Simulation-based testing

Part 1

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Packages and set seed

```
library(tidyverse)
library(infer)
```

```
set.seed(0917)
```

The hypothesis testing framework

Parameter vs. statistic

A **parameter** for is the "true" value of interest. We typically estimate the parameter using a **sample statistic** as a point estimate.

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Common population parameters of interest and their corresponding sample statistic:

Quantity	Parameter	Statistic
Mean	μ	$\bar{x}$
Variance	σ^2	s^2
Standard deviation	σ	s
Proportion	p	$\hat{p}$

How can we answer research questions using statistics?

Statistical hypothesis testing is the procedure that assesses evidence provided by the data in favor of or against some claim about the population (often about a population parameter or potential associations).

Motivating example: organ donors

People providing an organ for donation sometimes seek the help of a special medical consultant. These consultants assist the patient in all aspects of the surgery, with the goal of reducing the possibility of complications during the medical procedure and recovery. Patients might choose a consultant based in part on the historical complication rate of the consultant's clients.

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One consultant tried to attract patients by noting that the **average complication rate for liver donor surgeries in the US is about 10%**, but **her clients have only had 3 complications in the 62 liver donor surgeries she has facilitated**. She claims this is strong evidence that her work meaningfully contributes to reducing complications (and therefore she should be hired!).

Data

```
organ_donor %>%
  count(outcome)
```

```
## # A tibble: 2 x 2
##   outcome            n
##   <chr>          <int>
## 1 complication       3
## 2 no complication   59
```

Organ donors: Parameter vs. statistic

Parameter, p : true rate of complication

Statistic, $\hat{p}$: rate of complication in the sample = $\frac{3}{62}$ = 0.048

Correlation vs. causation

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No. The claim is that there is a causal connection, but the data are observational. For example, maybe patients who can afford a medical consultant can afford better medical care, which can also lead to a lower complication rate.

While it is not possible to assess the causal claim, it is still possible to test for an association using these data.

For this question we ask, **how likely is it that the low complication rate observed of $\hat{p}$ = 0.048 be due solely to chance?**

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Complication rate for this consultant is **lower** than the US average of 10%

In statistical hypothesis testing we always first assume that the null hypothesis is true and then see whether we reject or fail to reject this claim.

Hypothesis testing as a court trial

- **Null hypothesis**, H_0: Defendant is innocent
- **Alternative hypothesis**, H_a: Defendant is guilty

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Hypothesis testing as a court trial

- **Null hypothesis**, H_0: Defendant is innocent
- **Alternative hypothesis**, H_a: Defendant is guilty
- **Present the evidence:** Collect data
- **Judge the evidence:** "Could these data plausibly have happened by chance if the null hypothesis were true?"
  - Yes: Fail to reject H_0
  - No: Reject H_0

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1️⃣ Start with two hypotheses about the population: the null hypothesis and the alternative hypothesis.

2️⃣ Choose a (representative) sample, collect data, and analyze the data.

3️⃣ Figure out how likely it is to see data like what we observed, IF the null hypothesis were in fact true (called a **p-value**)

4️⃣ If our data would have been extremely unlikely if the null hypothesis were true, then we reject it in favor of the alternative hypothesis.

Otherwise, we cannot reject the null hypothesis

1 Defining the hypotheses

Remember, the null and alternative hypotheses are defined for **parameters,** not statistics

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1 Defining the hypotheses

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What will our null and alternative hypotheses be for this example?

- H_0: the true proportion of complications among her patients is **equal** to the US population rate
- H_a: the true proportion of complications among her patients is **lower** than the US population rate

Expressed in symbols:

- $H_0 : p = 0.10$
- $H_a : p < 0.10$

2 Collecting and summarizing data

With these two hypotheses, we now take our sample and summarize the data.

The choice of summary statistic calculated depends on the type of data. In our example, we use the sample proportion

$$\hat{p} = 3/62 \approx 0.048$$

3 Assessing the evidence observed

Next, we calculate the probability of getting data like ours, *or more extreme*, if H_0 were in fact actually true.

This is a conditional probability: "given that H_0 is true, $p = 0.1$, what would the the probability of observing $\hat{p} = 3/62$ or less?"

This probability is known as the **p-value**.

Calculate the p-value using simulation

Simulating the null distribution

Let's return to the organ transplant scenario.

Since $H_0 : p = 0.10$, we need to simulate a distribution for $\hat{p}$ under the null hypothesis such that the probability of complication for each patient is 0.10 for 62 patients.

This null distribution for $\hat{p}$ represents the distribution of the observed proportions we might expect, if the null hypothesis were true.

