CHAPTER 20

THE SPLIT-PLOT DESIGN

20.1 An alternative design for a two-factor experiment

Suppose the field plan of the 5 × 3 factorial design of Example 19.1 had been as follows:

	*B*1	*E*1	*A*1	*D*1	*C*1
Block 1	*D*2	*B*2	*C*2	*A*2	*E*2
	*A*3	*E*3	*C*3	*D*3	*B*3

	*A*3	*C*3	*E*3	*B*3	*D*3
Block 2	*D*1	*C*1	*E*1	*B*1	*A*1
	*D*2	*B*2	*E*2	*C*2	*A*2

	*E*3	*C*3	*B*3	*D*3	*A*3
Block 3	*B*2	*C*2	*E*2	*D*2	*A*2
	*E*1	*C*1	*A*1	*B*1	*D*1

	*E*1	*D*1	*C*1	*B*1	*A*1
Block 4	*E*2	*C*2	*D*2	*B*2	*A*2
	*B*3	*D*3	*E*3	*A*3	*C*3

It will be noticed that the levels of the factor "cultivation methods" are the same for all plots in any one row of any block. If this were an ordinary randomized blocks design, such a lay-out would constitute something of a freak randomization which the experimenter would probably reject (§ 12.8.8). However, the above lay-out was actually obtained under a different system of randomization, in which all treatment combinations involving the same cultivation method were restricted to appear in a single row in each block. The above is therefore not an ordinary randomized blocks design and is, in fact, a new type of design altogether.

20.2 Split plots

20.2.1 The above design could be arrived at by a two-stage process. Suppose that there is an existing design (on paper, not a field trial actually in progress) in which three methods of cultivation are to be tested in a randomized blocks design with 4 replications. (The number of Error D.F. for this design is too few, but let us ignore this point.) The plots of this design constitute the rows within each block, the boundaries of which are marked by the double lines. If now these plots are split into five in order to test 5 different varieties within each of the original plots, we have what is called a **split-plot design.** It was necessary to say in this example that the trial of the 3 cultivation methods must not already be in progress, since one variety would already have been planted and therefore could not be changed unless the experiment were to continue over more than one season. Fairly generally, however, it is possible to introduce treatments such as differential nitrogen dressings (in addition to any such dressings already included in a basal dressing) at any time during the course of an experiment, if such additional comparisons are desired.

20.2.2 Any field experiment on paper, and, provided there are no physical impediments, any field experiment in progress, can have an additional factor superimposed merely by dividing each plot (which is now termed a **whole-plot** or main plot) into a number of **sub-plots** or split-plots equal to the number of levels of the added factor. The sub-plot treatments are randomized to the sub-plots within each whole-plot so that each sub-plot treatment appears once and once only in each whole-plot, a separate randomization being carried out for each whole-plot. The randomization of treatments to the whole-plots must, of course, be that specified for the whole-plot design. In the above example methods of cultivation constitute the whole-plot factor and varieties the sub-plot factor; the whole-plot design is in randomized blocks.

20.2.3 An alternative way of looking at the split-plot design is to regard it (using the same example) as a randomized blocks design with 12 replications of 5 varieties, these 12 blocks being divided into groups of 3, within which the 3 cultivation treatments have been applied at random to whole blocks. From this point of view no plots have been split; the levels of an additional factor have been applied to whole blocks (now called whole-plots) of the original design, the plots of which are now regarded as sub-plots.

20.2.4 Clearly, the descriptions in §§ 20.2.2 and 20.2.3 amount to exactly the same thing. Nevertheless it is not necessary to regard either of the factors as "additional", and the split-plot design can be regarded simply as an alternative design for an experiment with two factors. The split-plot design is, however, much more literally "two experiments in one" than the ordinary factorial design. It even possesses, as we shall see, two distinct experimental errors.

20.3 Statistical analysis of the split-plot design

20.3.1 In line with the remark just made, the analysis of a split-plot design falls into two parts—the whole-plot analysis and the sub-plot analysis. To exemplify slightly more generally, let us assume that the whole-plot factor (A) has m levels, the whole-plot design being in randomized blocks with r replications, and that the sub-plot factor (B) has n levels. Initially, then, the Total S.S. may be partitioned on the following lines:

Table 20.1: Skeleton analysis of variance for the initial partitioning of the Total S.S. in a split-plot design with mr whole-plots and n sub-plot treatments

Source	D.F.
Between whole-plots	$mr - 1$
Within whole-plots	$mr(n - 1)$
Total	$mnr - 1$

This is, of course, the same partitioning as that of Table 10.3. Each of these two S.S.'s is now partitioned according to the respective designs of the two sections of the experiment.

20.3.2 Since each level of B appears once and once only in every whole-plot, the whole-plot and sub-plot analyses are orthogonal. Clearly, therefore, if we form total yields for each whole-plot (whole-plot totals), these can be analysed as if the sub-plot factor did not exist, except that the interpretation will be different to the extent that we are dealing with main effects of the whole-plot factor, not merely a set of whole-plot treatments. This analysis varies according to the whole-plot design.

20.3.3 In the standard split-plot design as given above, however, the type of basic analysis for the sub-plot section of the design is invariable in form. As is apparent from the randomization procedure and from the viewpoint of § 20.2.3, the whole-plots act as blocks for the sub-plot design, the analysis of which must therefore always follow that for a randomized blocks design. There is, however, a difference from the ordinary randomized blocks design, and consequently in the subsequent analysis, and this is that the "blocks" (whole-plots) have themselves been subjected to different treatments (levels of the whole-plot factor). Now the Error S.S. for a randomized blocks design is actually the Blocks × treatments interaction (§ 19.7.6) on the assumption that treatment differences do not vary from block to block—an assumption which is usually a very reasonable one, seeing that the blocks are supposed to be sited on a uniform piece of land and receive identical treatment. In the present situation, on the other hand, block (whole-plot) differences may be classified into two types, differences between whole-plots treated alike (i.e. receiving the same level of A) and differences between whole-plots receiving different levels of A. To these two types of block difference there correspond two components of the Blocks × treatment (actually whole-plots × factor B) interaction. The former gives rise to a S.S. representing pure error (on the same assumption as above), but that part of the Blocks S.S. (Whole-plot S.S.) which consists of treatment differences due to factor A gives rise to the S.S. for the interaction AB. This component is therefore separated out, and the sub-plot analysis takes the following form:

Table 20.2: Skeleton analysis of variance for sub-plot analysis in split-plot design with factors A (m levels—whole-plot factor) and B (n levels—sub-plot factor) and r replications

Source	D.F.
Blocks (whole-plots)	$mr - 1$
B	$n - 1$
AB	$(m - 1)(n - 1)$
Error	$m(n - 1)(r - 1)$
Total	$mnr - 1$

20.3.4 In this analysis the Blocks or Whole-plot S.S. will have a divisor n, since each whole-plot total is made up of n sub-plots. But the whole-plot totals give the Total S.S. for the whole-plot analysis. If, therefore, the two sections of the analysis are to be combined into a single analysis, *all the S.S.'s in the whole-plot analysis will have to be divided by an extra n* before being able to replace the Whole-plots S.S. in Table 20.2. This is the normal way of performing the analysis, which is said to be "on a sub-plot basis". What this amounts to is that *divisors are based on the number of sub-plots, irrespective of which section of the analysis the S.S. belongs to.* The whole-plot analysis is therefore carried out on whole-plot totals in exactly the same way as for any ordinary design of the same type as the whole-plot design except for this extra division by n, which affects even the C.F. and the Total S.S. The C.F. for whole-plots is then the same as for sub-plots and is used throughout the analysis. In the example where the whole-plot design is in randomized blocks the Blocks S.S. from this part of the analysis must not, of course, be confused with the "Blocks" S.S. of Table 20.2, the former being a component of the latter. The combined analysis in skeleton form is given in Table 20.3.

