Gov 50: 19. More Confidence Intervals

Matthew Blackwell

Harvard University

Roadmap

1. Bootstrap CIs for a difference in means
2. Bootstrap CIs for a difference in ATEs
3. Interpreting confidence intervals

1/ Bootstrap CIs for a difference in means

Comparison between groups

- Last time: confidence intervals for means.
- More interesting to compare across groups.
    - Differences in public opinion across groups
    - Difference between treatment and control groups.
- Bedrock of causal inference!

Trains experiment

- Back to the Boston trains example.
    - Boston commuter rail platform setting.
- Treatment group: presence of native Spanish-speaking confederates.
- Control group: no confederates.
- Outcome: X_i change in views on immigration.
    - Sample average in the treated group, $\overline{X}_T$
    - Sample average in the control group, $\overline{X}_C$
- Estimated **average treatment effect**

$$\widehat{\text{ATE}} = \overline{X}_T - \overline{X}_C$$

Inference for the difference

- Parameter: **population ATE** $\mu_T - \mu_C$
    - μ_T: Average outcome in the population if everyone received treatment.
    - μ_C: Average outcome in the population if everyone received control.
- Difference-in-means estimator: $\widehat{\text{ATE}} = \overline{X}_T - \overline{X}_C$
- $\overline{X}_T$ has a distribution centered on μ_T
- $\overline{X}_C$ has a distribution centered on μ_C
- $\rightsquigarrow \overline{X}_T - \overline{X}_C$ has a distribution centered on $\mu_T - \mu_C$
    - Sample difference in means is on average equal to the population difference in means.

Trains data

```r
library(gov50data)
trains
```

```
## # A tibble: 115 x 14
##      age  male income white college usborn treatment
##    <dbl> <dbl>  <dbl> <dbl>   <dbl>  <dbl>     <dbl>
##  1    31     0 135000     1       1      1         1
##  2    34     0 105000     1       1      0         1
##  3    63     1 135000     1       1      1         1
##  4    45     1 300000     1       1      1         1
##  5    55     1 135000     1       1      1         0
##  6    37     0  87500     1       1      1         1
##  7    53     0  87500     1       0      1         0
##  8    36     1 135000     1       1      1         1
##  9    54     0 105000     1       0      1         0
## 10    42     1 135000     1       1      1         1
## # i 105 more rows
## # i 7 more variables: ideology <dbl>, numberim.pre <dbl>,
## #   numberim.post <dbl>, remain.pre <dbl>,
## #   remain.post <dbl>, english.pre <dbl>,
## #   english.post <dbl>
```

Estimating the difference in means

```r
diff_in_means <- trains |>
  group_by(treatment) |>
  summarize(post_mean = mean(numberim.post)) |>
  pivot_wider(names_from = treatment, values_from = post_mean) |>
  mutate(ATE = `1` - `0`)
diff_in_means
```

```
## # A tibble: 1 x 3
##     `0`   `1`   ATE
##   <dbl> <dbl> <dbl>
## 1  2.73  3.12 0.383
```

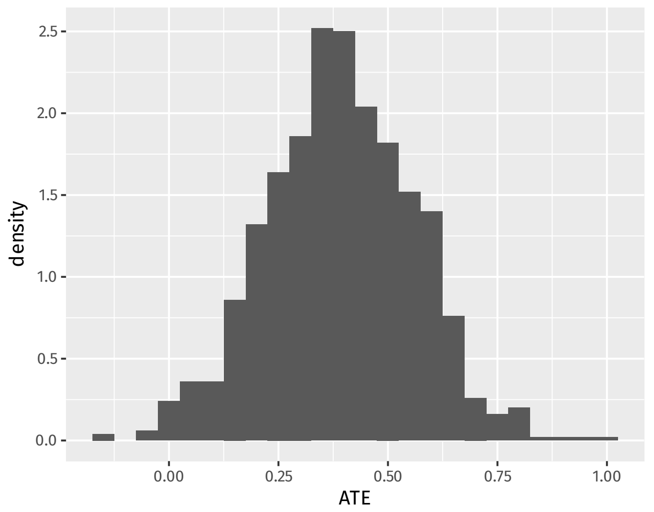
Bootstrap for the difference in means

```r
library(infer)
dim_boots <- trains |>
  rep_slice_sample(prop = 1, replace = TRUE, reps = 1000) |>
  group_by(replicate, treatment) |>
  summarize(post_mean = mean(numberim.post)) |>
  pivot_wider(names_from = treatment, values_from = post_mean) |>
  mutate(ATE = `1` - `0`)
dim_boots
```

```
## # A tibble: 1,000 x 4
## # Groups:   replicate [1,000]
##    replicate   `0`   `1`   ATE
##        <int> <dbl> <dbl> <dbl>
##  1         1  2.88  3.12 0.241
##  2         2  2.56  3.05 0.490
##  3         3  2.74  2.93 0.188
##  4         4  2.76  3.08 0.315
##  5         5  2.73  3.20 0.477
##  6         6  2.68  3.04 0.358
##  7         7  2.56  3.14 0.577
##  8         8  2.77  3.02 0.251
##  9         9  2.56  3.02 0.459
```

