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

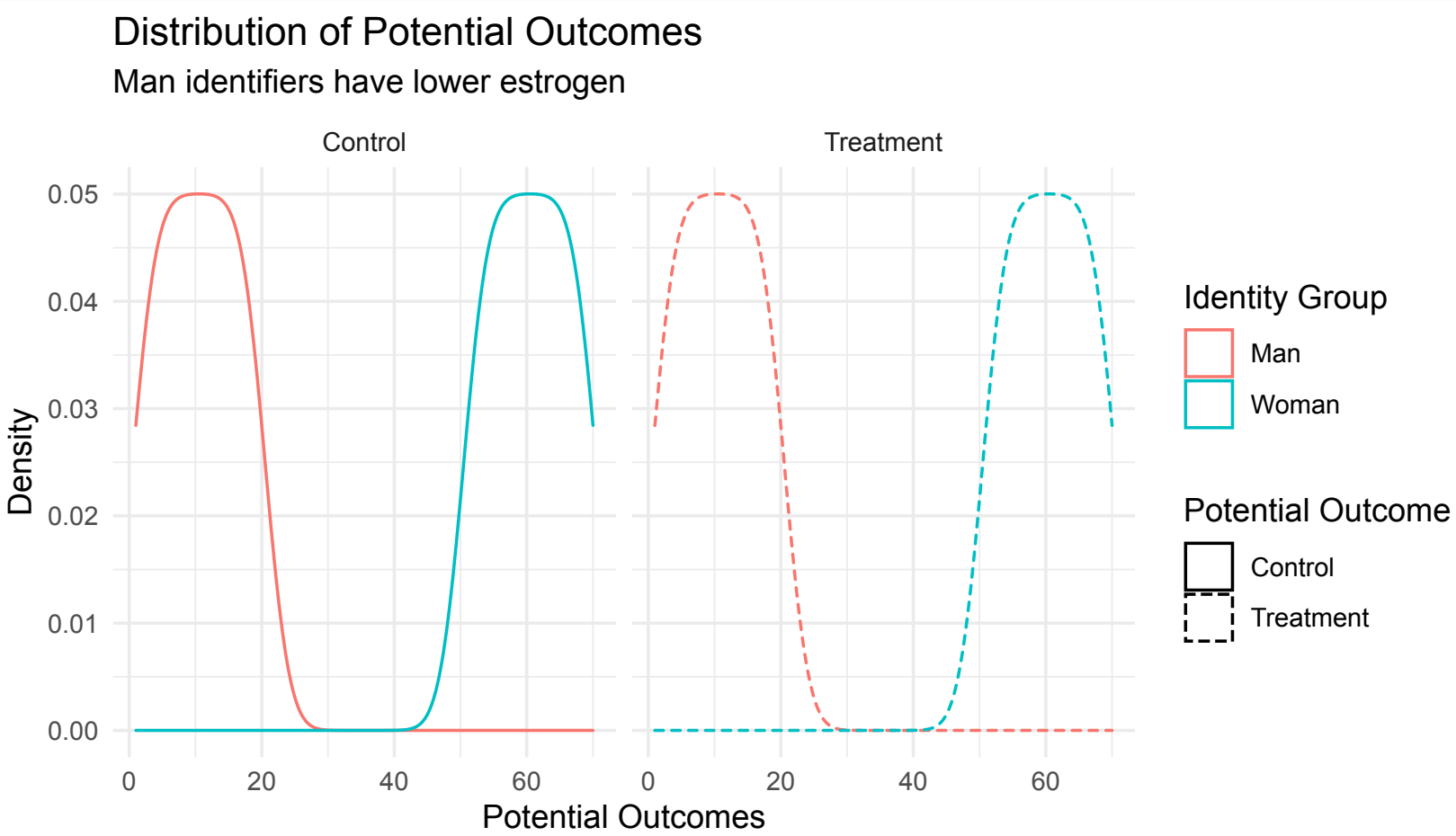
Example: An Experiment with no Effect

- 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.

```r
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] "Treatment" "Control"   "Control"   "Treatment" "Treatment" "Treatment" "Control"
```

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

```
## [1] "Treatment" "Treatment" "Control"   "Treatment" "Control"   "Control"   "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 56 57 58
```

