431 Class 15

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Today's Agenda

- The Analysis of Variance
  - Using Regression to Develop an ANOVA model
  - Methods for pairwise multiple comparisons
  - Examples Using the `ohio_20` data
- Some Comments on Project A
- Several ANOVA Examples for Home Study

Today's Packages

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

theme_set(theme_bw())
```

Analysis of Variance for Comparing Multiple Means

Today's Data (`ohio_2020`)

`ohio_2020.xlsx` rows describe Ohio's 88 counties:

- `FIPS` code (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 Donald Trump

Sources (these bullets are links)

- County Health Rankings (2020 Ohio Data)
- Wikipedia for 2016 Election Results

Importing the Data / Creating some Factors

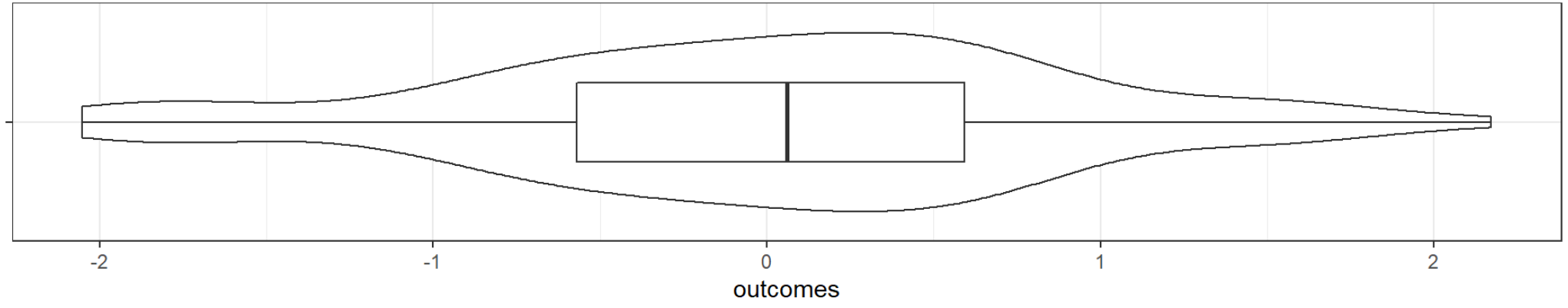
```
ohio20 <- read_xlsx("c15/data/ohio_2020.xlsx") |>
  mutate(behavior = Hmisc::cut2(rk_behavior, g = 4),
         clin_care = Hmisc::cut2(rk_clin_care, g = 3)) |>
  mutate(behavior = fct_recode(behavior,
           "Best" = "[ 1,23)", "High" = "[23,45)",
           "Low" = "[45,67)", "Worst" = "[67,88]")) |>
  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 × 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 = "")
```



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.

Key Measure Details

- **behavior** = (Best/High/Low/Worst) reflecting adult smoking, obesity, food environment, inactivity, exercise, drinking, alcohol-related driving deaths, sexually tranmitted infections and teen births.
  - Counties in the Best group had the best behavior results.

Key Measure Details

- **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.

Analytic Questions for Today's ANOVA

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?

K Samples: Comparing Means

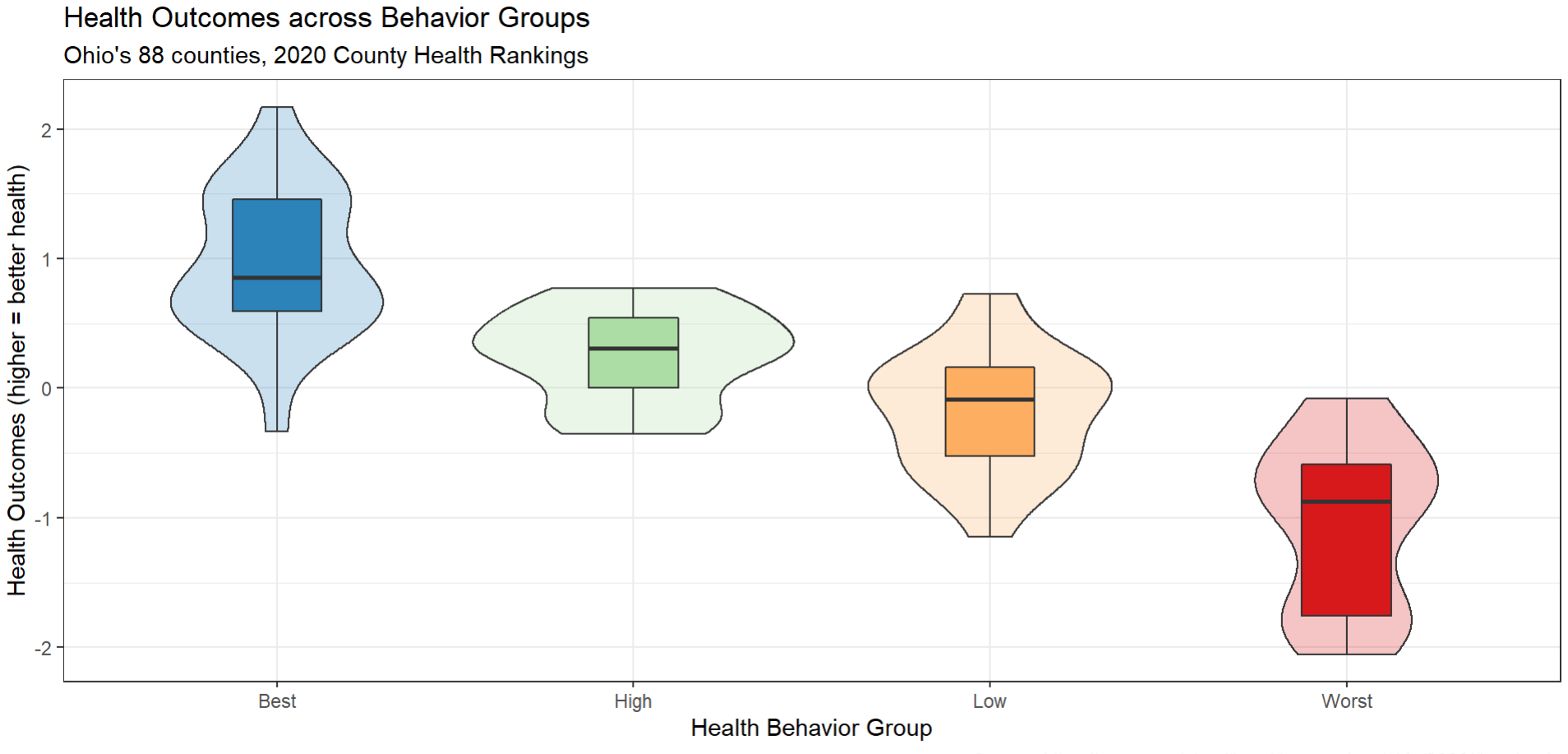
1. What is the outcome under study?
2. What are the (in this case, $K \geq 2$) treatment/exposure groups?
3. Were the data in fact collected using independent samples?
4. Are the data random samples from the population(s) of interest? Or is there at least a reasonable argument for generalizing from the 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 detectable 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?

Question 1

Do average health outcomes differ by health behavior?

```
ggplot(ohio20, aes(x = behavior, y = outcomes,
                   fill = behavior)) +
  geom_violin(alpha = 0.25) +
  geom_boxplot(width = 0.25) +
  guides(fill = "none") +
  scale_fill_brewer(palette = "Spectral", direction = -1) +
  labs(x = "Health Behavior Group",
       y = "Health Outcomes (higher = better health)",
       title = "Health Outcomes across Behavior Groups",
       subtitle = "Ohio's 88 counties, 2020 County Health Rankings",
       caption = "Source: https://www.countyhealthrankings.org/app/ohio/202
```

Question 1


Health Outcomes across Behavior Groups
Ohio's 88 counties, 2020 County Health Rankings
Health Outcomes (higher = better health)
2
1
0
-1
-2
Best
High
Low
Worst
Health Behavior Group
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) |> kbl(digits = 2) |> kable_classic_2(font_size = 28
```

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: Question 1

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

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

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.

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) |>
  kbl(digits = 2) |> kable_classic_2(font_size = 28)
```

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

```
extract_eq(model_one, use_coefs = T, operator_location = "start",
           terms_per_line = 1, wrap = T)
```

$$
\begin{aligned}
\operatorname{\widehat{outcomes}} &= 0.96 \\
&\quad - 0.71(\operatorname{behavior}_{\operatorname{High}}) \\
&\quad - 1.14(\operatorname{behavior}_{\operatorname{Low}}) \\
&\quad - 2.01(\operatorname{behavior}_{\operatorname{Worst}})
\end{aligned}
$$

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

```
outcomes = 0.96 - 0.71 behaviorHigh
           - 1.14 behaviorLow - 2.01 behaviorWorst
```

What predictions does the model make? Do these make sense?

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

Interpreting the Indicator Variables

```
outcomes = 0.96 - 0.71 behaviorHigh
           - 1.14 behaviorLow - 2.01 behaviorWorst
```

```
1 ohio20 |> group_by(behavior) |>
2   summarize(n = n(), mean = round_half_up(mean(outcomes),2)) |>
3   kbl(digits = 2) |> kable_classic_2(font_size = 28, full_width = F)
```

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?

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

```
1 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**.

```
1  anova(model_one)[1:2]
```

```
          Df Sum Sq
behavior   3 46.421
Residuals 84 22.519
```

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 df(behavior) + df(Residuals) = 3 + 84 = 87 = df(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.

