Hypothesis Testing for Population Mean (μ)

Case 1:

- Population mean is unknown
- Population standard deviation is known
- Sample size < 30
- Population is normally distributed

In this case, we can use normal distribution to run the hypothesis test

Case 2:

- Population mean is unknown
- Population standard deviation is known
- Sample size >= 30
- Population may or may not be normally distributed

In this case, we can use normal distribution to run the hypothesis test

Case 3:

- Population mean is unknown
- Population standard deviation is known
- Sample size < 30
- Population is not normally distributed

In this case, use non-parametric method.

Methods to run hypothesis test

There are two ways to run a hypothesis test.

1) Rejection region approach
2) P-value approach

For **Cases 1 and 2**, we use normal distribution to run the hypothesis test.

Suppose sample mean = $\bar{x}$. We first have to standardize this value:

$$Z_{\bar{X}} = \frac{\bar{x} - \mu}{\sigma / \sqrt{n}}$$

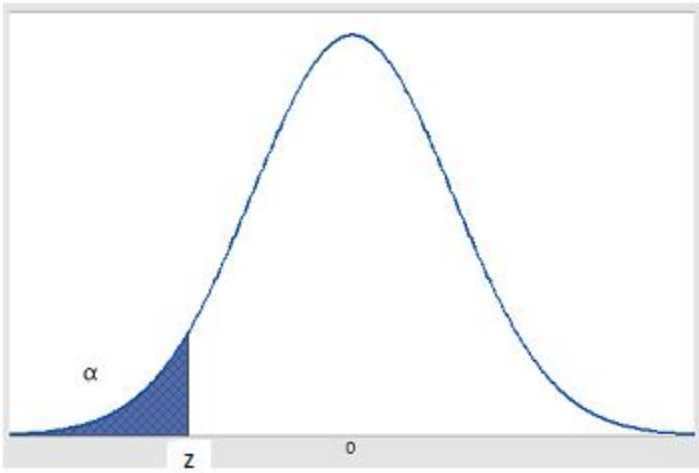
Significance level in hypothesis testing is the probability of falling into the rejection region: α (usually very small, like 0.1, 0.05, 0.025..)

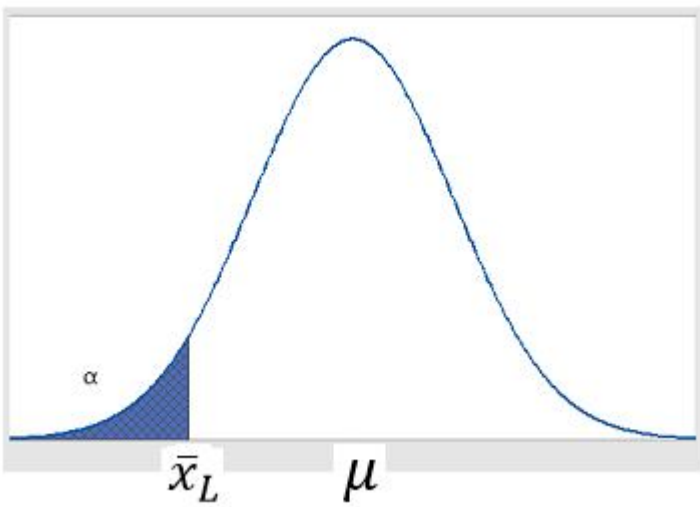
Left-tailed test

- Rejection Region Approach

We reject the null hypothesis if the sample mean $\bar{x}$ is less than equal to a threshold value $\bar{x}_L$. In a left-tailed test, $\bar{x}_L$ lies on the left tail of the normal distribution. To find $\bar{x}_L$ we need to find the z-critical value from the normal distribution table.

1. Find the z-critical value that has an area of α to the **left**.
2. Convert the z-critical value into $\bar{x}_L$. (use standardization formula backward)
3. Compare $\bar{x}$ to $\bar{x}_L$. Compare $Z_{\bar{X}}$ to the z-critical value.