Table 20.3: Skeleton analysis of variance for split-plot design with whole-plot factor A (m levels), sub-plot factor B (n levels), and r replications in randomized blocks

Source		D.F.	
Blocks	whole-plots	$r - 1$	$mr - 1$
A		$m - 1$	
Error (a)		$(m - 1)(r - 1)$	
B	sub-plots	$n - 1$	$mr(n - 1)$
AB		$(m - 1)(n - 1)$	
Error (b)		$m(n - 1)(r - 1)$	
Total		$mnr - 1$	

20.3.5 *Since each section of the analysis has its own Error S.S. the split-plot design has, in fact, two Error S.S.'s*, these being conventionally designated as Error (a) and Error (b). Error (a) is the whole-plot error and represents random variability between whole-plots; Error (b) is the sub-plot error and represents random variability of sub-plots within whole-plots. The latter variability is included in the former, so that ordinarily Error (a) M.S. $>$ Error (b) M.S. Another way of looking at this is that the whole-plots act as blocks for the sub-plot design, so that Error (a) represents this block variation excluding the effects of any superimposed treatments. Since the Blocks M.S. is as a rule greater than the Error M.S., Error (a) is usually greater than Error (b).

20.3.6 Since differences between levels of A belong to the whole-plot section of the analysis, the main effects of A are subject to the whole-plot error variance (estimated by Error (a)), so that the F-test for the significance of the main effect A must be referred to Error (a). The main effect of B and the interaction AB belong to the sub-plot section of the analysis and are subject to the sub-plot error variance (estimated by Error (b)). F-tests of these effects must therefore be referred to Error (b). The above holds good provided A and B effects are both assumed fixed; otherwise some amendment is necessary (see § 20.4.5).

20.3.7 The usual partitionings of the main effects and interaction S.S.'s may be made where appropriate in the manner explained in Chapter 19, and subsequent tests of differences between individual means follow in the same way except for certain differences in S.E.'s and test procedures to be discussed in §§ 20.6 and 20.7. The manner of presenting results is otherwise similar to that followed with an ordinary factorial design.

*One difficulty which may possibly occur in the partitioning of the main effects and interactions S.S.'s is that sometimes an alternative subdivision of the combined S.S. for one main effect and the interaction is required in such a way that the two classes of effects become intermingled. Where this type of subdivision is required in a split-plot design for $B + AB$, there is no difficulty, but if the subdivision is required for $A + AB$ (A = whole-plot factor), there are difficulties owing to the different error variances. Hence, when such a subdivision is known to be required, the main effect concerned should be made the sub-plot factor. An example of such a subdivision is that it is possible to subdivide the S.S.'s for $B + AB$ into S.S.'s for the effects of B at each separate level of A. In the notation of § 19.5.3 we have the following partitioning in accordance with [10.17]:

$$\underset{\text{Treatments}}{r\sum_i\sum_j(y_{ij} - \bar{y})^2} = \underset{A}{nr\sum_i(y_{i0} - \bar{y})^2} + \underset{B + AB}{r\sum_i\sum_j(y_{ij} - y_{i0})^2}$$

The latter S.S. with $m(n - 1)$ D.F. may be calculated as m separate S.S.'s corresponding to $i = 1, 2, \ldots m$, each with $n - 1$ D.F., representing S.S.'s for the effects of B at each level of A, and each of these M.S.'s can be separately tested. A corresponding subdivision of $A + AB$ is similarly made, but in the split-plot design we run into difficulties mentioned above when trying to apply this subdivision for statistical purposes.

20.3.8 In order to illustrate the analysis of the standard split-plot design when the whole-plot design is different from the example specified in Table 20.3, we give in Tables 20.4 and 20.5 skeleton analyses of variance for designs where the whole-plot design is (i) a Latin square, (ii) a two-factor arrangement in randomized blocks.

Table 20.4: Skeleton analysis of variance where whole-plots form a Latin square of order r and the sub-plot factor (B) has n levels

Source		D.F.	
Rows	whole-plots	$r - 1$	$r^2 - 1$
Columns		$r - 1$	
A		$r - 1$	
Error (a)		$(r - 1)(r - 2)$	
B	sub-plots	$n - 1$	$r^2(n - 1)$
AB		$(r - 1)(n - 1)$	
Error (b)		$r(r - 1)(n - 1)$	
Total		$nr^2 - 1$	

Table 20.5: Skeleton analysis of variance of split-plot design where whole-plots comprise r randomized blocks with two factors, A and B, at m and n levels, and the sub-plot factor C has p levels

Source		D.F.	
Blocks	whole-plots	$r - 1$	$mnr - 1$
A		$m - 1$	
B		$n - 1$	
AB		$(m - 1)(n - 1)$	
Error (a)		$(mn - 1)(r - 1)$	
C	sub-plots	$p - 1$	$mnr(p - 1)$
AC		$(m - 1)(p - 1)$	
BC		$(n - 1)(p - 1)$	
ABC		$(m - 1)(n - 1)(p - 1)$	
Error (b)		$mn(p - 1)(r - 1)$	
Total		$mnpr - 1$	

Notice that in Table 20.5 interactions of the sub-plot factor with all whole-plot treatment components must be included in the sub-plot analysis. This is a special case of the procedure which is followed whenever the whole-plot treatments S.S. is subdivided into components.

20.3.9 Only the basic analysis of variance of the split-plot design will be illustrated by a numerical example. The rest of the analysis will then be on the same lines as in the examples of Chapter 19, except for the differences mentioned in the first paragraph of § 20.3.7, which will be explained in §§ 20.6 and 20.7. As an example we take the same plot yields as those of Example 19.1, but assume that they come from the field lay-out given in § 20.1. It will be found that most of the S.S.'s will be the same as in Example 19.1, but the full computation sheet will be given so as to make it clear where the differences lie. Attention must be directed to the remarks of § 9.8.4. The present data comprise a different set from the data of Example 19.1, even if the figures are artificially kept the same. The figures really belong to the lay-out and design of Example 19.2.

Example 20.1 On the assumption that the plot yields of Example 19.1 belong to the lay-out given in § 20.1, calculate the basic analysis of variance table for the data.

