

Statistics 305/605: Introduction to Biostatistical Methods for Health Sciences

Chapter 14 : Inference for Proportions

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Inference for Proportions (Chapter 14)

- ▶ Instead of quantitative measurements, we classify each sampled individual into one of two categories.
 - ▶ success, failure (canonical)
 - ▶ breast cancer, no breast cancer
 - ▶ Etc.
- ▶ Want to make inference about the proportion p of successes in a population, or about the difference between the proportions p_1 and p_2 of successes in two populations.

Example: Women's Health Initiative (WHI)

- ▶ A randomized controlled trial, called the Women's Health Initiative, randomized 16,608 post-menopausal women aged 50-79 years to receive either hormone replacement therapy in the form of estrogen plus progestin (EP; $n_1 = 8506$), or a placebo ($n_2 = 8102$).
- ▶ After five years, 166 of those in the EP group had developed invasive breast cancer, compared to 122 in the placebo group.
- ▶ The populations to compare are postmenopausal women aged 50-79 years, who are taking EP (population 1) or placebo (population 2).
- ▶ The sample proportions are $\hat{p}_1 = 166/8506 = 0.0195$ and $\hat{p}_2 = 122/8102 = 0.0151$
- ▶ It looks like the EP group has a higher risk of breast cancer, but could this difference be due to chance?

Outline of Approach

- ▶ Similar approach to inference of population means (quantitative outcomes), with some minor differences.
- ▶ Inference is based on the sampling distribution of $\hat{p}_1 - \hat{p}_2$
- ▶ Two-stage reasoning:
 1. Transform the statistic $\hat{p}_1 - \hat{p}_2$ into an initial pivotal quantity, Z_1 , whose denominator depends on the unknown parameters p_1 and p_2 .
 2. Get a final pivotal quantity, Z , by replacing the unknown p_i 's in the denominator of Z_1 with estimates.
- ▶ CIs and hypothesis tests follow from the approximate sampling distribution of the final pivotal quantity, Z .
- ▶ Note: Not covering *Inference for a single proportion* (text, sections 14.2 – 14.5).

Pivotal Quantity Z

$$Z = \frac{(\hat{p}_1 - \hat{p}_2) - (p_1 - p_2)}{\sqrt{\hat{p}_1(1 - \hat{p}_1)/n_1 + \hat{p}_2(1 - \hat{p}_2)/n_2}}$$

- ▶ What is the distribution of Z ?
 - ▶ Under certain conditions (see below) it is reasonable to assume that Z is approximately normal.

Rule of Thumb for Normal Approximation

- ▶ The normal approximation to the distribution of Z is considered reliable when the sample sizes n_1 and n_2 are “large”
- ▶ The definition of large depends on the underlying p_j 's. The text (page 324) suggests:
 - ▶ $n_1 p_1 \geq 5$ and $n_1(1 - p_1) \geq 5$ and
 - ▶ $n_2 p_2 \geq 5$ and $n_2(1 - p_2) \geq 5$
- ▶ The parameters p_1 and p_2 are not known so we insert the estimates $\hat{p}_1 = (\text{number of successes in sample 1})/n_1$ and $\hat{p}_2 = (\text{number of successes in sample 2})/n_2$.
- ▶ After inserting estimates, one can simplify the requirements to the following rule:
 - ▶ The normal approximation is reliable when there are at least 5 successes *and* 5 failures in both sample 1 and sample 2.

Checking rule of thumb for WHI Data

- ▶ At least 5 successes and failures in both samples.
 - ▶ True: 166 cancer, 8340 cancer-free in the EP group; 122 cancer, 7980 cancer-free in the placebo group.

Confidence Intervals

- ▶ The level- C CI for $p_1 - p_2$ is of the form:

estimate \pm margin of error

- ▶ The estimate is $\hat{p}_1 - \hat{p}_2$
- ▶ The margin of error is $z^* \times SE$ where
 - ▶ z^* is the upper $(1 - C)/2$ critical value of the standard normal distribution.
 - ▶ SE is the estimated SD of $\hat{p}_1 - \hat{p}_2$ in the denominator of Z ; namely, $SE = \sqrt{\hat{p}_1(1 - \hat{p}_1)/n_1 + \hat{p}_2(1 - \hat{p}_2)/n_2}$

Example (WHI)

- ▶ Recall: 16,608 women aged 50-79 years randomized to receive either estrogen plus progestin (EP; $n_1 = 8506$), or a placebo ($n_2 = 8102$). After five years, 166 in the EP group developed invasive breast cancer, compared to 122 in placebo group.
- ▶ For EP, $\hat{p}_1 = 166/8506$ and, for placebo, $\hat{p}_2 = 122/8102$.
- ▶ 95% CI is estimate \pm margin of error, where
 - ▶ estimate of $p_1 - p_2$ is $\hat{p}_1 - \hat{p}_2 = 0.0044$
 - ▶ margin of error is a critical value times standard error of difference.
- ▶ The critical value is 1.96 (see R demo).
- ▶ The standard error is
$$\sqrt{\hat{p}_1(1 - \hat{p}_1)/n_1 + \hat{p}_2(1 - \hat{p}_2)/n_2} = 0.002$$
- ▶ The margin of error is therefore $1.96 * .002 = 0.00392$.
- ▶ Putting it all together, the CI is 0.0044 ± 0.00392 or approximately (0.0005, 0.008).

