YData: Introduction to Data Science



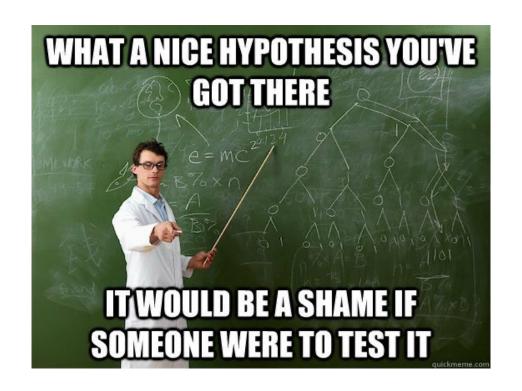
Class 21: Hypothesis tests continued

Overview

Quick review of parameters, statistics, sampling, and hypothesis tests for a single proportion

Hypothesis tests for multiple proportions

Hypothesis tests assessing causality



Project timeline

Tuesday, April 11th

- Projects are due on Gradescope at 11pm on
- Also, email a pdf of your project to your peer reviewers
 - A list of whose paper you will review will be posted to Canvas

That went as planned, said no project ever.

Wednesday, April 19th

- Jupyter notebook files with your reviews need to be sent to the authors
- A template for doing your review will be available

Sunday, April 30th

- Project is due on Gradescope
 - Add peer reviews to an Appendix of your project

Project peer review

A template for your project peer review has been posted

- import YData
- YData.download.download_class_file('reviewer_template.ipynb, 'homework')

Please review the projects by 11pm on Wednesday April 19th and:

- 1. Post a pdf of each of your reviews to Gradescope
- 2. Send a filled out Jupyter Notebook with your review to the project author

In your final project, please add the three reviews in the Appendix section, and discuss how you addressed the reviewers' comments

Review of Statistical Inference

Review: Statistical Inference

Statistical Inference: Making conclusions about a population based on data in a random sample

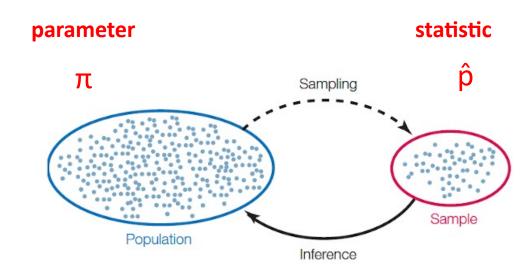
A parameter is number associated with the population

- e.g., population proportion π
- e.g., the proportion of voters who voted for Biden

A **statistic** is number calculated from the sample

- e.g., sample proportion \hat{p}
- e.g., the proportion of Biden's vote out of 1,000 people in our sample

