The Analysis of Square Lattice Designs Using R and SAS

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1 INTRODUCTION

For experiments using randomized block designs, all treatment combinations may not be run in each block because of shortages of experimental units or facilities. Yates (1936a) formally introduced balanced incomplete block (BIB) designs in which every treatment is not present in every block, but the number of pairs of each treatment occurring together is the same. A BIB design can reduce the number of experimental units used in experiment as we already knew. Although BIB designs are efficient designs, these designs are still not appropriate for experiments with a large number of treatments such as animal breeding experiments. Moreover, the minimum number of blocks required for a BIB design may be too large to be practical. In the same year, Yates (1936b) proposed a new method of arranging agricultural variety trials involving a large number of crop varieties. These types of arrangements were named a quasi-factorial or lattice designs. His paper contained numerical examples based on the results of a uniformity trial on orange trees. A special feature of lattice designs is that the number of treatments, t, is related to the block size, k, in one of three forms: $t = k^2$, $t = k^3$, or $t = k(k + 1)$. Even though the number of possible treatments is limited, a lattice design may be an ideal design for field experiments with a large number of treatments. Although lattice designs have been frequently used, there is limited software that performs an appropriate statistical analysis for a lattice design.

The SAS package is one of the most commonly-used packages for the design and analysis of experiments. The use of SAS for analyzing a lattice design was first discussed in a colloquium on horticulture (Stroup and Paparozzi, 1989). At that time, PROC MATRIX, PROC IML, and PROC LATTICE, which can analyze experiments using lattice designs, were only found on main-frame computers. Fernandez G. C.J. (1990) presented a PC-SAS program for the analyses of data obtained from a lattice design. His program consisted of two parts. In the first part, PROC GLM was used to calculate unadjusted block sum of squares (SS), adjusted block SS, unadjusted treatment SS, and intra-block error. In the second part, PROC MEANS and the MERGE option were used to calculate many statistics such as adjusted block values and treatment totals. Now PROC LATTICE is available in PC-SAS and will analyze data from balanced square lattices, partially balanced square lattices, and some rectangular lattices.

Besides SAS software, R, a free software environment for statistical computing and graphics is capable of analyzing experimental design data. Groemping (2011) provides a summary of R packages related to the design and analysis of experimental data. The

R package "agricolae" has the capability to analyze data obtained from lattice designs. Although it was not specifically created for lattice designs, there is one function which can be applied to use with lattice designs. Felipe de Mendiburu (2010) wrote the"agricola" package as a master's degree project, and it offers extensive functionality on experimental design especially for plant breeding and agricultural experiments. The strength of this package is that it allows for the randomization of treatments in lattice designs, factorial designs, randomized complete block designs, latin square designs, balanced incomplete block designs, alpha designs, cyclic, augmented block, and split and strip plot designs. Moreover, this package can also perform an analysis of variance for many designs. The R "agricolae" package is the newest tool for the analysis of lattice design data. More details are in a document by Felipe de Mendiburu (2010).

This paper provides a review of the analysis of two types of square lattice designs: balanced and partially balanced lattices, as well as numerical examples and the R and SAS computer code needed to analyze the experimental data. In the last section, the R function are written to give the complete analysis of variance which both SAS and R do not provide.

2 SQUARE LATTICE DESIGNS

The feature of balanced square lattices is that the number of treatments, t, is equal to the square of the number of units per block, k or $t = k^2$. The numbers of replication of partially balanced square lattices are similar to balanced square lattices, but only some replications are selected. If the number of replications is less than required for a balanced design, the analysis follows the same procedure as for a balanced design, but some formulas are changed.

2.1 A Balanced Square Lattice Design

A balanced square lattice design is similar to a balanced incomplete block design with k^2 treatments arranged in $k(k+1)$ blocks with k runs per block and $r = k+1$ replications. So, each replication has k blocks and contains every treatment. In this design, every pair of treatments occurs together once in the same incomplete block. This property holds for all plans having an odd number of treatments which is also a perfect square (e.g. 9, 25, 49, 81, 121, and 169 treatments). Let λ be an integer number indicating how many times each treatment occurs together in same block, and the relationship among the number of treatments t, block size k, and number of replications r. Numerically, it is defined as $\lambda = r(k-1)/(t-1)$ (Montgomery, 2005).

In balanced square lattice designs, $r = k+1$ or $t = k^2$, implying $\lambda = 1$. Because the designs are balanced, all treatment differences have the same estimated variance or the same precision. Hinkelmann and Kempthorne (2005) referred to the number of replications, r, as the number of different systems of confounding. Designs with $r = 2$ are called simple (or double) lattices; designs with $r = 3$ are called triple lattices; designs with $r = 4$ are called quadruple lattices, and balanced square lattices require $r = k+1$.

2.1.1 Lattice Design Construction

Assume there are t treatments labeled as $1, 2, \ldots, k^2$ with treatment numbers arranged in a $k \times k$ square. For example, in a 3×3 square forming Replication I (see Table 1), there are nine treatment numbers arranged in a specific order such that each row of the square array is considered as a block containing three treatments. To construct Replication II, each column of the array for Replication I is taken to form the three blocks in Replication II (see Table 1). Replications III and IV are based on two orthogonal latin squares. Two latin squares are orthogonal if, when superimposed, all ordered pairs are distinct (See Table 2). From the standard array, the treatment numbers that fall on the same letter in a latin square are taken to form a block. For example, from latin square 1 (See Table 2), treatment numbers 1, 6 and 8 fall on the letter A, so treatments 1, 6 and 8 are in the same block in Replication III (See Table 1). Analogous to Replication III, Replication IV is constructed from the second latin square. Another method of constructing lattice square designs can be found in Federer and Wright (1988) who proposed a simple method for constructing lattice square designs when the number of treatments is greater than 3.

Table 1: 3×3 balanced lattice $(t = 9, k = 3, r = 4, \lambda = 1)$

Block	Replication I		
1	1	2	3
2	4	5	6
3	7	8	9

Block	Replication II		
4	1	4	7
5	2	5	8
6	3	6	9

Block	Replication III		
7	1	6	8
8	2	4	9
9	3	5	7

Block	Replication IV		
10	1	5	9
11	2	6	7
12	3	4	8

Table 2: Two orthogonal latin squares of order 3.

Latin Square 1			Latin Square 2			Superimposed		
A	B	C	A	B	C			
($\underline{1}$)	(2)	(3)	(1)	(2)	(3)	(A,A)	(B,B)	(C,C)
B	C	A	C	A	B			
(4)	(5)	($\underline{6}$)	(4)	(5)	(6)	(B,C)	(C,A)	(A,B)
C	A	B	B	C	A			
(7)	($\underline{8}$)	(9)	(7)	(8)	(9)	(C,B)	A,C)	(B,A)

2.1.2 Randomization

Randomization is always important when designing an experiment. The randomization procedure gives an equal chance for each assignment of treatments to the experimental units. Randomization consists of the following steps: (1) randomly allotting the treatments to the treatment numbers (labels), (2) randomizing the replications, and (3) randomizing the blocks separately and independently within each replication.

2.1.3 Statistical Analysis

Although the following procedure can be applied to partially balanced designs, there are some differences which will be discussed later. We will adopt the following notation. Let

t denote the total number of treatments,

k denote the number of units per block or block size,

s denote the number of blocks per replication which is equal to k,

r denote the number of replications (for balanced designs, $r = k + 1$).

Let $y_{ij(l)}$ denotes the response value of the jth treatment in the lth block within ith replication, $i = 1, 2, \ldots, k + 1$, $j = 1, 2, \ldots, k^2$, $l = 1, 2, \ldots, rk$. The model is

$$y_{ij(l)} = \mu + \pi_i + \beta_{i(l)} + \tau_j + \varepsilon_{ij(l)}.$$

where $\mu, \pi_i, \beta_{i(l)}$, and τ_j represent the effect of the mean, the replicate, the incomplete block, and the treatment, respectively. $\varepsilon_{ij(l)}$ is the intra-block residual, assumed to be normally and independently distributed with mean 0 and variance σ_e^2.

Various ANOVA sums of squares are now presented:

1. Total Sum of Squares:

$$SSTot = \sum y_{ij(l)}^2 - CF \tag{1}$$

, where $CF = (\sum y_{ij(l)})^2/(rk^2)$, $\sum y_{ij(l)}$ is the grand total.

2. Unadjusted treatment sum of squares:

$$SSTrt_U = \frac{\sum T_j^2}{r} - CF \tag{2}$$

where T_j is the sum of observations for treatment j.

