

Gov 50: 19. More Confidence Intervals

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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, \bar{X}_T
 - Sample average in the control group, \bar{X}_C
- Estimated **average treatment effect**

$$\widehat{ATE} = \bar{X}_T - \bar{X}_C$$

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: $\widehat{ATE} = \bar{X}_T - \bar{X}_C$
- \bar{X}_T is a r.v. with mean $\mathbb{E}[\bar{X}_T] = \mu_T$
- \bar{X}_C is a r.v. with mean $\mathbb{E}[\bar{X}_C] = \mu_C$
- $\rightsquigarrow \bar{X}_T - \bar{X}_C$ is a r.v. with mean $\mu_T - \mu_C$
 - Sample difference in means is on average equal to the population difference in means.

Trains data

```
library(gov50data)
trains
```

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

Estimating the difference in means

```
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
```

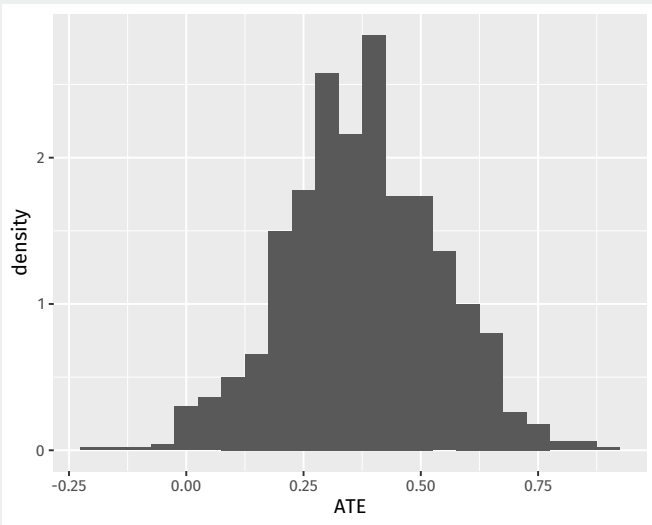

Bootstrap for the difference in means

```
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  2.83  3.02 0.194
## 2           2  2.67  3.07 0.406
## 3           3  2.74  3.09 0.346
## 4           4  2.79  3.19 0.398
## 5           5  2.76  3.13 0.376
## 6           6  2.62  3.14 0.520
## 7           7  2.87  3.27 0.395
## 8           8  2.71  3.07 0.360
## 9           9  3.03  3.26 0.229
```

Visualizing the bootstraps

```
dim_boots |>  
  ggplot(aes(x = ATE)) +  
  geom_histogram(aes(y = ..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    0.0514    0.685
```

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    0.0157    0.613
```

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      0.634
```

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

```
##    upper_ci  
## 1      0.597
```

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:

```
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    0.0569    0.720
```

2/ Bootstrap CIs for a difference in ATEs

Interactions

We have also estimated conditional ATEs:

$$\begin{aligned}ATE_{\text{college}} &= \bar{X}_{T,\text{college}} - \bar{X}_{C,\text{college}} \\ATE_{\text{noncollege}} &= \bar{X}_{T,\text{noncollege}} - \bar{X}_{C,\text{noncollege}}\end{aligned}$$

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.

```
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 Treat~1
##           <dbl>           <dbl>           <dbl>    <dbl>
## 1           2.63           3.57           3.11     3.14
## # ... with abbreviated variable name 1: Treated_Noncollege
```

Estimating the interaction

```
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