Rejection Rule for left tailed test:

Reject H_0 if $\bar{x} \leq \bar{x}_L$

Do not reject H_0 if $\bar{x} > \bar{x}_L$

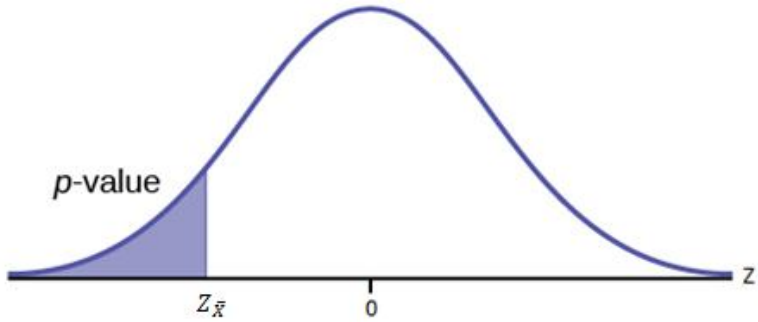
OR

Reject H_0 if $Z_{\bar{X}} \leq$ z critical value

Do not reject H_0 if $Z_{\bar{X}} >$ z critical value

- P-value Approach

For left tailed test, find the area to the left of $Z_{\bar{X}}$



Reject H_0 if p-value < α

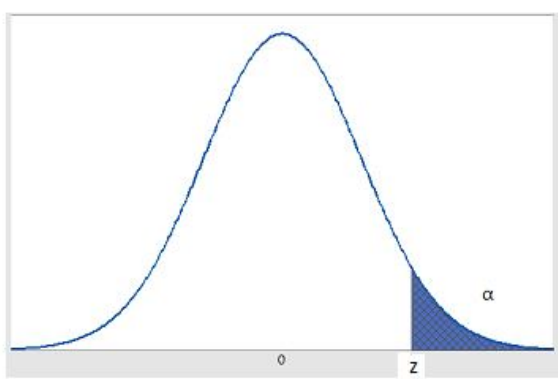
Do not reject H_0 if p-value > α

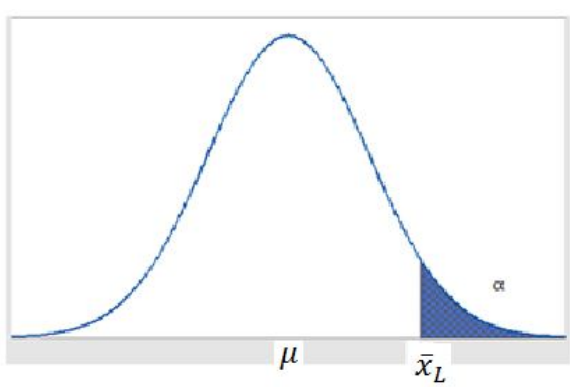
Right-tailed test

- Rejection Region Approach

We reject the null hypothesis if the sample mean $\bar{x}$ is greater than equal to a threshold value $\bar{x}_L$. In a right-tailed test, $\bar{x}_L$ lies on the right tail of the normal distribution. To find $\bar{x}_L$ we need to find the z-critical value from the normal distribution table.

1. Find the z-critical value that has an area of α to the **right**
2. Convert the z-critical value into $\bar{x}_L$. (use standardization formula backward)
3. Compare $\bar{x}$ to $\bar{x}_L$. Compare $Z_{\bar{X}}$ to the z-critical value.





Rejection Rule for right tailed test:

Reject H_0 if $\bar{x} \geq \bar{x}_L$

Do not reject H_0 if $\bar{x} < \bar{x}_L$

OR

Reject H_0 if $Z_{\bar{X}} \geq$ z critical value

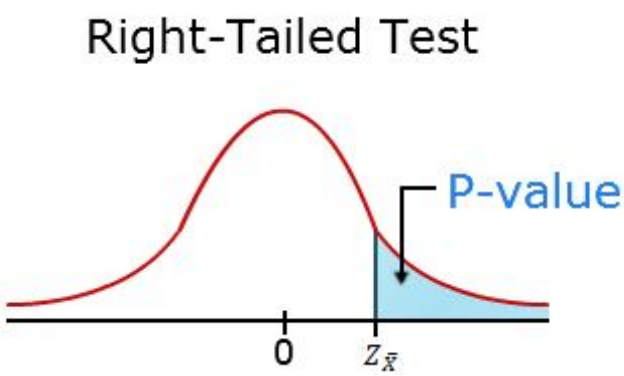
Do not reject H_0 if $Z_{\bar{X}} <$ z critical value

- P-value Approach

For a right-tailed test, p-value is the area to the right of $Z_{\bar{X}}$.

