

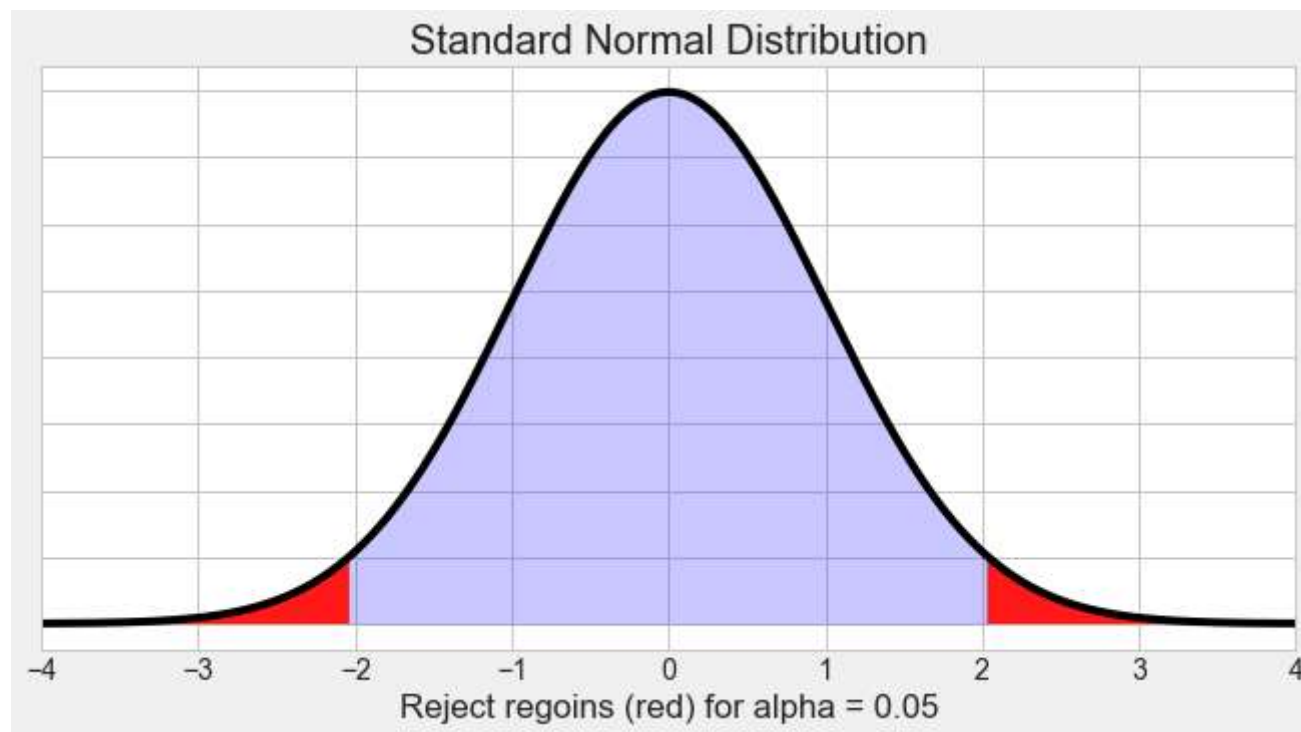
What is Z-Test?

It is a statistical hypothesis test used to determine whether there is a significant difference between the mean of a sample and the population mean. It is particularly useful when the population standard deviation is known. The test statistic follows a standard normal distribution (Z-distribution) under the null hypothesis.

Significance Level, α

It is a critical threshold used in hypothesis testing to determine whether to reject the null hypothesis. It represents the maximum probability of making a Type I error, which occurs when we incorrectly reject the null hypothesis when it is actually true.

Commonly used significance levels include 0.05 (5%), 0.01 (1%), and 0.10 (10%).



