1 Sample *t*-Test

Suppose you have a sample of 30 (n=30) rib lengths in cm from a site that looks like an antelope (*Antilocapra americanus*) kill dating to around 1200 BP, from the Southern High Plains. We are interested in whether this sample differs significantly from the modern population mean of pronghorn, as a significant difference might have some paleoenvironmental implications.

Let $\overline{Y}$ = the sample mean of antelope rib lengths in cm, and μ = the population mean of modern antelope rib lengths, where μ = 12.3. To test the hypothesis of interest we shall conduct a 1 sample *t*-test stating that there is no significant difference between the sample mean and the hypothesized population mean. We choose to test the hypothesis by putting confidence limits at the 95% level (a = 0.05) around $\overline{Y}$.

Formally, we are interested in testing the hypothesis:

$$H_O : \overline{Y} - \mu = 0$$
$$H_A : \overline{Y} - \mu \neq 0$$

Here are the data:

11.8843	11.7983	13.1594
12.7797	10.5240	12.3171
12.1933	12.1730	12.3902
13.8384	13.7647	11.7518
11.5809	11.7373	12.0339
13.0889	11.3124	11.6815
10.7319	12.1283	11.8447
12.0781	12.1219	12.0989
10.7204	12.5919	12.9757
11.9428	11.5474	13.6249

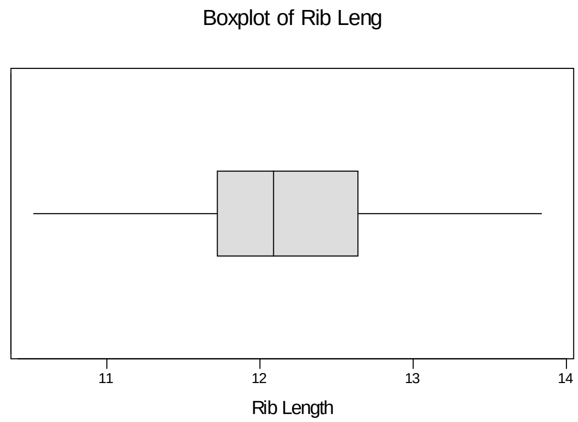
The descriptive statistics of this sample look like:

Descriptive Statistics

```
Variable          N      Mean    Median  Tr Mean     StDev  SE Mean
Rib Length       30    12.147    12.089   12.137     0.828    0.151

Variable        Min       Max        Q1       Q3
Rib Length   10.524    13.838    11.723   12.639
```

As the mean and median look pretty similar, looking at a boxplot below we conclude that the data is pretty much normally distributed.



Remembering to use the *standard error* as we are dealing with a sample and an unknown population variance, we use the following standard equations to establish the upper and lower confidence limits:

$$L_L = \overline{Y} - t\left(s / \sqrt{n}\right)$$
$$L_U = \overline{Y} + t\left(s / \sqrt{n}\right)$$

Where t = the table t_{CRIT} value obtained from the table (df = 29, a = 0.05, t_{CRIT} = 2.045). Calculating the standard error (or getting it from the descriptive statistics output), we see SE = 0.151. Plugging these values into the above equation we find

$$L_L = 12.147 - 2.045(0.151) = 11.838$$
$$L_U = 12.147 + 2.045(0.151) = 12.456$$

As our hypothesized μ = 12.3, we see that this value falls within the confidence limits established around the sample and we conclude that at the a = 0.05 level, we fail to reject the null hypothesis that there is no statistical difference between a sample mean of 12.147 cm for prehistoric late Holocene antelope, and an established population mean of modern antelope of 12.3 cm.

The MINITAB procedure for this test is straightforward:

>STAT

>BASIC STATS

>1 SAMPLE t

>Double click on your data column to get it into VARIABLES

>To establish CONFIDENCE INTERVALS select the test and choose the significance level (usually 95%). To test a MEAN, choose that test and input the appropriate hypothesized mean and choose the alternative hypothesis

