w241: Experiments and Causality

Unit 3

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Sampling Distribution and Randomization Inference

Standard Errors

- Standard deviation of the sampling distribution
- How spread out is the sampling distribution?
- How large are the typical chance differences?
- Later, we'll examine statistical power
    - The spread of the sampling distribution is the standard error
    - In what kinds of experiments are large and small differences likely to arise by chance?

Sampling Distributions and RI

- Groups may differ by chance, even if the treatment has no effect.
    - How much would the groups differ if the treatment had no effect?
    - How large of an "effect estimate" would we reach by chance?
- Distribution of estimates one would reach if treatment had no effect.
    - How likely is this estimate to have just arisen by chance?
- Similar to observational studies, but:
    - Intuition easy to see in experiments.
    - Testing a hypothesis about our sample, not a population.
    - Example code to walk through intuition on slides to follow

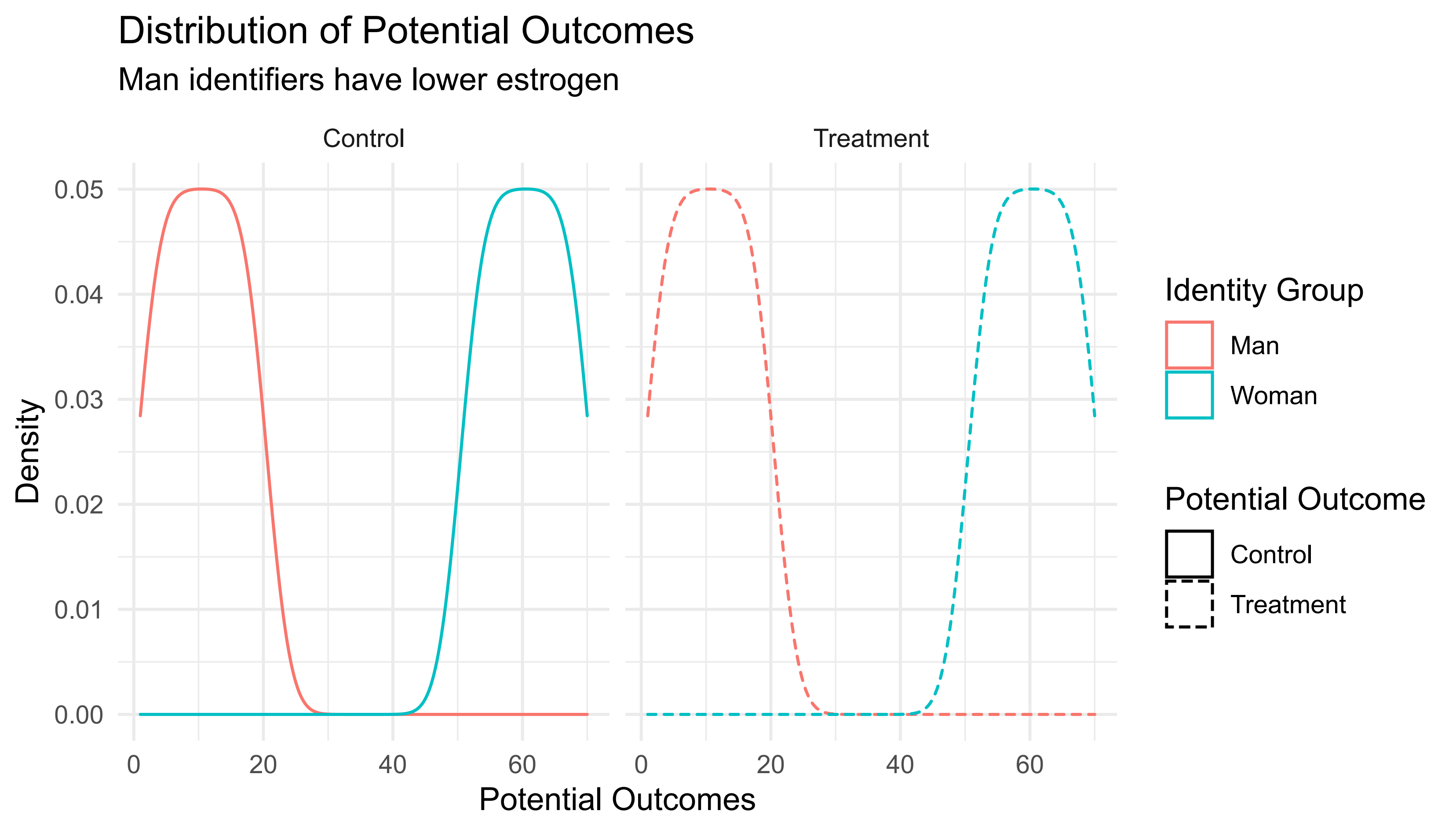
Example: An Experiment with no Effect

- Does eating soybeans affect estrogen levels?
- 40 individuals: 20 men, 20 women.
- Simulate the potential outcomes of the control group.
- Simulate the potential outcomes of the treatment group.
- A simulated experiment with no effect.

```
group ← c(rep("Man",20),rep("Woman",20))

po_control ← c(
  seq(from = 1, to = 20),
  seq(from = 51, to = 70)
  )

## Suppose there is no effect.
## Then, the potential outcomes to control are equal
## to the potential outcomes to treatment.

po_treatment ← po_control + 0

d ← data.frame(
  'Control'   = po_control,
  'Treatment' = po_treatment,
  'group'        = group
  )
```

```
d %>%
  head()
```

```
##   Control Treatment group
## 1       1         1   Man
## 2       2         2   Man
## 3       3         3   Man
## 4       4         4   Man
## 5       5         5   Man
## 6       6         6   Man
```


Distribution of Potential Outcomes
Man identifiers have lower estrogen
Control
Treatment
Density
0.05
0.04
0.03
0.02
0.01
0.00
0
20
40
60
Potential Outcomes
Identity Group
Man
Woman
Potential Outcome
Control
Treatment