Computation sheet

(A) Treatment	Blocks 1	2	3	4	Whole-plot (C) treatment totals
1*A*	56	45	43	46	
1*B*	61	58	55	56	
1*C*	63	53	49	48	
1*D*	65	61	60	63	
1*E*	60	61	50	53	
(B) Whole-plot totals	305	278	257	266	1,106
2*A*	66	57	50	50	
2*B*	59	55	51	52	
2*C*	66	58	52	55	
2*D*	53	53	48	55	
2*E*	73	77	77	65	
(B) Whole-plot totals	317	300	278	277	1,172
3*A*	60	50	45	48	
3*B*	60	59	54	54	
3*C*	65	56	50	50	
3*D*	60	58	56	60	
3*E*	62	68	67	60	
(B) Whole-plot totals	307	291	272	272	1,142
(C) Block totals	929	869	807	815	3,420

(D) Method of cultivation	Varieties *A*	*B*	*C*	*D*	*E*	Methods totals
1	190	230	213	249	224	1,106
2	223	217	231	209	292	1,172
3	203	227	221	234	257	1,142
Variety totals	616	674	665	692	773	3,420

Whole-plot analysis (E)

C.F. = 194,940·0 (F)

Whole-plots S.S. = 195,702·8 (G)
194,940·0
762·8

S.S. Blocks = 195,578·4 (H)
194,940·0
638·4

S.S.(M) = 195,049·2 (I)
194,940·0
109·2

S.S. Error (a) = 15·2 (J)

Skeleton analysis of variance

	D.F.	
Blocks	3	whole-plots
M	2	whole-plots
Error (a)	6	whole-plots
V	4	sub-plots
MV	8	sub-plots
Error (b)	36	sub-plots
Total	59	

Sub-plot analysis **(K)**

$$\text{Total S.S.} = \begin{array}{r} 198{,}184\cdot 0 \\ 194{,}940\cdot 0 \\ \hline 3{,}244\cdot 0 \end{array}$$

$$\text{S.S.}(V) = \begin{array}{r} 196{,}029\cdot 2 \\ 194{,}940\cdot 0 \\ \hline 1{,}089\cdot 2 \end{array} \qquad \text{S.S. body of table (treatments)} = \begin{array}{r} 197{,}013\cdot 5 \\ 194{,}940\cdot 0 \\ \hline 2{,}073\cdot 5 \end{array}$$

Analysis of variance

Source	D.F.	S.S.	M.S.	*F*
Blocks	3	638·4		
M	2	109·2	54·60	21·6** **(N)**
Error (a)	6	15·2	2·53 **(P)**	
V	4	1,089·2	272·30	18·96**
MV	8	875·1 **(L)**	109·39	7·62** **(O)**
Error (b)	36	516·9 **(M)**	14·36	
Total	59	3,244·0		

S.E. of single sub-plot = 3·789 **(Q)**

$$\textbf{(R)}\ \text{C.V. (sub-plots)} = \frac{3\cdot 789}{3420} \times 60 \times 100 = 6\cdot 65\%$$

Notes on the computations

(A) The data are set down in such a way as to facilitate the calculations required in the whole-plot analysis. The treatment combinations are grouped according to levels of the whole-plot factor.

(B) Whole-plot totals are formed by adding yields of plots with the same level of the whole-plot factor within each block. The whole-plot totals comprise the yields to be analysed in the whole-plot analysis.

(C) *From the whole-plot totals* block and whole-plot treatment totals are obtained in the usual manner and checked down and across to the G.T.

(D) *The check just made is only partial, since it does not check any mistakes in calculating the whole-plot totals.* As the next step, therefore, it is best to calculate the interaction table, even though it will not be required for the whole-plot analysis. The entries in this table (which is identical with the table in Example 19.1) are treatment totals obtained as totals of the separate rows in the table above, e.g. 190 = 56 + 45 + 43 + 46. The row totals of the interaction table are totals for levels of *M* and must therefore check with the whole-plot treatment totals previously obtained. If the variety totals also check to the G.T., the checking of the totals is now complete.

(E) One may proceed to analyse the whole-plot totals as a randomized blocks design with 4 replications and 3 treatments, except that the C.F. and all S.S.'s must be divided by an extra 5, the number of sub-plots per whole-plot. It will be found that the C.F. and all S.S.'s are the same as their counterparts in Example 19.1, and one will soon become used to *basing divisors on the number of sub-plots making up the various totals*, rather than thinking about an extra divisor.

(F) $\text{C.F.} = \frac{(3{,}420)^2}{12 \times 5} = \frac{(3{,}420)^2}{60}$ (60 = total number of sub-plots in the experiment).

(G) Whole-plots S.S. = $\frac{1}{5}(305^2 + 278^2 + \cdots + 272^2) - C.F.$

Do not call this the "Total S.S." (which it is for the whole-plot analysis), since this can lead to confusion.

(H) $\frac{1}{3 \times 5}(929^2 + \cdots + 815^2) - C.F.$ Or obtain divisor from the fact that 15 sub-plots make up each block total.

(I) $\frac{1}{4 \times 5}(1{,}106^2 + 1{,}172^2 + 1{,}142^2) - C.F.$ Or obtain divisor from the fact that 20 sub-plots make up each *M* total.

(J) 15.2 = 762·8 − 638·4 − 109·2.

(K) All divisors here are based on the number of sub-plots making up a total (as is, of course, also the case for the whole-plot analysis).

(L) S.S.(MV) = S.S. Body of table − S.S.(M) − S.S.(V).

(M) By subtraction.

(N) $21 \cdot 6 = \frac{54 \cdot 60}{2 \cdot 53}$.

(O) $18 \cdot 96 = \frac{272 \cdot 30}{14 \cdot 36}$; $7 \cdot 62 = \frac{109 \cdot 39}{14 \cdot 36}$.

(P) In this example Error (*a*) M.S. is not as great as Error (*b*) M.S. (see § 20.3.5), but it must be remembered that the example is artificial and is not really a split-plot design.

(Q) $3 \cdot 789 = \sqrt{14 \cdot 36}$.

(R) There are actually two C.V.'s, one for sub-plots and one for whole-plots. Presentation of the former is usually sufficient. Should the latter be required, however, there is a trick about it in that the Error (*a*) M.S. is rightly $5 \times 2 \cdot 53$ (restoring the whole-plot basis) and that a whole-plot mean (mean of whole-plot totals) is 5 × (sub-plot mean). Hence

$$\text{C.V. for whole-plots} = \frac{\sqrt{5 \times 2 \cdot 53}}{3{,}420} \times 12 \times 100 = 1 \cdot 25\%.$$

This is exceptionally low, owing to the low Error (*a*) M.S. Nevertheless it is not unusual for the C.V. for whole-plots to be *lower* than the C.V. for sub-plots, because larger plots tend to have a lower C.V. (§ 12.11.4). The reason this can happen even though the Error (*a*) M.S. is usually the higher is that $\sqrt{\text{Error } (a) \text{ M.S.}}$ is not on a whole-plot basis and needs to be *divided* by $\sqrt{n}$ (n = no. of sub-plots per whole plot) before being expressed as a percentage of the *sub-plot* mean.

