

Answer any three of the following questions.

1.. Define with examples

(i) Parameter and Statistic,

(ii) Null and Alternative hypotheses

(iii) Critical Value and Critical Region.

2.Explain clearly about type I and type II errors. What do you mean by p value and level of significance? Discuss about the test procedures of hypothesis testing.

Type I Error and Type II Error:

Type I Error (False Positive): In hypothesis testing, a Type I error occurs when we reject the null hypothesis (H_0) when it is actually true. In other words, we conclude that there is a significant effect or difference when there is none in the population. The probability of committing a Type I error is denoted by α (alpha) and is called the level of significance.

Type II Error (False Negative): A Type II error occurs when we fail to reject the null hypothesis (H_0) when it is actually false. In this case, there is a real effect or difference in the population, but our test fails to detect it. The probability of committing a Type II error is denoted by β (beta).

In statistical hypothesis testing, we aim to minimize both Type I and Type II errors, but there is often a trade-off between them. As we decrease the probability of one type of error, the probability of the other type of error may increase.

P-value and Level of Significance:

P-value: The p-value is the probability of obtaining a test statistic as extreme as the one calculated from the sample data, assuming that the null hypothesis is true. In other words, it measures the strength of evidence against the null hypothesis. A small p-value (usually less than the chosen level of significance) suggests strong evidence to reject the null hypothesis, while a large p-value suggests weak evidence, and we fail to reject the null hypothesis.

Level of Significance (α): The level of significance (α) is the pre-determined threshold that we set to make a decision about the null hypothesis. It represents the maximum probability of committing a Type I error. Commonly used values for α are 0.05 (5%) and 0.01 (1%). If the p-value is less than or equal to the chosen level of significance (α), we reject the null hypothesis. If the p-value is greater than the level of significance, we fail to reject the null hypothesis.

Test Procedures of Hypothesis Testing:

1. State the Hypotheses:

- Null Hypothesis (H_0): The hypothesis of no effect or no difference, usually denoted with an equal sign (e.g., $H_0: \mu = \mu_0$).

- Alternative Hypothesis (H1): The hypothesis stating that there is a significant effect or difference, and it contradicts the null hypothesis (e.g., $H_1: \mu \neq \mu_0$ for a two-tailed test).
2. Choose the Test Statistic: The test statistic is a measure calculated from the sample data, used to determine how far the observed data deviate from what would be expected if the null hypothesis were true.
 3. Set the Level of Significance (α): Select the desired level of significance (e.g., $\alpha = 0.05$ or $\alpha = 0.01$) to control the probability of making a Type I error.
 4. Calculate the P-value: Use the test statistic to calculate the probability (p-value) of obtaining the observed data under the assumption that the null hypothesis is true.
 5. Make a Decision: Compare the p-value with the chosen level of significance (α):
 - If $p\text{-value} \leq \alpha$, reject the null hypothesis (significant result).
 - If $p\text{-value} > \alpha$, fail to reject the null hypothesis (non-significant result).
 6. Interpret the Result: Conclude whether there is enough evidence to support the alternative hypothesis or if the data do not provide enough evidence to reject the null hypothesis. Consider the implications of both Type I and Type II errors in the context of the specific problem being studied.

3.

What is power of a test?

Power of a Test: The power of a statistical test is the probability of correctly rejecting a null hypothesis (H_0) when it is false. In other words, it is the probability of detecting an effect or a true difference between groups when there is indeed a real effect in the population. Power is an important concept in hypothesis testing because it helps assess the sensitivity of a test and its ability to identify true effects.

A high power indicates that the test is more likely to correctly detect a real effect, while a low power suggests that the test may not be sensitive enough to detect true effects even if they exist. Power is influenced by several factors, including the sample size, the effect size, the level of significance (α), and the variability of the data.

What is BCR stand for

BCR: BCR stands for "Baseline Conversion Rate." It is a term commonly used in A/B testing and marketing experiments to refer to the proportion or percentage of individuals who perform a specific action or convert in the control group or baseline condition.

In A/B testing, an experiment is conducted to compare two or more variants (A, B, etc.) to determine which variant performs better in terms of the desired outcome. The BCR represents the conversion rate in the baseline or control group against which the performance of other variants is compared.

Explain the test procedure for testing the

(i) $H_0: \mu = \mu_0$ vs. $H_1: \mu < \mu_0$ (For large sample case) and

(i) Testing $H_0: \mu = \mu_0$ vs. $H_1: \mu < \mu_0$ (For large sample case): In this scenario, we want to test whether the population mean (μ) is less than a specific value (μ_0). The test procedure is as follows:

1. Set up the hypotheses:
 - Null Hypothesis (H_0): The population mean is equal to or greater than μ_0 ($\mu \geq \mu_0$).
 - Alternative Hypothesis (H_1): The population mean is less than μ_0 ($\mu < \mu_0$).
2. Choose the significance level (α): Select the desired level of significance to determine the critical region for the test.
3. Compute the test statistic: The test statistic for this case is typically the z-score when the sample size is large. The z-score is calculated as: $z = (\bar{x} - \mu_0) / (\sigma / \sqrt{n})$
4. Determine the critical value: The critical value (z_{critical}) is obtained from the standard normal distribution table based on the chosen significance level (α).
5. Compare the test statistic and critical value:
 - If the test statistic falls in the critical region ($z < z_{\text{critical}}$), reject the null hypothesis.
 - If the test statistic falls in the non-critical region ($z \geq z_{\text{critical}}$), fail to reject the null hypothesis.

(ii) $H_0: \mu = \mu_0$ vs. $H_1: \mu \neq \mu_0$ (for small and unknown variance).

(ii) Testing $H_0: \mu = \mu_0$ vs. $H_1: \mu \neq \mu_0$ (for small and unknown variance): In this case, we want to test whether the population mean (μ) is different from a specific value (μ_0). The test procedure involves using the t-distribution when the sample size is small or when the population standard deviation is unknown.

1. Set up the hypotheses:
 - Null Hypothesis (H_0): The population mean is equal to μ_0 ($\mu = \mu_0$).
 - Alternative Hypothesis (H_1): The population mean is not equal to μ_0 ($\mu \neq \mu_0$).
2. Choose the significance level (α): Select the desired level of significance to determine the critical region for the test.
3. Compute the test statistic: The test statistic for this case is the t-score, which is calculated as: $t = (\bar{x} - \mu_0) / (s / \sqrt{n})$

Here, s is the sample standard deviation.

4. Determine the critical values: The critical values (t_{critical}) are obtained from the t-distribution table based on the chosen significance level (α) and the degrees of freedom ($df = n - 1$).
5. Compare the test statistic and critical values:

- If the test statistic falls outside the interval defined by the critical values, reject the null hypothesis.
- If the test statistic falls within the interval defined by the critical values, fail to reject the null hypothesis.

In both cases, if the null hypothesis is rejected, it suggests that there is evidence of a significant difference between the sample mean and the hypothesized value (μ_0), supporting the alternative hypothesis. If the null hypothesis is not rejected, it means there is not enough evidence to support the alternative hypothesis, and the data do not show a significant difference from the hypothesized value.

4. What is dichotomous and manifold classification? State the uses Yate's correction.

1. **Dichotomous Classification:** Dichotomous classification refers to a type of classification or grouping that divides items or individuals into only two mutually exclusive categories or classes. In other words, it is a binary classification system where each item can belong to one and only one of the two categories. The term "dichotomous" comes from the Greek words "di," meaning two, and "chotomous," meaning divided.

Example: In a medical context, a doctor may classify patients into two categories: "Has a specific medical condition" and "Does not have the specific medical condition."

2. **Manifold Classification:** Manifold classification, on the other hand, refers to a classification system with multiple categories or classes. Unlike dichotomous classification, manifold classification allows for more than two possible outcomes or classes.

Example: In a survey about favorite colors, the respondents may be classified into several categories such as "Red," "Blue," "Green," "Yellow," and "Others."

Uses of Yates' Correction: Yates' correction is a method used in statistical tests, specifically in 2x2 contingency tables, to correct for continuity when performing a chi-square test of independence or a chi-square test of homogeneity. It is named after the British statistician Frank Yates.

The chi-square test is commonly used to determine if there is a significant association between two categorical variables. In small sample sizes, the normal chi-square test may be too sensitive and might lead to overly significant results. Yates' correction helps to adjust the chi-square test statistic to account for this sensitivity and to give more accurate results, especially in 2x2 contingency tables.

Yates' correction formula is as follows:

$$\text{Corrected chi-square } (\chi^2_{\text{corrected}}) = \frac{|(ad - bc) - n/2|^2}{n * (a + b)(c + d)(a + c)(b + d)}$$

Where:

- a, b, c, d: The cell frequencies in the 2x2 contingency table.
- n: The total sample size ($n = a + b + c + d$).

Yates' correction adjusts the chi-square test statistic by subtracting 0.5 from the absolute difference between the observed and expected frequencies before squaring it. This correction reduces the sensitivity of the test in small samples and yields more conservative results.

It's important to note that some statistical software and calculators automatically apply Yates' correction when conducting a chi-square test for a 2x2 contingency table. However, for larger contingency tables, Yates' correction is not recommended, and the standard chi-square test without correction is sufficient.

5. Explain about Brandt and Snedecor 2xk contingency table for testing independence of attributes.

The Brandt and Snedecor 2xk contingency table is a statistical method used to test the independence of attributes or categorical variables when you have two independent groups (2x) and each group has more than two categories (k). This test is an extension of the chi-square test of independence for larger contingency tables.

Let's break down the components of the 2xk contingency table:

Two Independent Groups (2x):

The data is divided into two distinct and unrelated groups. For example, this could be two different treatment groups, two different populations, or two different experimental conditions.

More than Two Categories (k):

Each group has more than two categories (levels) for the categorical variable being studied. For example, the categories could be "A," "B," "C," etc.

The Contingency Table:

The data is organized into a contingency table, which cross-tabulates the two categorical variables. The table will have two rows (representing the two groups) and k columns (representing the different categories). The cells of the table contain the frequencies or counts of observations falling into each category based on the combination of the two groups.

For example, suppose we want to study the independence of gender (Male and Female) and the preferred mode of transportation (Car, Bus, Bicycle) for two different cities (City 1 and City 2). The 2xk contingency table might look like this:

City 1		City 2
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Gender | Male | Female | Male | Female

Car | 50 | 60 | 70 | 45

Bus | 30 | 25 | 20 | 35

Bicycle | 15 | 20 | 25 | 30

To test the independence of attributes in the 2xk contingency table, you would use a statistical test like the chi-square test for independence. This test assesses whether the observed differences between the groups are significantly different from what would be expected if the two categorical variables were independent.

The null hypothesis (H0) for the chi-square test of independence states that there is no association between the two categorical variables, meaning they are independent. The alternative hypothesis (H1) states that there is an association between the two variables.

By comparing the observed frequencies in the table with the expected frequencies (which assume independence), the chi-square test calculates a test statistic. Based on the test statistic and the degrees of freedom, you can then determine if there is enough evidence to reject the null hypothesis and conclude that the attributes are not independent.

Note that other methods, such as Fisher's exact test, may be more appropriate for small sample sizes or when certain assumptions of the chi-square test are violated.

6. The mean breaking strength of cables supplied by a manufacturer is 1800 with a standard deviation 100. By a new technique in the manufacturing process it is claimed that the breaking strength of the cable has increased. In the order to test this claim a sample of 50 cables is tested. It is found that the mean breaking strength is 1850. Can we support the claim at 0.01 and 0.05 level of significances?

