



## R CODE FOR PARAMETRIC AND NON- PARAMETRIC TESTS

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## ABSTRACT

Statistics serves as the foundation for various domains such as businesses, policy makers, markets and other sectors involved in activities such as data collection, planning, design, analysis, interpretation and reporting of the research findings. Moreover, the findings obtained from a research project carry greater significance when subjected to analysis using statistical techniques. Various methods are employed to ensure precise data interpretation within the realm of research. Considering the data parameters, we have two methodologies – Parametric tests and Nonparametric tests. Parametric test depends on the presence of normal distributions within the data, whereas Nonparametric tests are suitable for analysing continuous data in any format. This article provides an explanation of a range of Parametric and Nonparametric tests along with R code.

**KEYWORDS :** Parametric, Nonparametric, Statistical tool, R code.

## INTRODUCTION

The subject Statistics is widely used in almost all fields like Education, commerce, Biology, Botany, Medicine, Bio-Technology, Psychology, Zoology, etc. While doing research in the above fields, the researchers should have some knowledge in using the statistical tools which helps them in drawing rigorous and good conclusions. For every hypothesis testing problem, it requires a test which may be Parametric or Nonparametric test. Statistical methods typically centre on population parameters or probability distribution characteristics, and these are commonly known as parametric methods. Nonparametric methods are those statistical techniques that necessitate fewer assumption regarding a population or probability distribution.

Parametric tests are characterized by their assumption that the sample data originates from a population adhering to a particular probability distribution, namely the normal distribution, with a predetermined set of parameters. Prominent examples of parametric tests comprise the z-test, t-test and ANOVA.

## Parametric test

Parametric tests exhibit significant statistical power. These tests are suitable for quantitative data measured on a metric scale (interval or ratio) and conforming to normal distribution with a mean  $\mu$  and standard deviation  $\sigma$ .

Below is the list of fundamental parametric tests that can be conducted.

- One-sample Z – test
- Independent - samples Z – test
- One sample t – test
- Independent – samples t-test
- Paired – sample t – test
- F – test
- One – way ANOVA
- Bartlett test

## One-sample Z - test:

The Z-test is a hypothesis test employed to evaluate the mean of a sample against a predefined value. It is used when the standard deviation of the distribution is known and the sample size is typically large (usually 30 and above).

## Assumptions:

The population data is continuous, and it adheres to a normal distribution with known population mean and standard deviation. Samples must be both independent of each other

and randomly drawn from the population.

Consider a sample size  $n$  drawn from a population with mean  $\mu$  and standard deviation  $\sigma$ , then the test statistic to test sample mean is given by

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

## R code for one-sample Z-test:

A researcher wants to ascertain if the mean student score is 61 in the exam or not. The researcher collected the data of 30 students by using random samples and got following data: 67, 73, 54, 67, 48, 80, 69, 56, 59, 62, 70, 66, 64, 71, 65, 49, 80, 60, 56, 70, 68, 55, 58, 70, 70, 69, 52, 65, 66, 79. The S.D of student score is 10.

The scores are distributed in accordance with normal distribution. The test is conducted at 5% level of significance.

$H_0$ : Average score of students is 61,  $\mu = 61$ .

$H_1$ : Average score of students is not 61,  $\mu \neq 61$ .

R code

```
> dataset <- c(67,73,54,67,48,80,69,56,59,62,70,66,64,71,65,49,80,60,56,70,68,55,58,70,70,69,52,65,66,79)
```

```
> z.test (dataset, mu = 61,sd = 10, sigma.x = 8.3849, alternative = "two.sided", conf.level = 0.95)
```

## One sample Z-test results:

$z = 1.9718$ ,

$p\text{-value} = 0.04863$

The test statistic for one sample Z – test is 1.9718 and the corresponding  $p$  – value is 0.04863. since this  $p$  – value is less than 0.05, The researcher has the sufficient evidence to reject the null hypothesis. Thus, the conclusion is that the average score of students is not 61 in the exam.

## Independent-samples Z - test:

A parametric test called the two-sample test is used to compare the means of two separate groups of samples taken from normally distributed populations. In simpler terms, it helps to determine whether the means of two populations are identical or distinct.

## Assumptions:

The population data is continuous and conforms to normal distribution. The population's standard deviation is known,

and there is uniform variability among the groups, indicating homogeneity of variance. Moreover, both samples should be randomly drawn from the population.

Consider a sample of size  $n_1$  and  $n_2$  drawn from the population with sample means  $(\bar{x}_1)$  and  $(\bar{x}_2)$  and the population variances  $\sigma_1^2$  and  $\sigma_2^2$  of the first and second group respectively, then to compare means of two different samples the test statistic is given by

$$Z = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}}$$

**R-code for Independent sample Z-test:**

A professor desires to determine if there is a difference in mean IQ level of boys and girls in the class with 5% level of significance. She selects two random samples of girls and boys each of size 40. The population standard deviations of girls and boys are 25. The samples are as follows:

Girls:  
99,128,89,107,99,104,119,112,105,93,84,91,113,129,100,105,94,115,114,106,113,116,116,131,117,123,134,128,112,101,105,89,101,118,124,72,104,119,145,133.

Boys:  
79,118,99,117,98,102,112,111,102,73,114,97,114,122,90,115,84,105,84,105,84,126,83,96,111,151,147,103,104,118,132,108,95,118,121,88,94,109,105,123.

$H_0: \mu_1 = \mu_2$ , IQ of girls and boys are equal.  
 $H_1: \mu_1 \neq \mu_2$ , IQ of girls and boys are not equal.

**R code:**

```
>boys_dataset = c( 79,118,99,117,98,102, 112,111, 102,73,114,97,114,122,90,115,84,105,84,126,83,96,111,151,147,103,104,118,132,108,95,118,121,88,94,92,94,109,105,123)
```

```
>girls_dataset = c(99,128,89,107,99,104,119,112,105,93,84,91,113,129,100,105,94,115,114,106,
```

```
113,116,116,131,117,123,134,128,112,101,105,89,101,118,124,72,104,119,145,133)
```

```
>z.test(x=boys_dataset, y=girls_dataset, alternative = "two.sided", mu = 0, sigma.x = 25, sigma.y = 25, conf.level = 0.95)
```

**Two-sample z-test result:**

$z = -0.68424$ ,  $p\text{-value} = 0.4938$   
The test statistic for independent sample Z – test is  $-0.6842$  and the corresponding  $p$  – value is  $0.4938$ . since this  $p$  – value is greater than  $0.05$ , The professor has the sufficient evidence to accept the null hypothesis. Thus, the conclusion is that the IQ of boys and girls are equal.

**One-sample t-test:**

When the sample size falls below 30, it qualifies as a small sample. The One-sample t-test is a statistical hypothesis test employed to assess the mean of a small sample extracted from a population in comparison to a specified value.

**Assumptions:**

Data is continuous and quantitative at the scale level (ratio or interval), should follow normal probability distribution. The samples should be chosen at random from the population and must exhibit independence from one another.

When assessing whether the mean of a sample  $(\bar{x}_i)$  drawn from a normal population significantly differs from the stated value (hypothetical value of the population mean  $\mu_0$ ), and the variance of the population is unknown, the test statistic is as

follows:

$$t = \frac{\bar{x}_i - \mu_0}{s_i / \sqrt{n}}$$

**R-code for one-sample t-test:**

Using field experiments, it was anticipated that a new variety of green gram would yield 12 quintals per hectare. In order to verify whether the actual yield confirms the expectations, the variety was tested on 10 randomly selected farmers field. The yield (quintals/hectare) was recorded as 14.3, 12.6, 13.7, 10.9, 13.7, 12, 11.4, 12, 12.6, 13.1

Do the results conform the expectations.

$H_0: \mu_1 = 12$ , The average yield of new variety of green gram is 12 quintals/hectare.

$H_1: \mu_1 \neq 12$ , The average yield is not 12 quintals/hectare.

**R code**

```
>greengram_dataset<-c(14.3,12.6,13.7, 10.9,13.7, 12,11.4,12,12.6,13.1)
>set.seed(123)
>greengram_dataset<- rnorm (10, mean = 12.63, sd = 1.02961)
>t.test(greengram_dataset, mu = 12)
```

**One Sample t-test result:**

$t = 2.2761$ ,  $p\text{-value} = 0.04887$   
The test statistic for  $t$  – test is  $2.2761$  and the corresponding  $p$  – value is  $0.04887$ . since this  $p$  – value is greater than  $0.05$ , The researcher has sufficient evidence to accept the null hypothesis. Thus, the conclusion is that the average yield of the new variety of green gram is 12 quintal/hectare.

**Independent-samples t-test:**

A two sample tests, often referred to as an independent t-test, is employed to assess the disparity between the means of two unknown populations. This test is applied when two distinct populations are sampled, and their means are compared using small sample sizes.

**Assumptions:**

The samples should be chosen randomly from the two separate populations, and both samples should have a normal distribution with independence between them. Additionally, each sample sizes must be less than 30.

When examining whether the samples originate from the common normal population, we work with two separate, independent random samples. These samples have sizes  $n_1$  and  $n_2$  with means  $\bar{x}_1$  and  $\bar{x}_2$  and standard deviations  $s_1$  and  $s_2$ , in testing the hypothesis that the samples come from the same normal population.

To compare the means of two different samples the test statistic is given by

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\frac{n_1 s_1^2 + n_2 s_2^2}{(n_1 + n_2 - 2)} \left( \frac{1}{n_1} + \frac{1}{n_2} \right)}}$$

**R-code for Independent sample t-test:**

To evaluate the efficacy of medicines A and B, a group of 5 patients were treated with medicine A. Their weights were 42,39,38,60,41 kgs. Second group of 7 patients from the same hospital were treated with medicine B. Their weights were 38,42,56,64,68,69,62 kgs.

$H_0: \mu_1 = \mu_2$ , There is no significant difference in the outcomes between the medicines A and B.

$H_1: \mu_1 \neq \mu_2$ , There is significant difference in the outcomes between the medicines A and B.

**R code**

```
>medicineA_dataset<- c(42,39,38,60,41)
```

```
> medicineB_dataset <- c(38,42,56,64,68,69,62) >
t.test(medicineA_dataset,medicineB_dataset, var.equal =
TRUE, alternative = "two.sided")
```

**Two Sample t-test result:**

t = -1.981, p-value = 0.07574

The test statistic for t – test is -1.981 and the corresponding p – value is 0.0757. since this p – value is greater than 0.05, the researcher have the sufficient evidence to accept the null hypothesis. Thus, the conclusion is that there is no significant difference between the medicines A and B in terms of efficacy.

**Paired-sample t-test:**

A paired t-test is a statistical technique used to assess whether there is a notable distinction between two related groups by examining their means and standard deviations. Essentially, it evaluates whether the average difference between paired measurements is statistically significant from zero.

**Assumptions:**

Paired samples t-test can have only two groups (Use ANOVA for more than two measures) and assumes no extreme outliers. The dependent variable must be quantitative and is continuous measure at the interval or ratio. For accurate analysis, it is essential that the sampling distribution of the dependent variable exhibits a normal distribution.

When dealing with paired observations, such as a measurement taken before being matched with a measurement taken after, the objective is to compare the means of two distinct samples. The test statistic is given by

$$t = \frac{\bar{d}}{s_d / \sqrt{n}}$$

- d - sample mean of the differences
- s<sub>d</sub> - sample standard deviation of the differences
- n - sample size

**R-code for paired sample t-test:**

20 mice received a treatment X during 3 months. The researcher wants to know whether the treatment X has an impact on the weight of the mice. The weights have been measured before and after the treatment. The weights are as follows:

Before: 200.1, 190.9, 192.7, 213, 241.4, 196.9, 172.2, 185.5, 205.2, 193.7.

After: 392.9, 393.2, 345.1, 393, 434, 427.9, 422, 383.9, 392.3, 352.2.

H<sub>0</sub>: μ<sub>1</sub> = μ<sub>2</sub>, There is no difference in weights of mice before and after treatment.

H<sub>1</sub>: μ<sub>1</sub> ≠ μ<sub>2</sub>, There is difference in weights of mice before and after treatment.

**R code :**

```
>before <-c(200.1, 190.9, 192.7, 213, 241.4, 196.9, 172.2, 185.5,
205.2, 193.7)
>after <-c(392.9, 393.2, 345.1, 393, 434, 427.9, 422, 383.9,
392.3, 352.2)
>t.test(before, after, paired = TRUE)
```

**Paired t-test result:**

t = -20.883, p-value = 6.2e-09

The test statistic for t – test is -20.883 and the corresponding p – value is 6.2e-09. since this p – value is less than 0.05. The researcher has the sufficient evidence to reject the null hypothesis. Thus, the conclusion is that there is difference in weights of mice before and after treatment.

**F-test:**

The F test is utilised to assess whether two distinct samples

have varying variances, examining the hypothesis that they are drawn from populations with different variances. The value of the F-test is determined by the ratio of the variances in two samples.

**Assumptions:**

Both the populations are independent and exhibit a normal distribution in relation to each other.

The test statistic is given by

$$F = \frac{s_1^2}{s_2^2} \quad (s_1^2 \geq s_2^2)$$

$$s^2 = \frac{\sum_{i=1}^n (x_i - \bar{x})^2}{n-1}$$

**R-code for F-test:**

A scientist wants to test the weight progress on pigs by giving a different diet on different randomly selected pigs. For that, a random sample of 10 pigs were fed on diet A. The increase in weight in pound in certain period were, 10,6,16,17,13,12,8,14,15,9

For another random sample of 12 pigs fed on diet B, the increase in weight in pounds in the same period were, 7,13,22,15,12,14,18,8,21,23,10,17

To test whether both the samples come from the population having same variance.

H<sub>0</sub>: σ<sub>1</sub><sup>2</sup> = σ<sub>2</sub><sup>2</sup>, Both the samples come from the same population having the same variance.

H<sub>1</sub>: σ<sub>1</sub><sup>2</sup> ≠ σ<sub>2</sub><sup>2</sup>, Both the samples does not come from the same population having the same variance.

**R code:**

```
>Diet_A <-c(10,6,16,17,13,12,8,14,15,9)
>Diet_B <-c(7,13,22,15,12,14,18,8,21,23,10,17)
>var.test(Diet_B,Diet_A)
```

**F test to compare two variances result:**

F = 2.1409, p-value = 0.2629

The test statistic for F – test is 2.1409 and the corresponding p – value is 0.2629. since this p – value is greater than 0.05, The scientist has the sufficient evidence to accept the null hypothesis. Thus, the conclusion is that both the samples come from same population having the same variance.

**One-way ANOVA:**

ANOVA is a statistical test employed to assess whether samples drawn from various populations share the same mean or if there is a significant difference in the population means.

**Assumptions:**

Every sample should be derived from a population that follows a normal distribution, and it should also be independent of the other samples, Additionally, the variance of the data in different groups should be consistent or equal.

The test statistic is given by

If F<sub>1</sub> > F<sub>2</sub>

$$F = \frac{F_1}{F_2} \sim F(n_1, n_2)$$

If F<sub>2</sub> > F<sub>1</sub>

$$F = \frac{F_2}{F_1} \sim F(n_2, n_1)$$

$$F = \frac{\text{variation between sample means}}{\text{variation within the samples}}$$

**R-code for one-way ANOVA:**

The following are the yield of paddy (quintals) with three treatments in five different plots. A researcher wants to test whether there is significant difference between the three groups of yield obtained.

Group1	Group2	Group3
2	10	10
3	8	13
7	7	14
2	5	13
6	10	15

H<sub>0</sub>: There is no significant difference between three groups.  
 H<sub>1</sub>: There is significant difference between the three groups.

```
R code:
group1 <- c(2,3,7,2,6)
group2 <- c(10,8,7,5,10)
group3 <- c(10,13,14,13,15)
```

```
combined_groups <- data.frame (cbind(group1, group2,
group3))
stacked_groups <- stack(combined_groups)
Anova_Results <- aov(values ~ ind, data = stacked_groups)
```

**One-way ANOVA-Results:**

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
ind	2	203.3	101.7	22.59	8.54e-05 ***
Residuals	12	54.0	4.5	---	---

F(2,12) = 22.59, p value is less than 0.05. Thus, the researcher conclude that the null hypothesis is rejected. There is significant difference between the yield of paddy in the three groups.

**Bartlett test:**

This is often referred to as the homogeneity of variance test, which examines homoscedasticity or the equality of variances among multiple samples originating from different populations. Several statistical methods rely on the assumption that these population variances are Uniform. Bartlett's test is a tool used to evaluate this assumption by testing the null hypothesis that the variances of the populations are equal.

To assess the importance of variance differences among k normally distributed populations, independent samples are collected from each of these populations. We denote S<sub>2j</sub> as the variance of a sample containing n<sub>j</sub> items from the jth population (j = 1,2,3.....k).