Random Assignment

- Define function to randomly assign units to treatment and control.
- Randomly pick 20 for treatment and 20 for control.
- Concatenate the two vectors.
- Get a different vector when you run it again.

```
randomize ← function(units_per_group) {
  ## an (unnecessary) function to randomize units into
  ## treatment and control
  ## ---
  ## args:
  ##  - units_per_group: how many zero and one should be returned

  assignment_vector ← rep(c('Control', 'Treatment'), each = units_per_group)
  sample(assignment_vector)
}
```

Random Assignment

```
randomize(units_per_group = 4)
```

```
## [1] "Control"   "Control"   "Treatment" "Treatment" "Treatment" "Treatment"
## [7] "Control"   "Control"
```

```
randomize(units_per_group = 4)
```

```
## [1] "Treatment" "Control"   "Control"   "Treatment" "Control"   "Control"
## [7] "Treatment" "Treatment"
```

Realized Outcomes

- Treatment outcome for those randomized to treatment and control outcome for those randomized to control.
- Assign for each person in the vector.
- Same because we had an experiment with no effect.
- R code is often written in a compact manner; could also have been done separately for each group.
- Why are we doing this when there is no treatment effect?
- Because it should also work when there is one. We're looking at what happens when we randomly assign people to control and treatment groups.

Realized Outcomes

```
treatment_assigned <- randomize()

outcomes <- po_treatment * I(treatment_assigned == "Treatment") +
  po_control * I(treatment_assigned == "Control")

outcomes
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 51 52 53 54 55
## [26] 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70
```

Function to Estimate the Average

- Subtract the mean outcome for the control group from the mean outcome of the treatment group.
- How much higher is the average in the treatment group versus the control group?
- We may have randomly selected someone with a higher or lower level of estrogen.
- Even though we know the effect is 0, we see chance differences.

Function to Estimate the Average

```r
estimate_ate <- function(y_values, treatment) {

  treatment_group_mean <- mean(y_values[treatment == 'Treatment'])
  control_group_mean   <- mean(y_values[treatment == 'Control'])

  ate <- treatment_group_mean - control_group_mean

  return(
    list(
      "tg_mean" = treatment_group_mean,
      "cg_mean" = control_group_mean,
      "ate" = ate)
  )
}
```

```r
## In fact, there is _no_ effect, but ... sampling!
estimate_ate(y_values = outcomes, treatment = treatment_assigned)
```

```
## $tg_mean
## [1] 36
##
## $cg_mean
## [1] 35
##
## $ate
## [1] 1
```

```r
## To pull a single part of this, because it is a list, R indexes with .[[
estimate_ate(y_values = outcomes, treatment = treatment_assigned)[['ate']]
```

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

The Null Hypothesis

Rhetorical Posture of the Null

- You want to argue against a skeptic that a treatment has an effect.
- Assume the skeptic is right.

> Treatment has no effect.

- What is the chance that we would see this estimate by chance in that scenario?

> This is p-value.

- We’ll see where it comes from visually.

Average Size of the Difference

Because this demonstration is based on a stochastic simulation, the *specific* values that are in the slides might not match what we're narrating aloud.

What we're reading aloud are the results for the trial that we conducted.

Average Size of the Difference

- Simulate this a few times to get a sense of how much our treatment effect estimate would vary by chance.
- We created an estimate function with the outcomes and the treatment group.
- Outcome vector will look the same regardless of the treatment vector.

```
treatment_assigned_one ← randomize(units_per_group = 20)
estimate_ate(y_values = outcomes, treatment = treatment_assigned_one)[['ate']]
```

```
## [1] 7.5
```

```
treatment_assigned_two ← randomize(units_per_group = 20)
estimate_ate(y_values = outcomes, treatment = treatment_assigned_two)[['ate']]
```

```
## [1] -3.9
```

```
treatment_assigned_three ← randomize(units_per_group = 20)
estimate_ate(y_values = outcomes, treatment = treatment_assigned_three)[['ate']]
```

```
## [1] 4
```

Outcome With Different Assignments

- Similar to re-sampling from a population.
- Re-randomizing from within the original population. Testing the null hypothesis from within the sample we already have.

- Re-shuffle the 40 people between treatment and control. Assuming the treatment effect for everyone is zero.

