Causal Inference I Day 2 In-Class Exercise

Tyler Rongxuan Chen

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```
knitr::opts_chunk$set(echo = TRUE)
```

```
acorn <- read.csv("acorn03.csv")
```

```
library("MASS")
library("sandwich")
library("lmtest")
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
options(digits = 3)
```

Let's start with our original model:

```
model <- lm(vote03 ~ z, data = acorn)
summary(model)
```

```
##
## Call:
## lm(formula = vote03 ~ z, data = acorn)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.10199 -0.04229  0.00437  0.04575  0.16400
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.2885     0.0172   16.73  1.9e-15 ***
## z             0.0363     0.0244    1.49     0.15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0645 on 26 degrees of freedom
## Multiple R-squared:  0.0785, Adjusted R-squared:  0.0431
## F-statistic: 2.22 on 1 and 26 DF,  p-value: 0.149
```
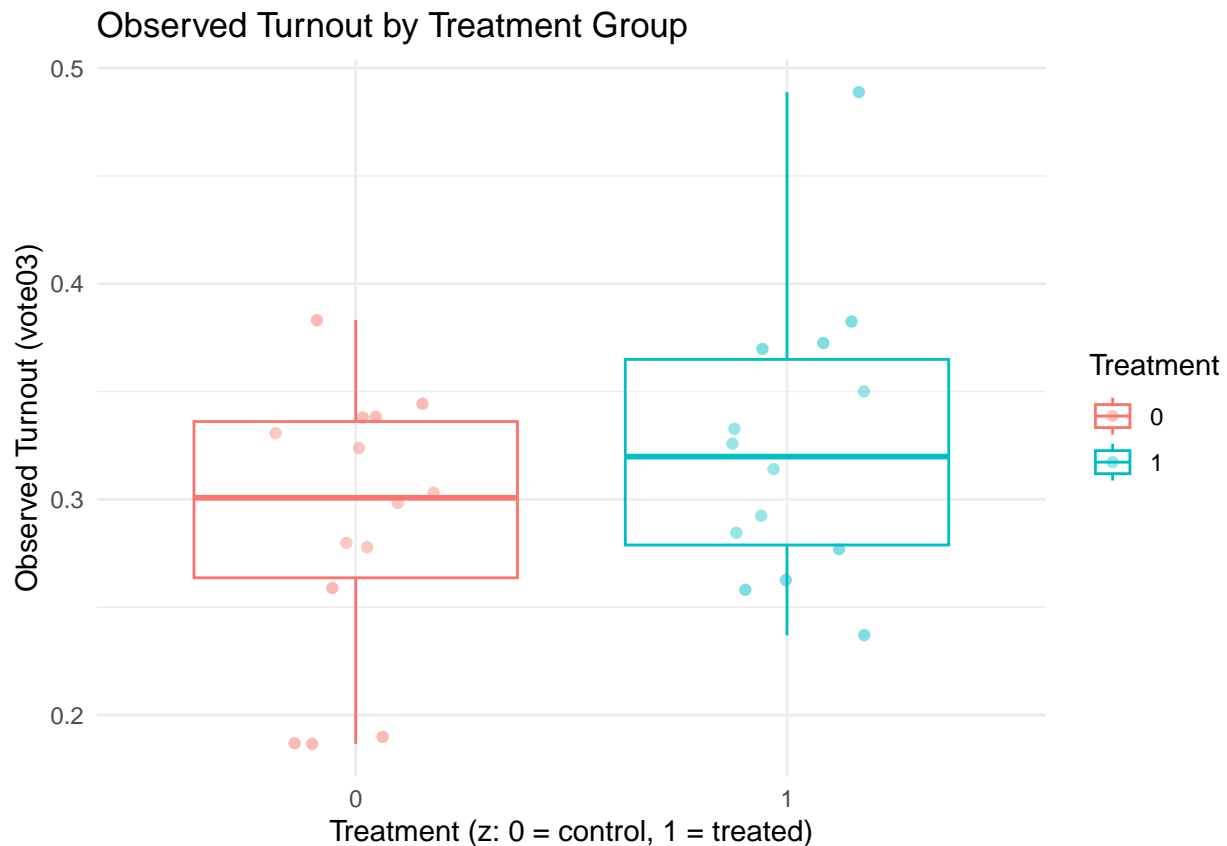
```
library(ggplot2)

ggplot(acorn, aes(x = as.factor(z), y = vote03, color = as.factor(z))) +
  geom_jitter(width = 0.2, alpha = 0.5) +
  geom_boxplot(alpha = 0.2, outlier.shape = NA) +
  labs(
    x = "Treatment (z: 0 = control, 1 = treated)",
    y = "Observed Turnout (vote03)",
    color = "Treatment",
    title = "Observed Turnout by Treatment Group"
  ) +
  theme_minimal()
```

Observed Turnout by Treatment Group

What we have seen in previous classes is regressing directly on z, as shown above. This gives us the observed difference in average turnout between the treatment $(z = 1)$ and control $(z = 0)$ groups.

It answers: "Did the treatment group have higher turnout than the control group?"

BUT: This only tests whether there's a difference, it does not test if a specific hypothesized effect size fits the data.

Here, we created some new versions of the outcome variable (yc_moe0, yc_moe1, yc_moe2) for each model of effect (MOE).

Each transformation answers: "If the effect of treatment were exactly what this model assumes, what would the data look like after we 'remove' that effect from the treated units?"

After applying the transformation, if the assumed effect is correct, the treated and control groups should look similar—there should be no systematic difference left.

If there is still a difference (especially in the "wrong" direction), our model of the effect is not supported by the data.

With this mindset, let's look at the exercise.

