# Day 04: Analyzing experimental data

Erin Rossiter

January 25, 2022

# Today's plan

1. Tidy up
   - Abigail, will you:
     - remind me to take a break at 4:30-4:45
     - jot notes on typos & email after class
   - Note that HW4 will ask for a one-pager on your research topic, question, and hypothesis(es)
2. Lecture part 1 and lab 1 (hypothesis testing)
3. Lecture part 2 and lab 2 (covariates in design)

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# Recap

# ATE

- The average treatment effect (ATE) is often an interesting, important, useful estimand.
- Difference-in-means is an **unbiased** estimator of the ATE assuming:

  1. Randomization of treatment

     » $E[Y_i(1)|D_i = 1] = E[Y_i(1)]$
     » $E[Y_i(0)|D_i = 0] = E[Y_i(0)]$
     » We can estimate left-hand terms using our observed data!

  2. Excludability
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- What about **uncertainty**?

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# Standard error

To be clear:

- a **sampling distribution** is a distribution of a statistic (e.g., $\hat{ATE}$)
- a **standard deviation** is a single value quantifying variability for any variable $X$
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There's a true standard error: $SE(\hat{ATE})$

- How much might our estimate vary across all hypothetical random assignments?
- Our design choices influence this!
  - $N$ size
  - Potential outcome variability
  - Randomization routine (blocking, clustering)
- Beneficial to reduce standard error in design phase.

Of course, we must estimate the standard error: $\hat{SE}(\hat{ATE})$

- DeclareDesign helps understand both true standard error and how we plan to estimate it
  - Is our estimation strategy getting a standard error that's too big? Meaning, we'd fail to reject a false null? No stars when there should be?!

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✓ Uncertainty associated with the $\hat{ATE}$

Today → Hypothesis testing

1. (Typical) null hypotheses of no *average* effect and hypothesis testing with approximate p-values based on assumptions about sampling distributions
2. Sharp null hypotheses and randomization inference hypothesis testing with exact p-values

Today → More talk about covariates

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# Hypothesis testing

## “Traditional” hypothesis testing

# Refresher on hypothesis testing

1. We state a null hypothesis
   - e.g., $H_0$: $ATE = 0$
   - No average treatment effect
   - The claim we'd like to reject
2. We choose a test statistic
   - e.g., $t$-value
3. Determine the distribution of the test statistic under the null
   - A thought experiment. If the null is true, what data would we expect to see? (board)
   - e.g., Student's $t$
4. Calculate the probability ($p$-value) of our test statistic under the null
   - Continuing our thought experiment. If the null is true, how surprising is our data? (board)

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# Example

- Data from page 65 of GG
- Treatment is encouragement to make a charitable donation
- Outcome is how much money donated

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df <- data.frame("Donation" = c(500, 100, 100, 50,
                               25, 25, 0, 0, 0, 0,
                               25, 20, 15, 15, 10,
                               5, 5, 5, 0, 0),
                 "Treatment" = c(rep(1,10),
                                 rep(0, 10)))
head(df)
```

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##   Donation Treatment
## 1      500         1
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2. Choose the $t$ value as our test statistic
3. Assume sampling distribution of $t$ follows Student's $t$ under the null
   - *We're assuming sampling dist of DIM estimator has a certain shape*
4. Calculate probability of observing our test statistic (from #2) given assumed sampling distribution under the null (from #3)

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# t-test by hand

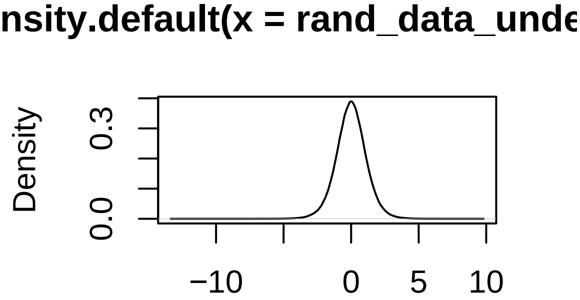
```
# 1. state null
h_not <- 0

# 2. choose test statistic (t-test with unequal variances)
s1 <- sd(df$Donation[df$Treatment == 0])^2
s2 <- sd(df$Donation[df$Treatment == 1])^2
t <- (70-h_not)/sqrt(s1/10 + s2/10)
t
```

```
## [1] 1.44776
```

# t-test by hand

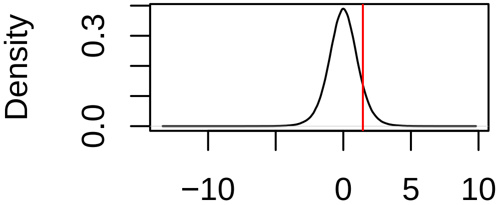
```
# 3. think about data we'd observe if the null is true
# (Notice the assumption about the sampling
# distribution we're making here!)
rand_data_under_null <- rt(n = 1000000, df = 9.0558)
plot(density(rand_data_under_null),
     xlab = "", cex = .25)
```



# t-test by hand

