

# SPLIT PLOT AND STRIP PLOT DESIGNS

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## 1. Split Plot Design

### 1.1 Introduction

In conducting experiments, sometimes some factors have to be applied in larger experimental units while some other factors can be applied in comparatively smaller experimental units. Further some experimental materials may be rare while the other experimental materials may be available in large quantity or when the levels of one (or more) treatment factors are easy to change, while the alteration of levels of other treatment factors are costly, or time-consuming. One more point may be that although two or more different factors are to be tested in the experiment, one factor may require to be tested with higher precision than the others. In all such situations, a design called the split plot design is adopted.

A split plot design is a design with at least one blocking factor where the experimental units within each block are assigned to the treatment factor levels as usual, and in addition, the blocks are assigned at random to the levels of a further treatment factor. The designs have a nested blocking structure. In a block design, the experimental units are nested within the blocks, and a separate random assignment of units to treatments is made within each block. In a split plot design, the experimental units are called split-plots (or sub-plots), and are nested within whole plots (or main plots).

In split plot design, plot size and precision of measurement of effects are not the same for both factors, the assignment of a particular factor to either the main plot or the sub-plot is extremely important. To make such a choice, the following guidelines are suggested:

***Degree of Precision-*** For a greater degree of precision for factor B than for factor A, assign factor B to the sub-plot and factor A to the main plot e.g. a plant breeder who plans to evaluate ten promising rice varieties with three levels of fertilization, would probably wish to have greater precision for varietal comparison than for fertilizer response. Thus, he would designate variety as the sub-plot factor and fertilizer as the main plot factor. Or, an agronomist would assign variety to main plot and fertilizer to sub-plot if he wants greater precision for fertilizer response than variety effect.

***Relative Size of the Main effects-*** If the main effect of one factor (A) is expected to be much larger and easier to detect than that of the other factor (B), factor A can be assigned to the main plot and factor B to the sub-plot. This increases the chance of detecting the difference among levels of factor B which has a smaller effect.

***Management Practices-*** The common type of situation when the split plot design is automatically suggestive is the difficulties in the execution of other designs, i.e. practical execution of plans. The cultural practices required by a factor may dictate the use of large

plots. For practical expediency, such a factor may be assigned to the main plot e.g. in an experiment to evaluate water management and variety, it may be desirable to assign water management to the main plot to minimize water movement between adjacent plots, facilitate the simulation of the water level required, and reduce border effects. Or, if ploughing is one of the factors of interest, then one cannot have different depths of ploughing in different plots scattered randomly apart.

## 1.2 Randomization and Layout

There are two separate randomization processes in a split plot design – one for the main plot and another for the sub-plot. In each replication, main plot treatments are first randomly assigned to the main plots followed by a random assignment of the sub-plot treatments within each main plot. This procedure is followed for all replications. A possible layout of a split plot experiment with four main plot treatments ( $a=4$ ), three sub-plot treatments ( $b=3$ ), and four replications ( $r=4$ ) is given below:

Rep. I				Rep. II				Rep. III				Rep. IV			
b <sub>1</sub>	b <sub>3</sub>	b <sub>2</sub>	b <sub>2</sub>	b <sub>3</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>1</sub>	b <sub>3</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>	b <sub>2</sub>	b <sub>3</sub>	b <sub>3</sub>	b <sub>1</sub>
b <sub>3</sub>	b <sub>2</sub>	b <sub>1</sub>	b <sub>3</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>1</sub>	b <sub>3</sub>	b <sub>2</sub>	b <sub>3</sub>	b <sub>3</sub>	b <sub>2</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>1</sub>	b <sub>2</sub>
b <sub>2</sub>	b <sub>1</sub>	b <sub>3</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>	b <sub>3</sub>	b <sub>2</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>1</sub>	b <sub>1</sub>	b <sub>3</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>
a <sub>4</sub>	a <sub>2</sub>	a <sub>1</sub>	a <sub>3</sub>	a <sub>1</sub>	a <sub>4</sub>	a <sub>2</sub>	a <sub>3</sub>	a <sub>3</sub>	a <sub>2</sub>	a <sub>4</sub>	a <sub>1</sub>	a <sub>1</sub>	a <sub>4</sub>	a <sub>3</sub>	a <sub>2</sub>

The above layout has the following important features –

- The size of the main plot is  $b$  times the size of the sub-plot,
- Each main plot treatment is tested  $r$  times whereas each sub-plot treatment is tested  $ar$  times, thus the number of times a sub-plot treatment is tested will always be larger than that for the main plot and is the primary reason for more precision for the sub-plot treatments relative to the main plot treatments.