Rejection Region

Rejection Region

In hypothesis testing, the rejection region (also known as the critical region) is the range of values of the test statistic for which the null hypothesis is rejected. It is determined based on the chosen significance level (α) and the sampling distribution of the test statistic under the null hypothesis.

```
In [2]: # Import the necessary libraries
import numpy as np
import scipy.stats as stats
```

1. Z-test for One-Sample Mean:

This test is used when you have a single sample and want to compare its mean to a known population mean. The null hypothesis typically states that there is no difference between the sample mean and the population mean.

The formula for the test statistic in a one-sample Z-test is:

Z-statistic

Based on CLT: $\bar{X} \sim N(\mu, \sigma^2/n)$

Under H_0 , $Z \sim N(0, 1)$

$$Z = \frac{\bar{X} - \mu_0}{\sigma/\sqrt{n}}$$

if σ is unknown (the case in almost all applications) and the sample size is large, we can replace it with the sample standard deviation s , then:

$$Z = \frac{\bar{X} - \mu_0}{s/\sqrt{n}} \text{ where } s = \sqrt{\frac{\sum_{i=1}^n (X_i - \bar{X})^2}{n-1}}$$

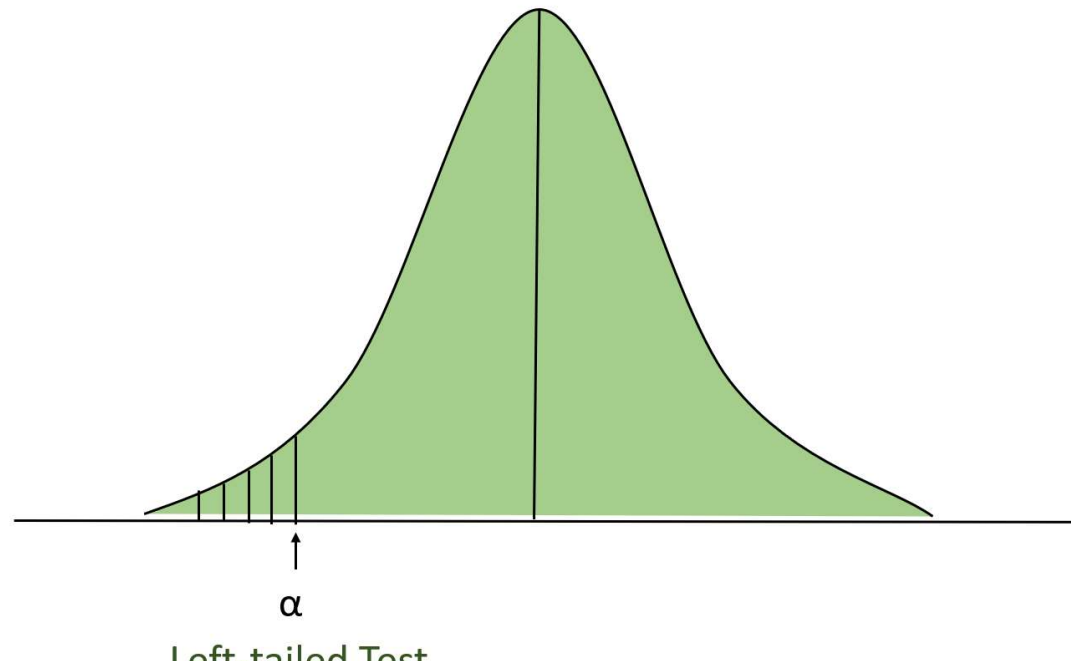
where:

- \bar{X} is the sample mean
- μ is the population mean
- σ is the population standard deviation
- n is the sample size