When sampling from the null distribution, what is the expected proportion of complications?

Data

```
glimpse(organ_donor)
```

```
## Rows: 62
## Columns: 1
## $ outcome <chr> "complication", "complication", "complication", "no compli
```

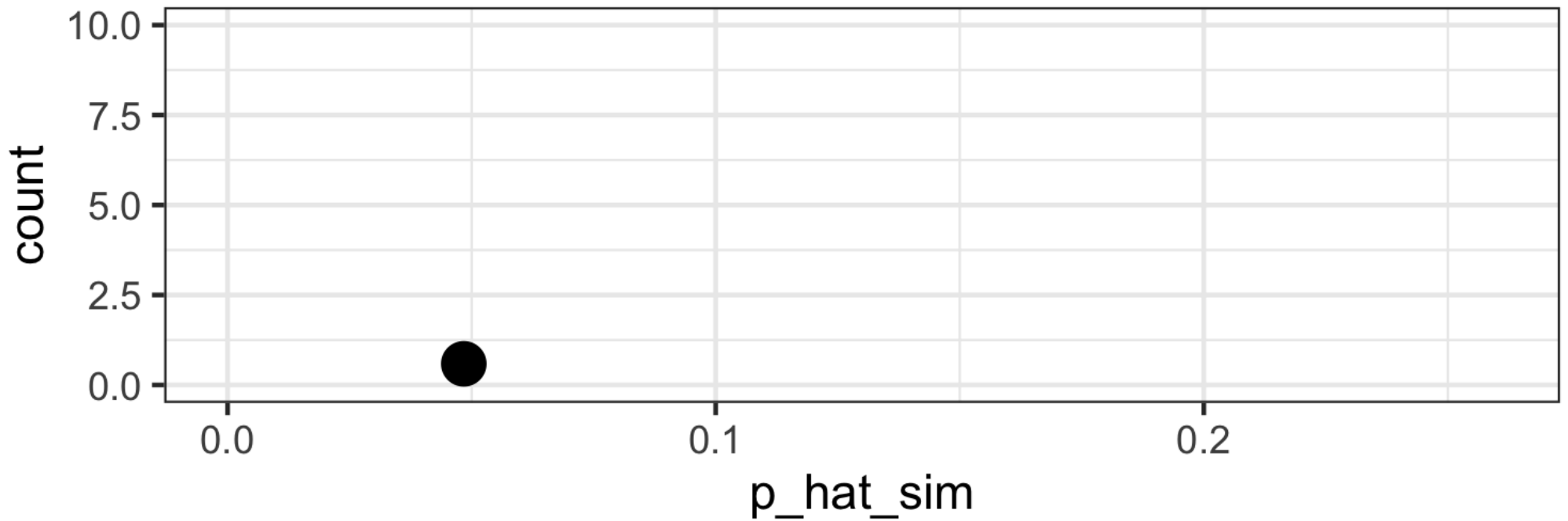
```
organ_donor %>%
  count(outcome)
```

```
## # A tibble: 2 x 2
##   outcome              n
##   <chr>            <int>
## 1 complication         3
## 2 no complication     59
```

Simulation #1

```
## sim1
##    complication no complication
##               3               59

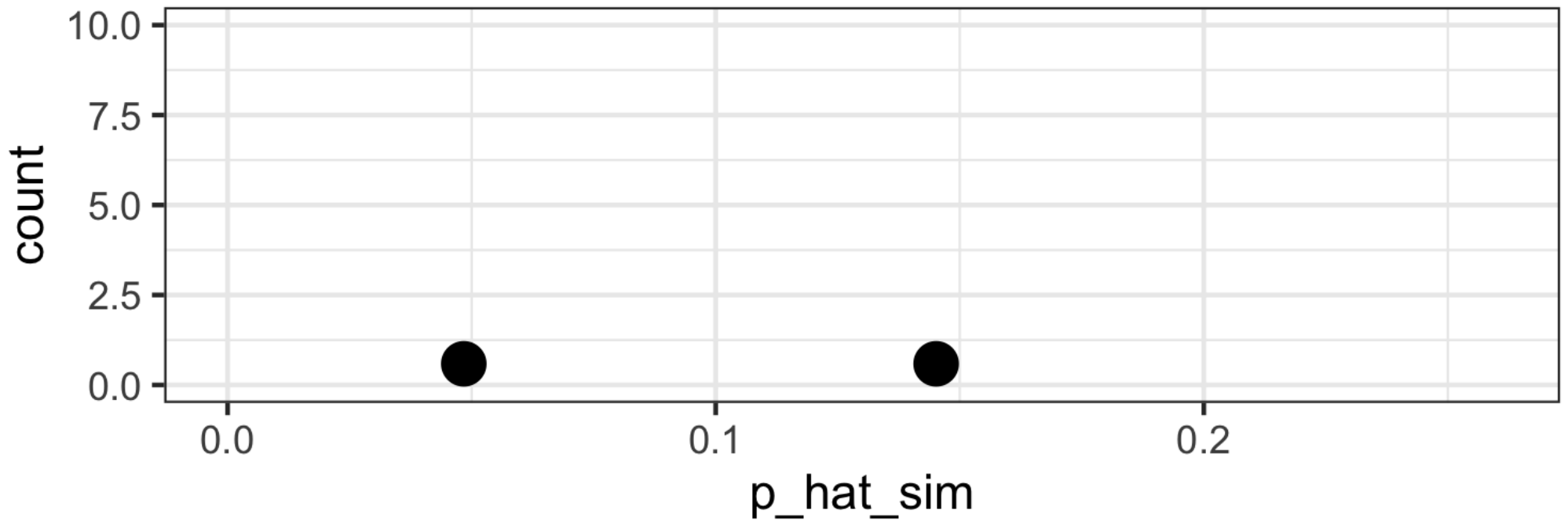
## [1] 0.0483871
```