This concept of splitting each plot may be extended further to accommodate the application of additional factors. An extension of this design is called the split-split plot design where the sub-plot is further divided to include a third factor in the experiment. The design allows for 3 different levels of precision associated with the 3 factors. That is, the degree of precision associated with the main factor is lowest, while the degree of precision associated with the sub-sub plot is the highest.

### 1.3 Model

The model for simple split plot design is

$$Y_{ijk} = \mu + \rho_i + \tau_j + \delta_{ij} + \beta_k + (\tau\beta)_{jk} + \varepsilon_{ijk} \quad \forall i = 1, 2, \dots, r, j = 1, 2, \dots, a, k = 1, 2, \dots, b,$$

where,

$Y_{ijk}$  : observation corresponding to  $k^{\text{th}}$  level of sub-plot factor(B),  $j^{\text{th}}$  level of main plot factor(A) and the  $i^{\text{th}}$  replication.

- $\mu$  : general mean
- $\rho_i$  :  $i^{\text{th}}$  block effect
- $\tau_j$  :  $j^{\text{th}}$  main plot treatment effect
- $\beta_k$  :  $k^{\text{th}}$  sub-plot treatment effect
- $(\tau\beta)_{jk}$  : interaction between  $j^{\text{th}}$  level of main-plot treatment and the  $k^{\text{th}}$  level of sub-plot treatment

The error components  $\delta_{ij}$  and  $\varepsilon_{ijk}$  are independently and normally distributed with means zero and respective variances  $\sigma_{\delta}^2$  and  $\sigma_{\varepsilon}^2$ .

### 1.4. Analysis

*Whole-Plot analysis:*

This part of the analysis is based on comparisons of whole-plot totals:

- The levels of A are assigned to the whole plots within blocks according to a randomized complete block design, and so the sum of squares for A needs no block adjustment. There are  $a - 1$  degrees of freedom for A, so the sum of squares is given by

$$ssA = \sum_j y_{.j.}^2 / rb - y_{...}^2 / rab$$

[ The “dot” notation means “add over all values of the subscript replaced with a dot” ]

- There are  $r - 1$  degrees of freedom for blocks, giving a block sum of squares of
- $$ssR = \sum_i y_{i..}^2 / ab - y_{...}^2 / rab$$
- There are  $a$  whole plots nested within each of the  $r$  blocks, so there are, in total,  $r(a - 1)$  whole-plot degrees of freedom. Of these,  $a - 1$  are used to measure the effects of A leaving  $(r - 1)(a - 1)$  degrees of freedom for whole-plot error. Equivalently, this can be obtained by the subtraction of the block and A degrees of freedom from the whole-plot total degrees of freedom i.e.  $(ra - 1) - (r - 1) - (a - 1) = (r - 1)(a - 1)$ .

So, the whole plot error sum of squares, is obtained as

$$ssE_1 = \sum_i \sum_j y_{ij.}^2 / b - y_{...}^2 / rab - ssR - ssA$$

- The whole plot error mean square  $msE_1 = ssE_1 / (r - 1)(a - 1)$ , is used as the error estimate to test the significance of whole plot factor(A).