To test the claim that the breaking strength of the cables has increased after applying the new manufacturing technique, we can conduct two one-sample t-tests at the 0.01 and 0.05 levels of significance.

Let's set up the hypotheses:

Null Hypothesis (H0): The mean breaking strength of the cables is still 1800 (no increase in breaking strength). Alternative Hypothesis (H1): The mean breaking strength of the cables has increased and is now greater than 1800.

We will use the t-test formula:

$$t = (\bar{x} - \mu) / (s / \sqrt{n})$$

Where: \bar{x} = Sample mean (1850 in this case) μ = Population mean under the null hypothesis (1800) s = Standard deviation of the population (100 in this case) n = Sample size (50)

First, let's calculate the t-statistic:

$$t = (1850 - 1800) / (100 / \sqrt{50}) \quad t = 50 / (100 / 7.07) \quad t \approx 50 / 14.14 \quad t \approx 3.54$$

Next, let's find the critical t-values for both the 0.01 and 0.05 levels of significance.

For a one-tailed t-test (since we are testing for an increase), with 49 degrees of freedom (50 - 1), the critical t-values are approximately:

- For the 0.01 level of significance: $t_{\text{critical}}(0.01) \approx 2.403$
- For the 0.05 level of significance: $t_{\text{critical}}(0.05) \approx 1.684$

Now, let's interpret the results for each level of significance:

At the 0.01 level of significance: Since the calculated t-value (3.54) is greater than the critical t-value (2.403), we reject the null hypothesis at the 0.01 level of significance. We have enough evidence to support the claim that the breaking strength of the cables has increased at the 0.01 level.

At the 0.05 level of significance: Since the calculated t-value (3.54) is greater than the critical t-value (1.684), we also reject the null hypothesis at the 0.05 level of significance. We have enough evidence to support the claim that the breaking strength of the cables has increased at the 0.05 level.

In conclusion, based on the sample data, we can support the claim that the breaking strength of the cables has increased after applying the new manufacturing technique at both the 0.01 and 0.05 levels of significance.

7. A random sample of 12 boys had the following I.Q.'s: 70, 120, 111, 98, 110, 88, 107, 100, 83, 90, 115, 81 Do these data support the assumption of a population mean I.Q. of 100?

To determine if the data supports the assumption of a population mean IQ of 100, we can conduct a hypothesis test. We'll use a one-sample t-test since we have a sample of IQ scores and want to test if the population mean is significantly different from 100.

Let's set up the null and alternative hypotheses:

Null Hypothesis (H_0): The population mean IQ is equal to 100. Alternative Hypothesis (H_1): The population mean IQ is not equal to 100.

Next, we'll calculate the sample mean and sample standard deviation from the given data:

$$\text{Sample mean } (\bar{x}) = (70 + 120 + 111 + 98 + 110 + 88 + 107 + 100 + 83 + 90 + 115 + 81) / 12 \approx 100.17$$

$$\text{Sample standard deviation } (s) \approx 15.15$$

Now, we can perform the t-test. The t-statistic is given by:

$$t = (\bar{x} - \mu) / (s / \sqrt{n})$$

Where: \bar{x} = Sample mean μ = Population mean (null hypothesis value, which is 100 in this case) s = Sample standard deviation n = Sample size

$$t = (100.17 - 100) / (15.15 / \sqrt{12}) \approx 0.08$$

Now, we need to find the critical t-value for a significance level (α) of our choice. Let's assume a significance level of 0.05 (5%).

For a two-tailed t-test with 11 degrees of freedom ($12 - 1$), the critical t-value is approximately ± 2.201 from the t-distribution table.

Since the calculated t-value (0.08) is within the range of -2.201 to +2.201, we fail to reject the null hypothesis. There is not enough evidence to support that the population mean IQ is different from 100 at the 5% significance level. Therefore, based on this sample, the data do support the assumption of a population mean IQ of 100.