*20.3.10 There is some simplification possible in the above computations if (as is not uncommon) there are only 2 levels of the sub-plot factor. In addition to forming whole-plot totals one may form differences between the two levels of the sub-plot factor (in a consistent direction) in each whole-plot. The totals are analysed with divisor 2 as ordinarily, but the S.S. within whole-plots is the uncorrected S.S., with divisor 2, of the sub-plot differences. Since this is calculated directly, there is a check obtained by summing the S.S.'s between whole-plots and within whole-plots to the Total S.S. The C.F. for the differences is the S.S. for the main effect of the sub-plot factor. If the differences are analysed in exactly the same way as the whole-plot totals the "Treatments" S.S. of the differences is the Interaction S.S., the method being equivalent to that explained in § 19.11.2.

20.4 Statistical model for the split-plot design

20.4.1 Suppose that we have the particular design specified in § 20.3.1. Then, if y_{ijk} represents the yield associated with the k^{th} level of the sub-plot factor within the whole-plot in the j^{th} block which receives the i^{th} level of the whole-plot factor, we may take the model as

$$y_{ijk} = \mu + \rho_j + \alpha_i + \beta_k + (\alpha\beta)_{ik} + \eta_{ij} + \epsilon_{ijk}, \qquad [20.1]$$

where μ represents a component of yield common to all sub-plots, ρ_j is a component common to all sub-plots in the j^{th} block, α_i is the main effect component on a sub-plot basis of the i^{th} level of A, β_k is the similar component due to the k^{th} level of B, $(\alpha\beta)_{ik}$ is the interaction component common to all sub-plots with the i^{th} level of A and the k^{th} level of B, η_{ij} is a random component common to all sub-plots in the $(i, j)^{\text{th}}$ whole-plot, and ϵ_{ijk} is a random component peculiar to the sub-plot with the k^{th} level of B in the $(i, j)^{\text{th}}$ whole-plot. On the assumption that all treatment effects represent fixed effects we may take $\sum_i \alpha_i = \sum_k \beta_k = \sum_i (\alpha\beta)_{ik} = \sum_k (\alpha\beta)_{ik} = 0$. It is immaterial whether the block effects ρ_j are fixed or random, so long as additivity of block and treatment effects is assumed (§ 13.5.4). We further assume the η_{ij} to be N.I.D.(0, σ_w^2) and the ϵ_{ijk} to be N.I.D.(0, σ^2), the η_{ij} also being assumed independent of the ϵ_{ijk}.

20.4.2 The special feature of this model is the appearance of two random error components, η_{ij} and ϵ_{ijk}. The latter, of course, represents the random variability of sub-plot yields within a whole-plot, and has variance σ^2, the sub-plot error variance, estimated in the analysis by the Error (*b*) M.S., which we shall designate as s_b^2. The Error (*a*) M.S., designated as s_a^2, is an estimate of the error variance of a single whole-plot total yield, except that in the analysis it is divided by n (= no. of sub-plots per whole-plot). The random components in the total for the $(i, j)^{\text{th}}$ whole-plot are $n\eta_{ij} + \sum_k \epsilon_{ijk}$, η_{ij} being common to all sub-plots in this whole-plot. The error variance of a single whole-plot total is therefore $n^2\sigma_w^2 + n\sigma^2$, and hence s_a^2 is an estimate of $n\sigma_w^2 + \sigma^2$ (= σ_a^2). Equating s_a^2 to $n\sigma_w^2 + \sigma^2$ and s_b^2 to σ^2, we obtain an estimate of σ_w^2, the **whole-plot component of error variance,** as $\frac{1}{n}(s_a^2 - s_b^2)$. The whole procedure here follows very closely that described in § 10.7.4.

20.4.3 As explained in § 10.7.7, σ_w^2 cannot be negative under the present theoretical approach, so that if s_a^2 is actually less than s_b^2, it is usually assumed to be only because of sampling fluctuations, and σ_w^2 is estimated as zero. There are, however, instances when there are physical reasons why s_a^2 is less than s_b^2, e.g. when there is "competition" between sub-plot units, which could cause s_b^2 to be increased relative to s_a^2. Quenouille gives as an example an animal experiment with a number of animals per cage, the available food being limited. Here an animal is a "sub-plot" and cages are "whole-plots". If there were two animals per cage the more aggressive might dominate the other and by obtaining an unfair share of the food show a higher weight gain than the other. Differences would thereby be created between sub-plots within a whole-plot without being reflected in any extra variability between whole-plots, the totals of which would be more or less unchanged compared with a state of no competition.

20.4.4 If Example 20.1 had been a genuine split-plot design, we would have taken σ_w^2 as zero and the problems discussed in § 20.6 would not arise. In order to be able to give numerical examples of the situation when $s_a^2 > s_b^2$, *we shall henceforth assume that* s_a^2 *was* $25{\cdot}30$ *instead of* $2{\cdot}53$. The estimate of σ_w^2 is then $\frac{1}{5}(25{\cdot}30 - 14{\cdot}36) = 2{\cdot}188$. Actually the formulae for S.E.'s presented in § 20.6 are all expressed directly in terms of s_a^2 and s_b^2, so that no explicit estimation of σ_w^2 is required.

*20.4.5 If the levels of *A* represent random instead of fixed effects, then, in accordance with the arguments of § 19.12.7, the test of significance of the main effect of *B* should be made against the M.S. for the interaction *AB*. On the other hand, if the levels of *B* represent random effects, there is no M.S. immediately available for testing the main effect of *A*. This is because σ_w^2 does not appear in the expected value of the M.S. for *AB* (within whole-plots), but does in the expected value of the M.S. for *A*.

20.5 Algebraic partitioning of Total S.S. in the split-plot design.

20.5.1 The algebraic partitioning of the Total S.S. justifies the analysis of variance outlined in § 20.3. We once again use as an example the design specified in § 20.3.1, and adopt y_{ijk} as the notation for a sub-plot yield in the same manner as in § 20.4.1. Means are indicated by zero suffices in the usual way.

20.5.2 Initially we have

$$\sum_i\sum_j\sum_k(y_{ijk}-\bar{y})^2 = n\sum_i\sum_j(y_{ij0}-\bar{y})^2 + \sum_i\sum_j\sum_k(y_{ijk}-y_{ij0})^2, \qquad [20.2]$$

which represents the partitioning of the Total S.S. into that between whole-plots and that within whole-plots as in Table 20.1.