A statistic can be used as an estimate of a parameter



	Sample Statistic	Population Parameter
Mean	χ̄	μ
Proportion	p̂	π

Probability distribution of a statistic

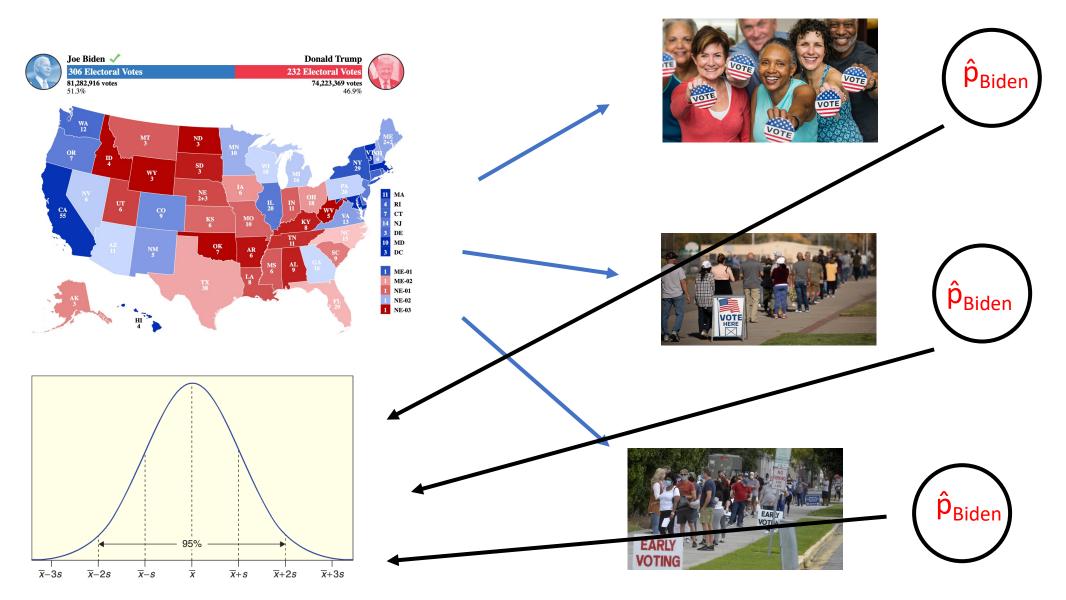
Values of a statistic vary because random samples vary

A **sampling distribution** is a probability distribution of *statistics*

- All possible values of the statistic and all the corresponding probabilities
- We can approximate a sampling distribution by simulating statistics

 π_{Biden}

n = 1,000

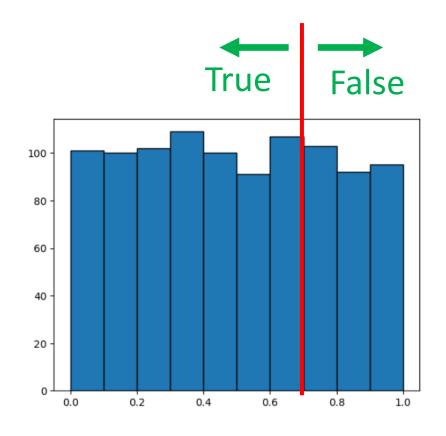


Sampling distribution!

Simulating random proportions (p's)

We can simulate random proportions \hat{p} consistent with a population proportion π by:

- 1. Generated n random numbers uniformly distributed between 0 and 1
 - rand_nums = np.random.rand(1000)
- 2. Marking points less than π as being True, and greater π than as being False
 - rand_binary = rand_nums <= pi_value
- 3. Calculating the proportion of points to get a p̂
 - rand_phat = np.mean(rand_binary)

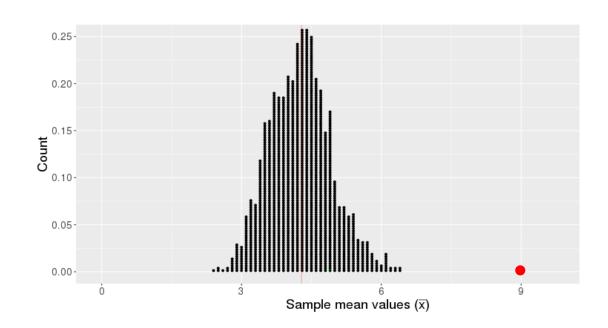


Hypothesis tests

Basic hypothesis test logic

We start with a claim about a population parameter

This claim implies we should get a certain distribution of statistics



If our observed statistic is highly unlikely, we reject the claim

Null and Alternative hypotheses

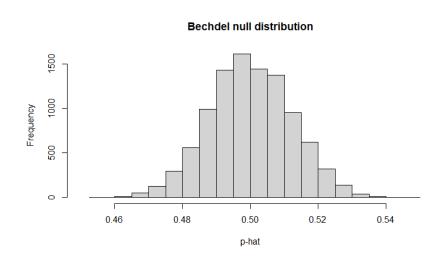
Null hypothesis

- A hypothesis where "nothing interesting" happened
 - E.g., our experiment failed
- We can simulate data under the assumptions of this model to get a "null distribution" of statistics