ANOVA table: Sum of Squares

```
1  anova(model_one)[1:3]
```

```
          Df Sum Sq Mean Sq
behavior   3 46.421 15.4736
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(factor) + SS(Residuals) = SS(Total) in a one-factor ANOVA table.
- We describe the proportion of variation explained by a one-factor ANOVA model with \(\eta^2\) (“eta-squared”: same as Multiple \(R^2\))

\[\eta^2 = \frac{SS(\mbox{behavior})}{SS(\mbox{Total})} = \frac{46.421}{46.421+22.519} = \frac{46.421}{68.94} \approx 0.673 \]

ANOVA table: (Mean Square, F ratio)

```
1  anova(model_one)[1:4]
```

```
          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

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

- 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**.

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

ANOVA Table p value

```
tidy(anova(model_one)) |> kbl(digits = 3) |>
  kable_classic_2(font_size = 28, full_width = F)
```

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…

```
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, p.value)
  kbl() |> kable_minimal(font_size = 28)
```

r.squared	statistic	df	df.residual	p.value
0.673348	57.71815	3	84	0

```
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?

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.

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?

```
1 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.

```
1 pairwise.t.test(ohio20$outcomes, ohio20$behavior,
2                 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

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

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 \(\alpha\) 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…

```
1 pairwise.t.test(ohio20$outcomes, ohio20$behavior,
2                 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

P value adjustment method: bonferroni
```

We still detect a meaningful difference between each pair of groups.

Better Approach: Holm-Bonferroni

Suppose you have m comparisons, with p-values sorted from low to high as p_1, p_2, ..., p_m.

- Is $P_1 < \alpha/m$? If so, reject H_1 and continue, otherwise STOP.
- Is $P_2 < \alpha/(m-1)$? If so, reject H_2 and continue, else STOP.
- and so on...

Holm-Bonferroni Approach

This is uniformly more powerful than Bonferroni, while preserving the overall false positive rate at \(\alpha\).

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

```
    Pairwise comparisons using t tests with pooled SD

data:  ohio20$outcomes and ohio20$behavior

      Best    High    Low
High  3.5e-05 -       -
Low   5.5e-10 0.007   -
Worst < 2e-16 7.9e-12 1.1e-06

P value adjustment method: holm
```

Tukey's Honestly Significant Differences

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)
```

Tukey's Honestly Significant Differences

```
  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 Tukey HSD 99% CIs

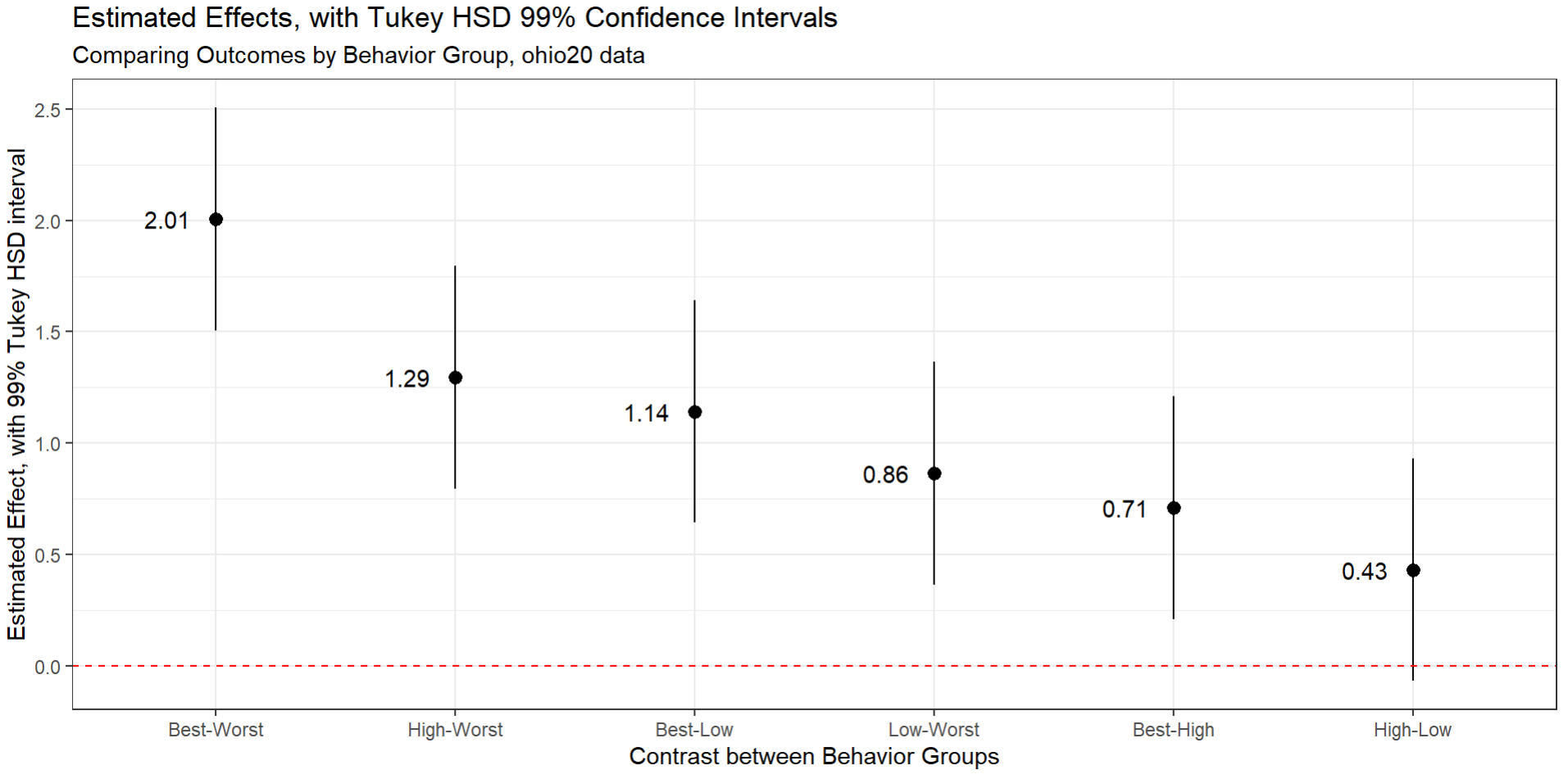
```
model_one <- lm(outcomes ~ behavior, data = ohio20)
tukey_one <- tidy(TukeyHSD(aov(model_one), ordered = TRUE, conf.level = 0.9
tukey_one |> rename(null = null.value) |>
  kbl(digits = 3) |> kable_classic_2(font_size = 28)
```

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

Plot Tukey HSD intervals