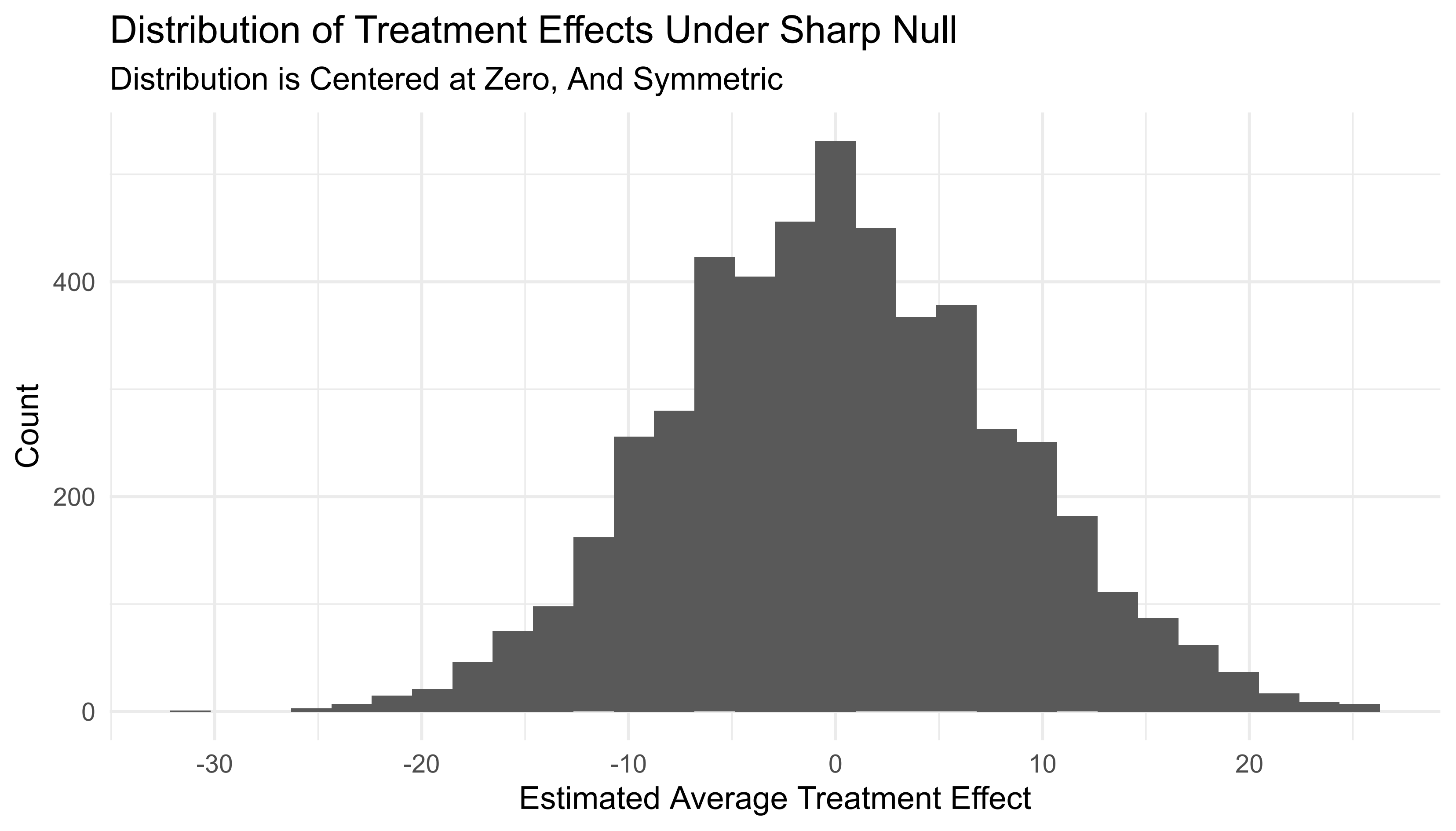
Sharp null hypothesis: For every unit, there is no effect.

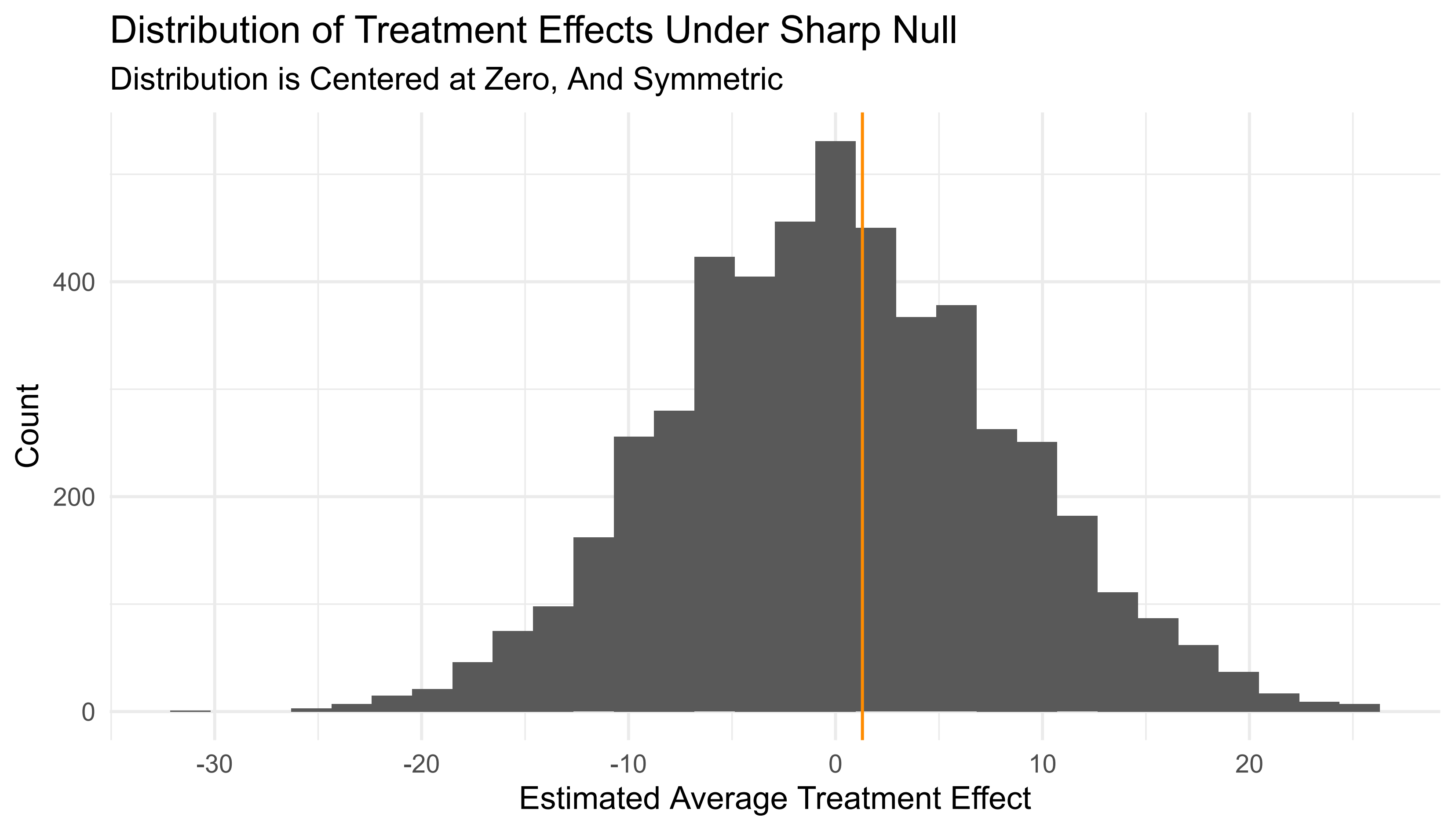
- Repeat this process to generate a synthetic distribution of effects if the sharp null hypothesis *were true*.