3. Replication sum of squares:

$$SSR = \frac{\sum R_i^2}{k^2} - CF \tag{3}$$

where R_i is the sum of observations in replication i.

4. For computing the adjusted block sum of squares, SSB_{Adj}, several quantities are required to be computed first. Let
B_j denote the sum of block totals for the blocks with treatment j, $j = 1, 2, \ldots, t$,
T_j denote the total of the jth treatment total from all replications,
W_j denote the weight for the jth treatment which is used for adjustment for block,
$$W_j = kT_j - (k+1)B_j + G \tag{4}$$
where $G = \sum y_{ij(l)}$, or the grand total. Note that $\sum W_j = 0$. The sum of squares for blocks within replication, adjusted for treatment effects, SSB_{Adj}, is defined as
$$SSB_{Adj} = \frac{\sum W_j^2}{k^3(k+1)}. \tag{5}$$

5. Intra-block error sum of squares:
$$SSE = SST - SSR - SSTrt_U - SSB_{Adj}. \tag{6}$$
Using the various sums of squares above, the analysis of variance (ANOVA) table is given in Table 3.

Table 3: Analysis of Variance for the balanced square lattice design

Source of variation	Degree of freedom	Sum of squares	Mean squares
Replication	$r-1$	SSR	MSR
Treatment(Unadjusted)	k^2-1	$SSTrt_U$	$MSTrt_U$
Block within replication(Adj)	k^2-1	SSB_{Adj}	$MSB_{Adj} = E_b$
Intra-block Error	$(k^2-1)(k-1)$	SSE	$MSE = E_e$
Total	rk^2-1	SST	

It is important to note that the mean square of the unadjusted treatment cannot be used for testing against the mean square of intra-block error because the mean square of unadjusted treatment still contains block effects. The adjusted treatment sum of the squares is defined as

$$SSTrt_{Adj} = \frac{\sum(T_j + \mu W_j)^2}{r} - CF = \frac{\sum(T_j^{'})^2}{r} - CF \tag{7}$$

where $T_j^{'}$ is the adjusted treatment total defined as $T_j + \mu W_j$, and μ is the adjustment factor for error and treatment means defined as

$$\mu = \frac{MSB_{Adj} - MSE}{k^2 MSB_{Adj}} = \frac{E_b - E_e}{k^2 E_b} \tag{8}$$

If dividing the $SSTrt_{Adj}$ by its degree of freedom, $k^2 - 1$, we will get the $MSTrt_{Adj}$. So, the F-statistics is the $MSTrt_{Adj}$ divided by the the intra-block error mean square. For t-test, the mean square of intra-block error, E_e, needs to be adjusted to take into account the sampling error. The new mean square is called the "effective error mean squar", or $E_e^{'}$, which is defined as

$$E_e^{'} = E_e(1 + k\mu) = E_e[1 + (r-1)\mu]. \tag{9}$$

The F-statistic is

$$F = \frac{MSTrt_{Adj}}{E_e} \tag{10}$$

The degrees of freedom of the numerator and denominator for the F statistic are $k^2 - 1$ and $(k-1)(k^2-1)$, respectively.
The variance of the adjusted treatment mean is $E_e^{'}/r$, and the error variance of the difference between two adjusted treatment means in the same block is

$$\frac{2E_e[1 + (r-1)\mu]}{r} = \frac{2E_e^{'}}{r} \tag{11}$$

The square root of error variance of the difference between two treatment means is the standard error used for t-tests between pairs of treatments.

If, however, E_b is less than E_e, then we conclude the blocks have no effect, and the data will be analyzed as if it were a randomized block design but using the replications as the blocks. One numerical value that summarizes the potential advantage or disadvantage of one specific experimental design relative to another is called a "relative efficiency". The relative efficiency is expressed as an unbiased estimator of the error variance that would have been present if the experiment had been conducted as a randomized block divided by effective error mean square, $E_e^{'}$. The sum of the SSB_{Adj} and SSE, $SSB_{Adj} + SSE$, is called the "randomized complete block design (RCBD) error sum of squares" which is an estimate of the block sum of squares in a randomized block design. The degrees of freedom for RCBD sum of squares is the sum of the degrees of freedom of SSB_{Adj} and SSE , or $(k^2 - 1) + (k^2 - 1)(k - 1) = rk(k - 1)$.

2.2 Partially Balanced Square Lattice

Partially balanced square lattices are similar to balanced square lattices, but are more flexible with respect to the number of replications. Partially balanced designs do not use all replications of the basic plan. For example, for 3×3 lattice designs, we need 4 replications for a balanced design, but if we have only two or three replications, these are partially balanced designs. The designs using only the first two replications from the basic plan are called *simple lattices*, and designs using the first three replications from the basic plan are called *triple lattices*.

2.2.1 Construction and Randomization

After construction of a balanced lattice design, the number of replications is selected. The function named "design.lattice" in the R package "agricolae" can automatically create partially balanced lattice designs, but only simple and triple lattice designs. For example, the code for creating a 4×4 triple lattice is:

```
library(agricolae)
design.lattice(4,type="triple")
```

and the R results are:

```
$square1
     [,1] [,2] [,3] [,4]
[1,]    6    3    8   12
[2,]   11   13   10   15
[3,]   14    7    2    5
[4,]    9    1    4   16
$square2
     [,1] [,2] [,3] [,4]
[1,]   15    5   12   16
[2,]   13    7    3    1
[3,]   10    2    8    4
[4,]   11   14    6    9
$square3
     [,1] [,2] [,3] [,4]
[1,]   11    7    8   16
[2,]   13    5    6    4
[3,]   10   14   12    1
[4,]   15    2    3    9
```

2.2.2 Statistical Analysis for Partially Balanced Lattices

Computations for the analysis of variance for a partially balanced lattice design is more complicated than it is for a balanced design. Actually, the partially balanced square lattices could be considered as partially balanced incomplete block designs (PBIB). This was shown by Bose and Nair (1939). Nair (1952) used the method of analysis of a PBIB design for the simple square lattice design. However, this paper actually presents the method from Cochran and Cox (1950) who simplified the original method by Yates (1936b). In the analysis, let

t denote the total number of treatments,

k denote the number of units per block (i.e., the block size),

s denote the number of blocks per replication (which equals k), and

r denote the number of replications.

The analysis procedure involves the following steps:

1. The total sum of squares ($SSTot$), the unadjusted treatment sum of squares ($SSTrt_U$), and the replication sum of squares (SSR) are computed in the same way as those in balanced designs.

2. Find (1) the block total, B_l , $l = 1, 2, \ldots, rk$, (2) the replication total, R_i, $i = 1, 2, \ldots, r$, (3) the treatment total, T_j, $j = 1, 2, \ldots, k^2$, and (4) the grand total G.

3. For each block,
   (1) calculate $C_l = \sum T_{j(l)} - rB_l$, $l = 1, 2, \ldots, rk$, where $\sum T_{j(l)}$ is the sum of the treatment totals which are in block l.
   (2) calculate the total of $C's$, $RC_i = \sum C_{l(i)}$, in the ith replication (e.g. $i = 1, 2$ for a simple lattice).

4. Calculate the adjusted block sum of squares, SSB_{Adj}, given by

$$SSB_{Adj} = \frac{\sum_{l=1}^{rk} C_l^2}{rk(r-1)} - \frac{\sum_{i=1}^{allrep} (RC_i)^2}{rk^2(r-1)}. \tag{12}$$

5. Calculate the intra-block error sum of squares given by

$$SSE = SST - SSR - SSTrt_U - SSB_{Adj} \tag{13}$$

From these sums of squares, the analysis of variance table is shown in Table 4. From Table 4, the mean square of the unadjusted treatment, however, cannot be

Table 4: Analysis of Variance for the partially balanced square lattice design

Source of variation	Degree of freedom	Sum of squares	Mean squares
Replication	$r-1$	SSR	MSR
Treatment(Unadjusted)	k^2-1	$SSTrt_U$	$MSTrt_U$
Block within replication(Adj)	$r(k-1)$	$SSB_{Adj} = B_a$	$MSB_{Adj} = E_b$
Intra-block Error	$(rk-k-1)(k-1)$	SSE	$MSE = E_e$
Total	rk^2-1	SST	

used for testing against the mean square of intra-block error in an F test. Instead, the unadjusted treatment mean square can be used for testing the data as if the experiment were in randomized block. The denominator for the F-test is the pooled mean square for adjusted blocks and intra-block error. For lattice designs, if we want a test for the treatment effects, the treatment totals must be adjusted. The adjustment factor, similar to the weight in a balanced lattice, is

$$\mu = \frac{MSB_{Adj} - MSE}{k(r-1)MSB_{Adj}} = \frac{E_b - E_e}{k(r-1)E_b}. \tag{14}$$

Then, the adjusted treatment total, $T_j^{'}$, is defined as

$$T_j^{'} = T_j + \mu \sum_{i=1}^{r} C_i(\text{in Block l containing Trt j}). \tag{15}$$

Then, for a simple lattice, $T_j^{'} = T_j + \mu[C_1^* + C_2^*]$, where C_1^* and C_2^* are the values of C's in the particular blocks containing the treatment jth in the replication 1, and 2, respectively. The procedure to obtain the adjusted treatment sum of squares (Cochran and Cox, 1950) in a simple lattice is the following:

1. Calculate the unadjusted sum of squares for blocks within replication,

$$SSB(Within\ Rep)_{Unadj} = \underbrace{(\frac{\sum B_l^2}{k} - CF_1)}_{replication\ 1} + \underbrace{(\frac{\sum B_l^2}{k} - CF_2)}_{replication\ 2} = B_u \tag{16}$$

   where CF_i is the correction factor in ith replication.