*Sub-plot analysis:*

This part of the analysis is based on the observations arising from the split-plots within whole plots:

- There are  $rab - 1$  total degrees of freedom, and the total sum of squares is

$$sstot = \sum_i \sum_j \sum_k y_{ijk}^2 - y_{...}^2 / rab$$

- Due to the fact that all levels of B are observed in every whole plot as in a randomized complete block design, the sum of squares for B needs no adjustment for whole plots, and is given by -

$$ssB = \sum_k y_{..k}^2 / ra - y_{...}^2 / rab, \text{ corresponding to } b-1 \text{ degrees of freedom.}$$

- The interaction between the factors A and B is also calculated as part of the split-plot analysis. Again, due to the complete block structure of both the whole-plot design and the split-plot design, the interaction sum of squares needs no adjustment for blocks. The number of interaction degrees of freedom is  $(a-1)(b-1)$ , and the sum of squares is

$$ss(AB) = \sum_j \sum_k y_{.jk}^2 / r - y_{...}^2 / rab - ssA - ssB$$

- Since there are  $b$  split plots nested within the  $ra$  whole plots, there are, in total,  $ra(b-1)$  split-plot degrees of freedom. Of these,  $b-1$  are used to measure the main effect of B, and  $(a-1)(b-1)$  are used to measure the AB interaction, leaving  $ra(b-1) - (b-1) - (a-1)(b-1) = a(r-1)(b-1)$  degrees of freedom for error. Equivalently, this can be obtained by subtraction of the whole plot, B, and AB degrees of freedom from the total i.e.  $(rab-1) - (ra-1) - (b-1) - (a-1)(b-1) = a(r-1)(b-1)$ .

The split-plot error sum of squares can be calculated by subtraction:

$$ssE_2 = sstot - ssR - ssA - ssE_1 - ssB - ss(AB).$$

- The split-plot error mean square  $msE_2 = ssE_2 / a(r-1)(b-1)$  is used as the error estimate in testing the significance of split-plot factor(B) and interaction(AB).
- The analysis of variance table is outlined as follows:

ANOVA				
Source of Variation	Degrees of Freedom	Sum of Squares	Mean Square	F
<i>Whole plot analysis</i>				
Replication	r-1	ssR	-	-
Main plot treatment(A)	a-1	ssA	MsA	msA/msE <sub>1</sub>
Main plot error(E <sub>1</sub> )	(r-1)(a-1)	ssE <sub>1</sub>	msE <sub>1</sub> = E <sub>a</sub>	
<i>Sub-plot analysis</i>				
Sub-plot treatment(B)	b-1	ssB	MsB	msB/msE <sub>2</sub>
Interaction (AxB)	(a-1)(b-1)	ss(AB)	ms(AB)	ms(AB)/msE <sub>2</sub>
Sub-plot error(E <sub>2</sub> )	a(r-1)(b-1)	ssE <sub>2</sub>	msE <sub>2</sub> = E <sub>b</sub>	
Total	rab-1	sstot		

### 1.5. Standard Errors and Critical Differences:

Estimate of S.E. of difference between two main plot treatment means =  $\sqrt{\frac{2E_a}{rb}}$

Estimate of S.E. of difference between two sub-plot treatment means =  $\sqrt{\frac{2E_b}{ra}}$

Estimate of S.E. of difference between two sub-plot treatment means at the same level of main plot treatment =  $\sqrt{\frac{2E_b}{r}}$

Estimate of S.E. of difference between two main plot treatment means at the same or different levels of sub-plot treatment =  $\sqrt{\frac{2[(b-1)E_b + E_a]}{rb}}$

Critical difference is obtained by multiplying the S.E.<sub>d</sub> by t<sub>5%</sub> table value for respective error d.f. for (i), (ii) & (iii). For (iv), as the standard error of mean difference involves two error terms, we use the following equation to compute the weighted t values:

$$t = \frac{(b-1)E_b t_b + E_a t_a}{(b-1)E_b + E_a}$$

where t<sub>a</sub> and t<sub>b</sub> are t-values at error d.f. (E<sub>a</sub>) and error d.f.(E<sub>b</sub>) respectively.

**Example:** In a study carried by agronomists to determine if major differences in yield response to N fertilization exist among different varieties of jowar, the main plot treatments were three varieties of jowar (V<sub>1</sub>: CO-18, V<sub>2</sub>: CO-19 and V<sub>3</sub>: C0-22), and the sub-plot treatments were N rates of 0, 30, and 60 Kg/ha. The study was replicated four times, and the data gathered for the experiment are shown in Table 1.

