

One-sample z -test

1. Assumptions

- **Experimental Design:** The sample forms a single treatment group.
- **Null Hypothesis:** The population mean of the treatment group is not significantly different from a hypothesized constant c .
- **Population Distribution:** Arbitrary.
- **Sample Size:** Greater than or equal to 30.

2. Inputs for the z -test

- Sample size: n
- Sample mean: \bar{x}
- Sample standard deviation: s_x
- Standard error of mean: $SE_{\text{mean}} = \frac{s_x}{\sqrt{n}}$
- Null hypothesis value: c
- The level of the test: α

3. Five Steps for Performing the Test of Hypothesis

1. State null and alternative hypotheses:

$$H_0 : \mu = c, \quad H_1 : \mu \neq c$$

2. Compute test statistic:

$$z = \frac{\bar{x} - \mu}{SE_{\text{mean}}},$$

assuming the null hypothesis value for μ .

3. Compute $100(1 - \alpha)\%$ confidence interval I for z .
4. If $z \in I$, accept H_0 ; if $z \notin I$, reject H_1 and accept H_0 .
5. Compute p -value.

4. Discussion

Since we are assuming that $n \geq 30$, the sample standard deviation s_x is a close approximation to the population standard deviation σ_x ; we will assume that σ_x is known and equal to s_x . Furthermore, since SE_{mean} is constant, $E(\bar{x}) = \mu_x$, and $SE_{\text{mean}} = s_x/\sqrt{n} = \sigma_x/\sqrt{n}$,

$$E(z) = E\left(\frac{\bar{x} - \mu_x}{SE_{\text{mean}}}\right) = \frac{E(\bar{x}) - \mu_x}{SE_{\text{mean}}} = \frac{\mu_x - \mu_x}{SE_{\text{mean}}} = 0$$

and

$$\text{Var}(z) = \text{Var}\left(\frac{\bar{x} - \mu_x}{SE_{\text{mean}}}\right) = \frac{\text{Var}(\bar{x} - \mu_x)}{SE_{\text{mean}}^2} = \frac{\text{Var}(\bar{x})}{SE_{\text{mean}}^2} = \frac{SE_{\text{mean}}^2}{SE_{\text{mean}}^2} = 1.$$

Thus, by the central limit theorem, z has an approximately standard normal distribution and we can use the standard normal table to compute confidence intervals and p -values for z .

4. A Sample Problem

Mendenhall and Sincich, p. 45: Humerus bones from the same species of animal have approximately the same length-to-width ratios. It is known that Species A has a mean ratio of 8.5. Suppose that 41 fossil humerus bones were unearthed at a site where Species A is known to have flourished. (We assume that all bones are from the same species.) The length-to-width ratios of these bones has sample mean 9.26 and sample standard deviation 1.20. Can we conclude that these bones belong to Species A? Perform a level 0.05 z -test to check.

Solution: We have these inputs:

$$n = 41 \quad \bar{x} = 9.26 \quad s_x = 1.20 \quad c = 8.5 \quad \alpha = 0.05$$

and compute

$$SE_{\text{mean}} = \frac{\sigma_x}{\sqrt{n}} = \frac{1.20}{\sqrt{41}} = 0.187.$$

Here are the five steps of the z -test:

1. State the null and alternative hypotheses:

$$H_0 = 8.5, \quad H_1 \neq 8.5$$

2. Compute the test statistic:

$$z = \frac{\bar{x} - \mu}{\text{SE}_{\text{mean}}} = \frac{9.26 - 8.5}{0.188} = 4.03$$

3. Find a $100(1-\alpha)\%$ confidence interval I : use the standard normal table to show that $[-1.96, 1.96]$ is a 95% confidence interval for z , which is $N(0, 1)$.
4. Determine whether to accept or reject H_0 : $4.03 \notin [-1.96, 1.96]$, so reject H_0 .
5. Compute the p -value: if u is standard normal,

$$P(u \leq -z) = P(u \leq -4.03) = 0.000028.$$

By the symmetry of the normal curve,

$$P(z \leq u) = P(4.03 \leq u) = 0.000028.$$

Thus $p = 0.000028 + 0.000028 = 0.000054$.

Note: although the confidence interval produced by the z -test is fairly accurate when compared to the t -test for the same problem if $n > 30$, the p -value produced by a z -test can be very much smaller than the p -value computed by the corresponding t -test, especially when the p -value is very small.