- Randomly sample the vector of assignments 5,000 times to generate an unbiased sample of all the effects.

- Literally, replicate 5,000 times, and save to a vector.

```r
## going to move the randomization inside the `estimate_ate` function
## for compactness

sharp_null <- replicate(
  n = 5000,
  expr = estimate_ate(
    y_value = outcomes,
    treatment = randomize(units_per_group = 20))[['ate']]
)
```


Distribution of Treatment Effects Under Sharp Null
Distribution is Centered at Zero, And Symmetric
Count
400
200
0
-30
-20
-10
0
10
20
Estimated Average Treatment Effect


Distribution of Treatment Effects Under Sharp Null
Distribution is Centered at Zero, And Symmetric
Count
400
200
0
-30
-20
-10
0
10
20
Estimated Average Treatment Effect

Size of the Observed Difference

- The p-value.
- How often did I get a randomization under the sharp null where the estimate was larger than my actual estimate?
- For each, is it larger than the average treatment effect estimate?
- This is a sampling distribution.
- How big is my estimate relative to the distribution of estimates?

Size of the Observed Difference

In this particular case,

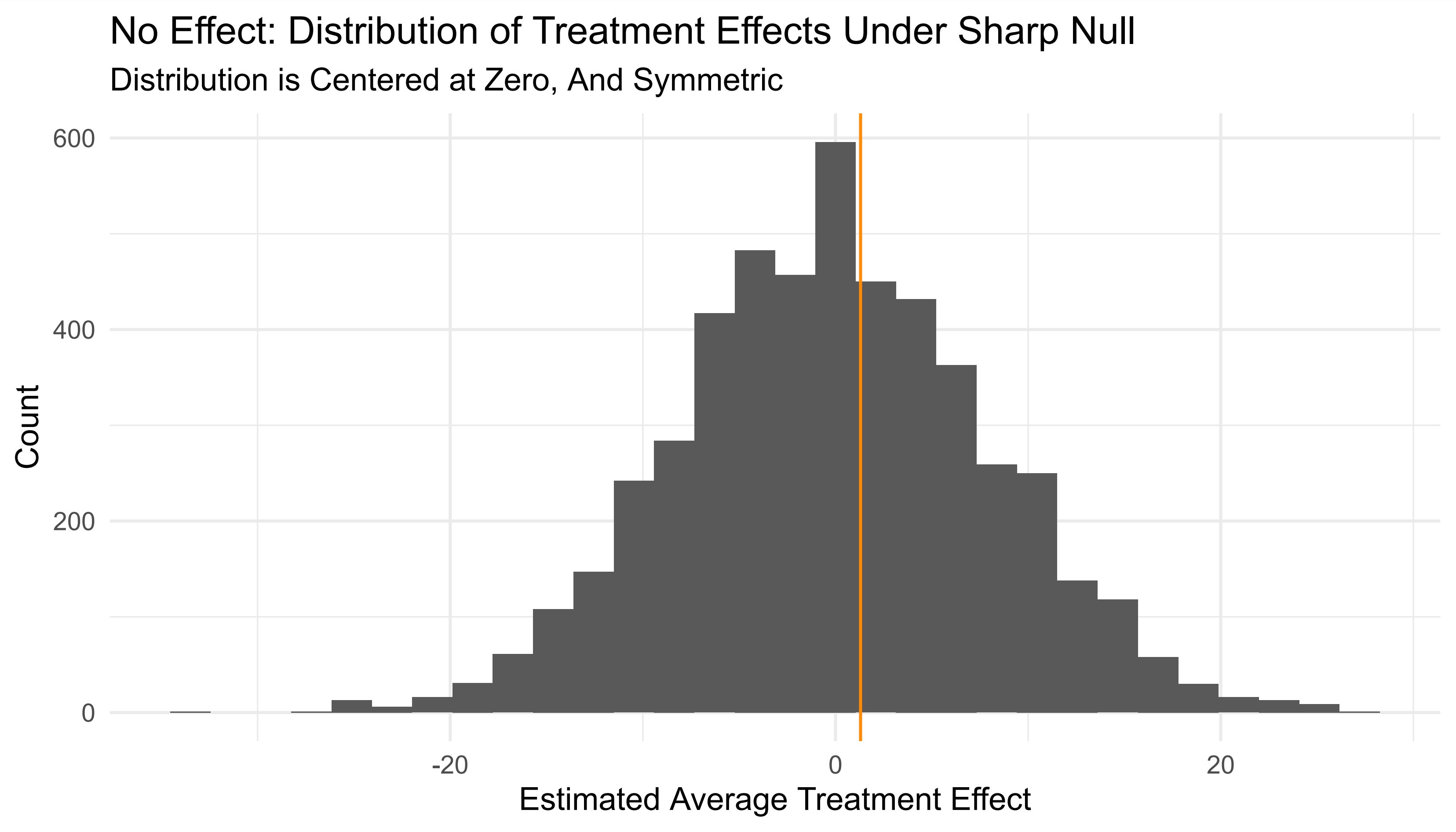
```
experimental_randomization <- randomize(units_per_group = 20)

sharp_null <- replicate(
  n = 5000,
  expr = estimate_ate(
    y_value = outcomes,
    treatment = randomize(units_per_group = 20))[['ate']]
)

mean(abs(sharp_null) > abs(experimental_ate))
```

```
## [1] 0.8512
```

Size of the Observed Difference

```
histogram_no_effect <- ggplot() +
  aes(x = sharp_null) +
  geom_histogram() +
  geom_vline(xintercept = experimental_ate, color = 'darkorange') +
  labs(
    title = "No Effect: Distribution of Treatment Effects Under Sharp Null",
    subtitle = "Distribution is Centered at Zero, And Symmetric",
    x = "Estimated Average Treatment Effect",
    y = "Count"
  )
```

Size of the Observed Difference


No Effect: Distribution of Treatment Effects Under Sharp Null

Distribution is Centered at Zero, And Symmetric

P-Values and Hypothesis Tests

P-Values

- If the treatment had no effect, how likely is it that the data would generate a difference this extreme, *just by chance*?
- What is the difference between the mean in the control and treatment groups?
- Different from how likely it is the treatment has an effect
- Convention is to reject the null with p-value under 0.05.
- p-values don't tell you for sure that the treatment has an effect.
- They just tell you how likely it is you would have gotten that result by chance.
- The sampling distribution tells us how large the differences are we find by chance.
- Can find p-values < 0.05 even when the null hypothesis is correct.

Simulating an Experiment with a Large

- Vector of outcomes and control
- 40-row table with potential outcomes in control and treatment.
- This time, with a difference of 25

Simulating an Experiment with a Large

```r
po_control   <- c(1:20, 51:70)
po_treatment <- po_control + 25

treatment_assigned <- randomize(units_per_group = 20)

outcomes <- po_treatment * I(treatment_assigned == "Treatment") +
  po_control * I(treatment_assigned == "Control")
outcomes
```

```
##  [1] 26  2 28 29  5  6  7  8 34 35 11 12 38 39 40 16 42 43 19 45 76 52 78 79 80
## [26] 56 57 58 59 60 86 62 63 89 65 91 67 68 94 95
```

```r
experimental_ate_big_effect <- estimate_ate(
  y_values = outcomes,
  treatment = treatment_assigned
  )[['ate']]
experimental_ate_big_effect
```

```
## [1] 20.7
```

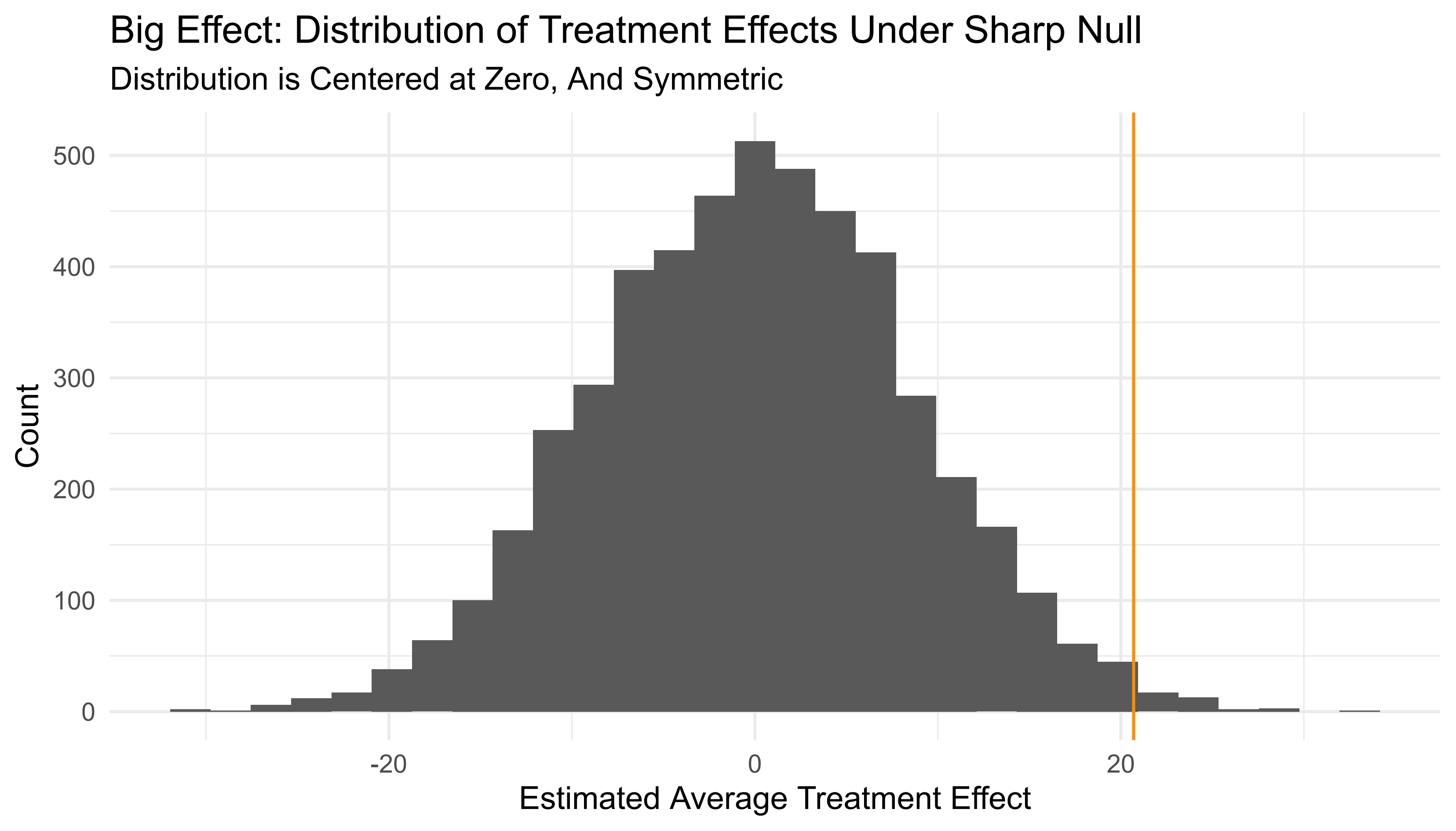
Simulating an Experiment with a Large

```r
sharp_null_big_effect <- replicate(
  n = 5000,
  expr = estimate_ate(
    y_values = outcomes,
    treatment = randomize(units_per_group = 20))[['ate']]
  )
```

