SciencesPo
DEPARTMENT OF ECONOMICS

ScPoEconometrics

Confidence Intervals and Hypothesis Testing

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Quick "Quiz" on Last Week's Material

1. From your ***computer*** 👉 connect to ***www.wooclap.com/SCPOSAMP***

   OR

2. From your ***phone*** 👉 flash QR code below

Today - Deeper dive into ***statistical inference*** [1]

- *Confidence intervals*: providing plausible ***range*** of values
- *Hypothesis testing*: comparing statistics between groups

[1]: This lecture is based on the wonderful confidence interval and hypothesis testing chapters of ModernDive

Back to reality (there goes gravity 😜)

- In real life we only get to take ***one*** sample from the population (not *1000*!).
- Also, we obviously don't know the true population parameter, that's what we are interested in!
- So what on earth was all of this good for? Fun only?! 😦

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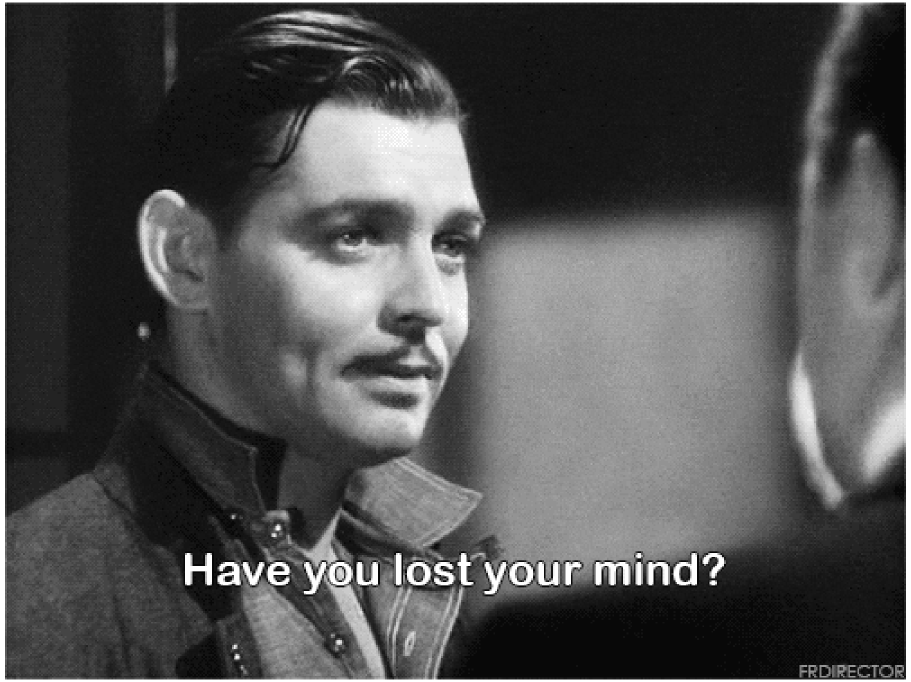

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- Even unobserved, we ***know*** that the sampling distribution does exist, and even better, we know how it behaves!
- Let's see what we can do with this...

Confidence Intervals

From Point Estimates to Confidence Intervals

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- We know that this ***sample statistic*** differs from the ***true population parameter*** due to ***sampling variation***.
- Rather than a point estimate, we could give a ***range of plausible values*** for the population parameter.
- This is precisely what a ***confidence interval*** (CI) provides.

Constructing Confidence Intervals

There are several approaches to constructing confidence intervals:

1. *Theory*: use mathematical formulas (***Central Limit Theorem***) to derive the sampling distribution of our point estimate under certain conditions $\rightarrow$ ***what `R` does under the hood!***

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We'll focus on simulation to give you the intuition and come back to the maths approach next week.

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In practice, you ***don't*** need to compute your confidence intervals using *bootstrap*, `R` uses statistical theory to do it for you.

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- How could we study the effect of sampling variation with a single sample? 👉 ***bootstrap resampling with replacement***!
- Let's start by drawing one random sample of size $n = 50$ from our bowl.

```
library(tidyverse)
bowl <- read.csv("https://www.dropbox.com/s/qpjsk0rfgc0gx80/pasta.csv?dl=1")

my_sample = bowl %>%
  mutate(color = ifelse(color == "green","green","non-green")) %>%
  rep_sample_n(size = 50) %>%
  ungroup() %>%
  select(pasta_ID, color)
```

```
head(my_sample,3)
```

```
## # A tibble: 3 x 2
##   pasta_ID color
##      <int> <fct>
## 1        4 non-green
## 2       41 non-green
## 3       79 non-green
```

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```

```
p_hat = mean(my_sample$color == "green")
p_hat
```

```
## [1] 0.46
```

The proportion of green pasta in this sample is: $\hat{p} = 0.46$.

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3. Repeat steps 1 and 2 49 times, i.e. ***until the new sample is of the same size as the original sample***.

4. Compute the proportion of green pasta in the bootstrap sample.

This procedure is called ***resampling with replacement***:

- *resampling*: drawing repeated samples from a sample.
- *with replacement*: each time the drawn pasta is put back in the sample.

Resampling our Pasta Sample

Here is one bootstrap sample:

```
one_bootstrap = my_sample %>%
  rep_sample_n(size = 50, replace = TRUE) %>%
  arrange(pasta_ID)

head(one_bootstrap, 8)
```

```
## # A tibble: 8 x 3
## # Groups:   replicate [1]
##   replicate pasta_ID color
##       <int>    <int> <fct>
## 1         1        4 non-green
## 2         1       41 non-green
## 3         1       41 non-green
## 4         1       79 non-green
## 5         1       79 non-green
## 6         1      103 non-green
## 7         1      103 non-green
## 8         1      103 non-green
```

```
nrow(one_bootstrap)
```

```
## [1] 50
```

Resampling our Pasta Sample

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## 6         1      103 non-green
## 7         1      103 non-green
## 8         1      103 non-green
```

```
nrow(one_bootstrap)
```

```
## [1] 50
```

Several pasta have been drawn multiple times. How come?

What's the proportion of green pasta in this bootstrap sample?

```
mean(one_bootstrap$color == "green")
```

```
## [1] 0.4
```

The proportion is different than that in our sample! This is due to resampling ***with replacement***.

What if we repeated this resampling procedure many times? Would the proportion be the same each time?

Obtaining the Bootstrap Distribution

- Let's repeat the resampling procedure 1,000 times: there will be 1,000 bootstrap samples and 1,000 bootstrap estimates!

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We use the `infer` package to ease the bootstrapping procedure.

```
library(infer)

bootstrap_distrib = my_sample %>%
  # specify the variable and level of interest
  specify(response = color, success = "green") %>%
  # generate 1000 bootstrap samples
  generate(reps = 1000, type = "bootstrap") %>%
  # calculate the proportion of green pasta for each
  calculate(stat = "prop")
```

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  # calculate the proportion of green pasta for each
  calculate(stat = "prop")
```

Here are the first 6 rows:

```
head(bootstrap_distrib)
```

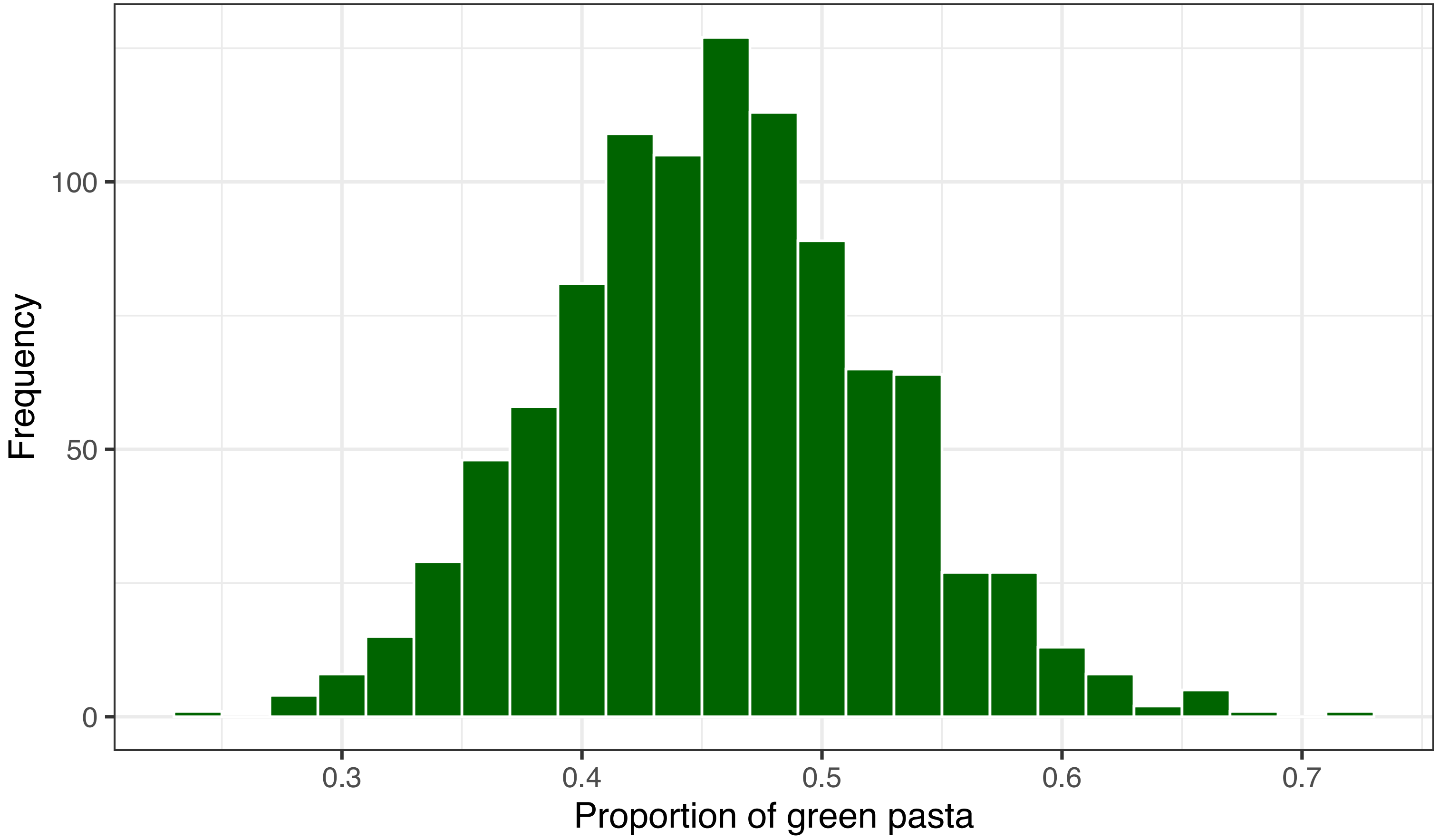
```
## Response: color (factor)
## # A tibble: 6 x 2
##   replicate  stat
##       <int> <dbl>
## 1         1  0.44
## 2         2  0.36
## 3         3  0.46
## 4         4  0.46
## 5         5  0.52
## 6         6  0.52
```

```
nrow(bootstrap_distrib)
```

```
## [1] 1000
```

