukey_one %>% rename(null = null.value) %>% kable(dig = 3)
```

term	contrast	null	estimate	conf.low	conf.high	adj.p.value
behavior	Low-Worst	0	0.863	0.362	1.364	0.000
behavior	High-Worst	0	1.295	0.794	1.796	0.000
behavior	Best-Worst	0	2.006	1.505	2.507	0.000
behavior	High-Low	0	0.431	-0.070	0.932	0.035
behavior	Best-Low	0	1.142	0.641	1.643	0.000
behavior	Best-High	0	0.711	0.210	1.212	0.000

Plotting Your Tukey HSD intervals, Approach 1

Estimated Effects, with Tukey HSD 99% Confidence Intervals

Comparing Outcomes by Behavior Group, ohio20 data



Code for Plot on Previous Slide

```
ggplot(tukey_one, aes(x = reorder(contrast, -estimate),  
                      y = estimate)) +  
  geom_pointrange(aes(ymin = conf.low, ymax = conf.high)) +  
  geom_hline(yintercept = 0, col = "red",  
            linetype = "dashed") +  
  geom_text(aes(label = round(estimate,2)), nudge_x = -0.2) +  
  theme_bw() +  
  labs(x = "Contrast between Behavior Groups",  
       y = "Estimated Effect, with 99% Tukey HSD interval",  
       title = "Estimated Effects, with Tukey HSD 99% Confidence",  
       subtitle = "Comparing Outcomes by Behavior Group, ohio2010")
```


Question 2: 90% Tukey HSD intervals, tidying

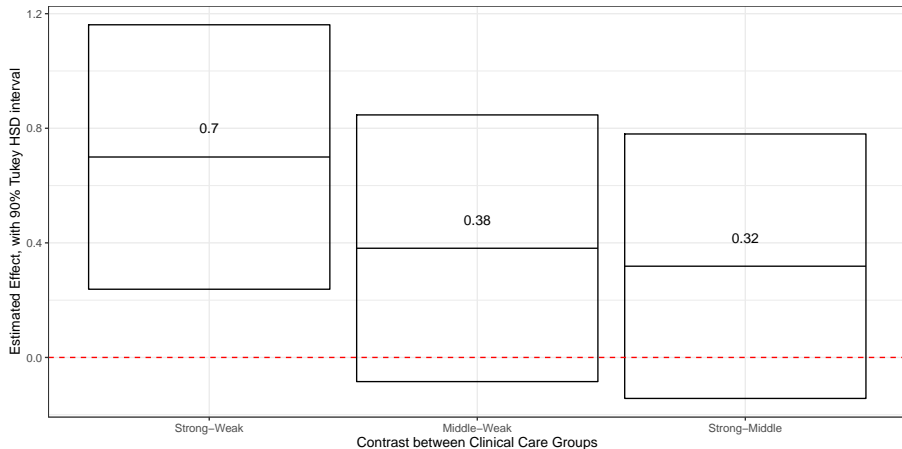
```
model_two <- lm(outcomes ~ clin_care, data = ohio20)
tukey_two <- tidy(TukeyHSD(aov(model_two),
                           ordered = TRUE,
                           conf.level = 0.90))
tukey_two %>% select(-term, -null.value) %>% kable(dig = 3)
```

contrast	estimate	conf.low	conf.high	adj.p.value
Middle-Weak	0.381	-0.084	0.847	0.210
Strong-Weak	0.700	0.238	1.161	0.006
Strong-Middle	0.319	-0.143	0.780	0.327

Plotting Question 2 Tukey HSD intervals

Estimated Effects, with Tukey HSD 90% Confidence Intervals

Comparing Outcomes by Clinical Care Group, ohio20 data



Code for Question 2 Tukey HSD plot

