11.2: Hypothesis Tests for the Difference Between Two Proportions

Often, instead of comparing a sample's proportion to a benchmark value, we want to compare the proportions of two different samples, drawn from two different populations.

If the sample sizes are sufficiently large, we can assume that the difference between the two sample proportions, $\hat{p}_1 - \hat{p}_2$, is normally distributed.

Suppose we have two samples, Sample A and Sample B, of sizes n_1 and n_2, respectively.
In Sample A, x_1 is the number of the n_1 observations that possess the characteristic of interest.
In Sample B, x_2 is the number of the n_2 observations that possess the characteristic of interest.

Then the sample proportions are $\hat{p}_1 = \frac{x_1}{n_1}$ and $\hat{p}_2 = \frac{x_2}{n_2}$.

We'll follow this rule of thumb: For sample sizes to be sufficiently large to assume the difference in proportions is normally distributed, all of the quantities x_1, $n_1 - x_1$, x_2, $n_2 - x_2$ should be at least 10.
Another way to say this: All four cells (groups) in a contingency table must contain at least 10 data points.

Example 1: Suppose we are comparing the number of successful treatments for two groups. Treatment A is given to 20 patients, and is successful in 16 patients. Treatment B is given to 18 patients, and is successful in 12 patients. Can we assume a normal distribution for the difference between proportions?

	Successful	Not Successful	Total
Treatment A	16	4	20
Treatment B	12	6	18
Total			

2x2 contingency table

No, cannot assume a normal distribution for the difference, because some cells have less than 10.

Sampling distribution for the difference between two sample proportions:

Suppose independent samples of sizes n_1 and n_2 are taken from two populations, in which the proportions of observations possessing a characteristic are p_1 and p_2.

Then the mean and standard deviation of the difference between sample proportions are:

$$\mu_{\hat{p}_1-\hat{p}_2} = p_1 - p_2$$

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

Also, the shape of the sampling distribution of $\hat{p}_1 - \hat{p}_2$ is approximately normal, provided that the sample sizes are sufficiently large.

<u>Rule of thumb</u>: to assume the difference between sample proportion is normally distributed, all of x_1, $n_1 - x_1$, x_2, $n_2 - x_2$ should be at least 10.

However, we will almost never know the population proportions p_1 and p_2, so we cannot calculate the above mean and standard deviation.

Instead, we use statistics from the samples to calculate <u>point estimates</u> for $\mu_{\hat{p}_1-\hat{p}_2}$ and $\sigma_{\hat{p}_1-\hat{p}_2}$.

<u>Point estimates for the mean and standard deviation of the difference between sample proportions</u>:

$\hat{p}_1 - \hat{p}_2$ is an unbiased estimate for $\mu_{\hat{p}_1-\hat{p}_2} = p_1 - p_2$.

For a point estimate of $\sigma_{\hat{p}_1-\hat{p}_2}$, we use the <u>pooled sample proportion</u> $\hat{p}$:

$$\hat{p} = \frac{x_1 + x_2}{n_1 + n_2},$$

where n_1 and n_2 are the sample sizes, and x_1 and x_2, respectively, are the numbers of observations possessing the characteristic of interest. Then the standard error is approximately

$$\sigma_{\hat{p}_1-\hat{p}_2} \approx \sqrt{\hat{p}(1-\hat{p})\left(\frac{1}{n_1} + \frac{1}{n_2}\right)} = \sqrt{\frac{\hat{p}(1-\hat{p})}{n_1} + \frac{\hat{p}(1-\hat{p})}{n_2}}.$$

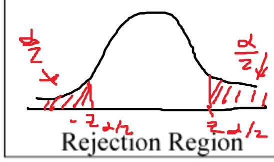
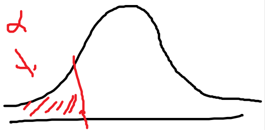
Hypothesis Testing for Two Population Proportions:

Step 1: Determine the significance level α.

Step 2: Check that the assumptions are satisfied.

- Simple random sample
- Samples are independent (observations from one sample are not paired with observations from the other sample).
- x_1, $n_1 - x_1$, x_2, $n_2 - x_2$ are all at least ~~5~~ 10.

Step 3: Determine the null and alternative hypotheses.