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

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

- 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] -16.7
```

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

```
## [1] -1.5
```

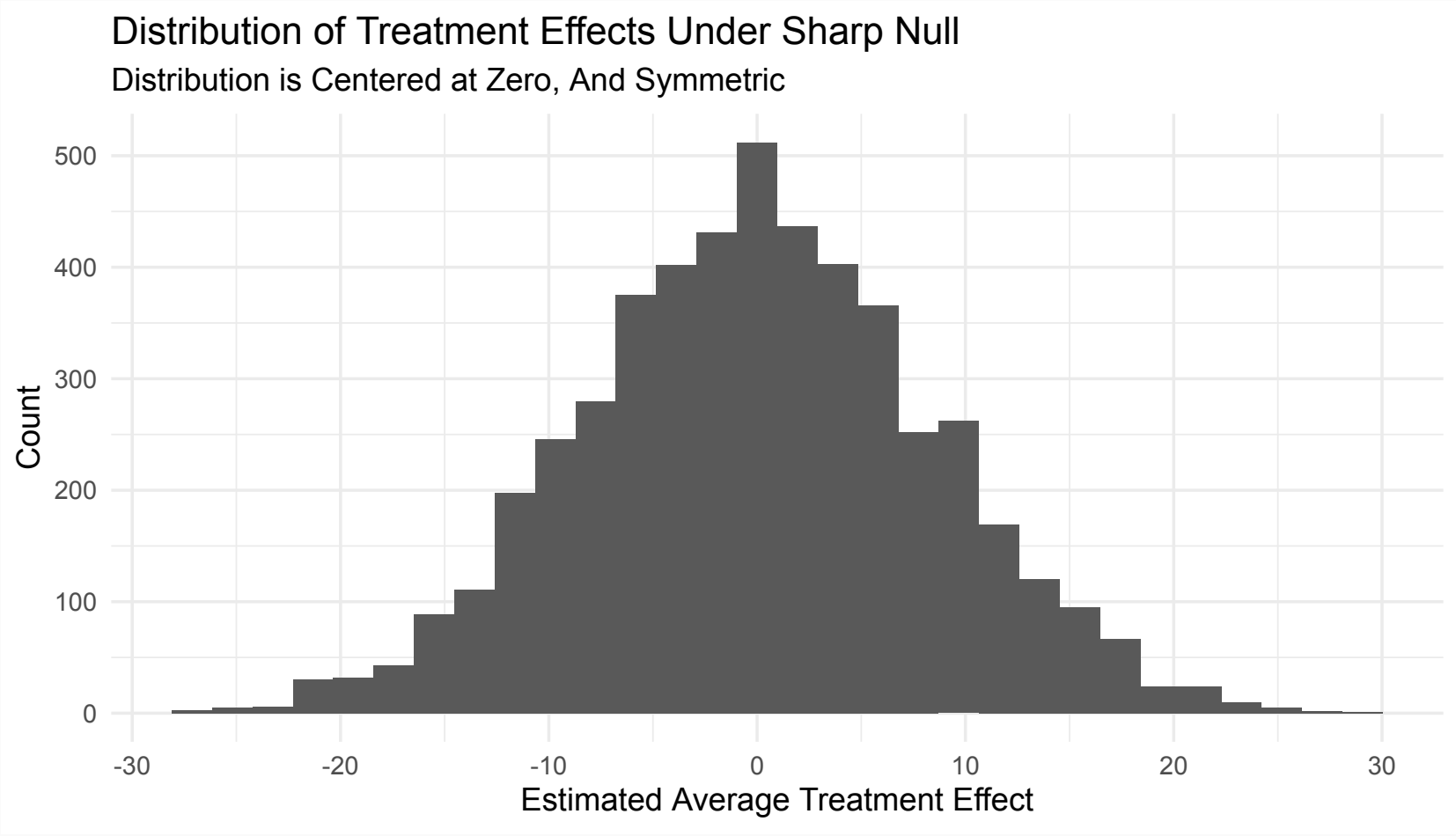
```
treatment_assigned_three ← randomize(units_per_group = 20)
estimate_ate(y_values = outcomes, treatment = treatment_assigned_three)[['ate']]
```

```
## [1] 0.2
```

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.

```
## 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
500
400
300
200
100
0
-30
-20
-10
0
10
20
30
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,

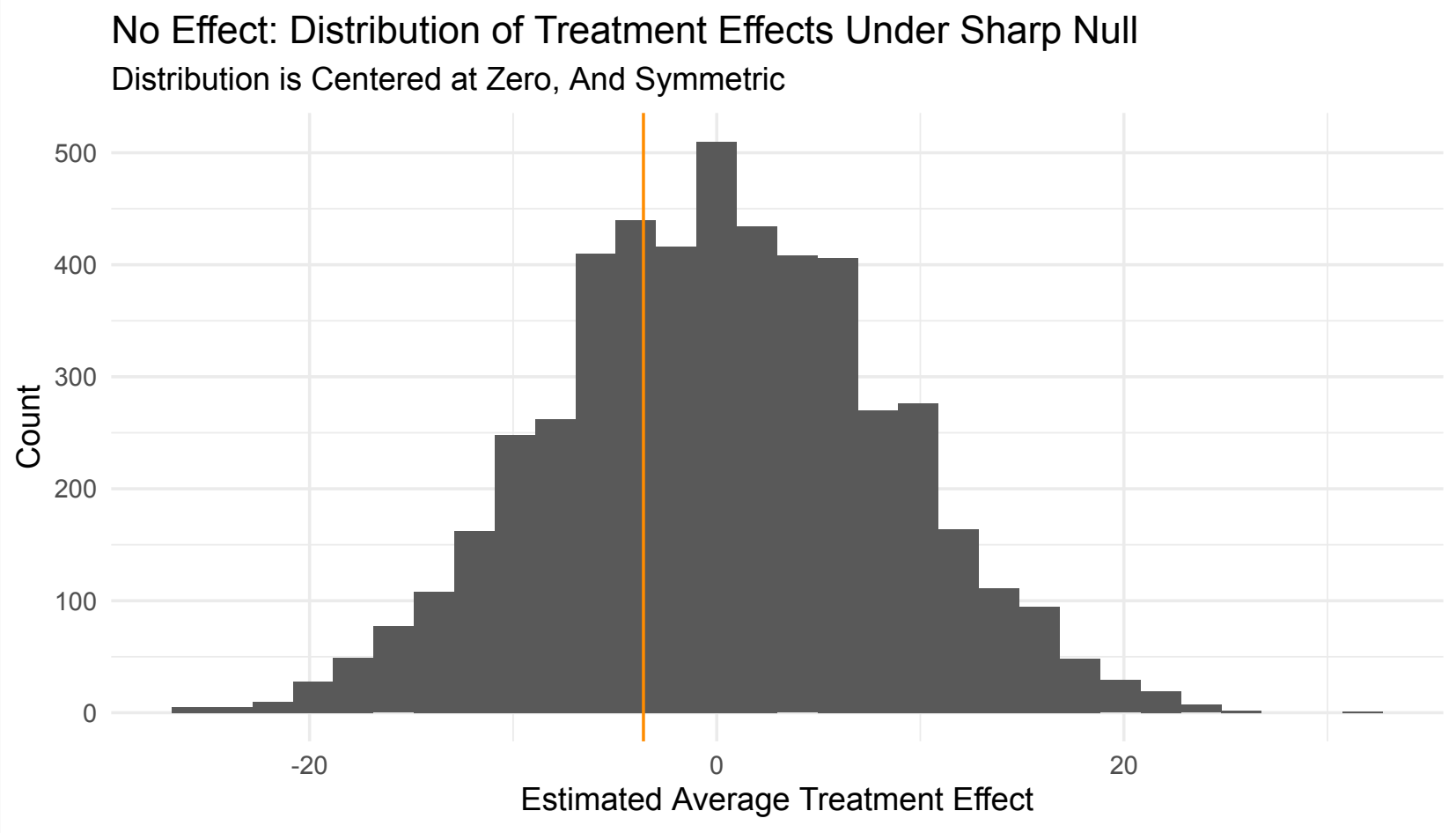
```
experimental_randomization ← randomize(units_per_group = 20)
experimental_ate ← estimate_ate(
  y_values = outcomes,
  treatment = experimental_randomization)[['ate']]

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] 0.6704
```

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



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

```
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")

experimental_ate_big_effect ← estimate_ate(
  y_values = outcomes,
  treatment = treatment_assigned
  )[['ate']]
```

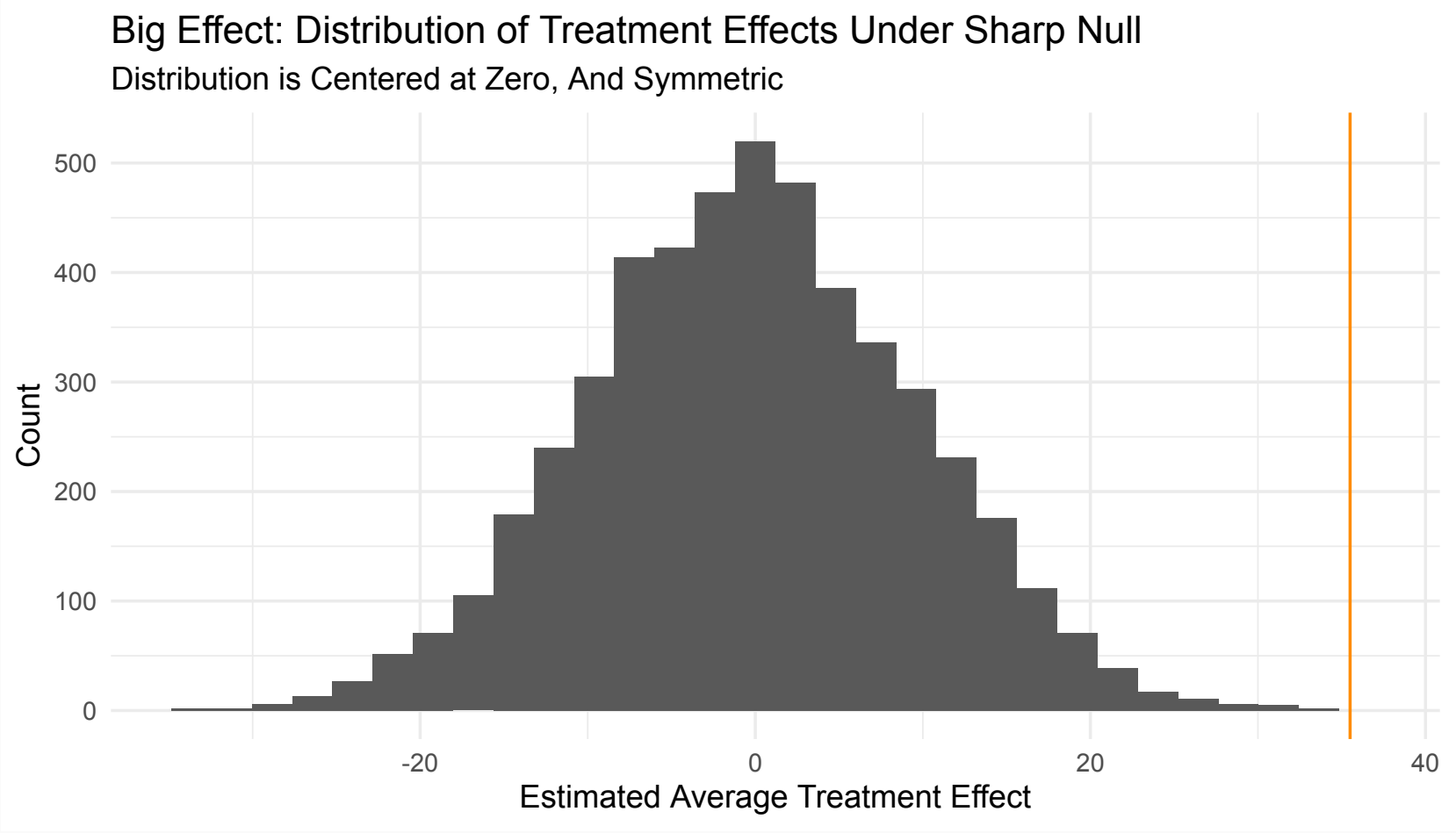
Simulating an Experiment with a Large

```
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

```
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

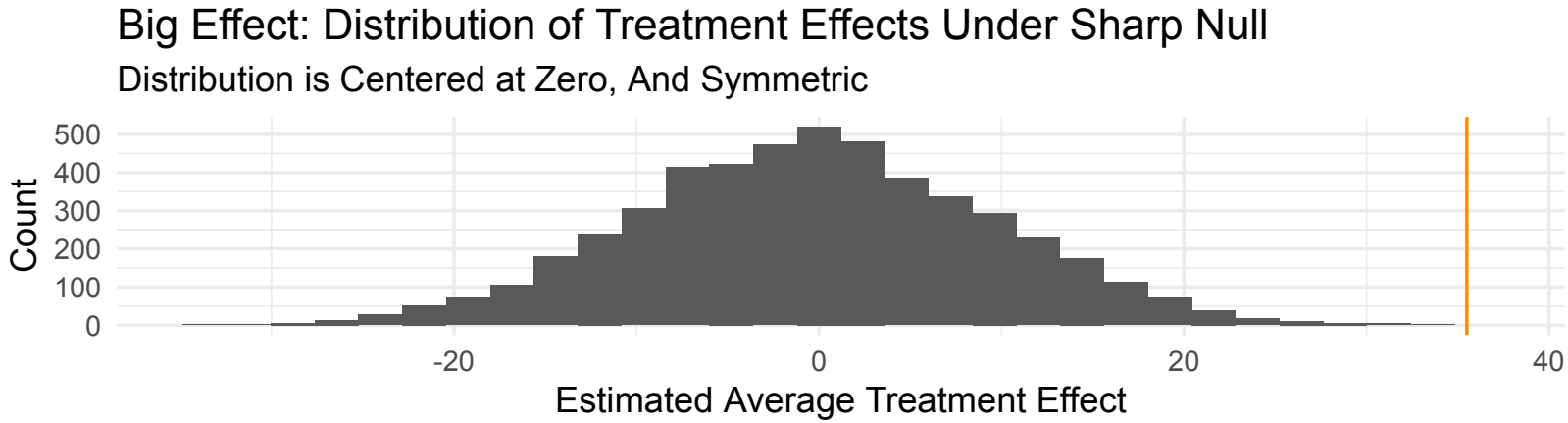


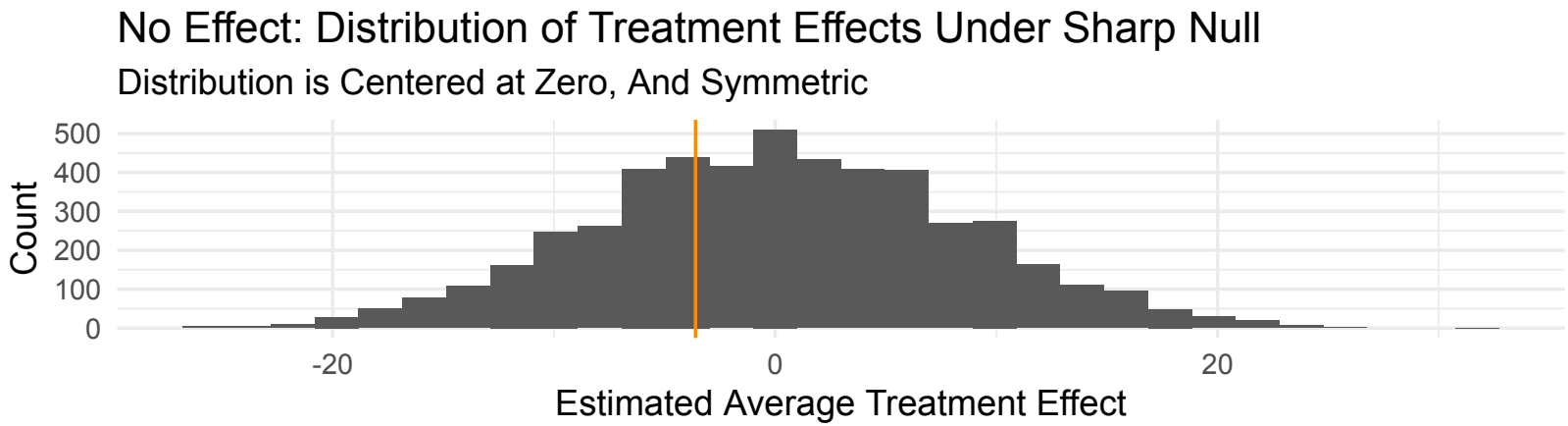
Simulating an Experiment with a Large

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

```
## [1] 0
```

Compare Big Effect and No Effect Sharp





Statistical Power

Detecting Non-Zero Treatment Effects

Suppose the treatment effect is 10.

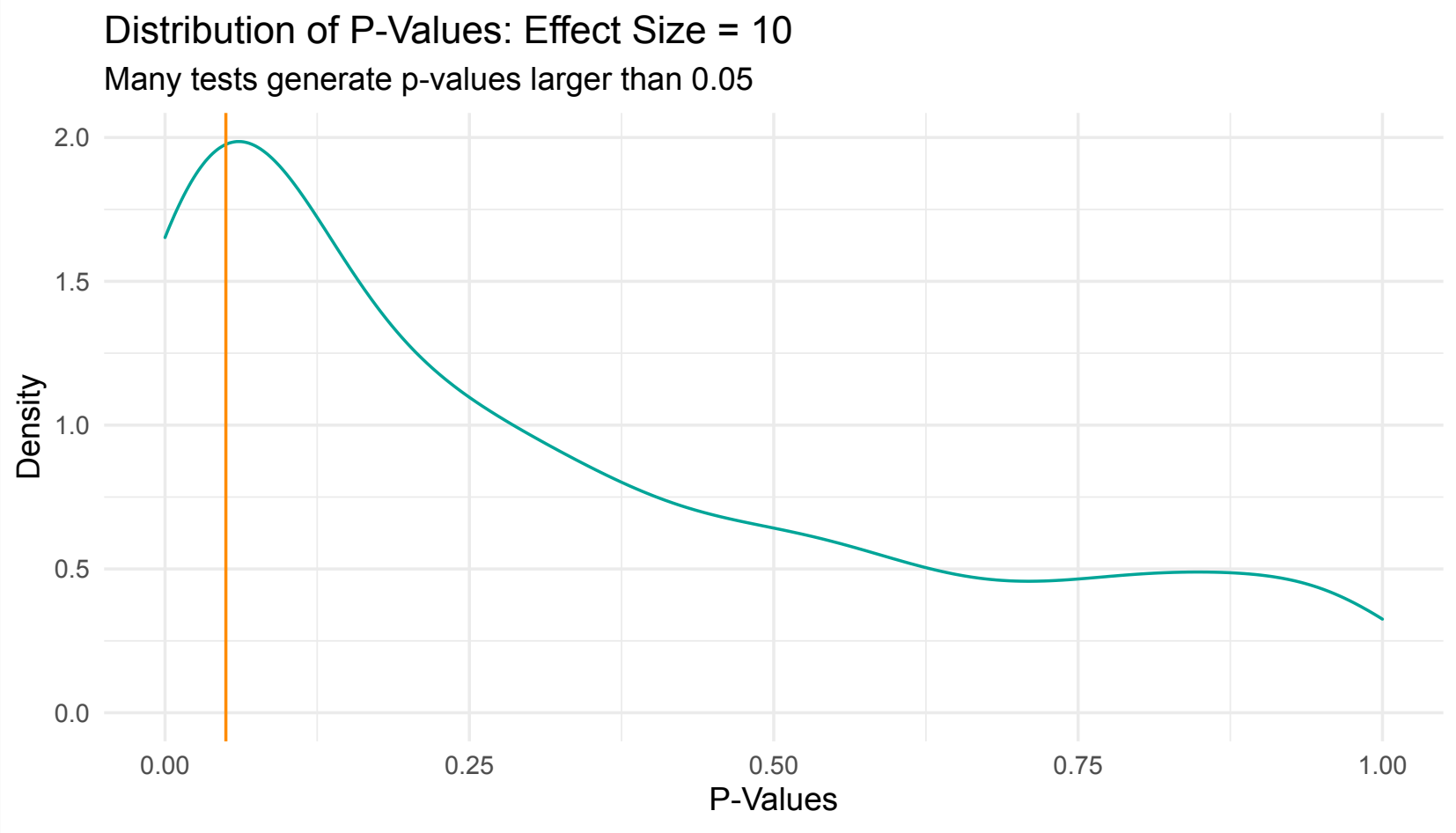
Create Whole Study Function

```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

```
## 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']]
)
```

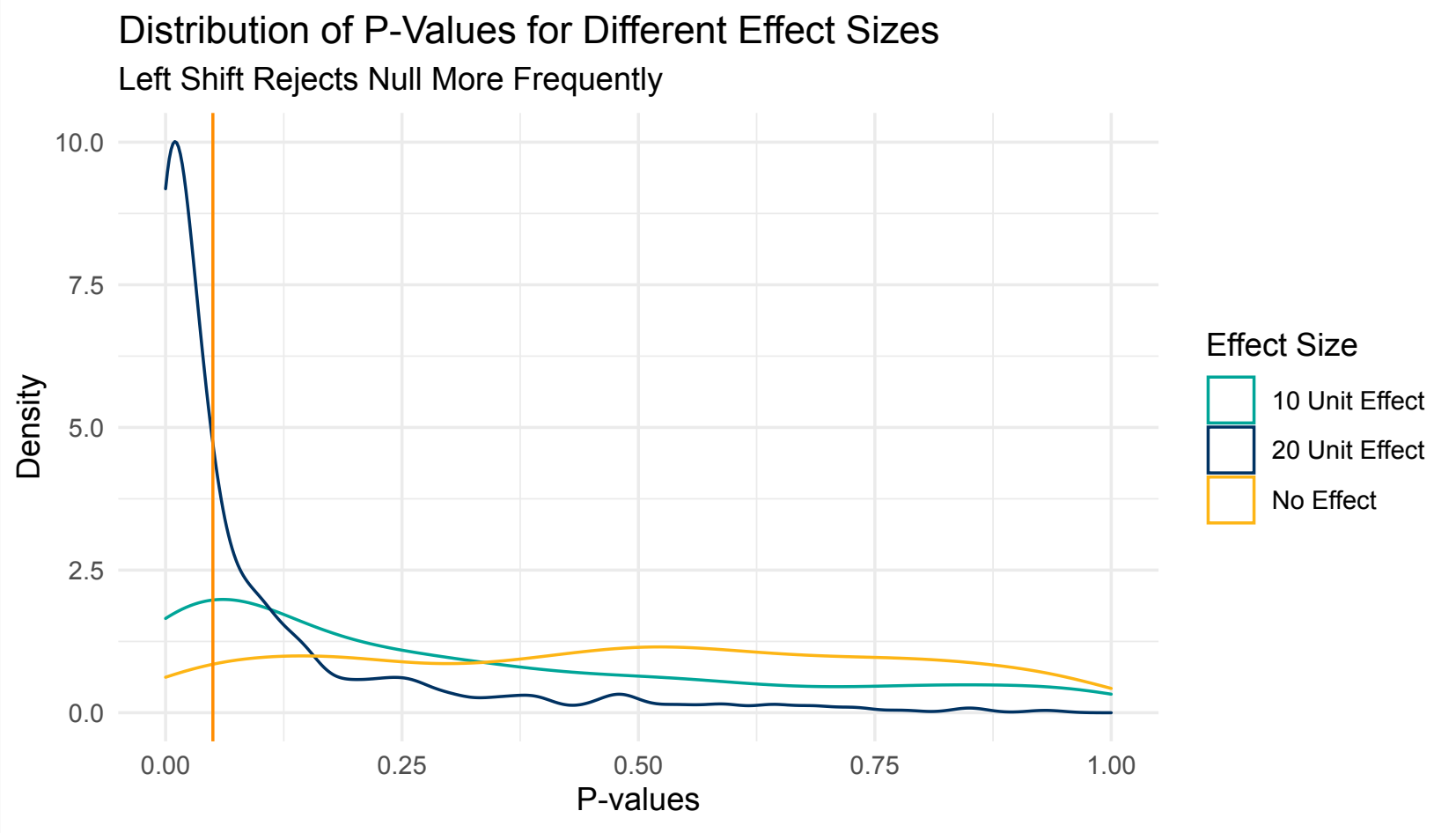
Power for 10 Unit Effect



Power Sim: 0 & 20 Unit Effect

```
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:

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