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A Graphical Approach as Multiple Comparison Method for the Balanced and Partially Balanced Lattice Designs

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ABSTRACT

This study proposes a reliable and easy understandable statistical solution for the selection of varieties in the balanced and partially balanced lattice experiments, which are widely used in plant breeding studies. For this purpose, the Analysis of Means (ANOM) was adapted to the balanced, simple and triple lattice designs and an R function is developed for it. The adapted ANOM approach was compared with the Tukey, Duncan and Fisher's LSD tests with respect to the actual type I error rate in all of the balanced, simple and triple lattice designs. In addition to this, the ANOM approach and Tukey test were examined comparatively using a hypothetical example. According to the simulation results, LSD and Duncan could not maintain the actual type I error rate at 5.00% under any conditions. This situation became more dramatic with the increase in the number of groups. While the actual type I error rate for LSD and Duncan tests varied between 54.36%-100.00% and 37.49%-99.96%, respectively, for ANOM and Tukey tests it varied between 4.64%-6.08% and 4.62%-6.45%, respectively. ANOM and Tukey tests were quite successful in terms of maintaining the actual type I error rate. However, since the number of groups in lattice designs was quite high, the given hypothetical example showed that it would be more understandable to use the ANOM method.

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Introduction

Due to the soil structure, the experimental designs containing blocks are widely used in agricultural studies. The completely randomized block design is the leading of these experimental designs. In the completely randomized block design, each treatment or group takes place once in each block at equal intervals. The purpose of blocking is to separate the heterogeneous material of the experiment into homogeneous parts within itself. However, as the number of groups compared increases, it is almost not possible to find homogeneous blocks that can contain all groups. As in areas such as the stock market, medical research, and automotive industry, also in some cases in agriculture, the number of groups (varieties or treatments) compared especially in breeding studies is quite large (Wu & Liao, 2004). Therefore, it is not appropriate to use completely randomized block design. As a solution to this situation, Yates (1936a) proposed Balanced Incomplete Block (BIB) design, where not every group takes part in each block, but the number of pairs of each group taking part together is equal. Although balanced incomplete block designs are effective, they are not suitable. Because the minimum number of blocks required is impractical when the number of groups is large. Hence, Yates (1936b) developed a new experimental design called Lattice or Quasi-factorial for cases where the number of groups is large. As with all experimental designs, also in Lattice, the analysis of variance only shows whether the factor (such as variety, treatment or application) is statistically effective (Glass & Hakstian, 1969). However, it does not show the difference stems from which group or groups (levels of the factor) (Duncan, 1955). Therefore, if the effect of the factor as a result of the analysis of variance is statistically significant, multiple comparison tests are used. Numerous multiple comparison tests have been developed to compare group averages. At this point, it is very important to determine which multiple comparison tests should be used. Multiple comparison tests are divided into categories such as all-contrast comparisons (ACC), all-pairwise multiple comparisons (MCP) (Duncan, 1955; Fisher, 1937; Tukey, 1949) multiple comparisons with the best (MCB) (Hsu,

1996), multiple comparisons with the control (MCC) (Dunnett, 1955), and multiple comparisons with the overall average (MCA), depending on the purpose of use (Hsu, 1996). MCP tests can be used easily when the number of groups compared is not large. However, as the number of groups (k) increases, the number of pairwise comparisons (kC2) also increases rapidly. For example, when k = 3, 5, 10, and 50, the number of pairwise comparisons are 3, 6, 10, 45, and 1225, respectively. Absorbing the results becomes increasingly difficult when the number of groups being compared is large. Therefore, in such cases, it is much more understandable to compare the groups with the best group, the control group, or the overall average rather than comparing them with each other. Especially in experimental designs such as lattice where breeding or selection studies are carried out, the differences of quite a large number of varieties from the population average are examined. Therefore, using MCA may be much more useful than MCP, MCB, and MCC. The multiple comparisons with the overall average is also called the Analysis of Means (ANOM). ANOM is a graphical method used to compare groups in terms of averages, variances, rates or proportions, correlation coefficients, and regression coefficients (Ott, 1983; Nelson, 1983, 1985, 1989, 1993; Wludyka & Nelson, 1997; Nelson & Dudewicz, 2002; Pran Kumar & Rao, 1998; Rao, 2005; Nelson et al., 2005). Since it is a graphical method, the results are very easy to understand. The use of ANOM is detailed by Nelson et al.(2005). In this study, ANOM test was adapted to the balanced and partially balanced lattice designs. Also, an user friendly function was developed with the R programming language to use the improved ANOM approach for the balanced and partially balanced lattice designs. The adapted ANOM was compared with Tukey (Tukey, 1949), Duncan (Duncan, 1955) and LSD (Fisher, 1937) tests which are common multiple comparison tests in practice (Genç & Soysal, 2018), in terms of the actual type I error rate via monte carlo simulation technique. Finally, the use and interpretation of the ANOM approach were explained by comparing it with the Tukey test through a hypothetical example. The aim of this study is to provide a reliable solution based on statistical approaches for the selection of varieties in the balanced and partially balanced lattice experiments, which are widely used in plant breeding studies.

Materials and Methods

The Balanced Lattice Designs

Every replication must be an absolute square in balanced and partially balanced lattice desings. The number of blocks (k) in each replication must be equal to the square root of the number of groups (k2). Also, in balanced lattice designs, the number of replications (r = k + 1) must be one more than the number of blocks. Calculation steps for balanced lattice designs are as follows.