```
ggplot(tukey_two, aes(x = reorder(contrast, -estimate),  
                      y = estimate)) +  
  geom_crossbar(aes(ymin = conf.low, ymax = conf.high),  
                fatten = 1) +  
  geom_hline(yintercept = 0, col = "red",  
             linetype = "dashed") +  
  geom_text(aes(label = round(estimate,2)), nudge_y = 0.1) +  
  theme_bw() +  
  labs(x = "Contrast between Clinical Care Groups",  
       y = "Estimated Effect, with 90% Tukey HSD interval",  
       title = "Estimated Effects, with Tukey HSD 90% Confidence",  
       subtitle = "Comparing Outcomes by Clinical Care Group,
```

Coming Up Next Time: Comparisons using Paired/Matched Samples

FOR SELF-STUDY: ANOVA Examples about President Trump's 2016 Votes by County

Question 3 (Education)

We have some additional variables in `ohio20`, specifically:

- `trump16` = proportion of the vote cast in 2016 in the county that went to President Trump
- `somecollege` = percentage of adults ages 25-44 with some post-secondary education in the county

Let's break Ohio's counties into 5 groups based on `somecollege`...

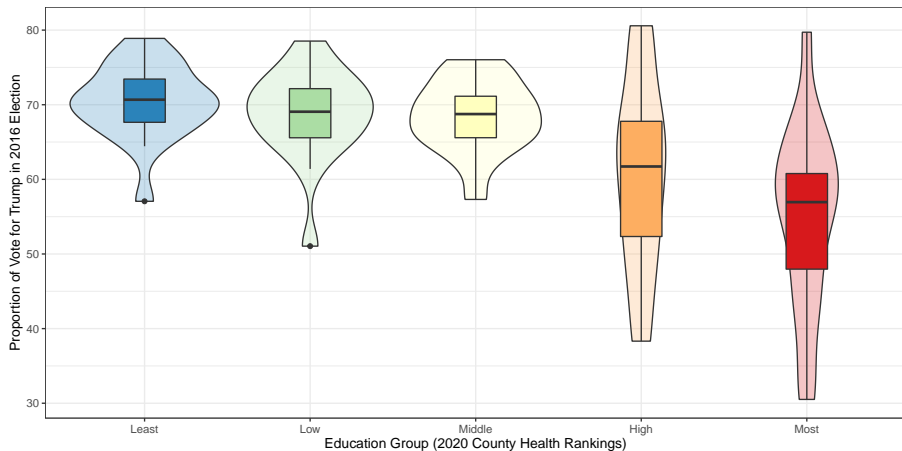
```
ohio20 <- ohio20 %>%  
  mutate(trump16 = 100*trump16) %>%  
  mutate(educ = Hmisc::cut2(somecollege, g = 5)) %>%  
  mutate(educ = fct_recode(educ, "Least" = "[20.4,50.3)",  
    "Low" = "[50.3,54.3)", "Middle" = "[54.3,59.7)",  
    "High" = "[59.7,67.1)", "Most" = "[67.1,85.1)"))
```

Did President Trump's vote percentage in 2016 vary meaningfully across groups of counties defined by educational attainment?

Trump 2016 % by Educational Attainment

Proportion of Trump Vote by 'Some College' Group

Ohio's 88 counties



Numerical Comparison

```
mosaic::favstats(trump16 ~ educ, data = ohio20) %>%  
  rename(na = missing) %>% kable(digits = 2)
```

educ	min	Q1	median	Q3	max	mean	sd	n	na
Least	57.06	67.64	70.67	73.44	78.89	70.34	5.06	18	0
Low	51.05	65.57	69.06	72.16	78.53	68.72	6.17	18	0
Middle	57.31	65.58	68.75	71.14	76.03	68.39	4.89	17	0
High	38.32	52.34	61.72	67.78	80.58	60.42	12.83	18	0
Most	30.51	47.97	56.95	60.78	79.72	55.08	12.51	17	0

Analysis of Variance (ANOVA) testing: Question 3

Does the mean trump16 result differ detectably across the educ groups?

```
model_3 <- lm(trump16 ~ educ, data = ohio20)
```

```
tidy(model_3, conf.int = 0.90) %>%  
  select(term, estimate, std.error,  
         conf.low, conf.high, p.value) %>% kable(dig = 2)
```

term	estimate	std.error	conf.low	conf.high	p.value
(Intercept)	70.34	2.13	66.11	74.58	0.00
educLow	-1.62	3.01	-7.61	4.37	0.59
educMiddle	-1.95	3.05	-8.02	4.13	0.52
educHigh	-9.92	3.01	-15.91	-3.93	0.00
educMost	-15.26	3.05	-21.33	-9.18	0.00

ANOVA for the Linear Model: Question 3