Visualizing the bootstraps

```
dim_boots |>
  ggplot(aes(x = ATE)) +
  geom_histogram(aes(y = after_stat(density)), binwidth = 0.05)
```



Calculating the percentile CI

You can use `get_confidence_interval()` with your “hand-rolled” bootstraps, but you have to make sure you only pass it the variable of interest using `select`:

```
dim_ci_95 <- dim_boots |>
  select(replicate, ATE) |>
  get_confidence_interval(level = 0.95, type = "percentile")

dim_ci_95
```

```
## # A tibble: 1 x 2
##   lower_ci upper_ci
##      <dbl>    <dbl>
## 1   0.0627    0.709
```

What about change in views as the outcome?

```
change_ci_95 <- trains |>
  rep_slice_sample(prop = 1, replace = TRUE, reps = 1000) |>
  group_by(replicate, treatment) |>
  summarize(change_mean = mean(numberim.post - numberim.pre)) |>
  pivot_wider(names_from = treatment, values_from = change_mean) |>
  mutate(ATE = `1` - `0`) |>
  select(replicate, ATE) |>
  get_confidence_interval(level = 0.95, type = "percentile")
change_ci_95
```

```
## # A tibble: 1 x 2
##   lower_ci upper_ci
##      <dbl>    <dbl>
## 1   0.0243    0.626
```

What’s different?

Let’s look at the width of the two confidence intervals:

```
## Post outcome width
dim_ci_95[2]-dim_ci_95[1]
```

```
##   upper_ci
## 1    0.647
```

```
## Change outcome width
change_ci_95[2] - change_ci_95[1]
```

```
##   upper_ci
## 1    0.602
```

Width of CI depends on outcome variability

Change CI is narrower! Why? Because the change is less variable than the post outcome:

```
trains |> summarize(sd_post = sd(numberim.post),
                    sd_change = sd(numberim.post - numberim.pre))
```

```
## # A tibble: 1 x 2
##   sd_post sd_change
##     <dbl>     <dbl>
## 1   0.917     0.826
```

`infer` workflow

For `infer`, we have to do a bit of massaging. It wants the treatment variable to be a vector and we have to tell it what order we take the difference:

```r
dim_boots_infer <- trains |>
  mutate(treatment = if_else(treatment == 1, "Treated", "Control")) |>
  specify(numberim.post ~ treatment) |>
  generate(reps = 1000, type = "bootstrap") |>
  calculate(stat = "diff in means", order = c("Treated", "Control"))
dim_boots_infer |>
  get_confidence_interval(level = 0.95, type = "percentile")
```

```
## # A tibble: 1 x 2
##   lower_ci upper_ci
##      <dbl>    <dbl>
## 1   0.0671    0.695
```

2/ Bootstrap CIs for a difference in ATEs

Interactions

We have also estimated conditional ATEs:

$$ATE_{\text{college}} = \overline{X}_{T,\text{college}} - \overline{X}_{C,\text{college}}$$
$$ATE_{\text{noncollege}} = \overline{X}_{T,\text{noncollege}} - \overline{X}_{C,\text{noncollege}}$$

An **interaction** between treatment and college is the difference between these two effects:

$$ATE_{\text{college}} - ATE_{\text{noncollege}}$$

This is a random variable and has a **sampling distribution**.

Estimating the interaction

To estimate the interaction, we need to pivot both treatment and college to the columns.

```r
trains |>
  mutate(
    treatment = if_else(treatment == 1, "Treated", "Control"),
    college = if_else(college == 1, "College", "Noncollege")
  ) |>
  group_by(treatment, college) |>
  summarize(post_mean = mean(numberim.post)) |>
  pivot_wider(
    names_from = c(treatment, college),
    values_from = post_mean
  )
```

```
## # A tibble: 1 x 4
##   Control_College Control_Noncollege Treated_College
##             <dbl>              <dbl>           <dbl>
## 1            2.63               3.57            3.11
## # i 1 more variable: Treated_Noncollege <dbl>
```

Estimating the interaction

```r
trains |>
  mutate(
    treatment = if_else(treatment == 1, "Treated", "Control"),
    college = if_else(college == 1, "College", "Noncollege")
  ) |>
  group_by(treatment, college) |>
  summarize(post_mean = mean(numberim.post)) |>
  pivot_wider(
    names_from = c(treatment, college),
    values_from = post_mean
  ) |>
  mutate(
    ATE_c = Treated_College - Control_College,
    ATE_nc = Treated_Noncollege - Control_Noncollege,
    interaction = ATE_c - ATE_nc
  ) |>
  select(ATE_c, ATE_nc, interaction)
```

```
## # A tibble: 1 x 3
##   ATE_c ATE_nc interaction
##   <dbl>  <dbl>       <dbl>
## 1 0.482 -0.429       0.911
```