```
# (from step 3)
plot(density(rand_data_under_null), main = "", xlab = "", cex =

# 4. how odd is our data (or something bigger) given the null?
abline(v = t, col = "red")
```




```
pt(t, df = 9.0558, lower.tail = F) #or...
```

```
## [1] 0.09070126
```

```
sum(rand_data_under_null > t)/1000000
```

```
## [1] 0.090729
```

# t-test in R using `t.test()`

```
t.test(df$Donation[df$Treatment == 1],
       df$Donation[df$Treatment == 0],
       var.equal = F, alternative = "greater")
```

```
##
##  Welch Two Sample t-test
##
## data:  df$Donation[df$Treatment == 1] and df$Donation[df$Trea
## t = 1.4478, df = 9.0558, p-value = 0.0907
## alternative hypothesis: true difference in means is greater t
## 95 percent confidence interval:
##  -18.56994       Inf
## sample estimates:
## mean of x mean of y
##        80        10
```

# t-test in R using `difference_in_means()`

Identical, but

- no one-sided tests
- allows for easy design-based estimation when you use blocking and clustering (see homework)
- *I encourage this package since it's built with experiments in mind*

```
options(width = 60)
estimatr::difference_in_means(Donation ~ Treatment,
                              data = df)
```

```
## Design:  Standard
##           Estimate Std. Error t value  Pr(>|t|)  CI Lower
## Treatment       70   48.35057 1.44776 0.1814026 -39.27398
##           CI Upper      DF
## Treatment  179.274 9.05578
```

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# t-test big picture

- We're making assumptions about sampling distribution
  - sampling dist for DIM estimate follows $t$ distribution
- Good assumption when...
  - Outcomes distributed normally, or
  - Outcome distributed non-normally, but big sample (invoke CLT for sampling distribution to be approximately normal)
- In general, we should be wary when we're using small and/or skewed samples
  - "Rules of thumb" are hard...

Next, an alternative approach that starts from a different null hypothesis...

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# Randomization inference

# Sharp null hypothesis of no effect

$$H_0 : \tau_i = Y_i(1) - Y_i(0) = 0 \quad \forall i$$

- Think, "no effect means no effect"
- Different than no **average** treatment effect
  - No average treatment effect does not imply sharp null.
- Example on board

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# Recall our hypothesis testing steps

1. We state a null hypothesis
   - $H_0 : \tau_i = Y_i(1) - Y_i(0) = 0 \quad \forall i$
   - Or simply, $H_0 : Y_i(1) = Y_i(0)$
2. We choose a test statistic
   - Keep in mind, many to choose from
   - Let's stick with DIM
3. Determine the distribution of the test statistic under the null
   - **This is where we shake things up!** Example next.
   - Null hypothesis is about *individual* rather than *average* effect
   - We have a link between observed data and the potential outcomes.
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# How do we determine the distribution of the test statistic under the null?

1. What do we know about potential outcomes from what we *observe*?

| Unit | $d_i$ | $Y_i$ | $Y_i(0)$ | $Y_i(1)$ |
|---|---|---|---|---|
| 1 | 0 | 1 | ? | ? |
| 2 | 0 | 4 | ? | ? |
| 3 | 0 | 2 | ? | ? |
| 4 | 0 | 1 | ? | ? |
| 5 | 1 | 5 | ? | ? |
| 6 | 1 | 7 | ? | ? |
| 7 | 1 | 3 | ? | ? |
| 8 | 1 | 3 | ? | ? |

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- $Y_i(0)|d_i = 0$
- $Y_i(1)|d_i = 1$

| Unit | $d_i$ | $Y_i$ | $Y_i(0)$ | $Y_i(1)$ |
|---|---|---|---|---|
| 1 | 0 | 1 | 1 | ? |
| 2 | 0 | 4 | 4 | ? |
| 3 | 0 | 2 | 2 | ? |
| 4 | 0 | 1 | 1 | ? |
| 5 | 1 | 5 | ? | 5 |
| 6 | 1 | 7 | ? | 7 |
| 7 | 1 | 3 | ? | 3 |
| 8 | 1 | 3 | ? | 3 |

# How do we determine the distribution of the test statistic under the null?

2. What do we know about potential outcomes from what we *assume*?

| Unit | $d_i$ | $Y_i$ | $Y_i(0)$ | $Y_i(1)$ |
|---|---|---|---|---|
| 1 | 0 | 1 | 1 | ? |
| 2 | 0 | 4 | 4 | ? |
| 3 | 0 | 2 | 2 | ? |
| 4 | 0 | 1 | 1 | ? |
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| 8 | 1 | 3 | ? | 3 |

# How do we determine the distribution of the test statistic under the null?

2. What do we know about potential outcomes from what we *assume*?

- We can use the sharp null to fill in remaining potential outcomes
- $Y_i(1) - Y_i(0) = 0$

| Unit | $d_i$ | $Y_i$ | $Y_i(0)$ | $Y_i(1)$ |
|---|---|---|---|---|
| 1 | 0 | 1 | 1 | (1) |
| 2 | 0 | 4 | 4 | (4) |
| 3 | 0 | 2 | 2 | (2) |
| 4 | 0 | 1 | 1 | (1) |
| 5 | 1 | 5 | (5) | 5 |
| 6 | 1 | 7 | (7) | 7 |
| 7 | 1 | 3 | (3) | 3 |
| 8 | 1 | 3 | (3) | 3 |

# How do we determine the distribution of the test statistic under the null?

3. Since we have *all* potential outcomes, we can calculate test-statistic for all hypothetical randomizations!!!

– What is this called?

# How do we determine the distribution of the test statistic under the null?

3. Since we have *all* potential outcomes, we can calculate test-statistic for all hypothetical randomizations!!!

- What is this called? **Sampling distribution**
- Also called "randomization distribution"

4. Compare our test statistic to all possible test statistics under the null to get p-value.

# Example

| Unit | $d_i$ | $Y_i$ | $Y_i(0)$ | $Y_i(1)$ |
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```
df <- data.frame(Z = c(0,0,0,0,1,1,1,1),
                 Y = c(1,4,2,1,5,7,3,3))
```

