Hypothesis Testing I

Nate Wells

Math 141, 3/16/22

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Outline

In this lecture, we will...

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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 Framework

Framework for Hypothesis Testing

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

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

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```
coin %>% rep_sample_n(size = 8, replace = T, reps = 2000) %>%
summarize(n_heads = sum(face == "Heads")) %>% mutate(p_hat = n_heads/8)
```

##	# A t	ibble: 2,0	00 x 3	
##	re	plicate n_	heads p_hat	
##		<int></int>	<int> <dbl></dbl></int>	
##	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 1,99	0 more rows	

Visualizing the Null Distribution

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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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null_stats %>% mutate(extreme = ifelse(p_hat >=1.0, "yes", "no")) %>%
group_by(extreme) %>% summarize(n = n()) %>%
mutate(proportion = n/sum(n))
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```
## # A tibble: 2 x 3
## extreme n proportion
## <chr> <int> <dbl>
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## 2 yes 7 0.0035
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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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Null Distribution, right-tailed test

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Null Distribution, left-tailed test

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- Does the specific alternative hypothesis play any role in calculating the p-value?
 - Yes! The **direction** of the alternative hypotheses determines which "tail(s)" of the null distribution correspond to *extreme* values.
- **(2)** If H_a is of the form parameter \neq null value, then the p-value is twice the proportion of simulated statistics more extreme than the test statistic (i.e. both tails)



Null Distribution, two-tailed test
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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.

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- We should always choose the value of α prior to conducting an experiment and observing data. Usually the choice is made for us depending on conventions in our field of study.
- Choosing a significance level of $\alpha = 0.05$ means that we treat any result that would have occurred by chance alone less than 5% of the time as good evidence that the null hypothesis is false.

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 - The coin is actually fair. But we saw an unlikely event and claimed the coin was biased.
- A Type 2 Error occurs when we fail to reject H_0 when it is in fact false.
 - The coin was indeed biased. But we withheld judgment since unlikely events do happen from time to time.

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With great power comes...greater chance of Type I error.

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.

Suppose a person walks into a medical clinic with 6 of the 10 symptoms of COVID, and medical personnel are concerned the person may have COVID.

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- What significance level are you willing to use for this COVID test? *Remember, decreasing significance level also decreases the power of the test.*

DNA Tests

DNA testing allows researchers to compare markers in a person's DNA to those found at crime scene. Suppose the DNA found at a crime scene will **always** match the perpetrator of the crime. However, there is a small chance that the crime scene DNA will also match the markers for another innocent person.

Suppose a person is on trial for a crime. Forensic scientists attest that the person's DNA matches that found at the crime scene.

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DNA testing allows researchers to compare markers in a person's DNA to those found at crime scene. Suppose the DNA found at a crime scene will **always** match the perpetrator of the crime. However, there is a small chance that the crime scene DNA will also match the markers for another innocent person.

- What are the Null and Alternate Hypotheses in this case?
- What 'statistic' is being used to determine whether the person has committed the crime.
- In the context of this problem, what does a Type I error represent? What are some possible consequences of a Type I error?
- Ø Similarly, what does a Type II error represent? What are some possible consequences of a Type II error?

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- In the context of this problem, what does a Type I error represent? What are some possible consequences of a Type I error?
- ② Similarly, what does a Type II error represent? What are some possible consequences of a Type II error?
- What significance level are you willing to use for this DNA test? *Remember*, *decreasing significance level also decreases the power of the test.*