To approach this problem, we should consider the concepts of sampling distribution and hypothesis testing. We are given the population mean (\(\mu = 12.3\) inches) and the population standard deviation (\(\sigma = 3\) inches). We also have a sample of size \(n = 100\) with a sample mean (\(\bar{x} = 11.2\) inches).

The standard error of the mean (SEM) for the sample is calculated using the formula:

\[

\text{SEM} = \frac{\sigma}{\sqrt{n}} = \frac{3}{\sqrt{100}} = 0.3

\]

We want to test whether the sample mean is significantly different from the population mean. To do this, we can use a z-test for the mean:

\[

z = \frac{\bar{x} - \mu}{\text{SEM}} = \frac{11.2 - 12.3}{0.3} = \frac{-1.1}{0.3} \approx -3.67

\]

A z-value of -3.67 indicates that the sample mean is 3.67 standard errors below the population mean. We now should look up this z-value in standard normal distribution tables (or use a calculator) to find the p-value. A z-value of -3.67 corresponds to a very small p-value, much less than 0.05, typically regarded as the threshold for significance in hypothesis testing.

This means we reject the null hypothesis (\(H\_0: \mu = 12.3\)) in favor of the alternative hypothesis (\(H\_a: \mu < 12.3\)), concluding that the mean length of adult largemouth bass in Silver Lake this year is statistically significantly smaller than the established normal mean.

Thus, the most appropriate statistical conclusion is:

(C) The researchers can conclude that the fish are smaller than what is normal because the difference between 12.3 inches and 11.2 inches is much larger than the expected sampling error.