# Example

- For randomization inference (often called RI), you need exact randomization procedure
- Why is this so important?

```
random_assignment <- randomizr::declare_ra(N = 8, m = 4)
random_assignment
```

```
## Random assignment procedure: Complete random assignment
## Number of units: 8
## Number of treatment arms: 2
## The possible treatment categories are 0 and 1.
## The number of possible random assignments is 70.
## The probabilities of assignment are constant across units:
## prob_0 prob_1
##    0.5    0.5
```

# Example

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## prob_0 prob_1
##    0.5    0.5
```

# Example

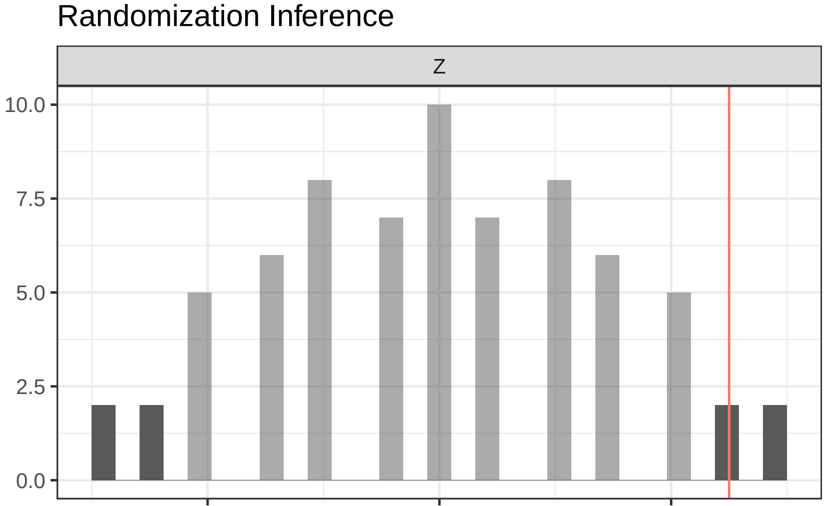
```r
out <- ri2::conduct_ri(formula = Y ~ Z,
                       data = df,
                       declaration = random_assignment)
out
```

```
##   term estimate two_tailed_p_value
## 1    Z      2.5          0.1142857
```

# Example

```
plot(out)
```

```
## Warning: It is deprecated to specify `guide = FALSE` to
## remove a guide. Please use `guide = "none"` instead.
```



# Example 2

Let's re-do the GG t-test example

```
df <- data.frame("Donation" = c(500, 100, 100, 50,
                                25, 25, 0, 0, 0, 0,
                                25, 20, 15, 15, 10,
                                5, 5, 5, 0, 0),
                 "Treatment" = c(rep(1,10),
                                 rep(0, 10)))
head(df)
```

```
##   Donation Treatment
## 1      500         1
## 2      100         1
## 3      100         1
## 4       50         1
## 5       25         1
## 6       25         1
```

# Example 2

```
random_assignment <- randomizr::declare_ra(N = 20)
random_assignment
```

```
## Random assignment procedure: Complete random assignment
## Number of units: 20
## Number of treatment arms: 2
## The possible treatment categories are 0 and 1.
## The number of possible random assignments is 184756.
## The probabilities of assignment are constant across units:
## prob_0 prob_1
##    0.5    0.5
```

# Example 2

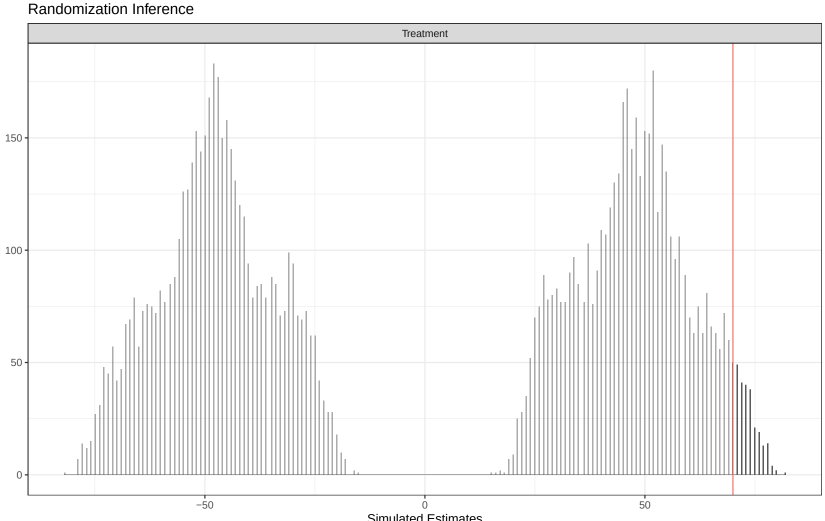
```r
out <- ri2::conduct_ri(formula = Donation ~ Treatment,
                       outcome = "Donation",
                       assignment = "Treatment",
                       p = "upper",
                       sims = 10000,
                       data = df,
                       declaration = random_assignment)
out
```

```
##        term estimate upper_p_value
## 1 Treatment       70        0.0292
```

# Example 2

```
plot(out)
```

```
## Warning: It is deprecated to specify `guide = FALSE` to
## remove a guide. Please use `guide = "none"` instead.
```



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- good when assumptions about sampling distribution are worrisome
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- good when we have complicated randomization procedures
  - blocking, clustering, etc.
- it's simple and exact!
- but null hypothesis might be less interesting
- regardless, it forces you to take a moment to think carefully about what the null hypothesis is and how it should be tested

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# Lab 1

# Covariates in experimental design

# Big picture

Recall,

- Randomization addresses the problem of omitted variables that plagues observational data
- Therefore, covariates are not a primary concern for causal inference
  - However, covariates can have important roles in design and analysis (or can be mis-used!)
  - Incorporation of covariates is best though-out during the design of experiments
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- "Supplementary variables that predict outcomes" GG pg 95
- We assume that they are fixed pre-treatment
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Experimenters bear the burden to demonstrate the soundness of their experimental procedures:

- Give details of the random assignment procedure and any instances in which subjects are lost or excluded after allocation
- Concerned about **imbalances**
  - When a covariate is correlated with treatment/control assignment
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  - Present a table decribing the degree of similarity between treatment and control groups in terms of covariates
- Adjustment using covariates (next slide) re-established balance in case of chance (or error) imbalance

# Use #3. Regression adjustment

Switching equation $Y_i = Y_i(0)(1 - d_i) + Y_i(1)d_i$

Rearrange $Y_i = Y_i(0) + (Y_i(1) - Y_i(0))d_i$

Rename $Y_i = \mu_{Y(0)} + [\mu_{Y(1)} - \mu Y(0)]d_i + u_i,$

- see definition of $u_i$ in text and see it matches how we think of disturbance in DeclareDesign

Rename $Y_i = a + bd_i + u_i$

- $a$ is average value of untreated potential outcomes for all units
- $b$ is average shift in average potential outcomes for i.e., ATE
- OLS estimator produces equivalent $A\hat{T}E$ as DIM

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# Readjustment

Including covariate(s) on RHS

$$Y_i = Y_i(0) + (Y_i(1) - Y_i(0))d_i = a + bd_i + cX_i + (u_i - cX_i)$$

- When $X_i$ predicts the outcome, we reduce amount of unexplained variation in $Y_i$!
  - Doing so reduces the standard error of $\hat{b}$ like we talked about last time :)
- Restablishes balance if an unlucky randomization, administrative error, etc.

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# Summary on using covariates

- Use pre-treatment covariates identified by other researchers, pilot testing, or theory to influence outcome of interest (blocking, adjustment, re-scaling outcome)
- Helps to reduce variability in our estimate
- Including covariates that does not predict outcomes does nothing to the sampling variability of our estimates
- Avoid waiting to determine which covariates to include (tie your hands using a PAP)
- Report both unadjusted estimates of the causal estimates along with adjusted estimates

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# Lab 2