>GRAPHS; choose a graphic output, either boxplot or histogram, or both

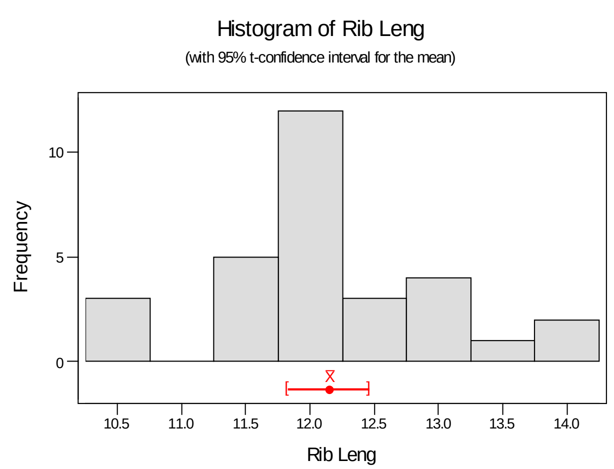
>OK

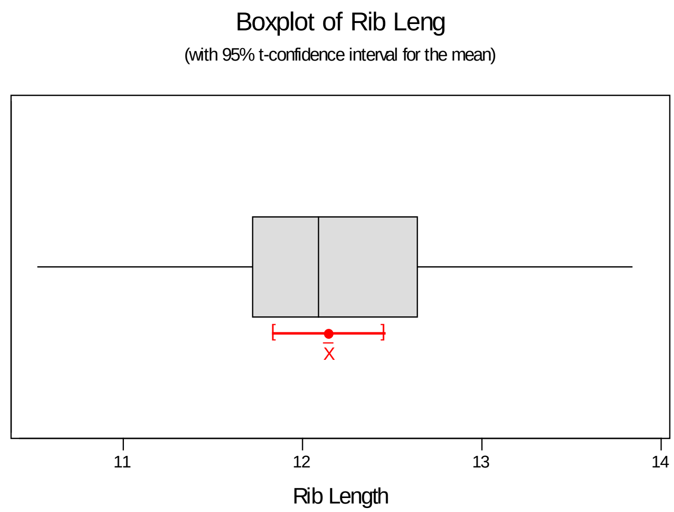
The output for a confidence limit test is as follows:

Confidence Intervals

```
Variable       N      Mean     StDev  SE Mean        95.0 % CI
Rib Length    30    12.147     0.828    0.151   (  11.838,   12.456)
```

With the graphics:





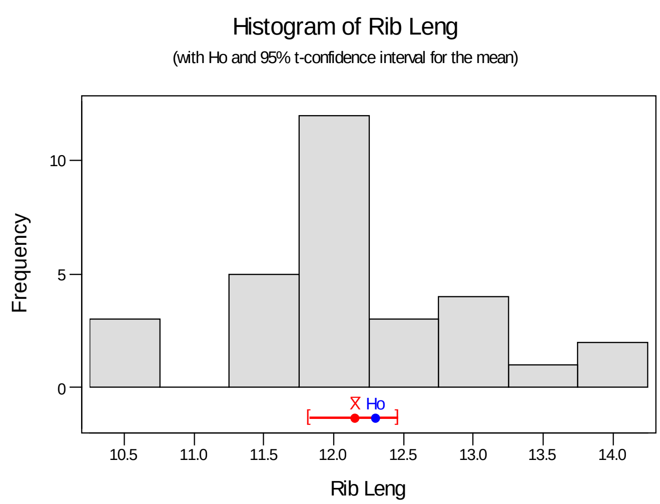
The output for the test of the mean is:

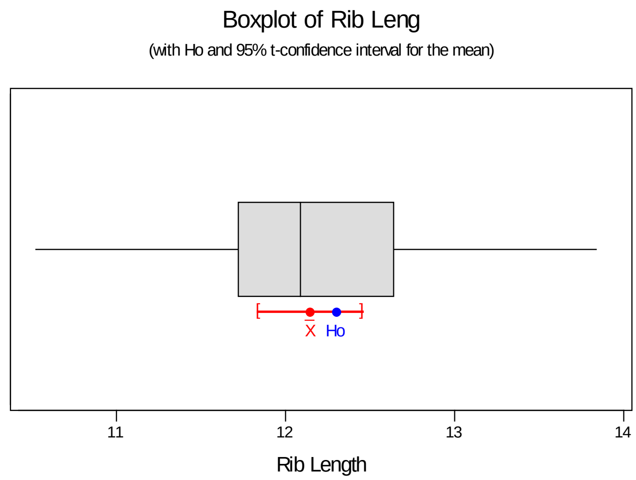
T-Test of the Mean

```
Test of mu = 12.300 vs mu not = 12.300

Variable      N      Mean     StDev    SE Mean        T           P
Rib Length   30    12.147     0.828      0.151    -1.01        0.32
```

With the graphical output:





You will notice that the two testing methods agree (of course!), but you get no *p* value with the confidence limit method. Also, with the test of the mean method, on the graphical output we get both the confidence limits established around the sample mean and the hypothesized population mean, labled H_O in blue.

If you choose to perform a *t*-test, choose one method over the other based on the question you are interested in; DO NOT PRESENT BOTH!