```
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) +
  labs(x = "Contrast between Behavior Groups",
       y = "Estimated Effect, with 99% Tukey HSD interval",
       title = "Estimated Effects, with Tukey HSD 99% Confidence Intervals"
       subtitle = "Comparing Outcomes by Behavior Group, ohio20 data")
```

Plot Tukey HSD intervals



ANOVA Assumptions

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

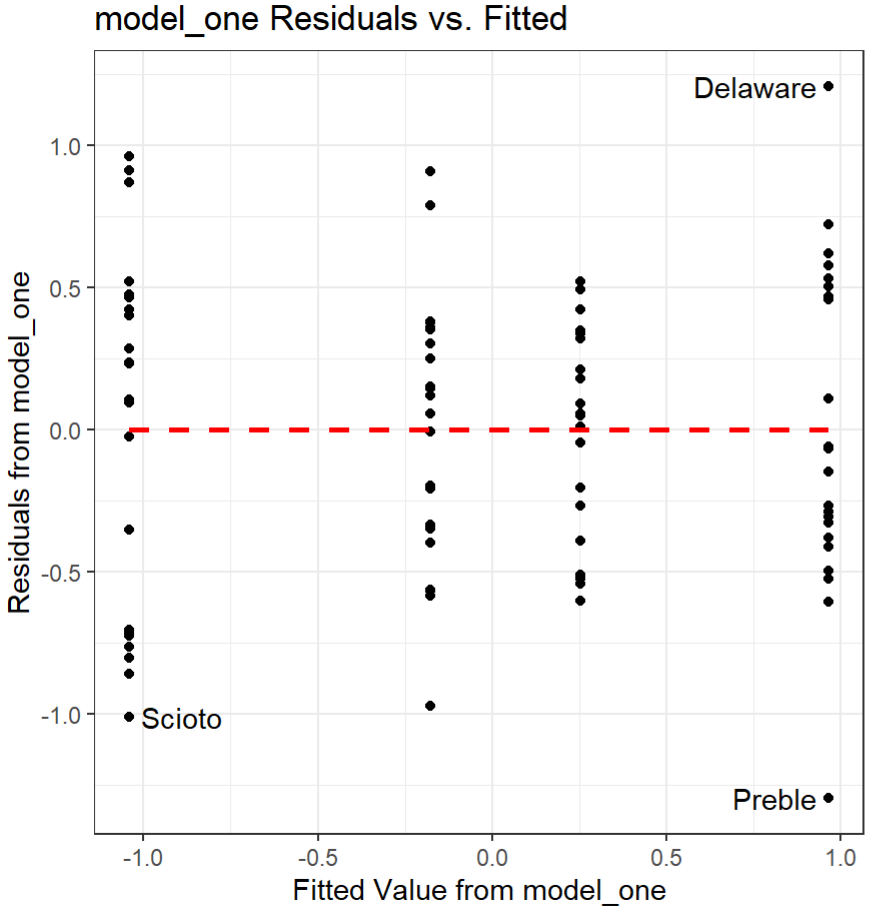
- The samples obtained from each group are independent.
- Ideally, the samples from each group are a random sample from the population described by that group.
- In the population, the variance of the outcome in each group is equal. (This is less of an issue if our study involves a balanced design.)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

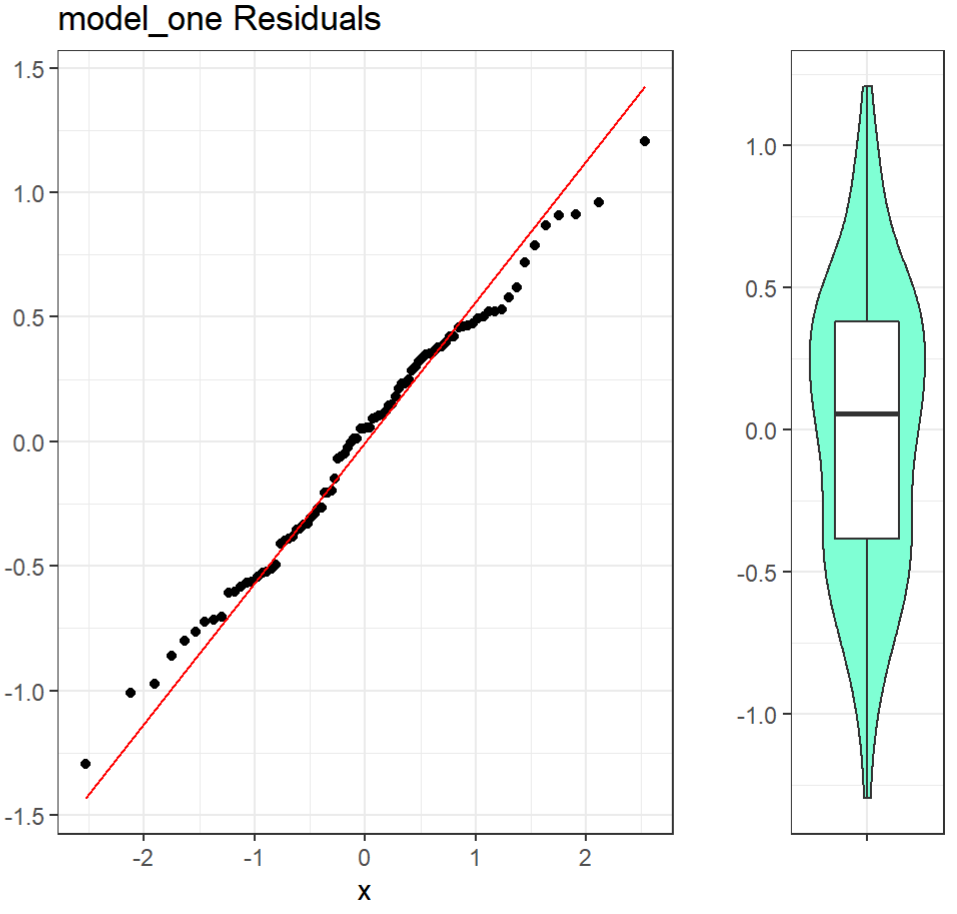
Happily, the ANOVA F test is fairly robust to violations of the Normality assumption.

Residual Plots for `model_one`

```
aug_one <- augment(model_one, ohio20)

p1 <- ggplot(aug_one, aes(x = .fitted, y = .resid)) +
  geom_point() +
  geom_smooth(method = "lm", formula = y ~ x, se = F,
              lty = "dashed", col = "red") +
  geom_text_repel(data = aug_one |>
                    slice_max(abs(.resid), n = 3),
                  aes(label = county)) +
  labs(title = "model_one Residuals vs. Fitted",
       x = "Fitted Value from model_one",
       y = "Residuals from model_one")

p2 <- ggplot(aug_one, aes(sample = .resid)) +
  geom_qq() + geom_qq_line(col = "red") +
  labs(title = "model_one Residuals",
       y = "")

p3 <- ggplot(aug_one, aes(x = .resid, y = "")) +
```

Residual Plots for `model_one`





Can we avoid assuming equal population variances?

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

```
1 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:

```
1 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?

K Samples: 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 detectable 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?

On Project A

Deliverables on 2022-10-31 at 9 PM

- To Canvas: R Markdown and HTML report
- To Canvas: Video (has outsized importance)
- Google Form (self-evaluation) submitted after the Canvas stuff is in

Working with a Partner?

- The submitting investigator submits Rmd, HTML and video to Canvas, and then submits the Google Form.
- The partner submits the one-sentence text document to Canvas (yes, again), and then submits the Google Form.

On the R Markdown and HTML Report

Please review the checklist for the final report, listing things the TAs will be looking for in evaluating your project. Details matter.

- The most important part of your analyses are the research questions, and your paragraphs about conclusions and limitations. This is the only part Dr. Love will read before he reviews your video, although he'll come back and read other things after grading the videos.
  - We are NOT looking for separate training and testing samples. We want you to use your whole sample for all elements of this Project.

Dealing with Missing Data

You can absolutely use complete cases in each of the three analyses, but these should have explicitly specified and different sample sizes if you have missing data in something other than your outcome.

- Be certain to specify what you are assuming (MCAR, MAR or MNAR) about the missing data mechanism in developing your models.

If you decide instead to use single imputation (with the `simputation` package), great.

If you impute... (1/2)

This would mean that you are making a different assumption about the missing data mechanism than if you were using complete cases, and this should be explicitly specified.

- It's fine to use `rlm` or `pmm` to impute quantitative predictors, and to use `pmm` or `cart` for categorical ones.
- Use (at least) all other variables included in your planned model to help with the imputation, and you are also welcome to use other variables from your tidy data set, if you like. Be sure to state explicitly what you are doing.

If you impute... (2/2)

- Be sure to set a seed just before you do any imputation.
- For Project A, you can impute predictors, but not the outcome. Use complete cases for your outcome, regardless of any other decisions you make.

Your Job in the Rmd / HTML report

Your job is to provide reasonable research questions (one question per analysis) and reasoned conclusions and clear, compelling logical motivations for those conclusions.

- All of the material from your proposal should be included in your final report. Some needs to be augmented, and, of course, may have changed in light of what you've done since your proposal was improved.
- Don't fight our example. Use it to make sure you've covered everything we need to see, and so that you make it as easy for us to review as possible.

The Analyses

Create a section called Analysis 1, another called Analysis 2, and another called Analysis 3, **using the outline (including subsections) we've provided** for all of your headings.

1. Analysis 1 - predict your outcome using one of your quantitative predictors
2. Analysis 2 - predict your outcome using one of your categorical predictors
3. Analysis 3 - predict your outcome using one of your quantitative predictors (can be same as Analysis 1, or different) as well as `state`.

Using Variables?

Many of you will only use four variables: your outcome, one quantitative predictor, one categorical one, and the `state`, in these analyses. Some will use five.

Don't use language to suggest causality if your data and model cannot justify that.

Analysis 2 with a binary predictor (1/2)

If you're using a binary predictor here, then this regression model boils down to a pooled t test. You should complete that regression model (with whatever transformation you like) and obtain an appropriate regression-based analysis.

- If you are unsatisfied with the adherence of the situation to regression assumptions, and want to ALSO develop an alternative confidence interval based on a Welch's t procedure, or a bootstrap comparison, that would be a good idea.

Analysis 2 with a binary predictor (2/2)

- Be sure to justify your final choice of approach (pooled t or other) with results from the output, and a description of what you're doing. Draw clear conclusions.
- Be certain that you address the issue of what population is being described by the confidence interval you develop in this setting.

Analysis 2 with a multi-categorical predictor

If you're using a multi-categorical predictor here, then this regression model boils down to an analysis of variance (ANOVA).

- That's what we just did. Also, see Chapter 24 in the Course Notes.
- A set of formal pairwise comparisons should be a part of your analysis should your multi-categorical predictor demonstrate meaningful predictive value for your outcome.

Analysis 3 (1/2)

Does `state` have a large impact on the model between your outcome and your quantitative predictor, and what does this imply about that outcome-quant predictor relationship?

- I suppose you could fit a model using `state` only to affect the intercept of the relationship between your outcome and your quantitative predictor, but …

Analysis 3 (2/2)

- We'd far prefer that you fit a model where the `state` also can affect the slope of that relationship.
  - This implies that you should be fitting a model with an interaction term between `state` and your quantitative predictor, and that model requires careful interpretation.
  - A part of that interpretation should be a clear and appropriate visualization explaining what the impact of the `state` is on the regression line describing the outcome based on the quantitative predictor.

On the Video, I

The video has more weight on your project grade than you might think, despite the fact that it is short.

- Do what we ask you to do in the video. (See the Final Report instructions.)
- Dr. Love will review all videos in detail **before** he looks at (most of) your report.

On the Video, II

All videos should include a clear statement of the research questions for both analyses you present, and justify the responses to those questions with results from the analyses.

- The video must stand on its own, in the sense that it must be completely understandable to someone who has not read your report, but who is generally familiar with County Health Rankings and its measurements.

On the Video, III

You need to tell us everything we need to know to evaluate your claims, and no more.

- Don’t use causal or sloppy language in your video unless you can back that up.
- Make sure we can clearly see everything you want us to see in the video.

On the Video, IV

- Building the video is going to take more than the time to record it. Leave that time in your planning. It's a very bad idea to try to toss this together in the last 30 minutes.
- Make smart choices about what to present in the video. You cannot possibly include everything you put in your main report. What are the conclusion-driving things to show us?

The Self-Evaluation

The Google Form is available at https://bit.ly/431-projectA-self-evaluation-2022.

Fill it out AFTER you have submitted the other materials to Canvas. This way, you'll have completed that work before you submit the self-evaluation, which is what we want.

- Again, if you're working with a partner for the rest of the project, you still do this part completely on your own.
- Same deadline as everything else: October 31 at 9 PM.

Session Information