Let's visualize this sampling variation!

Bootstrap Distribution



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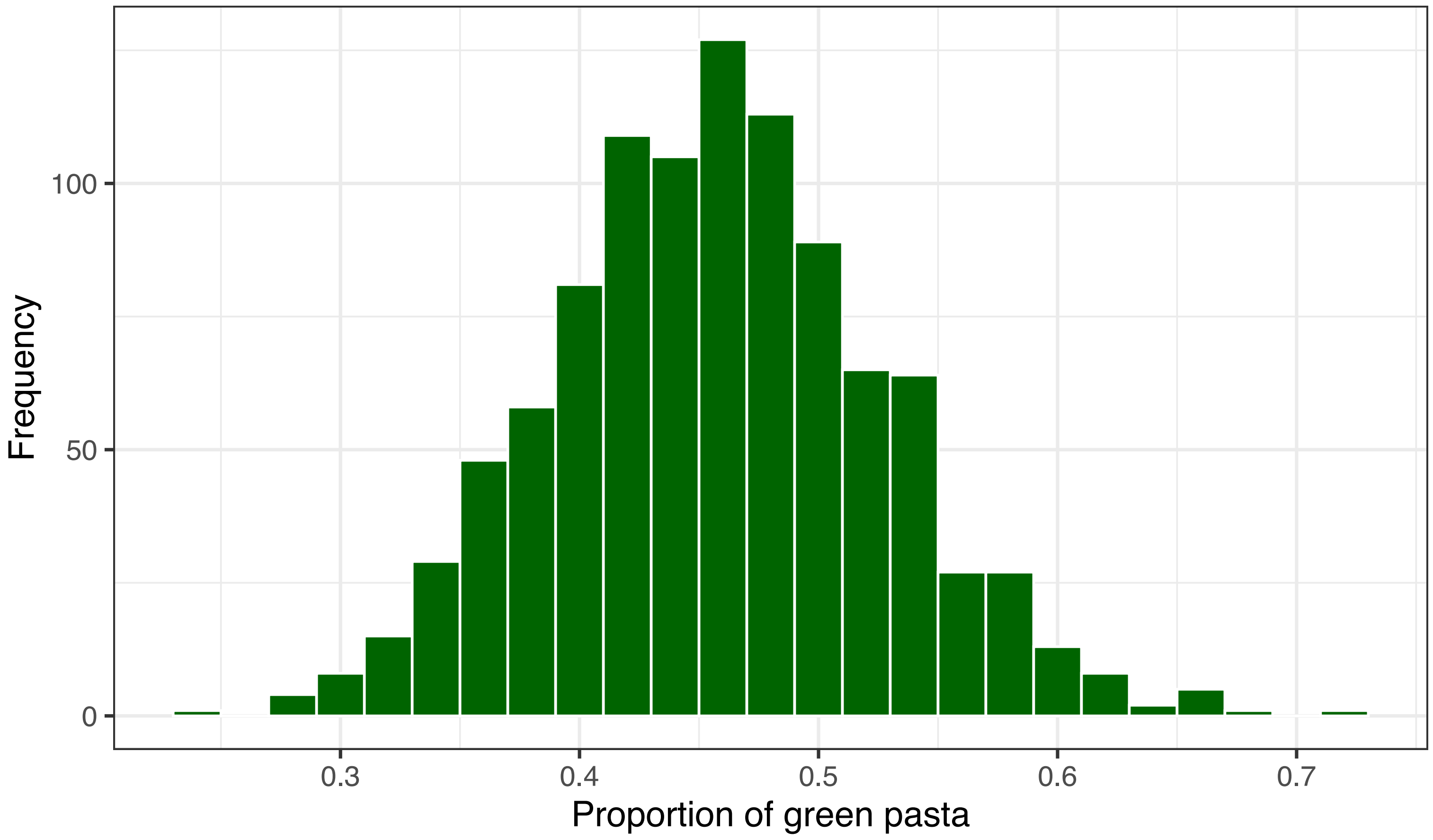
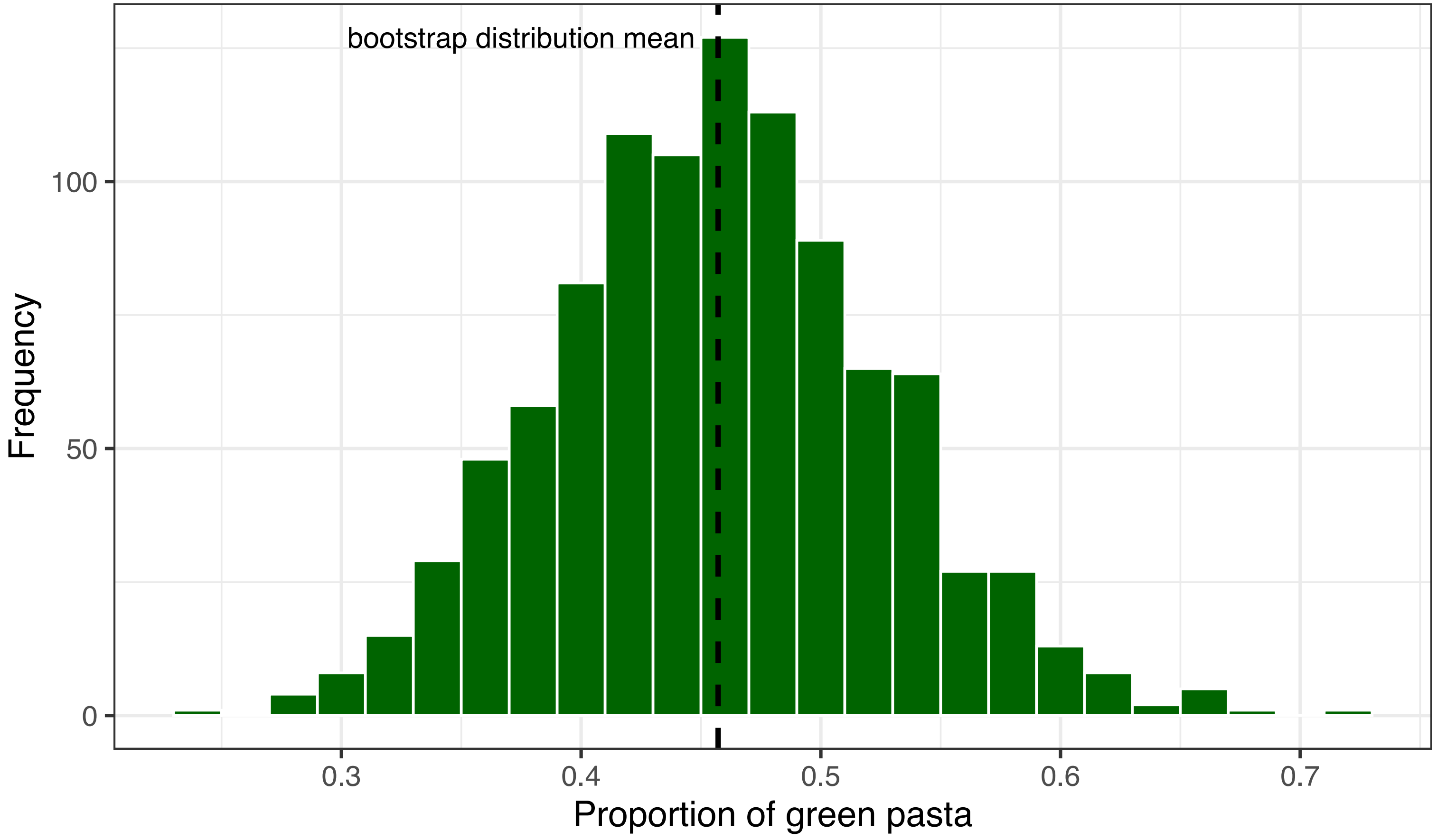


The ***bootstrap distribution*** is an approximation of the ***sampling distribution***.