2. Let B_a be the adjusted sum of squares for blocks within replication, or SSB_{Adj} (see Table 4). The adjusted treatment sum of squares, $SSTrt_{Adj}$ is calculated

by

$$SSTrt_{Adj} = SSTrt_{Unadj} - k(r-1)\mu[\frac{r}{(r-1)(1+k\mu)}B_u - B_a] \tag{17}$$

Like the adjusted mean square error in balanced designs, the "effective error mean square", or $E_e^{'}$, is defined as

$$E_e^{'} = E_e[1 + \frac{rk\mu}{k+1}]. \tag{18}$$

The effective error mean square is used for estimating the gain in accuracy over randomized blocks. However, the F-statistic for testing the treatment effect uses the intra block mean square as the denominator.

$$F = \frac{MSTrt_{Adj}}{E_e} \tag{19}$$

with the degrees of freedom $(k^2 - 1)$ and $(rk - k - 1)(k + 1)$.

The formula for the error variance of the difference between two treatment means in the same block is the same as those in for a balanced lattice design which is $2E_e[1+(r-1)\mu]/r$. Because of the partial balance, the error variance of the difference between two treatment means in the same block is slightly smaller than the error variance of the difference between two treatment means in different blocks which is

$$\frac{2E_e}{r}[1 + r\mu]. \tag{20}$$

Except for small designs, we can use the average variance given by

$$\frac{2E_e}{r}\left(1 + \frac{r\mu k}{k+1}\right). \tag{21}$$

To estimate the gain in accuracy over the randomized block designs, the effective error mean square is used to compare with the error mean square in randomized block analysis.

3 NUMERICAL EXAMPLES

3.1 Example of a balanced square lattice design

In the following example, the original data appeared in a paper by Comstock *et al* (1948). They studied the effects of nine feeding treatments on the growth rates of pigs. The experimental unit in this study was a pair of pigs which were fed in the same pen. The 3×3 balanced lattice design is used, so six pigs were required for each block. From past experience, the litter has an effect on the variance in the growth rate; hence, two sets of three uniform littermates were assigned to each block. Within a block, each treatment was applied to only one member of each set. The response variable is the sum of gains in weight for 2 pigs. The data is given in Table 5. In this example, we have $r = k + 1 = 4$ replications, block size of $k = 3$, k^2=3^2 treatments, and $3^2 - 1 = 8$ blocks.

Table 5: Gain in weight for 2 pigs

Block	Replication I			Total	Block	Replication II			Total
1	(1)	(2)	(3)		4	(3)	(4)	(8)	
	2.20	1.84	2.18	6.22		1.71	1.57	1.13	4.41
2	(4)	(5)	(6)		5	(2)	(6)	(7)	
	2.05	0.85	1.86	4.76		1.76	2.16	1.80	5.72
3	(7)	(8)	(9)		6	(1)	(5)	(9)	
	0.73	1.60	1.76	4.09		1.81	1.16	1.10	4.08
Block	Replication III			Total	Block	Replication IV			Total
7	(1)	(4)	(7)		10	(3)	(5)	(7)	
	1.19	1.20	1.15	3.54		2.04	0.93	1.78	4.75
8	(2)	(5)	(8)		11	(2)	(4)	(9)	
	2.26	1.07	1.45	4.78		1.50	1.60	1.42	4.52
9	(3)	(6)	(9)		12	(1)	(6)	(8)	
	2.12	2.03	1.63	5.78		1.77	1.57	1.43	4.77

The total sum of squares, the unadjusted treatment sum of squares, the unadjusted block sum of squares, and the replication sum of squares are computed below:
from equation (1), $SST = (2.20^2 + 1.84^2 + \ldots + 1.43^2) - CF = 97.55 - 91.58 = 5.97$;

from equation (2),

$$SSTrt_U = \frac{\sum T_j^2}{r} - CF = \frac{6.97^2 + 7.36^2 + \ldots + 5.92^2}{4} - 91.58$$

$$= \frac{379.24}{4} - 91.58 = 3.23;$$

from (3),

$$SSR = \frac{15.07^2 + 14.21^2 + 14.10^2 + 14.04^2}{3^2} - 91.58 = 91.66 - 91.58 = 0.08$$

Then, to find the adjusted sum of squares for blocks, (1) the sum of block totals for block with the jth treatment, B_j, (2) the total of treatment j for all replications, T_j, and (3) the weights for treatment j, W_j, are required. For example, for treatment 7,
$T_7 = 0.73 + 1.80 + 1.15 + 1.78 = 5.46$,
$B_7 = 4.09 + 5.72 + 3.54 + 4.75 = 18.10$,
and from equation (4), $W_7 = 3(5.46) - 4(18.10) + G = 1.40$, where G is the grand total. The values of B_j, T_j, and W_j are summarized in Table 6. From Table 6, we

Table 6: Treatment Totals and Adjustment Factors

Trt j	T_j	B_j	$W_j = kT_j - (k+1)B_j + G$
1	6.97	18.61	3.89
2	7.36	21.24	-5.46
3	8.05	21.16	-3.07
4	6.42	17.23	7.76
5	4.01	18.37	-4.03
6	7.62	21.03	-3.84
7	5.46	18.10	1.40
8	5.61	18.05	2.05
9	5.92	18.47	1.30

can find SSB_{Adj} from equation (5):

$$SSB_{Adj} = \frac{\sum W_j^2}{k^3(k+1)} = \frac{3.89^2 + (-5.46)^2 + \ldots + 1.30^2}{3^3(3+1)} = \frac{153.43}{108} = 1.42;$$

the intra-block error sum of squares,
$SSE = SST - SSR - SSTrt_U - SSB_{Adj} = 5.97 - 0.08 - 3.23 - 1.42 = 1.24$. The complete ANOVA table is summarized in Table 7.

Table 7: Analysis of Variance for the balanced square lattice design example

Source of variation	Degree of freedom	Sum of squares	Mean squares
Replication	$4-1=3$	0.08	0.026
Treatment(Unadjusted)	$3^2-1=8$	3.23	0.404
Block within replication(Adj)	$3^2-1=8$	1.42	$0.178 = E_b$
Intra-block Error	$(3^2-1)(3-1)=16$	1.24	$0.077 = E_e$
Total	$4(3^2)-1=35$	5.97	

To test for a treatment effect, the adjustment factor for treatment means is calculated as follows:

$$E_b = MSB_{Adj} = \frac{1.42}{3^2-1} = 0.178$$

$$E_e = MSE = \frac{1.24}{(3^2-1)(3-1)} = 0.078.$$

From equation (8), we can calculate the adjustment factor,

$$\mu = \frac{E_b - E_e}{k^2 E_b} = \frac{0.178 - 0.078}{3^2(0.178)} = 0.062.$$

So, using the adjustment factor to calculate the adjusted treatment total, $T_j^{'} = T_j + \mu W_j,\ j = 1, 2, \ldots, 9$; all adjusted treatment totals are summarized in Table 8.

Table 8: The adjusted treatment totals

Adjusted treatment totals								
$T_1^{'}$	$T_2^{'}$	$T_3^{'}$	$T_4^{'}$	$T_5^{'}$	$T_6^{'}$	$T_7^{'}$	$T_8^{'}$	$T_9^{'}$
7.21	7.01	7.85	6.90	3.76	7.38	5.55	5.74	6.00

Thus, the adjusted treatment sum of squares (see equation (7)) is

$$SSTrt_{Adj} = \frac{\sum (T_j^{'})^2}{r} - CF = \frac{7.21^2 + 7.01^2 + \ldots + 6.00^2}{4} - 91.58$$

$$= \frac{379.02}{4} - 91.58 = 3.16,$$

and the effective error mean squares, equation (9), is $E_e^{'} = E_e(1 + k\mu) = E_e[1 + (r-1)\mu] = 0.078[1 + 3(0.062)] = 0.092$. The adjusted treatment mean square which equals to $SSTrt_{Adj}/(k^2 - 1) = 3.16/8 = 0.395$. Therefore, the F-ratio equals to $0.395/0.092 = 4.30$ having 8 and 16 degrees of freedom. Normally, the intra-error mean square is the denominator of F-statistic, but in this example the effective mean square is used instead to take account of sampling errors. The standard error of the adjusted treatment mean is $\sqrt{E_e^{'}/r} = \sqrt{0.092/4} = 0.151$; and the standard error of the difference between 2 adjusted means in the same block (see equation (11)) is $\sqrt{2E_e^{'}/r} = \sqrt{(2 \times 0.092)/4} = 0.215$.

The randomized complete block design error sum of squares is $SSB_{Adj} + SSE = 1.42 + 1.24 = 2.66$ with 24 degrees of freedom. So, the unbiased estimate of error variance for a randomized block design is 2.66/24, or 0.1108, and the efficiency of the experiment relative to a randomized complete block design is 0.1108/0.092, or 120%.

3.2 Example of a partially balanced square lattice design

This example is from Cochran and Cox (1967). The data are yields in bushels per acre of 25 varieties of soybeans. The data are collected in two replications of 25 varieties in five blocks. Each block contains 5 varieties. So, this is a simple lattice design. The data is given in Table 9. In this example, we have $r = 2$ replications, block size of $k = 5$, k^2=5^2 = 25 treatments, and $rk = 2(5) = 10$ blocks.

From the data in Table 9, the total sum of squares, the unadjusted treatment sum of squares, the unadjusted block sum of squares, and the replication sum of squares are calculated from equation(1),

$SST = (6^2 + 7^2 + \ldots + 14^2) - CF = 10,767 - 9,275.22 = 1,491.78$

and from equation (2),

$$SSTrt_U = \frac{\sum T_j^2}{r} - CF = \frac{30^2 + 28^2 + \ldots + 33^2}{2} - 9,275.22$$

$$= 9,834.50 - 9,275.22 = 559.28$$

The jth treatment totals are summarized in the Table 10. For example, $T_1 = 6 + 24 = 30$.

From equation (3),

$$SSR = \frac{289^2 + 392^2}{5^2} - 9,275.22 = 9,487.4 - 9,275.22 = 212.8$$

, where CF is the correction factor, $681^2/50 = 9,275.22$. To calculate the adjusted block sum of squares (equation (12)) we need C_l and RC_i. For example, for block 2

Table 9: Data of yields in bushels per acre of 25 varieties of soybeans

Bk	Replication I					TotalB_l	Bk	Replication II					TotalB_l
1	(1)	(2)	(3)	(4)	(5)		6	(1)	(6)	(11)	(16)	(21)	
	6	7	5	8	6	32		24	13	24	11	8	80
2	(6)	(7)	(8)	(9)	(10)		7	(2)	(7)	(12)	(17)	(22)	
	16	12	12	13	8	61		21	11	14	11	23	80
3	(11)	(12)	(13)	(14)	(15)		8	(3)	(8)	(13)	(18)	(23)	
	17	7	7	9	14	54		16	4	12	12	12	56
4	(16)	(17)	(18)	(19)	(20)		9	(4)	(9)	(14)	(19)	(24)	
	18	16	13	13	14	74		17	10	30	9	23	89
5	(21)	(22)	(23)	(24)	(25)		10	(5)	(10)	(15)	(20)	(25)	
	14	15	11	14	14	68		15	15	22	16	19	87
					Total	289						Total	392

Table 10: Treatment totals

T_1	T_2	T_3	T_4	T_5	T_6	T_7	T_8	T_9	T_{10}	T_{11}	T_{12}	T_{13}
30	28	21	25	21	29	23	16	23	23	41	21	19
T_{14}	T_{15}	T_{16}	T_{17}	T_{18}	T_{19}	T_{20}	T_{21}	T_{22}	T_{23}	T_{24}	T_{25}	
39	36	29	27	25	22	30	22	38	23	37	33	

(which is in replication 1) $C_2 = \sum T_{j(2)} - rB_2 = \underbrace{(T_6 + T_7 + T_8 + T_9 + T_{10})}_{see\,Table\,10} - 2(61) =$ $(29 + 23 + 16 + 23 + 23) - 2(61) = -8$. Other C_l's, $l = 1, 2, \dots, 10$ are computed in the same way. The complete set of values of C_l's are in Table 11.

Then, calculate the total of C_ls in each replication:
for replication 1, $RC_1 = C_1 + C_2 + C_3 + C_4 + C_5 = 61 + (-8) + 48 + (-15) + 17 = 103$;
for replication 2, $RC_2 = C_6 + C_7 + C_8 + C_9 + C_{10} = (-9) + (-23) + (-8) + (-32) + (-31) = -103$.

Table 11: Value of C_l for each block

C_1	C_2	C_3	C_4	C_5	C_6	C_7	C_8	C_9	C_{10}
61	-8	48	-15	17	-9	-23	-8	-32	-31

From the equation (12), the adjusted block sum of squares is calculated:

$$SSB_{Adj} = \frac{\sum_{l=1}^{rk} C_l^2}{rk(r-1)} - \frac{\sum_{i=1}^{allrep} (RC_i)^2}{rk^2(r-1)}$$

$$= \frac{61^2 + (-8)^2 + \ldots + (-31)^2}{2(5)(2-1)} - \frac{103^2 + (-103)^2}{2(5^2)(2-1)} = 501.84.$$

The intra-block error sum of square (equation (13)) is

$$SSE = SST - SSR - SSTrt_U - SSB_{Adj} = 1,491.78 - 212.18 - 559.28 - 501.84 = 218.48.$$

The complete ANOVA table is summarized in Table 12.

Table 12: Analysis of variance table for example of yield data

Source of variation	Degree of freedom	Sum of squares	Mean squares
Replication	$2-1=1$	212.18	212.18
Treatment(Unadjusted)	$5^2-1=24$	559.28	23.30
Block within replication(Adj)	$2(5-1)=8$	$501.84 = B_a$	$62.73 = E_b$
Intra-block Error	16 (Substraction)	218.48	$13.66 = E_e$
Total	$2(5^2)-1=49$	$1,491.78$	

To get the adjusted treatment total, the adjustment factor, equation (14), is calculated:

$$\mu = \frac{E_b - E_e}{k(r-1)E_b} = \frac{62.73 - 13.66}{5(2-1)62.73} = 0.1564.$$

After getting the the adjustment factor, this quantity is used for calculating the adjusted treatment total (see equation (15)). For example, the adjusted treatment total 2, treatment 2 are in the blocks 1 and 7 in replications 1 and 2 , respectively. So,

$$T_2' = T_2 + \mu[\underbrace{C_1^*}_{in\,block\,1} + \underbrace{C_2^*}_{in\,block\,7}] = \underbrace{28}_{from\,Table\,10} + 0.1564[\underbrace{61 + (-23)}_{see\,Table\,11}] = 33.945.$$

Another example for treatment 23 which are in the blocks 5 and 8 in replications 1 and 2 , respectively. So,

$$T'_{23} = T_{23} + \mu[\underbrace{C_1^*}_{in\,block\,5} + \underbrace{C_2^*}_{in\,block\,8}] = \underbrace{23}_{from\,Table\,10} + 0.1564[\underbrace{17 + (-8)}_{see\,Table\,11}] = 24.41.$$

The complete set of values of T'_j's are in Table 13.

Table 13: Adjusted treatment totals

T'_1	T'_2	T'_3	T'_4	T'_5
38.14	33.95	29.29	29.54	25.70
T'_6	T'_7	T'_8	T'_9	T'_{10}
26.34	18.15	13.50	16.74	16.90
T'_{11}	T'_{12}	T'_{13}	T'_{14}	T'_{15}
47.10	24.91	25.26	41.50	38.66
T'_{16}	T'_{17}	T'_{18}	T'_{19}	T'_{20}
25.24	21.05	21.40	14.65	22.80
T'_{21}	T'_{22}	T'_{23}	T'_{24}	T'_{25}
23.25	37.06	24.41	34.65	30.81

To test the treatment effect, we need the adjusted treatment sum of squares, equation (17). Equations (16) and (17) would be used to obtain $SSTrt_{Adj}$. First, calculate the unadjusted sum of squares for blocks within replication:

$$B_u = \underbrace{(\frac{\sum B_l^2}{k} - CF_1)}_{replication\,1} + \underbrace{(\frac{\sum B_l^2}{k} - CF_2)}_{replication\,2}$$

$$= [\frac{32^2 + 61^2 + 54^2 + 74^2 + 68^2}{5} - \frac{289^2}{25}] + [\frac{80^2 + 80^2 + 56^2 + 89^2 + 87^2}{5} - \frac{392^2}{25}]$$

$$= 211.36 + 138.64 = 350.$$

Next, calculate the adjusted treatment sum of squares (equation (17)) in the following:

$$SSTrt_{Adj} = SSTrt_{UnAdj} - k(r-1)\mu[\frac{r}{(r-1)(1+k\mu)}B_u - B_a]$$

$$= 559.28 - 5(2-1)(0.1564)[\frac{2}{(2-1)(1+5(0.1564))}(350) - 501.84]$$

$$= 559.28 - (-85.26) = 644.54.$$

The effective error mean square, $E_e^{'}$, is

$$E_e^{'} = E_e[1 + \frac{rk\mu}{k+1}] = 13.66[1 + \frac{2(5)(0.1564)}{5+1}] = 17.2144.$$

Therefore, the F-ratio equals to $MSTrt_{Adj}/E_e = (644.54/24)/13.66 = 1.966$ having 24 and 8 degrees of freedom. The standard error of the adjusted treatment mean is $\sqrt{E_e^{'}/r} = \sqrt{17.2144/2} = 2.933$; and the standard error of the difference between 2 adjusted means in the same block is $\sqrt{2E_e[1+(r-1)\mu]/r} = \sqrt{2(13.66)[1+(2-1)(0.1564)]/2} = \sqrt{15.796} = 3.975$; the standard error of the difference between two adjusted treatment means in different blocks (equation (20)) is

$$\sqrt{\frac{2E_e}{r}(1+r\mu) = \frac{2(13.66)}{2}(1+2(0.1564))} = 4.235.$$

The average of variance, equation (21), is

$$\frac{2E_e}{r}[1 + \frac{r\mu k}{k+1}] = \frac{2(13.66)}{2}[1 + \frac{2(0.1564)(5)}{5+1}] = 17.22.$$

The randomized complete block design error sum of squares is $SSB_{Adj} + SSE = 501.84 + 218.48 = 720.32$ with 24 degrees of freedom. While the mean square of error variance for randomized block design is $720.32/24 = 30.01$, the effective error mean square in this design is 17.22. The efficiency of the experiment relative to a randomized complete block design is 30.01/17.22, or 174.27%.

4 R AND SAS PROGRAMS

4.1 R and SAS Programs for a balanced lattice design

4.1.1 R Program

In R Package "agricolae", although there is no function that can directly analyze data obtained from a lattice design, there are 2 useful functions for use with lattice designs. The function "design.lattic" can randomize treatments into a $k \times k$ lattice, but only for a partially balanced lattice design (simple and triple lattice designs). This function, however, does not generate the analysis of variance. The function "PBIB.test" which is aimed at the analysis of the partially balanced incomplete block design (PBIB) can be applied to resoluble designs (lattice and alpha designs). For the previous example of the study of the effects of nine feeding treatments on the growth rates of pigs by Comstock *et al* (1948), the data in Table 5 must be structured in an appropriate form for use in R. Variables referring to replications, blocks, treatments, response values must be created. Sample R code is given below:

First, we have to load packages "agricolae" and MASS". Package "MASS" is also required because package "agricolae" needs a function "ginv" from the MASS package.

```
library(agricolae)
library(MASS)
```

Second, create column vectors for the replication, the block, treatment, and response which are the argument of the function "PBIB.test". In Table 5, we have 4 replications, 12 blocks, and 9 treatments.

```
# Creates a replication vector
rep<-rep(1:4,each=9)
# Creates a block vector
block<-rep(1:12,each=3)
# Creat a treatment vector
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)
# Creat a response vector
gain.wt
<-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)
```

Now, specify the value of k , the block size. For this example, $k = 3$.

```
model<- PBIB.test(block,trt,rep,gain.wt,k=3)
```

After running the above program and display "data", the following output is generated:

```
ANALYSIS PBIB:  gain.wt

Class level information
Blocks:  12
Trts  :  9

Number of observations:  36
Analysis of Variance Table
Response: gain.wt
                      Df Sum Sq Mean Sq F value   Pr(>F)
replication            3 0.0774 0.02580  0.3337 0.801132
trt.unadj              8 3.2261 0.40326  5.2168 0.002467 **
replication:block.adj  8 1.4206 0.17758  2.2972 0.074630 .
Residuals             16 1.2368 0.07730
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

coefficient of variation: 17.4 %
gain.wt Means: 1.595

Treatments

Parameters PBIB
treatmeans : 9
Block size : 3
Blocks/rep : 3
Replication: 4

Efficiency factor 0.75
```

The mean sums of squares corresponds to those in Table 7 except for the F tests. As we saw in the previous calculations, to test the treatment effect, both the treatment sum of squares and the error mean square have to be adjusted. The actual F value is 4.30 instead of 5.21. The function "PBIB.test" also gives the adjusted treatment means which are presented below (and correspond to adjusted treatment totals in Table 8).

```
model$means
<<< to see the objects: comparison and means  >>>
trt  means  mean.adj  N     std.err
1  1.7425  1.8035178  4  0.1554838
2  1.8400  1.7543554  4  0.1554838
3  2.0125  1.9643445  4  0.1554838
4  1.6050  1.7267220  4  0.1554838
5  1.0025  0.9392861  4  0.1554838
6  1.9050  1.8447665  4  0.1554838
7  1.3650  1.3869601  4  0.1554838
8  1.4025  1.4346559  4  0.1554838
9  1.4800  1.5003916  4  0.1554838
```

The standard error above does not exactly corresponds to the $\sqrt{E'_e/r} = \sqrt{0.092/4} = 0.151$. We can ask "PBIB.test" to show the difference between 2 adjusted mean in the same block. This follows from equation (11) as well as the previous example.

```
model$comparison
Comparison between treatments means
<<< to see the objects: comparison and means  >>>

       Difference     stderr    pvalue
1 - 2  0.04916241  0.2143020  0.821460
3 - 1  0.16082670  0.2143020  0.463868
1 - 4  0.07679588  0.2143020  0.724764
1 - 5  0.86423169  0.2143020  0.000964
6 - 1  0.04124861  0.2143020  0.849788
1 - 7  0.41655769  0.2143020  0.069722
1 - 8  0.36886191  0.2143020  0.104484
1 - 9  0.30312627  0.2143020  0.176386
3 - 2  0.20998911  0.2143020  0.341734
2 - 4  0.02763347  0.2143020  0.899008
2 - 5  0.81506928  0.2143020  0.001562
6 - 2  0.09041103  0.2143020  0.678722
2 - 7  0.36739528  0.2143020  0.105760
2 - 8  0.31969950  0.2143020  0.155200
2 - 9  0.25396386  0.2143020  0.253292
3 - 4  0.23762257  0.2143020  0.283896
3 - 5  1.02505839  0.2143020  0.000204
3 - 6  0.11957808  0.2143020  0.584576
3 - 7  0.57738439  0.2143020  0.015958
3 - 8  0.52968860  0.2143020  0.025060
3 - 9  0.46395297  0.2143020  0.045852
4 - 5  0.78743581  0.2143020  0.002050
6 - 4  0.11804449  0.2143020  0.589358
```

```
4 - 7  0.33976181  0.2143020  0.132432
4 - 8  0.29206603  0.2143020  0.191798
4 - 9  0.22633039  0.2143020  0.306596
6 - 5  0.90548031  0.2143020  0.000644
7 - 5  0.44767400  0.2143020  0.053044
8 - 5  0.49536978  0.2143020  0.034454
9 - 5  0.56110542  0.2143020  0.018634
6 - 7  0.45780631  0.2143020  0.048454
6 - 8  0.41011052  0.2143020  0.073720
6 - 9  0.34437489  0.2143020  0.127616
8 - 7  0.04769578  0.2143020  0.826692
9 - 7  0.11343142  0.2143020  0.603860
9 - 8  0.06573564  0.2143020  0.762994
Done.
```

The P-values are based on a t statistic. For example, for comparing treatments 1 and 2, $t = 0.049/0.214 = 0.229$ with an associated P-value of $2P(t_{16} > 0.229) = 0.821$.