```
1 sessionInfo()
```

```
R version 4.2.1 (2022-06-23 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 10 x64 (build 22000)

Matrix products: default

locale:
[1] LC_COLLATE=English_United States.utf8
[2] LC_CTYPE=English_United States.utf8
[3] LC_MONETARY=English_United States.utf8
[4] LC_NUMERIC=C
[5] LC_TIME=English_United States.utf8

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base
```

This is the last of today's slides that will be discussed live.

The remaining slides provide three more examples (using the same data) designed for self-study. Use these and the example in Chapter 25 of the Course Notes to guide your work.

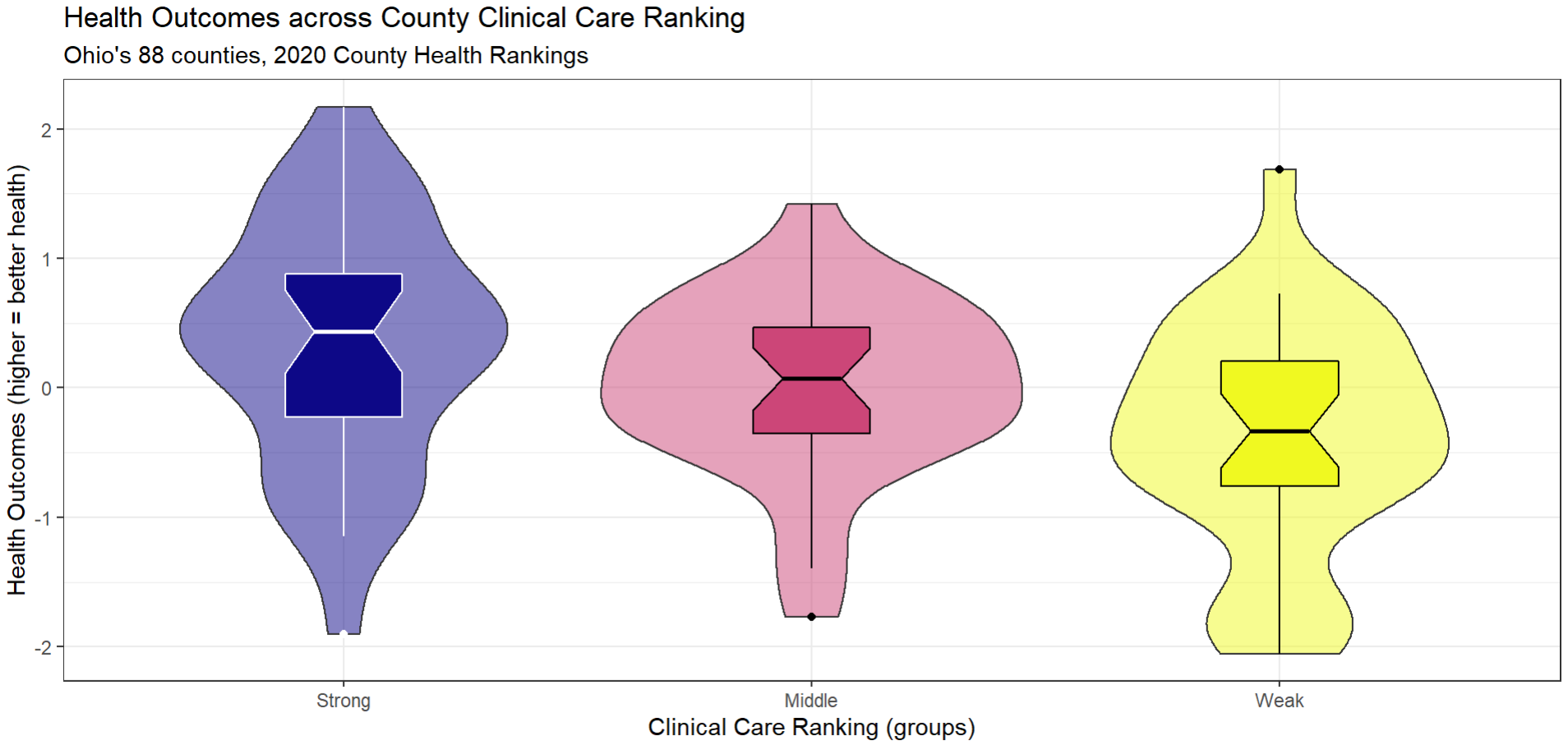
For Self-Study: Health Outcomes compared across Clinical Care Groups

Question 2

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

```
ggplot(ohio20, aes(x = clin_care, y = outcomes,
                   fill = clin_care)) +
  geom_violin(alpha = 0.5) +
  geom_boxplot(width = 0.25, notch = TRUE,
               col = c("white", "black", "black")) +
  guides(fill = "none") +
  scale_fill_viridis_d(option = "C") +
  labs(x = "Clinical Care Ranking (groups)",
       y = "Health Outcomes (higher = better health)",
       title = "Health Outcomes across County Clinical Care Ranking",
       subtitle = "Ohio's 88 counties, 2020 County Health Rankings",
       caption = "Source: https://www.countyhealthrankings.org/app/ohio/202
```

Question 2



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?

```
1 mosaic::favstats(outcomes ~ clin_care, data = ohio20) |>
2   rename(na = missing) |> kbl(digits = 2) |> kable_classic_2(font_size = 28
```

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

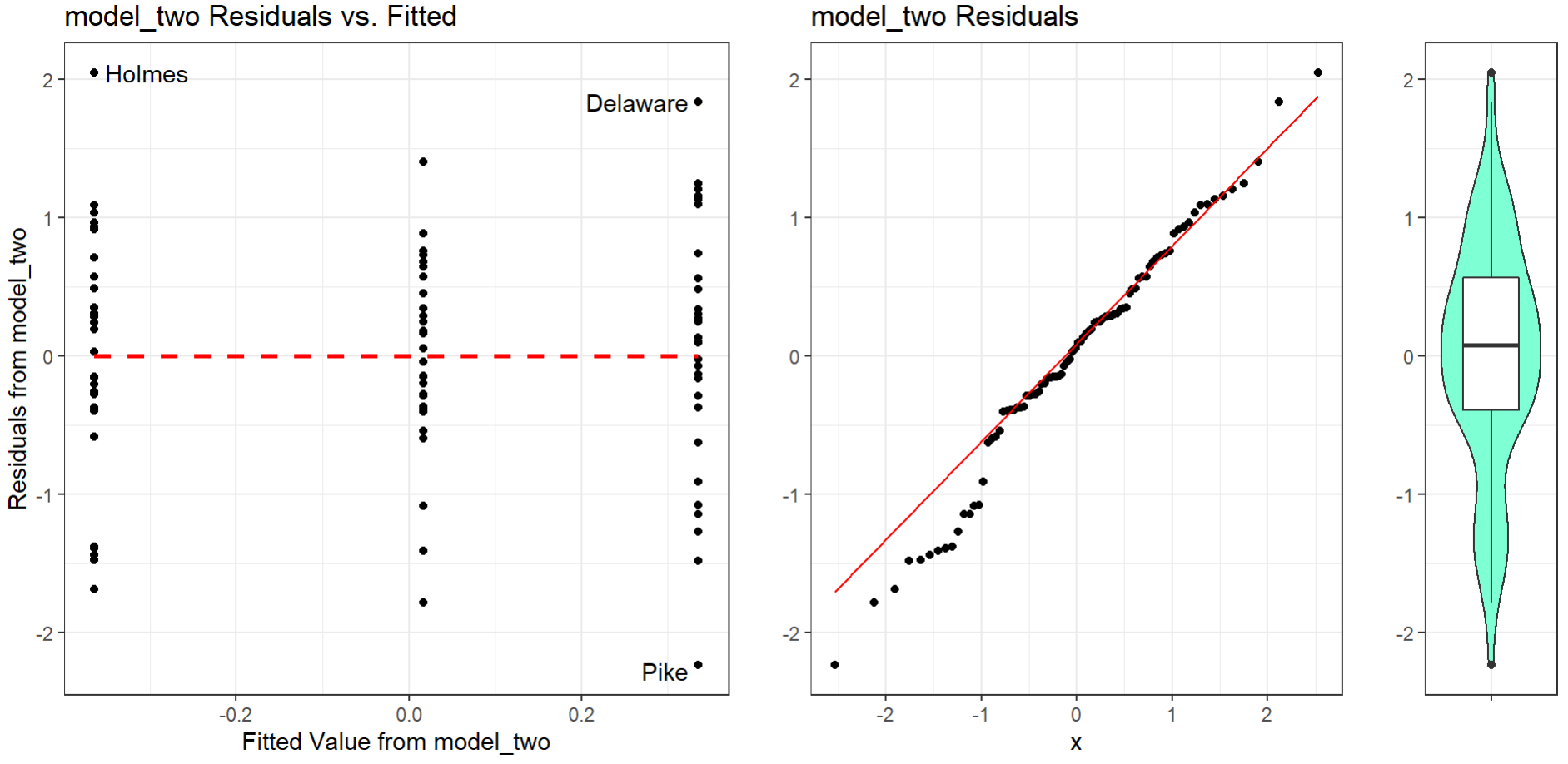
```
1 model_two <- lm(outcomes ~ clin_care, data = ohio20)
2
3 anova(model_two)
```

