Hypothesis Testing Procedures for Two-sample Data

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- $1. \ \mbox{One-sample vs. two-sample testing}$
- 2. Testing a difference in proportions
- 3. Testing a difference in means
- 4. Paired study designs

One-sample testing uses a single sample in an attempt to falsify a hypothesis about a population (ie: H₀ : p = p₀ or H₀ : μ = μ₀)
 Notice, the null hypothesis must specify a specific numeric value (ie: p = 0.5 or μ = 0)

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 - Notice, the null hypothesis must specify a specific numeric value (ie: p = 0.5 or µ = 0)
- ► **Two-sample testing** looks to compare two subgroups within a population (ie: $H_0: p_1 p_2 = 0$ or $H_0: \mu_1 \mu_2 = 0$)
 - Here, the null hypothesis is relational and be satisfied in many different ways (ie: p₁ and p₁ could both be 0.1, or could both be 0.6)
 - This will require us to make some minor adjustments in order to utilize Z and T tests



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- At the time, many experts believed these infections were due to "bad air"
 - Hospitals had policies that required their wards open their windows at midday to air out
- It was customary for surgeons to move quickly from patient to patient with out any sort of special precautions
 - In fact, many took pride the accumulated stains on their surgical gowns as a measure of experience



Motivating example - surgical site infections

- In 1862, Louis Pasteur discovered food spoilage was caused by the proliferation of harmful micro-organisms
- Pasteur identified three methods for eliminating these micro-organisms: heat, filtration, and chemical disinfectants
 - His heating method became known as *pasteurization* and is widely applied to milk, beer, and many other food products



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 - His heating method became known as *pasteurization* and is widely applied to milk, beer, and many other food products
- Joseph Lister, a Professor of Surgery at the Glasgow Royal Infirmary, became aware of Pasteur's work and hypothesized that it might explain the infections that frequently occurred following surgery
 - How would you recommend Lister evaluate his hypothesis?



- Lister proposed a "sterile" protocol that required surgeons to wash their hands, wear clean gloves, and disinfect their instruments with a carbolic acid solution
 - He randomly assigned 75 patients to the "sterile" procedure or a control group
 - He then tracked how many patients survived until their discharage from the hospital

	Died	Survived
Control	16	19
Sterile	6	34



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- 2) Confounding variables?



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- Bias? Unlikely, even though double-blinding wasn't possible, it's unlikely the measurement of the outcome (survival) was biased. It's also unlikely that this is a non-representative group of patients (sampling bias)
- Confounding variables? No, we'd expect any problematic variables to be balanced across the two groups due to random assignment
- 3) Random chance? ... This is where hypothesis testing is useful

- ► In Lister's experiment, we're interested in H₀ : p₁ p₂ = 0, which implies the survival rates for the treatment and control groups are the same
- In our introduction to hypothesis testing, we evaluated the null hypothesis by *simulating outcomes* that would be expected if the null hypothesis were true
 - In particular, we used "coin flips" to model the toy choices of the study's 16 infants
 - Can we apply a similar approach to Lister's experiment?



- A major challenge is that there are many different ways in which the treatment and control groups could have the same survival rate, and each would satisfy the null hypothesis
 - However, most realistic is to assume that a *pooled proportion* applies to each group
- ▶ In Lister's experiment, $\hat{p}_0 = \frac{19+34}{75} = 0.707$ is the overall survival rate, regardless of group

We can use pooled proportion to simulate the survival outcomes we'd expect to see in each group if H_0 were true:

```
## Set seed (for replication purposes)
set.seed(15)
nsim = 1000
## Simulate survival for the control group
control <- rbinom(nsim, size = 35, prob = 0.707)
## Simulate survival for the sterile group
sterile <- rbinom(nsim, size = 40, prob = 0.707)</pre>
```



These simulated outcomes can be used to estimate the *p*-value, or the probability of a difference in survival that's at least as large as 19/35 - 34/40 = -0.307

```
## Simulated differences in proportions
diffs <- control/35 - sterile/40
## Estimate the two-sided p-value
2*sum(diffs <= (19/35 - 34/40))/nsim</pre>
```

[1] 0.004

So, a difference in survival as large as the one seen in Lister's experiment would only happen 0.4% of the time if the "sterile" protocol made no difference.