```
anova(model_3)
```

Analysis of Variance Table

Response: trump16

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
educ	4	2997.1	749.27	9.1867	3.401e-06 ***
Residuals	83	6769.5	81.56		

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

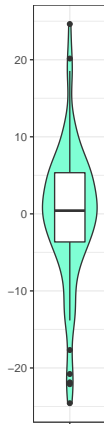
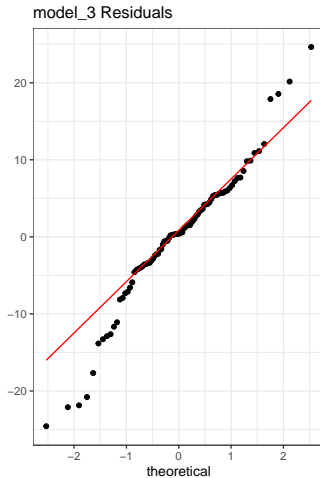
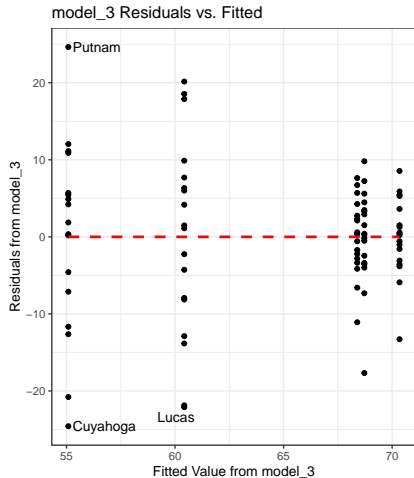
```
glance(model_3) %>%
```

```
  select(r.squared, statistic, df, df.residual, p.value)
```

A tibble: 1 x 5

r.squared	statistic	df	df.residual	p.value
<dbl>	<dbl>	<dbl>	<int>	<dbl>

Residual Plots for model_3



Does Kruskal-Wallis give a very different result?

```
kruskal.test(trump16 ~ educ, data = ohio20)
```

Kruskal-Wallis rank sum test

data: trump16 by educ

Kruskal-Wallis chi-squared = 25.759, df = 4,

p-value = 3.539e-05

Tukey HSD 90% confidence intervals: Example 3

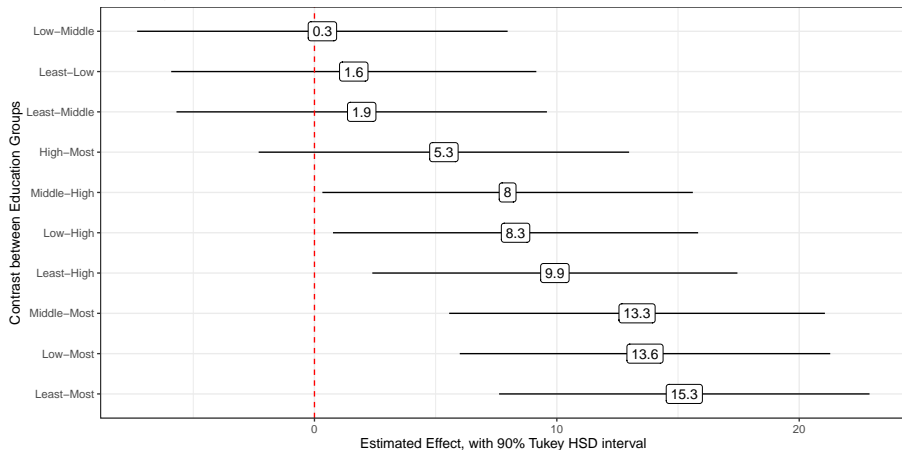
```
tukey_3 <- tidy(TukeyHSD(aov(model_3),  
                        ordered = TRUE,  
                        conf.level = 0.90))  
tukey_3 %>% select(-null.value) %>% kable(dig = 3)
```

term	contrast	estimate	conf.low	conf.high	adj.p.value
educ	High-Most	5.340	-2.302	12.982	0.411
educ	Middle-Most	13.309	5.559	21.060	0.000
educ	Low-Most	13.638	5.995	21.280	0.000
educ	Least-Most	15.259	7.617	22.901	0.000
educ	Middle-High	7.969	0.327	15.611	0.078
educ	Low-High	8.297	0.765	15.829	0.054
educ	Least-High	9.919	2.387	17.451	0.012
educ	Low-Middle	0.328	-7.314	7.970	1.000
educ	Least-Middle	1.950	-5.692	9.592	0.968
educ	Least-Low	1.622	-5.911	9.154	0.983

Plotting Tukey HSD intervals for Example 3

Estimated Effects, with Tukey HSD 90% Confidence Intervals

Comparing Trump16 Vote % by Education Group, ohio20 data



Code for Previous Slide