Bootstrap Distribution with Mean



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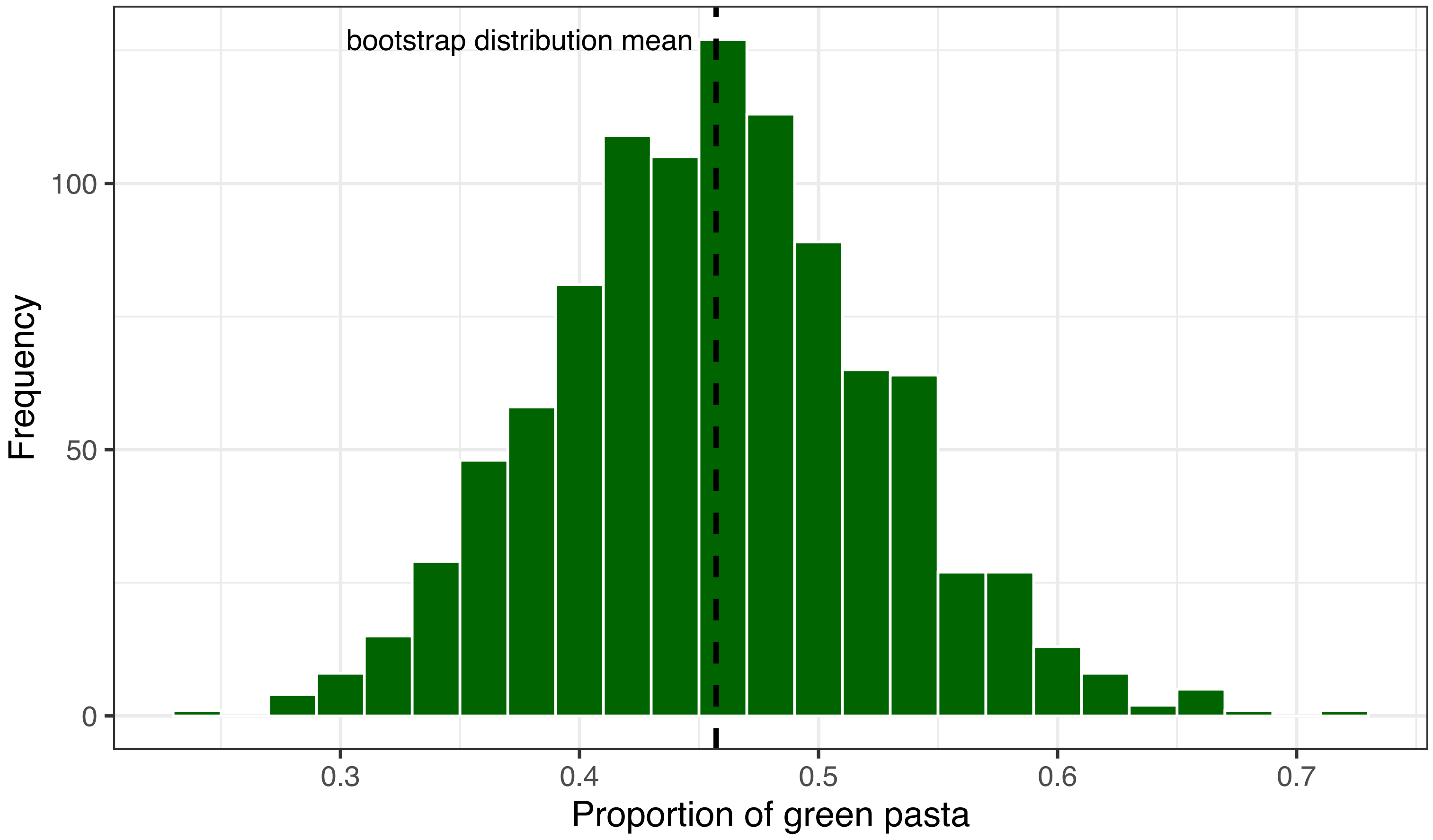
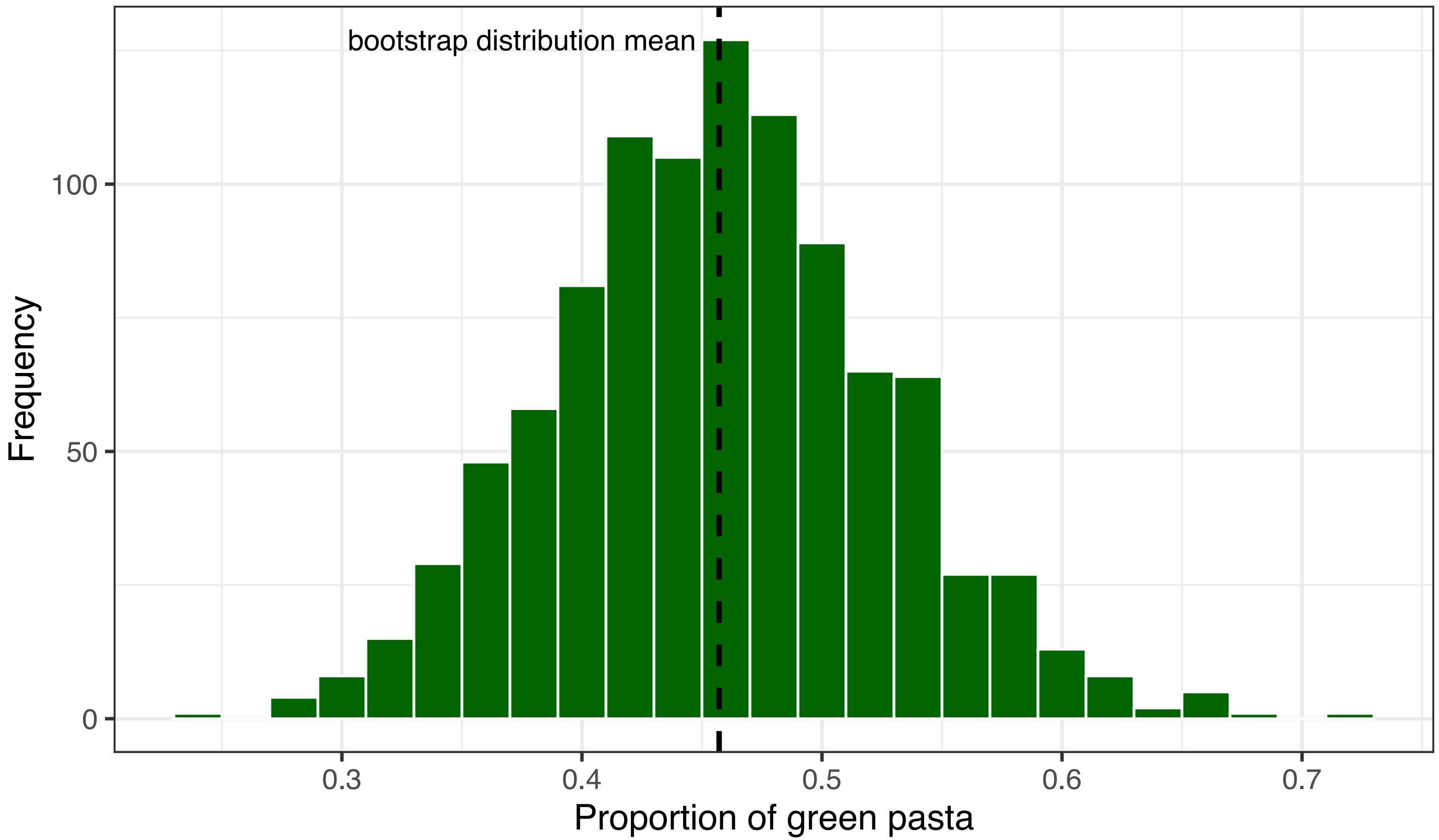


The ***bootstrap distribution*** mean is very close to the original sample proportion.

Bootstrap Distribution with Mean



Let's use this ***bootstrap distribution*** to construct confidence intervals!

Understanding Confidence Intervals

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  - *point estimate*: fishing with a spear.

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- The *confidence interval*: from the previous bootstrap distribution, ***where do most proportions lie?***
- Method for confidence interval construction: ***percentile method***.
- Requires specifying a ***confidence level***: 90%, 95%, and 99% are the most common.

Percentile Method: 95% Confidence Interval

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- For that, we compute the 2.5% and 97.5% percentile:

```
quantile(bootstrap_distrib$stat,0.025)
```

```
## 2.5%
## 0.32
```

```
quantile(bootstrap_distrib$stat,0.975)
```

```
## 97.5%
##   0.6
```

- Therefore the 95% confidence interval is $[0.32; 0.6]$.