4.1.2 SAS Program

The LATTICE procedure in SAS can analyze data from balanced square lattices, partially balanced square lattices, and some rectangular lattices. The LATTICE procedure determines the type of lattice design from the data set. It also checks whether the data is valid and gives the message if it is not working. The data that we will create must consist of variables named "Group", "Block", "Treatmnt", and "Rep". The variable Group indicates which orthogonal replication in the basic plan (balanced design) includes the experimental unit. The values of "Group" are $1, 2, \ldots, r$ where r is the number of replicates for a balanced design. The variable "Rep" is needed when there are more than 1 repetition of the entire basic plan. The values of "Rep" are $1, 2, \ldots, p$, where p is the number of replications of the entire basic plan. Hence, the experiment has a total of $r \times p$ replications. Then, for a balanced square lattice design, there will be a variable "Rep". More details are in SAS/STAT 9.2 (2008). A sample program for the pig data example is given below.
First, create a dataset with variables Group, Treatmnt, Rep, and response Weight.

```
data pigs;
input Group Block Treatmnt Weight @@;
cards
1 1 1 2.20  1 1 2 1.84  1 1 3 2.18  1 2 4 2.05
1 2 5 0.85  1 2 6 1.86  1 3 7 0.73  1 3 8 1.60
1 3 9 1.76  2 1 1 1.19  2 1 4 1.20  2 1 7 1.15
2 2 2 2.26  2 2 5 1.07  2 2 8 1.45  2 3 3 2.12
```

```
2 3 6 2.03  2 3 9 1.63  3 1 1 1.81  3 1 5 1.16
3 1 9 1.11  3 2 2 1.76  3 2 6 2.16  3 2 7 1.80
3 3 3 1.71  3 3 4 1.57  3 3 8 1.13  4 1 1 1.77
4 1 6 1.57  4 1 8 1.43  4 2 2 1.50  4 2 4 1.60
4 2 9 1.42  4 3 3 2.04  4 3 5 0.93  4 3 7 1.78
;
```

Second, use PROC LATTICE to generate the analysis of variance.

```
proc lattice data = pigs;
var Weight;
run;
```

The results are the following:

```
The Lattice Procedure
               Analysis of Variance for Weight

                                                Sum of        Mean
Source                                   DF     Squares       Square

Replications                              3     0.07739       0.02580
Blocks within Replications (Adj.)         8      1.4206       0.1776
Component B                               8      1.4206       0.1776
Treatments (Unadj.)                       8      3.2261       0.4033
Intra Block Error                        16      1.2368       0.07730
Randomized Complete Block Error          24      2.6574       0.1107
Total                                    35      5.9609       0.1703

              Additional Statistics for Weight

Variance of Means in Same Block        0.04593
LSD at .01 Level                        0.6259
LSD at .05 Level                        0.4543
Efficiency Relative to RCBD             120.55

      Adjusted Treatment
       Means for Weight

    Treatment      Mean

         1       1.8035
         2       1.7544
         3       1.9643
         4       1.7267
         5       0.9393
```

```
        6       1.8448
        7       1.3870
        8       1.4347
        9       1.5004
```

The mean sums of squares are the same as those from function PBIB.test in R except that PROC LATTICE did not perform the F tests. PROC LATTICE also gives the randomized complete block error, the pooled sums of squares for blocks and intra-block error. The relative efficiency of the lattice design was 120.5. However, both SAS and R did not give the adjusted treatment sum of squares. Therefore, we cannot obtain the test of treatment effect from both R and SAS.

4.2 R and SAS Programs for a partially balanced lattice design

4.2.1 R Program

We use the same function as we did for a balanced lattice design. Column vectors are created for the replication, the block, treatment, and response which are the arguments of the function "PBIB.test". The example in Table 9 has 2 replications, 10 blocks, and 25 treatments.

```
library(agricolae)
library(MASS)
rep<-rep(1:2,each=25)
block<-rep(1:10,each=5)
trt<-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)
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)
PBIB.test(block,trt,rep,yield,k=5)
```

The results from R are the following:

```
ANALYSIS PBIB:  yield
Class level information
Blocks:  10
Trts  :  25
Number of observations:  50

Analysis of Variance Table
```

```
Response: yield
                     Df Sum Sq Mean Sq F value   Pr(>F)
replication           1 212.18 212.180 15.5386 0.001166 **
trt.unadj            24 559.28  23.303  1.7066 0.135789
replication:block.adj  8 501.84  62.730  4.5939 0.004629 **
Residuals            16 218.48  13.655
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

coefficient of variation: 27.1 %
yield Means: 13.62

Treatments

Parameters PBIB
treatmeans : 25
Block size : 5
Blocks/rep : 5
Replication: 2
Efficiency factor 0.75
```

All mean squares are the same as those in Table 12 except for the F statistics. Again, the estimates of adjusted treatment means which are obtained by dividing the adjusted treatment totals (in Table 13) by 2 (the number of replications) are given below. The standard error below is not exactly the same as $\sqrt{E_e'/r} = 2.933$.

```
PBIB.test(block,trt,rep,yield,k=5)$means
Comparison between treatments means

<<< to see the objects: comparison and means  >>>
trt  means   mean.adj  N   std.err
1    15.0  19.068070  2  2.993997
2    11.5  16.972820  2  2.993997
3    20.5  14.646302  2  2.993997
4    10.5  14.768731  2  2.993997
5     9.5  12.846963  2  2.993997
6    19.5  13.170054  2  2.993997
7    18.0   9.074805  2  2.993997
8    14.5   6.748286  2  2.993997
9    13.5   8.370716  2  2.993997
10   12.5   8.448948  2  2.993997
11   11.0  23.551052  2  2.993997
12   14.0  12.455803  2  2.993997
13    15.0  12.629284  2  2.993997
```

```
14   11.0  20.751714  2  2.993997
15   19.0  19.329946  2  2.993997
16   11.5  12.622429  2  2.993997
17   18.5  10.527180  2  2.993997
18   16.5  10.700662  2  2.993997
19   10.5   7.323091  2  2.993997
20   12.5  11.401323  2  2.993997
21   10.5  11.625857  2  2.993997
22   14.5  18.530607  2  2.993997
23   11.5  12.204089  2  2.993997
24    8.0  17.326518  2  2.993997
25   11.5  15.404751  2  2.993997
```

Again, we can generate the estimates of differences in treatment effects from PBIB.test. There are 2 standard errors (see below). For example, treatments 1 and 2 are in the same block (see Table 9), and formula (11) is applied. Treatments 1 and 7 are in different blocks, and formula (20) is applied.

```
PBIB.test(block,trt,rep,yield,k=5)$comparison[1:24,]
```

```
         Difference    stderr    pvalue
1 - 2     2.095249   3.973854  0.605248
1 - 3     4.421768   3.973854  0.282270
1 - 4     4.299338   3.973854  0.295332
1 - 5     6.221106   3.973854  0.137026
1 - 6     5.898015   3.973854  0.157188
1 - 7     9.993265   4.234151  0.031300
1 - 8    12.319783   4.234151  0.010234
1 - 9    10.697354   4.234151  0.022446
1 - 10   10.6191216  4.234151  0.023298
11 - 1    4.4829826  3.973854  0.275902
1 - 12    6.6122669  4.234151  0.137930
1 - 13    6.4387853  4.234151  0.147856
14 - 1    1.6836442  4.234151  0.696154
15 - 1    0.2618763  4.234151  0.951450
1 - 16    6.4456400  3.973854  0.124338
1 - 17    8.5408895  4.234151  0.060780
1 - 18    8.3674079  4.234151  0.065638
1 - 19   11.7449785  4.234151  0.013552
1 - 20    7.6667464  4.234151  0.089006
1 - 21    7.4422127  3.973854  0.079486
1 - 22    0.5374621  4.234151  0.900574
1 - 23    6.8639806  4.234151  0.124534
1 - 24    1.7415511  4.234151  0.686302
```