1. Compute the block totals, the replication totals, the group totals (t) and grand total (G).
2. For each group, compute totals (B_t) for all blocks in which the groups are located.
3. $W = kt - (k+1)B_t + G$
4. Sum of squares (s.s.) for the total, replications and groups are found classically.
5. Compute the adjusted sum of squares for the blocks, $SSB_{adj}=(\sum W^2)/(k^3+k^4)$
6. Compute the adjustment factor, $\mu = (E_b - E_e)/(k^2 E_b)$
7. $E_b = SSB_{adj}/(k^2-1)$ and $E_e = SSE/(k-1)(k^2-1)$, SSE is found by subtracting replications s.s., groups s.s. and adjusted blocks s.s. from total s.s.
8. The adjusted group total is $t + \mu W$.
9. Compute sum of squares for the groups based on the adjusted group total.
10. Effective error (E_e') is $E_e(1 + k\mu)$
11. Compute the F-value by dividing the adjusted groups s.s. by the effective error (Cochran & Cox, 1960).

The Partially Balanced Lattice Designs

In the partially balanced lattice, the number of replications does not have to be more than the number of blocks. A partially balanced lattice designs are named according to the number of replications. When the number of replications (r) are 2, 3, 4, etc., it is called as simple lattice, triple lattice, quadruple lattice, etc., respectively. In this study also, simple and triple lattice are emphasized. Calculation steps for partially balanced lattice designs are as follows.

1. Compute the block totals (B), the replication totals, the group totals (t) and grand total (G).
2. For each block compute,
   $C = \text{Sum (OR) of all groups in the block} - rB$
   OR: overall replicates
3. All sum of squares are computed classically.
4. Compute the adjusted sum of squares for the blocks,
   $SSB_{adj} = (\sum C^2)/[kr(r-1)] - (\sum R_c^2)/[k^2 r(r-1)]$,
   R_c *is* is the sum of C values in each replication.
5. The adjustment factor (μ) is $(E_b - E_e)/[k(r-1)E_b]$
6. $E_b = SSB_{adj}/r(k-1)$ and E_e is found like in the balanced lattice designs.
7. The adjusted group total is $t + \mu c$
8. Compute sum of squares for the groups based on the adjusted group total.
9. Effective error (E_e') is $E_e[1 + (rk\mu)/(k+1)]$
10. Compute the F-value like in the balanced lattice designs (Cochran & Cox, 1960).

The Basic Anom Procedure

The basic ANOM procedure is introduced for balanced one-way analysis of variance. In the ANOM chart, there are two decision lines, namely lower (LDL) and upper (UDL).

$$LDL = \bar{X}_{..} - h(\alpha, k, v)\sqrt{MSE}\sqrt{(k-1)/(kn)} \quad (1)$$

$$UDL = \bar{X}_{..} + h(\alpha, k, v)\sqrt{MSE}\sqrt{(k-1)/(kn)} \quad (2)$$

If the average of which group is outside of these decision lines, it is understood that the average of that group is statistically significantly different from the overall average. This is corresponding to comparing with h(α, k, v).

$$|T_i| = |\bar{X}_{i.} - \bar{X}_{..}| / \left[\sqrt{MSE}\sqrt{(k-1)/(kn)}\right] \quad (3)$$

The assumption that $X_{ij} \sim N(\mu_i, \sigma^2)$ are independent are met and if $H_0: \mu_1 = \mu_2 = \cdots = \mu_k$, $(T_1, T_2, \ldots, T_k)$ has a multivariate t distribution with equicorrelations $\rho = -1/(k-1)$ and $v = k(n-1)$ df. Under H_0, the critical values $h(\alpha, k, v)$ meet,

$$P[|T_1| \leq h(\alpha, k, v), |T_2| \leq h(\alpha, k, v), \ldots, |T_k| \leq h(\alpha, k, v)] = 1 - \alpha$$

Where, $\bar{X}_{i.}$ is average of i*th* group, $\bar{X}_{..}$ is the overall average, MSE is the mean square error, α is significance level, k is the number of groups (treatments or varieties), n is the number of replications (Nelson, 1993).

Adaptation of ANOM for the Balanced and Partially Balanced Lattice Designs

Lattice designs adjust E_e and group totals so as to take account of sampling errors in the block correction. Therefore, the ANOM method should be applied to adjusted means. The Adjusted overall average is

$$\tilde{X}_{...} = \left(\sum \tilde{X}_{i..}\right)/k^2$$

The Adjusted average of i*th* group is

$\tilde{X}_{i..} = (t_i + \mu W_i)/(k+1)$ for the balanced lattice,

$\tilde{X}_{i..} = (t_i + \mu c)/r$ for the partially balanced lattice.

Therefore, the variance for difference of the adjusted averages of the groups from the adjusted overall average is

$Var(\tilde{X}_{i..} - \tilde{X}_{...}) = E'_e\,(k^2-1)/(k^3+k^2)$ for the balanced lattice,

$Var(\tilde{X}_{i..} - \tilde{X}_{...}) = E'_e\,(k^2-1)/(rk^2)$ for the partially balanced lattice.

Thus,

$|T_i| = \left|\tilde{X}_{i..} - \tilde{X}_{...}\right| / \sqrt{E'_e(k^2-1)/(k^3+k^2)}$ for the balanced lattice,

$|T_i| = \left|\tilde{X}_{i..} - \tilde{X}_{...}\right| / \sqrt{E'_e(k^2-1)/(rk^2)}$ for the partially balanced lattice.

The assumption that $X_{ijk} \sim N(\mu_i, \sigma^2)$ are independent is met and if $H_0: \mu_1 = \mu_2 = \cdots = \mu_k$, $(T_1, T_2, \ldots, T_k)$ has a multivariate t distribution with equicorrelations $\rho = -1/(k^2-1)$ and degree of freedom $v = (k-1)(k^2-1)$ for the balanced lattice and $v = (k-1)(rk-k-1)$ for the partially balanced lattice. Under H_0, the critical values $h(\alpha, k^2, v)$ are

$$P[|T_1| \leq h(\alpha, k^2, v), |T_2| \leq h(\alpha, k^2, v), \ldots, |T_{k^2}| \leq h(\alpha, k^2, v)] = 1 - \alpha$$

Accordingly, decision lines are

$$\left.\begin{aligned} LDL &= \tilde{X}_{...} - h(\alpha, k^2, v)\sqrt{E'_e}\sqrt{(k^2-1)/(k^3+k^2)} \\ UDL &= \tilde{X}_{...} + h(\alpha, k^2, v)\sqrt{E'_e}\sqrt{(k^2-1)/(k^3+k^2)} \end{aligned}\right\}$$

for the balanced lattice,

$$\left.\begin{aligned} LDL &= \tilde{X}_{...} - h(\alpha, k^2, v)\sqrt{E'_e}\sqrt{(k^2-1)/(rk^2)} \\ UDL &= \tilde{X}_{...} + h(\alpha, k^2, v)\sqrt{E'_e}\sqrt{(k^2-1)/(rk^2)} \end{aligned}\right\}$$

for the partially balanced lattice.

If an adjusted average of group falls outside these decision lines, it is statistically significantly different from the adjusted overall average.

Also, the required $h(\alpha, k^2, v)$ values according to different significance levels (α = 0.25, 0.10, 0.05, 0.01, 0.001) for all available the balanced, simple and triple lattice experimental designs were given in the appendix B (Table 8, 9 and 10).

The R Function for ANOM Approach

The function (ANOMLattice) developed using the R programming language (R Core Team, 2021) for the ANOM approach were given in appendix C. While writing the "ANOMLattice" function, "agricolae" (de Mendiburu, 2021), "MASS" (Venables & Ripley, 2002), "ggplot2" (Wickham, 2016) and "mvtnorm" (Genz et al., 2021) packages were used. Therefore, the aforementioned packages must be installed in order to use the "ANOMLattice" function. Then the following steps should be applied.

Firstly, installed packages must be loaded.

```
library(agricolae)
library(MASS)
library(ggplot2)
library(mvtnorm)
```

Secondly, it should be loaded by running the "ANOMLattice" function given in the appendix C.

Thirdly, the block, group, replication and response vectors required for "ANOMLattice" function should be created and the alpha value should be determined according to the desired significance level.

The "ANOMLattice" function were explained through two different examples for the balanced and partially balanced lattice designs.

An Example for The Balanced Lattice Designs

An application of the balanced lattice design were examined in a study investigating the effect of 9 feeding treatments on the growth rates of pigs by Comstock et al. (1948). The use of the "ANOMLattice" function for the balanced lattice were also explained through the same study. The R function is

"ANOMLattice(block,treat,rep,response,alpha)".

Vectors must be created for all inputs required by the function.

```
library(agricolae)
library(MASS)
library(ggplot2)
library(mvtnorm)
blk   =rep(1:12,each=3)
trt  = c(1,2,3,4,5,6,7,8,9,
         3,4,8,2,6,7,1,5,9,
         1,4,7,2,5,8,3,6,9,
         3,5,7,2,4,9,1,6,8)
rep = rep(1:4, each=9)
growth = c(2.20,1.84,2.18,2.05,0.85,1.86,0.73,1.60,1.76,
           1.71,1.57,1.13,1.76,2.16,1.80,1.81,1.16,1.11,
           1.19,1.20,1.15,2.26,1.07,1.45,2.12,2.03,1.63,
           2.04,0.93,1.78,1.50,1.60,1.42,1.77,1.57,1.43)
ANOMLattice(blk, trt, rep, growth, alpha = 0.05)
```

When the codes written above are run, figure 1 was generated directly.

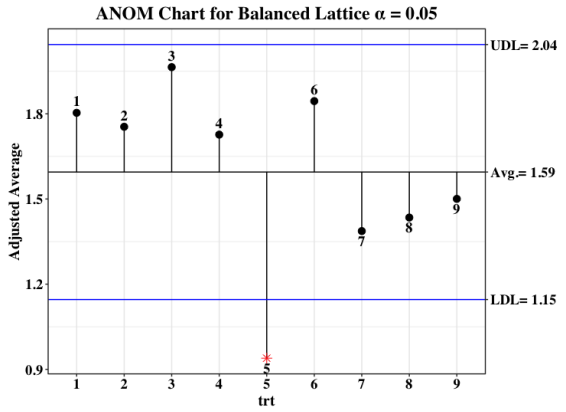

Figure 1. ANOM Chart for Balanced Lattice Design

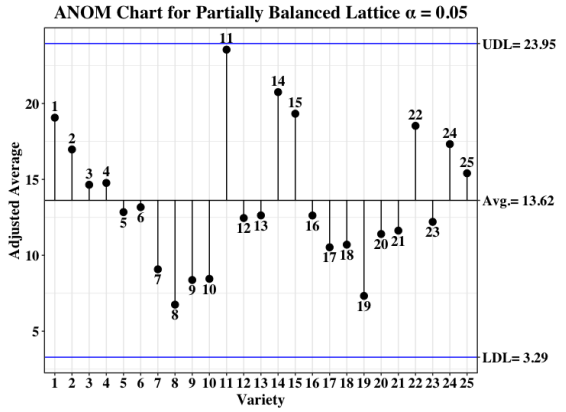

Figure 2. ANOM Chart for Partially Balanced Lattice Design

Figure 1 just showed that the average of the treatment 5 was statistically significantly smaller than the overall average, while the other treatment averages were not statistically significantly different from the overall average.

An Example for The Partially Balanced Lattice Designs

The use of the "ANOMLattice" function for the partially balanced lattice designs were explained through an example given by Cochran and Cox (1960). In this example, 25 soybean varieties are compared with respect to yield in a simple lattice design.

```
library(agricolae)
library(MASS)
library(ggplot2)
library(mvtnorm)
block = rep(1:10,each=5)
Variety =
c(1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,
21,22,23,24,25,1,6,11,16,21,2,7,12,17,22,3,8,13,18,23,
4,9,14,19,24,5,10,15,20,25)
rep = rep(1:2,each=25)
yield =
c(6,7,5,8,6,16,12,12,13,8,17,7,7,9,14,18,16,13,13,14,14,15,
11,14,14,24,13,24,11,8,21,11,14,11,23,16,4,12,12,12,17,10,
30,9,23,15,15,22,16,19)
ANOMLattice(block, Variety, rep, yield, alpha = 0.05)
```

When the codes written above are run, figure 2 was generated directly.

Figure 2 showed that the average of any variety was not different from the overall average in terms of yield. However, variety 11 was fairly close to UDL. This situation can be practically important (Nelson et al., 2005).

Design of the Simulation Study

ANOM approach together with Tukey (Tukey, 1949), Duncan (Duncan, 1955) and Fisher's LSD (Fisher, 1937) tests, which are widely used in practice, were examined in terms of the actual type I error rates in the balanced and partially balanced lattice designs under the assumptions of normality and homogeneity of variances. Random numbers which were generated using "rnorm" function of R project (R Core Team, 2021) were used in order to examine the all tests in terms of the actual type I error rates. Six different designs (k=3, 4, 5, 7, 8 and 9) for the balanced lattice and nine different designs (k=3, 4, 5, 6, 7, 8, 9, 10 and 12) for partially balanced lattice were considered in the study. Each experimental condition was repeated 10,000 times. The actual type I error rates for all tests were estimated as

$$\frac{\text{The number of falsely rejected } H_0 \text{ hypothesis}}{10{,}000}$$

Bradley (1978) reported that the actual type I error rate of a robust test should be between 4.50% and 5.50% when testing at the 5.00% level. In this work, Bradley's conservative criterion was taken into account as a measure of robustness.

Results and Discussion

Results of the Simulation Study

The actual Type I error rates were obtained as a result of simulation trials were given in Tables 1, 2 and 3. The actual type I error rates within Bradley's limits were written in bold.

In the balanced lattice designs, the actual type I error rates for the ANOM approach, Tukey, Duncan and LSD tests were in the range of 4.64-5.71%, 4.62-5.74%, 37.49-98.31% and 54.36 100.00%, respectively. Bradley's criterion was met for the ANOM approach and Tukey test in the all balanced lattice designs except 3x3 design. In the 3x3 design also, the actual type I error rates for ANOM and Tukey which were 5.76% and 5.74%, respectively deviated negligibly from Bradley's criterion. However, performances of the Duncan and LSD tests were dramatically badness under the same experimental conditions (Table 1).

In simple lattice designs, the actual type I error rates varying between 4.76-6.08% for ANOM, 4.75-6.45% for Tukey, 44.59-99.96% for Duncan and 44.31-100.00% for LSD were estimated. The ANOM and Tukey could not meet Bradley's criteria only in 3x3 and 4x4 designs. However, this situation was negligibly compared to the Duncan and LSD (Table 2). The actual type I error rates for the ANOM (6.04%) and Tukey (6.33%) fallen outside Bradley's limits only in 3x3 triple lattice design. However, the actual type I error rates for the Duncan and LSD tests could not met Bradley's criterion in any triple lattice designs (Table 3).

Table 1. The actual type I error rates for the balanced lattices.

k×k	ANOM	Tukey	Duncan	LSD
3×3	5.71	5.74	37.49	54.36
4×4	**4.82**	**4.96**	55.01	81.63
5×5	**4.94**	**4.91**	71.45	95.31
7×7	**4.82**	**4.99**	90.86	99.95
8×8	**4.64**	**4.62**	95.94	100.00
9×9	**5.03**	**5.05**	98.31	100.00

Table 2. The actual type I error rates for the simple balanced lattices.

k×k	ANOM	Tukey	Duncan	LSD
3×3	6.08	6.45	44.59	44.31
4×4	5.98	5.97	63.06	74.10
5×5	**5.49**	**5.50**	77.22	91.19
6×6	**5.16**	**5.35**	86.74	97.80
7×7	**5.07**	**5.19**	92.90	99.66
8×8	**5.19**	**5.23**	97.01	99.96
9×9	**4.97**	**4.94**	98.70	99.99
10×10	**4.98**	**4.75**	99.36	100.00
12×12	**4.76**	**4.75**	99.96	100.00

Table 3. The actual type I error rates for the triple balanced lattices.

k×k	ANOM	Tukey	Duncan	LSD
3×3	6.04	6.33	40.74	53.34
4×4	**5.11**	**5.25**	58.29	79.45
5×5	**5.07**	**5.14**	73.31	93.97
6×6	**5.10**	**5.07**	84.92	98.64
7×7	**5.00**	**5.14**	92.59	99.76
8×8	**4.95**	**4.95**	96.72	99.98
9×9	**4.73**	**4.74**	98.46	100.00
10×10	**5.24**	**4.93**	99.55	100.00
12×12	**5.10**	**4.98**	99.91	100.00

As the number of groups increases, the total number of observations increases, so the effect of the number of replications on the actual type I error rate decreases. Since the number of groups is less in 3×3 and 4×4 designs compared to the other designs, the actual type I error rates for the ANOM and Tukey deviated slightly. On the other hand, the actual type I error rates for the Duncan and LSD tests were seriously high under all experimental conditions.

A Numerical Example

A hypothetical example was given in which averages of 49 varieties (groups) from any plant species (for example wheat, barley, oat, etc.) were compared in terms of any traits (for example yield, length, etc.) in the balanced lattice design (Table 7 in appendix A). Calculations can be made easily by applying the formulas given in section 3 for the partially balanced lattices. While creating this example, the balanced lattice plan given by Cochran and Cox was used (1960). Since the number of varieties compared (k^2) was 49, the number of blocks must be $k = \sqrt{49} = 7$ and the number of replications must be r=7+1 = 8.

B_t and W for Treatment 3,

First, the blocks in which variety 3 was located were determined. These were blocks 1, 10, 17, 24, 31, 38, 45 and 52.

The sum of these blocks given the Bt for Variety 3.

$B_t = 76 + 68 + 65 + 75 + 75 + 73 + 81 + 66 = 579$

$W = kt - (k+1)B_t + G$

$W = (7)93 - (7+1)579 + 3921 = -60$

Similarly, B_t and W were calculated for all treatments (Table 4). After the Bt andWvalues were obtained, the analysis of variance table (Table 5) were easily created by using the formulas given in section 2.

The adjusted mean square for treatment (23.29) was found by dividing the adjusted sum of squares for treatment (1117.95) by degrees of freedom (d.f.) for treatment ($k^2 - 1 = 48$). The effective error was found by $E'_e = E_e(1 + k\mu) = (2.07)[1 + (7)(0.0029)] = 2.11.$ An approximately F value, 23.29/2.11 or 11.04, had 48 and 288 d.f. . Because the F value (11.04) was greater than $F_{0.05,48,288}$ critical table value (1.40), at least the average of one variety was statistically significantly different from the others. Therefore, after this point, it was necessary to determine which variety or varieties caused the difference. For this purpose, the ANOM approach and the Tukey test, which was quite common in practice, were used in this study. Variety averages were compared with both Tukey and ANOM approach at 0.05 significance level. The results of the Tukey test and ANOM approach were given in the table 6 and figure 3, respectively.

Table 6 showed that Tukey test results were highly complex. Since the number of varieties with common letters was considerably large, it was very difficult to select varieties based on Tukey test results. For example, the varieties with the highest average (31, 45 and 22) shared a letter with the 26 varieties that follows itself, and the variety with the lowest average (24) shared a letter with the 22 varieties whose average was higher. On the other hand, variety 20 shared letters with all the other varieties. When this was the case, it became very complicated to distinguish between varieties.

Therefore, it was more understandable and useful to compare with the general average using the ANOM method instead of pair-wise comparison. After obtaining the results of the analysis of variance, it was quite simple to apply the ANOM method. What needs to be done was to calculate the UDL and LDL.

Table 4. t, B_t, W and adjusted total values

Treat.	t	B_t	W	Adj. Tot.	Treat.	t	B_t	W	Adj. Tot.	Treat.	t	B_t	W	Adj. Tot.
1	88	558	73	88.21	18	87	567	-6	86.98	34	67	561	-98	66.72
2	95	571	18	95.05	19	94	568	35	94.10	35	61	538	44	61.13
3	93	579	-60	92.83	20	79	559	2	79.01	36	62	562	-141	61.59
4	82	559	23	82.07	21	59	544	-18	58.95	37	62	545	-5	61.99
5	74	564	-73	73.79	22	100	569	69	100.20	38	72	549	33	72.10
6	83	568	-42	82.88	23	92	587	-131	91.62	39	80	562	-15	79.96
7	65	550	-24	64.93	24	56	542	-23	55.93	40	74	538	135	74.39
8	69	556	-44	68.87	25	81	590	-232	80.33	41	88	560	57	88.17
9	83	583	-162	82.53	26	73	547	56	73.16	42	94	570	19	94.06
10	76	551	45	76.13	27	62	531	107	62.31	43	91	552	142	91.41
11	70	543	67	70.19	28	75	562	-50	74.85	44	96	563	89	96.26
12	96	577	-23	95.93	29	94	567	43	94.12	45	100	557	165	100.48
13	65	551	-32	64.91	30	69	551	-4	68.99	46	65	542	40	65.12
14	92	574	-27	91.92	31	102	573	51	102.15	47	62	526	147	62.43
15	58	543	-17	57.95	32	80	565	-39	79.89	48	98	591	-121	97.65
16	95	570	26	95.08	33	96	573	9	96.03	49	91	569	6	91.02
17	75	570	-114	74.67										

$G = 3921, \sum B_t = 27447, \sum(t + \mu W) = 3921, \bar{X}_{...} = 10.00$

Table 5. Results of the analysis of variance.

Source	d.f.	s.s.	m.s.	F	P
Replications	$k = 7$	18.92			
Treatments (adj.)	$k^2 - 1 = 48$	1117.95	23.29	23.29/2.11=11.04	0.000
Blocks (adj.)	$k^2 - 1 = 48$	115.60	2.41		
Intra-block error	$(k - 1)(k^2 - 1) = 288$	594.86	2.07		
Total	$k^3 + k^2 - 1 = 391$	1843.00			

Table 6. Results of the Tukey test.

Variety	$\bar{X}$	Grouping	Variety	$\bar{X}$	Grouping	Variety	$\bar{X}$	Grouping
31	12.77	a	1	11.03	a b c d e f g	38	9.01	d e f g h i j k
45	12.56	a	41	11.02	a b c d e f g	11	8.77	e f g h i j k
22	12.53	a	18	10.87	a b c d e f g	30	8.62	f g h i j k
48	12.21	a b	6	10.36	a b c d e f g h	8	8.61	f g h i j k
44	12.03	a b c	9	10.32	a b c d e f g h	34	8.34	g h i j k
33	12.00	a b c	4	10.26	a b c d e f g h i	46	8.14	g h i j k
12	11.99	a b c	25	10.04	a b c d e f g h i j	7	8.12	g h i j k
16	11.88	a b c d	39	9.99	a b c d e f g h i j	13	8.11	g h i j k
2	11.88	a b c d	32	9.99	a b c d e f g h i j	47	7.80	h i j k
29	11.77	a b c d	20	9.88	a b c d e f g h i j k	27	7.79	h i j k
19	11.76	a b c d	10	9.52	b c d e f g h i j k	37	7.75	h i j k
42	11.76	a b c d	28	9.36	b c d e f g h i j k	36	7.70	h i j k
3	11.60	a b c d e	17	9.33	b c d e f g h i j k	35	7.64	h i j k
14	11.49	a b c d e f	40	9.30	b c d e f g h i j k	21	7.37	i j k
23	11.45	a b c d e f	5	9.22	c d e f g h i j k	15	7.24	j k
43	11.43	a b c d e f	26	9.15	c d e f g h i j k	24	6.99	k
49	11.38	a b c d e f						

$$LDL=10.00-3.31\sqrt{2.11(7^2-1)/(7^3+7^2)}=8.32$$

$$UDL=10.00+3.31\sqrt{2.11(7^2-1)/(7^3+7^2)}=11.68$$

3.31 value was found easily from table 8 in appendix B. Then, the varieties that were outside and within the decision lines were determined. Thus, varieties were divided into three groups as statistically superior, equal, and inferior to the overall average.

The ANOM method does not compare the average of varieties with each other. It compares the average of varieties with the overall average. Therefore, this situation should not be overlooked in the interpretations. When the ANOM chart was examined, it was seen that the varieties numbered 2, 12, 16, 19, 22, 29, 31, 33, 42, 44, 45 and 48 were statistically significantly higher than the overall average. Varieties numbered 7, 13, 15, 21, 24, 27, 35, 36, 37, 46 and 47were statistically significantly smaller than the overall average.

However, the differences of the other varieties from the overall average were not statistically significant. The ANOM chart provided information not only about statistical significance but also about practical significance. For example, it was seen that varieties numbered 3, 14, 23, 43 and relatively 49 were very close to UDL, and varieties numbered 8, 11, 30 and 34 to LDL. Therefore, the varieties in question were very close to statistical significance compared to other varieties. This situation can be of practical significance. As can be seen, the ANOM method has allowed statistical inferences in a very simple and understandable way.

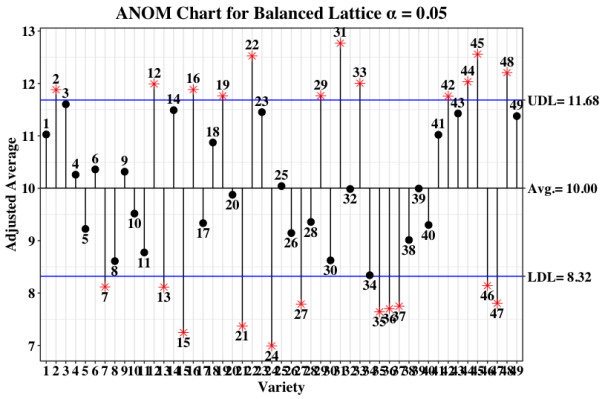

Figure 3. ANOM Chart for example of the balanced lattice design.

Conclusion

Multiple comparison tests have an important place in comparing group averages. When the number of groups is small, it is easy and understandable pair-wise comparisons. However, the increase in the number of groups compared brings some problems. For example, Fisher's LSD test is widely used in practice. However, the LSD (Hayter, 1986) and Duncan tests (Hsu, 1996; Tukey, 1991) are very negatively affected by the increase in the number of groups. In the lattice designs, the number of groups is generally higher than the classical trial designs (completely randomized design, randomized block design, etc.). Simulation experiments in this study also, showed that the actual type I errors of LSD and Duncan tests were frighteningly high. This means that as the number of groups increases, the LSD and Duncan tests are more likely to find a result that there is a difference between the group averages while there is actually no difference between the group averages. For example, in every experiment set up in 8x8 balanced lattice design, the LSD test will certainly find that at least one group mean is different from the others, even though there is actually no difference between the group averages (Table 1). The Duncan test is almost exactly the same to the LSD test. Therefore, using the LSD and Duncan tests will cause misleading results. On the other hand, ANOM approach and Tukey test have almost excellent performance in terms of preserving the actual type I error rate. Regardless of the number of groups, both tests are very reliable. However, another problem is that arises with the increase in the number of groups is the difficulties in interpreting the results. When the number of groups increases, the number of pair-wise comparisons also increases significantly. The rapid increase in the number of pair-wise comparisons makes very complex and difficult to the interpretation of the results. At this point, it can be a very useful and reliable solution to compare the group averages with the overall average using the ANOM approach rather than comparing them with each other. Since the results of the ANOM can be presented graphically, both statistical and practical significance can be easily understood. As a result, the use of the ANOM test can be recommended when the number of groups compared is large so that researchers can easily understand reliable results.

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Appendices

A. Plan and Data for 7×7 The Balanced Lattice Design

Table 7. Plan and data for 7×7 balanced lattice design.

Block	Replication I							Totals	Block	Replication II							Totals
(1)	(1)	(2)	(3)	(4)	(5)	(6)	(7)		(8)	(1)	(8)	(15)	(22)	(29)	(36)	(43)	
	12	14	11	9	10	11	9	76		11	8	7	13	11	6	10	66
(2)	(8)	(9)	(10)	(11)	(12)	(13)	(14)		(9)	(2)	(9)	(16)	(23)	(30)	(37)	(44)	
	11	12	10	10	10	7	14	74		12	8	12	12	10	7	14	75
(3)	(15)	(16)	(17)	(18)	(19)	(20)	(21)		(10)	(3)	(10)	(17)	(24)	(31)	(38)	(45)	
	7	13	9	11	14	11	7	72		11	8	8	5	12	10	14	68
(4)	(22)	(23)	(24)	(25)	(26)	(27)	(28)		(11)	(4)	(11)	(18)	(25)	(32)	(39)	(46)	
	12	13	8	11	10	9	10	73		11	9	12	9	11	9	8	69
(5)	(29)	(30)	(31)	(32)	(33)	(34)	(35)		(12)	(5)	(12)	(19)	(26)	(33)	(40)	(47)	
	9	9	15	9	13	8	10	73		7	11	11	11	11	6	7	64
(6)	(36)	(37)	(38)	(39)	(40)	(41)	(42)		(13)	(6)	(13)	(20)	(27)	(34)	(41)	(48)	
	10	9	10	9	8	11	10	67		8	9	8	6	10	14	13	68
(7)	(43)	(44)	(45)	(46)	(47)	(48)	(49)		(14)	(7)	(14)	(21)	(28)	(35)	(42)	(49)	
	10	9	13	8	9	10	10	69		6	10	7	9	9	13	12	66
								504									476
	Replication III									Replication IV							
(15)	(1)	(9)	(17)	(25)	(33)	(41)	(49)		(22)	(1)	(37)	(24)	(11)	(47)	(34)	(21)	
	11	10	12	10	15	11	13	82		12	8	8	9	6	6	8	57
(16)	(43)	(2)	(10)	(18)	(26)	(34)	(42)		(23)	(15)	(2)	(38)	(25)	(12)	(48)	(35)	
	11	12	10	10	8	6	13	70		9	12	9	11	15	13	8	77
(17)	(36)	(44)	(3)	(11)	(19)	(27)	(35)		(24)	(29)	(16)	(3)	(39)	(26)	(13)	(49)	
	7	10	9	10	11	10	8	65		13	10	10	13	7	9	13	75
(18)	(29)	(37)	(45)	(4)	(12)	(20)	(28)		(25)	(43)	(30)	(17)	(4)	(40)	(27)	(14)	
	11	7	12	10	13	10	8	71		13	8	8	10	11	6	9	65
(19)	(22)	(30)	(38)	(46)	(5)	(13)	(21)		(26)	(8)	(44)	(31)	(18)	(5)	(41)	(28)	
	13	8	11	9	10	7	5	63		8	12	14	11	8	13	9	75
(20)	(15)	(23)	(31)	(39)	(47)	(6)	(14)		(27)	(22)	(9)	(45)	(32)	(19)	(6)	(42)	
	8	11	12	10	7	13	11	72		11	8	14	12	12	10	13	80
(21)	(8)	(16)	(24)	(32)	(40)	(48)	(7)		(28)	(36)	(23)	(10)	(46)	(33)	(20)	(7)	
	7	13	7	12	11	11	8	69		9	11	10	8	14	12	8	72
								492									501
	Replication V									Replication VI							
(29)	(1)	(30)	(10)	(39)	(19)	(48)	(28)		(36)	(1)	(23)	(45)	(18)	(40)	(13)	(35)	
	11	7	10	11	12	13	8	72		10	10	12	11	12	6	7	68
(30)	(22)	(2)	(31)	(11)	(40)	(20)	(49)		(37)	(29)	(2)	(24)	(46)	(19)	(41)	(14)	
	13	11	12	7	9	8	9	69		12	12	8	7	11	9	13	72
(31)	(43)	(23)	(3)	(32)	(12)	(41)	(21)		(38)	(8)	(30)	(3)	(25)	(47)	(20)	(42)	
	14	11	13	7	11	10	9	75		9	8	13	11	10	10	12	73
(32)	(15)	(44)	(24)	(4)	(33)	(13)	(42)		(39)	(36)	(9)	(31)	(4)	(26)	(48)	(21)	
	6	13	7	10	12	8	10	66		9	13	15	10	10	13	7	77
(33)	(36)	(16)	(45)	(25)	(5)	(34)	(14)		(40)	(15)	(37)	(10)	(32)	(5)	(27)	(49)	
	7	15	13	8	11	9	14	77		7	9	11	9	10	8	10	64
(34)	(8)	(37)	(17)	(46)	(26)	(6)	(35)		(41)	(43)	(16)	(38)	(11)	(33)	(6)	(28)	
	10	7	9	7	11	10	7	61		9	13	9	9	11	10	10	71
(35)	(29)	(9)	(38)	(18)	(47)	(27)	(7)		(42)	(22)	(44)	(17)	(39)	(12)	(34)	(7)	
	12	9	8	9	7	9	8	62		14	12	11	8	12	9	10	76
								482									501
	Replication VII									Replication VIII							
(43)	(1)	(16)	(31)	(46)	(12)	(27)	(42)		(50)	(1)	(44)	(38)	(32)	(26)	(20)	(14)	
	11	10	10	10	12	7	10	70		10	13	7	10	9	9	9	67
(44)	(36)	(2)	(17)	(32)	(47)	(13)	(28)		(51)	(8)	(2)	(45)	(39)	(33)	(27)	(21)	
	8	12	7	10	8	11	12	68		8	10	11	9	10	7	9	64
(45)	(22)	(37)	(3)	(18)	(33)	(48)	(14)		(52)	(15)	(9)	(3)	(46)	(40)	(34)	(28)	
	14	7	15	11	10	12	12	81		8	12	11	8	9	9	9	66
(46)	(8)	(23)	(38)	(4)	(19)	(34)	(49)		(53)	(22)	(16)	(10)	(4)	(47)	(41)	(35)	
	8	13	8	12	11	10	12	74		10	9	8	10	8	10	6	61
(47)	(43)	(9)	(24)	(39)	(5)	(20)	(35)		(54)	(29)	(23)	(17)	(11)	(5)	(48)	(42)	
	13	11	5	11	10	11	6	67		15	11	11	7	8	13	13	78
(48)	(29)	(44)	(10)	(25)	(40)	(6)	(21)		(55)	(36)	(30)	(24)	(18)	(12)	(6)	(49)	
	11	13	9	12	8	10	7	70		6	9	8	12	12	11	12	70
(49)	(15)	(30)	(45)	(11)	(26)	(41)	(7)		(56)	(43)	(37)	(31)	(25)	(19)	(13)	(7)	
	6	10	11	9	7	10	7	60		11	8	12	9	12	8	9	69
								490									406

B. Critical Table Values For The Balanced, Simple And Triple Lattice Designs

Table 8. Critical table values for the balanced lattice designs.

α	Experimental Design (k×k)					
	3×3	4×4	5×5	7×7	8×8	9×9
0.25	2.2751	2.4262	2.5611	2.7695	2.8517	2.9231
0.10	2.7853	2.8308	2.9230	3.0939	3.1655	3.2284
0.05	3.1405	3.1007	3.1631	3.3089	3.3743	3.4338
0.01	5.0886	3.6700	3.6618	3.7588	3.8135	3.8609
0.001	13.3087	4.4066	4.3034	4.3336	4.3662	4.4042

Table 9. Critical table values for the simple lattice designs.

α	E×perimental Design (k×k)								
	3×3	4×4	5×5	6×6	7×7	8×8	9×9	10×10	12×12
0.25	2.7140	2.6684	2.7264	2.7971	2.8668	2.9305	2.9896	3.0429	3.1374
0.10	3.7789	3.3168	3.2366	3.2391	3.2679	3.3035	3.3420	3.3807	3.4543
0.05	4.6933	3.7992	3.5929	3.5421	3.5368	3.5544	3.5804	3.6088	3.6682
0.01	7.3911	4.9533	4.3986	4.1980	4.1176	4.0866	4.0815	4.0877	4.1174
0.001	13.4869	6.8589	5.5596	5.0874	4.8944	4.7884	4.7355	4.7106	4.6985

Table 10. Critical table values for the simple lattice designs.

α	E×perimental Design (k×k)								
	3×3	4×4	5×5	6×6	7×7	8×8	9×9	10×10	12×12
0.25	2.3578	2.4961	2.6173	2.7200	2.8077	2.8839	2.9514	3.0111	3.1133
0.10	2.9586	2.9637	3.0266	3.0954	3.1611	3.2208	3.2754	3.2556	3.4138
0.05	3.4002	3.2869	3.3020	3.3458	3.3972	3.4467	3.4926	3.5369	3.6172
0.01	4.4253	3.9976	3.8894	3.8790	3.8919	3.9191	3.9509	3.9817	4.0433
0.001	6.0289	4.9666	4.6716	4.5706	4.5371	4.5312	4.5385	4.5519	4.5900

C. The R Code Of The 'ANOMLattice' Function

```
ANOMLattice=function(block,treat,rep,response,alpha){
   nr=nlevels(factor(rep))
   k=nlevels(factor(block))/nr
   corr=matrix(NA,k^2,k^2)
   for (i in 1:k^2) {
      for(j in 1:k^2){
         corr[i,j]=1
         if (i!=j){corr[i,j]=-(1/((k^2)-1))}}}
y=response
sink("NUL")
output=PBIB.test(block,treat,rep,y,k=k,method = "VC")
sink()
nr=output$parameters$r
Eb=output$ANOVA$`Mean Sq`[3]
Ee=output$ANOVA$`Mean Sq`[4]

if(nr==(k+1)){
Mu=(Eb-Ee)/(k*k*Eb)
Ee1=Ee*(1+k*Mu)
title="ANOM Chart for Balanced Lattice"
v=(k-1)*((k^2)-1)}
else{Mu=(Eb-Ee)/(k*(nr-1)*Eb)
   Ee1=Ee*(1+(nr*k*Mu)/(k+1))
title="ANOM Chart for Partially Balanced Lattice"
v=(k-1)*(nr*k-k-1)}
Gmean=output$statistics$Mean
h=qmvt(1-alpha,df=v,corr=corr,tail = "both")$quantile
LDL=Gmean-h*sqrt(Ee1)*sqrt(((k^2)-1)/((k^2)*nr))
UDL=Gmean+h*sqrt(Ee1)*sqrt(((k^2)-1)/((k^2)*nr))
labeludl=paste('UDL=',format(round(UDL,2),nsmall=2))
labelavg=paste('Avg.=',format(round(Gmean,2),nsmall=2))
labelldl=paste('LDL=',format(round(LDL,2),nsmall=2))
a1=expression(alpha)
a2=paste("=",format(round(alpha,2),nsmall=2))
Xmean=output$means[,2]
color=NULL
label=NULL
alig=NULL
shape=NULL
XX=as.character(rep(1:k^2))
XX=factor(XX,levels = XX)
YY=Xmean[1:k^2]
ZZ=data.frame(XX,YY)
for (i in 1:k^2) {
   if ((Xmean[i]>=UDL)||(Xmean[i]<=LDL)){
      color[i]='red'
      shape[i]=8
   }else{color[i]='black';shape[i]=19}

   if (Xmean[i]>mean(Xmean)){alig[i]=-0.7}
   if (Xmean[i]<mean(Xmean)){alig[i]=1.5}
}
font='Times'
chart=ggplot(ZZ, aes(x=XX, y=Xmean)) +
   ylab("Adjusted Average")+
   xlab(substitute(treat))+
   geom_segment(aes(xend=XX), yend=Gmean, colour="gray50") +
   geom_hline(yintercept = c(LDL,UDL,Gmean),
```

```
            colour=c('blue','blue','black'))+
   scale_y_continuous(sec.axis = sec_axis(~ ., breaks = c(LDL,Gmean,UDL),
                    labels = c(labelldl,labelavg,labeludl)))+
   geom_point(shape=shape,size=1,color= color)+
   geom_text(size=3,aes(label=XX,family=font),vjust=alig)+
   theme_bw() +
   theme(panel.grid.major.y = element_blank(), # No horizontal grid lines
        legend.position=c(1, 0.55), # Put legend inside plot area
        legend.justification=c(1, 0.5),
        plot.margin = unit(c(0.2,0.2,0.2,0.2), "cm"),
        axis.title = element_text(family = font),
        axis.text.x = element_text(colour='black',size = 6,
                                   hjust = .5,vjust = .5,
                                   family = font),
        axis.text.y = element_text(colour='black',
                                   hjust = .5,vjust = .5,
                                   family = font))+
   ggtitle(label = paste(title,sep=" ","\u03b1",a2))+
   theme(plot.title = element_text(hjust=0.5,
      family = font))+
   coord_cartesian(clip = "off")
return(chart)
}
```