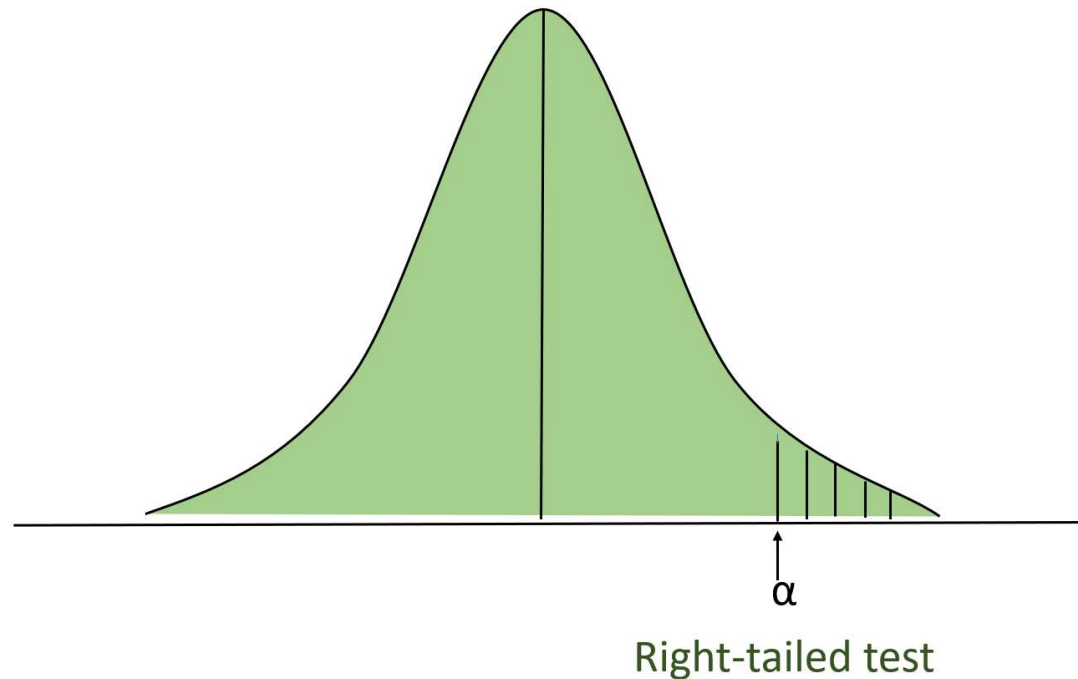
One-Tail Z-Test

In a one-tail (or one-sided) Z-test, the critical region (rejection region) is located entirely in one tail of the sampling distribution.

Left-tailed Test: In this test, our region of rejection is located to the extreme left of the distribution. Here our null hypothesis is that the claimed value is less than or equal to the mean population value.



Right-tailed Test: In this test, our region of rejection is located to the extreme right of the distribution. Here our null hypothesis is that the claimed value is less than or equal to the mean population value.



The decision to reject the null hypothesis occurs when the test statistic falls in the critical region corresponding to the specified direction.

Note: One-tail tests are appropriate when there is a specific hypothesis about the direction of the difference between the sample mean and the population mean.

Question:

Suppose a company is evaluating the impact of new training program on productivity of its employees $\mu = 50$ and $\sigma = 5$. After training from sample_size 30, sample mean is 53. The company wants to know if new training program has any significance on productivity increase.

Null Hypothesis $H_0 : \mu = 50$

Alternative Hypothesis $H_a : \mu > 50$

```
In [3]:  $\bar{X}$  = 53 # sample_mean
 $\mu$  = 50 # population_mean
n = 30 # sample_size
 $\sigma$  = 5 # population_std
```

```
In [4]: # compute the z-score
z_score = ( $\bar{X}$ - $\mu$ )/( $\sigma$ /np.sqrt(n))
print('Z-Score : ',z_score)
```

Z-Score : 3.2863353450309964

Confidence interval for a population mean

Let X_1, \dots, X_n be independent samples from a population with mean μ and suppose that $n > 30$ so that we can apply the CLT. If the standard deviation is known, then a level $(1 - \alpha) * 100\%$ confidence interval for μ is

$$\bar{X} \pm z_{\alpha/2} \frac{\sigma}{\sqrt{n}}$$

Point estimate: \bar{X}

Margin of error: $z_{\alpha/2} \frac{\sigma}{\sqrt{n}}$

If σ is unknown to us, we can use the sample standard deviation s .