Two-Tailed Test (most common)	Left-Tailed Test (rare)	Right-Tailed Test (rare)
$H_0: p_1 = p_2$ $H_a: p_1 \neq p_2$	$H_0: p_1 = p_2$ $H_a: p_1 < p_2$	$H_0: p_1 = p_2$ $H_a: p_1 > p_2$
 Rejection Region	 Rejection Region	 Rejection Region

Note: One tailed tests assume that the scenario not listed ($p_1 < p_2$ for a left-tailed test or $p_1 > p_2$ for a right-tailed test) is not possible or is of zero interest.

Step 4: Using your α level and hypotheses, sketch the rejection region.

Step 5: Use a normal curve table to determine the critical value for z associated with your rejection region.

Step 6: Compute the test statistic:

$$z = \frac{\hat{p}_1 - \hat{p}_2}{\sqrt{\hat{p}(1-\hat{p})\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}.$$

$\hat{p}$ = Pooled sample proportion

Step 7: Determine whether the value of z calculated from your sample (in Step 6) is in the rejection region.

- If z is in the rejection region, reject the null hypothesis.
- If z is not in the rejection region, do not reject the null hypothesis.

Step 8: State your conclusion and interpret the results of the hypothesis test.

Example 2: Suppose that a clinical trial for two different cancer drugs is conducted. For drug A, 637 of 2095 patients were cured. For drug B, 702 of 2119 patients were cured. Does this trial provide evidence that Drug B cures a higher percentage of patients than Drug A? Use a 5% level of significance.

1-tailed

Check assumptions:

	Cured	Not Cured	Total
Drug A	637	1458	2095
Drug B	702	1417	2119
Total	1339	2875	4214

All cells have at least 10, so can assume difference in proportions is normally distributed.

Sample info

Drug A: $n_1 = 2095$

$\hat{p}_1 = \frac{x_1}{n_1} = \frac{637}{2095} \approx 0.304$

Drug B:

$n_2 = 2119$

$\hat{p}_2 = \frac{x_2}{n_2} = \frac{702}{2119} \approx 0.331$

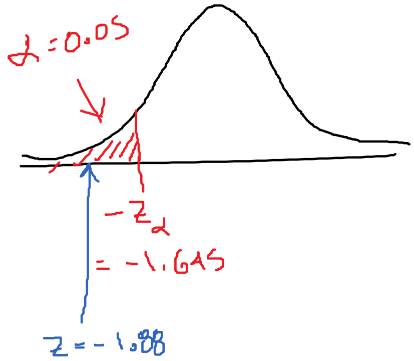
Hypotheses

$H_0: p_1 = p_2$

$H_1: p_1 < p_2$

$\alpha = 0.05$

Picture



From normal table, critical value is $-z_{0.05} = -1.645$

Calculate test statistic

Pooled sample proportion: $\hat{p} = \hat{p}_p = \frac{x_1 + x_2}{n_1 + n_2} = \frac{637 + 702}{2095 + 2119}$

$= \frac{1339}{4214} \approx 0.318$

$1 - \hat{p} = 1 - 0.318 = 0.682$

Std error: $\sigma_{\hat{p}_1 - \hat{p}_2} \approx \sqrt{\frac{\hat{p}(1-\hat{p})}{n_1} + \frac{\hat{p}(1-\hat{p})}{n_2}} = \sqrt{\frac{0.318(0.682)}{2095} + \frac{0.318(0.682)}{2119}}$

$= \sqrt{0.318(0.682)\left(\frac{1}{2095} + \frac{1}{2119}\right)} \approx 0.01435$ store in calculator

11.2 Example 2 Continued.

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$$Z = \frac{\hat{p}_1 - \hat{p}_2}{\text{std error}} = \frac{0.304 - 0.331}{0.01435} \approx -1.88$$

This is in the rejection region, so we $\boxed{\text{reject } H_0}$.

This sample provides evidence that Drug B cures a higher proportion of patients.

There is a statistically significant difference in favor of Drug B.

Confidence intervals:

We construct the confidence interval for the difference between two population proportions in the usual way: Start with a point estimate of the difference between the proportions, then add and subtract a margin of error, created by multiplying the critical value of *z* by the standard error.

This results in:

$$\hat{p}_1 - \hat{p}_2 \pm z_{\alpha/2}\sqrt{\hat{p}(1-\hat{p})\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}$$