The former may be further subdivided according to the randomized blocks partitioning of [13.2] as

$$n\sum_i\sum_j(y_{ij0}-\bar{y})^2 = \overset{A}{nr\sum_i(y_{i00}-\bar{y})^2} + \overset{\text{Blocks}}{mn\sum_j(y_{0j0}-\bar{y})^2}$$
$$+ \overset{\text{Error }(a)}{n\sum_i\sum_j(y_{ij0}-y_{i00}-y_{0j0}+\bar{y})^2}. \qquad [20.3]$$

The latter may also be subdivided. Applying [10.15], we have for a particular value of k

$$\sum_i\sum_j(y_{ijk}-y_{ij0})^2 = mr(y_{00k}-\bar{y})^2 + \sum_i\sum_j(y_{ijk}-y_{ij0}-y_{00k}+\bar{y})^2,$$

and for all values of k

$$\sum_i\sum_j\sum_k(y_{ijk}-y_{ij0})^2 = \overset{B}{mr\sum_k(y_{00k}-\bar{y})^2} + \overset{\text{Residuals}}{\sum_i\sum_j\sum_k(y_{ijk}-y_{ij0}-y_{00k}+\bar{y})^2}. \qquad [20.4]$$

This residual S.S. may now be partitioned further in accordance with [19.16] as

$$\sum_i\sum_j\sum_k(y_{ijk}-y_{ij0}-y_{00k}+\bar{y})^2 = \overset{AB}{r\sum_i\sum_k(y_{i0k}-y_{i00}-y_{00k}+\bar{y})^2}$$
$$+ \overset{\text{Error }(b)}{\sum_i\sum_j\sum_k(y_{ijk}-y_{ij0}-y_{i0k}+y_{i00})^2}. \qquad [20.5]$$

Substituting in [20.2] in terms of [20.3], [20.4], and [20.5], we obtain the full partitioning.

*20.5.3 That the final S.S. does in fact represent Error (b) may be confirmed by expressing any Error (b) residual in terms of [20.1]. Thus

$$\begin{aligned} &y_{ijk}-y_{ij0}-y_{i0k}+y_{i00} \\ &= [\mu+\rho_j+\alpha_i+\beta_k+(\alpha\beta)_{ik}+\eta_{ij}+\epsilon_{ijk}] - [\mu+\rho_j+\alpha_i+\eta_{ij}+\epsilon_{ij0}] \\ &\quad -[\mu+\alpha_i+\beta_k+(\alpha\beta)_{ik}+\eta_{i0}+\epsilon_{i0k}] + [\mu+\alpha_i+\eta_{i0}+\epsilon_{i00}] \\ &= \epsilon_{ijk}-\epsilon_{ij0}-\epsilon_{i0k}+\epsilon_{i00}, \qquad \text{(the suffix 0 indicating a mean as usual)} \end{aligned}$$

and hence is a reflection solely of the random variation of sub-plots within a whole-plot.

20.6 S.E.'s of linear functions of treatment totals in the split-plot design

20.6.1 We consider the following symbolic interaction table of treatment *totals*:

Table 20.6: Treatment totals in a two-factor split-plot design with r replications

Level of B (sub-plot factor)	Level of A (whole-plot factor) a_1	a_2	$\cdots$	a_m	Totals
b_1	Y_{101}	Y_{201}	$\cdots$	Y_{m01}	Y_{001}
b_2	Y_{102}	Y_{202}	$\cdots$	Y_{m02}	Y_{002}
.	.	.	$\cdots$	.	.
.	.	.	$\cdots$	.	.
b_n	Y_{10n}	Y_{20n}	$\cdots$	Y_{m0n}	Y_{00n}
Totals	Y_{100}	Y_{200}	$\cdots$	Y_{m00}	Y

The difficulties mentioned earlier, which cause differences from a two-factor experiment not in split-plots, arise from the fact that there are two error variances. The following very simple principle is of assistance: If a pair of totals is such that their yields come from the same whole-plots, then their difference is unaffected by the whole-plot component of error variance. If, however, they cōme from different whole-plots, then the variance of their difference must involve the whole-plot component. This will be clarified in each instance by means of the statistical model, which in any case is needed for working out the appropriate variances. As a simple illustration, two totals in the same column of Table 20.6 come from the same whole-plots, but two totals in the same row come from different whole-plots (receiving different levels of the whole-plot factor). A single treatment total therefore has two S.E.'s according to the type of comparison, unless $\sigma_w^2 = 0$.

20.6.2 *Marginal totals.* S.E.'s and least significant differences may be obtained as usual except that s_a^2 must be used for levels of A and s_b^2 for levels of B. Thus

S.E. of difference of two marginal totals (levels of whole-plot factor)

$$= \sqrt{2nrs_a^2}; \qquad [20.6]$$

S.E. of difference of two marginal totals (levels of sub-plot factor)

$$= \sqrt{2mrs_b^2}. \qquad [20.7]$$

In terms of Model [20.1], two A-totals, e.g. for a_1 and a_2, may be represented as

$$Y_{100} = nr\mu + nr\alpha_1 + n\sum_j \eta_{1j} + \sum_j\sum_k \epsilon_{1jk},$$
$$Y_{200} = nr\mu + nr\alpha_2 + n\sum_j \eta_{2j} + \sum_j\sum_k \epsilon_{2jk};$$

hence

$$Y_{100} - Y_{200} = nr(\alpha_1 - \alpha_2) + n\sum_j(\eta_{1j} - \eta_{2j}) + \sum_j\sum_k(\epsilon_{1jk} - \epsilon_{2jk}),$$

with variance $2n^2r\sigma_w^2 + 2nr\sigma^2 = 2nr(n\sigma_w^2 + \sigma^2) = 2nr\sigma_a^2$. Replacing σ_a^2 by its estimate s_a^2 and taking the square root, we arrive at [20.6].

Similarly, two B-totals, e.g. for b_1 and b_2, may be represented as

$$Y_{001} = mr\mu + mr\beta_1 + \sum_i\sum_j \eta_{ij} + \sum_i\sum_j \epsilon_{ij1},$$
$$Y_{002} = mr\mu + mr\beta_2 + \sum_i\sum_j \eta_{ij} + \sum_i\sum_j \epsilon_{ij2}.$$

Here the whole-plot component of error vanishes on subtraction (since each B-total involves one sub-plot from *every* whole-plot), and

$$Y_{001} - Y_{002} = mr(\beta_1 - \beta_2) + \sum_i \sum_j (\epsilon_{ij1} - \epsilon_{ij2}),$$

with variance $2mr\sigma^2$. Hence we obtain [20.7].