Alternative hypothesis

• The hypothesis we believe in (would like to see true)

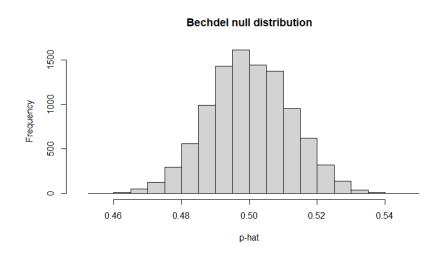
A test statistic is the statistic we choose to simulate in order decide between the two hypotheses



Testing the null hypothesis

To resolve choice between null and alternative hypotheses:

- We compare the observed test statistic to the statistic values in the null distribution
- If the observed statistic is not consistent with the null distribution, then we can reject the null hypothesis
 - And we accept the alternative hypothesis



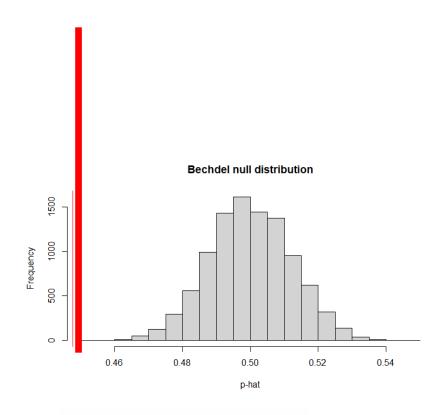
The p-value

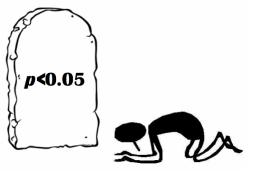
The p-value is the probability, that we get a statistic as or more extreme than the observed statistic from the null distribution

P(Null_Stat ≥ obs_stat | H₀)

If the P-value is small, this is evidence against the null hypothesis and the results are often called "statistically significant"

• Convention, p-value < 0.05



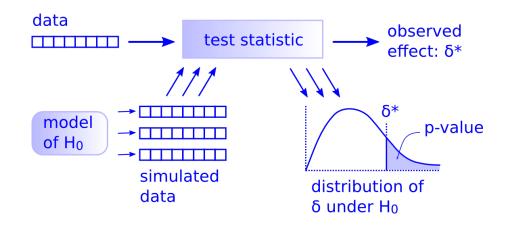


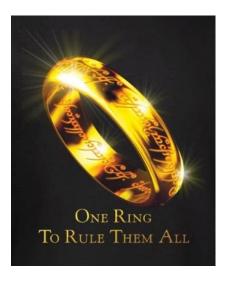
Steps needed to run a hypothesis test

To run a hypothesis test, we can use 5 steps:

- 1. State the null and alternative hypothesis
- 2. Calculate the observed statistic of interest
- Create the null distribution
- 4. Calculate the p-value
- Make a decision

Let's go through these steps now...





Bechdel (hypothesis) test

1. State the null hypothesis and the alternative hypothesis

- 50% of the movies pass the Bechdel test: H_0 : $\pi = 0.5$
- Less than 50% of movies pass the: H_A : π < 0.5



803 out of 1794 movies passed the Bechdel test

3. Create a null distribution that is consistent with the null hypothesis

• i.e., the statistics we expect if 50% of the movies passed the Bechdel test

4. Examine how likely the observed statistic is to come from the null distribution

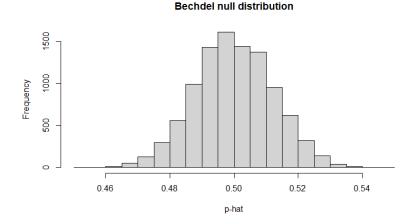
- What is the probability that only 803 of 1794 movies would pass the Bechdel test ($\hat{p} = .448$) if the null hypothesis was true?
- i.e., what is the p-value?

