R Coding Demonstration Week 11: Hypothesis Tests (Tidy)

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Introduction

- Today we're going to cover some tools for exploring bivariate relationships.
- We'll use the data from the Broockman & Kalla (2016) transphobia study.
- Basic summary of experiment:
    - Randomly assigned door-to-door canvassers to two conditions
    - Conditions: perspective-taking script (treatment) or recycling script (placebo)
    - Follow up surveys at 3 days, 3 weeks, 6 weeks, and 3 months.

Data

```
library(tidyverse)
phobia <- read.csv("data/transphobia_all.csv")
```

Variable Name	Description
age	Age of the respondent in years
female	1=respondent marked “Female” on voter registration, 0 otherwise
voted_gen_14	1 if respondent voted in the 2014 general election
voted_gen_12	1 if respondent voted in the 2012 general election
treat_ind	1 if respondent was assigned to treatment, 0 for control
racename	character name of racial identity indicated on voter file
democrat	1 if respondent is a registered Democrat
therm_trans_t0	0-100 feeling therm. about transgender people at baseline
therm_trans_tX	0-100 feeling therm. about transgender people in Wave X after treatment
therm_obama_t0	0-100 feeling therm. about Barack Obama at baseline
therm_obama_tX	0-100 feeling therm. about Barack Obama in Wave X after treatment

Permutation tests

- A common way to conduct inference in an experiment is called a **permutation test**.
    - Null hypothesis of no treatment effect: $H_0 : Y_i(1) = Y_i(0)$
    - Doesn't matter if we flip treatment for someone.
    - But different allocation of treatment will lead to different estimated ATEs by random chance.
- Permutation test:
    1. Calculate observed difference in means.
    2. Randomly shuffle treatment indicator across units.
    3. Calculate difference in means of shuffled data.
    4. Repeat 2-3 many times and compare observed effect to this distribution.
- Shuffled distribution = reference distribution.
    - p-value: what proportion of effects would we see if treatment had no effect?

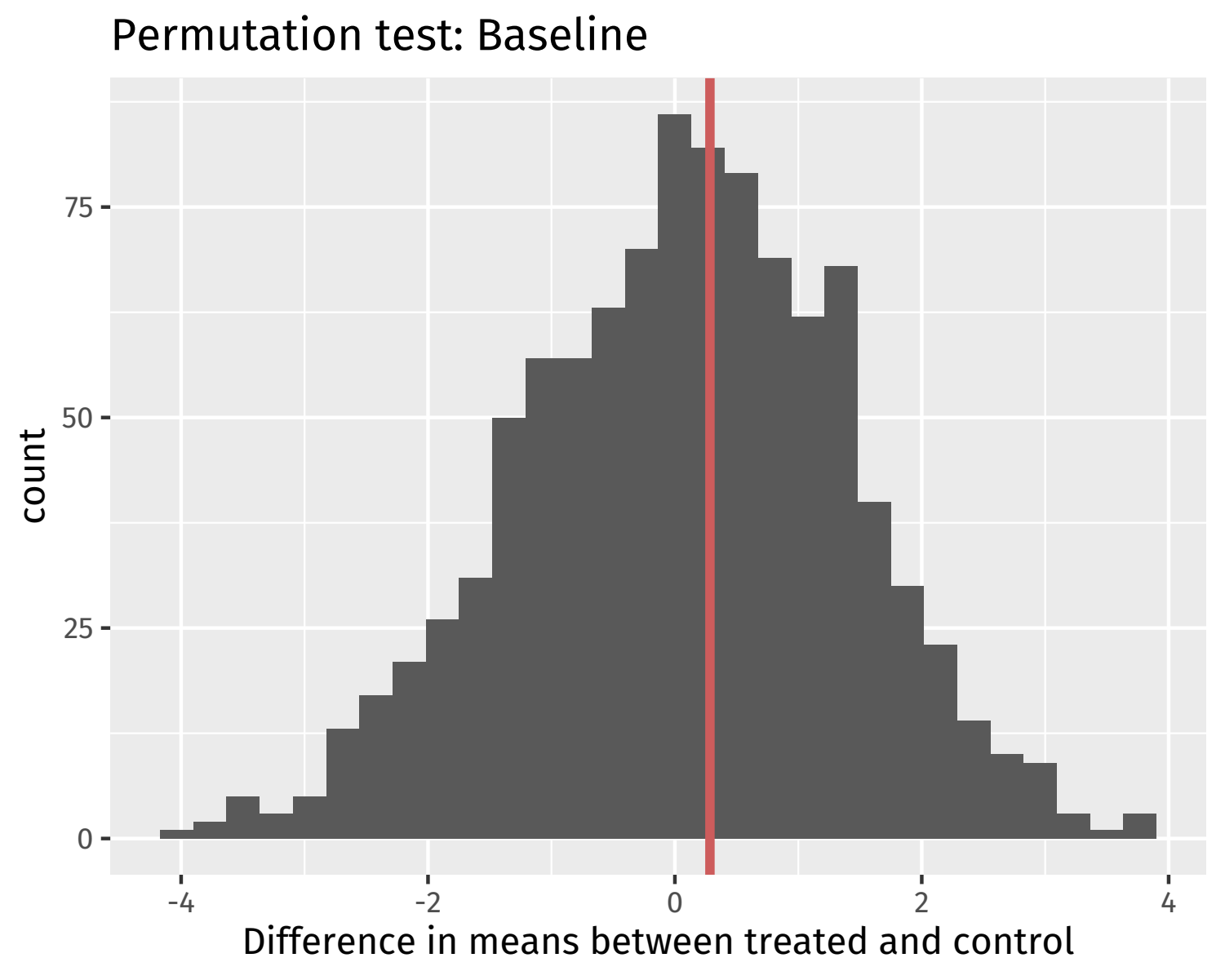
Question 1

Conduct a permutation test for the “effect” of treatment on baseline thermometer scores for transgender people. Show a histogram of the reference distribution and plot a line that indicates where the observed difference in means is.

Answer 1

```
n_sims <- 1000
n_obs <- nrow(phobia)
trans_t0_test <- rep(NA, times = n_sims)

treated <- phobia %>% filter(treat_ind == 1)
control <- phobia %>% filter(treat_ind == 0)

trans_t0_est <- mean(treated$therm_trans_t0) -
  mean(phobia$therm_trans_t0)

for (i in 1:n_sims) {
  phobia <- phobia %>% mutate(
    shuff_treat = sample(treat_ind)
  )
  shuff_treated <- phobia %>% filter(shuff_treat == 1)
  shuff_control <- phobia %>% filter(shuff_treat == 0)
  trans_t0_test[i] <- mean(shuff_treated$therm_trans_t0) -
    mean(shuff_control$therm_trans_t0)
}

ggplot(mapping = aes(x = trans_t0_test)) + geom_histogram() +
  labs(title = "Permutation test: Baseline",
    x = "Difference in means between treated and control") +
  geom_vline(xintercept = trans_t0_est, size = 1.3, col = "indianred")
```

Answer 1 (plot)