Simulating an Experiment with a Large

```r
histogram_big_effect <- ggplot() +
  aes(x = sharp_null_big_effect) +
  geom_histogram() +
  geom_vline(xintercept = experimental_ate_big_effect, color = 'darkorange') +
  labs(
    title = "Big Effect: Distribution of Treatment Effects Under Sharp Null",
    subtitle = "Distribution is Centered at Zero, And Symmetric",
    x = "Estimated Average Treatment Effect",
    y = "Count"
  )
```

Simulating an Experiment with a Large

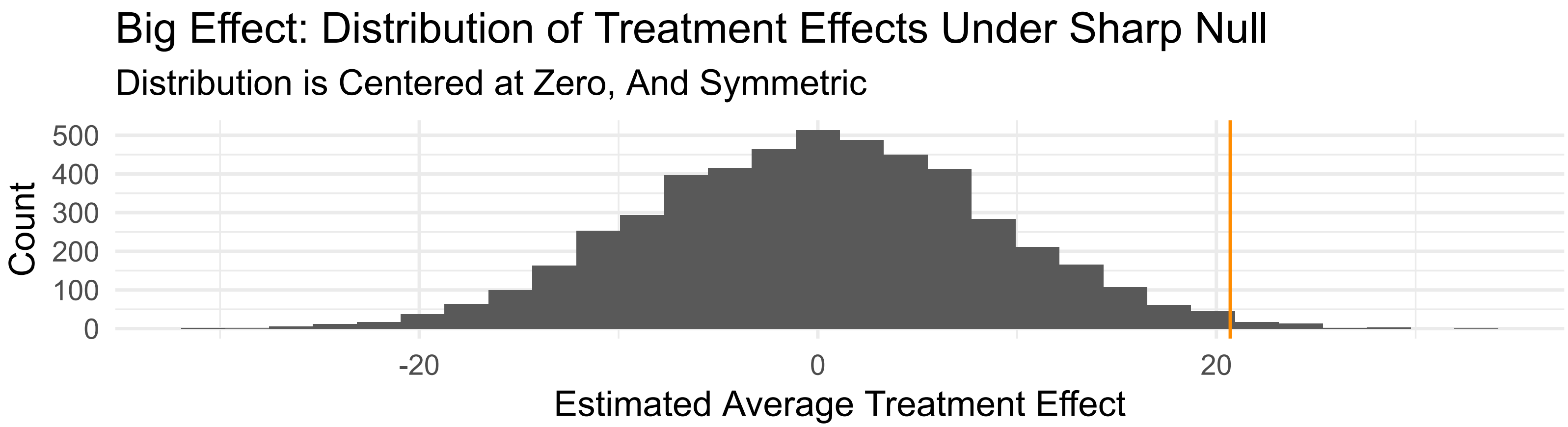


Simulating an Experiment with a Large

```
mean(abs(sharp_null_big_effect) > abs(experimental_ate_big_effect))
```

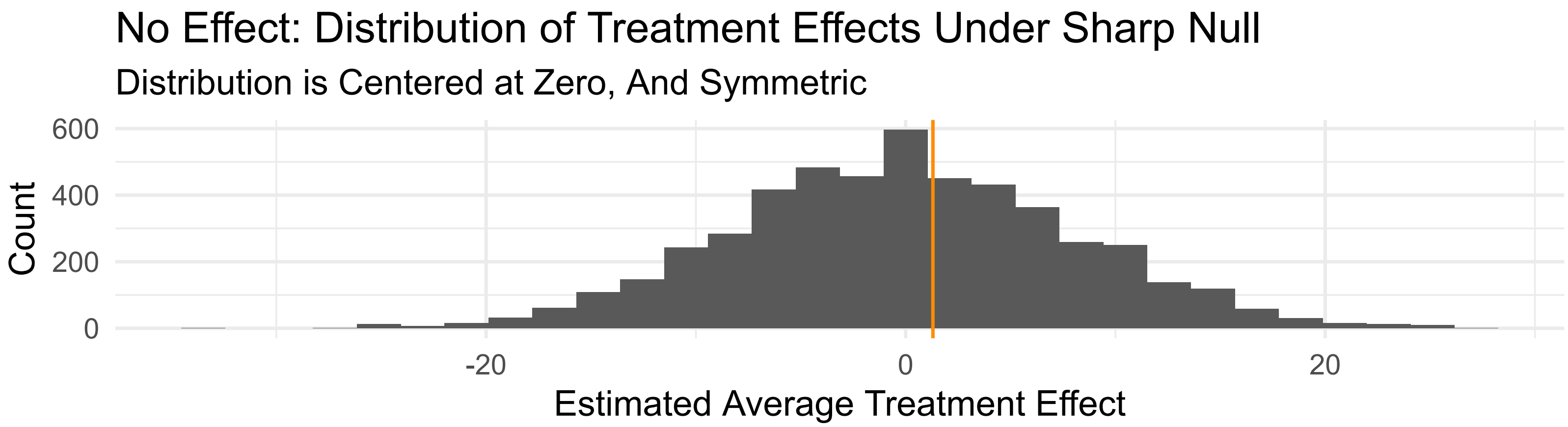
```
## [1] 0.0166
```

Compare Big Effect and No Effect Sharp



Big Effect: Distribution of Treatment Effects Under Sharp Null

Distribution is Centered at Zero, And Symmetric



No Effect: Distribution of Treatment Effects Under Sharp Null

Distribution is Centered at Zero, And Symmetric

Statistical Power

Detecting Non-Zero Treatment Effects

Suppose the treatment effect is 10.