The test statistic is

$$B = \frac{(N-k) \ln \left( \frac{\sum_{j=1}^k (n_j - 1) s_j^2}{N-k} \right) - \sum_{j=1}^k (n_j - 1) \ln(s_j^2)}{1 + \frac{1}{2(k-1)} \left[ \left( \sum_{j=1}^k \frac{1}{n_j - 1} \right) - \frac{1}{N-k} \right]}$$

This test statistic follows Chi-Square distribution with k-1 degrees of freedom.

**R-code for Bartlett test:**

A professor intends to investigate whether three distinct study methods result in varying exam scores. To do this, the professor randomly allocates 10 students to each of the techniques (A, B, or C) for one week and subsequently administers an exam of equivalent difficulty to all the students.

The exam scores of 30 students are:  
 81, 86, 88, 75, 78, 94, 98, 79, 71, 80, 96, 93, 93, 85, 87, 84, 72, 88, 97, 96, 74, 88, 84, 94, 99, 95, 83, 88, 85, 81.

H<sub>0</sub>: Three groups have no different variances.  
 H<sub>1</sub>: Three groups have different variances.

**R code:**

```
> df <- data.frame(group = rep(c('A','B','C'), each=10),
score = c(81, 86, 88, 75, 78, 94, 98, 79, 71, 80, 96, 93, 93, 85, 87,
84, 72, 88, 97, 96, 74, 88, 84, 94, 99, 95, 83, 88, 85, 81))
> bartlett.test(score ~ group, data = df)
```

**Bartlett test of homogeneity of variances result:**

Bartlett's Chi-squared (χ<sup>2</sup>) = 0.16336, p-value = 0.9216  
 Since the p-value is not less than 0.05, the professor will not reject the null hypothesis.

The professor does not have sufficient evidence to say that the three groups have different variances.

**Non-Parametric tests:**

Non-parametric tests are statistical analysis techniques that do not demand adherence to specific distribution assumptions, particularly when dealing with non-normally distributed data. It is important to note that the term "non-parametric" does not imply the absence of parameters in these models. In reality, the nature and quantity of parameters are quite adaptable and not predetermined. Hence, these models are often referred to as distribution-free models.

**Assumptions:**

Non parametric tests are utilised when either of the sample lacks a normal distribution and when the sample size is small. These tests are suitable for variables measured on a nominal or ordinal scale.

The basic Non parametric tests that can be carried out are listed below:

- Mann – Whitney U test
- Wilcoxon Signed Rank test
- Kruskal – Wallis test
- Friedman test
- Chi – square test

**Mann-Whitney U test:**

This non-parametric test is similar to independent sample t-tests. To perform this test, the dataset must consist of ordinal data and is also commonly referred to as the Wilcoxon rank sum test. The test statistic is U should be smaller of U<sub>1</sub> and U<sub>2</sub>

$$U_1 = n_1 n_2 + \frac{n_1(n_1+1)}{2} - R_1$$

$$U_2 = n_1 n_2 + \frac{n_2(n_2+1)}{2} - R_2$$

Where R<sub>1</sub> is the sum of ranks in group1 and R<sub>2</sub> is the sum of ranks in group2

Mann-Whitney U test is used for every field, but it is frequently in psychology, healthcare, nursing, business, and other disciplines.

**R-code for Mann-Whitney U test:**

Researchers want to know whether or not a new drug is effective at preventing panic attacks. To test this a total of 12 patients are randomly split into two groups of 6 and assigned to receive the new drug or the placebo. The patients then record how many panic attacks they have over the course of one month. The results are shown below:

New drug: 8 5 7 4 3 5  
 Placebo: 4 9 3 2 1 9

Mann-Whitney U test was conducted to determine if there is a difference in the number of panic attacks for the patients in the placebo group compared to the new group. At 0.05 level of significance.

H<sub>0</sub>: The panic attacks experienced by patients in the placebo group is not different from the new drug group.

H<sub>1</sub>: The panic attacks experienced by patients in the placebo



group is different from the new drug group.

**R code:**

```
>new <- c(8, 5, 7, 4, 3, 5)
placebo <- c(4, 9, 3, 2, 1, 9)
>wilcox.test(new, placebo, alternative="less")
```

**Wilcoxon rank sum test result:**

W = 22, p-value = 0.766  
 The test statistic W is 22 and the corresponding p – value is 0.766. since this p – value is greater than 0.05, The researcher has the sufficient evidence to accept the null hypothesis. Thus, the researcher concluded that the number of panic attacks experienced by patients in the new drug was less than that of the patients in the Placebo group.

**Wilcoxon Signed Rank test:**

This is the non-parametric test, which can be considered the equivalent of the parametric paired t-test. It is applied to compare two dependent samples containing ordinal data. The Wilcoxon signed-rank test operates under the assumption that the data is derived from a symmetric distribution.

$$W = \sum_{i=1}^{N_r} \left[ \text{sgn} \left( x_{2,i} - x_{1,i} \right) \cdot R_i \right]$$

W – test statistic  
 Nr - sample size excluding pairs where  $x_1 = x_2$   
 $x_{2,i}, x_{1,i}$  - corresponding ranked pairs from two distributions  
 Ri - rank i

**R-code for Wilcoxon Signed Rank test:**

A throwball coach is interested in determining whether a specific training program enhances the number of successful free throws made by their players wants to know if a certain training program increases the number of free throws made by his players. To test this, he has 15 players shoot 20 free throws each before and after the training program.

Before: 13,18,13,16,15,9,12,14,14,16,20,17,14,14,16  
 After: 16,18,15,15,18,15,10,14,11,16,18,20,20,11,17  
 Wilcoxon signed rank test was conducted to determine whether there is an improvement in throws after training.

$H_0$ : There is no significant difference in the number of free throws before and after players participate in the training program.

$H_1$ : There is increase in number of free throws of the players after the training program.

```
R code for Wilcoxon signed Rank test:
>before <- c(13, 18, 13, 16, 15, 9, 12, 14, 14, 16, 20, 17, 14, 14, 16)
>after <- c(16, 18, 15, 15, 18, 15, 10, 14, 11, 16, 18, 20, 20, 11, 17)
>wilcox.test(before, after, paired=TRUE, alternative="greater")
```

**Wilcoxon signed rank test result:**

V = 25.5, p-value = 0.8664  
 The test statistic value, V is 25.5 and the p value is 0.8664. Since p value is greater than 0.05, The coach has the sufficient evidence to accept the null hypothesis.

Thus, the coach concluded that, there is no significant difference in the number of free throws before and after players participate in the training program.

**Kruskal-Wallis test:**

This is a rank-based nonparametric test, making it suitable as a versatile option for comparing more than two independent samples. Its utility lies in assessing whether these samples originate from a common distribution, rendering it a robust alternative to one-way analysis of variance.

N – Total no of observations in all observations combined.  
 k - No of samples.  
 $R_i$  - Sum of ranks for ith sample.  
 $n_i$  - No of observations

**R-code for Kruskal-Wallis test:**

A researcher aims to investigate whether three distinct fertilizers yield varying levels of plant growth. To explore this, they employ a random selection of 30 different plants, dividing them into three groups of 10, with each group receiving a different fertilizer. After one month, they measure the height of each plant. A Kruskal-Wallis test was employed to ascertain whether the median growth across the three groups is equivalent. The heights are given below:  
 9, 14, 16, 13, 12, 9, 6, 14, 12, 9, 15, 18, 13, 15, 15, 18, 9, 14, 10, 8, 6, 8, 10, 9, 5, 14, 13, 9, 10, 9

$H_0$ : The median is equal across all groups.  
 $H_1$ : The median is not equal across all groups.

**R code:**

```
>df <- data.frame(group=rep(c('A', 'B', 'C'), each=10),
height=c(9, 14, 16, 13, 12, 9, 6, 14, 12, 9, 15, 18, 13, 15, 15, 18, 9, 14, 10, 8, 6, 8, 10, 9, 5, 14, 13, 9, 10, 9))
>kruskal.test(height ~ group, data = df)
```

**Kruskal-Wallis rank sum test result:**

Kruskal-Wallis chi-squared ( $\chi^2$ ) = 6.7706, p-value = 0.03387  
 The test statistic value is 6.7706 and the p value is 0.03387. Since p value is less than 0.05, the researcher has the sufficient evidence to reject the null hypothesis. The conclusion is that, the type of fertilizer used leads to statistically significant differences in plant growth. The median plant growth is not the same for all three fertilizers.

**Friedman test:**

Fredman’s test is also called Friedman’s two-way ANOVA, shares similarities with the Kruskal-Wallis test and can be considered an extension of the sign test. Unlike traditional repeated measures ANOVA, the Friedman test offers an alternative approach. It operates by utilizing ranked data, rather than raw data, in the calculation of the test statistic. This non-parametric test is particularly useful for comparing three or more dependent samples. It is most applicable when dealing with ranked data in a randomised block design, resembling a two-way ANOVA setup. The Friedman test is the preferred choice when the data significantly deviates from a normal distribution, making it a robust alternative to ANOVA in such cases. Moreover, it is the go-to option among non-parametric tests when assessing the same parameter under various conditions in a repeated measure design. For instance, in scenarios like monitoring a subject’s blood glucose levels before treatment, after one month of treatment, and after three months of treatment.

**Assumptions of the Friedman Test:**

The group under consideration represents a randomly selected subset of the population, and it comprises one group of test subjects who are measured on three or more distinct occasions. It is important that there is no discernible interaction between the various subgroups (blocks or rows) and the treatment conditions (columns). Additionally, the dependent variable must, at a minimum, exhibit ordinal or continuous characteristics. There is no requirement for the samples to adhere to a normal distribution.

The test statistic of Friedman’s test statistic is given by

$$H = \frac{12}{N(N+1)} \left[ \frac{R_1^2}{n_1} + \frac{R_2^2}{n_2} + \frac{R_3^2}{n_3} + \dots + \frac{R_k^2}{n_k} \right] - 3(N+1)$$

Where  $R_j$  is the sum of the ranks for sample j.  
 n is the number of independent blocks

K is the number of groups or treatment levels  
 DF – number of groups -1(k – 1)

**R-code for Friedman’s test:**

A researcher wants to test the reaction time of five patients on 4 different drugs. Each patient is measured on each of the 4 drugs. Friedman test is conducted to determine if the mean reaction time differs between drugs. The scores are below: 30, 28, 16, 34, 14, 18, 10, 22, 24, 20, 18, 30, 38, 34, 20, 44, 26, 28, 14, 30.

H<sub>0</sub>: The mean response time is same for all the four drugs.  
 H<sub>1</sub>: The mean response time is different for all four drugs.

**R code:**

```
> data <- data.frame(person = rep(1:5, each=4),
  drug = rep(c(1, 2, 3, 4), times=5),
  score = c(35, 28, 16, 34, 16, 18, 10, 23, 24, 20, 18, 30, 38, 34, 28,
  44, 26, 28, 16, 30))
> friedman.test(y = data$score, groups = data$drug,
  blocks = data$person)
```

**Friedman rank sum test result:**

Friedman chi-squared = 12.12, p-value = 0.006983  
 The Chi-squared (χ<sup>2</sup>) test statistic is 12.12 and the p-value is 0.006983. Since the p value is less than 0.05, The researcher has all the evidence to reject the null hypothesis. Thus, the researcher concluded that the type of drug used lead to statistically significant differences in response time.

**Chi-Square Test:**

Chi-square distribution is a direct derivation from the normal distribution. It represents the outcome of adding up the squares of n independent standard normal variables and is referred to as a Chi-square variable with n degrees of freedom.

Applications of Chi-square distribution:

1. To assess if a population exhibits a specified variance.
2. To examine the Independence of Attributes within a contingency table.
3. To evaluate the degree to which a theoretical distribution aligns with an observed distribution, often referred to as a test for 'Goodness of Fit'.

**Chi-square test for variance:**

The chi-square test variance is a statistical method employed to compare the variance of a sample with a known population variance. Its primary purpose is to evaluate a hypothesis regarding the population’s variance. This test relies on the assumption that the sample is drawn from a population that follows normal distribution.

Assumptions:

The sample should be selected through a random process from the population, and each observation within the sample should be unrelated to the others. The distribution of the population should closely resemble a normal distribution.

A random sample has been drawn from a population with mean μ and variance σ<sup>2</sup>, to test whether the population variance is σ<sup>2</sup>,

The test statistic is given by,

$$\chi^2 = \frac{(n-1)s^2}{\sigma^2}$$

**R-code for Chi-square test for Variance:**

A researcher wants to test whether the standard deviation of strength of rods is more than 8 tons. To study this, the strength of 8 rods were selected and the values are 18,13,12,4,17,13,19,6.

H<sub>0</sub>: The standard deviation of strength of the rod is 8 tons.  
 H<sub>1</sub>: The standard deviation of strength of the rod is more than 8 tons.