The simulation approach described on the previous few slides is an approximation of a method known as **Fisher's exact test**:

```
##
## Fisher's Exact Test for Count Data
##
## data: table
## p-value = 0.005018
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
## 1.437621 17.166416
## sample estimates:
## odds ratio
## 4.666849
```

Fisher's exact test should be used to test for a difference in categorical outcomes across two groups. You can view it as a generalization of the exact binomial test.



Another way to use the pooled proportion is within the *standard error* suggested by the Central Limit theorem result:

$$\hat{p}_1 - \hat{p}_2 \sim N\left(p_1 - p_2, \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}\right)$$

This approach allows us to calculate a Z-value and perform a Z-test:

$$Z = \frac{\text{Observed-Null}}{SE} = \frac{(\hat{p}_1 - \hat{p}_2) - 0}{\sqrt{\frac{\hat{p}_0(1 - \hat{p}_0)}{n_1} + \frac{\hat{p}_0(1 - \hat{p}_0)}{n_2}}}$$

Remember that \hat{p}_0 is the *pooled proportion*, it represents the most likely survival rate when the null hypothesis is true



For Lister's experiment:

1)
$$H_0: p_1 - p_2 = 0$$
 vs. $H_a: p_1 - p_2 \neq 0$
2) The pooled proportion that best reflects H_0 is:
 $\hat{p}_0 = \frac{19+34}{75} = 0.707$
3) $Z = \frac{Observed-Null}{SE} = \frac{(19/35-34/40)-0}{\sqrt{\frac{0.707(1-0.707)}{35} + \frac{0.707(1-0.707)}{40}}} = -2.916$

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4) The two-sided *p*-value is 0.0035 (see R code below). Thus, we can conclude that Lister's sterilization protocol *causes* an improvement in survival.

2*pnorm(-2.916, mean = 0, sd = 1, lower.tail = TRUE)

[1] 0.003545505



- Fisher's exact test is computationally expensive (especially for larger samples)
 - The two-sample Z-test is generally recommended when the "success-failure condition" is met for both groups (ie: the sample data contain at least 10 "successes" and 10 "failures" in each group)
 - However, modern computing has made it feasible to use Fisher's exact test in most circumstances
- Both tests produce a similar *p*-value for large samples, but the two-sample Z-test can be unreliable when the success-failure condition is not met



In 2015-16, the Golden State Warriors set an NBA record for most wins in a season. The table below shows a breakdown of the Warrior's wins and losses by whether the game was played on their home court, or on their opponent's court:

```
gsw = read.csv("https://remiller1450.github.io/data/GSWarriors.csv")
table(gsw$Location, gsw$Win)
```

L W ## Away 7 34 ## Home 2 39

- 1) Perform a two-sample Z-test to evaluate whether the observed difference in the Warrior's home vs. away success could be explained by random chance.
- Briefly explain why a two-sample Z-test might be inappropriate, then analyze these data using Fisher's exact test (the preferred approach in this application)

Practice (solution)

1) $H_0: p_1 - p_2 = 0$, where p_1 is the proportion of wins at home and p_2 is the proportion wins on the road. Then, $Z = \frac{(34/41-39/41)-0}{0.069} = 1.77$, where 0.069 is the standard error calculated using the pooled proportion. The two-sided *p*-value corresponding to this *Z*-value is 0.077, so there's borderline evidence of better performance at home.

2) The null hypothesis is still $H_0: p_1 - p_2 = 0$, see the R code below for the *p*-value:

```
gsw = read.csv("https://remiller1450.github.io/data/GSWarriors.csv")
fisher.test(table(gsw$Location, gsw$Win))$p.value
```

[1] 0.1549418



Hypothesis testing for two-sample quantitative data

In order to test for a difference in means, we can begin with the same general approach as the two-sample Z-test:

• Propose
$$H_0: \mu_1 - \mu_2 = 0$$

Find the corresponding sample outcome, $\bar{x}_1 - \bar{x}_2$

• Using CLT, estimate $SE = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$, where s_1 and s_2 are the sample standard deviations of each group

At this point we've estimated *two extra population parameters* using the sample data, so we must use the T-distribution:

$$T = \frac{\text{Observed-Null}}{SE} = \frac{(\bar{x}_1 - \bar{x}_2) - 0}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

Degrees of freedom are complicated, we'll either use R or take the smaller of $n_1 - 1$ and $n_2 - 1$ if forced to work "by hand"

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 - Of these 25 new records, 23 were set by swimmers using a wetsuit known as the LZR Racer, a suit produced by Speedo whose design involved scientists at NASA
- But is this convincing evidence that LZR Racer provides an unfair advantage?
 - Are there any alternative explanations for 23 of 25 records being set by swimmers who wore LZR Racers?