Bootstrapping the interaction

```r
int_boots <- trains |>
  mutate(
    treatment = if_else(treatment == 1, "Treated", "Control"),
    college = if_else(college == 1, "College", "Noncollege")
  ) |>
  rep_slice_sample(prop = 1, replace = TRUE, reps = 1000) |>
  group_by(replicate, treatment, college) |>
  summarize(post_mean = mean(numberim.post)) |>
  pivot_wider(
    names_from = c(treatment, college),
    values_from = post_mean
  ) |>
  mutate(
    ATE_c = Treated_College - Control_College,
    ATE_nc = Treated_Noncollege - Control_Noncollege,
    interaction = ATE_c - ATE_nc
  ) |>
  select(replicate, ATE_c, ATE_nc, interaction)
```

```
int_boots
```

```
## # A tibble: 1,000 x 4
## # Groups:   replicate [1,000]
##    replicate ATE_c  ATE_nc interaction
##        <int> <dbl>   <dbl>       <dbl>
##  1         1 0.445 -0.429        0.873
##  2         2 0.509 -0.5          1.01
##  3         3 0.560 -0.375        0.935
##  4         4 0.387 -0.75         1.14
##  5         5 0.411 -0.0794       0.490
##  6         6 0.628 -0.583        1.21
##  7         7 0.673 -0.0333       0.706
##  8         8 0.523 -0.375        0.898
##  9         9 0.244 -1            1.24
## 10        10 0.704 -0.375        1.08
## # i 990 more rows
```

Getting the confidence interval

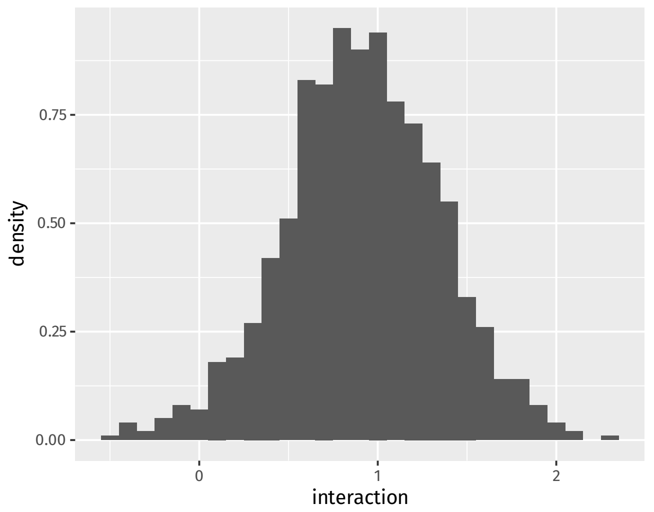
We have to drop NA values because sometimes the bootstrap gets a draw of all college or all noncollege and we can’t calculate the interaction:

```
int_boots |>
  select(replicate, interaction) |>
  drop_na() |>
  get_confidence_interval(level = 0.95)
```

```
## # A tibble: 1 x 2
##   lower_ci upper_ci
##      <dbl>    <dbl>
## 1   0.0221     1.77
```

Visualizing the bootstrap

```
int_boots |>
  ggplot(aes(x = interaction)) +
  geom_histogram(aes(y = ..density..), binwidth = 0.1)
```



3/ Interpreting confidence intervals

Interpretation and simulation

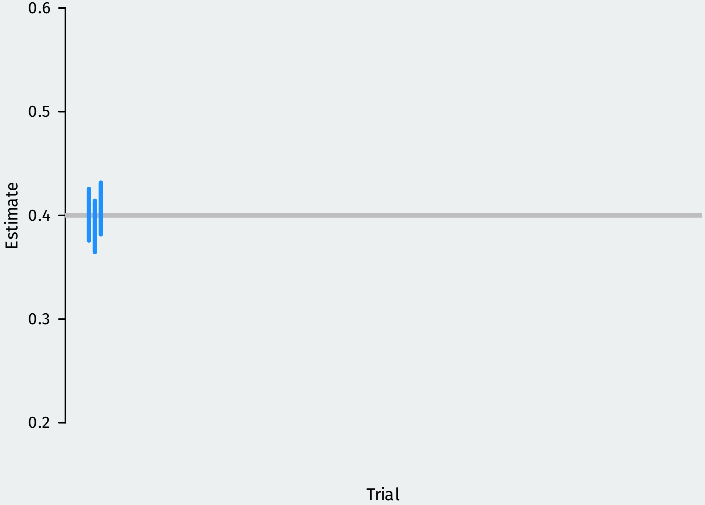
- Be careful about interpretation:
    - A 95% confidence interval will contain the true value in 95% of repeated samples.
    - For a particular calculated confidence interval, truth is either in it or not.
- A simulation can help our understanding:
    - Draw samples of size 1500 assuming population approval for Biden of $p = 0.4$.
    - Calculate 95% confidence intervals in each sample.
    - See how many overlap with the true population approval.

Plotting the CIs

Plotting the CIs

Plotting the CIs

Plotting the CIs



Plotting the CIs