4.2.2 SAS Program

The following SAS code is similar to the code used for a balanced design:

```
data Soy;
    do Group = 1 to 2;
     do Block = 1 to 5;
      do Plot = 1 to 5;
        input Treatmnt Yield @@;output;
      end;
     end;
    end;
cards;
    1   6    2   7   3   5   4   8   5   6
    6   16   7   12  8  12   9   13  10  8
   11   17   12  7   13  7   14  9   15  14
   16   18   17  16  18  13  19  13  20  14
   21   14   22  15  23  11  24  14  25  14
    1   24   6   13  11  24  16  11  21  8
    2   21   7   11  12  14  17  11  22  23
    3   16   8   4   13  12  18  12  23  12
    4   17   9   10  14  30  19  9   24  23
    5   15   10  15  15  22  20  16  25  19
;
proc lattice data=Soy;
run;
```

The following SAS output was generated by the code above:

```
The Lattice Procedure

Analysis of Variance for Yield

                                                 Sum of        Mean
Source                                  DF      Squares      Square

Replications                             1       212.18      212.18
Blocks within Replications (Adj.)        8       501.84     62.7300
  Component B                            8       501.84     62.7300
Treatments (Unadj.)                     24       559.28     23.3033
Intra Block Error                       16       218.48     13.6550
Randomized Complete Block Error         24       720.32     30.0133
Total                                   49      1491.78     30.4445

Additional Statistics for Yield
```

Variance of Means in Same Block	15.7915
Variance of Means in Different Bloc	17.9280
Average of Variance	17.2159
LSD at .01 Level	12.1189
LSD at .05 Level	8.7959
Efficiency Relative to RCBD	174.34

The mean sums of squares are the same as those in Table 12 as well as the results from R. PROC LATTICE provides the variances of the mean differences in the same block and in different blocks. Their square roots are equal to standard errors in R output. Unlike the PBIB.test in R, PROC LATTICE also gives the average variance corresponding to formula (21). The following results are the estimates of adjusted treatment means.

Adjusted Treatment
Means for Yield

Treatment	Mean
1	19.0681
2	16.9728
3	14.6463
4	14.7687
5	12.8470
6	13.1701
7	9.0748
8	6.7483
9	8.3707
10	8.4489
11	23.5511
12	12.4558
13	12.6293
14	20.7517
15	19.3299
16	12.6224
17	10.5272
18	10.7007
19	7.3231
20	11.4013
21	11.6259
22	18.5306
23	12.2041
24	17.3265
25	15.4048

5 R PROGRAMS FOR SQUARE LATTICE DESIGNS

The function PBIB.test in library agricolae did not give the right F-test because the mean square of unadjusted treatment still contains block effects. PROC LATTICE in SAS did not give the F-test for the treatment effect. Therefore, in this paper the R function, named “lattice.design” is written for balanced and partially balanced square lattice designs. The arguments for this function are exactly the same as those for the function PBIB.test. The R code for the function “lattice.balance” is in appendix.

5.1 A Balanced lattice design

Using the same data in section 3.1 (gain in weight in pigs), the result generated by the lattice.balance function is below.

```
> lattice.design(block,trt,rep,y,3)

S.E.Adjusted Treatment Mean    :  0.1515
S.E.Diff of Adj Treatment Mean :  0.2143
Effective error mean square    :  0.0919
Efficiency Relative to RCBD    :  120.5494

Analysis of Variance Table: Balanced

                  Df Sum Sq Mean Sq F value   Pr(>F)
Replication        3 0.0774 0.02580  0.3337
Block.Adj          8 1.4206 0.17758  2.2972 0.074630 .
Treatment.Adj      8 3.1717 0.39646  5.1289 0.002689 **
Intra-block Error 16 1.2368 0.07730
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

5.2 A Partially balanced lattice design

Using the same data in section 3.2 (yield data), the result generated by the lattice.balance function is below.

```
> lattice.design(block,trt,rep,y,5)

S.E.Adjusted Treatment Mean                : 2.9339
S.E.Diff of Adj Trt Mean                   : 3.9739
S.E.Diff of Adj Trt Mean (not the same bk): 4.2342
The average variance                       : 17.2159
Efficiency Relative to RCBD                : 174.3353

Analysis of Variance Table: Partially Balanced

                  Df Sum Sq Mean Sq F value   Pr(>F)
Replication        1 212.18 212.180 15.5386
Block.Adj          8 501.84  62.730  4.5939 0.004629 **
Treatment.Adj     24 644.63  26.859  1.9670 0.082442 .
Intra-block Error 16 218.48  13.655
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The class of the lattice.balance is the list. In this object, the sums of squares, their degrees of freedom, and the adjusted treatment means can be extracted. The function "names" gives all objects in the "lattice.balance".