Reject H_0 if p-value < α

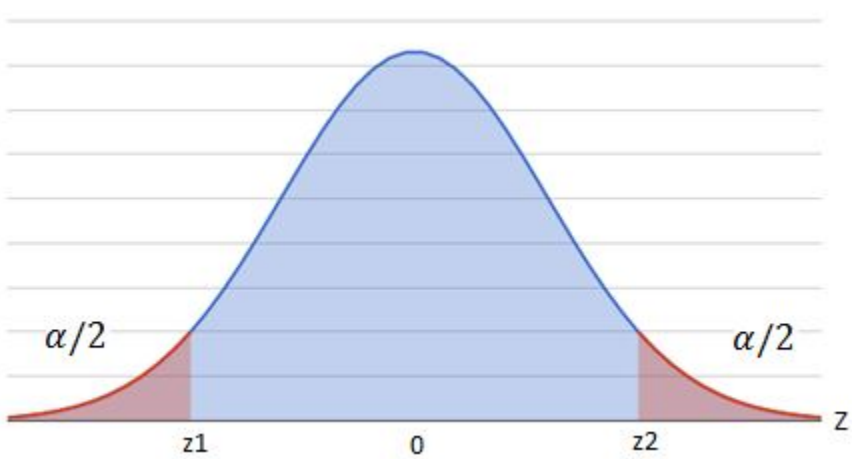
Do not reject H_0 if p-value > α

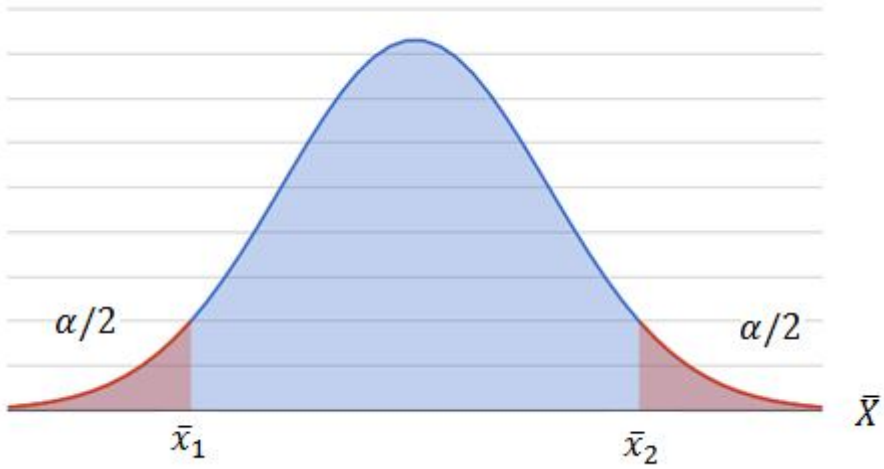


Two-tailed test

- Rejection Region Approach

1. Find two z-critical values. One that has an area of $\alpha/2$ to the **right**, and one that has an area of $\alpha/2$ to the **left.**
2. Compare $Z_{\bar{X}}$ to the z-critical values





Rejection Rule:

Reject H_0 if $\bar{x} \leq \bar{x}_1$ or $\bar{x} \geq \bar{x}_2$

Do not reject H_0 if $\bar{x}_1 < \bar{x} < \bar{x}_2$

OR

Reject H_0 if $Z_{\bar{X}} \leq z_1$ or if $Z_{\bar{X}} \geq z_2$

Do not reject H_0 if $z_1 < Z_{\bar{X}} < z_2$

- P-value Approach

For two-tailed tests, p-value is calculated as follows:

If $Z_{\bar{X}} < 0$, then p-value is $2 \times P(Z < Z_{\bar{X}})$

If $Z_{\bar{X}} > 0$, then p-value is $2 \times P(Z > Z_{\bar{X}})$

Reject H_0 if p-value < α

Do not reject H_0 if p-value > α