**Table 1: Replication-wise yield data.**

Replication	Variety	N rate, Kg/ha		
		0	30	60
		Yield, kg per plot		
I	V <sub>1</sub>	15.5	17.5	20.8
	V <sub>2</sub>	20.5	24.5	30.2
	V <sub>3</sub>	15.6	18.2	18.5
II	V <sub>1</sub>	18.9	20.2	24.5
	V <sub>2</sub>	15.0	20.5	18.9
	V <sub>3</sub>	16.0	15.8	18.3
III	V <sub>1</sub>	12.9	14.5	13.5
	V <sub>2</sub>	20.2	18.5	25.4
	V <sub>3</sub>	15.9	20.5	22.5
IV	V <sub>1</sub>	12.9	13.5	18.5
	V <sub>2</sub>	13.5	17.5	14.9
	V <sub>3</sub>	12.5	11.9	10.5

Analyze the data and draw conclusions.

**Steps of analysis:** Calculate the replication totals(R), and the grand total(G) by first constructing a table for the replication × variety totals shown in Table 1.1, and then a second table for the variety × nitrogen totals as shown in Table 1.2.

**Table 1.1 Replication × variety (RA) - table of yield totals.**

Replication	Variety			Rep.Total(R)
	V <sub>1</sub>	V <sub>2</sub>	V <sub>3</sub>	
I	53.8	75.2	52.3	181.3
II	63.6	54.4	50.1	168.1
III	40.9	64.1	58.9	163.9
IV	44.9	45.9	34.9	125.7
Variety Total(A)	203.2	239.6	196.2	
Grand Total(G)				639.0

**Table 1.2: Variety × Nitrogen (AB) - table of yield totals.**

Nitrogen	Variety			Nitrogen Total(B)
	V <sub>1</sub>	V <sub>2</sub>	V <sub>3</sub>	
N <sub>0</sub>	60.2	69.2	60.0	189.4
N <sub>1</sub>	65.7	81.0	66.4	213.1
N <sub>2</sub>	77.3	89.4	69.8	236.5

- Compute the various sums of squares for the main plot analysis by first computing the correction factor:

$$C.F. = \frac{G^2}{rab} = \frac{(639)^2}{4 \times 3 \times 3} = 11342.25$$

$$\begin{aligned} \text{Total S.S. (sstot)} &= [ (15.5)^2 + (20.5)^2 + \dots + (10.5)^2 ] - C.F. \\ &= 637.97 \end{aligned}$$

$$\begin{aligned} \text{Replication S.S. (ssR)} &= \frac{\sum R^2}{ab} - C.F. \\ &= \frac{(181.3)^2 + (168.1)^2 + (163.9)^2 + (125.7)^2}{3 \times 3} - 11342.25 \\ &= 190.08 \end{aligned}$$

$$\begin{aligned} \text{S.S. due to Variety (ssA)} &= \frac{\sum A^2}{rb} - C.F. \\ &= \frac{(203.2)^2 + (239.6)^2 + (196.2)^2}{4 \times 3} - 11342.25 \\ &= 90.487 \end{aligned}$$

$$\begin{aligned} \text{Main plot error S.S. (ssE}_1) &= \frac{\sum (\text{RA})^2}{b} - \text{C.F.} - \text{ssR} - \text{ssA} \\ &= \frac{(53.8)^2 + (63.6)^2 + \dots + (34.9)^2}{3} - 11342.25 - 190.08 - 90.487 \\ &= 174.103 \end{aligned}$$

- Compute the various sums of squares for sub-plot analysis:

$$\begin{aligned} \text{S.S. due to Nitrogen (ssB)} &= \frac{\sum \text{B}^2}{ra} - \text{C.F.} \\ &= \frac{(189.4)^2 + (213.1)^2 + (236.5)^2}{4 \times 3} - 11342.25 \\ &= 92.435 \end{aligned}$$

$$\begin{aligned} \text{S.S. due to Interaction (A} \times \text{B)} &= \frac{\sum (\text{AB})^2}{r} - \text{C.F.} - \text{ssA} - \text{ssB} \\ &= \frac{(60.2)^2 + (65.7)^2 + \dots + (69.8)^2}{4} - 11342.25 - 90.487 - 92.435 \\ &= 9.533 \end{aligned}$$

$$\begin{aligned} \text{Sub-plot error S.S. (ssE}_2) &= \text{Total S.S.} - \text{All other sum of squares} \\ &= 637.97 - (190.08 + 90.487 + 174.103 + 92.435 + 9.533) \\ &= 81.332 \end{aligned}$$