5. Make a judgement

- If we have a small p-value, this means that $\pi = .5$ is unlikely and so $\pi < .5$
- i.e., we say our results are 'statistically significant'



$$\hat{p} = .448$$





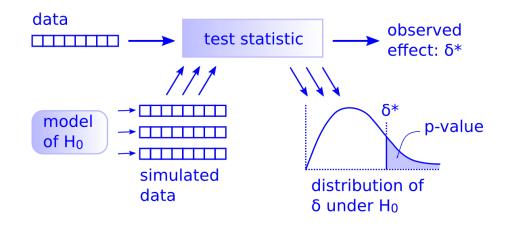
Hypothesis tests multiple proportions

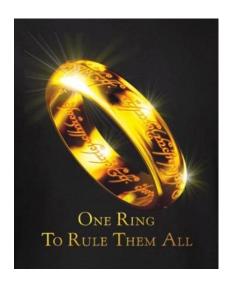
Steps needed to run a hypothesis test

To run a hypothesis test, we can use 5 steps:

- 1. State the null and alternative hypothesis
- 2. Calculate the observed statistic of interest
- 3. Create the null distribution
- 4. Calculate the p-value
- Make a decision

The only difference is the parameters we are testing in step 1, and consequently the statistics we use...

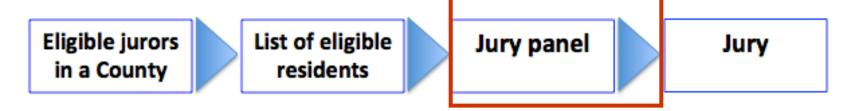




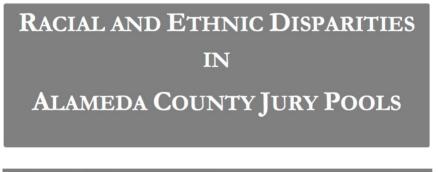
Example: Jury selection in Alameda county

Section 197 of California's Code of Civil Procedure says:

"All persons selected for jury service shall be selected at random, from a source or sources inclusive of a representative cross section of the population of the area served by the court."



In 2010, the American Civil Liberties Union (ACLU) of Northern California presented a report that concluded that certain racial and ethnic groups are underrepresented among jury panelists in Alameda County.



Step 1: Null and Alternative hypothesis

The null hypothesis is that the proportion of people on jury panels matches the underlying demographics.

We can write the null hypothesis in symbols using:

- $\pi_{Asian-on-panels} = .15$
- $\pi_{Black-on-panels} = .18$
- etc.

Proportions in the population

The alternative hypothesis that the proportion of at least one ethnicity does not match the underlying population.

We can write this using symbols as: at least one π_i is not as specified

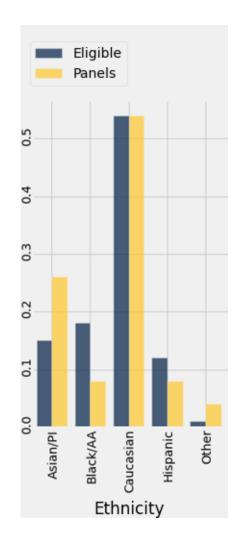
Step 2: Calculating the observed statistic

The ACLU compiled data on the composition of 1453 people who were on jury panels from in the years 2009 and 2010.

People on the panels are of multiple ethnicities

Distribution of ethnicities is categorical

To see whether the distribution of ethnicities of the panels is close to that of the eligible jurors, we have to measure the distance between two categorical distributions



Total variation distance

To run a hypothesis test we need to select a statistic

A statistic we can use to measure the deviation of two distributions of proportions is the **Total Variation Distance** (TVD) which can be calculated using:

- For each category, compute the difference in proportions between two distributions
- Take the absolute value of each difference
- Sum the values

$$TVD = \sum_{i=1}^{k} |\pi_i - \hat{p}_i|$$

Eligible Panels Ethnicity

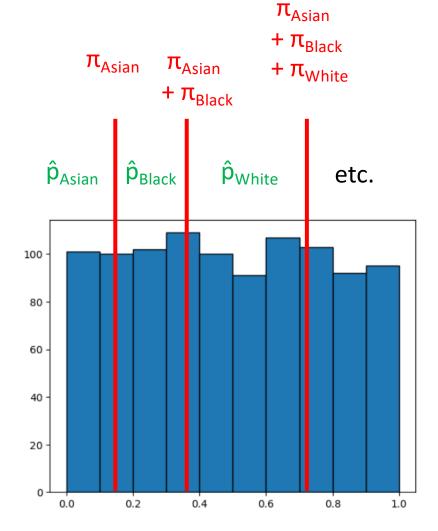
The value of the TVD statistic for Almeda county is 0.28

Step 3: Creating a null distribution

To create a null distribution, we need to randomly generate several proportions consistent with the null hypothesis

• i.e., \hat{p}_{Asian} , \hat{p}_{Black} etc.

We can do this by randomly generating numbers between 0 and 1, and then splitting the data at the cumulative sums of the proportions specified by the null hypothesis



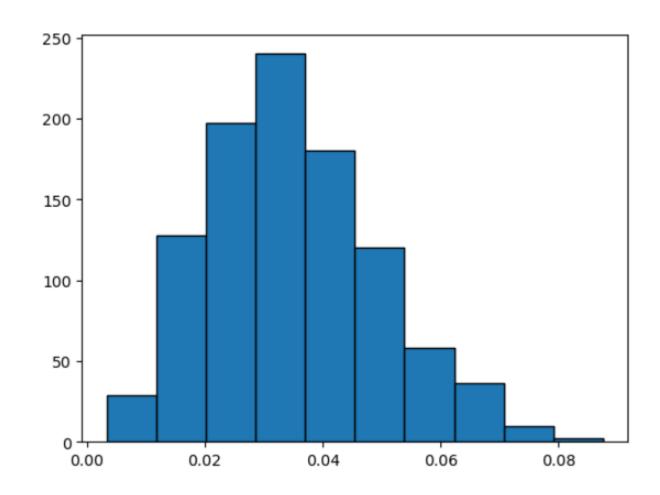
Step 3: Creating a null distribution

One we have generated \hat{p}_{Asian} , \hat{p}_{Black} etc. consistent with the null hypothesis, we can then calculate the TVD between these random and the true \hat{p} 's and the π_i 's specified by the null hypothesis

$$TVD = \sum_{i=1}^{k} |\pi_i - \hat{p}_i|$$

We can repeat this 10,000 times to get a null distribution...

Step 3: Creating a null distribution

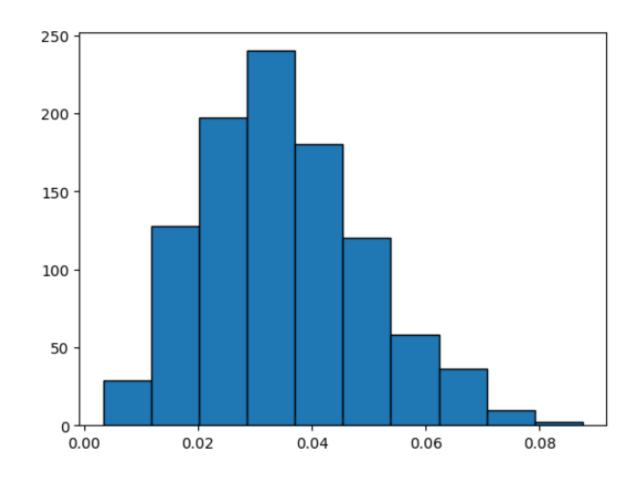


Step 4: Calculate the p-value

The p-value is the proportion of statistics in the null distribution more extreme than our observed statistic

Our observed statistic TVD value was 0.28

What is the p-value?