Simulation #2

```
## sim2
##    complication no complication
##                9               53

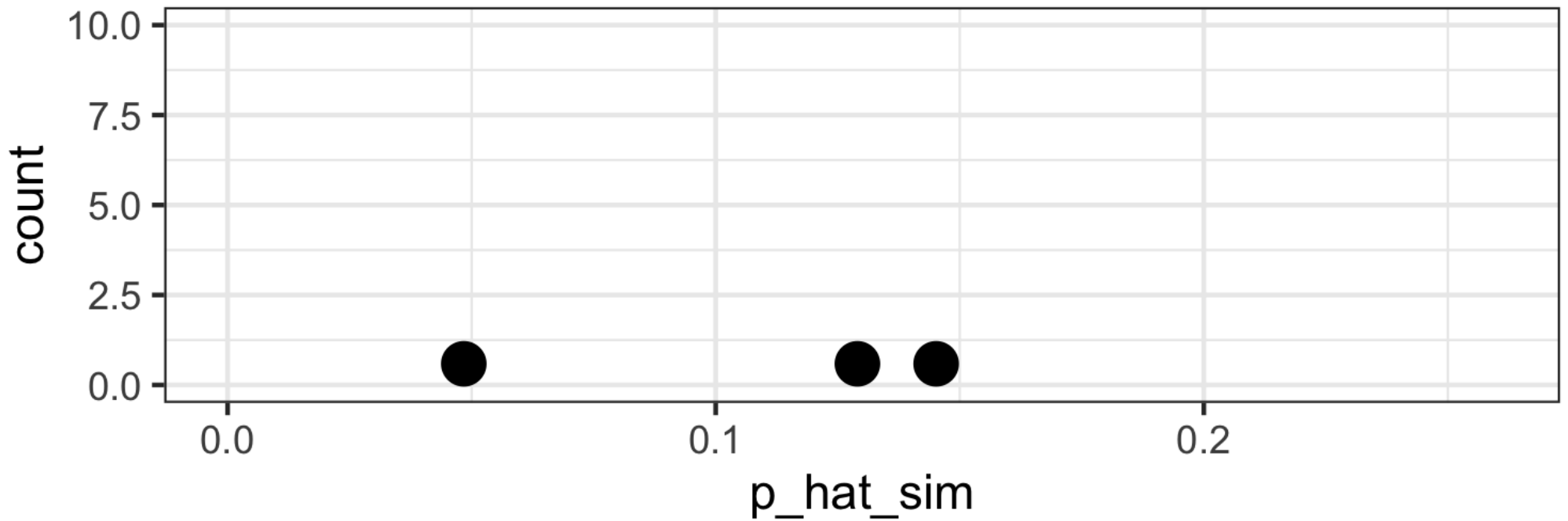
## [1] 0.1451613
```



Simulation #3

```
## sim3
##    complication no complication
##                 8               54

## [1] 0.1290323
```



This is getting boring...

We need a way to automate this process!