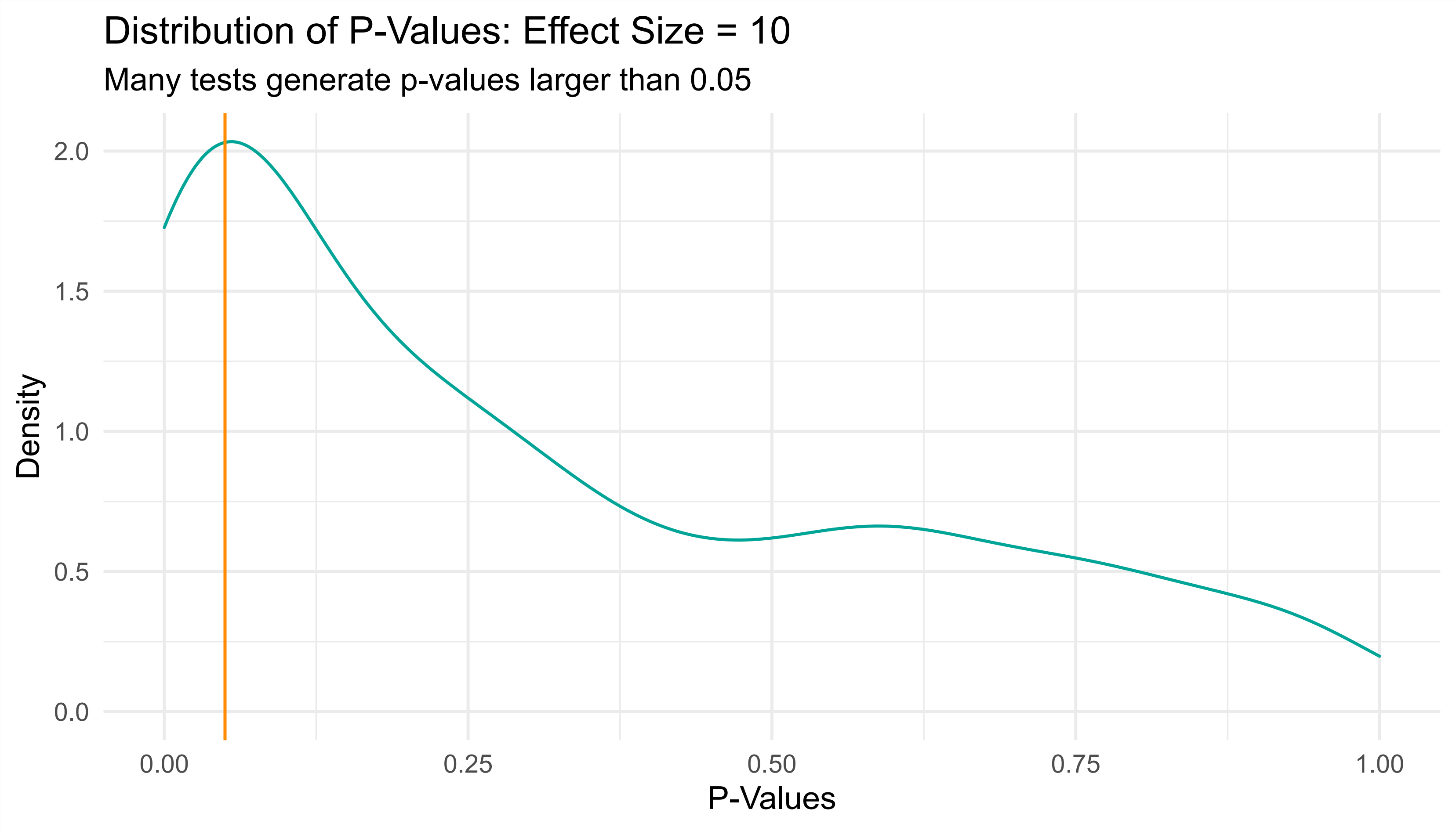
Create Whole Study Function

```r
simulate_study <- function(effect_size) {
  # generate world
  po_control   <- c(1:20, 51:70)
  po_treatment <- po_control + effect_size

  # assign treatment and measure outcomes
  treatment_assigned <- randomize(20)
  outcomes <- po_treatment * I(treatment_assigned == "Treatment") +
    po_control * I(treatment_assigned == "Control")

  # estimate ate
  estimated_ate <- estimate_ate(y_values = outcomes, treatment = treatment_assigned)[[

  # generate sharp null distribution
  sharp_null <- replicate(
    n = 100,
    expr = estimate_ate(y_values = outcomes, treatment = randomize(20))[['ate']])

  p_value <- mean(abs(sharp_null) > abs(estimated_ate))
  return(list(
    'estimated_ate' = estimated_ate,
    'mean_sharp_null' = mean(sharp_null),
    'p_value' = p_value)
  )
}
```

Simulate Study, Effect Size: 10

```r
## notice: we now have two loops:
  ## - We're running 500 simulations;
  ## - In each simulation, there are 1,000 sharp nulls drawn out
  ## - So get some coffee if you're running this at home

distribution_of_p_values_10 <- replicate(
  n = 500,
  expr = simulate_study(effect_size = 10)[['p_value']]
)
```