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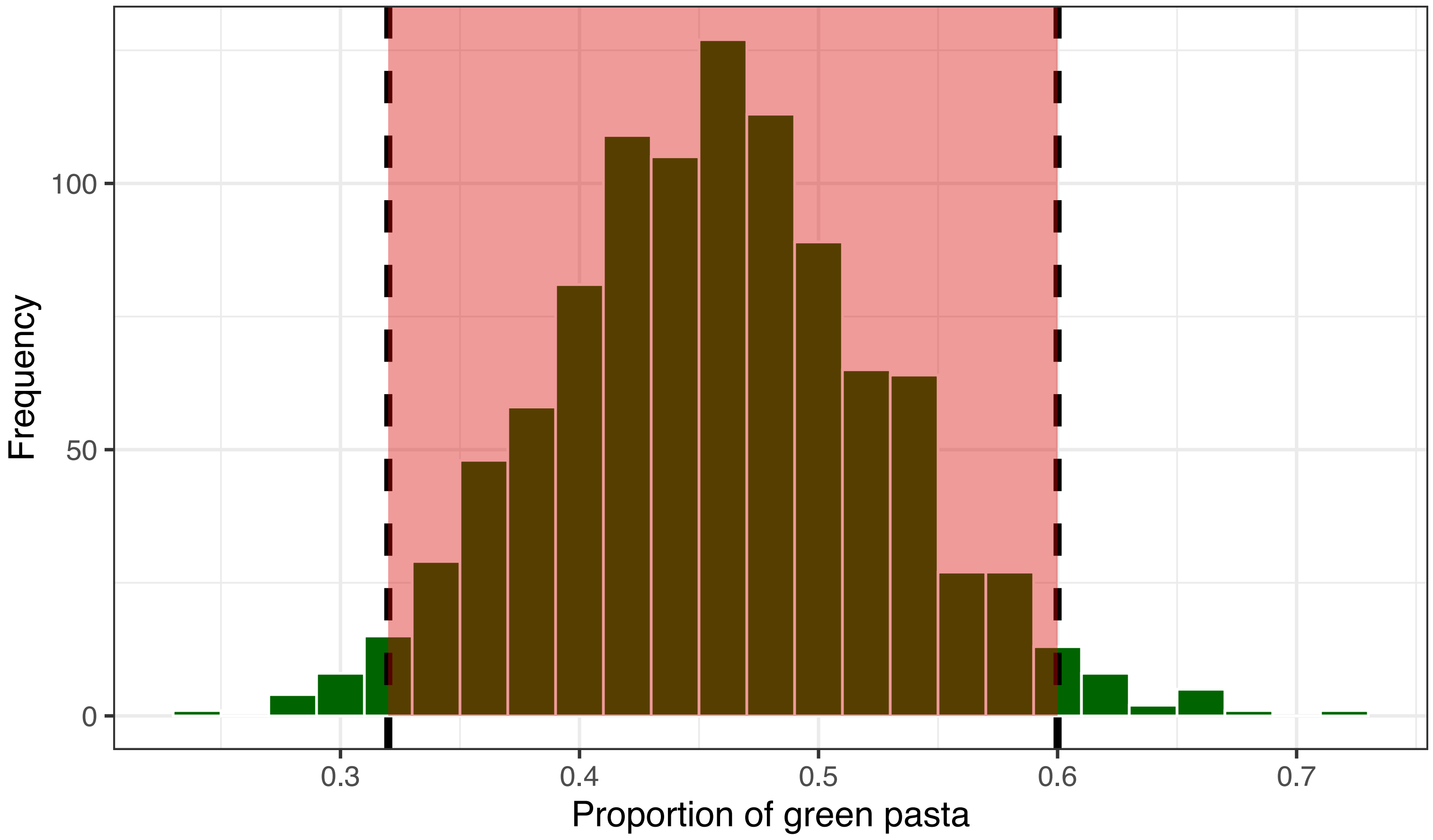
- Therefore the 95% confidence interval is $[0.32; 0.6]$.
- It is a ***range*** of values.
- Let's see this confidence interval on the sampling distribution.

Percentile Method: 95% Confidence Interval Visually



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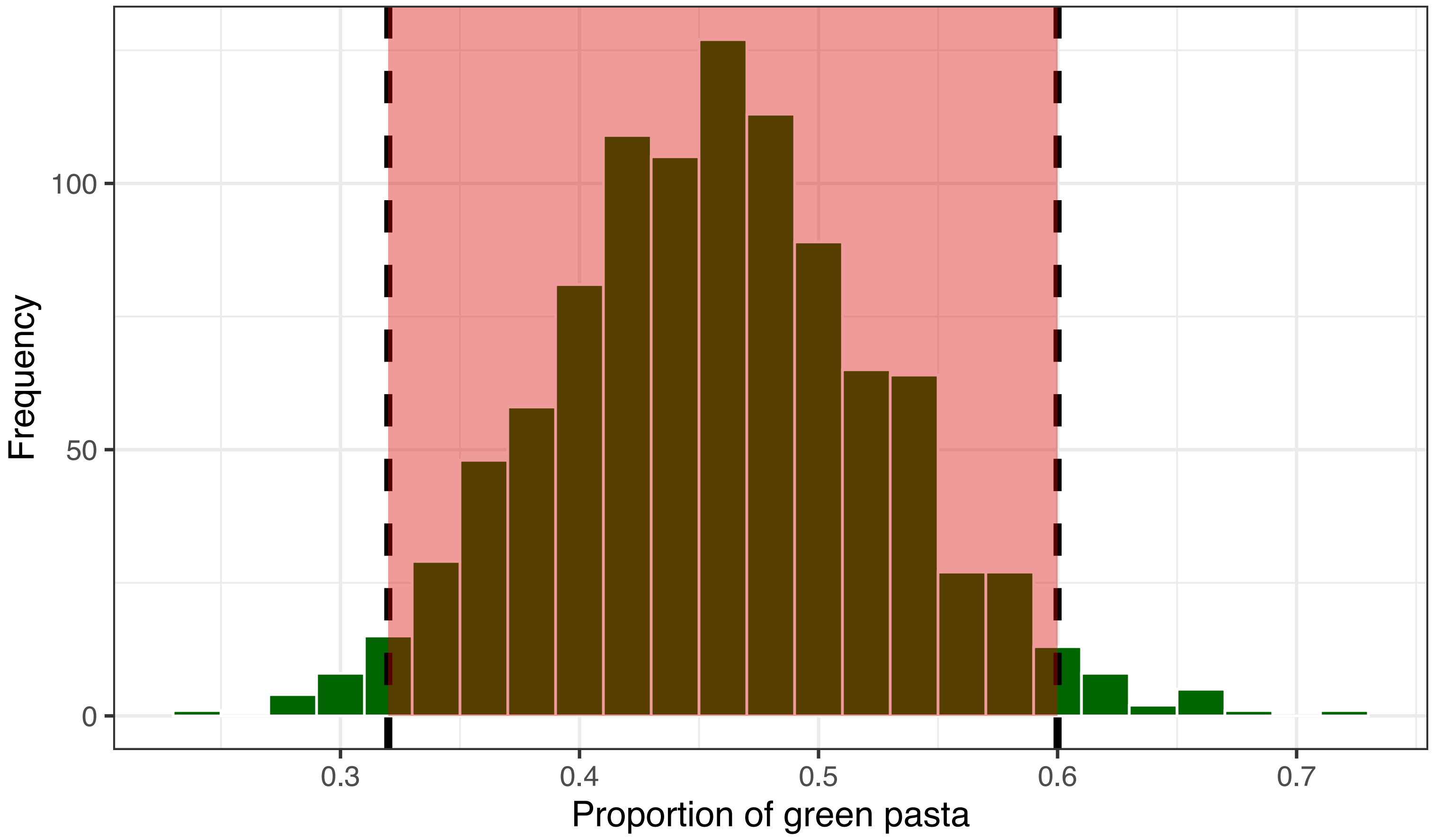

Does the interval contain the true population proportion?

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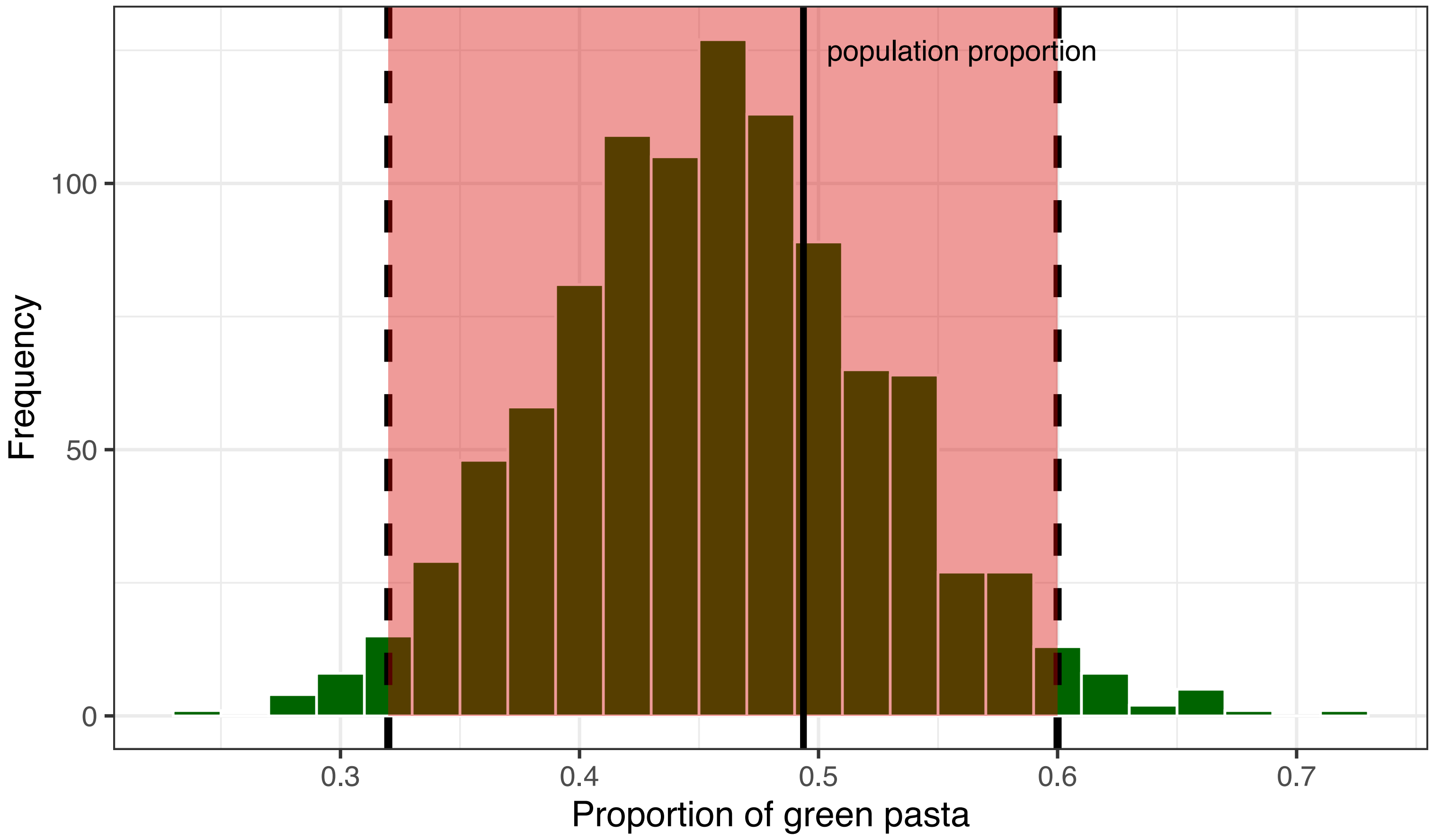

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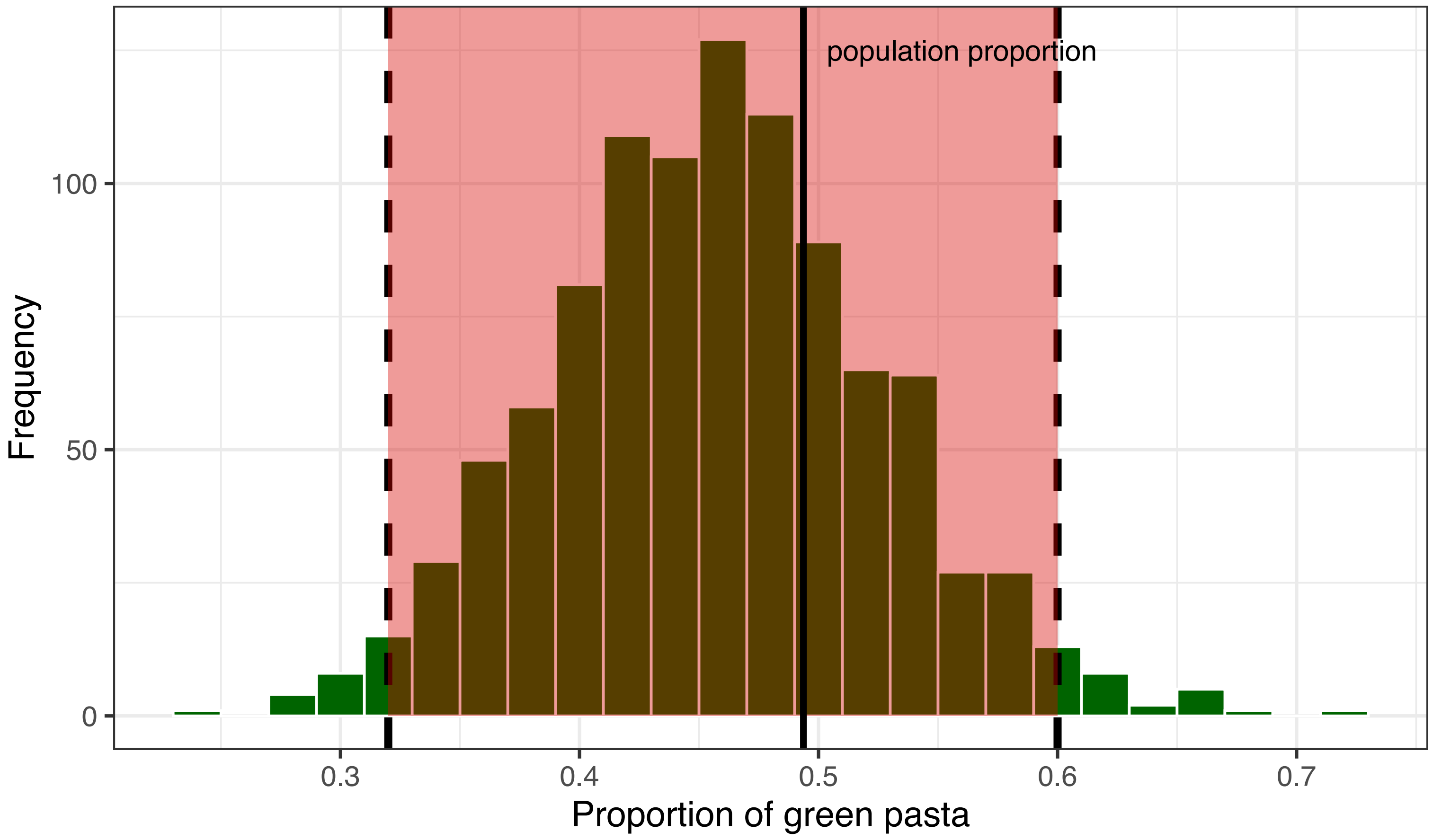

True population parameter is indeed in our 95% interval! Will it always be?

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How many confidence intervals contain the true parameter? Why?

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> *Precise interpretation:* If we repeated our sampling procedure ***a large number of times***, we ***expect about 95%*** of the resulting confidence intervals to capture the value of the population parameter.

In other words, 95% of the time, the 95% confidence interval will contain the true population parameter.

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Questions:

- How does the width of the confidence interval change as the ***confidence level*** increases?
- How does the width of the confidence interval change as the ***sample size*** increases?

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Impact of confidence level: the greater the confidence level, the wider the confidence intervals.

- *Intuition*: a greater confidence level means the confidence interval needs to contain the true population parameter more often, and thus needs to be wider to ensure this.

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Impact of sample size: the greater the sample size, the narrower the confidence intervals.

- *Inutuition*: a larger sample size leads to less sampling variation and therefore a narrower boostrap distribution, which in turn leads to thiner confidence intervals.

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- What if we want to ***compare*** a sample statistic for two groups?
    - *Example*: differences in average wages between men and women. Are the observed differences ***significant***?

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- What if we want to ***compare*** a sample statistic for two groups?
  - *Example*: differences in average wages between men and women. Are the observed differences ***significant***?
- These comparisons are the realm of ***hypothesis testing***.
- Just like confidence intervals, hypothesis tests are used to make claims about a population based on information from a sample.
- However, we'll see that the framework for making such inferences is slightly different.

Hypothesis Testing

Is There Gender Discrimination In Promotions?

- We will use data from an article published in the *Journal of Applied Psychology* in 1974 which investigated whether female employees at banks were discriminated against.
- 48 (male) supervisors were given *identical* candidate CVs, differing only with respect to the first name, which was male or female.
  - Each CV was "*in the form of a memorandum requesting a decision on the promotion of an employee to the position of branch manager.*"

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- The data from the experiment are provided in the `promotions` dataset from the `moderndive` package.

```
library(moderndive)
head(promotions)
```

```
## # A tibble: 6 x 3
##      id decision gender
##   <int> <fct>    <fct>
## 1     1 promoted male
## 2     2 promoted male
## 3     3 promoted male
## 4     4 promoted male
## 5     5 promoted male
## 6     6 promoted male
```

Evidence of Discrimination?

How many men and women were offered a promotion (and not)?

```
promotions %>%
  group_by(gender, decision) %>%
  tally() %>%
  mutate(percentage = 100 * n / sum(n))
```

```
## # A tibble: 4 x 4
## # Groups:   gender [2]
##   gender decision     n percentage
##   <fct>  <fct>    <int>      <dbl>
## 1 male   not          3       12.5
## 2 male   promoted    21       87.5
## 3 female not         10       41.7
## 4 female promoted    14       58.3
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There is a ***29.2 percentage points difference*** in promotions between men and women!

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Question: Is this difference ***conclusive evidence*** of differences in promotion rates between men and women? Could such a difference have been observed ***by chance***?

Imposing A Hypothetical World: No Gender Discrimination

- Suppose we lived in a world without gender discrimination: the promotion decision would be completely ***independent*** from gender.
- Let's randomly reassign `gender` to each row and see how this affects the result.

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- Suppose we lived in a world without gender discrimination: the promotion decision would be completely ***independent*** from gender.

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```
promotions_shuffled %>%
  group_by(gender, decision) %>%
  tally() %>%
  mutate(percentage = 100 * n / sum(n))
```

```
## # A tibble: 4 x 4
## # Groups:   gender [2]
##   gender decision     n percentage
##   <fct>  <fct>    <int>      <dbl>
## 1 male   not          6       25
## 2 male   promoted    18       75
## 3 female not          7       29.2
## 4 female promoted    17       70.8
```

The difference is much lower: ***4.2 percentage points***!

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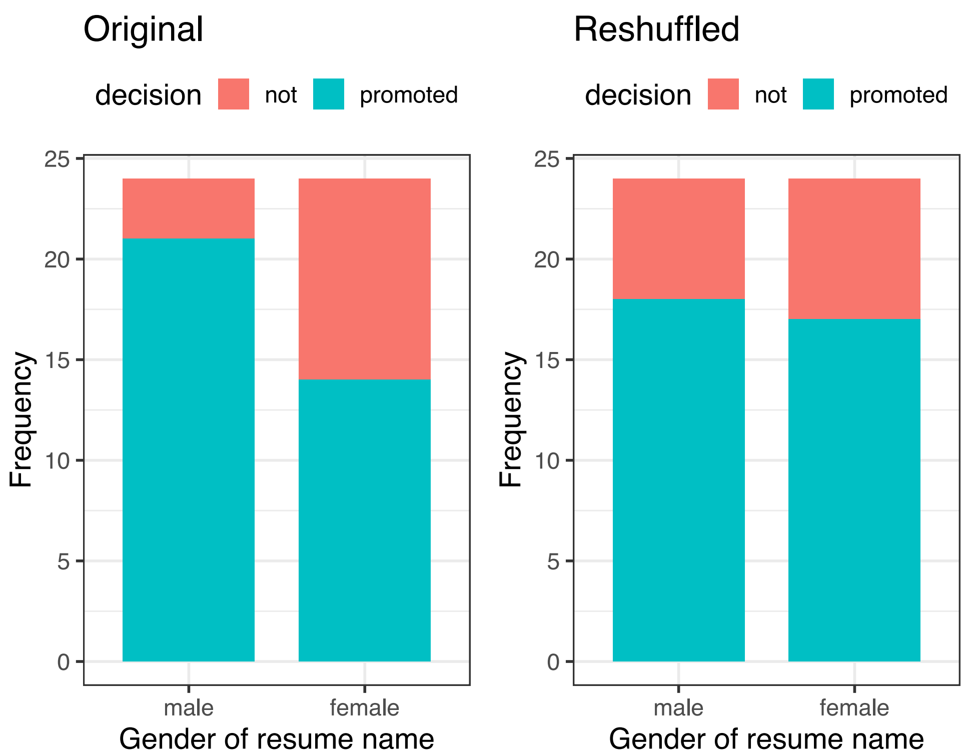

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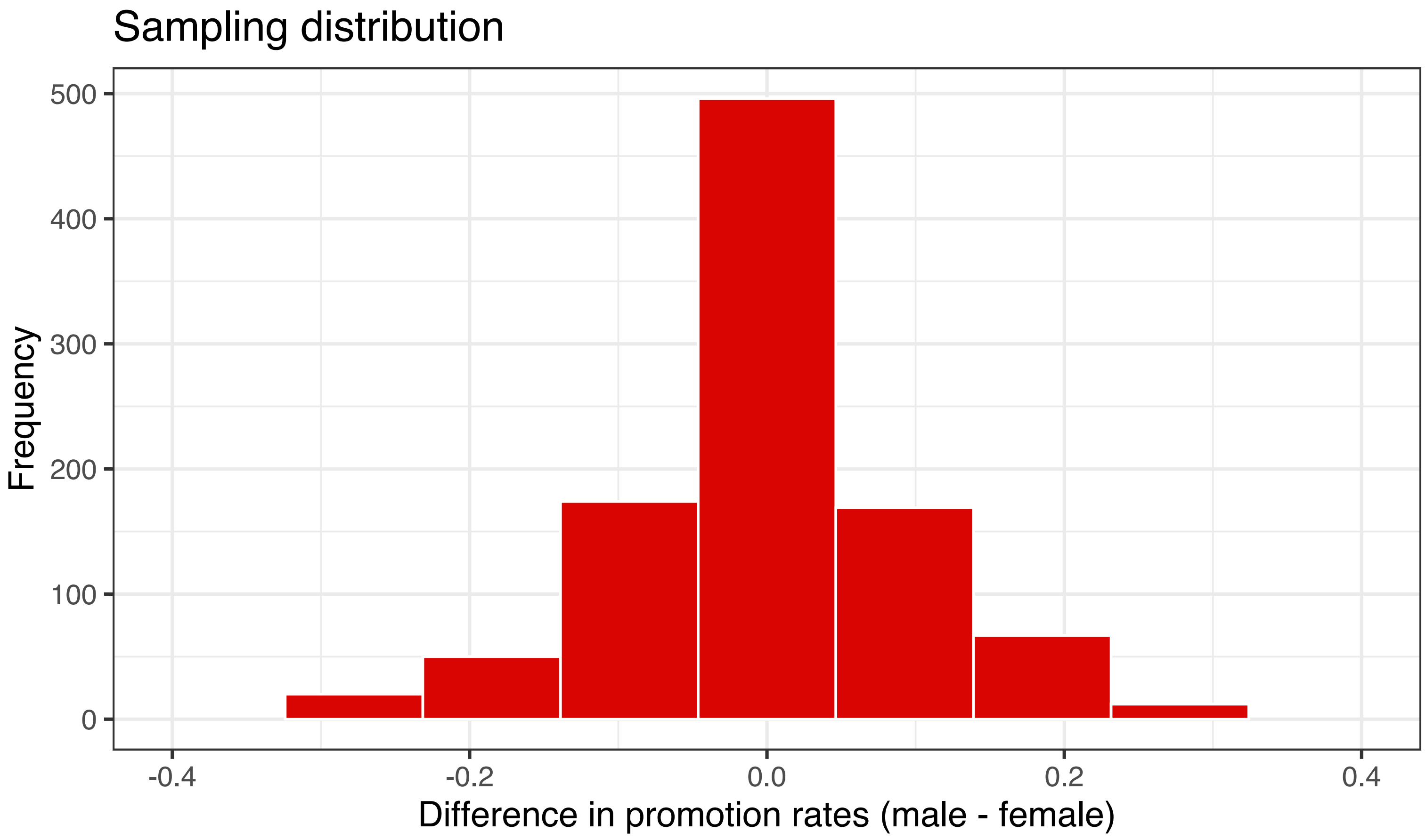
- We need to know about the whole sampling distribution under the *no discrimination* hypothesis.
- How? Just by redoing the reshuffling a large number of times, and computing the difference each time.

Sampling Distribution with 1000 Reshufflings



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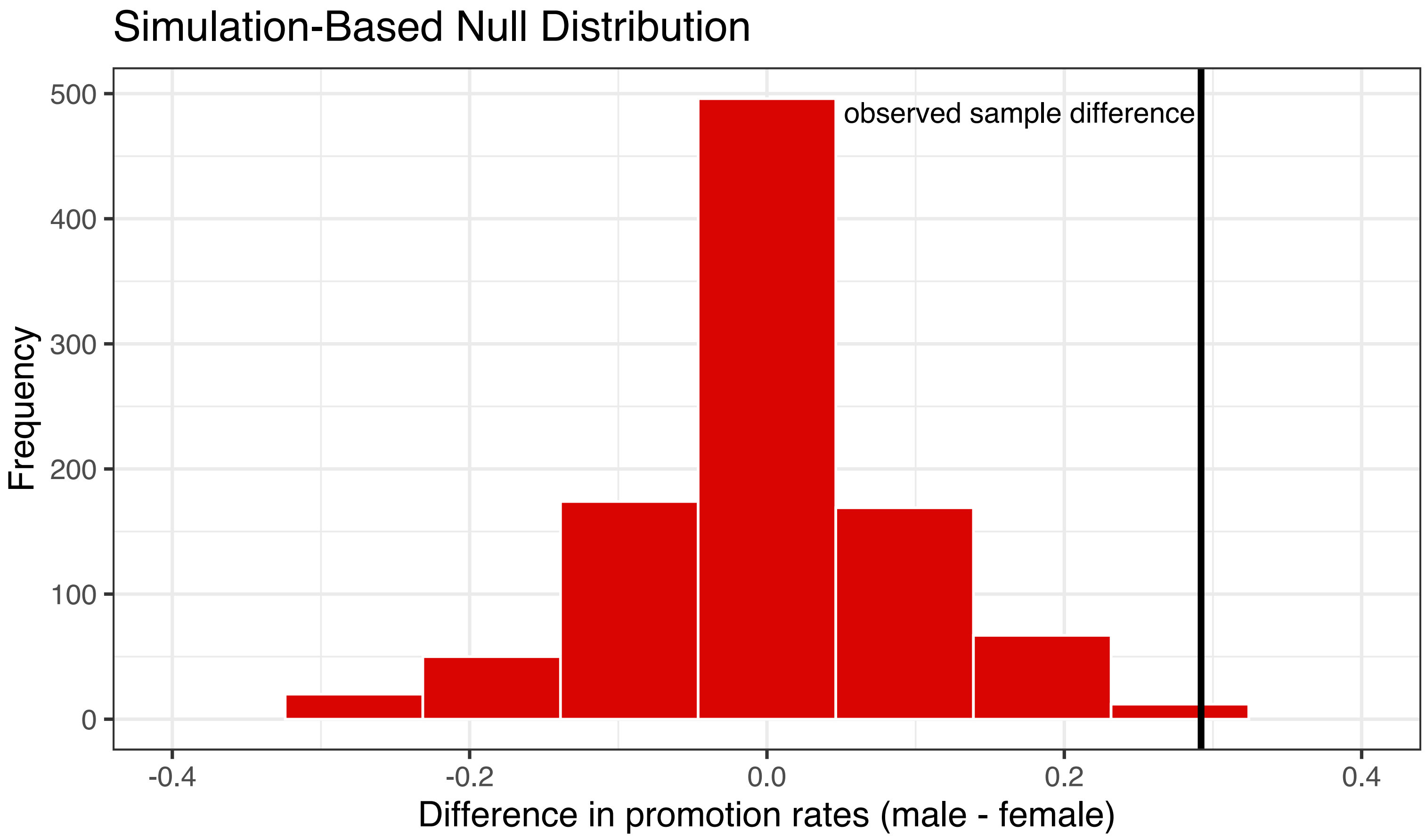

