

Gov 50: 23. More Hypothesis testing

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Roadmap

1. Reviewing hypothesis testing

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Difference-in-means

```
library(gov50data)
trains <- trains |>
  mutate(treated = if_else(treatment == 1, "Treated", "Untreated"))
trains
```

```
## # A tibble: 115 x 15
```

```
##       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 8 more variables: ideology <dbl>, numberim.pre <dbl>,
## #   numberim.post <dbl>, remain.pre <dbl>,
## #   remain.post <dbl>, english.pre <dbl>,
```

Calculating the ATE

```
library(infer)
ate <- trains |>
  specify(numberim.post ~ treated) |>
  calculate(stat = "diff in means",
            order = c("Treated", "Untreated"))
ate
```

```
## Response: numberim.post (numeric)
## Explanatory: treated (factor)
## # A tibble: 1 x 1
##   stat
##   <dbl>
## 1 0.383
```

Difference in means hypotheses

Hypotheses:

$$H_0 : \mu_T - \mu_C = 0$$

$$H_1 : \mu_T - \mu_C \neq 0$$

Observed difference in means:

$$\widehat{ATE} = \overline{Y}_T - \overline{Y}_C$$

How can we approximate the **null distribution**? **Permute** the outcome/treatment variables.

Permuting the treatment

Let's do 2 permutations to see how things vary:

```
set.seed(02138)
perm <- trains |>
  specify(numberim.post ~ treated) |>
  hypothesize(null = "independence") |>
  generate(reps = 1000,
           type = "permute")
```

`generate(type = "permute")` shuffles to the outcomes, keeping treatment the same:

```
perm |> filter(replicate == 1)
```

```
## # A tibble: 115 x 3
## # Groups:   replicate [1]
##   numberim.post treated replicate
##   <dbl> <fct>         <int>
## 1         3 Treated         1
## 2         2 Treated         1
## 3         5 Treated         1
## 4         3 Treated         1
## 5         3 Untreated       1
## 6         3 Treated         1
## 7         2 Untreated       1
## 8         2 Treated         1
## 9         3 Untreated       1
## 10        3 Treated         1
## # i 105 more rows
```

```
perm |> filter(replicate == 2)
```

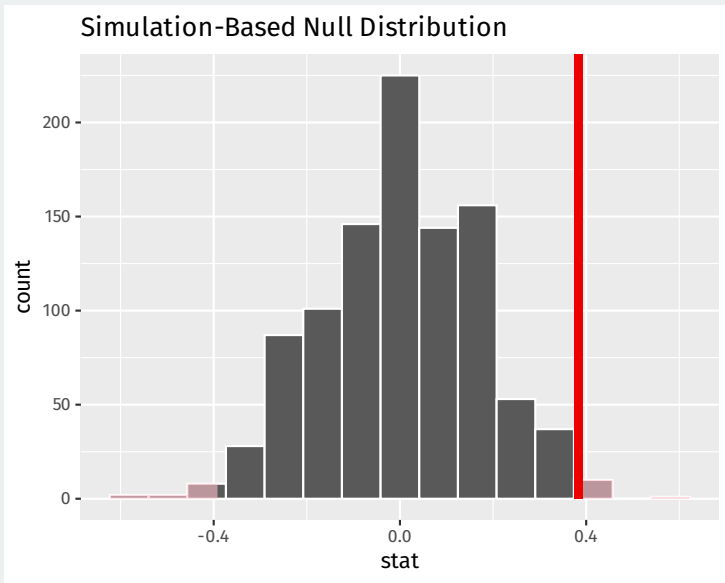
```
## # A tibble: 115 x 3
## # Groups:   replicate [1]
##   numberim.post treated replicate
##   <dbl> <fct>         <int>
## 1         2 Treated         2
## 2         3 Treated         2
## 3         3 Treated         2
## 4         3 Treated         2
## 5         3 Untreated       2
## 6         4 Treated         2
## 7         2 Untreated       2
## 8         3 Treated         2
## 9         3 Untreated       2
## 10        2 Treated         2
## # i 105 more rows
```


Null distribution

The distribution of the differences-in-means under permutation will be mean 0 because shuffling the outcomes means that the outcomes in each permutation's treated and control group are coming from the same distribution.

```
null_dist <- trains |>
  specify(numberim.post ~ treated) |>
  hypothesize(null = "independence") |>
  generate(reps = 1000,
           type = "permute") |>
  calculate(stat = "diff in means", order = c("Treated", "Untreated"))
```

```
null_dist |>  
  visualize() +  
  shade_p_value(obs_stat = ate, direction = "both")
```



Interpreting p-values

```
get_p_value(null_dist, obs_stat = ate, direction = "both")
```

```
## # A tibble: 1 x 1  
##   p_value  
##   <dbl>  
## 1    0.022
```

Hypotheses:

$$H_0 : \mu_T - \mu_C = 0$$

$$H_1 : \mu_T - \mu_C \neq 0$$

Observed difference in means:

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

p-value: probability of an estimated ATE as big as $|\widehat{ATE}|$ by random chance if there is no treatment effect.

Rejecting the null

Decision rule: “reject the null if the p-value is below the **test level α** ”

Rejecting the null in two-sample tests: there is a true difference in means.

Test level α controls the amount of false positives:

	Null False (True difference)	Null True (No true difference)
Reject Null	True Positive	False Positive (Type I error)
Retain Null	False Negative (Type II error)	True Negative

Tests and confidence intervals

- There is a deep connection between confidence intervals and tests.
- Any value outside of a $100 \times (1 - \alpha)\%$ confidence interval would have a p-value less than α if we tested it as the null hypothesis.
 - 95% CI for social pressure experiment: $[0.016, 0.124]$
 - \rightsquigarrow p-value for $H_0 : \mu_T - \mu_C = 0$ less than 0.05.
- Confidence intervals are all of the null hypotheses we **can't reject** with a test.

CI in the trains example

```
trains |>
  specify(numberim.post ~ treated) |>
  generate(reps = 1000, type = "bootstrap") |>
  calculate(stat = "diff in means",
            order = c("Treated", "Untreated")) |>
  get_ci(level = 0.95)
```

```
## # A tibble: 1 x 2
##   lower_ci upper_ci
##   <dbl>     <dbl>
## 1    0.0893    0.698
```