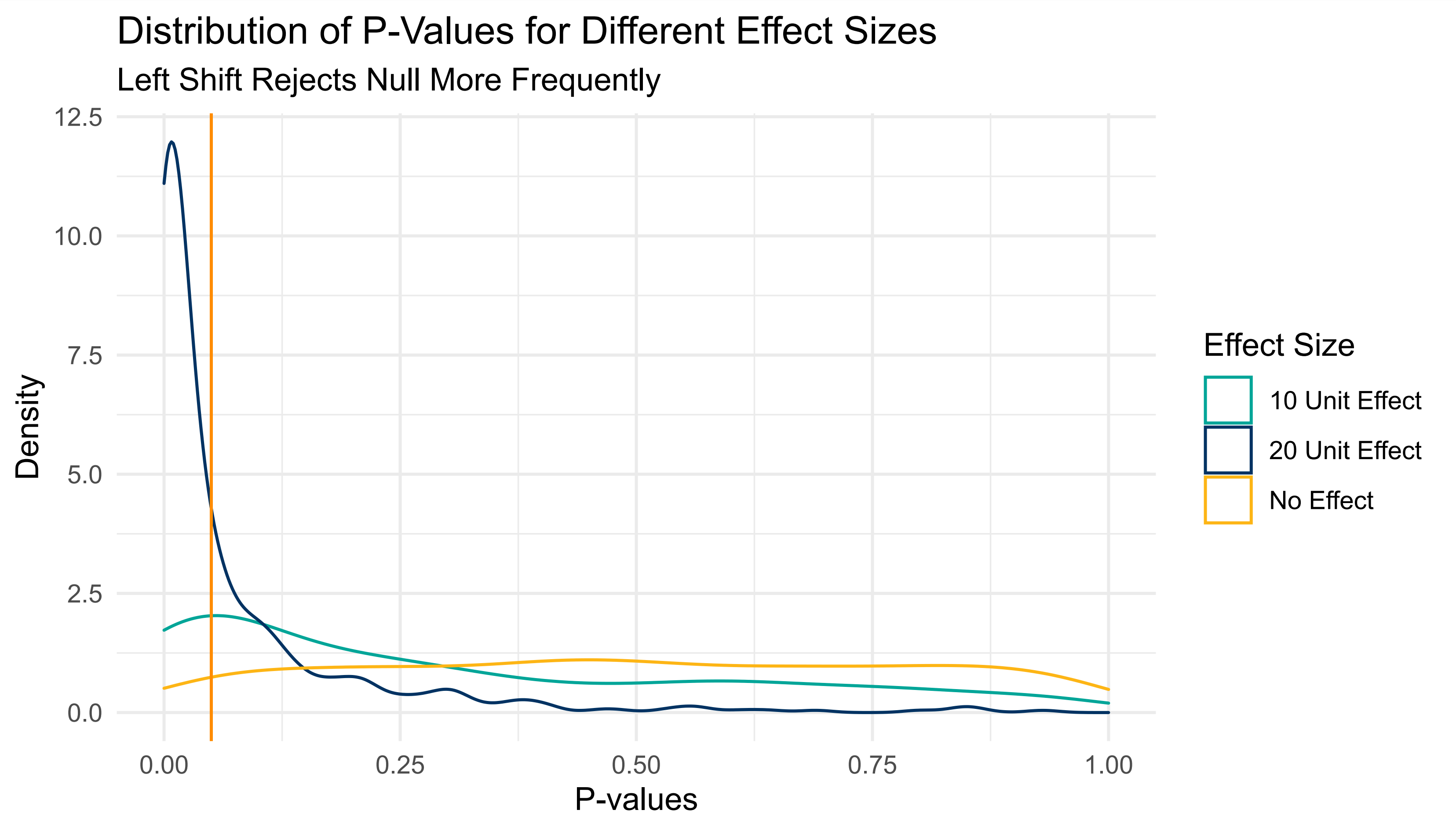
Power for 10 Unit Effect



Power Sim: 0 & 20 Unit Effect

```r
distribution_of_p_values_0 <- replicate(
  n = 500,
  expr = simulate_study(effect_size = 0)[['p_value']]
)

distribution_of_p_values_20 <- replicate(
  n = 500,
  expr = simulate_study(effect_size = 20)[['p_value']]
)
```

Power Curves for All Effects



Increasing Statistical Power

Power Increases With:

- Size of the effect -- *larger effects are easier to detect!*
- Square root of the sample size, $\sqrt{N}$.
    - To detect an effect twice as small (or equivalently half as large) requires a sample size 4 times larger;
- Precision of the measurement
- Reduction of variance within groups (e.g. removing individuals pre-test; or block randomizing)

Statistical Power:

> "The probability that a particular {experiment design & measurment & test} will reject the null hypothesis in a world where it *should* reject that null hypothesis."

Concentrated Tests

Suppose the FDA is testing the effect of soybeans on estrogen

- **Study One**: Give one soybean to 1,000,000 people.
- **Study Two**: Give 10 soybeans to 10,000 people.
    - If there is a linear effect of soybeans, then these two design have equivalent power
    - However, *Study Two* has used 1/10 as many soybeans in the study.=
    - If the input is the expensive part of the experiment, then this saves cost on the input
    - If the recruitment of subjects is the expensive part of the experiment, then this has *also* saved cost on the recruitment.
- (**Study Three**): Give 100 soybeans to 100 people has the same power as the above two experiments as well!

Concentrated Tests

- Often, it is a good idea to decrease the sample size and give a higher "dosage" to the treatment group
- Concentrated tests increase statistical power by exposing a smaller number of people to a larger dose of treatment.

Decreasing Statistical Power

Power Decreasese With:

- Larger amounts of variation in the measured outcomes
    - More diverse populations create more differences in baseline differences; relative to the effect size, this "mutes" the ability to measure an effect
    - More "noise" in the measurement raises the "floor" of what one must detect to look different from that noise; precise measurements are preferred to imprecise measurements
- Standard deviation, σ, of the outcome

Key Concept:

- The ratio of the true treatment effect to the standard error of the estimated effect:

$$\text{test statistic} = \frac{\hat{\tau}}{SE(\hat{\tau})} = \frac{\hat{\tau}}{\left(\frac{\sigma_{\hat{\tau}}}{\sqrt{N}}\right)}$$

Recap of the Week

Recap of the Week, Part I

Sampling Distribution

- A **sharp null sampling distribution** is a distribution of estimates that we would receive by chance if there really were *no effect*
  - The "sharp null distribution" then simulates the range of outcomes our experiment and estimate system can produce, even when there is *no effect*
  - The proportion of these simulations that are *more-extreme* than the treatment effect observed in the experiment is the **randomization inference p-value**.

Recap of the Week, Part II

P-Values

- **P-values** provide a statement about $P(\textbf{data}|\textbf{sharp-null is true})$.
- What we would *ideally* like to know is $P(\textbf{alternative is true}|\textbf{data})$, but this isn't provided by randomization inference, or Frequentest inference.

Recap of the Week, Part III

Statistical Power

- Simply increasing sample size of an experiment can improve **statistical power** which is the *the probability that a test will reject the sharp-null hypothesis when the sharp null is* actually *true*.
- Careful design can also improve statistical power.