```
ggplot(tukey_3, aes(x = reorder(contrast, -estimate),  
                    y = estimate)) +  
  geom_pointrange(aes(ymin = conf.low, ymax = conf.high)) +  
  geom_hline(yintercept = 0, col = "red",  
             linetype = "dashed") +  
  geom_label(aes(label = round_half_up(estimate,1))) +  
  coord_flip() +  
  labs(x = "Contrast between Education Groups",  
       y = "Estimated Effect, with 90% Tukey HSD interval",  
       title = "Estimated Effects, with Tukey HSD 90% Confidence Interval",  
       subtitle = "Comparing Trump16 Vote % by Education Group, on the basis of 2012 data")
```

Question 4 ()

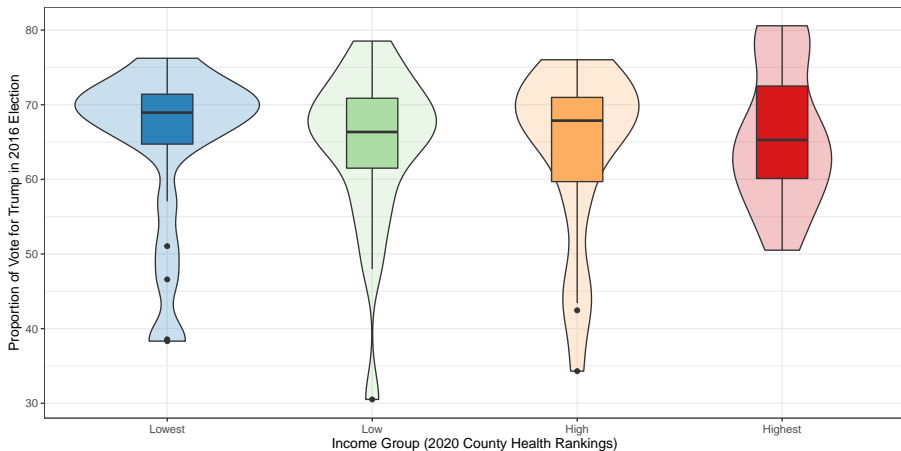
Let's break Ohio's counties into 4 groups based on their median income...

```
ohio20 <- ohio20 %>%  
  mutate(income = Hmisc::cut2(income, g = 4)) %>%  
  mutate(income = fct_recode(income, "Lowest" = "[40416, 48792)",  
    "Low" = "[48792, 53904)", "High" = "[53904, 60828)",  
    "Highest" = "[60828,103536]"))
```

Did President Trump's vote percentage in 2016 vary meaningfully across income?

Trump 2016 % by Income

Proportion of Trump Vote by Income Group
Ohio's 88 counties



Numerical Comparison

```
mosaic::favstats(trump16 ~ income, data = ohio20) %>%  
  rename(na = missing) %>% kable(digits = 2)
```

income	min	Q1	median	Q3	max	mean	sd	n	na
Lowest	38.32	64.72	68.94	71.41	76.23	64.71	11.18	22	0
Low	30.51	61.50	66.35	70.87	78.53	64.40	10.71	22	0
High	34.30	59.70	67.87	70.98	76.03	63.73	11.75	22	0
Highest	50.51	60.12	65.28	72.51	80.58	65.80	9.21	22	0

Analysis of Variance (ANOVA) testing

Does the mean trump16 result differ detectably across the income groups?

```
model_4 <- lm(trump16 ~ income, data = ohio20)
```

```
tidy(model_4, conf.int = 0.90) %>%  
  select(term, estimate, std.error,  
         conf.low, conf.high, p.value) %>% kable(dig = 2)
```

term	estimate	std.error	conf.low	conf.high	p.value
(Intercept)	64.71	2.29	60.15	69.27	0.00
incomeLow	-0.31	3.24	-6.75	6.14	0.93
incomeHigh	-0.98	3.24	-7.42	5.47	0.76
incomeHighest	1.09	3.24	-5.36	7.54	0.74

ANOVA for the Linear Model