```
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`

```
aug_two <- augment(model_two, ohio20)

p1 <- ggplot(aug_two, aes(x = .fitted, y = .resid)) +
  geom_point() +
  geom_smooth(method = "lm", formula = y ~ x, se = F,
              lty = "dashed", col = "red") +
  geom_text_repel(data = aug_two |>
                    slice_max(abs(.resid), n = 3),
                  aes(label = county)) +
  labs(title = "model_two Residuals vs. Fitted",
       x = "Fitted Value from model_two",
       y = "Residuals from model_two")

p2 <- ggplot(aug_two, aes(sample = .resid)) +
  geom_qq() + geom_qq_line(col = "red") +
  labs(title = "model_two Residuals",
       y = "")

p3 <- ggplot(aug_two, aes(x = .resid, y = "")) +
```

Residual Plots for `model_two`



Question 2 Kruskal-Wallis test

```
1 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 Samples: 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?

Question 2: 90% Tukey HSD intervals, tidying

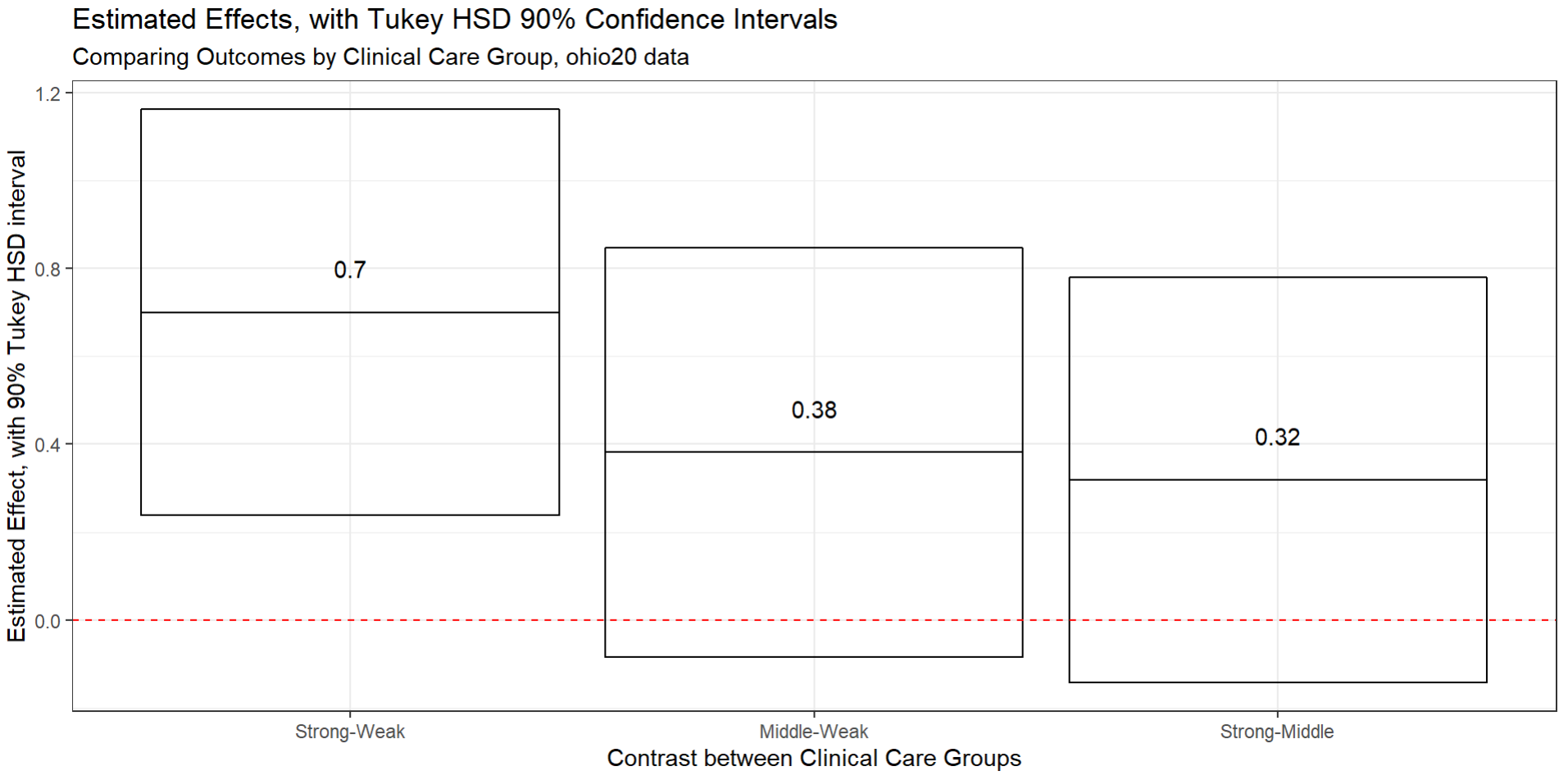
```
model_two <- lm(outcomes ~ clin_care, data = ohio20)
tukey_two <- tidy(TukeyHSD(aov(model_two),
                           ordered = TRUE,
                           conf.level = 0.90))
tukey_two |> select(-term, -null.value) |> kbl(digits = 3) |> kable_classic
```

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

```
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) +
  labs(x = "Contrast between Clinical Care Groups",
       y = "Estimated Effect, with 90% Tukey HSD interval",
       title = "Estimated Effects, with Tukey HSD 90% Confidence Intervals",
       subtitle = "Comparing Outcomes by Clinical Care Group, ohio20 data")
```

Plotting Question 2 Tukey HSD intervals



For Self-Study: ANOVA Examples about 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 Former President Trump
- `somecollege` = percentage of adults ages 25-44 with some post-secondary education in the county

Question 3 (Education)

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

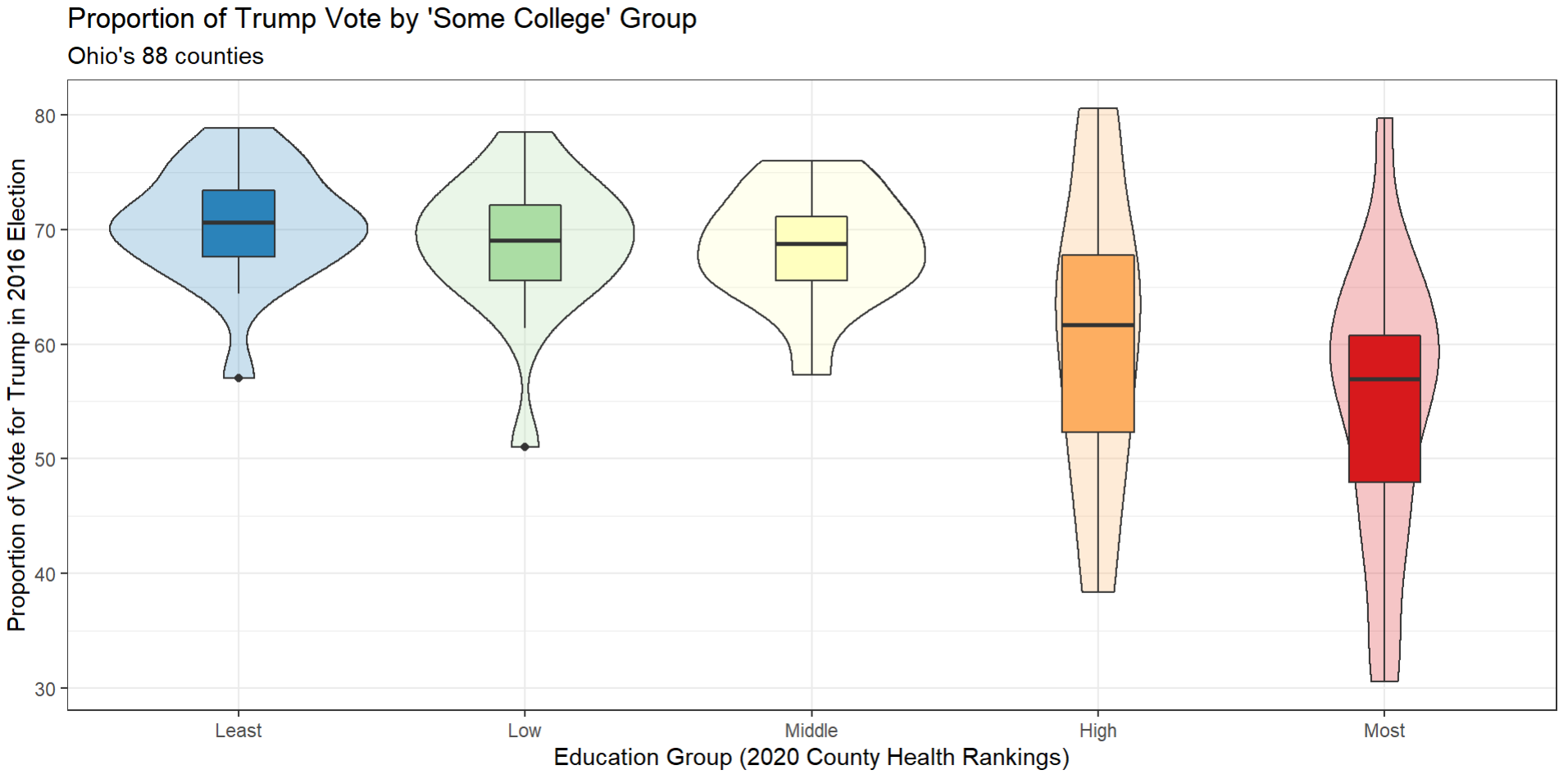
```
ohio20 <- ohio20 |>
  mutate(trump16 = 100*trump16) |>
  mutate(educ = Hmisc::cut2(somecollege, g = 5)) |>
  mutate(educ = fct_recode(educ, "Least" = "[20.4,50.3)",
           "Low" = "[50.3,54.3)", "Middle" = "[54.3,59.7)",
           "High" = "[59.7,67.1)", "Most" = "[67.1,85.1]"))
```

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

Trump 2016 % by Educational Attainment