$$s = \sqrt{\frac{\sum_{i=1}^n (X_i - \bar{X})^2}{n-1}}$$

```
In [5]: alpha = 0.05
```

```
In [8]: # Critical Z-Score
def z_test(alpha, z_score):
    z_critical = stats.norm.ppf(1-alpha)
    print('Critical Z-Score : ', z_critical)

    # Hypothesis
    if z_score > z_critical:
        print("Reject Null Hypothesis")
    else:
        print("Fail to Reject Null Hypothesis")
```

```
In [9]: z_test(alpha, z_score)
```

Critical Z-Score : 1.6448536269514722
Reject Null Hypothesis

```
In [10]: # P-Value : Probability of getting less than a Z-score
def p_value(z_score):
    p_value = 1-stats.norm.cdf(z_score)

    print('p-value : ', p_value)

    # Hypothesis
    if p_value < alpha:
        print("Reject Null Hypothesis")
    else:
        print("Fail to Reject Null Hypothesis")
```

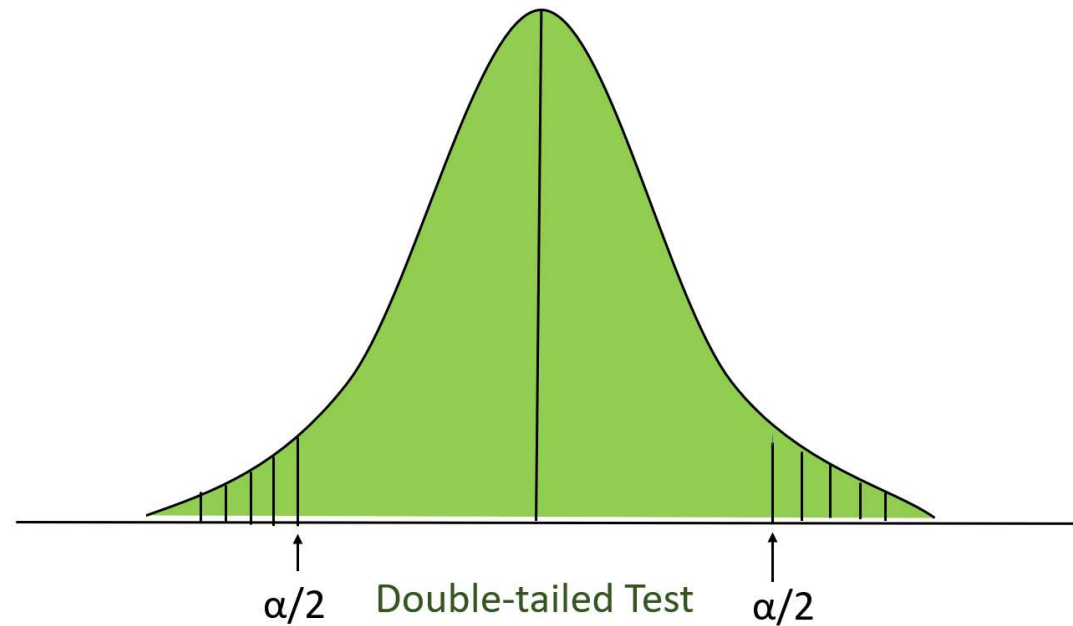
```
In [11]: p_value(z_score)
```

p-value : 0.0005075004735565214
Reject Null Hypothesis

Two-tail Z-test:

In a two-tail (or two-sided) Z-test, the critical region is divided into two tails of the sampling distribution, representing extreme

In a two-tail (or two-sided) Z-test, the critical region is divided into two tails of the sampling distribution, representing extreme values in either direction from the population mean.



The decision to reject the null hypothesis occurs when the absolute value of the test statistic falls in either tail of the critical region.