20.6.3 *Difference of two treatment totals with the same level of the whole-plot factor.* Such a comparison is between two totals in the same column of Table 20.6, and clearly cannot involve the whole-plot component of variance. Taking Y_{i01} and Y_{i02} as an example, we have in terms of [20.1]:

$$Y_{i01} = r\mu + r\alpha_i + r\beta_1 + r(\alpha\beta)_{i1} + \sum_j \eta_{ij} + \sum_j \epsilon_{ij1}$$

$$Y_{i02} = r\mu + r\alpha_i + r\beta_2 + r(\alpha\beta)_{i2} + \sum_j \eta_{ij} + \sum_j \epsilon_{ij2}$$

The difference $Y_{i01} - Y_{i02} = r[\beta_1 - \beta_2 + (\alpha\beta)_{i1} - (\alpha\beta)_{i2}] + \sum_j (\epsilon_{ij1} - \epsilon_{ij2})$, which has variance $2r\sigma^2$. We therefore have:

S.E. of difference of two treatment totals with same level of whole-plot factor

$$= \sqrt{2r.s_b^2} \qquad [20.8]$$

20.6.4 *Difference of two treatment totals with the same level of the sub-plot factor.* Such a comparison is between two totals in the same row of Table 20.6, and must involve the whole-plot component of variance. Taking Y_{10k} and Y_{20k} as an example, we have in terms of [20.1]:

$$Y_{10k} = r\mu + r\alpha_1 + r\beta_k + r(\alpha\beta)_{1k} + \sum_j \eta_{1j} + \sum_j \epsilon_{1jk}$$

$$Y_{20k} = r\mu + r\alpha_2 + r\beta_k + r(\alpha\beta)_{2k} + \sum_j \eta_{2j} + \sum_j \epsilon_{2jk}$$

The difference

$$Y_{10k} - Y_{20k} = r[\alpha_1 - \alpha_2 + (\alpha\beta)_{1k} - (\alpha\beta)_{2k}] + \sum_j (\eta_{1j} - \eta_{2j}) + \sum_j (\epsilon_{1jk} - \epsilon_{2jk}), \qquad [20.9]$$

which has variance

$$2r\sigma_w^2 + 2r\sigma^2 = 2r(\sigma_w^2 + \sigma^2). \qquad [20.10]$$

Since, as explained in § 20.4.2, σ_w^2 is estimated from the analysis as $\frac{1}{n}(s_a^2 - s_b^2)$, the variance of $Y_{10k} - Y_{20k}$ is estimated as

$$2r\left\{\frac{1}{n}(s_a^2 - s_b^2) + s_b^2\right\} = \frac{2r}{n}\left\{s_a^2 + (n-1)s_b^2\right\}.$$

Hence

S.E. of difference of two treatment totals with same level of sub-plot factor

$$= \sqrt{\frac{2r}{n}\left\{s_a^2 + (n-1)s_b^2\right\}}. \qquad [20.11]$$

This same S.E. with the factor 2 deleted and with r as divisor instead of multiplier will apply to a single treatment mean standing on its own, e.g. if fiducial limits are required.

20.6.5 *Difference of two treatment totals without a level of either factor in common,* e.g. $Y_{101} - Y_{202}$. In terms of [20.1]

$$Y_{101} = r\mu + r\alpha_1 + r\beta_1 + r(\alpha\beta)_{11} + \sum_j \eta_{1j} + \sum_j \epsilon_{1j1},$$

$$Y_{202} = r\mu + r\alpha_2 + r\beta_2 + r(\alpha\beta)_{22} + \sum_j \eta_{2j} + \sum_j \epsilon_{2j2}.$$

The difference $Y_{101} - Y_{202}$

$$= r[\alpha_1 - \alpha_2 + \beta_1 - \beta_2 + (\alpha\beta)_{11} - (\alpha\beta)_{22}] + \sum_j (\eta_{1j} - \eta_{2j}) + \sum_j (\epsilon_{1j1} - \epsilon_{2j2}),$$

which has the same variance as that given by [20.10]. Hence [20.11] provides the S.E. for this case as well.

*20.6.6 *Difference of linear functions at two different levels of the whole-plot factor*, e.g.

$(\lambda_1 Y_{101} + \lambda_2 Y_{102} + \cdots + \lambda_n Y_{10n}) - (\lambda_1 Y_{201} + \lambda_2 Y_{202} + \cdots + \lambda_n Y_{20n})$.

We may rewrite this as

$$\lambda_1(Y_{101} - Y_{201}) + \lambda_2(Y_{102} - Y_{202}) + \cdots + \lambda_n(Y_{10n} - Y_{20n}) = \sum_k \lambda_k(Y_{10k} - Y_{20k}), \qquad [20.12]$$

which in terms of [20.1] contains error components

$$(\sum_k \lambda_k)\{\sum_j (\eta_{1j} - \eta_{2j})\} + \sum_j \sum_k \lambda_k(\epsilon_{1jk} - \epsilon_{2jk}). \qquad [20.13]$$

This can be seen from [20.9], if it is borne in mind that the part involving the η_{ij} is the same for all values of k in [20.12]. The variance of [20.13] and hence of [20.12] is

$$(\Sigma\lambda)^2\, 2r\sigma_w^2 + (\Sigma\lambda^2)2r\sigma^2 = 2r\{(\Sigma\lambda)^2\sigma_w^2 + (\Sigma\lambda^2)\sigma^2\}.$$

In the analysis this is estimated by

$$2r\{(\Sigma\lambda)^2\left[\frac{s_a^2 - s_b^2}{n}\right] + (\Sigma\lambda^2)s_b^2\} = \frac{2r}{n}\{(\Sigma\lambda)^2 s_a^2 + [n(\Sigma\lambda^2) - (\Sigma\lambda)^2]s_b^2\},$$

giving the required S.E.:

$$\sqrt{\frac{2r}{n}\{(\Sigma\lambda)^2 s_a^2 + [n(\Sigma\lambda^2) - (\Sigma\lambda)^2]s_b^2\}} \qquad [20.14]$$

Formula [20.6] may be obtained from this by putting all the λ_k equal to 1, so that $\Sigma\lambda = n = \Sigma\lambda^2$; the term involving s_b^2 in [20.14] then vanishes. Formula [20.11] may also be obtained from [20.14] by putting one value of λ equal to 1 and all the others zero, so that $\Sigma\lambda = \Sigma\lambda^2 = 1$.

A special case of some interest is where a mean of the totals of any p levels of B in any one column of Table 20.6 is compared with the corresponding mean for the same levels of B in another column, e.g. $\frac{1}{3}(Y_{101} + Y_{102} + Y_{103}) - \frac{1}{3}(Y_{201} + Y_{202} + Y_{203})$. Here we put p of the λ's equal to $1/p$ and the rest zero, so that $\Sigma\lambda = p(1/p) = 1$ and $\Sigma\lambda^2 = p(1/p^2) = 1/p$, and [20.14] becomes

$$\sqrt{\frac{2r}{n}(s_a^2 + \frac{n-p}{p} s_b^2)}. \qquad [20.15]$$

If we put p equal to 1 in this, we obtain [20.11].

With the factor 2 deleted [20.14] gives the correct S.E. for a single linear function of treatment totals at any one level of the whole-plot factor, e.g. $\lambda_1 Y_{101} + \lambda_2 Y_{102} + \cdots + \lambda_n Y_{10n}$. Likewise for the special case covered by [20.15].

20.6.7 An additional special case of more importance is when $\Sigma\lambda = 0$. Formula [20.14] then reduces to

$$\sqrt{2r(\Sigma\lambda^2) . s_b^2}, \qquad [20.16]$$

which is clearly correct since any difference of sub-plots within a whole-plot does not involve the whole-plot component of error. Deletion of the factor 2 gives the S.E. for a single linear function in this special case, of which [20.8] is the simplest example.

20.6.8 *Difference of linear functions at two different levels of the sub-plot factor*, e.g.

$(\lambda_1 Y_{101} + \lambda_2 Y_{201} + \cdots + \lambda_m Y_{m01}) - (\lambda_1 Y_{102} + \lambda_2 Y_{202} + \cdots + \lambda_m Y_{m02})$.
Rewriting this as

$$\lambda_1(Y_{101} - Y_{102}) + \lambda_2(Y_{201} - Y_{202}) + \cdots + \lambda_m(Y_{m01} - Y_{m02}),$$

we see from § 20.6.3, that no whole-plot error component enters any of the bracketed terms. The S.E. for this comparison is therefore

$$\sqrt{2r(\Sigma\lambda^2)s_b^2}, \qquad [20.17]$$

the same as [20.16], but this coincidence is only when $\Sigma\lambda = 0$. By putting all the λ's equal to 1 in [20.17] ($\Sigma\lambda^2 = m$), we obtain [20.7].

There is a special case similar to that discussed in the second paragraph of § 20.6.6 which is of some interest, namely the S.E. for the comparison of the mean of the totals of any q levels of A in any one row of Table 20.6 with the corresponding mean for the same levels of A in another row, e.g.

$$\tfrac{1}{3}(Y_{101} + Y_{201} + Y_{301}) - \tfrac{1}{3}(Y_{102} + Y_{202} + Y_{302}).$$

In this case each $\lambda = 1/q$, so that $\Sigma\lambda^2 = 1/q$ and [20.17] becomes

$$\sqrt{\frac{2r}{q}s_b^2}. \qquad [20.18]$$

If we put q equal to 1 in this, we obtain [20.8].

20.6.9 *Linear function of treatment totals at any single level of the sub-plot factor*, e.g. $\lambda_1 Y_{101} + \lambda_2 Y_{201} + \cdots + \lambda_m Y_{m01}$. This time deletion of the factor 2 in [20.17] does not provide the correct S.E. From § 20.6.4 we see that each term in the linear function contains distinct components of whole-plot error, and hence the variance of the linear function is

$$r(\Sigma\lambda^2)(\sigma_w^2 + \sigma^2) \qquad [20.19]$$

The S.E. is therefore

$$\sqrt{\frac{r\Sigma\lambda^2}{n}\{s_a^2 + (n-1)s_b^2\}}. \qquad [20.20]$$

In practice this is only likely to be useful when $\Sigma\lambda = 0$; [20.11] is a special case of this.

20.6.10 All the formulae for S.E.'s given in this section can easily be put in terms of treatment means. For [20.6] and [20.7], the given S.E.'s must be divided by nr and mr respectively (so that these now appear as divisors instead of multipliers under the root sign). All the other formulae for S.E.'s must be divided by r to give the corresponding formula for means, i.e. r must be changed from a multiplier to a divisor under the root sign.

20.6.11 If s_a^2 is less than s_b^2, we take $\sigma_w^2 = 0$, i.e. we put $s_a^2 = s_b^2$ in all formulae where s_a^2 appears, and the S.E.'s all reduce to those of an ordinary two-factor experiment without split-plots with s_b^2 as the Error M.S.

20.6.12 Numerical applications to Example 20.1 would consist only of straightforward applications of [20.6] and [20.7], and, on the assumption that $s_a^2 = 25{\cdot}30$ (see § 20.4.4), of [20.8] and [20.11]. These are the only S.E.'s which ordinarily need to be presented with the interaction table, and usually the factor 2 is dropped to give the S.E.'s of single marginal means and single means in the body of the interaction table. In the latter case [20.8] provides an effective S.E. only, and so it must be stipulated which S.E. applies to comparisons in the same row and which to comparisons in the same column, of the table.

An example of the use of [20.17] and [20.20] would occur if the whole-plot factor of Example 20.1 were actually 3 equally spaced levels of a factor S and it were desired to present values of S' for each variety as in the presentation of results given with Example 19.2. Here the linear function would be determined by coefficients $[-1 \quad 0 \quad 1]$, so that $\Sigma\lambda^2 = 2$. The S.E. for the difference of S' (as obtained from treatment totals) for any two varieties would be, from [20.17], $\sqrt{2 \times 4 \times 2 \times 14{\cdot}36} = 15{\cdot}16$. The S.E. for a value of S' (as obtained from treatment totals) for any single variety would be, from [20.20] (which actually reduces to [20.11] in this case),

$$\sqrt{\frac{4 \times 2}{5}\{25.30 + (4 \times 14.36)\}} = 11.51.$$

The S.E. for the difference is less than $\sqrt{2 \times 11.51}$ because of the whole-plot component of error variance. In presenting results these S.E.'s would be divided by $\Sigma\lambda^2$ and multiplied by the appropriate conversion factor (cf. Example 19.2, Note K).

An example of the application of [20.16] can be given if we assume that 3 of the varieties were of one type and 2 of another, so that it were desired to evaluate the linear function determined by coefficients $[\,2 \quad 2 \quad 2 \; -3 \; -3]$ for each level of M. Here $\Sigma\lambda = 0$, $\Sigma\lambda^2 = 30$. Hence, as explained in § 20.6.7, the S.E. of this linear function for a single level of M would be

$$\sqrt{4 \times 30 \times 14.36} = 41.51.$$

The S.E. of the difference for any two levels of M would be $\sqrt{2}$ times this ([20.16]).

20.7 Tests of significance for linear functions of treatment totals or means in the split-plot design

20.7.1 Where the S.E. of the linear function to be tested involves only s_a^2 or s_b^2 (e.g. [20.6], [20.7], [20.8], [20.16], [20.17], and [20.18]), the usual t-test is made with the D.F. of s_a^2 $(=f_a)$ when [20.6] is used, or with the D.F. of s_b^2 $(=f_b)$ in all the other instances.

20.7.2 Where the S.E. involves both s_a^2 and s_b^2, there is doubt whether to make the test with f_a D.F. or f_b D.F. Actually, the ratio of the linear function to its S.E. does not in general follow the t-distribution in a case like this where the S.E. is a combination of two estimates of variance. However, if we continue to regard the ratio as a t-ratio we can allot it a number of D.F. in such a way that a close approximation to the exact test can be made using the t-tables.

20.7.3 Formulae have been given for working out this approximate number of D.F., which always lies between f_a and f_b. Looking at this in a different way, we see that we require a least significant value of t which lies between that for f_a D.F. and that for f_b D.F., and Cochran and Cox give a formula of this type. If the least significant values of t are t_a (f_a D.F.) and t_b (f_b D.F.) for a given level of significance, and if the S.E. is $\sqrt{k_a s_a^2 + k_b s_b^2}$, then the required least significant value of t is given by

$$t' = \frac{k_a s_a^2 t_a + k_b s_b^2 t_b}{k_a s_a^2 + k_b s_b^2}. \qquad [20.21]$$

This is a weighted mean of t_a and t_b. In practice k_a and k_b need not be the actual coefficients of s_a^2 and s_b^2, but only two quantities in the same ratio as the coefficients. Thus, with [20.11] we can take $k_a = 1, k_b = n - 1$; there is no need to take $k_a = \frac{2r}{n}$ and $k_b = \frac{2r(n-1)}{n}$, since the factor $\frac{2r}{n}$ cancels in [20.21]. This test gives an approximation which errs on the conservative side, i.e. the level of significance is really slightly higher than the ostensible 5% or 1% level.