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- But is this convincing evidence that LZR Racer provides an unfair advantage?
 - Are there any alternative explanations for 23 of 25 records being set by swimmers who wore LZR Racers?
- Recognize that these data are observational, so it could be that all of the best swimmers were wearing this suit. Therefore, an *experimental* study should be performed



Practice

- The wetsuits data contains the results of an experiment involving 12 competitive swimmers
 - Each swam 1500m for time under two conditions: wearing a high-tech wetsuit, or wearing a placebo suit identical in appearance
 - It was randomly determined which condition the participant experienced first
- The columns Wetsuit and NoWetsuit record the respective velocities (in m/s) over the 1500m swim

wet <- read.csv("https://remiller1450.github.io/data/Wetsuits2.csv")</pre>

Use R to find the sample mean and standard deviation of each group, then perform a two-sample T-test "by hand"



Practice (solution)

- ► Consider H₀ : µ₁ − µ₂ = 0, where µ₁ is the average velocity when wearing a wetsuit and µ₂ is the average velocity when wearing a normal swimsuit.
- We observed $\bar{x}_1 = 1.507$, $\bar{x}_2 = 1.429$, $s_1 = 0.136$, and $s_2 = 0.141$
- ► Thus, the *T*-value relating the sample data to the null hypothesis is $T = \frac{(1.507 1.429) 0}{\sqrt{0.136^2/12 + 0.141^2/12}} = 1.379$
- Comparing this against a *t*-distribution with *df* = 11, the two-sided *p*-value is 0.195, indicating insufficient evidence of any difference in velocity



We can use the t.test function in R to perform this test using the precise degrees of freedom:

```
t.test(x = wet$Wetsuit, y = wet$NoWetsuit, alternative = "two.sided")
```

```
##
## Welch Two Sample t-test
##
## data: wet$Wetsuit and wet$NoWetsuit
## t = 1.3688, df = 21.974, p-value = 0.1849
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.03992937 0.19492937
## sample estimates:
## mean of x mean of y
## 1.506667 1.429167
```

Notice the actual degrees of freedom are slightly below $n_1 + n_2 - 2 = 22$, which why the "by hand" approach uses the lower bound min $(n_1 - 1, n_2 - 1)$



The two-sample *t*-test is designed to work in two settings:

- 1) Small, Normally distributed samples
- 2) Large samples of any distributional shape (ie: $n_1 \ge 30$ and $n_2 \ge 30$)

Outside of these settings, the Wilcoxon Rank-Sum test can be used to test whether the medians of each group are equal:

```
## Warning in wilcox.test.default(x = wet$Wetsuit, y = wet$NoWetsuit, alternative =
## "two.sided"): cannot compute exact p-value with ties
##
## Wilcoxon rank sum test with continuity correction
##
## data: wet$Wetsuit and wet$NoWetsuit
## W = 95.5, p-value = 0.1838
## alternative hypothesis: true location shift is not equal to 0
```



The "Wetsuits" study used a **paired design** where each subject served as their own control. Therefore, we should treat it as *one-sample data* and analyze the *paired differences*:

```
t.test(wet$Difference, mu = 0)$p.value
## [1] 8.885414e-08
t.test(x = wet$Wetsuit, y = wet$NoWetsuit, mu = 0)$p.value
```

[1] 0.1848961

Paired designs can provide a tremendous statistical advantage (variability within individuals tends to be lower than variability between individuals), and they also help control for confounding variables!



This presentation covered two new hypothesis testing scenarios:

- 1) Two-sample categorical data, where we evaluate $H_0: p_1 p_2 = 0$ using either Fisher's exact test or a two-sample Z-test
- 2) Two-sample quantitative data, where we evaluate $H_0: \mu_1 \mu_2 = 0$ using either a two-sample *T*-test or the Wilcoxon Rank-Sum test

All of the fundamental concepts we've previously covered apply to these new situations, but we must be aware of when and how to implement these new statistical tests.