```
acorn_e <- transform(acorn,
                     yc_moe0 = vote03,
                     yc_moe1 = vote03 - contact/10,
                     yc_moe2 = vote03 - contact/5)
```

Exercise 1

Since we already have three different model of effect above, we are now heading to the fourth model.

Let's say our new model assumes the effect is proportional to the square root of contacts (maybe: more contacts, but with diminishing returns). Here's an example formula:

Model: Each contact increases votes by 0.3 times the square root of contacts (rounded, as an example).

```
acorn_e <- transform(acorn_e,
  yc_moe3 = vote03 - 0.3 * sqrt(contact)
)
```

Let's take a look at what is happening here:

```
library(tidyr)

acorn_long <- acorn_e |>
  pivot_longer(
    cols = starts_with("yc_moe"),
    names_to = "model",
    values_to = "yc"
  )

ggplot(acorn_long, aes(x = as.factor(z), y = yc, color = as.factor(z))) +
  geom_jitter(width = 0.2, alpha = 0.5) +
  geom_boxplot(alpha = 0.2, outlier.shape = NA) +
  facet_wrap(~ model, ncol = 2) +
  labs(
    x = "Treatment (z: 0 = control, 1 = treated)",
    y = "Reconstructed Outcome (yc)",
    color = "Treatment",
    title = "Scatter plots by Model of Effect"
  ) +
  theme_minimal()
```

Scatter plots by Model of Effect
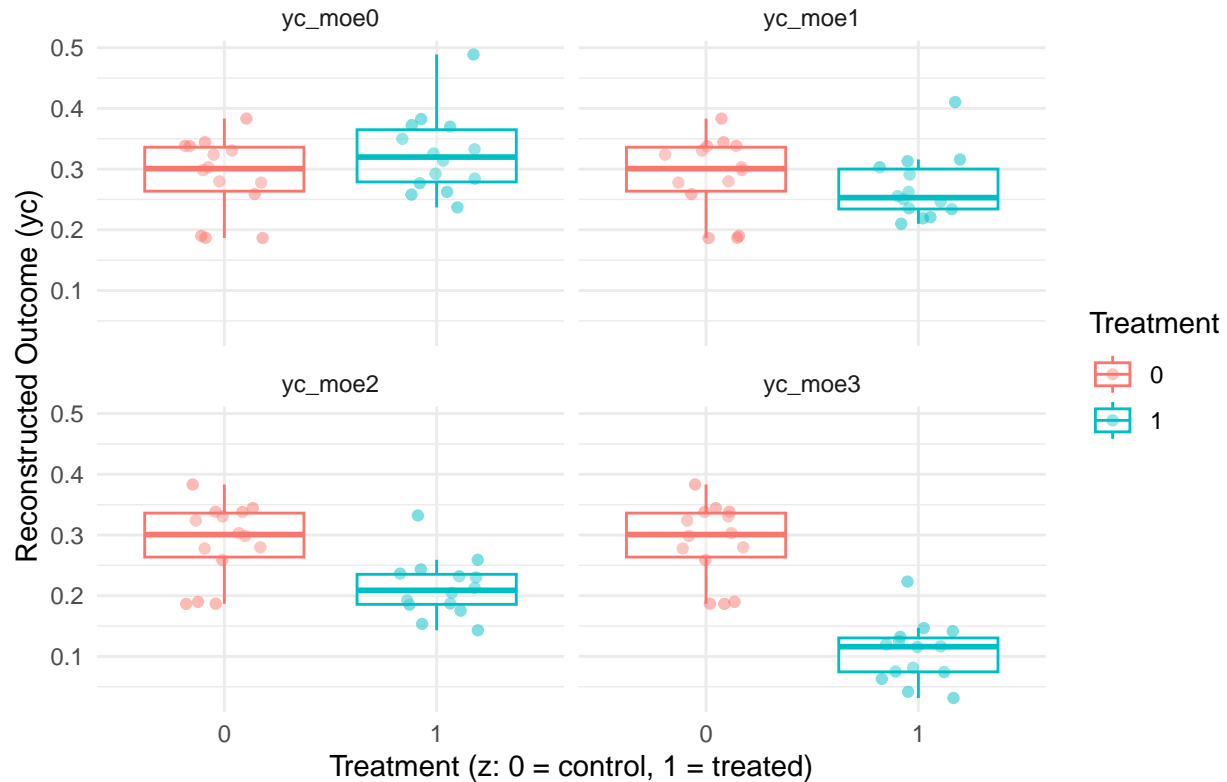
What This Plot Shows

- **Each panel** represents one hypothesis about the treatment's effect (the four different `yc_moe*` variables).
- **X-axis: z** (Treatment assignment: 0 = control, 1 = treated)
- **Y-axis:** The reconstructed outcome (`yc`) under each hypothesis/model.
- **Points:** Each precinct's reconstructed outcome.
- **Boxplot:** Summary (median, quartiles) of reconstructed outcomes for treated vs. control.
- **Facets:** Each hypothesis/model.

---

(1) `yc_moe0` ("No Effect" Model)

The treated group (1) is slightly higher than control (0), but the boxplots overlap.

This implies that there is Some, but not strong, difference between treated and control.

Statistically, this model suggests little evidence for a large treatment effect.

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(2) `yc_moe1` ("1 Vote Per 10 Contacts" Model)

The model assumes too much effect. If this were the real effect, treated and control should look the same. Instead, treated is lower, so this model probably overestimates the effect.

Statistically, this model is not supported.

---

(3) `yc_moe2` ("1 Vote Per 5 Contacts" Model)

This is way too much adjustment—the data do not support this strong an effect.

The difference is significant, but in the wrong direction: this model "over-removes" the effect, suggesting it is too aggressive.

---

(4) `yc_moe3` (Our Custom Model, e.g., Proportional to sqrt(contact))

Now the treated group is much, much lower than control, almost all the values for treated are below those for control.

This model over-adjusts more than any other.

If this were the true effect, the treated and control should have the same distribution. But now, treated is dramatically lower, and clearly, the model is not supported by the data.

Exercise 2