How *likely* is it to observe a 0.292 difference in a world with no discrimination?

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- The question is how likely the observed difference in promotion rates is to occur in a hypothetical universe with no discrimination.
- We concluded ***rather not***, i.e. we tended to ***reject*** the no discrimination hypothesis.
- Let's introduce the formal framework of hypothesis testing now.

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- Here, we considered a *one-sided* alternative, stating that $p_m > p_f$, i.e. women are discriminated against.
- The *two-sided* formulation is just $H_A : p_m - p_f \neq 0$.

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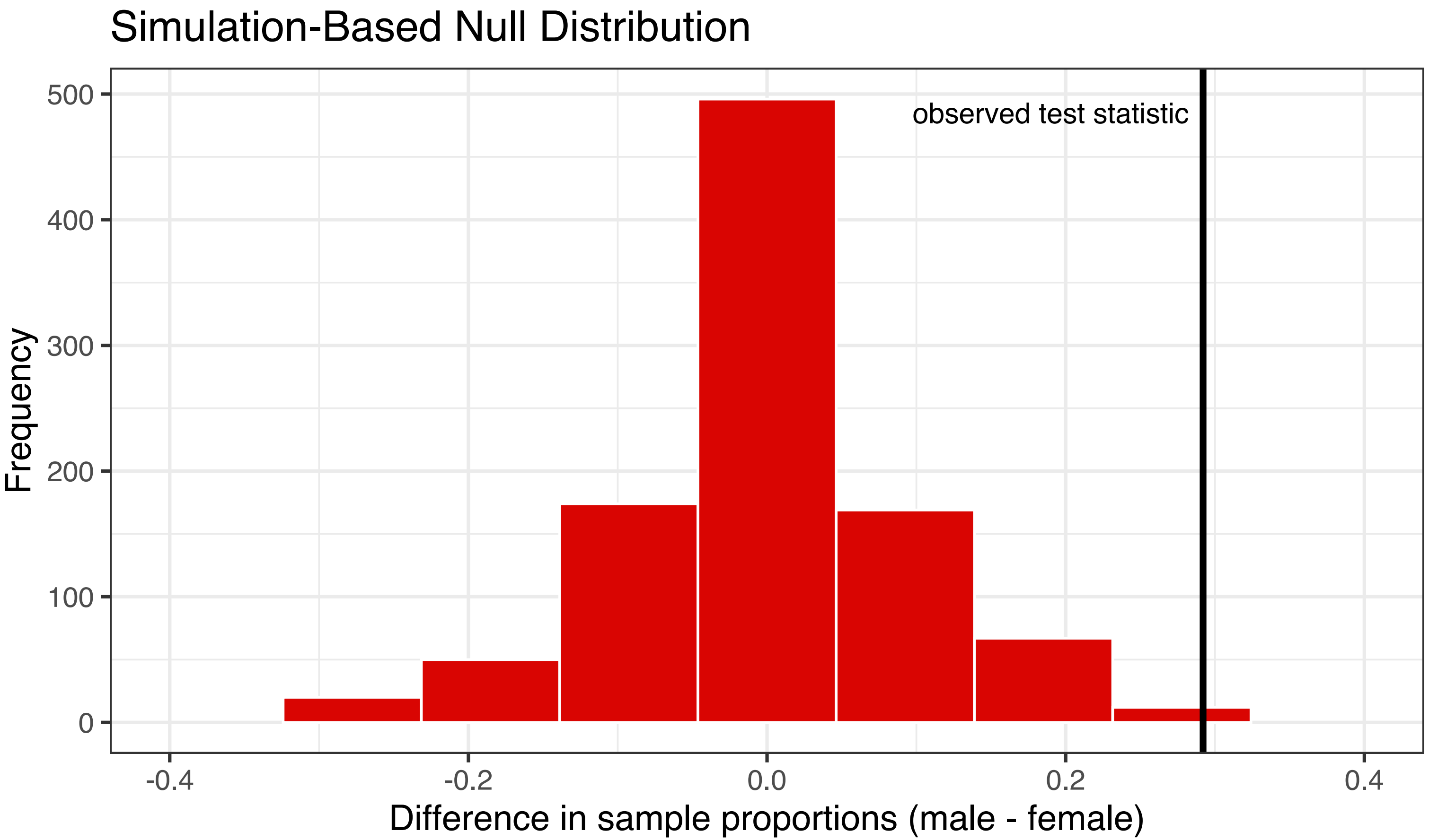
  - That's the distribution we have seen just before.

Null Distribution



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- When do we decide to ***reject*** H_0 or not?

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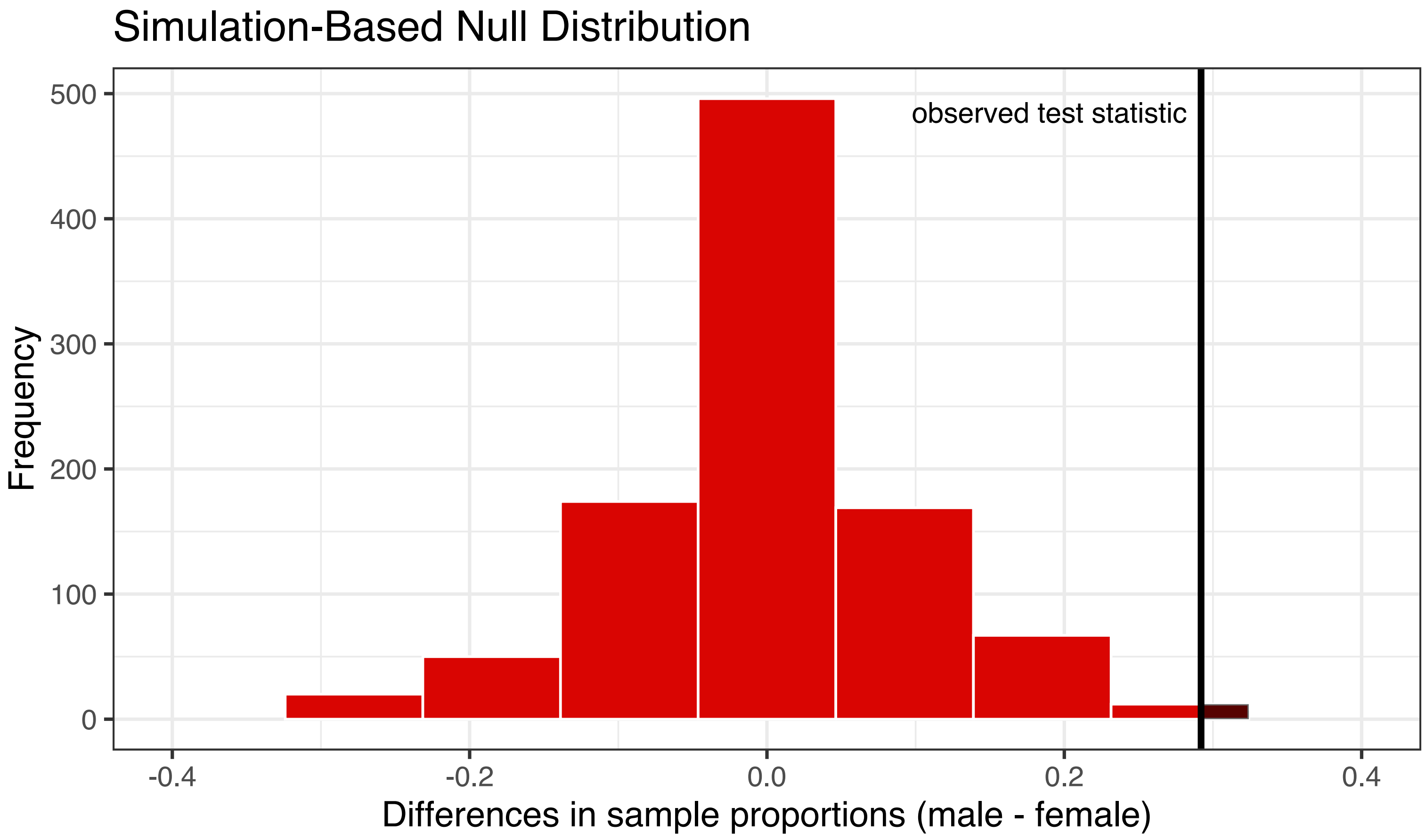
- Let's illustrate how it works in our example.