A R Code for lattice.design

```
lattice.design<- function(block,trt,rep,y,bksize.sclar)
{
if(max(rep)==(bksize.sclar+1)){
############## FIND Adj SSB ####################
k<-bksize.sclar
Total.InBj<- as.matrix(tapply(y,list(block),sum))
Tj<- as.matrix(tapply(y,list(trt),sum))
NumOfBlock<- max(dim(Total.InBj))
NumOfTrt<- max(dim(Tj))
BTotal.long<-rep(Total.InBj,each=k)
dat<-as.data.frame(cbind(BTotal.long,trt,block))
Bj<-matrix(0,ncol=1,nrow=NumOfTrt)

for(i in 1:NumOfTrt){
SumVec<-rep(0,(NumOfBlock*k))
dat<-as.data.frame(cbind(BTotal.long,trt,block,SumVec))
Bj[i]<-sum(ifelse(dat$trt==i,dat$SumVec<- dat$BTotal.long,dat$SumVec<- 0))
}
    ##############################################
FindW<-as.data.frame(cbind(Tj,Bj))
FindW$W<- k*FindW$V1-(k+1)*FindW$V2+sum(y)
FindW$WSquare<-(FindW$W)^2
SSB.Adj<-sum(FindW$WSquare)/((k^3)*(k+1))
#############################################

MSB.Adj<-SSB.Adj/(max(trt)-1)
SSRep<- anova(lm(y~factor(rep)))$"Sum Sq"[1]
MSRep<- SSRep/(max(rep)-1)
SSTrt.UnAdj<- anova(lm(y~factor(trt)))$"Sum Sq"[1]
MSTrt.UnAdj<- SSTrt.UnAdj/(max(trt)-1)
SSTotal<- sum(anova(lm(y~factor(trt)))$"Sum Sq")
SSE<- SSTotal-SSRep-SSTrt.UnAdj-SSB.Adj
MSE<- SSE/((max(trt)-1)*(sqrt(max(trt))-1))

mu<- (MSB.Adj-MSE)/(max(trt)*MSB.Adj)

CF<- (sum(y))^2/length(rep)
Adj.Total<-FindW$V1+mu*FindW$W
Adj.Trt.Mean<- Adj.Total/(k+1)

SSTrt.Adj<- sum(Adj.Total^2)/max(rep)-CF
MSTrt.Adj <- SSTrt.Adj/(max(trt)-1)

RBD.MSE<-(SSB.Adj+SSE)/((max(trt)-1)+(max(trt)-1)*(sqrt(max(trt))-1))
EffectiveMSE2<-MSE*(1+sqrt(max(trt))*mu)
EffectiveSSE2<-EffectiveMSE2*(k^2-1)*(k-1)
Efficiency<- (RBD.MSE/EffectiveMSE2)*100
F.Trt <- MSTrt.Adj/EffectiveMSE2
pval<-pf(F.Trt, df1=max(trt)-1, df2=(max(trt)-1)*(sqrt(max(trt))-1),lower.tail = FALSE)
se.Adj.trtMean<- sqrt(EffectiveMSE2/(sqrt(max(trt))+1))
se.Diff.same<- sqrt(2*EffectiveMSE2/(sqrt(max(trt))+1))
```

```
############# bar plot ####################
#mp<-barplot(Adj.Trt.Mean, names.arg=seq(1:max(trt)),xlab="Treatments",
#ylab="Adjusted Means",col=terrain.colors(max(trt)),
#main="Balanced Square Lattice Design")
#tot <- round(colMeans(t(Adj.Trt.Mean)),2)
#text(mp, tot + 0.05, format(tot), xpd = TRUE, col = "black",cex=1)
 #legend("bottomright",legend=paste(c("F-statistic=","p-value=","Efficiency="),
#               c(format(F ,digits=4,justify = "right", scientific = TRUE)
    #                ,format(pval,digits=4,justify = "right", scientific = TRUE)
#  ,format(Efficiency*100,,digits=4,justify = "right",
#  scientific = TRUE)
# )
# ),bg="white",box.col="grey")

#error.bar <- function(x, y, upper, lower=upper, length=0.1,...){
    #if(length(x) != length(y) | length(y) !=length(lower) | length(lower) != length(upper))
    #stop("vectors must be same length")
    #arrows(x,y+upper, x, y-lower, angle=90, code=3, length=length, ...)
    #}
    #error.bar(mp,Adj.Trt.Mean,rep(se.Adj.trtMean,length(Adj.Trt.Mean))


############## Make a  Table Output (ANOVA)###############
ssrep<-SSRep
repdf<- k

SSBAdj<-SSB.Adj
SSBAdjrep<- max(trt)-1

    SSTrt.Adj<-SSTrt.Adj
SSTrt.Adjdf<- max(trt)-1


SSE.Effective<-EffectiveSSE2
Errordf<-(max(trt)-1)*(k-1)

Df <- c(repdf, SSBAdjrep, SSTrt.Adjdf,Errordf,Errordf)
ssq <- c(ssrep, SSBAdj,SSTrt.Adj,SSE, SSE.Effective)

frep<-MSRep/MSE
fb<-MSB.Adj/MSE
pval.B<-pf(fb, df1=max(trt)-1, df2=(max(trt)-1)*(sqrt(max(trt))-1),lower.tail = FALSE)


ftrt<-MSTrt.Adj/EffectiveMSE2
fsse<-1

Fval<-c(frep,fb,ftrt,NA,NA)
Means.Adj<-Adj.Trt.Mean

Pvalue<-c(NA,pval.B,pval,NA,NA)


anovadf <- data.frame(Df, ‘Sum Sq‘=ssq, ‘Mean Sq‘=ssq/Df,
```

```
'F value'=Fval ,'Pr(>F)' = Pvalue, check.names=FALSE)
rownames(anovadf) <- c("Replication","Block.Adj[a]","Treatment.Adj[b]","Error[a]",
"Effective.Error[b]")
class(anovadf) <- c("anova","data.frame")
print(list(Adj.means=Means.Adj))
cat(c("                          \n"))
cat(c("                          \n"))
cat(c("S.E.Adjusted Treatment Mean    : "),round(se.Adj.trtMean,4),"\n")
    cat(c("Efficiency Relative to RCBD    : "),round(Efficiency,4),"\n")
cat(c("S.E.Diff of Adj Treatment Mean : "),round(se.Diff.same,4),"\n")
cat(c("                          \n"))
cat(c("Analysis of Variance Table: Balanced\n"))
cat(c("                          \n"))
    return(anovadf)
}
else{
k<-bksize.sclar

tmp<-as.data.frame(cbind(rep,block,trt,y))
class(tmp$block)


SSTrt.UnAdj<-anova(lm(y~factor(trt),data=tmp))$"Sum Sq"[1]
SSRep<-anova(lm(y~factor(rep),data=tmp))$"Sum Sq"[1]
SSTot<-anova(lm(y~factor(rep),data=tmp))$"SumSq"[1]+anova(lm(y~factor(rep),
data=tmp))$"Sum Sq"[2]

Total.InBj<- as.matrix(tapply(y,list(block),sum))
Tj<- as.matrix(tapply(y,list(trt),sum))

SumTj.L<-matrix(0,ncol=1,nrow=max(block))
for(i in 1:max(block)){
SumTj.L[i,1] <- sum(Tj[tmp[block==i,][,3]])
}
r<-max(rep)
CL<-SumTj.L-r*Total.InBj

RCi<-matrix(0,ncol=1,nrow=r)
for(j in 1:r){
RCi[j,1]<-sum(CL[unique(tmp[rep==j,][,2])])
}

SSB.Adj<- (sum(CL^2)/(r*k*(r-1)))-(sum(RCi^2)/(r*(k^2)*(r-1)))
SSE<- SSTot-SSRep-SSTrt.UnAdj-SSB.Adj

Df.Rep<- (r-1)
Df.Trt<- k^2-1
Df.Block<- r*(k-1)
Df.Error<- (r*k-k-1)*(k-1)


MSTrt.UnAdj<-SSTrt.UnAdj/Df.Trt
MSRep<-SSRep/Df.Rep
MSB.Adj<-SSB.Adj/Df.Block
```

```
MSE<-SSE/Df.Error

mu<-(MSB.Adj-MSE)/(k*(r-1)*MSB.Adj)

Adj.Total<-matrix(0,ncol=1,nrow=k^2)


for(i in 1:(k^2)){
Adj.Total[i,1]<- Tj[i]+ mu*sum(CL[tmp[trt==i,][,2]])
}
Adj.means<-Adj.Total/r

BuI<-matrix(0,ncol=1,nrow=r)
for(i in 1:r){
BuI[i,1]<-(sum(Total.InBj[unique(tmp[rep==i,][,2])]^2)/k)-
(sum(Total.InBj[unique(tmp[rep==i,][,2])])^2)/(k^2)
}
Bu<-sum(BuI)

SSTrt.Adj<- SSTrt.UnAdj-k*(r-1)*mu*(r/((r-1)*(1+k*mu))*Bu-SSB.Adj)

Effective.Error <- MSE*(1+((r*mu*k)/(k+1)))
SSE.Effective <- (Effective.Error)*Df.Error

F.Trt<- (SSTrt.Adj/Df.Trt)/Effective.Error
se.Adj.Mean<- sqrt(Effective.Error/r)
se.Adj.Mean.Same<- sqrt((2*MSE*(1+(r-1)*mu))/r)
se.Adj.Mean.DiffB<- sqrt((2*MSE*(1+r*mu))/r)
averg.var<- 2*MSE*(1+(r*mu*k)/(k+1))/r


RBD.SSE<-SSB.Adj+SSE
RBD.MSE<- RBD.SSE/(Df.Block+Df.Error)

Efficiency<- (RBD.MSE/Effective.Error)*100

######################################
#  MSTrt.UnAdj<-SSTrt.UnAdj/Df.Trt   #
#  MSRep<-SSRep/Df.Rep               #
#  MSB.Adj<-SSB.Adj/Df.Block         #
#  MSE<-SSE/Df.Error                 #
######################################



Df <- c(Df.Rep, Df.Block, Df.Trt,Df.Error,Df.Error)
ssq <- c(SSRep, SSB.Adj,SSTrt.Adj,SSE, SSE.Effective)

frep <- MSRep/MSE
fb<- MSB.Adj/MSE
ftrt<- F.Trt

Fval<-c(frep,fb,ftrt,NA,NA)
pval.B<-pf(fb, df1= Df.Block, df2= Df.Error,lower.tail = FALSE)
```

```
pval.trt<-pf(ftrt, df1= Df.Trt, df2= Df.Error,lower.tail = FALSE)

Pvalue<-c(NA,pval.B,pval.trt,NA,NA)

anovadf <- data.frame(Df, ‘Sum Sq‘=ssq, ‘Mean Sq‘=ssq/Df,
‘F value‘=Fval ,‘Pr(>F)‘ = Pvalue, check.names=FALSE)
rownames(anovadf) <- c("Replication","Block.Adj[a]","Treatment.Adj[b]","Error[a]"
,"Effective.Error[b]")class(anovadf) <- c("anova","data.frame")


print(list(Adj.means=Adj.means))
cat(c("                        \n"))
cat(c("S.E.Adjusted Treatment Mean                : "),round(se.Adj.Mean,4),"\n")
cat(c("S.E.Diff of Adj Trt Mean                   : "),round(se.Adj.Mean.Same,4),"\n")
cat(c("S.E.Diff of Adj Trt Mean (not the same bk): "),round(se.Adj.Mean.DiffB,4),"\n")
cat(c("The average variance                       : "),round(averg.var,4),"\n")
cat(c("Efficiency Relative to RCBD                : "),round(Efficiency,4),"\n")
cat(c("                        \n"))
cat(c("Analysis of Variance Table: Partially Balanced\n"))
cat(c("                        \n"))
return(anovadf)
}
}

############################################################################
####################### BALANCED LATTICE DESIGN ############################
############################################################################
# Creates a replication vector
rep<-rep(1:4,each=9)
# Creates a block vector
block<-rep(1:12,each=3)
# Creat a treatment vector
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)

# Creat a response vector
y<-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)

lattice.design(block,trt,rep,y,3)


############################################################################
############# PARTIALLY BALANCED LATTICE DESIGN ############################
############################################################################

rep<-rep(1:2,each=25)
block<-rep(1:10,each=5)
trt<-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)
y<-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)
lattice.balance(block,trt,rep,y,5)
```

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