

Hypothesis Testing II

Prof. Wells

STA 209, 4/3/23

Outline

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- Use P-values to quantify the strength of evidence against the null hypothesis
- Investigate significance level as means of making decisions
- Discuss decision errors and statistical power

Section 1

Hypothesis Testing Review

Framework for Hypothesis Testing

Hypothesis Testing represents a type of scientific experiment, and so should follow the general scientific method.

- 1 Present research question
- 2 Identify hypotheses
- 3 Obtain data
- 4 Calculate relevant statistics
- 5 Compute likelihood of observing statistic under original hypothesis
- 6 Determine statistical significance and make conclusion on research question

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 - H_0 : The probability of heads is 50%, or $p = 0.5$.
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 - H_a : The probability of heads is greater than 50%, or $p > 0.5$.
- The alternate hypothesis in a **two-sided hypothesis test** proposes that the population parameter is not equal null value. (i.e. $p \neq .5$)
- The alternate hypothesis in a **one-sided hypothesis test** proposes that the population parameter is less than (or greater than) the null value (i.e. one of $p > .5$ or $p < .5$)

Review: Hypotheses

Approximating the Null Distribution

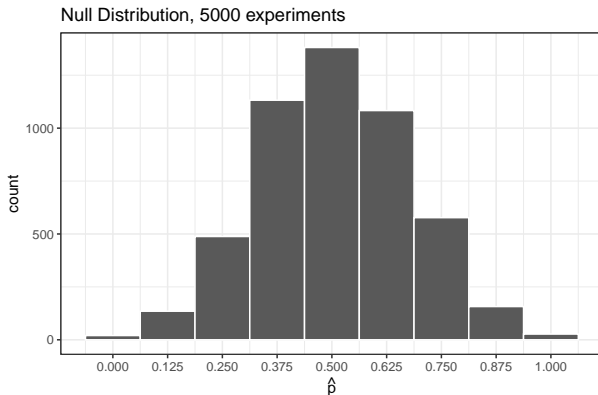
- The distribution of the statistic of interest, *if the null hypothesis were true*, is called the **Null Distribution**
- We can use R to approximate the null distribution by running 5000 experiments of 8 coin flips:

```
coin %>% rep_sample_n(size = 8, replace = T, reps = 5000) %>%  
  summarize(n_heads = sum(face == "Heads")) %>% mutate(p_hat = n_heads/8)
```

```
## # A tibble: 5,000 x 3  
##   replicate n_heads p_hat  
##   <int>    <int> <dbl>  
## 1         1      5 0.625  
## 2         2      5 0.625  
## 3         3      4 0.5  
## 4         4      4 0.5  
## 5         5      3 0.375  
## 6         6      3 0.375  
## 7         7      3 0.375  
## 8         8      2 0.25  
## 9         9      3 0.375  
## 10        10      2 0.25  
## # ... with 4,990 more rows  
## # i Use `print(n = ...)` to see more rows
```

Visualizing the Null Distribution

- We can use a histogram to visualize the Null Distribution of the sample proportion \hat{p}
- ```
null_stats %>% ggplot(aes(x = p_hat))+geom_histogram(bins = 9, color = "white")
```



## Section 2

### Strength of Evidence

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  - P-values very close to 0 represent statistics that were very unlikely to arise by chance, if the null hypothesis were true.

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 summarize(n = n()) %>%
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  - Then use the model to calculate the theoretical probability of observing a sample statistic as extreme as the test statistic.
  - Assuming that coin flips heads with probability 0.5 and that each flip is independent of the others, then the probability of 8 consecutive heads is

```
0.5^8
```

```
[1] 0.00390625
```