Test Statistic

- ▶ The null hypothesis is $H_0 : p_1 - p_2 = 0$.
- ▶ Numerator of the test statistic is therefore the estimated difference $(\hat{p}_1 - \hat{p}_2)$ minus 0.
- ▶ Denominator of the test statistic is

$$SE = \sqrt{\hat{p}_1(1 - \hat{p}_1)/n_1 + \hat{p}_2(1 - \hat{p}_2)/n_2}$$

- ▶ BUT, under H_0 , we have $p_1 = p_2$. Call this common value p .
- ▶ Assuming a common proportion p in the two populations, we pool the 2 samples to obtain an estimate \hat{p} ; i.e.,

$$\hat{p} = (\text{number of cancers in both samples}) / (n_1 + n_2).$$

- ▶ The formula for the SE of $\hat{p}_1 - \hat{p}_2$ simplifies to $\sqrt{\hat{p}(1 - \hat{p}) \times (1/n_1 + 1/n_2)}$
- ▶ So the statistic for testing $H_0 : p_1 - p_2 = 0$ is

$$Z = \frac{(\hat{p}_1 - \hat{p}_2)}{\sqrt{\hat{p}(1 - \hat{p}) (1/n_1 + 1/n_2)}}$$

Example (WHL, continued)

- ▶ $H_0 : p_1 - p_2 = 0$.
- ▶ Test statistic numerator is $\hat{p}_1 - \hat{p}_2 = 0.0044$.
- ▶ Test statistic denominator is the SE based on the pooled estimate of $p = p_1 = p_2$.
 - ▶ Pooled estimate of the common population proportion is $\hat{p} = (166 + 122)/(8506 + 8102) = 0.0173$.
 - ▶ So the SE is

$$\begin{aligned} & \sqrt{\hat{p}(1 - \hat{p})(1/n_1 + 1/n_2)} \\ &= \sqrt{0.0173(1 - 0.0173)(1/8506 + 1/8102)} \\ &= 0.002. \end{aligned}$$

- ▶ The test statistic value is $z = 0.0044/0.002 = 2.2$.

p -value

- ▶ The p -value is the chance of a value of the test statistic that is as or more extreme than what we did observe in our data, when the null hypothesis is true.
- ▶ Same logic as we saw earlier for inference of population means (Chapter 11).
- ▶ Let Z be a standard normal random variable and z be the observed value of the test statistic.
- ▶ For $H_a : p_1 - p_2 \neq 0$, the p -value is $p = 2P(Z \geq |z|)$.

Example (WHI, continued)

- ▶ Suppose we wish to test
 $H_0: p_1 - p_2 = 0$ vs. $H_a: p_1 - p_2 \neq 0$ at level $\alpha = 0.05$.
- ▶ For an observed value of the test statistic $z = 2.2$, computer software calculates a pvalue of about 0.03 (see R demo)
- ▶ We therefore reject H_0 at the 5% level: There is statistical evidence that women taking EP have a higher risk of invasive breast cancer than those taking the placebo.
 - ▶ Note: The EP group appears to have a higher risk of breast cancer than the placebo group because \hat{p}_1 (for EP) is greater than \hat{p}_2 (for placebo), as reflected by $z = 2.2$ being greater than zero.

Summary

- ▶ Inference for the difference $p_1 - p_2$ between two population proportions is based on a pivotal quantity.
- ▶ Confidence intervals are of the form **estimate** \pm **margin of error**, where
 - ▶ estimate is difference between sample proportions, and
 - ▶ margin of error is a critical value times the standard error of the difference in sample proportions
- ▶ To test the null hypothesis $H_0 : p_1 - p_2 = 0$ against an alternative H_a we calculate a test statistic and the p -value
 - ▶ The p -value is the chance of seeing a value of the test statistic as or more extreme than the value that was observed in our data, under the null hypothesis.
 - ▶ Compare the p -value to a significance level α to obtain a statistical hypothesis test
- ▶ The statistical inference is considered reliable when there are at least 5 successes and 5 failures in each sample.