Using infer to generate the null distribution

```
null_dist <- organ_donor %>%
  specify(response = outcome, success = "complication") %>%
  hypothesize(null = "point",
              p = c("complication" = 0.10, "no complication" = 0.90)
              ) %>%
  generate(reps = 100, type = "simulate") %>%
  calculate(stat = "prop")
```

Specify

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null_dist <- organ_donor %>%
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```

- **response**: **outcome** in the **organ_donor** data frame
- **success**: **"complication"**, the level of outcome we're interested in studying

Hypothesize

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- **`null`**: Since we're testing the point null hypothesis that $H_0 : p = 0.10$, we choose **`"point"`**
- Next, we provide the probability of "success" and "failure"
  - **`"complication" = 0.10, "no complication" = 0.90`**

Generate

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null_dist <- organ_donor %>%
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```

- **`reps`**: We will generate 100 repetitions here
- **`type`**: Choose **`"simulate"`** for testing a point null
  - Choose **`bootstrap`** for estimation
  - Choose **`permute`** for testing independence

Calculate

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null_dist <- organ_donor %>%
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```

- Calculate a sample statistic. Here, the sample proportion.
  - **`stat = "prop"`**

Store simulated null distribution

```
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```

```
## # A tibble: 100 x 2
##    replicate  stat
##        <dbl> <dbl>
##  1         1 0.048
##  2         2 0.097
##  3         3 0.081
##  4         4 0.081
##  5         5 0.161
##  6         6 0.081
##  7         7 0.081
```

Visualizing the null distribution

What would you expect the center of the null distribution to be?

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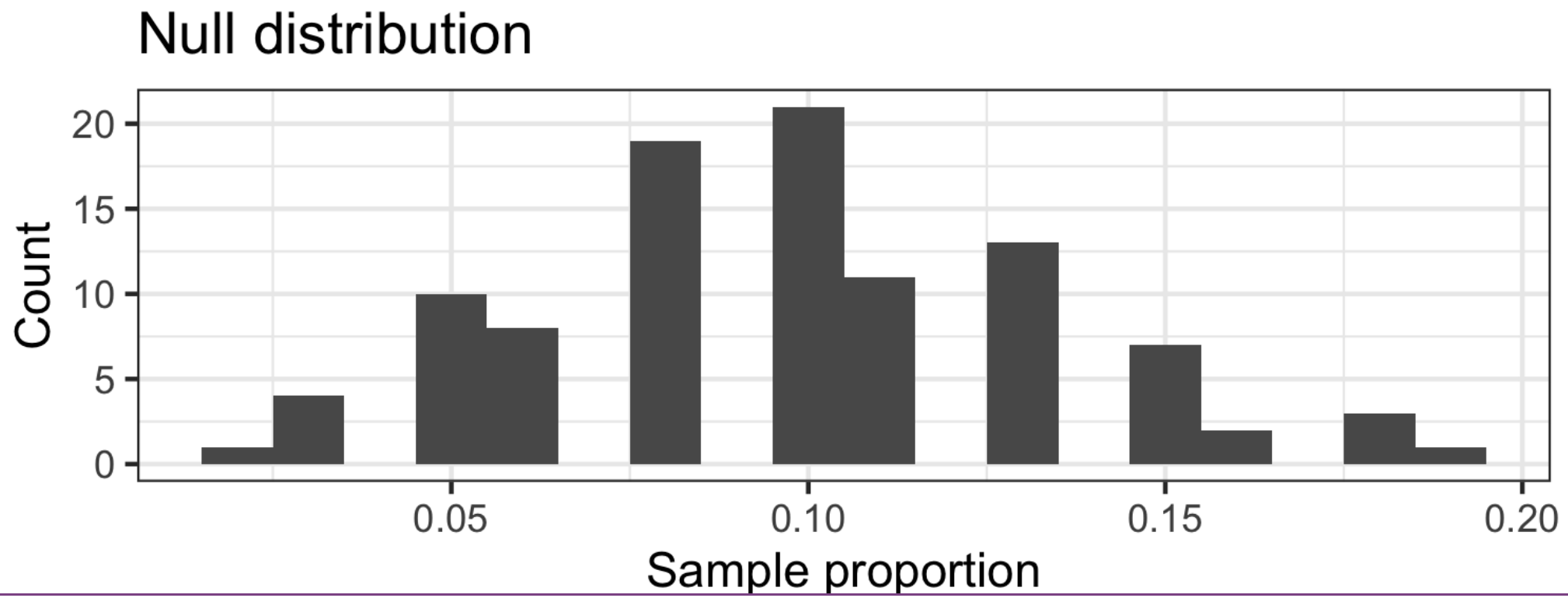
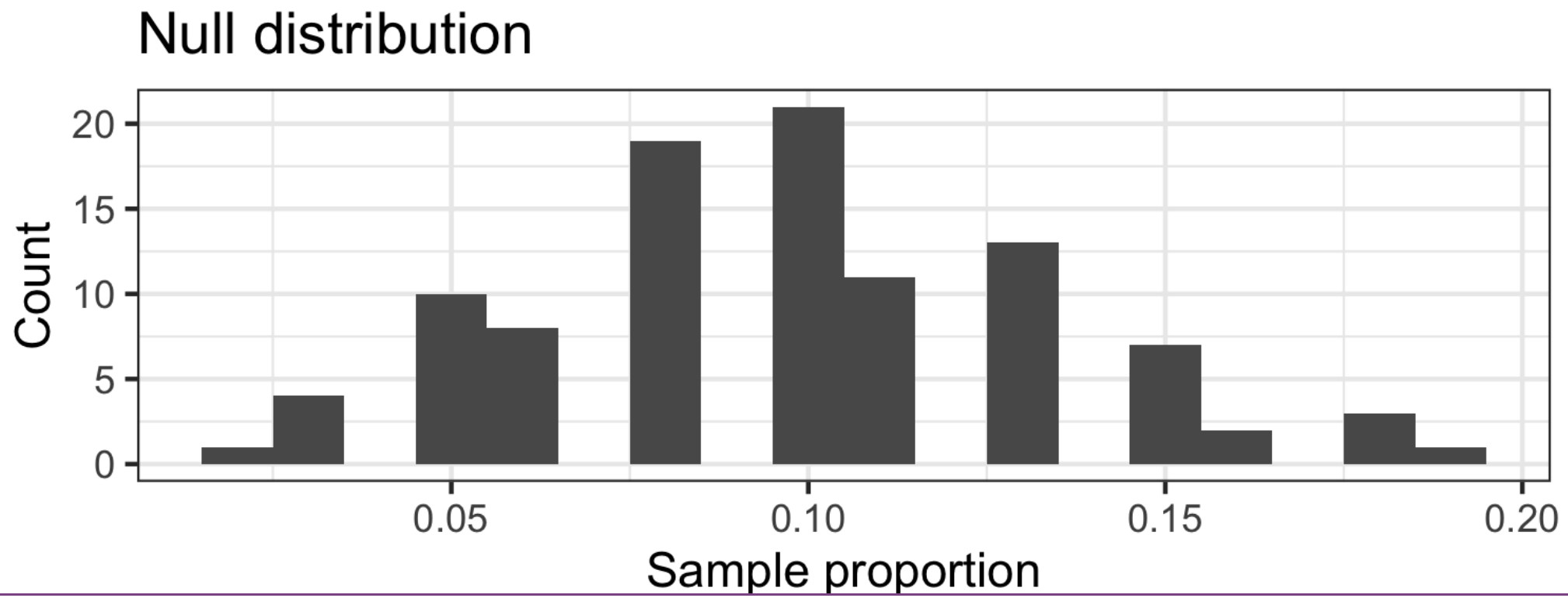


Calculating the p-value, visually

What is the p-value (just eyeball it)?



Calculating the p-value, directly