- Calculate the mean square for each source of variation by dividing the S.S. by its corresponding degrees of freedom and compute the F value for each effect that needs to be tested, by dividing each mean square by the corresponding error mean square, as shown in Table 1.3.

**Table 1.3 ANOVA results.**

Source of variation	of Degrees of freedom	Sum of Squares	Mean Square	F
Replication	3	190.08	63.360	
Variety(A)	2	90.487	45.243	1.56 <sup>ns</sup>
Error(a)	6	174.103	29.017(E <sub>a</sub> )	
Nitrogen(B)	2	92.435	46.218	10.23 <sup>**</sup>
Variety×Nitroge	4	9.533	2.383	<1
n				
(A×B)				
Error(b)	18	81.332	4.518 (E <sub>b</sub> )	
Total	35	637.97		

<sup>ns</sup> – not significant, <sup>\*\*</sup> - significant at 1% level.

- Compute the coefficient of variation for the main plot and sub-plot as:  

$$cv(a) = \frac{\sqrt{E_a}}{G.M.} \times 100, \text{ and } cv(b) = \frac{\sqrt{E_b}}{G.M.} \times 100 \text{ respectively.}$$
- Compute standard errors and to make specific comparisons among treatment means compute respective critical differences only when F-tests show significance differences and interpret.
- Conclusion: There was no significant difference among variety means. Yield was significantly affected by nitrogen. However, the interaction between N rate and variety was not significant. All the varieties gave significant response to 30 kg N/ha as well as to 60 kg N/ha.

## 2. Strip Plot Design

### 2.1 Introduction

Sometimes situation arises when two factors each requiring larger experimental units are to be tested in the same experiment, e.g., suppose four levels of spacing and three levels of methods of ploughing are to be tested in the same experiment. Here both the factors require large experimental units. If the combination of the two factors at all possible levels are allotted in a R.B.D. in the normal way, the experimental plots shall have to be very large thereby bringing heterogeneity. So, it will not be appropriate. On the other hand if one factor(spacing) is taken in main plots and other factor(methods of ploughing) is taken in sub-plots within main plots, the sub-plots shall have to be large enough. Hence split plot design also will not be appropriate. In such situations a design called Strip plot design is adopted.

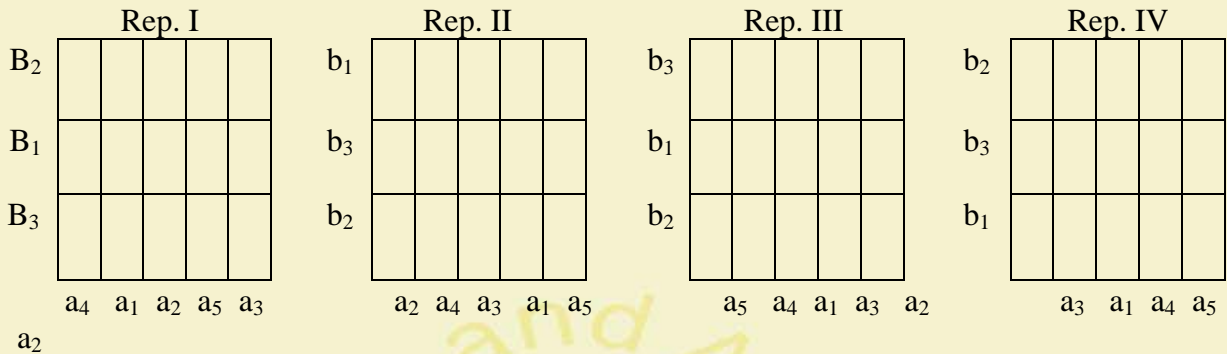
The strip plot is a 2-factor design that allows for greater precision in the measurement of the interaction effect while sacrificing the degree of precision on the main effects. The experimental area is divided into three plots, namely the vertical-strip plot, the horizontal-strip plot, and the intersection plot. We allocate factors A and B, respectively, to the vertical and horizontal-strip plots, and allow the intersection plot to accommodate the interaction between these two factors. As in the split plot design, the vertical and the horizontal plots are perpendicular to each other. However, in the strip plot design the relationship between the vertical and horizontal plot sizes is not as distinct as the main and sub-plots were in the split plot design. The sub-plot treatments instead of being randomized independently within each main plot as in the case of split plot design are arranged in strips across each replication. The intersection plot, which is one of the characteristics of the design, is the smallest in size.