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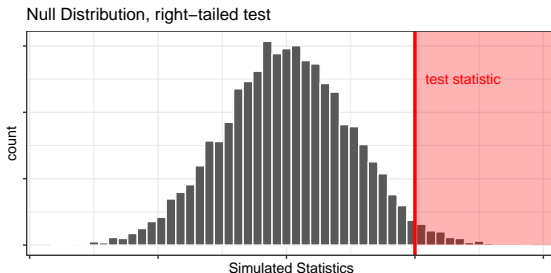
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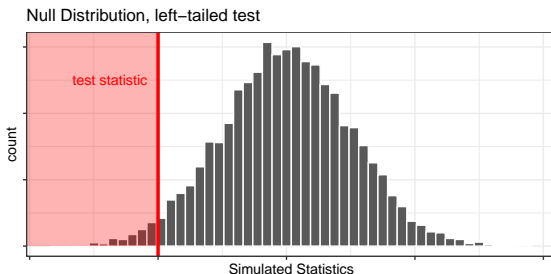
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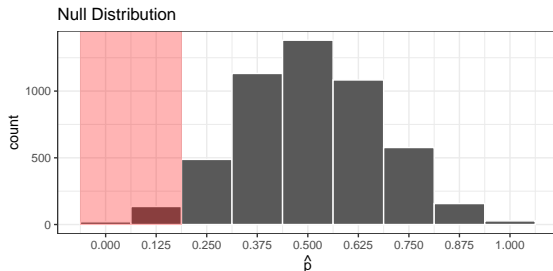
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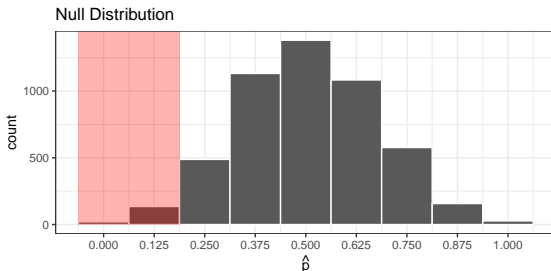


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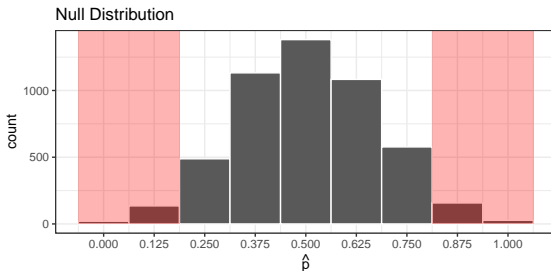
- We find the proportion of simulated statistics in the left tail is 0.034

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- We double this to include the right-tail as well, and get a p-value of 0.068.

## Section 3

### Decision Rules

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  - But if you are trying to determine whether pushing a crosswalk button more than once causes the stoplight to change faster, you might find a p-value of 0.25 compelling evidence.

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- In general, we should **always** choose the value of  $\alpha$  prior to conducting an experiment and observing data.
  - Otherwise, we are liable to choose a significance level that conforms to whichever decision we would prefer to make.

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  - The coin is actually fair. But we saw an unlikely event and claimed the coin was biased.

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  - Remember: Unlikely things happen. All of the time.
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- In general, we will never know we made an error at all (but we can still quantify the probability that we made a particular error)



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## Rapid COVID test

A quick and accessible (but unreliable) test for COVID-19 is to match a patient's symptoms to the 10 most common symptoms exhibited by victims of COVID.

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DNA testing allows researchers to compare the DNA profile of a suspect to the profile of DNA at the crime scene. Suppose that the perpetrator's DNA profile will **always** match profile of the DNA found at the crime scene. However, there is a small chance that profile of an innocent person matches the crime scene DNA profile, as well.

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## Section 4

### (Mis)Interpreting P-Values

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- This may be one cause of the *Reproducibility Crisis* currently faced in the fields of Psychology and Medicine (and to some extent, other natural and social sciences)

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- ⑤ A  $p$ -value does not measure the size of an effect, or the importance of a result.
- ⑥ By itself, a  $p$ -value does not provide a good measure of evidence regarding a model or hypothesis.



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  - No. We would also need to take into account our prior beliefs about the likelihood of this hypothesis.



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  - Effect size determines whether a result is *practically significant* (i.e. is noteworthy or worth changing behavior over).

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  - Can we deduce causal relationships from this investigation? (This is unrelated to significance and effect size)

## Conclusion

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