Visualizing the P-value



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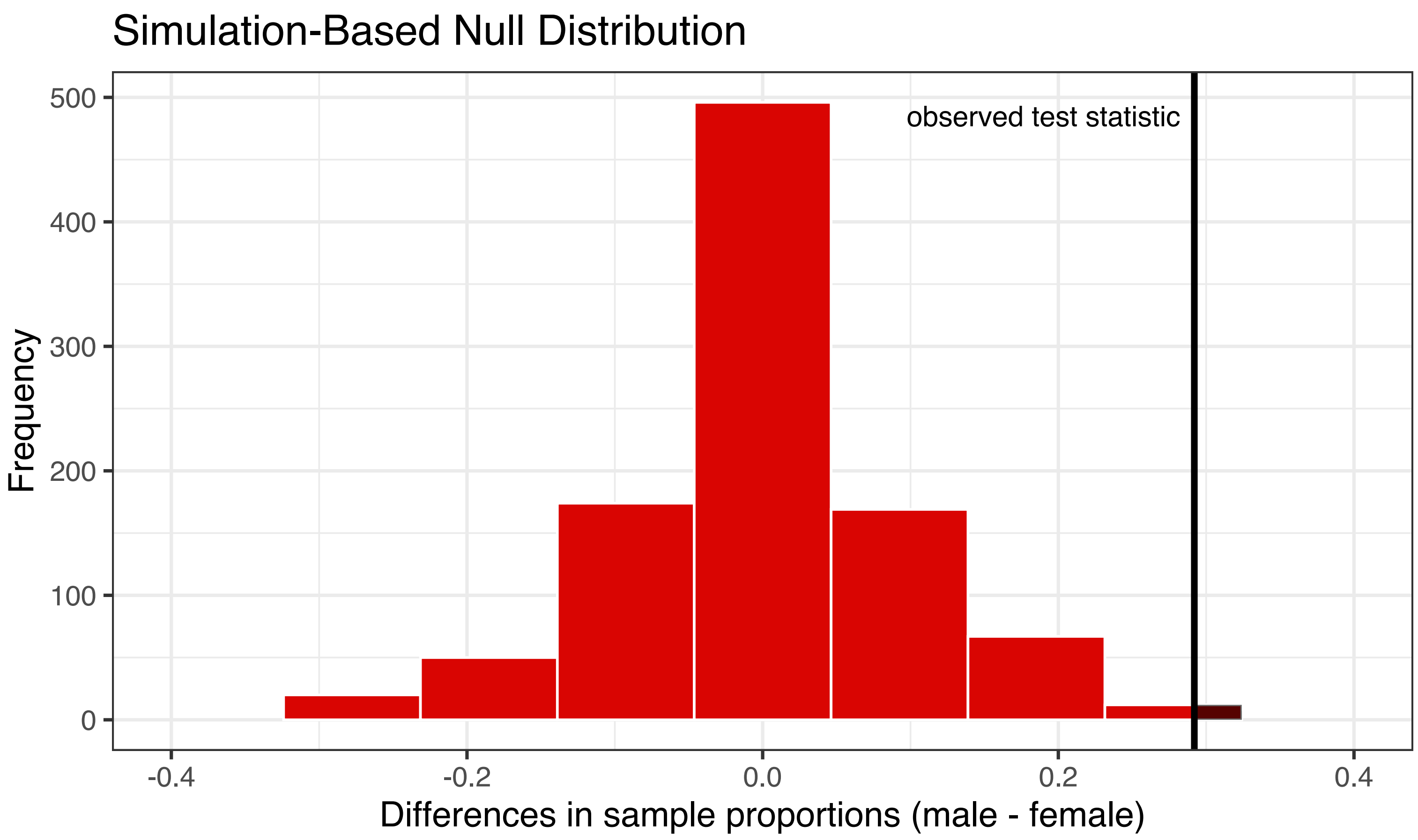

The shaded area correponds to the p-value!

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- So, we can reject H_0, i.e. the absence of discrimination, at the 5% significance level.
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- ***Question***: Suppose we had set $\alpha = 0.01 = 1\%$, would we have rejected the absence of discrimination at this level?

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- A 29%p difference may be *unlikely* under H_0, but that **doesn't mean it's *impossible* to occur**.
  - In fact, such a difference (or higher) would occur (approximately) in 0.007% of cases.
- So, it may happen that we sometimes reject H_0, when in fact it was true.
  - Setting 5% significance level, you make sure it won't happen more than 5% of the time.

Testing Errors

In hypothesis testing, there are ***two types of errors***:

	H0 true	HA true
Verdict		
Fail to reject H0	Correct	Type II error
Reject H0	Type I error	Correct

Type I error: reject the null hypothesis when in fact it was true. ***false positive***

Type II error: don't reject the null hypothesis when in fact it was false. ***false negative***

- In practice, we choose the frequency of a Type I error by setting α and try to minimize the type II error.

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- ***Question***: Is the estimated effect statistically significantly different from some value z?
- The answer in the next episode of *Introduction to Econometrics with R*! 🐵

On the way to causality

☑ How to manage data? Read it, tidy it, visualise it!

☑ How to summarise relationships between variables? Simple and multiple linear regression, non-linear regressions, interactions...

☑ What is causality?

☑ What if we don't observe an entire population? Sampling!

🚧 **Are our findings just due to randomness?** Confidence intervals and hypothesis testing...

❌ How to find exogeneity in practice?

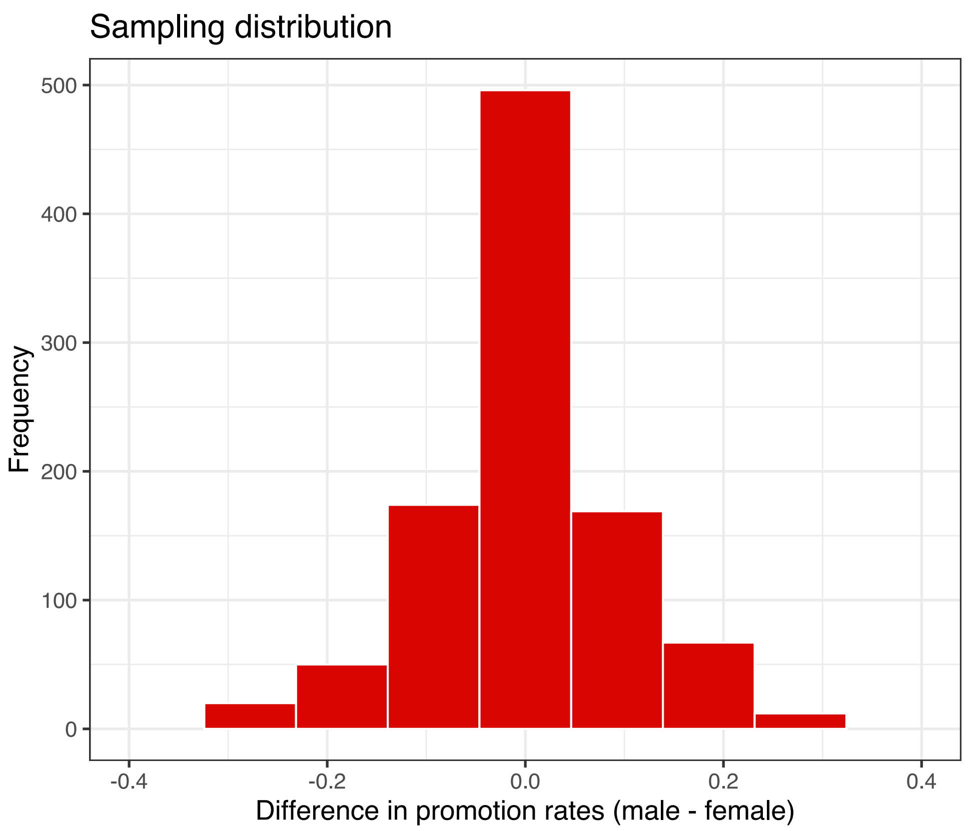
THANKS

To the amazing moderndive team!

Appendix: code to generate the null distribution

```
null_distribution <- promotions %>%
  # takes formula, defines success
  specify(formula = decision ~ gender,
          success = "promoted") %>%
  # decisions are independent of gender
  hypothesize(null = "independence") %>%
  # generate 1000 reshufflings of data
  generate(reps = 1000, type = "permute") %>%
  # compute p_m - p_f from each reshuffle
  calculate(stat = "diff in props",
            order = c("male", "female"))

visualize(null_distribution,
          bins = 10,
          fill = "#d90502") +
  labs(title = "Sampling distribution",
       x = "Difference in promotion rates (male - fema
       y = "Frequency") +
  xlim(-0.4, 0.4) +
  theme_bw(base_size = 14)
```



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