Note: Two-tail tests are appropriate when there is no specific hypothesis about the direction of the difference, and you want to test whether the sample mean is significantly different from the population mean, regardless of direction.

Question:

Suppose a snack food company claims that the packet of their wafers have average weight = 50 gms. To verify this a consumer watchdog organisation decided to do a test on random sample of 40 wafers packets. They find sample has average weight of 49 gms and known population standard deviation is 4 gms.

given and known population standard deviation is 4 given.

Null Hypothesis $H_0 : \mu = 50$

Alternative Hypothesis $H_a : \mu \neq 50$

In [12]:

```
 $\bar{X}$  = 49 # sample_mean  
 $\mu$  = 50 # population_mean  
n = 40 # sample_size  
 $\sigma$  = 4 # population_std
```

In [13]:

```
# compute the z-score  
z_score = ( $\bar{X}$ - $\mu$ )/( $\sigma$ /np.sqrt(n))  
print('Z-Score : ',z_score)
```

Z-Score : -1.5811388300841895

In [14]:

```
z_test(alpha, z_score)
```

Critical Z-Score : 1.6448536269514722

Fail to Reject Null Hypothesis

In [15]:

```
p_value(z_score)
```

p-value : 0.9430768509966709

Fail to Reject Null Hypothesis

2. Z-Test for Comparing the Means of Two Populations

This test is used to compare the means of two independent samples when the population standard deviations are known. The null hypothesis typically states that there is no difference between the means of the two populations.

The formula for the test statistic in a two-sample Z-test is similar to the one-sample Z-test, but it involves the difference between the means of the two samples

Let X_1 be a large random sample of size n_1 from a population with mean μ_1 and standard deviation σ_1 .

Let X_2 be a large random sample of size n_2 from a population with mean μ_2 and standard deviation σ_2 .

The population mean of interest becomes the difference of the population means: $\mu_1 - \mu_2$.

▼ Hypotheses

$$H_0 : \mu_1 = \mu_2,$$

$$H_1 : \mu_1 \neq \mu_2.$$

▼ Z-statistic

$$X_1 \sim N(\mu_1, \sigma_1^2)$$

$$X_2 \sim N(\mu_2, \sigma_2^2)$$

$$X_1 - X_2 \sim N(\mu_1 - \mu_2, \sigma_1^2 + \sigma_2^2)$$

$$\bar{X}_1 - \bar{X}_2 \sim N(\mu_1 - \mu_2, \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2})$$

$$\frac{\bar{X}_1 - \bar{X}_2 - (\mu_1 - \mu_2)}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}} \sim N(0, 1)$$

$$\text{Under } H_0, Z = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}} \sim N(0, 1)$$

where,

- \bar{X}_1 and \bar{X}_2 are the sample means of the two groups
- σ_1 and σ_2 are the population standard deviations of the two groups
- n_1 and n_2 are the sample sizes of the two groups

Question:

Does a new teaching method lead to a significant improvement in students' test scores compared to the traditional method?

```
# Generate random test scores for two groups
np.random.seed(123)
sample_size = 30
scores_new_method = np.random.normal(loc=75, scale=10, size=sample_size) # New teaching method
scores_traditional_method = np.random.normal(loc=70, scale=10, size=sample_size) # Traditional method

# Perform two-sample Z-test
z_stat, p_value = stats.ttest_ind(scores_new_method, scores_traditional_method)

# Set significance level
alpha = 0.05

# Print results
print("Two-sample Z-test results:")
print("Z-statistic:", z_stat)
print("P-value:", p_value)

# Interpret the results
if p_value < alpha:
    print("Reject the null hypothesis: There is a significant difference in test scores between the two groups.")
else:
    print("Fail to reject the null hypothesis: There is no significant difference in test scores between the two g
```

Two-sample Z-test results:

Z-statistic: 1.290510429939904

P-value: 0.2019944589487864

Fail to reject the null hypothesis: There is no significant difference in test scores between the two groups.

In []: