NSS

Neutrosophic Sets and Systems, Vol. 82, 2025

University of New Mexico

Estimating and Testing Augmented Randomized Complete Block Designs: The Neutrosophic Approach

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Abstract. In plant breeding programs, the augmented design is designated to screen numerous new treatments compared with a few check treatments, which in turn are required to estimate both of error variance and local control for new future treatments. It is well known that the classical augmented design is not suitable for data that are imprecise, uncertain, or undetermined, and these accordingly emerge because of many circumstances beyond humans control. As a result, there is a sever necessity to define a proper generalization for the augmented designs to handle uncertain environments. To be more specific, this work aims to propose an easy to apply approach to treat the augmented randomized complete block design under neutrosophic statistics (NS). This well-defined approach is based on building a neutrosophic ANOVA table, including deriving a suitable test statistics, F_N, to handle uncertain settings.This leads to the corresponding neutrosophic hypotheses and the necessary related decision rules. Real data and a series of simulation studies numerically assess the performance of the present method. It will be shown that the neutrosophic method outperforms the classical one, and in effect, it is more flexible than in the presence of indeterminacy.

Keywords: Augmented randomized complete block design; neutrosophic test statistics; indeterministic observations; NANOVA.

1. Introduction

Breeding programs worldwide are administered when numerous genotypes are the object of examination. As a result, the augmented design has been developed for comparing thousands of genotypes with only one plot per genotype. This statistical art was first introduced by Federer [17]. This design contains a small number of varieties, known as checks, which are

randomly replicated in the field to compute an estimate of error [17]. As Federer states, one can calculate the expected yield for the plots in the studied field by relying on those varieties, and then the observed yields of the genotypes can be adjusted. Besides, the augmented design can also be used in characterizing genotypes for assessing mean performances, assessing effects, and controlling the variability of genotypes (see Federer and Crossa [18]).

The augmented design is a special case of block design (like complete, incomplete, Latin squares, etc.) by enlarging the block size. For example, the augmented randomized block design (ARCBD) can be constructed as c replicated checks and n non-replicated new treatments in r blocks. To build this augmented design, a randomized complete block design (RCBD) with r blocks and c check genotypes is employed. Then, the blocks are expanded so that embrace all c checks and n new units, in a way that each block would contain n/r new genotypes. We may refer the interested reader to review many examples of augmented designs in Federer and Crossa [18].

On the other hand, the augmented row-column designs along with few checks were handled by Piepho and Williams [24]. Also, the augmented design in which all treatments are not replicated was discussed by Burgueño, et al. (Ch. 13) [10]. Further developments in augmented designs can also be found in [26, 28].

In today's real world studies, especially when the experimental units are either biological or breeding varieties, uncertain observations are plausible. What is known for sure is that the classical ARCBD model will fail in analyzing such indeterministic observations. So, the search aims to define a novel neutrosophic model to overcome all limitations in the literature of ARCBD, and to our knowledge, this is the first such study in this framework.

The statistical art of neutrosophic statistics (NS) has attracted many researchers in recent years, years after its first definition by Smarandache [32], to propose and define new approaches to deal with uncertain and imprecise information. Aslam [11] gives an explicit explanation for the differences between the fuzzy, neutrosophic, and classic statistics. Contributions by Aslam [12] in experimental design analysis, the neutrosophic ANOVA was completely highlighted. After that, Aslam and Albassam [15] introduced multiple comparison post hoc tests for NS. The neutrosophic ANCOVA's for varieties of block designs were suggested and developed by AlAita and Aslam [1]. Other NS applications to deal with imprecise data in split-plot design and augmented Latin square design are given in [8, 9], respectively. To stay on track, one may point out to the numerous NS applications that are sufficiently discussed in [2–6, 13, 14, 16, 20–22, 27, 30, 31, 33, 35].

The randomized complete design is, in fact, the most and popular design in agricultural studies and biological fields, and this design can be extended to uncertain environments by adopting the NS, which is suitable for estimating model parameters and compute all related sum of

squares. The suggested new approach, which is called the NARCBD, is a suitable generalization of the classic ARCBD in sense of dealing with both exact or vague information. The superiority of the proposed NARCBD over the ARCBD will be approved through real data study and simulation scenarios. It will be shown that the suggested design can completely discriminate between the null hypothesis and the alternatives, where the type I error is controlled at a given nominal level of α.

Following in this paper, first, we give a brief summary addressing the motivation for this current research in Section 2. After that, basic concepts and notions of the NS framework are introduced in Section 3. An overview of the addressed NARCBD is given in Section 4. Section 5 contains a numerical explanatory example of real case study, as well as a series of simulation studies to check and evaluate the performance of our proposed design. A wide conclusion and further discussions are presented in Section 6.

2. **Motivation, Necessity and Research Gap**

Imprecise data in real-world problems forces researchers to innovate corresponding statistical techniques to deal with such a situation. This motivated us to generalize the augmented designs consisting of imprecise observations and solve them under the NS setting. In this way, one can deal with interval-type observations or a set of neutrosophic data. In our point of view, this is a significant addition to previous classical experimental designs, and would close the gap between the two. In fact, our work was inspired by many previous literatures in NS, showing its flexibilty and efficiency in treating complex situations. In this paper, the main focus was made on presenting a new theoretical approach along with a series of simulation studies and a real case study.

3. **Preliminaries**

By reviewing some basic ideas of NS in this section, one can easily follow-up and comprehend the main results related to the subsequent sections.

The neutrosophic logic is a type of logic that extends both of classical and fuzzy logics to handle uncertain, vague and indeterminate data. As already known, fuzzy sets represent the uncertain part by a single-valued membership on [0, 1], whereas NS considers three possible outcomes: true, false and indeterminate. Consequently, the indeterminate part opens a wide window to accommodate uncertain and vague data more nuancedly.

The neutrosophic probability [34] is, in effect, a natural generalization of classical probability theory for dealing with incomplete and indeterminate data. The neutrosophic probability is the triple (T, I, F), where T and F are respectively for truth and falsity, and I stands for uncertainty.

A neutrosophic random variable includes two parts, defined by

$$X_N = X_L + X_U I_N$$

where X_L is classical and $X_U I_N$ is the indeterminate part for uncertainty level $I_N \in [I_L, I_U]$. In this way, the values of NRV can be true, false or indeterminate, simultaneously. Consider the neutrosophic normal random variable $X_N \in [X_L, X_U]$ with neutrosophic mean and variance $\mu_N \in [\mu_L, \mu_U\ ]$ and $\sigma_N^2 \in [\sigma_L^2, \sigma_U^2]$, where

$$\mu_N \in [\mu_L, \mu_U\ ] = \left[\frac{\sum_{i=1}^{N} X_{Li}}{N}, \frac{\sum_{i=1}^{N} X_{Ui}}{N}\right]$$
$$\sigma_N^2 \in [\sigma_L^2, \sigma_U^2] = \left[\frac{\sum_{i=1}^{N} (X_{Li} - \mu_L)^2}{N}, \frac{\sum_{i=1}^{N} (X_{Ui} - \mu_U)^2}{N}\right]$$

Now, let a neutrosophic random sample of size n is drawn from a population of size N including indeterminate observations. The observed neutrosophic sample mean $\overline{x}_N$ and variance s_N^2 are

$$\overline{x}_N \in [\overline{x}_L, \overline{x}_U\ ] = \left[\frac{\sum_{i=1}^{n} x_{Li}}{n}, \frac{\sum_{i=1}^{n} x_{Ui}}{n}\right]$$
$$s_N^2 \in [s_L^2, s_U^2] = \left[\frac{\sum_{i=1}^{n} (x_{Li} - \overline{x}_L)^2}{n-1}, \frac{\sum_{i=1}^{n} (x_{Ui} - \overline{x}_U)^2}{n-1}\right]$$

4. **The NARCBD**

The model of a design with b blocks, c checks and v new treatments can be written as

$$y_{Nhijg} = \mu_N + \alpha_{Ni} + \tau_{Nqj} + \tau_{Nlig} + \varepsilon_{Nhijg}, \quad \begin{cases} i = 1, 2, \ldots, b \\ j = 1, 2, \ldots, c \\ g = 1, 2, \ldots, n_{(li)} \end{cases} \tag{1}$$

where indices l and q for h are related to new treatments and checks, respectively, μ_N is the general mean, α_{Ni} is the i^{th} neutrosophic block effect, τ_{Nqj} is the j^{th} neutrosophic check effect, τ_{Nlig} is the g^{th} neutrosophic new treatment effect, and ε_{Nhijg} is the neutrosophic error with zero mean and variance σ_N^2. For $\mathrm{v} = \sum_{i=1}^{b} n_{(li)}$ new treatments and c checks, $e = \mathrm{v} + c$ is the total number of checks and new treatments; therefore, the total number of units in blocks is $n = \mathrm{v} + bc$.

It is worth mentioning here that the Equation (1) can be rewritten as

$$y_{Nhijg} = y_{Lhijg} + y_{Uhijg} I_N; \quad I_N \in [I_L, I_U] \tag{2}$$

In the neutrosophic ANOVA framework, the subscript N stands for the neutrosophic expression, and hence, the neutrosophic sum of squares (NSS) are denoted by SS_{NT}, SS_{NTr}, SS_{NB} and SS_{NE} to represent total, treatment, block, and error sum of squares, respectively.

4.1. *Estimating neutrosophic parameters*

After imposing the following two constraints

$$\sum_{i=1}^{b} \widehat{\alpha}_{Ni} = 0$$
$$\sum_{j=1}^{c} \widehat{\tau}_{Nqj} + \sum_{i=1}^{b} \sum_{g=1}^{n_{(li)}} \widehat{\tau}_{Nlig} = 0 \tag{3}$$

on the model (1), one can estimate model parameters by solving the least square normal equations and get

$$\widehat{\mu}_N = \frac{1}{\mathrm{v}+c}\left(y_{N...} - \frac{(b-1)}{b}\sum_{j=1}^{c} y_{Nq.j}\right) - \sum_{i=1}^{b} n_{(li)}\widehat{\alpha}_{Ni}; \quad \widehat{\mu}_N \in [\widehat{\mu}_L,\ \widehat{\mu}_U]$$
$$\widehat{\alpha}_{Ni} = \overline{y}_{Nqi.} - \frac{y_{Nq..}}{bc}; \quad \widehat{\alpha}_{Ni} \in [\widehat{\alpha}_{Li}, \widehat{\alpha}_{Ui}]$$
$$\widehat{\tau}_{Nqj} = \overline{y}_{Nq.j} - \widehat{\mu}_N; \quad \widehat{\tau}_{Nqj} \in [\widehat{\tau}_{Lqj}, \widehat{\tau}_{Uqj}] \tag{4}$$
$$\widehat{\tau}_{Nlig} = y_{Nlig} - \widehat{\alpha}_{Ni} - \widehat{\mu}_N; \quad \widehat{\tau}_{Nlig} \in [\widehat{\tau}_{Llig}, \widehat{\tau}_{Ulig}]$$

where $i = 1, 2, ..., b$, $j = 1, 2, ..., c$, and $g = 1, 2, ..., n_{(li)}$.
All parameter estimators in neutrosophic treatment models and block-reduced models can be obtained in a similar manner.

4.2. *The neutrosophic test statistics*

First of all, let us introduce some mathematical expressions for NSS, where "adj" and "unadj" stand for adjusted and unadjusted sums of squares, respectively.

$$SS_{NT} = \sum_{i=1}^{b}\sum_{j=1}^{c} y_{Nqij}^2 + \sum_{i=1}^{b}\sum_{g=1}^{n_{(li)}} y_{Nlig}^2 - \frac{y_{N...}^2}{n}; \quad SS_{NT} \in [SS_{LT},\ SS_{UT}]$$

$$SS_{NB(\text{unadj})} = \sum_{i=1}^{b} \frac{y_{N.i.}^2}{c + n_{(li)}} - \frac{y_{N...}^2}{n};\ SS_{NB(\text{unadj})} \in \left[SS_{LB(\text{unadj})},\ SS_{UB(\text{unadj})}\right]$$

$$SS_{NTr(\text{adj})} = \sum_{i=1}^{b}\left(\overline{y}_{Nqi.} - \frac{y_{Nq..}}{bc}\right) y_{Nqi.} + \frac{1}{b}\sum_{j=1}^{c} y_{Nq.j}^2 + \sum_{i=1}^{b}\sum_{g=1}^{n_{(li)}} y_{Nlig}^2 - \sum_{i=1}^{b} \frac{y_{N.i.}^2}{c + n_{(li)}};$$

$$SS_{NTr(\text{adj})} \in \left[SS_{LTr(\text{adj})},\ SS_{UTr(\text{adj})}\right]$$

$$SS_{NTr(\text{unadj})} = \frac{1}{b}\sum_{j=1}^{c} y_{Nq.j}^2 + \sum_{i=1}^{b}\sum_{g=1}^{n_{(li)}} y_{Nlig}^2 - \frac{y_{N...}^2}{n};$$

$$SS_{NTr(\text{unadj})} \in \left[SS_{LTr(\text{unadj})} SS_{UTr(\text{unadj})}\right],$$

$$SS_{NCheck} = \frac{1}{b}\sum_{j=1}^{c} y_{Nq.j}^2 - \frac{y_{Nq..}^2}{bc};\ SS_{NCheck} \in [SS_{LCheck},\ SS_{UCheck}]$$

$$SS_{Nnew} = \sum_{i=1}^{b}\sum_{g=1}^{n_{(li)}} y_{Nlig}^2 - \frac{y_{Nl..}^2}{\mathrm{v}}; SS_{Nnew} \in [SS_{Lnew},\ SS_{Unew}]$$

$$SS_{N\text{new and new} \times \text{ch}} = SS_{NTr(\text{adj})} - SS_{NCheck};$$

$$SS_{N\text{new and new} \times \text{ch}} \in [SS_{L\text{new and new} \times \text{ch}},\ SS_{U\text{new and new} \times \text{ch}}]$$

$$SS_{N\text{new} \times \text{check}} = SS_{NTr(\text{unadj})} - SS_{NCheck} - SS_{Nnew};$$

$$SS_{N\text{new} \times \text{check}} \in [SS_{L\text{new} \times \text{check}},\ SS_{U\text{new} \times \text{check}}]$$

$$SS_{NB(\text{adj})} = SS_{NB(\text{unadj})} - (SS_{NTr(\text{unadj})} - SS_{NTr(\text{adj})}); SS_{NB(\text{adj})} \in \left[SS_{LB(\text{adj})} SS_{UB(\text{adj})}\right]$$

$$SS_{NE} = SS_{NT} - SS_{NTr(\text{adj})} SS_{NB(\text{unadj})} SS_{NT} - SS_{NTr(\text{unadj})} SS_{NB(\text{adj})};$$

$$SS_{NE} \in [SS_{LE},\ SS_{UE}]$$

It is well known that mean squares are obtained by dividing the each corresponding sum of squares onto its degrees of freedom. As a result, the neutrosophic mean squares are as follows:

$$MS_{NTr(\text{adj})} = \frac{SS_{NTr(\text{adj})}}{c + \mathrm{v} - 1};\ MS_{NTr(\text{adj})} \in \left[MS_{LTr(\text{adj})} MS_{UTr(\text{adj})}\right]$$

$$MS_{NB(\text{adj})} = \frac{SS_{NB(\text{adj})}}{b-1};\ MS_{NB(\text{adj})} \in \left[MS_{LB(\text{adj})}, MS_{UB(\text{adj})}\right]$$

$$MS_{NCheck} = \frac{SS_{NCheck}}{c-1};\ MS_{NCheck} \in [MS_{LCheck}, MS_{UCheck}]$$

$$MS_{Nnew} = \frac{SS_{Nnew}}{\mathrm{v}-1};\ MS_{Nnew} \in [MS_{Lnew}, MS_{Unew}]$$

$$MS_{N\text{new and new} \times \text{ch}} = \frac{SS_{N\text{new and new} \times \text{ch}}}{\mathrm{v}};$$

$$MS_{N\text{new and new} \times \text{ch}} \in [MS_{L\text{new and new} \times \text{ch}}, MS_{U\text{new and new} \times \text{ch}}]$$

$$MS_{N\text{new} \times \text{check}} = \frac{SS_{N\text{new} \times \text{check}}}{1}; MS_{N\text{new} \times \text{check}} \in [MS_{L\text{new} \times \text{check}}, MS_{U\text{new} \times \text{check}}]$$

$$MS_{NE} = \frac{SS_{NE}}{(b-1)(c-1)};\ MS_{NE} \in [MS_{LE}, MS_{UE}]$$

Now, each of the following statistics represents a candidate neutrosophic test statistics F_N.

$$F_{NTr(\text{adj})} = \frac{MS_{NTr(\text{adj})}}{MS_{NE}};\ F_{NTr(\text{adj})} \in \left[F_{LTr(\text{adj})}, F_{UTr(\text{adj})}\right]$$

$$F_{NB(\text{adj})} = \frac{MS_{NB(\text{adj})}}{MS_{NE}};\ F_{NB(\text{adj})} \in \left[F_{LB(\text{adj})}, F_{UB(\text{adj})}\right]$$

$$F_{NCheck} = \frac{MS_{NCheck}}{MS_{NE}};\ F_{NCheck} \in [F_{LCheck}, F_{UCheck}]$$

$$F_{Nnew} = \frac{MS_{Nnew}}{MS_{NE}}; F_{Nnew} \in [F_{Lnew}, F_{Unew}]$$

$$F_{N\text{new and new} \times \text{ch}} = \frac{MS_{N\text{new and new} \times \text{ch}}}{MS_{NE}};$$

$$F_{N\text{new and new} \times \text{ch}} \in [F_{L\text{new and new} \times \text{ch}}, F_{U\text{new and new} \times \text{ch}}]$$

$$F_{N\text{new } \times \text{ check}} = \frac{MS_{N\text{new } \times \text{ check}}}{MS_{NE}}; F_{N\text{new } \times \text{ check}} \in [F_{L\text{new } \times \text{ check}}, F_{U\text{new } \times \text{ check}}]$$

The neutrosophic test statistics F_N, is defined as

$$F_N = F_L + F_U I_{F_N}; \quad I_{F_N} \in [I_{F_L}, I_{F_U}] \tag{5}$$

where F_L is the lower bound and F_L is the upper bound. Note that F_L represents the determinate part, and $F_U I_{F_N}$ represents the indeterminate part in each proposed test.
It is obvious that the test statistics (5) reduces to the classical approach when $I_{F_N} = 0$.

4.3. *Neutrosophic decision rules*

We list down the null and the alternative hypotheses which are needed to test block, check and new treatments effects:
$H_{N0} : \alpha_{Ni} = 0 \;\; vs \;\; H_{N1} : not\ all\ \alpha_{Ni} \neq 0, i = 1.\ 2.,,,.\ b,$
$H_{N0} : \tau_{Nbj} = 0 \;\; vs \;\; H_{N1} : not\ all\ \tau_{Nbj} \neq 0, j = 1.\ 2.,,,.\ c,$
$H_{N0} : \tau_{Nlig} = 0 \;\; vs \;\; H_{N1} : not\ all\ \tau_{Nlig} \neq 0, g = 1.\ 2.,,,.\ n_{(li)}$
According to Smarandache [32], the neutrosophic decision rules at level α are:

- Accept H_{N0} for $min\{p_N{-}value\} > \alpha$.
- Reject H_{N0} for $max\{p_N{-}value\} \leq \alpha$.
- If $min\{p_N{-}value\} < \alpha < max\{p_N{-}value\}$, then there is no decissive decission. But, in this special case one could compute the chance to reject H_{N0} to be the ratio of $\frac{\alpha - min\{p_N - value\}}{max\{p_N - value\} - min\{p_N - value\}}$. Likewise, the ratio $\frac{max\{p_N - value\} - \alpha}{max\{p_N - value\} - min\{p_N - value\}}$ represents the chance of accepting H_{N0}.

As usual classical ANOVA tables, building NANOVA tables for NARCBD as in Tables 1 and 2 is also straightforward.

Table 1. NANOVA Table (A) suitable for NARCBD

Sources of variation	**Ndf**	**NSS**	**NMS**	$\boldsymbol{F_N}$**-value**
Blocks unadjusted	$b-1$	$SS_{NB(\text{unadj})}$	$\frac{SS_{NB(\text{unadj})}}{b-1}$	–
Treatments adjusted	$c+\text{v}-1$	$SS_{NTr(\text{adj})}$	$\frac{SS_{NTr(\text{adj})}}{c+\text{v}-1}$	$\frac{MS_{NTr(\text{adj})}}{MS_{NE}}$
Checks	$c-1$	SS_{NCheck}	$\frac{SS_{NCheck}}{c-1}$	$\frac{MS_{NCheck}}{MS_{NE}}$
New and New × Check	v	$SS_{N\text{new and new } \times \text{ ch}}$	$\frac{SS_{N\text{new and new } \times \text{ ch}}}{\text{v}}$	$\frac{MS_{N\text{new and new } \times \text{ ch}}}{MS_{NE}}$
Error	$(b-1)(c-1)$	SS_{NE}	$\frac{SS_{NE}}{(b-1)(c-1)}$	–
Total	$n-1$	SS_{NT}	–	–

5. **Case and simulation studies**

In this section, we exclusively examine the performance of our proposed NARCBD approach by a real data set scenario, followed by an extensive simulation study.

Table 2. NANOVA Table (B) suitable for ARCBD

Sources of variation	**Ndf**	**NSS**	**NMS**	$\boldsymbol{F_N}$**-value**
Blocks adjusted	$b-1$	$SS_{NB(\text{adj})}$	$\frac{SS_{NB(\text{adj})}}{b-1}$	$\frac{MS_{NB(\text{adj})}}{MS_{NE}}$
Treatments unadjusted	$c+\text{v}-1$	$SS_{NTr(\text{unadj})}$	$\frac{SS_{NTr(\text{unadj})}}{c+\text{v}-1}$	–
Checks	$c-1$	SS_{NCheck}	$\frac{SS_{NCheck}}{c-1}$	$\frac{MS_{NCheck}}{MS_{NE}}$
New treatments	$\text{v}-1$	SS_{Nnew}	$\frac{SS_{Nnew}}{\text{v}-1}$	$\frac{MS_{Nnew}}{MS_{NE}}$
New $\times$ Check	1	$SS_{N\text{new } \times \text{ check}}$	$\frac{SS_{N\text{new } \times \text{ check}}}{1}$	$\frac{MS_{N\text{new } \times \text{ check}}}{MS_{NE}}$
Error	$(b-1)(c-1)$	SS_{NE}	$\frac{SS_{NE}}{(b-1)(c-1)}$	–
Total	$n-1$	SS_{NT}	–	–

5.1. *Real case study*

An experiment is ran in a research farm at Isfahan University of Technology to study the breeding program of safflower plant. This study included observing neutrosophic ninety-nine cultivars of safflower genotypes using an NARCBD with three blocks. Each block has neutrosophic eight control treatments (as checks) and twenty-five neutrosophic genotypes (as new treatments).

AlAita and Talebi [7] have listed all outcomes concerning oil seed actions resulted from plants. The two consecutive NANOVA Tables 3 and 4 show the related observed value of test statistics F_N-tests for our experiment.

The NANOVA Tables 3 and 4 clarify how to report the previously proposed test statistics. As an example, in NANOVA Table 3, the neutrosophic form for treatments is $1.328 + \ 1.346I_{F_N};\ I_{F_N} \in [0,\ 0.013]$, and this in turn states that the measure of indeterminacy for treatments equals 0.013. It is noted that, due to the partitioning neutrosophic treatment effects into check and new treatments, for each effect, F_N and $p_N - values$ are computed, separately.

5.2. *Simulation study*

Under uncertainty and imprecise data framework, the performance of the proposed NARCBD is assessed in sense of test power and controlling type I error at a given nominal level of α. Two significance levels were chosen, namely $\alpha = .05$ and $\alpha = .01$. It will be shown that this new approach dominates the classical one.

The simulated number of treatments and blocks were taken just as do exist in famous references like Federer [17]. The underlying null hypothesis states that data are generated from the centered standard Gaussian distribution $\mathcal{N}(0,1)$. Above all, it is presumed that the homogeneity assumption of neutrosophic variances is verified and that all planned neutrosophic

Table 3. NANOVA Table (A) suitable for real case study

Sources of variation	**Ndf**	**NSS**	**NMS**	F_N	**Neutrosophic form** F_N	p_N**-value**
Blocks (unadj)	2	[88934.145, 88147.245]	[44467.072, 44073.623]	–	–	–
Treatments (adj)	82	[3509029.746, 3521660.933]	[42793.046, 42947.085]	[1.328, 1.346]	$1.328 + 1.346I_{F_N};\ I_{F_N} \in [0,\ 0.013]$	[0.285, 0.274]
Checks	7	[338369.950, 339847.407]	[48338.564, 48549.630]	[1.501, 1.522]	$1.501 + 1.522I_{F_N};\ I_{F_N} \in [0,\ 0.014]$	[0.245, 0.238]
New and new × check	75	[3170659.05, 3181813.526]	[42275.454, 42424.180]	[1.312, 1.330]	$1.312 + 1.330I_{F_N};\ I_{F_N} \in [0,\ 0.014]$	[0.294, 0.284]
Error	14	[450984.022, 446662.361]	[32213.144, 31904.454]	–	–	–
Total	98	[4048947.913, 4056470.539]	–	–	–	–

Table 4. NANOVA Table (B) for real case study

Sources of variation	**Ndf**	**NSS**	**NMS**	F_N	**Neutrosophic form** F_N	p_N**-value**
Blocks (adj)	2	[396001.136, 391361.045]	[198000.568, 195680.522]	[6.147, 6.133]	$6.147 - 6.133I_{F_N};\ I_{F_N} \in [0,\ 0.002]$	[0.012, 0.012]
Treatments (unadj)	82	[3201962.755, 3218447.133]	[39048.326, 39249.354]	–	–	–
Checks	7	[338369.950, 339847.407]	[48338.564, 48549.630]	[1.501, 1.522]	$1.501 + 1.522I_{F_N};\ I_{F_N} \in [0,\ 0.014]$	[0.245, 0.238]
New treatments	74	[2780946.509, 2795211.248]	[36367.407, 36558.516]	[1.130, 1.146]	$1.130 + 1.146I_{F_N};\ I_{F_N} \in [0,\ 0.014]$	[0.422, 0.409]
New × Check	1	[82646.296, 83388.478]	[82646.296, 83388.478]	[2.566, 2.614]	$2.566 + 2.614I_{F_N};\ I_{F_N} \in [0,\ 0.018]$	[0.131, 0.128]
Error	14	[450984.022, 446662.361]	[32213.144, 31904.454]	–	–	–
Total	98	[4048947.913, 4056470.539]	–	–	–	–

designs are balanced.

Recall that, under the null hypothesis, the check treatments all have zero mean. In other words, $H_{N0} : (\mu_{N1}, \mu_{N2}, \mu_{N3}, \mu_{N4}) = (0, 0, 0, 0)$.

Next, we itemize the Monte Carlo (MC) generating steps in order to compute the neutrosophic empirical type I error rates as well as the test power.

- In each repetition of the $a = 10,000$ independent repetitions:
  (1) Generate the u^{th} random sample $x_{N1}^{(u)}, x_{N2}^{(u)}, ..., x_{Nn}^{(u)}$ under the null hypothesis, where $u = 1, 2, ..., a$.
  (2) In the u^{th} sample, extract the test statistics F_{Nu}.
  (3) Next, assign the value $I_{Nu} = 1$ for every rejected H_{N0} at α, and $I_{Nu} = 0$ otherwise.
- The empirical type I error rate is estimated by the ratio of significant tests.
- The empirical test power is estimated by $\widehat{\pi}(\mu_{Nu}) = \frac{1}{a}\sum_{u=1}^{a} I_{Nu}$, where at least one of the parameters $(\mu_{N1}, \mu_{N2}, \mu_{N3}, \mu_{N4})$ is not zero.

It is also helpful to demonstrate all previous steps as diagrams showing in Figures 1 and 2.

By choosing different values of $\delta = (\mu_1, \mu_2, \mu_3, \mu_4)$ in blocks, the results listed in Tables 5 and

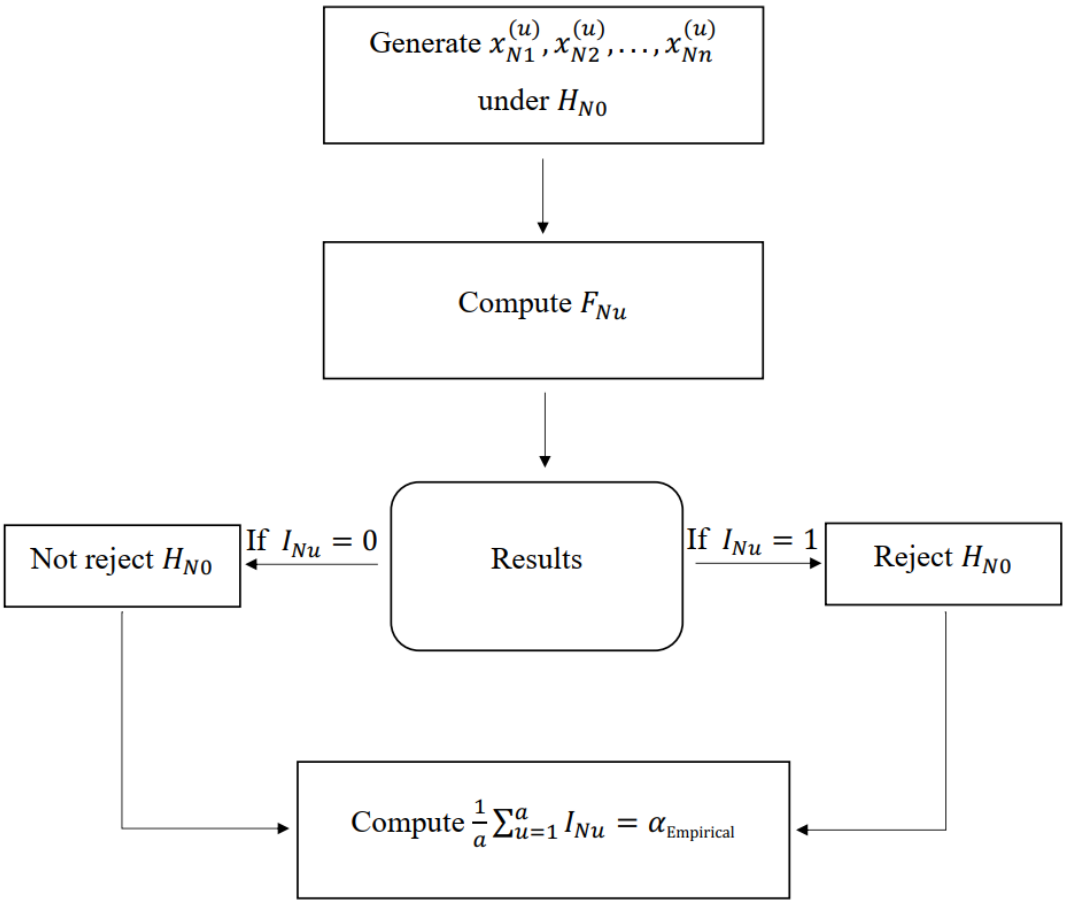

FIGURE 1. MC algorithm to find the empirical rejection rate $\alpha_{Empirical}$

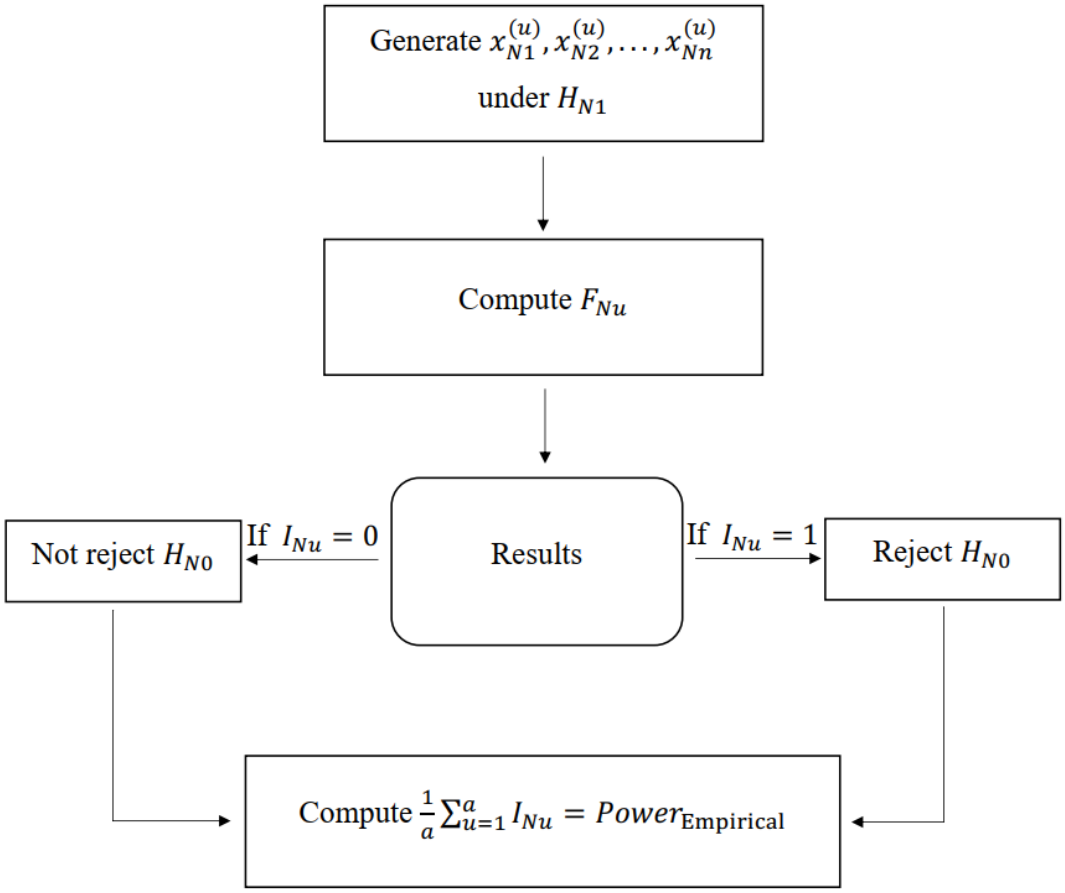

FIGURE 2. MC algorithm to find the empirical test power $Power_{Empirical}$

6 show each of empirical error rates and empirical tests power. Also, consider the following different values for δ such as, $(0,0,0,1)$, $(0,1,2,2)$, $(1,2,2,3)$, $(1,1,3,3)$, $(0,1,2,4)$, $(0,1,3,4)$, $(0,3,4,4)$, and $(0,2,4,6)$.

It is noted that the proposed NARCBD outperforms the classical design, since it controls the type I error much better and it also has a uniformly higher power. In light of these listed results, one concludes that the proposed F_N test is more informative and flexible than the existing classical F test under presence of uncertain data.

In addition, Figures 3 and 4 show that as number of treatments increases, a wide gap emerges which explicitly splits the two power curves to become far apart.

6. **Conclusions, further discussions and limitations**

In this work, we proposed an augmented randomized complete block design under NS which is suitable to analyze uncertain, indeterminate, and imprecise data. We defined an NARCBD model which provides several advantages over classical ARCBD model. It can surmount the indeterminacy in data, resulting in robust and flexible outcomes along with along with a

TABLE 5. MC NARCBD model findings assuming parameters of $(b = 3, c = 4, \mathrm{v} = 8, n = 20)$, *for means of check treatment* $\delta = (\mu_{N1}, \mu_{N2}, \mu_{N3}, \mu_{N4})$, *and different new treatments* $(\mu_{Ni} = 0, \mu_{Nj} = 1)$, $i = 1, ..., 4, j = 5, \ldots, 8$.

Test	$\boldsymbol{\alpha}$	**Mean empirical type I error**	**Mean empirical power**							
			$\boldsymbol{\delta_1 = (0,0,0,1)}$	$\boldsymbol{\delta_2 = (0,1,2,2)}$	$\boldsymbol{\delta_3 = (1,2,2,3)}$	$\boldsymbol{\delta_4 = (1,1,3,3)}$	$\boldsymbol{\delta_5 = (0,1,2,4)}$	$\boldsymbol{\delta_6 = (0,1,3,4)}$	$\boldsymbol{\delta_7 = (0,3,4,4)}$	$\boldsymbol{\delta_8 = (0,2,4,6)}$
NARCBD	0.01	[0.0093, 0.0098]	[0.0202, 0.0213]	[0.0542, 0.0632]	[0.0799, 0.0916]	[0.1138, 0.1342]	[0.1856, 0.2255]	[0.2398, 0.2856]	[0.3486, 0.4141]	[0.5914, 0.6617]
	0.05	[0.0510, 0.0517]	[0.0946, 0.1005]	[0.1985, 0.2261]	[0.2769, 0.3123]	[0.3615, 0.4091]	[0.5172, 0.5817]	[0.6046, 0.6668]	[0.7463, 0.8033]	[0.9216, 0.9504]

TABLE 6. MC NARCBD model findings assuming parameters of $(b = 6, c = 4, \mathrm{v} = 30, n = 54)$, *for means of check treatment* $\delta = (\mu_{N1}, \mu_{N2}, \mu_{N3}, \mu_{N4})$, *and different new treatments*$(\mu_{Ni} = 0, \mu_{Nj} = 1,\ \mu_{Nk} = 2)$, $i = 1, ..., 10, j = 11, \ldots, 20$, $k = 21, \ldots, 30$.

Test	$\boldsymbol{\alpha}$	**Mean empirical type I error**	**Mean empirical power**							
			$\boldsymbol{\delta_1 = (0,0,0,1)}$	$\boldsymbol{\delta_2 = (0,1,2,2)}$	$\boldsymbol{\delta_3 = (1,2,2,3)}$	$\boldsymbol{\delta_4 = (1,1,3,3)}$	$\boldsymbol{\delta_5 = (0,1,2,4)}$	$\boldsymbol{\delta_6 = (0,1,3,4)}$	$\boldsymbol{\delta_7 = (0,3,4,4)}$	$\boldsymbol{\delta_8 = (0,2,4,6)}$
NARCBD	0.01	[0.0095, 0.0108]	[0.1119, 0.1415]	[0.1441, 0.1791]	[0.2011, 0.2550]	[0.2962, 0.3619]	[0.4956, 0.5867]	[0.6029, 0.6985]	[0.7892, 0.8599]	[0.9705, 0.9874]
	0.05	[0.0478, 0.0492]	[0.3366 0.3824]	[0.4072, 0.4602]	[0.4803, 0.5505]	[0.6225, 0.6948]	[0.8093, 0.8712]	[0.8829, 0.9246]	[0.9623, 0.9807]	[0.9983, 0.9995]

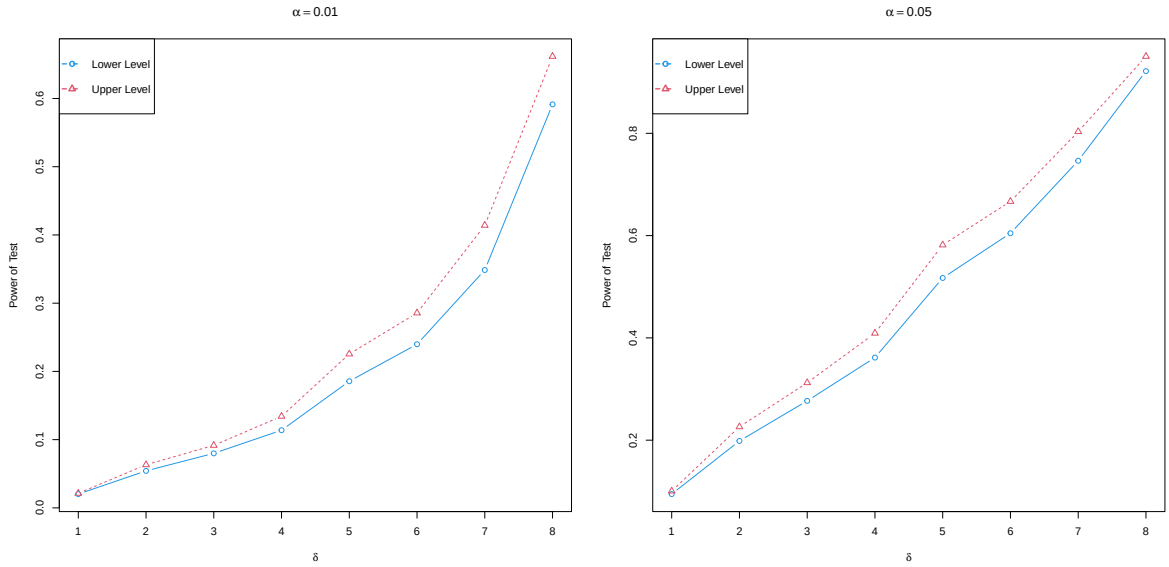

FIGURE 3. Plotting empirical power curves for NARCBD with parameters $(b = 3, c = 4, \mathrm{v} = 8, n = 20)$. The lower curve represents the classical design.

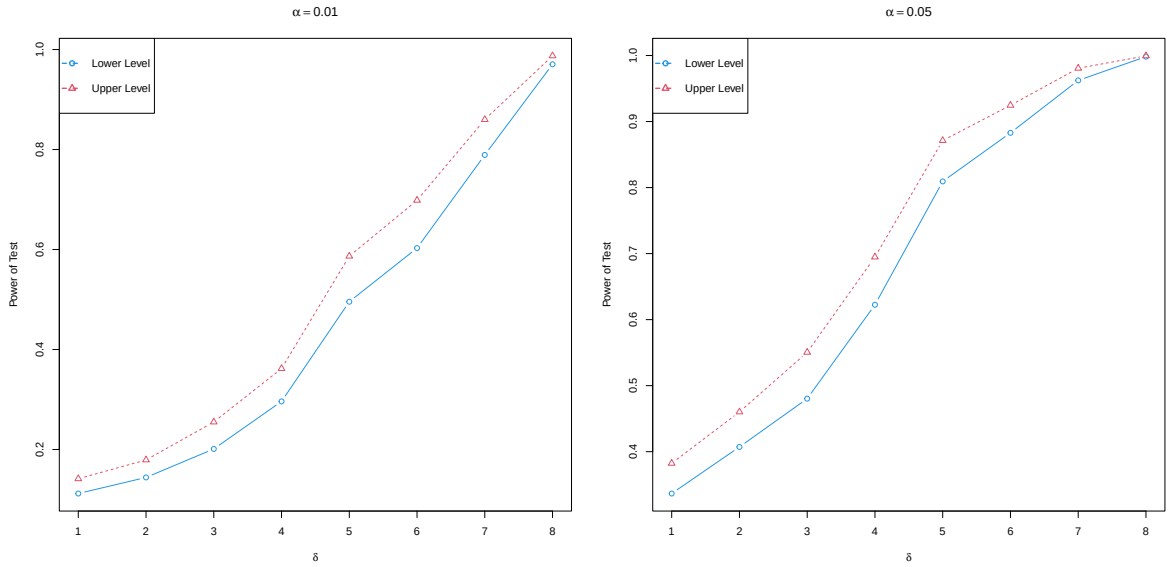

FIGURE 4. Plotting empirical power curves for NARCBD with parameters $(b = 6, c = 4, \mathrm{v} = 30, n = 54)$. The lower curve represents the classical design.

valuable increases in statistical precision, accuracy, and power. These are the basic tools in statistical inference. We believe that the NARCBD will emerge as a very useful model in different research fields, including farming, agricultural, and biological.

But the proposed NARCBD model has some limitations. It does require a larger sample size than the classical design to work perfectly, and this is of course, may lead to more time-consuming and more expensive experiments. The complex computational nature of NARCBD really requires a statistician who can give careful readings and interpretations in presence of indeterminacies.

After defining the neutrosophic hypotheses and the related decision rules, a neutrosophic test statistics was defined. All case study and simulation studies reflected the fact that the proposed method is the preferable model to work with uncertain environment.

Other extended directions

It is notably remarked that connecting the design of experiments with artificial intelligence is hardly found in specialized literatures but one may refer to a few great references, like [19, 23]. The need of developing an AI along with experimental designs comes from the fact that AI procedures can effectively reduce the repetitions and the time inquired to reach the best estimated parameters.

Funding: No external funding was recieved for this research.

Conflicts of Interest: The authors have no conflict of interests.

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Received: Oct 28, 2024. Accepted: March 18, 2025