### 2.2. Randomization and Layout:

In this design each block is divided into number of vertical and horizontal strips depending on the levels of the respective factors. Let A represent the vertical factor with  $a$  levels, B represent the horizontal factor with  $b$  levels and  $r$  represent the number of replications. To layout the experiment, the experimental area is divided into  $r$  blocks. Each block is divided into  $b$  horizontal strips and  $b$  treatments are randomly assigned to these strips in each of the  $r$  blocks separately and independently. Then each block is divided into  $a$  vertical strips and  $a$  treatments are randomly assigned to these strips in each of the  $r$  blocks separately and



independently. A possible layout of a strip plot experiment with  $a = 5$  ( $a_1, a_2, a_3, a_4,$  and  $a_5$ ),  $b = 3$  ( $b_1, b_2,$  and  $b_3$ ) and four replications is given below:



The strip plot design sacrifices precision on the main effects of both the factors in order to provide higher precision on the interaction which will generally be more accurately determined than in either randomized blocks or simple split plot design. Consequently this design is not recommended unless practical considerations necessitate its use or unless the interaction is the principle object of study.

### 2.3. Model

The model for strip plot design is

$$Y_{ijk} = \mu + \rho_i + \alpha_j + (\rho\alpha)_{ij} + \beta_k + (\rho\beta)_{ik} + (\alpha\beta)_{jk} + \varepsilon_{ijk} \quad \forall i = 1, 2, \dots, r, j = 1, 2, \dots, a, k = 1, 2, \dots, b$$

where,

$Y_{ijk}$  : observation corresponding to  $k^{\text{th}}$  level of factor A,  $j^{\text{th}}$  level of factor B and  $i^{\text{th}}$  replication.

$\mu$  : general mean

$\rho_i$  :  $i^{\text{th}}$  block effect

$\alpha_j$  : effect of  $j^{\text{th}}$  level of factor A

$\beta_k$  : effect of  $k^{\text{th}}$  level of factor B

$(\alpha\beta)_{jk}$  : interaction between  $j^{\text{th}}$  level of factor A and the  $k^{\text{th}}$  level of factor B

The error components  $(\rho\alpha)_{ij}$ ,  $(\rho\beta)_{ik}$  and  $\varepsilon_{ijk}$  are independently and normally distributed with means zero and respective variances  $\sigma_a^2$ ,  $\sigma_b^2$ , and  $\sigma_\varepsilon^2$ .

### 2.4. Analysis

In statistical analysis separate estimates of error are obtained for main effects of the factor, A and B and for their interaction AB. Thus there will be three error mean squares applicable for testing the significance of main effects of the factors and their interaction separately.

Suppose 4 levels of spacings(A) and 3 levels of methods(B) of ploughing are to be tested in the same experiment. Each replication is divided into 4 strips vertically and into 3 strips horizontally. In the vertical strips the four different levels of spacings are allotted randomly and in the horizontal strips three methods of ploughing are allotted randomly. Let there be 4

replications(R). The analysis of variance is carried out in three parts viz. vertical strip analysis, horizontal strip analysis and interaction analysis as follows:

- Form spacing × replication (A × R) table of yield totals and from this table compute the S.S. due to replication, S.S. due to spacings and S.S. due to interaction - Replication × Spacing i.e. error(a).
- Form method × replication (B × R) table of yield totals and from this table compute the S.S. due to methods and S.S. due to interaction - Replication × Method i.e. error(b).
- Form spacing × method (A × B) table of yield totals and from this table compute the S.S. due to interaction - Spacing × Method.
- Total S.S. will be obtained as usual by considering all the observations of the experiment and the error S.S. i.e. error(c) will be obtained by subtracting from total S.S. all the S.S. for various sources.
- Now, calculate the mean square for each source of variation by dividing each sum of squares by its respective degrees of freedom.
- Compute the F-value for each source of variation by dividing each mean square by the corresponding error term.
- The analysis of variance table is outlined as follows:

ANOVA				
Source of Variation	Degrees of Freedom	Sum of Squares	Mean Square	F
Replication(R)	(r-1)= 3	ssR	-	-
Spacing(A)	(a-1)= 3	ssA	MsA	msA/msE <sub>1</sub>
Error(a)	(r-1)(a-1)= 9	ssE <sub>1</sub>	msE <sub>1</sub> =E <sub>a</sub>	
Method(B)	(b-1)= 2	ssB	MsB	msB/msE <sub>2</sub>
Error(b)	(r-1)(b-1)= 6	ssE <sub>2</sub>	msE <sub>2</sub> =E <sub>b</sub>	
Spacing×Method (A×B)	(a-1)(b-1)= 6	ss(AB)	ms(AB)	ms(AB)/msE <sub>3</sub>
Error(c)	(r-1)(a-1)(b-1)=18	ssE <sub>3</sub>	msE <sub>3</sub> =E <sub>c</sub>	
Total	(rab-1)= 47	sstot		

### 2.5 Standard Errors and Critical Differences:

$$\text{Estimate of S.E. of difference between two A level means} = \sqrt{\frac{2E_a}{rb}}$$

$$\text{Estimate of S.E. of difference between two B level means} = \sqrt{\frac{2E_b}{ra}}$$

$$\text{Estimate of S.E. of difference between two A level means at the same level of B means} = \sqrt{\frac{2[(b-1)E_c + E_a]}{rb}}$$

Estimate of S.E. of difference between two B level means at the same level of A means =

$$\sqrt{\frac{2[(a-1)E_c + E_b]}{ra}}$$

Critical difference is obtained by multiplying the S.E.<sub>d</sub> by t<sub>5%</sub> table value for respective error d.f. for (i) & (ii). For (iii) & (iv), as the standard error of mean difference involves two error terms, we use the following equation to compute the weighted t values:

$$t = \frac{(b-1)E_c t_c + E_a t_a}{(b-1)E_c + E_a}, \text{ and } t = \frac{(a-1)E_c t_c + E_b t_b}{(a-1)E_c + E_b} \text{ respectively,}$$

where t<sub>a</sub>, t<sub>b</sub>, and t<sub>c</sub> are t-values at error d.f. (E<sub>a</sub>), error d.f.(E<sub>b</sub>) and error d.f.(E<sub>c</sub>) respectively.

### SAS input statements for the split plot experiment

```
data split plot;
input rep var nit yield;
cards;
1 1 0 15.5
1 1 1 17.5
1 1 2 20.8
1 2 0 20.5
1 2 1 24.5
1 2 2 30.2
1 3 0 15.6
1 3 1 18.2
1 3 2 18.5
2 1 0 18.9
2 1 1 20.2
2 1 2 24.5
2 2 0 15.0
2 2 1 20.5
2 2 2 18.9
2 3 0 16.0
2 3 1 15.8
2 3 2 18.3
3 1 0 12.9
3 1 1 14.5
3 1 2 13.5
3 2 0 20.2
3 2 1 18.5
3 2 2 25.4
3 3 0 15.9
3 3 1 20.5
3 3 2 22.5
4 1 0 12.9
4 1 1 13.5
4 1 2 18.5
4 2 0 13.5
```

```
4 2 1 17.5
4 2 2 14.9
4 3 0 12.5
4 3 1 11.9
4 3 2 10.5
;
proc print;
proc glm;
class rep var nit;
model yield = rep var rep* var nit var*nit;
test h = var e = rep*var;
mean var nit var*nit;
run;
```

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