```
anova(model_4)
```

Analysis of Variance Table

Response: trump16

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
income	3	48.8	16.272	0.1407	0.9354
Residuals	84	9717.8	115.688		

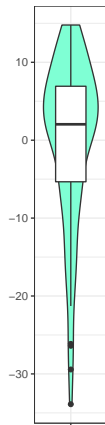
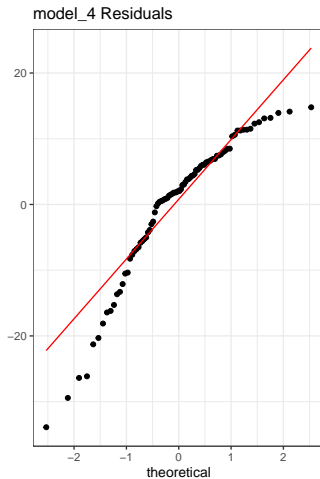
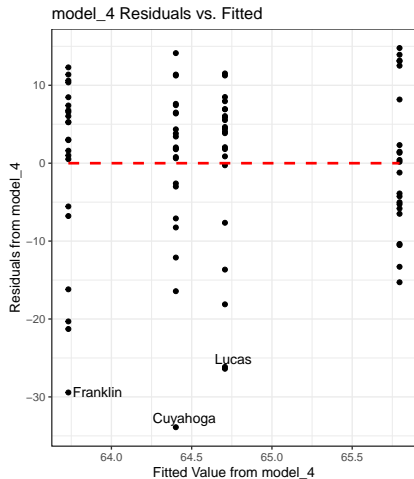
```
glance(model_4) %>%  
  select(r.squared, statistic, df, df.residual, p.value)
```

A tibble: 1 x 5

	r.squared	statistic	df	df.residual	p.value
	<dbl>	<dbl>	<dbl>	<int>	<dbl>
1	0.00500	0.141	3	84	0.935

So, what's the conclusion?

Residual Plots for model_4



Does Kruskal-Wallis give a different result?

```
kruskal.test(trump16 ~ income, data = ohio20)
```

Kruskal-Wallis rank sum test

data: trump16 by income

Kruskal-Wallis chi-squared = 0.35787, df = 3,

p-value = 0.9488

Tukey HSD 90% confidence intervals: Income Groups

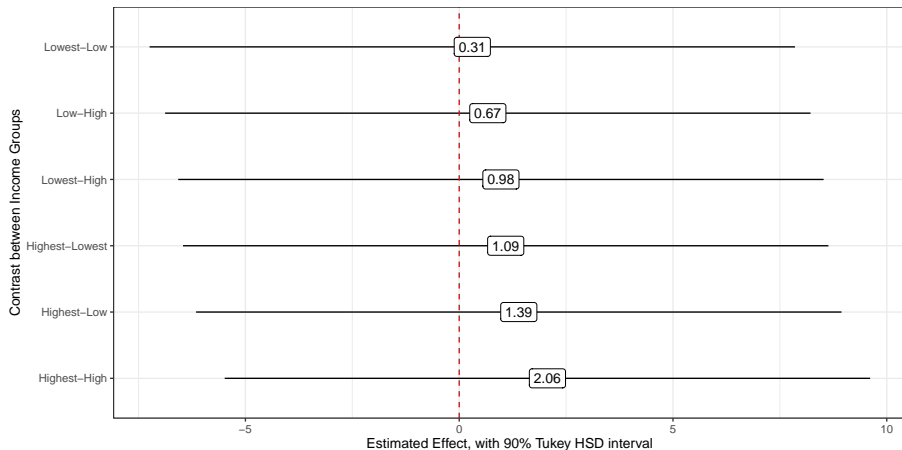
```
tukey_4 <- tidy(TukeyHSD(aov(model_4),  
                        ordered = TRUE,  
                        conf.level = 0.90))  
tukey_4 %>% select(-null.value) %>% kable(dig = 3)
```

term	contrast	estimate	conf.low	conf.high	adj.p.value
income	Low-High	0.670	-6.878	8.217	0.997
income	Lowest-High	0.975	-6.572	8.523	0.990
income	Highest-High	2.063	-5.484	9.611	0.920
income	Lowest-Low	0.306	-7.241	7.853	1.000
income	Highest-Low	1.394	-6.154	8.941	0.973
income	Highest-Lowest	1.088	-6.460	8.635	0.987

Plotting Tukey HSD intervals (Income Groups)

Estimated Effects, with Tukey HSD 90% Confidence Intervals

Comparing Trump16 Vote % by Income Group, ohio20 data



K-Sample Study Design, Comparing Means

- 1 What is the outcome under study?
- 2 What are the (in this case, $K \geq 2$) treatment/exposure groups?
- 3 Were the data in fact collected using independent samples?
- 4 Are the data random samples from the population(s) of interest? Or is there at least a reasonable argument for generalizing from the samples to the population(s)?
- 5 What is the significance level (or, the confidence level) we require?
- 6 Are we doing one-sided or two-sided testing? (usually 2-sided)
- 7 What does the distribution of each individual sample tell us about which inferential procedure to use?
- 8 Are there statistically meaningful differences between population means?
- 9 If an overall test rejects the null, can we identify pairwise comparisons of means that show detectable differences using an appropriate procedure that protects against Type I error expansion due to multiple comparisons?