Step 5: Draw a conclusion

A small p-value is evidence to reject the null hypothesis

• i.e., our data is not consistent with the null hypothesis

Thus, we can conclude that the ethnicities of members on jury panels do not accurately reflect the underlying demographics.



Potential reasons for bias in Alameda county jury selection

Rejection of model tells us the model doesn't accurately account for the data, but it doesn't tell us why

The ACLU identified several reasons for bias in jury selection including:

- The software didn't work well, contributing to biased selection
- Jurors were selected at random from everyone who is a registered voter and/or has a driver's license
- Hard to reach people who don't have permanent addresses
 - Can disproportionately affect people at lower income levels

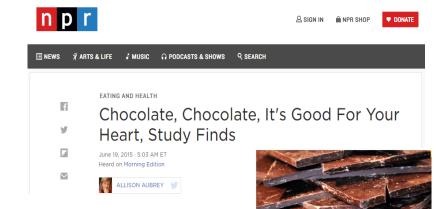
Let's explore this in Jupyter!

Assessing causal relationships

Review: Causality

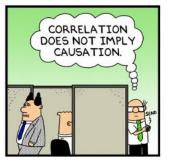
Recall from class 2:

- **An association** is the presence of <u>a reliable relationship</u> between the treatments an outcome
- A causal relationship is when changing the value of a treatment variable <u>influences</u> the value outcome variable
- A confounding variable (also known as a lurking variable) is a third variable that is associated with both the treatment (explanatory) variable and the outcome (response) variable
 - A confounding variable can offer a plausible explanation for an association between the other two variables of interest











Randomized Controlled Experiment

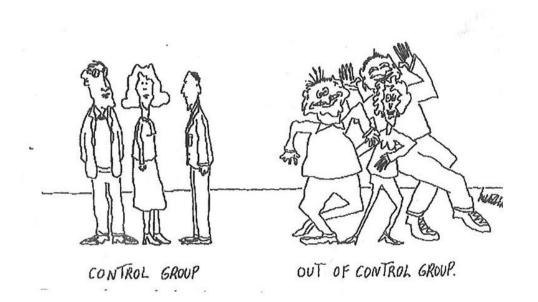
Sample A: control group

Sample B: treatment group

The treatment and control groups are selected at random; this allows causal conclusions!

Any difference in outcomes between the two groups could be due to:

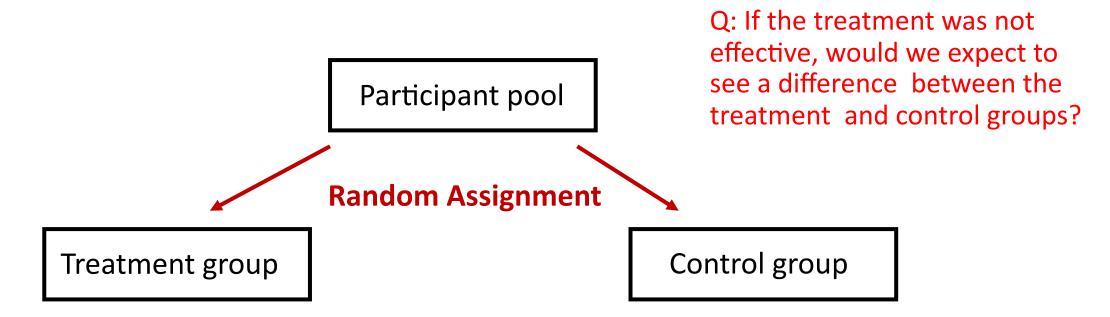
- Chance
- The treatment



Randomized Controlled Experiment

Take a group of participant and *randomly assign*:

- Half to a treatment group where they get chocolate
- Half in a control group where they get a fake chocolate (placebo)
- See if there is more improvement in the treatment group compared to the control group



Case study

RCT to study Botulinum Toxin A (BTA) as a treatment to relieve chronic back pain

- 15 patients in the treatment group (received BTA)
- 16 in the control group (normal saline)

Trials were run double-blind: neither doctors nor patients knew which group they were in.

