L31: Two sample proportions

CI for the difference in tw proportions

Two sample hypothesi testing in R

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April 20,2020

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Announcements

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- Lecture participation will now stay open through the following Tuesday (ie participation for today and tomorrow will be due by the 28th)
- ► Last Quiz this Friday (open for 24 hours)

Recipes for inference so far:

L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothes testing in R

Confidence intervals (margin of error): - calculate a measure of variability for the sample estimate - Use a theoretical distribution to get a critical value - Generate an estimate and interval

estimate \pm criticalvalue * variability

Hypothesis testing: - articulate a null hypothesis and alternative hypothesis - choose an appropriate statistical test - generate a statistic - compare to a critical value or p value - reject or fail to reject the null hypothesis

Roadmap

Part III started with continous outcomes and categorical predictors

How many groups?	Independent?	parametric?	test
1	yes	yes	Z or one sample T
2	yes	yes	Two sample T
2	yes	no	Wilcox rank sum
2	no	yes	Paired T
2	no	no	Wilcox sign rank
3 or more	yes	yes	ANOVA
3 or more	yes	no	Kruskal Wallis

Then we addressed continous outcomes with continous predictors (correlation and linear regression)

Last friday we introduced categorical outcomes (binary/proportions)

Today we will look at comparing two proportions.

L31: Two sample proportions

CI for the difference in two proportions

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Comparing two proportions (Chapter 20)

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CI for the difference in two proportions

Two sample hypothesi testing in R

► Two SRS from independent populations

Notation:

Population	Population proportion	Sample size	Sample proportion
1	ρ_1	n_1	$\hat{ ho}_1$
2	<i>p</i> ₂	n_2	\hat{p}_2

L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothesis testing in R

CI for the difference in two proportions

Large-sample confidence interval for the difference of two proportions

▶ Use when the number of observed successes and failures are > 10 for both samples

$$(\hat{p}_1 - \hat{p}_2) \pm z^* \sqrt{rac{\hat{p}_1(1-\hat{p}_1)}{n_1} + rac{\hat{p}_2(1-\hat{p}_2)}{n_2}}$$

- ▶ Just like for the difference between two means, the SE of the difference is the square root of the sum of the variances.
- ▶ This large-sample interval often has a lower confidence level than the one specified. That is, if you repeated the method several times < 95 of the 100 created intervals would contain the true value for the difference between the proportions for a 95% CI.

Example using the large sample method

L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothe testing in R

Patients in a randomized controlled trial were severely immobilized and randomly assigned to either Fragamin (to prevent blood clots) or to placebo. The number of patients experiencing deep vein thrombosis (DVT) was recorded

	DVT	no DVT	Total	ĝ
Fragamin	42	1476	1518	0.0277
Placebo	73	1400	1473	0.0496

We can apply the large study method because the sample sizes are large and the number of observed successes and failures are > 10 (i.e., 42, 73, 1476, and 1400 all > 10).

Example using the large sample method

L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothesis testing in R

$$(\hat{p}_1 - \hat{p}_2) \pm z^* \sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}$$

$$(0.0496 - 0.0277) \pm z^* \sqrt{\frac{0.0496_1(1-0.0496)}{1473} + \frac{0.0277(1-0.0277)}{1518}}$$

$$0.0219 \pm 1.96 \times 0.0071 = 0.008 \text{ to } 0.0358$$

- When the assumptions of the large sample method are not satisfied, we use the plus four method.
- ▶ When you have two samples this method says: add 4 observations, 1 success and 1 failure to each of the two samples.

$$\begin{split} \tilde{p}_1 &= \frac{\text{no. of successes in pop} 1+1}{n_1+2} \ \ \tilde{p}_2 = \frac{\text{no. of successes in pop} 2+1}{n_2+2} \\ (\tilde{p}_1 - \tilde{p}_2) &\pm z^* \sqrt{\frac{\tilde{p}_1(1-\tilde{p}_1)}{n_1+2} + \frac{\tilde{p}_2(1-\tilde{p}_2)}{n_2+2}} \end{split}$$

- ▶ Use when the sample size is at least five, with any counts of success and failure (can even use when number of successes or failures = 0)
- ▶ Much more accurate when the sample sizes are small
- May be conservative (giving a higher level of confidence than the one specified)

Example using the plus four method

L31:	Two	sample		
proportions				

CI for the difference in two proportions

Two sample hypothesis testing in R

	Flu	no Flu	Total	$\hat{\boldsymbol{p}}$
Vaccine	4	96	100	0.04
Placebo	11	89	100	0.11

Here, we don't have 10 "successes" (flu) in both groups, so we cannot use the Normal approximation method.

Example using the plus four method

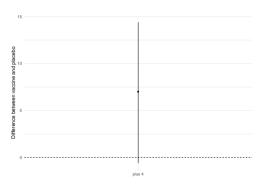
L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothesi testing in R

$$\begin{split} \tilde{p}_1 &= \frac{\text{no. of successes in pop1} + 1}{n_1 + 2} = \frac{5}{102} \\ \tilde{p}_2 &= \frac{\text{no. of successes in pop2} + 1}{n_2 + 2} = \frac{12}{102} \\ (\tilde{p}_1 - \tilde{p}_2) \pm z^* \sqrt{\frac{\tilde{p}_1(1 - \tilde{p}_1)}{n_1 + 2} + \frac{\tilde{p}_2(1 - \tilde{p}_2)}{n_2 + 2}} \\ (\frac{12}{102} - \frac{5}{102}) \pm 1.96 \times 0.0384 = -0.6\% \text{ to } 14.4\% \end{split}$$

The 95% CI of the difference ranged from -0.6 percentage points to 14.4% percentage points. While this CI contains 0 (the null hypothesized value for no difference) most of the values contained within it are positive, perhaps suggesting support for the alternative hypothesis. In this case, we might want to collect more data to create a more precise CI.



