

12.2: Hypothesis Tests for One Population Proportion

In a hypothesis test for one population proportion, we are testing the hypothesis that the population proportion p is equal to a benchmark value p_0 .

As long as $np \geq 5$ and $n(1-p) \geq 5$, we can assume that the sample proportion

$\hat{p} = \frac{x}{n}$ is normally distributed. Therefore the critical values come from the z -distribution.

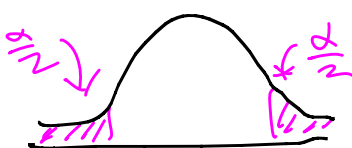


Hypothesis Testing for a Population Proportion:

Step 1: Determine the significance level α .

Step 2: Check that the assumptions are satisfied (simple random sample, $np \geq 5$ and $n(1-p) \geq 5$).

Step 3: Determine the null and alternative hypotheses.

$p_0 = \text{benchmark proportion}$

Two-Tailed Test (most common)	Left-Tailed Test (rare)	Right-Tailed Test (rare)
$H_0 : p = p_0$ $H_a : p \neq p_0$	$H_0 : p = p_0$ $H_a : p < p_0$	$H_0 : p = p_0$ $H_a : p > p_0$
		
Rejection Region	Rejection Region	Rejection Region

Note: One tailed tests assume that the scenario not listed ($p > p_0$ for a left-tailed test or $p < p_0$ for a right-tailed test) is not possible or is of zero interest.

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

Step 5: Use a normal curve table (Table C, on page 10) to determine the critical value for z associated with your rejection region.

or the shortcut critical values at bottom of t table

Step 6: Compute the test statistic $z = \frac{\hat{p} - p_0}{\sqrt{\frac{p_0(1-p_0)}{n}}}$.

← use benchmark p_0 here (not the sample proportion \hat{p})

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.

Example 1: A local police department claims that over 70% of false alarms from home security systems are caused by human error (e.g., a house-sitter or child sets off the alarm by mistake). A random sample of 450 police files for false alarm calls are analyzed. Of the 450 false alarms in the sample, 324 were caused by human error. Does this sample provide evidence to support the police department's claim? Use a 95% confidence level.

Characteristic of interest: alarm cause by human error

Sample info

$$n = 450$$

$$\hat{p} = \frac{x}{n} = \frac{324}{450} \approx 0.72$$

$$H_0: p = 0.70$$

$$H_a: p > 0.70$$

$$\alpha = 1 - 0.95 = 0.05$$

Check assumptions:

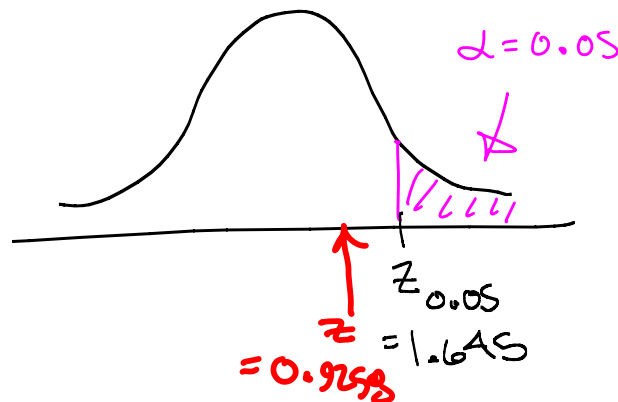
caused by
human error

$$324$$

not caused
by human error

$$126$$

(both ≥ 5 , so \hat{p} is normally distributed)



From table, critical value of
 z is $z_{0.05} = 1.645$

Find standard error:

$$\sigma_{\hat{p}} = \sqrt{\frac{p_0(1-p_0)}{n}} = \sqrt{\frac{0.7(0.3)}{450}} \approx 0.021602 \text{ (store in calculator)}$$

p_0 = benchmark
proportion = 0.7

$$q_0 = 1 - p_0 = 1 - 0.7 = 0.3$$

Calculate test statistic for our sample

$$z = \frac{\hat{p} - p_0}{\sigma_{\hat{p}}} \approx \frac{0.72 - 0.70}{0.021602} \approx 0.9258$$

↑ use stored value

This is not in
rejection region, so
Do not reject H_0

This sample does
not provide
evidence that
> 70% are human
error (does not provide
evidence for H_a)

Example 2: According to genetic theory, if two red/sorrel Appaloosa-spotted horses are mated, there is a 0.75 probability that the foal will be a red/sorrel Appaloosa (otherwise, the baby will be red/sorrel with no Appaloosa spotting). Suppose a genetic researcher analyzed a sample of 200 foals in which both the sire and dam were red/sorrel Appaloosas, and found that 135 of the foals were red/sorrel Appaloosas. Does this sample provide evidence that the proportion of Appaloosa foals from all such matings differs from 0.75? Use a 90% confidence level.

<http://www.animalgenetics.us/Equine/CCalculator3.asp>