```
null_dist %>%
  filter(stat <= (3/62)) %>%
  summarise(p_value = n()/nrow(null_dist))
```

```
## # A tibble: 1 x 1
##   p_value
##     <dbl>
## 1    0.15
```

4 Making a conclusion

We reject the null hypothesis if the p-value is probability is small enough, i.e. it is very unlikely to observe our data or more extreme if H_0 were actually true.

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What is "small enough"? We often consider a threshold (the **significance level** or α-level) defined *prior* to conducting the analysis.

Significance level

We often use 5% as the cutoff for whether the p-value is low enough that the data are unlikely to have come from the null model.

- If p-value < α, reject H_0 in favor of H_a:
  - The data provide convincing evidence against the null hypothesis
- If p-value $\geq \alpha$, fail to reject H_0 in favor of H_a
  - The data do not provide convincing evidence against the null hypothesis.

What if p-value $\geq \alpha$?

If p-value $\geq \alpha$ we fail to reject H_0.

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Importantly, we never "accept" the null hypothesis.

When we fail to reject the null hypothesis, we are stating that there is **insufficient evidence** to conclude that it is false. This could be due to any number of reasons:

- There truly is no effect
- There truly is an effect (and we happened to get unlucky with our sample or didn't have enough data to tell that there was one)

Organ donor example

The p-value 0.15 is greater than the significance level, $\alpha = 0.05$, so we **fail to reject the null hypothesis**.

The data **do not** provide sufficient evidence that the true complication rate for this consultant's clients is less than the US rate, $p = 0.1$.