L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothe testing in R

Hypothesis testing - two samples binary data

L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothesis testing in R

Hypothesis testing when you have two samples and binary data

L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothesis esting in R

$$H_0: p_1 = p_2 \text{ or } p_1 - p_2 = 0$$

 H_a :

- $ightharpoonup p_1
 eq p_2$ or $p_1 p_2
 eq 0$ (two-sided)
- $ho_1 > p_2$ or $p_1 p_2 > 0$ (one sided upper tail)
- $ightharpoonup p_1 < p_2 ext{ or } p_1 p_2 < 0 ext{ (one sided lower tail)}$

▶ If the null hypothesis is true, then p_1 is truly equal to p_2 . In this case, our best estimate of the underlying proportion that they are both equal to is

$$\hat{p} = \frac{\text{no. successes in both samples}}{\text{no. individuals in both samples}}$$

Also, our best guess at the SE for \hat{p} is:

$$\sqrt{rac{\hat{p}(1-\hat{p})}{n_1} + rac{\hat{p}(1-\hat{p})}{n_2}} \ \sqrt{\hat{p}(1-\hat{p})(rac{1}{n_1} + rac{1}{n_2})}$$

This is the formula for the SE for the difference between two proportions but we have substituted \hat{p} for p_1 and p_2 .

Using the information from the previous slide, we can create the z-test for the difference between two proportions as:

$$z = rac{\hat{
ho_1} - \hat{
ho_2}}{\sqrt{\hat{
ho}(1-\hat{
ho})ig(rac{1}{n_1} + rac{1}{n_2}ig)}}$$

Use this test when the counts of successes and failures are ≥ 5 in both samples

Example of hypothesis testing when you have two samples and binary data

Recall the RCT data on the occurrence of DVT between Fragamin vs. placebo groups:

	DVT	no DVT	Total	_p
Fragamin	42	1476	1518	0.0277
Placebo	73	1400	1473	0.0496

 $H_0: p_1 = p_2$, or that the rate of DVT is the same between Fragamin and placebo groups.

Suppose you're interested in knowing whether these two groups had different rates of DVT. Then, $H_a: p_1 \neq p_2$

L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothe testing in R

Example of hypothesis testing when you have two samples and binary data

- 1. Compute $\hat{p} = \frac{42+73}{1518+1473} = \frac{115}{2991} = 0.03844868$
- 2. Compute the SE: $\sqrt{0.0384(1-0.0384)(\frac{1}{1518}+\frac{1}{1473})}=0.007032308$
- 3. Compute the test statistic:

$$z = \frac{0.04955872 - 0.02766798}{0.007032308} = 3.11$$

4. Calculate the p-value

$$pnorm(q = 3.112881, lower.tail = F)*2$$

[1] 0.001852707

L31: Two sample proportions

CI for the difference in two proportions

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Two sample hypothesis testing in R

```
prop.test(x = c(42, 73), # x is a vector of number of successes
n = c(1518, 1473)) # n is a vector of sample sizes
```

```
L31: Two sample proportions
```

CI for the difference in two proportions

Two sample hypothesis testing in R

```
##
##
   2-sample test for equality of proportions with continuity
##
   correction
##
## data: c(42, 73) out of c(1518, 1473)
## X-squared = 9.107, df = 1, p-value = 0.002546
## alternative hypothesis: two.sided
## 95 percent confidence interval:
## -0.036376917 -0.007404562
## sample estimates:
##
      prop 1 prop 2
  0.02766798 0.04955872
```

Example of hypothesis testing when you have two samples and binary data

- L31: Two sample proportions
- CI for the difference in two proportions
- Two sample hypothesis testing in R

- ▶ R gives a slightly different p-value because it has a continuity correction.
- ► This is okay. If you want to use R to check your hand calculation, you need to add the argument correct = F to the calculation.

Next up

L31: Two sample proportions

CI for the difference in two proportions

Two sample hypothesis testing in R

The next lectures we will introduce the Chi-squared distribution and two tests - Goodness of fit - Chi-squared test of assiciation

This will be the end of new material for the semester. Bonus material on bootstrapping and permutations will be posted as notes, but has been dropped from the required material for the exam. It may be included as extra credit.

L31: Two sample proportions

Two sample hypothesis testing in R

ANOVA: ANALYSIS OF VALUE

IS YOUR RESEARCH WORTH ANYTHING?

Developed in 1912 by geneticist R.A. Fisher, the Analysis of Value is a powerful statistical tool designed to test the significance of one's work.



wasting my time?

Significance is determined by comparing one's research with the Dull Hypothesis:

$$H_0: \mu_1 = \mu_2$$
 ?

where

Ho: the Dull Hypothesis

μ₄: significance of your research

μ_a: significance of a monkey typing randomly on a typewriter in a forest where no one hears it

WWW. PHDCOMICS. COM JORGE CHAM @ 2007

The test involves computation of the F'd ratio:

sum(people who care about your research) F'd =

world population

This ratio is compared to the F distribution with I-1. N. degrees of freedom to determine a p(in your pants) value. A low p(in your pants) value means you're on to something good (though statistically improbable).

Type I/II Errors

The Analysis of Value must be used carefully to avoid the following two types of errors:

You incorrectly believe your Type I: research is not Dull.

Type II: No conclusions can be made Good luck graduating.

Of course, this test assumes both Independence and Normality on your part, neither of which is likely true, which means it's not your problem.