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# Missing Value Estimation and Analysis in Neutrosophic RBD

**Masum Raj[1], S. C. Malik[2*], Rahul Thakur[3]**

[1] Department of Mathematics, Institute of Applied Sciences and Humanities, G.L.A. University, Mathura, U.P., India; masum.raj@gla.ac.in

[2] Department of Statistics, Maharshi Dayanand University, Rohtak, Haryana, India (124001); thakurrahul3394@gmail.com

[3] Department of Statistics, Maharshi Dayanand University, Rohtak, Haryana, India (124001);sc_malik@rediffmail.com

* Correspondence: sc_malik@rediffmail.com

**Abstract:** The Randomized Block Design (RBD) is a fundamental experimental design widely utilized in agricultural and industrial research to control variation by grouping experimental units into homogeneous blocks. Moreover, real-world experiments are often subjected to various sources of uncertainty, including indeterminate, vague, imprecise, and erroneous data, which further complicate the analysis. To address these challenges, this paper introduces a novel neutrosophic analysis approach using Neutrosophic Logic for handling missing values in RBD under an uncertain environment. To further illustrate the practical application and effectiveness of the Neutrosophic Randomized Block Design (NRBD), an illustrative example from the medical field is presented. Further, simulation study is conducted to evaluate the performance of various parameters across different sample sizes. The analysis demonstrates the efficacy of Neutrosophic Randomized Block Design in preserving the statistical properties of the dataset and ensures more accurate and reliable experimental conclusions.

**Keywords:** Randomized Block Design, Neutrosophic Logic, Missing Value, Analysis of Variance, Neutrosophic Randomized Block Design.

## 1. Introduction

Randomized Block Design (RBD) is a fundamental technique to control variability and increase the precision of the outcomes of an experiment. It controls variability among experimental units by grouping them into homogeneous blocks. In many experiments, missing observations frequently occur, particularly when dealing with biological or breeding varieties. For example, consider a long-term study where different plant genotypes are evaluated for their resistance to fungal infections. The experiment might use a blocking design to account for variations in soil composition across the field. During the study, some plants might be lost due to disease, pest damage, or environmental stress, leading to missing data. Such gaps can substantially impact the accuracy and reliability of the experimental findings. In the field of biology, consider an experiment designed to study the growth rates of various bacterial strains under different temperature conditions. The experimental setup includes several blocks, each representing a specific temperature range. Due to unforeseen contamination or equipment failure, some bacterial cultures might not grow as expected, resulting in missing observations. This missing data can hinder the ability to draw accurate conclusions about the optimal growth conditions for each strain. In another example, a wildlife biologist might conduct a study to assess the impact of different feeding regimens on the reproductive success of a bird species. The study uses a blocking design to account for variations in habitat quality across different study sites. During the breeding season, some nests might be abandoned or predated, leading to missing data on reproductive success. This missing information can affect the validity of the study's conclusions. Missing data can lead to biased estimates and reduced statistical power thereby compromising the validity of the experimental conclusions. Addressing the issue of missing values is thus crucial for maintaining the integrity of the experimental analysis.

The issue of missing values has been extensively studied in various experimental designs[1]. Cornish [2]methods for estimating missing values in Incomplete Block Designs (IBD**)**, while Baird [3] focused on handling multiple missing values in Balanced IBDs. Beyond these estimation techniques, researchers have also proposed an exact approach to address missing values through the general regression significance test, a method primarily applied in the analysis of covariance. More recently, Sirikasemsuk et al**.** [4] investigated an exact approach for calculating the adjusted regression sum of squares in a Randomized Complete Block Design (RCBD) with missing observations. Despite these advancements, the issue of missing values remains underexplored in the Augmented Randomized Complete Block Design (ARCBD). Two key challenges arise in this context. First, estimating missing values becomes increasingly uncertain when the dataset contains inherent ambiguities and indeterminate information. Second, approximate methods for handling missing values may lack efficiency and reliability, leading to potential biases in statistical inference. The classic statistical approach does not account for uncertainty and indeterminacy, limiting its ability to accurately analyze genotype data. Similarly, conventional approximation methods may not always provide unbiased and precise results.

Traditional methods for handling missing values including mean substitution, listwise deletion and regression imputation often come with significant limitations. While various classes of augmented designs have been extensively studied using classical statistical methods, there remains a notable gap in their application within uncertain environments. Addressing this gap requires novel analytical frameworks that integrate uncertainty measures, ensuring more robust and reliable conclusions in experimental research. Uncertainty arises from incomplete knowledge about the data, while indeterminacy stems from conflicting or ambiguous information. Conventional statistical methods often struggle to address these aspects effectively which leads to less reliable results. Numerous researchers have utilized Fuzzy Sets (FSs)[5] and Intuitionistic Fuzzy Sets (IFSs) [6] in their studies to effectively address the uncertainty and ambiguity present in the data. Ali et al.[7] proposed a Fuzzy K-Top Matching Value (FKTM) method for imputing missing numerical and categorical data using fuzzy clustering and expectation-maximization, outperforming traditional methods like MICE in terms of accuracy, RMSE, and execution time. Malik et al.[8] proposed a new weighted correlation coefficient measure for IFSs, ranging between [-1, 1] in which the weights were assigned using the cosine entropy measure. Kumaran et al. [9]proposed a hybrid fuzzy clustering mean and majority vote method for imputing missing values in microarray gene expression data, demonstrating improved accuracy and reduced RMSE compared to traditional methods across multiple benchmark datasets. Khan et al. [10] proposed a missing value imputation method based on Fuzzy C-Means clustering to enhance classification accuracy by utilizing only the known feature values from a subset of selected instances. Although fuzzy sets and intuitionistic fuzzy sets extend classical set theory, neutrosophic sets offer an advancement by introducing a third parameter i.e. indeterminacy. This parameter evaluates the level of uncertainty or incompleteness in a statement, enhancing the representation of uncertainty by incorporating not just membership and non-membership degrees but also indeterminacy. The neutrosophic set (NS), first proposed by Smarandache [11] extends the concept of an intuitionistic fuzzy set (IFS) from a philosophical perspective. The benefits of neutrosophic logic compared to fuzzy logic and interval-based analysis were demonstrated by Smarandache and Khalid [12]. Some additional information on neutrosophic statistics, including relevant articles and books, are discussed [[13][14],[15],[16]]. Aslam [17] outlined the distinctions between fuzzy statistics, neutrosophic statistics and classical statistics. Aslam[18] discussed the neutrosophic ANOVA method, while AlAita and Aslam [19] emphasized the use of neutrosophic analysis of covariance in neutrosophic completely randomized designs, neutrosophic randomized complete block designs, and neutrosophic split-plot designs. Aslam and Albassam[20] proposed post hoc multiple comparison tests within the framework of neutrosophic statistics. Additionally, Salama et al. [21] explored neutrosophic correlation and simple linear regression. Thakur et al. [22] defined the method of testing of normality under uncertainty. In recent years, a substantial number of studies on neutrosophic statistics have been discussed [[23],[24],[25],[26],[27],[28],[29],[30]]. After

the thorough literature review, there appears to be a notable gap in the existing body of work concerning the estimation and analysis of missing values of Randomized Block Designs (RBD) under uncertainty.

### 1.1 Contribution

In this study, we address the issue of missing values in Randomized Block Design (RBD), highlighting key challenges such as indeterminacy, ambiguity in the number of treatments, estimation errors, and imprecision in statistical tests like the F-test. Conventional and fuzzy-based methods often struggle to effectively manage these uncertainties, motivating the use of a Neutrosophic Statistical (NS) framework. By incorporating neutrosophic logic, we propose a novel approach to estimate missing values in RBD which proposes deeper insight into uncertainty and enhancing reliability in analysis. This work marks the first integration of neutrosophic theory into RBD, leading to the formulation of the Neutrosophic Randomized Block Design (NRBD). Within this environment, we derive neutrosophic estimations, adjusted sums of squares, and construct an ANOVA table suitable for interpretation under uncertainty. The proposed method is demonstrated using a neutrosophic blood pressure dataset and further validated through simulation studies. Overall, this approach addresses a significant computational and methodological gap in the analysis of RBD with missing data under uncertain conditions.

Remaining paper are arranged in this manner. Section 2, consider some basic definitions of neutrosophic normal distribution (NND) and neutrosophic randomized block design (NRBD). In Section 3, we introduce a method for estimating missing values in neutrosophic observations within a randomized block design (NRBD). This section also includes the ANOVA table specifically developed for NRBD, along with a flowchart outlining the steps involved in the analysis. Section 4 presents an illustration to validate the applicability of the proposed method in the field of medical sciences, demonstrating its practical relevance. In Section 5, a simulation study is conducted to evaluate the performance and robustness of the method under various scenarios. Finally, the study concludes with a summary of findings and insights drawn from the analysis.

## 2. Preliminaries

### 2.1. Neutrosophic Normal Distribution (NND) [22]

Let $y_N = y_l + y_u i_N$ are the neutrosophic numbers where the $i_N \in [i_l, i_u]$ is an indeterminacy interval, follows that neutrosophic normal distribution (NND) with the neutrosophic mean $\mu_N = \mu_l + \mu_u i_N ; i_N \in [i_l, i_u]$ and neutrosophic variance $\sigma_N^2 = \sigma_l^2 + \sigma_u^2 i_N \; ; i_N \in [i_l, i_u]$. Then the probability density function of the NND is given by

$$f_N(y_N) = \frac{1}{\sigma_N \sqrt{2\pi}} exp\left\{-\frac{(y_N - \mu_N)^2}{2\sigma_N^2}\right\} ; \mu_N \in [\mu_l, \mu_u], \sigma_N^2 \in [\sigma_l^2, \sigma_u^2], i_N \in [i_l, i_u]$$

It is the generalized version of normal distribution. NND will reduce to the classical normal distribution if the $\boldsymbol{i_l = 0}$

## 3. Neutrosophic Randomized Block Design (NRBD)

The statistical model of the Neutrosophic Randomized Block Design with "$v$" number of treatments and "$r$" number of replications is given below:

$$y_{Nij} = \mu_N + t_{Ni} + b_{Nj} + \varepsilon_{Nij}, \quad i = 1,2, \dots, v \;\; and \; j = 1,2, \dots, r \tag{1}$$

The neutrosophic form of response variable can be represented as $y_{Nij} = y_{lij} + y_{uij} i_N \; ; \; i_N \in [i_l, i_u]$. $y_{Nij}$ is the neutrosophic response variable or the neutrosophic experimental unit receiving the $i^{th}$ treatment in $j^{th}$ block $\mu_N$ is the neutrosophic general mean effect, $t_{Ni}$ is the neutrosophic effect of $i^{th}$ treatment, $b_{Nj}$ is the neutrosophic effect of $j^{th}$ block and $\varepsilon_{Nij}$ is the random error term with neutrosophic zero mean and variance $\sigma_N^2$.

### 3.1 Estimation of Neutrosophic Missing Value

Let us consider that in the given observations, one neutrosophic observation $y_{Nij} = x_N$ in the $j^{th}$ block and receiving the $i^{th}$ treatment is missing.

| **Blocks** | **Treatments** | | | | | | **Totals** |
|---|---|---|---|---|---|---|---|
| ↓ | **1** | **2** | **….** | **i** | **…** | **v** | |
| 1 | $y_{N11}$ | $y_{N21}$ | …. | $y_{Ni1}$ | …. | $y_{Nv1}$ | $S_{N.1}{}'$ |
| 2 | $y_{N12}$ | $y_{N22}$ | …. | $y_{Ni2}$ | …. | $y_{Nv2}$ | $S_{N.2}{}'$ |
| . | | | | | | | |
| j | $y_{N1j}$ | $y_{N2j}$ | …. | $\boldsymbol{y_{Nij} = x_N}$ | …. | $y_{Nvj}$ | $S'_{N.j} + x_N$ |
| . | | | | | | | |
| r | $y_{N1r}$ | $y_{N2r}$ | …. | $y_{Nir}$ | …. | $y_{Nvr}$ | $S_{N.r}{}'$ |
| Totals | $S_{N1}.'$ | $S_{N2}.'$ | …. | $S_{Ni}.' + x_N$ | …. | $S_{Nv.}{}'$ | $S_{N}.. + x_N$ |

**Table 1: Missing Observation in Neutrosophic RBD.**

Here

- $S_{Ni.}{}'$ is the sum of the neutrosophic observations for the treatments without missing value.
- $S_{N.j}{}'$ is the sum of the neutrosophic observations in the blocks without missing value
- $S_{Ni.}$ is the sum of (r-1) known neutrosophic observations for the $i^{th}$ treatments with missing value.
- $S_{N.j}$ is the sum of (v-1) known neutrosophic observations in the $j^{th}$ block with the missing value.
- $S_{N..}$ is the sum of (vr-1) known neutrosophic observations.

Now, we will split the model given in equation (1) into two parts. First equation corresponding to known neutrosophic observations and another equation corresponding to missing observations as given below:

$$y_{Ni'j'} = \mu_N + t_{Ni'} + b_{Nj'} + \varepsilon_{Ni'j'} \quad (2)$$

$$x_N = \mu_N + t_{Ni} + b_{Nj} + \varepsilon_{Nij} \quad (3)$$

For the model NRBD,

$$SS_{NT} = \sum_{i'\neq i}\sum_{j'\neq j} y_{i'j'}^2 + x_N^2 - \frac{(S_{N..}+x_N)^2}{vr} \quad (4)$$

$$SS_{NTr} = \frac{1}{r}\sum_{i'\neq i} S_{i.'}^2 + \frac{(S_{Ni.}+x_N)^2}{r} - \frac{(S_{N..}+x_N)^2}{vr} \quad (5)$$

$$SS_{NBl} = \frac{1}{v}\sum_{j'\neq j} S_{.j'}^2 + \frac{(S_{N.j}+x_N)^2}{v} - \frac{(S_{N..}+x_N)^2}{vr} \quad (6)$$

$$SS_{NEr} = \sum_{i'\neq i}\sum_{j'\neq j} y_{i'j'}^2 + x_N^2 - \frac{(S_{N..}+x_N)^2}{vr} - \frac{1}{r}\sum_{i'\neq i} S_{i'}^2 - \frac{(S_{Ni.}+x_N)^2}{r} + \frac{(S_{N..}+x_N)^2}{vr} - \frac{1}{v}\sum_{j'\neq j} S_{i'}^2 - \frac{(S_{N.j}+x_N)^2}{v} + \frac{(S_{N..}+x_N)^2}{vr} \quad (7)$$

By using the principle of least square method we estimate the value of $x_N$ by minimising the sum of square due to error, we have

$$\frac{dSS_{NEr}}{dx} = 0 = 2x_N + \frac{2(S_{N..} + x_N)}{vr} - \frac{2(S_{N.j} + x_N)}{v} - \frac{2(S_{Ni.} + x_N)}{r}$$

$$x_N\left(1 + \frac{1}{vr} - \frac{1}{v} - \frac{1}{r}\right) - \frac{S_{Ni.}}{r} - \frac{S_{N.j}}{v} + \frac{S_{N..}}{vr} = 0$$

$$\widehat{x_N} = \frac{vS_{Ni.} + rS_{N.j} - S_{N..}}{(v-1)(r-1)} \tag{8}$$

**3.2 Analysis of Neutrosophic RBD After Estimation of Missing Value**

After estimating the missing Neutrosophic observation in NRBD, we have

$$SS_{NEr} = \sum_{i' \neq i}\sum_{j' \neq j} y_{i'j'}^2 + \widehat{x_N^2} - \frac{(S_{N..} + \widehat{x_N})^2}{vr} - \frac{1}{r}\sum_{i' \neq i} S_{i'}^2 - \frac{(S_{Ni.} + \widehat{x_N})^2}{r} + \frac{(S_{N..} + \widehat{x_N})^2}{vr} - \frac{1}{v}\sum_{j' \neq j} S_{i'}^2 - \frac{(S_{N.j} + \widehat{x_N})^2}{v} + \frac{(S_{N..} + \widehat{x_N})^2}{vr} \tag{9}$$

Under the null hypothesis of treatments i.e. $H_{oN}: t_{Ni} = 0 \ \forall \ i$ , the influence of Neutrosophic treatments disappears and contributes to the overall error term.

The model given in equation (2) and (3) reduces to

$$y_{Ni'j'} = \mu_N + b_{Nj'} + \varepsilon^*_{Ni'j'}$$
$$x'_N = \mu_N + b_{Nj} + \varepsilon^*_{Nij} \tag{10}$$

The least square estimates of the reduced models are

$$\widehat{\mu_N} = \overline{y_{N\cdot\cdot}} = \frac{(S_{N..} + \widehat{x'_N})}{vr} \tag{11}$$

$$\widehat{b_{Nj}} = \frac{(S_{N.j} + \widehat{x'_N})}{v} - \frac{(S_{N..} + \widehat{x'_N})}{vr} \tag{12}$$

Since there is one missing observation then we may take $\varepsilon^*_{Nij} = 0$ . By using estimates of $\mu_N \ and \ b_{Nj}$ in (10), we have

$$\widehat{x'_N} = \frac{(S_{N..} + \widehat{x'_N})}{vr} + \frac{(S_{N.j} + \widehat{x'_N})}{v} - \frac{(S_{N..} + \widehat{x'_N})}{vr}$$

$$\widehat{x'_N} = \frac{S_{N.j}}{v-1} \tag{13}$$

The Neutrosophic Sum of Square due to Error (NSSE) under $H_0$ is given by:

$$SS_{NErH_o} = \left[\sum_{i' \neq i}\sum_{j' \neq j} y_{i'j'}^2 + \widehat{x'_N}^2 - \frac{(S_{N..} + \widehat{x'_N})^2}{vr}\right] - \left[\frac{1}{v}\sum_{j' \neq j} S_{i'}^2 + \frac{(S_{N.j} + \widehat{x'_N})^2}{v} - \frac{(S_{N..} + \widehat{x'_N})^2}{vr}\right]$$

The Neutrosophic Adjusted Treatment Sum of Square (NATSS) is given by:

$$Adjusted\ SS_{NTr} = \sum_{i' \neq i}\sum_{j' \neq j} y_{i'j'}^2 + x_N^2 - \frac{(S_{N..} + x_N)^2}{vr} - \frac{(vS_{Ni.} + rS_{N.j} - S_{N..})^2}{v(v-1)(r-1)^2}$$

**Null and alternative hypothesis**

For Treatments:

$$H_{No}: \mu_1. = \mu_2. = \cdots = \mu_v.$$
$$H_{Na}: at\ least\ two\ \mu_i.'s\ are\ different.$$

For Blocks:

$$H_{No}: \mu_{.1} = \mu_{.2} = \cdots = \mu_{.r}$$

$$H_{Na}: at\ least\ two\ \mu'_j s\ are\ different.$$

Here, we define an ANOVA table in randomized block design for the neutrosophic observations after estimation of the missing value.

| Source of Variation | Degree of Freedom | Neutrosophic Sum of Squares | Neutrosophic Mean Square | Neutrosophic F value |
|---|---|---|---|---|
| Treatments (Adjusted) | v-1 | $Adjusted\ SS_{NTr}$ | $MS_{NTr} = \frac{Adjusted\ SS_{NTr}}{\mathrm{v}-1}$ | $F_{NTr} = \frac{MS_{NTr}}{MS_{NEr}}$ |
| Blocks | r-1 | $SS_{NBl}$ | $MS_{NBl} = \frac{SS_{NBl}}{\mathrm{r}-1}$ | $F_{NBl} = \frac{MS_{NBl}}{MS_{NEr}}$ |
| Error | (v-1)(r-1)-1 | $SS_{NEr}$ =By Subtraction | $MS_{NEr} = \frac{SS_{NEr}}{(v-1)(r-1)-1}$ | |
| Total | vr-2 | $SS_{NT}$ | | |

**Table 2: NANOVA table for RBD after Estimating Missing Value**

### 3.3. Flow Chart for Analysis of Neutrosophic RBD:

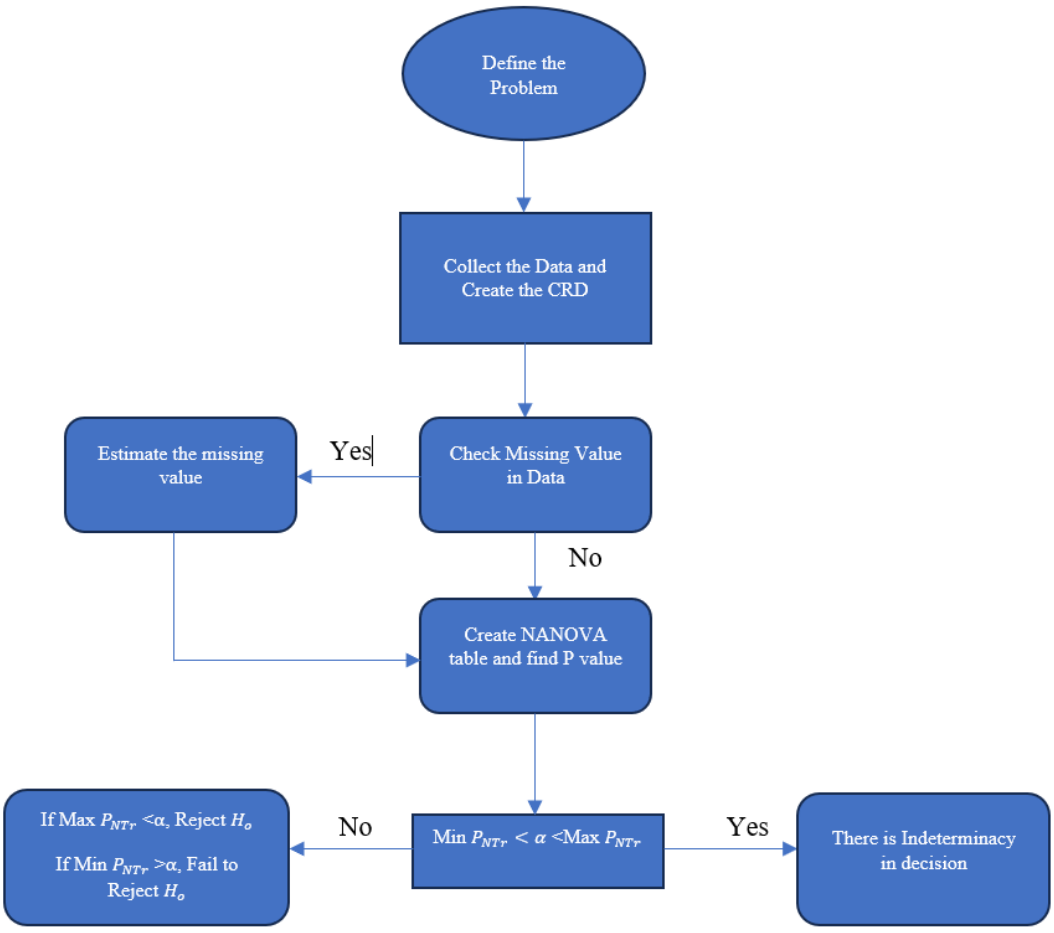


**Fig 1: Analysis Procedure for the Neutrosophic RBD**

**4. Illustration**

Consider a pharmaceutical company conducting a clinical trial to evaluate the efficacy of different drug formulations for treating a specific medical condition, such as hypertension. The company aims to employ a randomized block design (RBD) to control the patient variability and to ensure accurate assessment of treatment effects. The trial collects data on blood pressure reduction (response variable) as the primary outcome measure in neutrosophic form due to inaccuracy in the measurement of blood pressure. Patients are randomly assigned one of five different drug formulations (treatments) and monitored over a specified period. In case where patients miss scheduled visits or withdraw from the study prematurely is the reasons for missing data. There is one patient having ID 8 corresponding to which the data is missing (Appendix A, Table 5). The objective of the analysis is to estimate the missing observation and to assess the effectiveness of the different drug formulations in reducing blood pressure while considering the patient variability across medical centres. From the Table 5, $v = 5$ , $r = 4$ , $S_{Ni.} = (53, 55)$ , $S_{N.j} = (30, 40)$ , $S_{N..} = (244, 292)$

Using equation (8), The estimate of missing value corresponding to the patient ID 8 is $\widehat{x_N} = (9.83, 10.67)$. The Neutrosophic ANOVA table, which include Neutrosophic sums of squares (NSSN) and the observed F-test statistics (FN) with corresponding p-values ($p_N$), are calculated using both the proposed Neutrosophic RBD method for handling and analysis of missing values in RBD. The table is given below

The Neutrosophic ANOVA table is

| Source of Variation | Degree of Freedom | Neutrosophic Sum of Squares | Neutrosophic Mean Square | Neutrosophic F value | P value |
|---|---|---|---|---|---|
| Treatments (Adjusted) | 4 | (64.62, 65.41) | (16.16, 16.35) | (4.45, 35.36) | (0.0352, 0.5391) |
| Blocks | 3 | (1.04, 43.85) | (0.35, 14.62) | (0.76, 3.98) | (0, 0.0196) |
| Error | 12 | (5.48, 44.13) | (0.46, 3.68) | | |
| Total | 19 | (71.15, 153.39) | | | |

**Table 3: Neutrosophic ANOVA Table for RBD**

From Table 3, the value of significance level lies within the range of Neutrosophic p-value of the treatments. So, there is $\frac{0.05-0.0352}{0.5391-0.0352} = 0.0293$ chance of rejecting the null hypothesis and conclude that there are 2.93% chance that the blood pressure reduction in patients using different drug is not same. The maximum value of Neutrosophic p value for the blocks is less than the significance level so we reject the null hypothesis and conclude that the blood pressure reduction of the patients at different medical centres is not same.

**5. Simulation Study in Randomized Block Design with Neutrosophic Data:**

A comprehensive simulation study is conducted to assess the performance of the estimated parameter of Neutrosophic Randomized Block Design (NRBD). The dataset is generated from neutrosophic normal distribution. The data generation function creates a matrix of these observations for various sample sizes. For each generated dataset, the Neutrosophic grand mean, Neutrosophic

treatment effects and Neutrosophic block effects are estimated. The performance of these estimates is assessed in terms of Mean Squared Error (MSE). The simulation is repeated 1000 times for each sample size and the results are given in table 4.

| Sample Size | Grand Mean MSE | Treatments effect MSE | Block Effect MSE |
|---|---|---|---|
| 16 | (0.004996,0.019982) | (0.074744,0.298975) | (0.072379,0.289516) |
| 20 | (0.003286,0.013143) | (0.059720,0.238880) | (0.059590,0.238361) |
| 30 | (0.001359,0.005437) | (0.040962,0.163848) | (0.040182,0.160729) |
| 36 | (0.000931,0.003723) | (0.034127,0.136509) | (0.033745,0.134978) |
| 42 | (0.000711,0.002844) | (0.028917,0.115667) | (0.029164,0.116657) |
| 48 | (0.000548,0.002193) | (0.025404,0.101616) | (0.025626,0.102502) |
| 72 | (0.000246,0.000984) | (0.017169,0.068676) | (0.017124,0.068496) |
| 100 | (0.000124,0.000497) | (0.012432,0.049728) | (0.012385,0.049539) |

**Table 4: Performance of Neutrosophic MSE of Estimates at Different Sample Sizes**

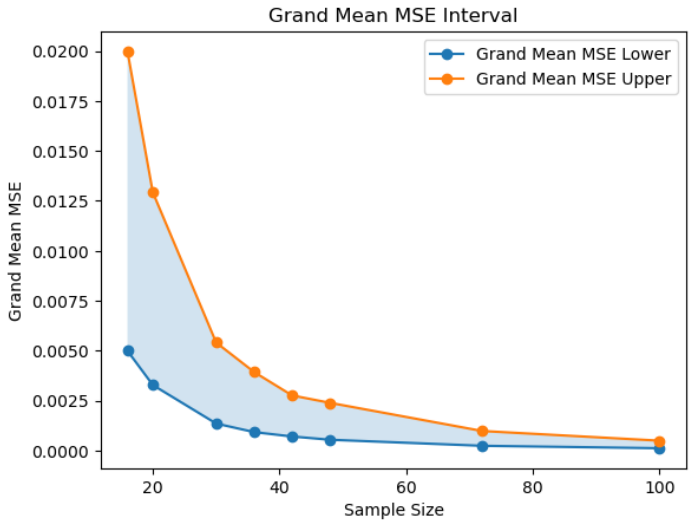


**Fig 2: Effect of Sample Size on the Grand Mean MSE**

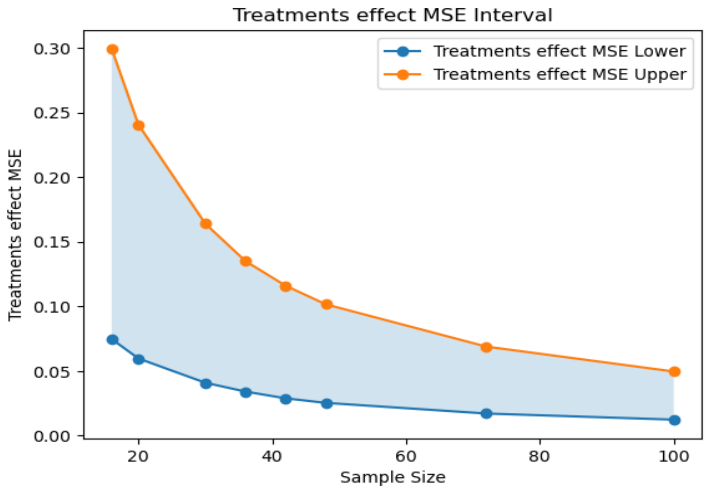


**Fig 3: Effect of Sample Size on the Treatment Effect MSE**

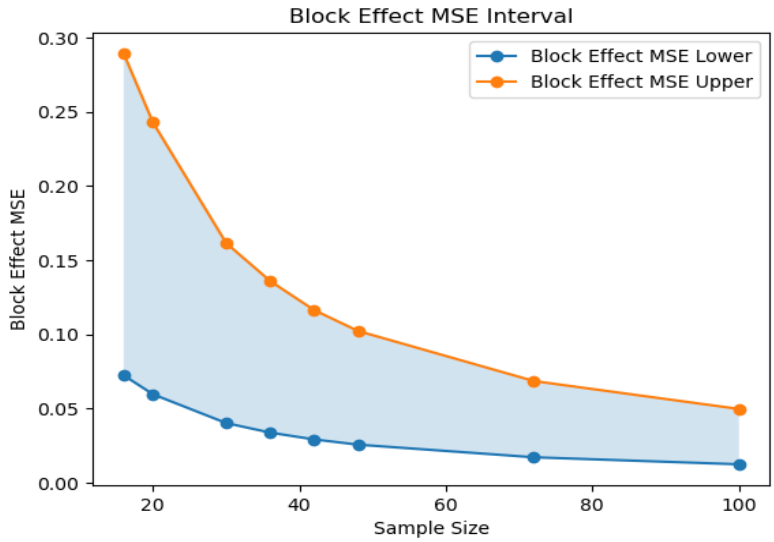


**Fig 4: Effect of Sample Size on the Block Effect MSE**

From Table 4, Fig 2, Fig 3 and Fig 4, it is evident that as the sample size increases, the MSE of Grand Mean, Treatment effect and Block effect decreases. It reveals that the larger the sample size in RBD tends to yield the more precise estimates in neutrosophic statistical analysis. From the above study we also conclude that the sample size improves the accuracy and reliability of the neutrosophic estimates in neutrosophic experimental designs.

## 6. Discussion

The findings from both the case study and the simulation study underscore the value of applying a neutrosophic framework to RBDs with missing values. The real-world medical illustration demonstrated that incorporating neutrosophic logic allows for a more nuanced understanding of variability across treatments and blocks, especially when dealing with incomplete or imprecise data. Notably, the neutrosophic p-value intervals provide a range that reflects the indeterminacy and uncertainty inherent in medical trials, rather than a binary decision from classical methods. For instance, the adjusted F-test values for treatments ranged widely, indicating possible sensitivity to uncertainty. This suggests that NRBD can be a more cautious and informative method for experimental conclusions. From the simulation results, we observed that larger sample sizes considerably reduce the mean squared error (MSE) of the estimated neutrosophic parameters, indicating improved estimation stability and precision. This implies that NRBD methods become more powerful with larger datasets, affirming their applicability in big-data experimental setups such as agricultural field trials or clinical trials. However, the study is not without limitations. The approach assumes the availability of bounds for neutrosophic observations, which may not always be feasible. Furthermore, the estimation formula used in this study handles only one missing observation; generalizing this method to multiple missing values is a crucial direction for future research.

## 7. Conclusion

In this study, we proposed the method of estimation of missing value and its analysis in Randomized Block Design (RBD) by introducing a Neutrosophic approach. The expressions for calculating Neutrosophic sum of squares, Neutrosophic Mean squares and Neutrosophic F values are also

provided. An illustration of this approach through a medical case study involving a clinical trial to evaluate drug formulations for hypertension. The results indicated that there is a 2.93% chance of rejecting the null hypothesis regarding the uniformity of blood pressure reduction across different drug formulations and a significant difference in blood pressure reduction across medical centers. Additionally, simulations conducted to assess the performance of Neutrosophic RBD showed that increasing the sample size leads to more precise estimates for Neutrosophic grand means, treatment effects, and block effects as decrease in Mean Squared Error (MSE). This highlights that larger sample sizes improve the accuracy and reliability of neutrosophic estimates in experimental designs. The Neutrosophic RBD approach proves an effective method for handling missing data and managing indeterminacy which offers valuable improvements in the analysis of neutrosophic datasets. In future, this work could be extended on other experimental designs.

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**Conflicts of Interest:** "The authors declare no Conflict of interest."

**Appendix A:**

| Patient ID | Medical Center (Block) | Treatment | Blood Pressure Reduction (mmHg) |
|---|---|---|---|
| 1 | 1 | 1 | (15,17) |
| 2 | 1 | 2 | (12,15) |
| 3 | 1 | 3 | 10 |
| 4 | 1 | 4 | (13,15) |
| 5 | 1 | 5 | (14,15) |
| 6 | 2 | 1 | 16 |
| 7 | 2 | 2 | 11 |
| 8 | 2 | 3 | - |
| 9 | 2 | 4 | (12,14) |
| 10 | 2 | 5 | 14 |
| 11 | 3 | 1 | (14,18) |
| 12 | 3 | 2 | (12,18) |
| 13 | 3 | 3 | (11,16) |
| 14 | 3 | 4 | 13 |
| 15 | 3 | 5 | (15,20) |
| 16 | 4 | 1 | (15,19) |
| 17 | 4 | 2 | (12,18) |
| 18 | 4 | 3 | (9,14) |
| 19 | 4 | 4 | 12 |
| 20 | 4 | 5 | (14,17) |

**Table 5: Data for Patients for Neutrosophic RBD**

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