

Hypothesis Testing Continued

Example: Humerus bones from the same species of animal tend to have approximately the same length-to-width ratios. When fossils of humerus bones are discovered, archeologists can often determine the species of animal by examining the length-to width ratios of the bones. It is known that species A exhibits a mean ratio of 8.5. Suppose 41 fossils of humerus bones were unearthed at an archeological site in East Africa, where species A is believed to have lived. (Assume that all the unearthed bones were from the same unknown species.) The length-to-width ratios of the bones were calculated and listed as shown in the following table:

We wish to decide whether or not we can believe the unearthed bones come from species A. Our null hypothesis is the presumption that the unknown species whose bones were unearthed have the same length-to-width ratios as species A.

10.73	9.84	9.29	9.98	6.66	10.48	8.17	11.67
8.89	9.59	9.94	8.52	9.35	10.39	8.93	8.30
9.07	8.48	8.07	8.87	8.86	9.39	8.80	9.17
9.20	8.71	8.37	6.23	9.93	9.17	10.02	12.00
10.33	9.57	6.85	9.41	8.91	9.89	8.38	9.38
11.77							

We will set up the test of hypothesis for this experiment using $\alpha = 0.01$. Our hypotheses are

$$H_0: \mu = 8.5 \text{ (Mean length-to-width ratio is 8.5)}$$

$$H_a: \mu \neq 8.5 \text{ (Mean length-to-width ratio is less than 8.5 or greater than 8.5)}$$

Note that we wish to test whether the mean length-to width ratio from the unearthed bones differs from the known mean of 8.5 for species A *in either direction* – that is $\mu < 8.5$ or $\mu > 8.5$. So, we will conduct a two-tailed statistical test. Using MINTAB, the descriptive statistics are

Results for: BONES.MTP Descriptive Statistics: RATIO

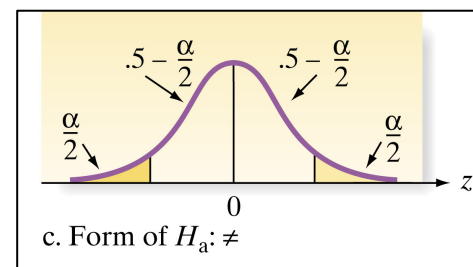
Variable	N	N*	Mean	SE Mean	StDev	Minimum	Q1	Median	Q3	Maximum
RATIO	41	0	9.258	0.188	1.204	6.230	8.615	9.200	9.935	12.000

Our test statistic measures the number of standard deviations between the observed value of \bar{x} and the null-hypothesized value $\mu = 8.5$.

$$z = \frac{\bar{x} - 8.5}{\sigma_{\bar{x}}} = \frac{\bar{x} - 8.5}{\sigma / \sqrt{n}} \approx \frac{\bar{x} - 8.5}{s / \sqrt{n}} \approx \frac{9.258 - 8.5}{1.204 / \sqrt{41}} \approx 4.03$$

The two-tailed rejection region for $\alpha = 0.01$ requires $\alpha/2 = 0.005$ in each tail of the z -distribution. The rejection region is $z < -2.58$ or $z > 2.58$. Since the test statistic falls in the rejection region, we reject H_0 . Hence, there is sufficient evidence, at the 0.01 level, to indicate that the true population mean of all bones of this particular (unknown) species differs from 8.5 at $\alpha = 0.01$.

The significance of this result is that the unknown species whose bones were unearthed is probably not species A.



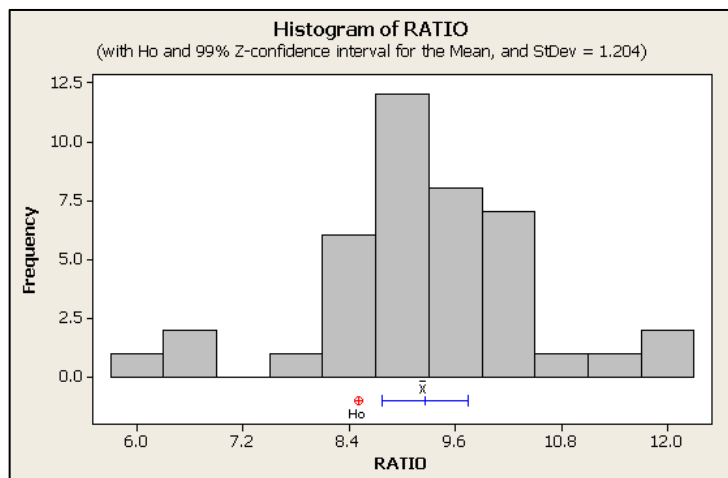
One-Sample Z: RATIO (MINITAB 1 Sample Z Output)

Test of mu = 8.5 vs not = 8.5
The assumed standard deviation = 1.204

Variable	N	Mean	StDev	SE Mean	99% CI	Z	P
RATIO	41	9.258	1.204	0.188	(8.773, 9.742)	4.03	0.000

Note the p-value in the last column of the MINITAB output on the previous page. The **p-value**, or observed significance level, is the smallest α that can be set that will result in the research hypothesis being accepted. Here are the steps in calculation the p-value:

- Determine value of test statistic z
- The p-value is the area to the right of z if H_a is one-tailed, upper tailed
- The p-value is the area to the left of z if H_a is one-tailed, lower tailed.
- The p-value is twice the tail area beyond z if H_a is two-tailed.



In the above example, $p\text{-value} = P(z < -4.03 \text{ or } z > 4.03) = 2P(z > 4.03) \approx 0.0000558$ (If H_0 is true 0.0000558 is the probability of observing a value of z that is as contradictory to H_0 , and supportive of the alternative hypothesis.) We can therefore interpret this p-value as a strong indication that $\mu \neq 8.5$.

Small Sample Test of Hypothesis about a Population Mean

Example: Suppose in the example above only 16 fossils of humerus bones were unearthed and the length-to-width ratios of those bones are displayed below.

10.48, 11.77, 6.66, 9.35, 6.23, 9.41, 9.93, 9.2, 8.71, 8.37, 9.84, 10.02, 12, 8.07, 8.93, 9.39

Variable	N	Mean	Median	TrMean	StDev	SE Mean
SmlSampl	16	9.273	9.370	9.295	1.533	0.383

As before, we specify $\alpha = 0.01$ (the probability that the test will lead to rejection of the null hypothesis when it is true) and find our rejection region. Consulting the t -table we find that when $\alpha = 0.01$, the two-tailed rejection region is determined by $t_{\alpha/2} = t_{0.005} = 2.947$ with $n - 1 = 15$ degrees of freedom so we reject H_0 if $t < -2.947$ or $t > 2.947$.

In the small sample case we must assume the population from which the sample is taken is approximately normal, and we use the t -distribution rather than the standard normal z -distribution. Our test statistics is

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}} = \frac{9.273 - 8.5}{1.533/\sqrt{16}} \approx 2.017$$

Since the calculated value of t does not fall in the rejection region, we cannot reject H_0 at the $\alpha = 0.01$ level of significance. So, we cannot conclude that $\mu \neq 8.5$. In this case we cannot conclude that the unearthed bones come from a species other than species A.

T-Test of the Mean

Test of $\mu = 8.500$ vs $\mu \text{ not } = 8.500$

Variable	N	Mean	StDev	SE Mean	T	P
SmlSampl	16	9.273	1.533	0.383	2.02	0.062