**R code:**

```
data <- c(18,13,12,4,17,13,19,6)
varTest(data, alternative = "greater", conf.level =
  0.95, sigma.squared = 8)
```

**chi-square test for variance result:**

Chi-Squared(χ<sup>2</sup>) = 25.9375, P-value is 0.0005167844  
 The test statistic for chi-square– test is 25.9375 and the corresponding p – value is 0.000516. since this p – value is less than 0.05, The researcher has the sufficient evidence to reject the null hypothesis. Thus, the researcher concluded that the standard deviation of the strength of the rod is more than 8 tons.

**Chi-square test for Independence of Attributes:**

A chi-square test for the independence of attributes is employed to ascertain if there exists a significant association between two categorical variables.

Assumption:

The total frequency N should be substantial (≥ 50). The observations should be independent.

**R-code for Chi-square test for Independence of Attributes:**

A researcher wants to study whether the examination result depends on special coaching. The following table shows the results.

Special Coaching	Examination Pass	Result Fail	Total
Taken	210	90	300
Not Taken	60	40	100
Total	270	130	400

H<sub>0</sub>: Examination result and special coaching are independent.  
 H<sub>1</sub>: Examination result and special coaching are not independent.

**R code:**

```
> data <- matrix(c(210,90,60,40), ncol=2, byrow = TRUE)
> colnames(data) <- c("Pass", "Fail")
> colnames(data) <- c("Pass", "Fail")
> rownames <- c("Coaching taken", "Coaching not taken")
> chisq.test(data)
```

**Pearson's χ<sup>2</sup>test result:**

Chi-squared (χ<sup>2</sup>) = 2.9782, p-value = 0.0844.  
 Since the p-value 0.0844 of the test is less than 0.05, the null hypothesis is rejected.

Thus, the researcher concluded that examination result and special coaching are not independent.

**Chi-square test for Goodness of Fit:**

The Chi-Square test is commonly referred to as the 'Goodness of Fit' test because it allows us to assess how closely theoretical distributions, like Binomial, Poisson, Normal, and others, match the empirical distribution derived from sample data. The chi-square value quantifies the extent of disparity between the theoretical and observed distributions.

Assumptions:

The total frequency N should be of a substantial magnitude. The theoretical frequencies E<sub>i</sub> should have a minimum value of 5. If any E<sub>i</sub> falls below this threshold, it should be pooled with the adjacent frequency. When estimating parameters based on the observed distribution, for each such estimation, one degree of freedom should be subtracted.

The test statistic is

O<sub>i</sub> - observed value

E<sub>i</sub> - Expected value

R-code for Chi-square test for Goodness of Fit:

Seven coins are tossed 128 times and the following distribution

is obtained:

Observed: 14 21 30 26 20 17

Expected: 8 21 35 35 21 8

To test whether Binomial distribution is a good fit at 5% level of significance,

H<sub>0</sub>: Binomial distribution is a good fit.

H<sub>1</sub>: Binomial distribution is not a good fit.

#### R code:

```
> chisq.test(x=c(14,21,30,26,20,17), p=c(8,21,35,35,21,8),rescale.p=TRUE)
```

#### Chi-squared $\chi^2$ test result:

chi-squared  $\chi^2 = 17.701$ , p-value = 0.003345

The test statistic for chi-square test is 17.701 and the corresponding p-value is 0.00334. since this p-value is less than 0.05, the researcher has the sufficient evidence to reject the null hypothesis. Thus, the researcher concluded that Binomial distribution is not a good fit.

#### CONCLUSION:

In conclusion, this discussion on parametric and nonparametric tests using R code highlights the importance of selecting the appropriate statistical method based on various factors, including research objectives, population size, and data scale. Both parametric and nonparametric tests have their strengths and weaknesses, and the choice between them should be made judiciously.

Parametric tests rely on specific distributional assumptions and can provide greater statistical power when these assumptions are met. Nonparametric tests, on the other hand, offer robustness in cases where normality assumptions are violated but may have lower power, especially with small sample sizes.

This resource not only clarifies the key considerations for choosing between these two types of tests but also provides valuable insights into their practical application through R code examples. Researchers can leverage this knowledge to make informed decisions and conduct rigorous statistical analysis in their own work, ultimately enhancing the quality and reliability of their research outcomes.

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