```
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 0.580 -0.175         0.755
## 2           2 0.515 -0.458         0.973
## 3           3 0.753 -0.812         1.57
## 4           4 0.339  0.125         0.214
## 5           5 0.355  0         0.355
## 6           6 0.465 -0.568         1.03
## 7           7 0.492 -0.75         1.24
## 8           8 0.382 -0.5         0.882
## 9           9 0.277  0.125         0.152
## 10          10 0.449 -0.633         1.08
## # ... with 990 more rows
```

Getting the confidence interval

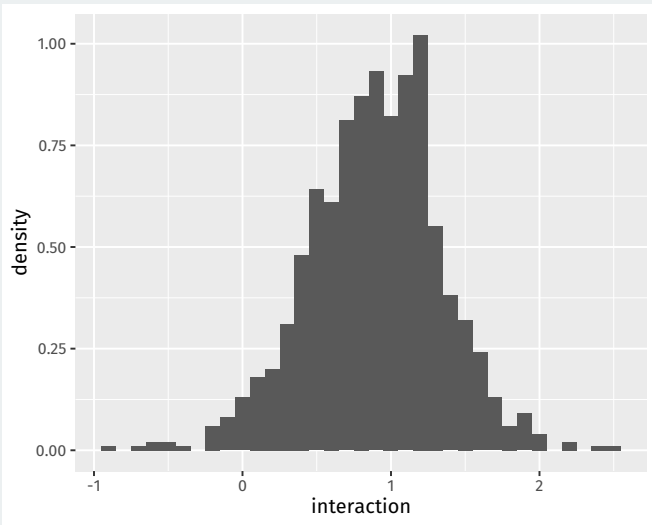
We have to drop NA values because sometimes the bootstrap gets a draw of all college or all noncollege and we can't calculate the interaction:

```
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 -0.00805    1.72
```

Visualizing the bootstrap

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

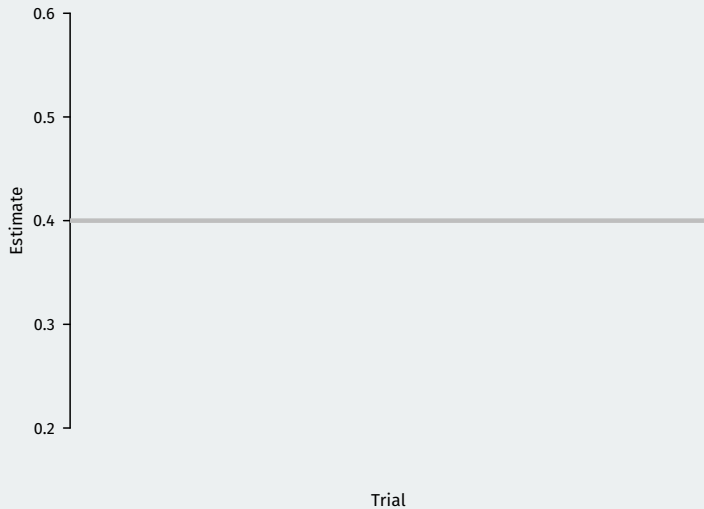


3/ Interpreting confidence intervals

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 Trump of $p = 0.4$.
 - Calculate 95% confidence intervals in each sample.
 - See how many overlap with the true population approval.

Plotting the CIs



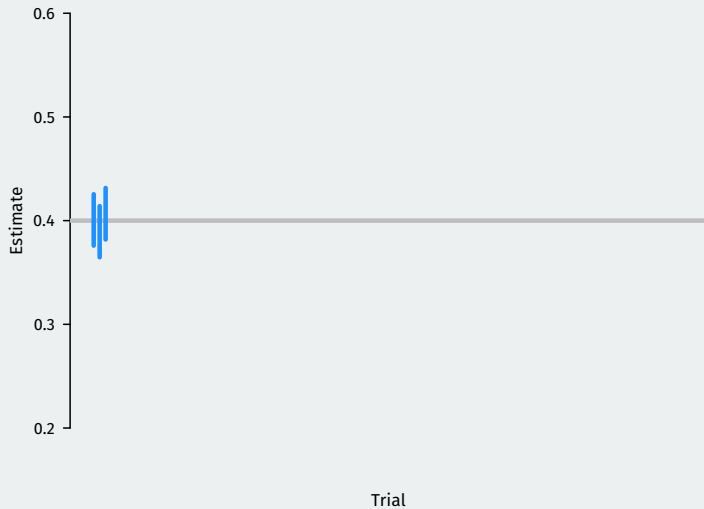
Plotting the CIs



Plotting the CIs



Plotting the CIs



Plotting the CIs