```
ggplot(ohio20, aes(x = educ, y = trump16, fill = educ)) +
  geom_violin(alpha = 0.25) +
  geom_boxplot(width = 0.25) +
  guides(fill = "none") +
  scale_fill_brewer(palette = "Spectral", direction = -1) +
  labs(x = "Education Group (2020 County Health Rankings)",
       y = "Proportion of Vote for Trump in 2016 Election",
       title = "Proportion of Trump Vote by 'Some College' Group",
       subtitle = "Ohio's 88 counties")
```

Trump 2016 % by Educational Attainment



Numerical Comparison

```
1 mosaic::favstats(trump16 ~ educ, data = ohio20) |>
2   rename(na = missing) |> kbl(digits = 2) |> kable_classic_2(font_size = 28
```

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: 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) |>
  kbl(digits = 2) |> kable_classic_2(font_size = 28)
```

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

```
1 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
```

```
1 glance(model_3) |>
2   select(r.squared, statistic, df, df.residual, p.value)
```

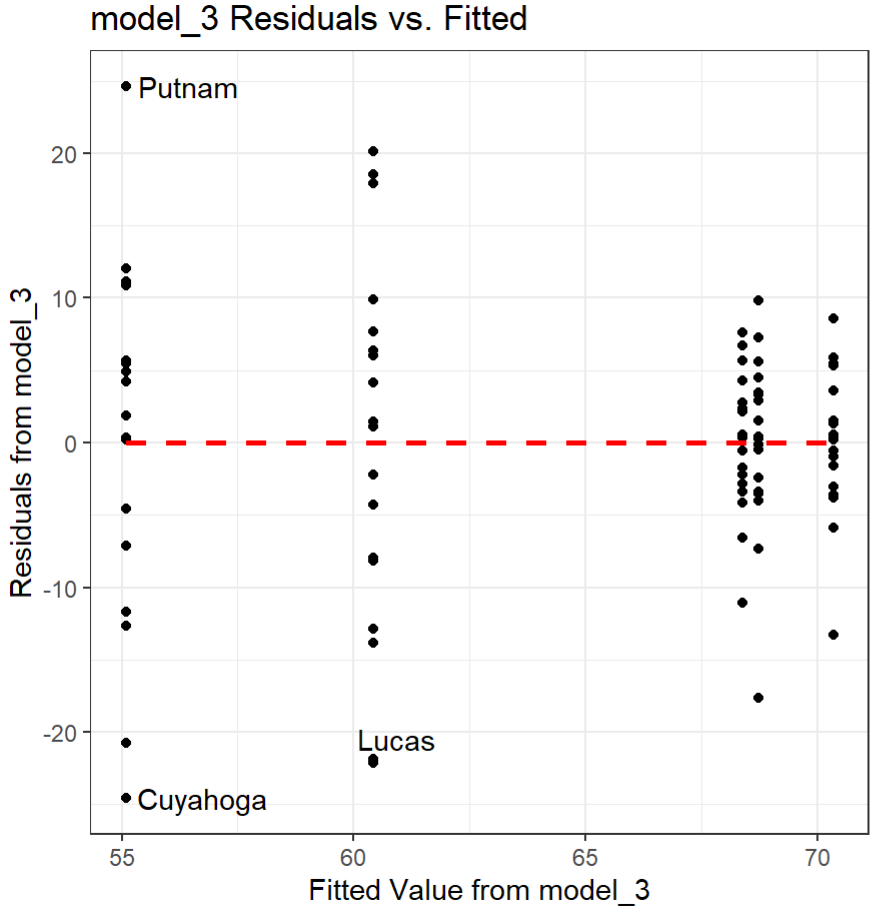
```
# A tibble: 1 × 5
  r.squared statistic    df df.residual    p.value
      <dbl>     <dbl> <dbl>       <int>      <dbl>
1     0.307      9.19     4          83 0.00000340
```

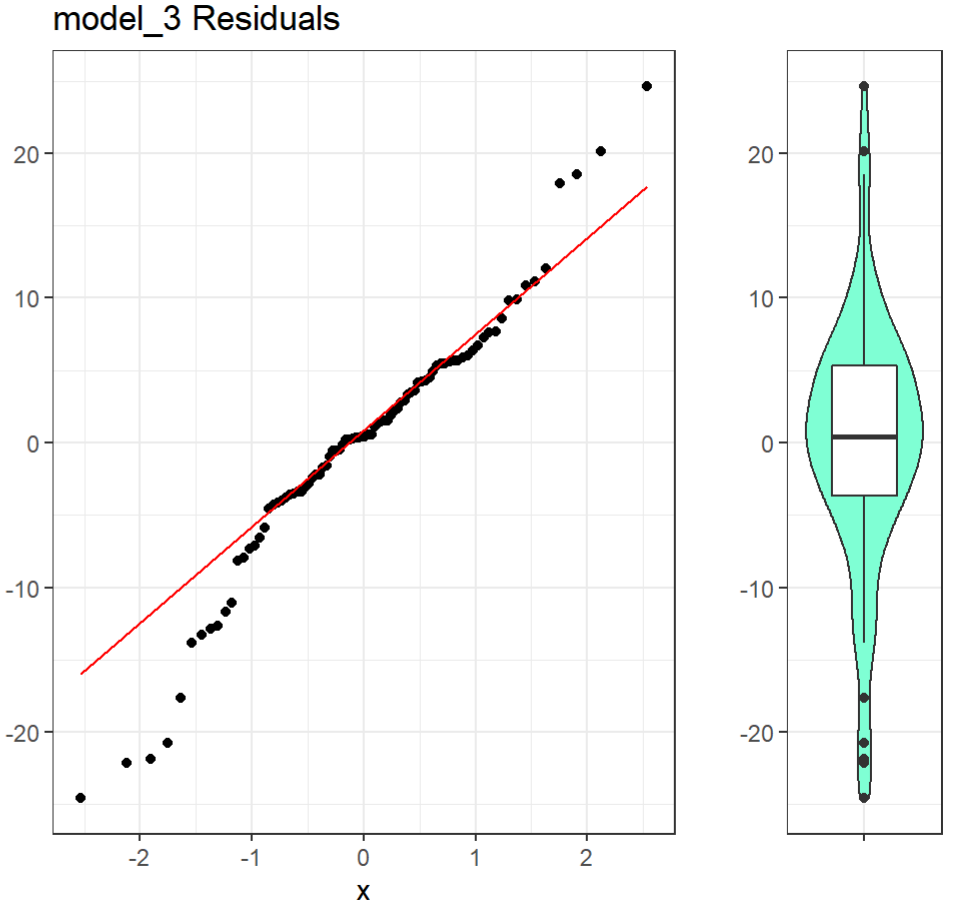
So, what's the conclusion?

Residual Plots for model_3

```
aug_3 <- augment(model_3, ohio20)

p1 <- ggplot(aug_3, aes(x = .fitted, y = .resid)) +
  geom_point() +
  geom_smooth(method = "lm", formula = y ~ x, se = F,
              lty = "dashed", col = "red") +
  geom_text_repel(data = aug_3 |>
                    slice_max(abs(.resid), n = 3),
                  aes(label = county)) +
  labs(title = "model_3 Residuals vs. Fitted",
       x = "Fitted Value from model_3",
       y = "Residuals from model_3")

p2 <- ggplot(aug_3, aes(sample = .resid)) +
  geom_qq() + geom_qq_line(col = "red") +
  labs(title = "model_3 Residuals",
       y = "")

p3 <- ggplot(aug_3, aes(x = .resid, y = "")) +
```