Results

- 2 patients in the control group had relief from pain (outcome=1)
- 9 patients in the treatment group had relief.

Can this difference be just due to chance?



May 22, 2001; 56 (10) ARTICLES

Botulinum toxin A and chronic low back pain

A randomized, double-blind study

Leslie Foster, Larry Clapp, Marleigh Erickson, Bahman Jabbari

First published May 22, 2001, DOI: https://doi.org/10.1212/WNL.56.10.1290

Step 1: The hypotheses

Null:

- BTA does not lead to an increase in pain relief
 - i.e., if many people were to get BTA and saline, the proportion of people who experienced pain relief would be the same in both groups.
 - H_0 : $\pi_{treat} = \pi_{control}$ or H_0 : $\pi_{treat} \pi_{control} = 0$

Alternative:

- BTA leads to an increase in pain relief
 - i.e., if many people were to get BTA and saline, the proportion of people who experienced pain relief would be higher for those who received BTA
 - H_A : $\pi_{treat} > \pi_{control}$ or H_0 : $\pi_{treat} \pi_{control} > 0$



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Step 2: The observed statistic

To calculate an observed statistic we need data:

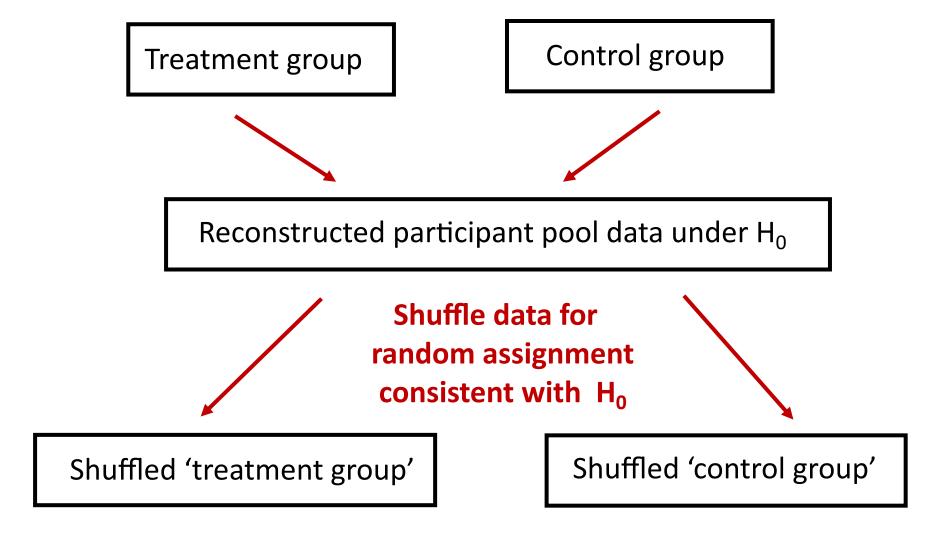
Let's have our observed statistic mirror our hypotheses

• H_0 : π_{treat} - $\pi_{control}$ = 0

Observed statistic is: \hat{p}_{treat} - $\hat{p}_{control}$

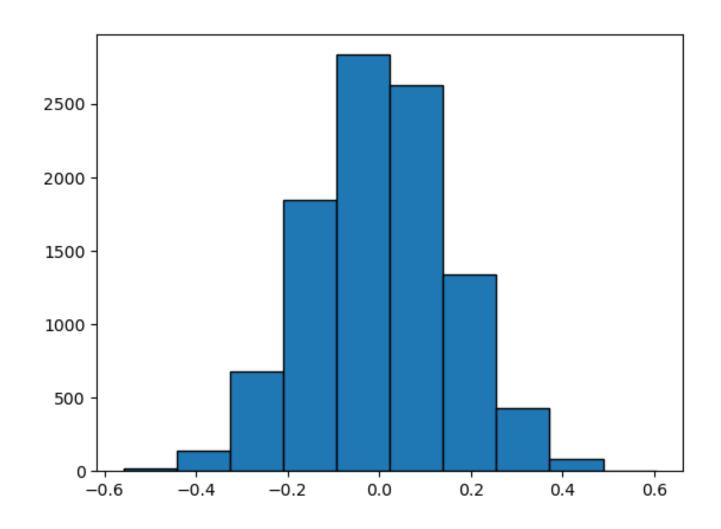
	Group	Result
19	Treatment	1.0
7	Control	0.0
6	Control	0.0
26	Treatment	0.0
17	Treatment	1.0
9	Control	0.0
13	Control	0.0
3	Control	0.0
1	Control	1.0
30	Treatment	0.0
28	Treatment	0.0