```
t.test(yc_moe0 ~ z, data = acorn_e)
```

```
##
##  Welch Two Sample t-test
##
## data:  yc_moe0 by z
## t = -1, df = 26, p-value = 0.1
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -0.0864  0.0138
## sample estimates:
## mean in group 0 mean in group 1
##           0.289           0.325
```

```
t.test(yc_moe1 ~ z, data = acorn_e)
```

Model	Mean (Control)	Mean (Treated)	t-stat	df	p-value	Interpretation
yc_moe0	0.289	0.325	-1.0	26	0.10	Reasonable
yc_moe1	0.289	0.269	0.9	25	0.40	Reasonable
yc_moe2	0.289	0.213	4.0	24	0.002	Over-adjusted
yc_moe3	0.289	0.106	8.0	25	$\ll 0.001$	Severely over-adjusted

Table 1: Welch Two Sample t-tests for Different Models of Effect.

```
##
##  Welch Two Sample t-test
##
## data:  yc_moe1 by z
## t = 0.9, df = 25, p-value = 0.4
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  -0.0262  0.0650
## sample estimates:
## mean in group 0 mean in group 1
##           0.289           0.269
```

```
t.test(yc_moe2 ~ z, data = acorn_e)
```

```
##
##  Welch Two Sample t-test
##
## data:  yc_moe2 by z
## t = 4, df = 24, p-value = 0.002
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  0.0313 0.1189
## sample estimates:
## mean in group 0 mean in group 1
##           0.289           0.213
```

```
t.test(yc_moe3 ~ z, data = acorn_e)
```

```
##
##  Welch Two Sample t-test
##
## data:  yc_moe3 by z
## t = 8, df = 25, p-value = 9e-09
## alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
## 95 percent confidence interval:
##  0.138 0.227
## sample estimates:
## mean in group 0 mean in group 1
##           0.289           0.106
```

```
model0 <- lm(yc_moe0 ~ z, data = acorn_e)
lmtest::coeftest(model0, sandwich::vcovHC, type = "HC2")
```

```
##
## t test of coefficients:
##
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.2885     0.0169   17.09  1.2e-15 ***
## z             0.0363     0.0244    1.49     0.15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
model1 <- lm(yc_moe1 ~ z, data = acorn_e)
lmtest::coeftest(model1, sandwich::vcovHC, type = "HC2")
```

```
##
## t test of coefficients:
##
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.2885     0.0169   17.09  1.2e-15 ***
## z            -0.0194     0.0222   -0.88     0.39
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
model2 <- lm(yc_moe2 ~ z, data = acorn_e)
lmtest::coeftest(model2, sandwich::vcovHC, type = "HC2")
```

```
##
## t test of coefficients:
##
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.2885     0.0169   17.09  1.2e-15 ***
## z            -0.0751     0.0212   -3.54   0.0015 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
model3 <- lm(yc_moe3 ~ z, data = acorn_e)
lmtest::coeftest(model3, sandwich::vcovHC, type = "HC2")
```

```
##
## t test of coefficients:
##
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.2885     0.0169   17.09  1.2e-15 ***
## z            -0.1823     0.0215   -8.48   5.8e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model	Estimate	Std. Error	t value	p-value	Interpretation
yc_moe0	0.0363	0.0244	1.49	0.15	Reasonable
yc_moe1	-0.0194	0.0222	-0.88	0.39	Reasonable
yc_moe2	-0.0751	0.0212	-3.54	0.0015	Over-adjusted
yc_moe3	-0.1823	0.0215	-8.48	5.8×10^{-9}	Severely over-adjusted

Table 2: Regression Estimates of Treatment Effect (z) for Different Models of Effect.