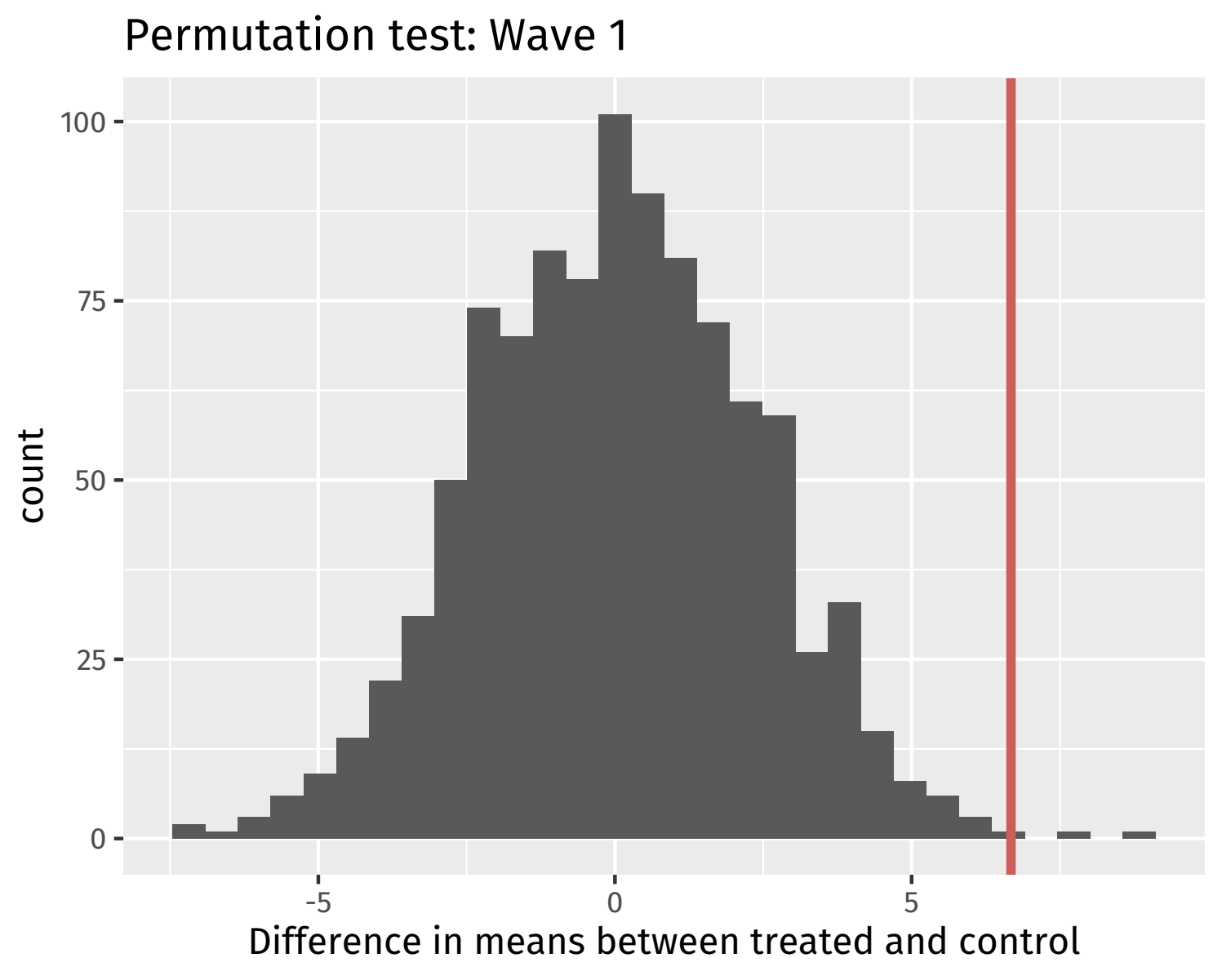
Question 2

Conduct a permutation test for the effect of treatment on thermometer scores for transgender people in wave 1 (`therm_trans_t1`). Note that there are missing values in wave 1, so be sure to drop those from your analyses.

Answer 2

```
trans_t1_test <- rep(NA, times = n_sims)

trans_t1_est <- mean(treated$therm_trans_t1, na.rm = TRUE) -
  mean(control$therm_trans_t1, na.rm = TRUE)

for (i in 1:n_sims) {
  phobia <- phobia %>% mutate(
    shuff_treat = sample(treat_ind)
  )
  shuff_treated <- phobia %>% filter(shuff_treat == 1)
  shuff_control <- phobia %>% filter(shuff_treat == 0)
  trans_t1_test[i] <- mean(shuff_treated$therm_trans_t1, na.rm = TRUE) -
    mean(shuff_control$therm_trans_t1, na.rm = TRUE)
}

ggplot(mapping = aes(x = trans_t1_test)) + geom_histogram() +
  labs(title = "Permutation test: Wave 1",
    x = "Difference in means between treated and control") +
  geom_vline(xintercept = trans_t1_est, size = 1.3, col = "indianred")
```

Answer 2 (plot)



Question 3

For the baseline thermometer score permutation test, calculate the one-sided and two-sided p-values for the estimated effect.

Answer 3

```
## one-sided
mean(trans_t0_test > trans_t0_est)
```

```
## [1] 0.44
```

```
## two-sided
mean(trans_t0_test > trans_t0_est) + mean(trans_t0_test < -trans_t0_est)
```

```
## [1] 0.823
```

Question 4

For the wave 1 thermometer score permutation test, calculate the one-sided and two-sided p-values for the estimated effect.

Answer 4

```
## one-sided
mean(trans_t1_test > trans_t1_est)
```

```
## [1] 0.002
```

```
## two-sided
mean(trans_t1_test > trans_t1_est) + mean(trans_t1_test < -trans_t1_est)
```

```
## [1] 0.005
```

Question 5

Conduct a t-test of the difference in average baseline thermometer scores between the treated and control group with the following null hypothesis:

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

where μ_T is the population mean of the potential outcomes under treatment. What are some differences between this null and the null hypothesis from the permutation test?

Answer 5

```
t.test(treated$therm_trans_t0, control$therm_trans_t0)
```

```
##
##  Welch Two Sample t-test
##
## data:  treated$therm_trans_t0 and control$therm_trans_t0
## t = 0.4, df = 1820, p-value = 0.7
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2.12  3.26
## sample estimates:
## mean of x mean of y
##      53.6      53.0
```

Question 6

Conduct a t-test of the difference in average wave 1 thermometer scores between the treated and control group.

Answer 6

```
t.test(treated$therm_trans_t1, phobia$therm_trans_t1)
```

```
##
##  Welch Two Sample t-test
##
## data:  treated$therm_trans_t1 and phobia$therm_trans_t1
## t = 2, df = 533, p-value = 0.1
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.758  7.656
## sample estimates:
## mean of x mean of y
##      60.7      57.3
```