Residual Plots for `model_3`





Does Kruskal-Wallis give a very different result?

```
1 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% CIs: Example 3

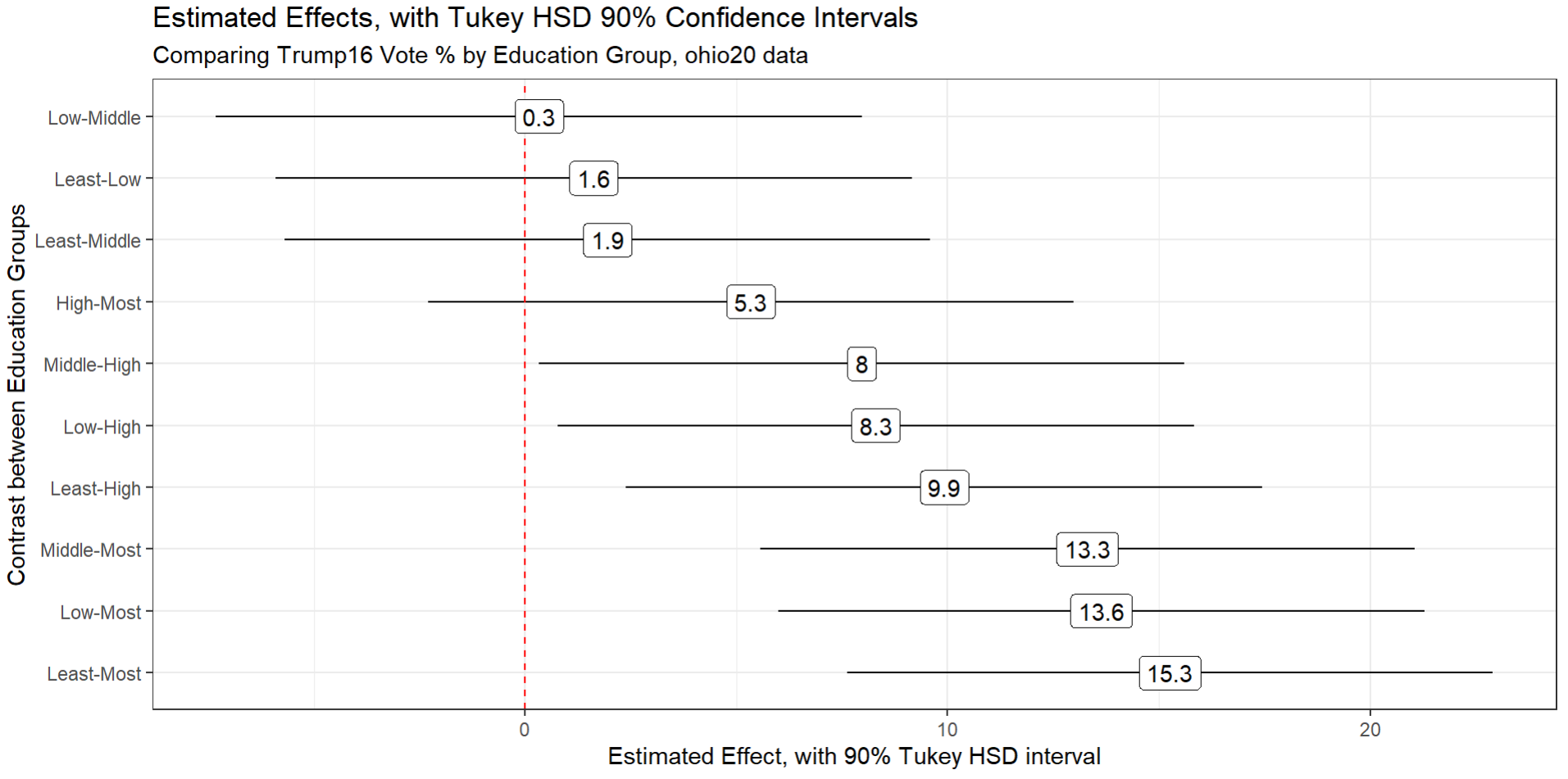
```
1 tukey_3 <- tidy(TukeyHSD(aov(model_3), ordered = TRUE, conf.level = 0.90))
2 tukey_3 |> select(-null.value) |>
3   kbl(digits = 3) |> kable_classic_2(font_size = 28)
```

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

```
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 Intervals"
       subtitle = "Comparing Trump16 Vote % by Education Group, ohio20 data
```

Plotting Tukey HSD intervals



Question 4

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

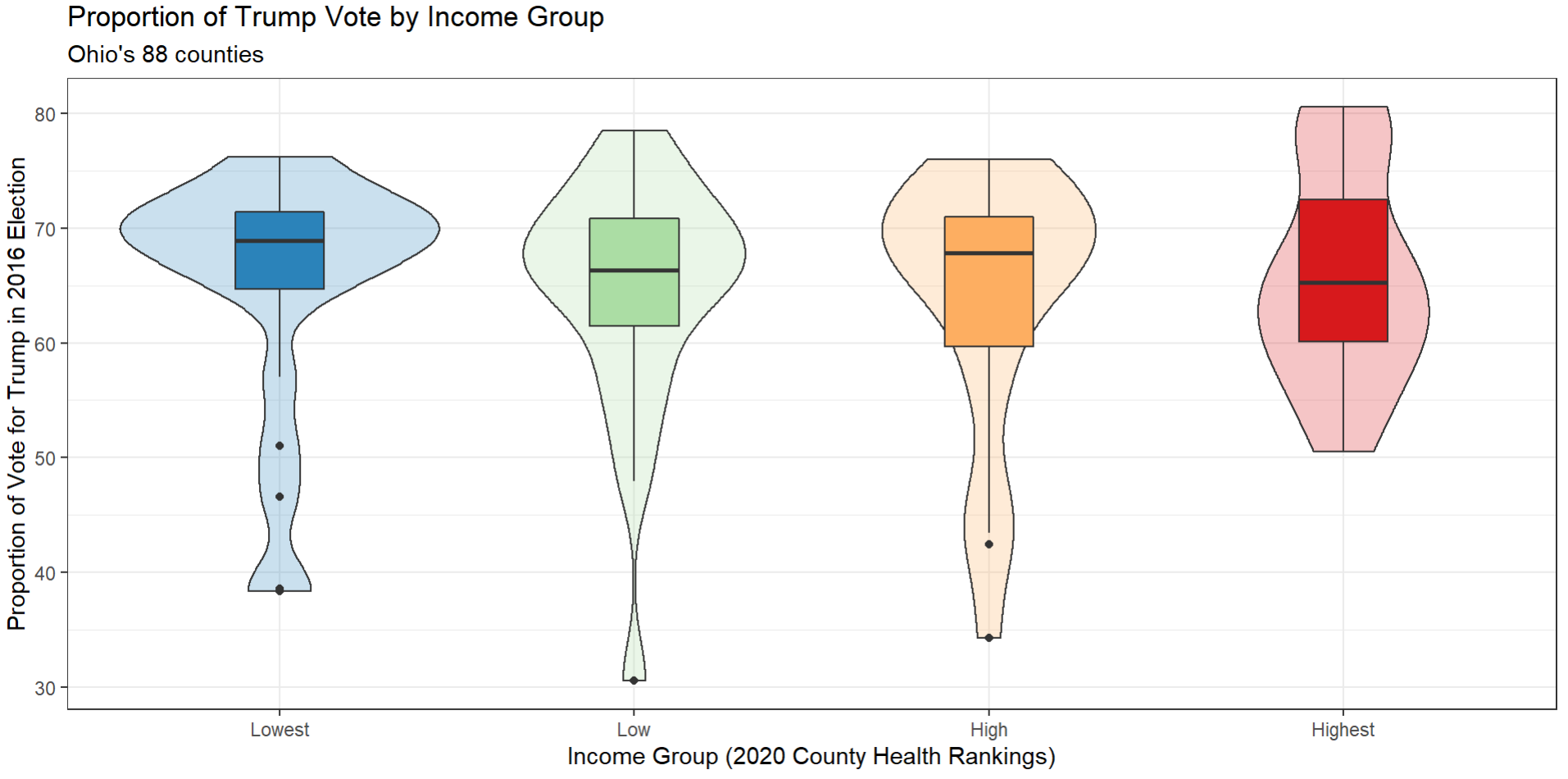
```
ohio20 <- ohio20 |>
  mutate(income = Hmisc::cut2(income, g = 4)) |>
  mutate(income = fct_recode(income, "Lowest" = "[40416, 48792)",
           "Low" = "[48792, 53904)", "High" = "[53904, 60828)",
           "Highest" = "[60828,103536]"))
```

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

Trump 2016 % by Income

```
ggplot(ohio20, aes(x = income, y = trump16, fill = income)) +
  geom_violin(alpha = 0.25) +
  geom_boxplot(width = 0.25) +
  guides(fill = "none") +
  scale_fill_brewer(palette = "Spectral", direction = -1) +
  labs(x = "Income Group (2020 County Health Rankings)",
       y = "Proportion of Vote for Trump in 2016 Election",
       title = "Proportion of Trump Vote by Income Group",
       subtitle = "Ohio's 88 counties")
```

Trump 2016 % by Income



Numerical Comparison

```
1 mosaic::favstats(trump16 ~ income, data = ohio20) |>
2   rename(na = missing) |> kbl(digits = 2) |> kable_classic_2(font_size = 28
```

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) |>
  kbl(digits = 2) |> kable_classic_2(font_size = 28)
```

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

```
1 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
```

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

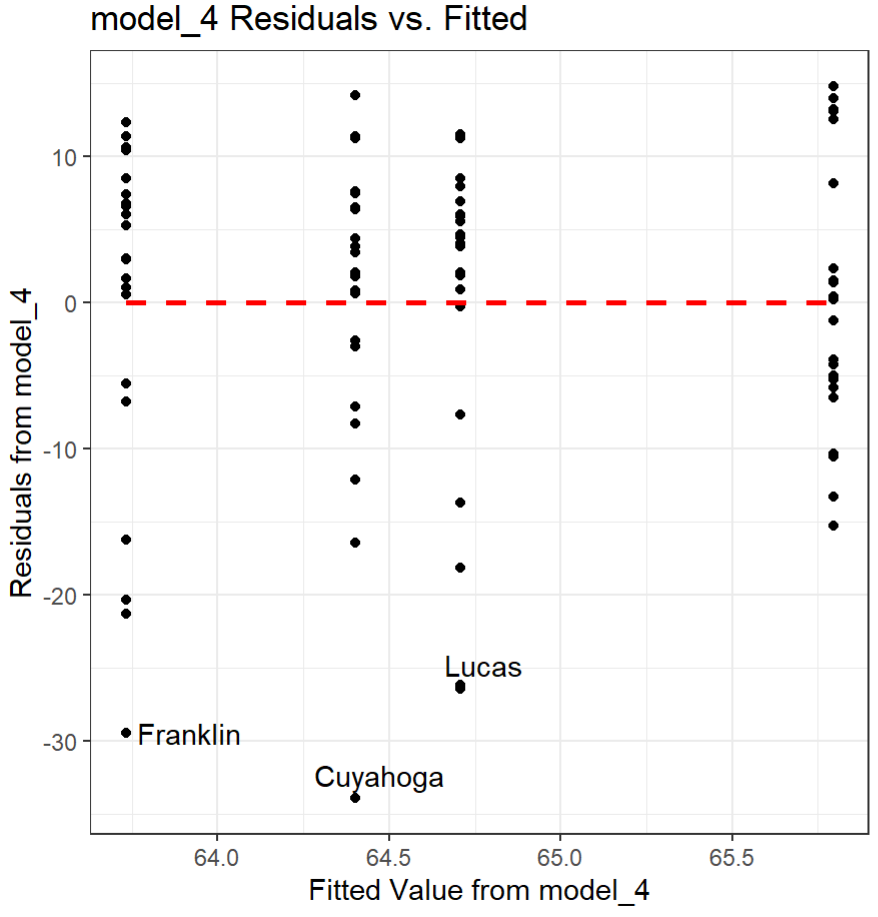
```
# A tibble: 1 × 5
  r.squared statistic    df df.residual p.value
      <dbl>     <dbl> <dbl>       <int>   <dbl>
1   0.00500     0.141     3          84   0.935
```