3. Create the null distribution!

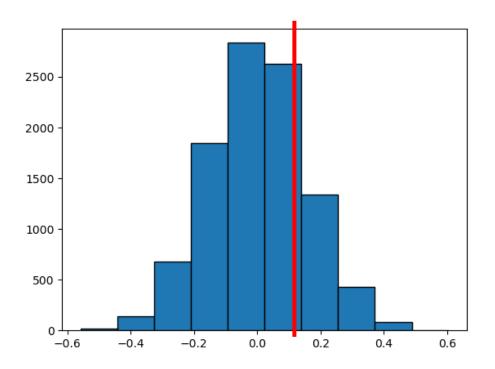


One null distribution statistic: $\hat{p}_{Shuff_Treatment} - \hat{p}_{Shuff_control}$

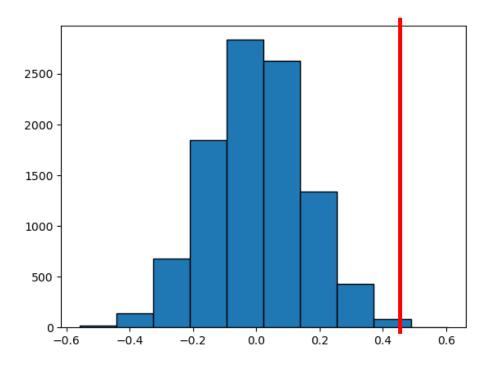
Step 3: Create a null distribution



Step 4: Calculate the p-value

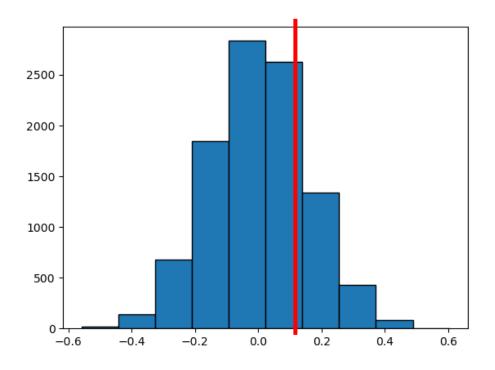


If \hat{p}_{treat} - $\hat{p}_{control}$ = 0.1 what would the p-value be?

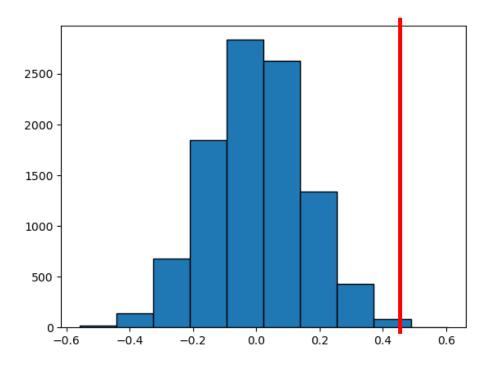


If \hat{p}_{treat} - $\hat{p}_{control}$ = 0.5 what would the p-value be?

Step 5: Draw a conclusion



If the p-value was 0.19 what would we conclude?



If the p-value was 0.0007 what would we conclude?



Let's explore this in Jupyter!