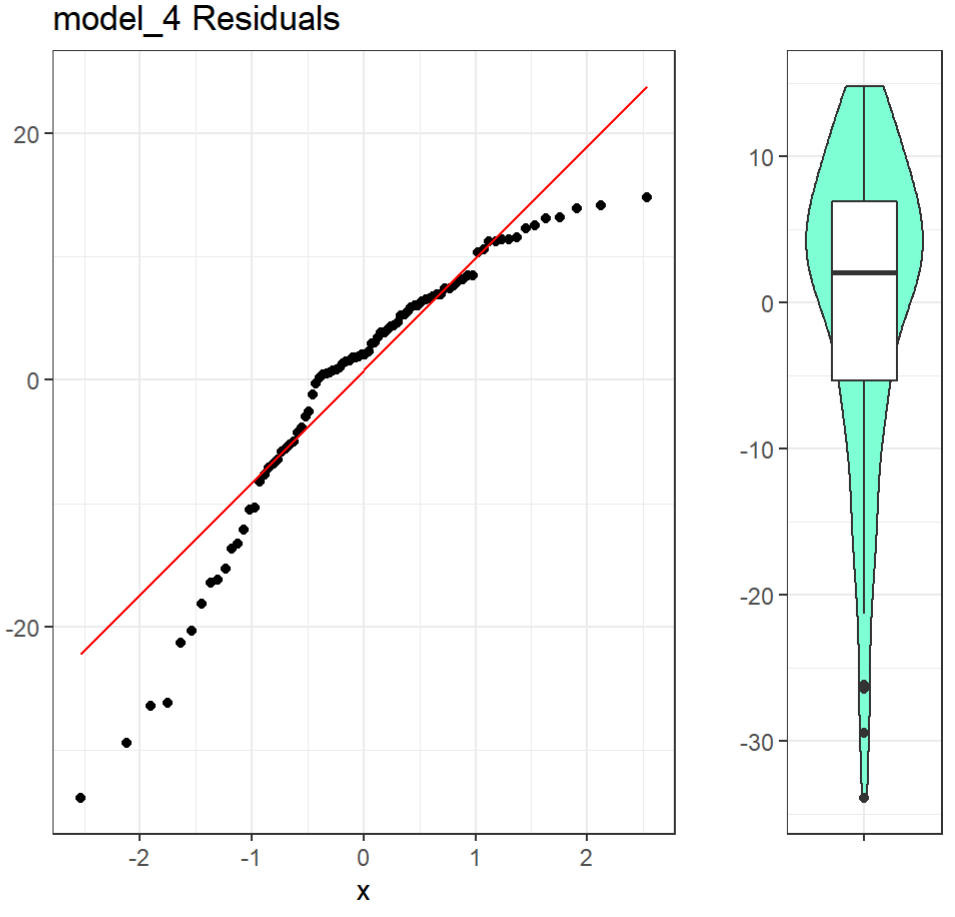
So, what's the conclusion?

Residual Plots for model_4

```
aug_4 <- augment(model_4, ohio20)

p1 <- ggplot(aug_4, aes(x = .fitted, y = .resid)) +
  geom_point() +
  geom_smooth(method = "lm", formula = y ~ x, se = F,
              lty = "dashed", col = "red") +
  geom_text_repel(data = aug_4 |>
                    slice_max(abs(.resid), n = 3),
                  aes(label = county)) +
  labs(title = "model_4 Residuals vs. Fitted",
       x = "Fitted Value from model_4",
       y = "Residuals from model_4")

p2 <- ggplot(aug_4, aes(sample = .resid)) +
  geom_qq() + geom_qq_line(col = "red") +
  labs(title = "model_4 Residuals",
       y = "")

p3 <- ggplot(aug_4, aes(x = .resid, y = "")) +
```

Residual Plots for `model_4`





Does Kruskal-Wallis give a different result?

```
1 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% CIs: Income Groups

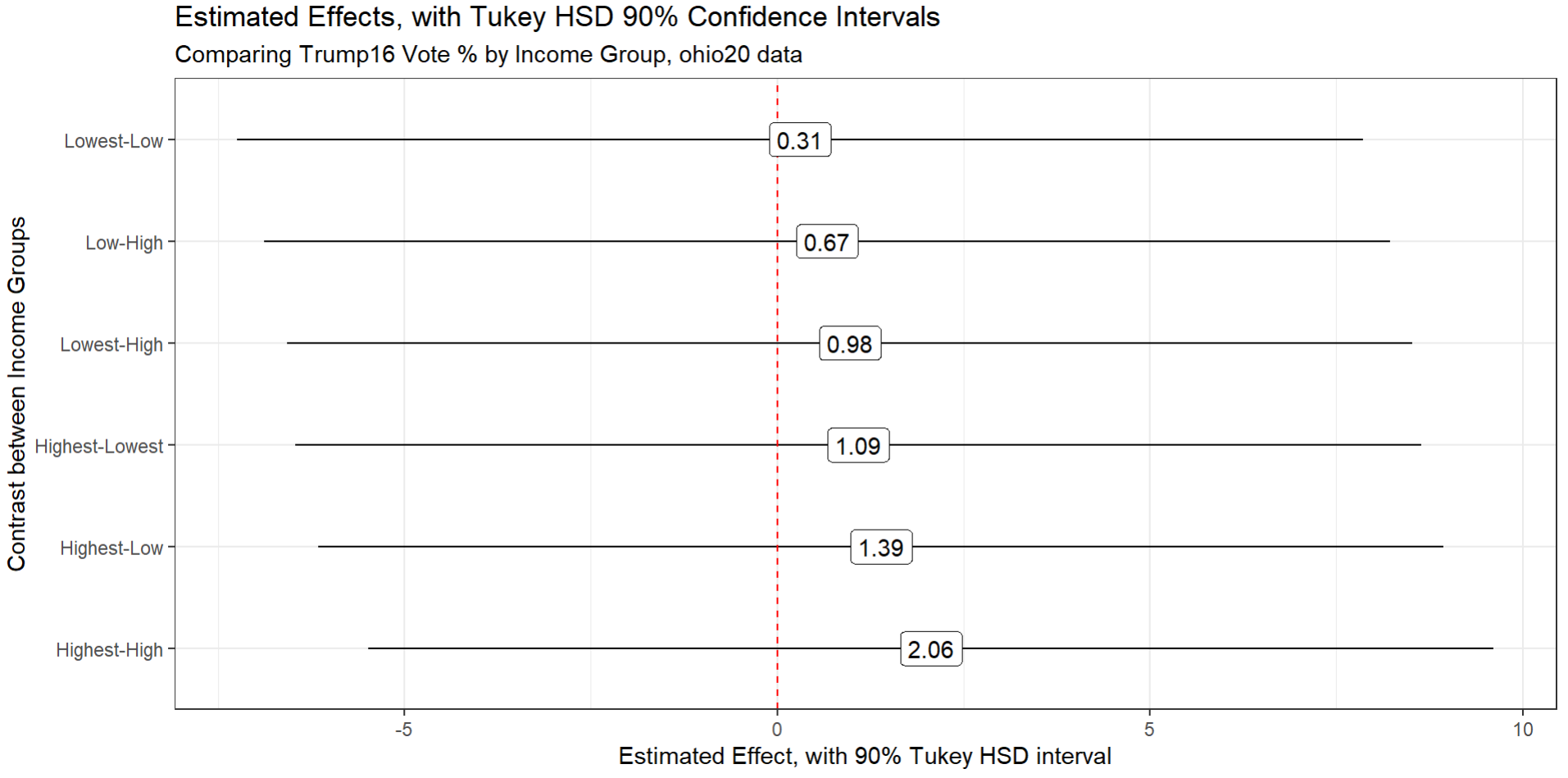
```
tukey_4 <- tidy(TukeyHSD(aov(model_4), ordered = TRUE, conf.level = 0.90))
tukey_4 |> select(-null.value) |>
  kbl(digits = 3) |> kable_classic_2(font_size = 28)
```

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)

```
ggplot(tukey_4, 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,2))) +
  coord_flip() +
  labs(x = "Contrast between Income Groups",
       y = "Estimated Effect, with 90% Tukey HSD interval",
       title = "Estimated Effects, with Tukey HSD 90% Confidence Intervals"
       subtitle = "Comparing Trump16 Vote % by Income Group, ohio20 data")
```

Plotting Tukey HSD intervals (Income Groups)



K Samples: 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 detectable 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?