20.7.4 Since t' as given by [20.21] always lies between t_a and t_b and since f_a is always less than f_b in the split-plot design, *there is most often no need to use [20.21] at all.* For example, if the ratio of the linear function to its S.E. exceeds t_a, then it must also exceed t', and the result is significant; likewise, if the ratio is less than t_b, then it must also be less than t', and the result is non-significant. It is only in border-line cases where the test is non-significant with f_a D.F. and significant with f_b D.F. that [20.21] need be used.

*20.7.5 *The Fisher-Behrens or d-test.* This is the exact test for the situation described in § 20.7.2. Suppose a linear function to be tested has S.E. $\sqrt{k_a s_a^2 + k_b s_b^2}$. Then the ratio of the linear function to its S.E. is formed. It is exactly the same as an ordinary t-ratio, but here it is called d. In addition, an auxiliary quantity θ must be evaluated from $\tan^2\theta = \frac{k_a s_a^2}{k_b s_b^2}$, i.e. $\theta = \tan^{-1}\sqrt{\frac{k_a s_a^2}{k_b s_b^2}}$, where θ is in degrees and lies between 0° and 90°. Fisher and Yates (Table V) give the least significant values of d for various values of θ, n_1, and n_2, where $n_1 = f_a$ and $n_2 = f_b$. Since this is a triple-entry table, only a few values of θ, f_a, and f_b can be given, but only seldom will the issue be in doubt. If this test is used, it should be used in conjunction with the quick method described in § 20.7.4.

20.7.6 The Fisher-Behrens test is the test referred to in § 9.7.7. It must be stated that there is considerable controversy as to the correctness or otherwise of the theoretical basis of the test. The approximate test of § 20.7.3 could also be used.

20.7.7 To exemplify the above tests, let us assume that in Example 20.1 there is reason for testing Variety A with Method 3 against Variety B with Method 1. The difference of their treatment totals is 27. The appropriate S.E. is given by [20.11] (as explained in § 20.6.5), and this was worked out in § 20.6.12 as 11.51. We therefore have $t = \frac{27}{11 \cdot 51} = 2 \cdot 35$ which is less than $t_{\cdot 01}$ (36 D.F.) and so cannot be significant at the 1% level, but which is not quite as high as $t_{\cdot 05}$ (6 D.F.). Significance at the 5% level is therefore in doubt.

By the approximate method (using a rough interpolation for t with 36 D.F.)

$$t' = \frac{(25 \cdot 30 \times 2 \cdot 447) + (4 \times 14 \cdot 36 \times 2 \cdot 028)}{25 \cdot 30 + 4 \times 14 \cdot 36} = 2 \cdot 16,$$

and so the difference is significant.

*Using the Fisher-Behrens test we have $d = 2 \cdot 35$ as before. Also $\tan^2 \theta = \frac{25 \cdot 30}{4 \times 14 \cdot 36} = 0 \cdot 44$, $\tan \theta = 0 \cdot 66$, $\theta = 34°$. In Fisher and Yates, Table V, we find the following adjacent entries for $n_1 = 6$ (D.F. of s^2), which luckily happens to be one of the values in the table:

	$\theta = 30°$	$\theta = 45°$
$n_2 = 24$	2·156	2·247
$n_2 = \infty$	2·082	2·201

Since the observed value of d is higher than the least favourable of these ($n_2 = 24$, $\theta = 45°$), it is clearly significant at the 5% level. The possibility of significance at the 1% level has already been ruled out, and this is borne out by the d-tables since the lowest of the corresponding four tabular values at this level is 2·803.

20.8 Comparison of the split-plot design and an ordinary factorial experiment in respect of efficiency

20.8.1 It is intuitively obvious (with one proviso) that there is no difference in over-all efficiency (in respect of estimation of main effects and interaction) between a split-plot design with the whole-plots in randomized blocks and a factorial experiment in ordinary randomized blocks. For the same number of replications the number of plots (or sub-plots) is the same, and the difference between the two designs merely amounts to a reshuffling of the same resources. In the split-plot design, however, the number of D.F. for error has to be dispersed over two Error M.S.'s and this does cause a loss of efficiency.

20.8.2 In a split-plot design with factors A (whole-plot) and B (sub-plot), since Error (a) is based on fewer D.F. than Error (b) and is usually larger than Error (b), the main effect of A is less precisely estimated than the main effect of B and the interaction AB. Relative to a randomized blocks design with the same sub-plots as plots, therefore, there is a loss of efficiency in respect of the main effect of A and a probable gain in efficiency in respect of the main effect of B and the interaction.

*20.8.3 It is sometimes said that the loss of efficiency on the whole-plot factor is because there are fewer replications of the whole-plot factor and the whole-plot error is higher. This is not, however, correct. It is true that, if we consider the whole-plot analysis carried out *on a whole-plot basis*, then, in the notation of § 20.3.1, there are only r replications of the whole-plot factor, compared with mr replications of the sub-plot factor. However, the variance of a whole-plot treatment mean is not then $\frac{\sigma_a^2}{r}$, but $\frac{n\sigma_a^2}{r}$ (restoring the division by n), which is, of course, larger, but which must be considered in relation to a mean of the order $n\bar{y}$, where $\bar{y}$ is the sub-plot mean. The ratio of mean to S.D. is then of the order $n\bar{y} \div \sqrt{\frac{n\sigma_a^2}{r}} = \bar{y} \div \sqrt{\frac{\sigma_a^2}{nr}}$, or in other words the number of replications is effectively nr. This merely confirms the formula for the S.E. of a whole-plot treatment mean, viz. $\sqrt{\frac{s_a^2}{nr}}$, given in § 20.6.10, and we see that in effect, the difference in the number of replications of the two factors depends only on the numbers of levels of each as in an ordinary factorial experiment. From another point of view, if we accept that A has fewer replications than B, then the ratio of mean to S.D. given above may be written as $\bar{y} \div \sqrt{\frac{\sigma_a^2/n}{r}}$. But if, as is not uncommon (see Example 20.1, Note R), the C.V. of the whole-plots is smaller than the C.V. of the smaller sub-plots, i.e. $\frac{\sqrt{n\sigma_a^2}}{n\bar{y}} < \frac{\sqrt{\sigma_b^2}}{\bar{y}}$ (cf. Example 20.1, Note R), then $\frac{1}{n}\sigma_a^2$, the comparable error variance if the number of replications of the whole-plot factor is regarded as r, is *less than* σ_b^2. We cannot, therefore, speak simultaneously of fewer replications and higher error, except only in so far as by the former we imply fewer D.F. for Error (a).

20.8.4 In assessing the relative efficiency of the split-plot and the ordinary factorial, a point to remember is that with the former it may be possible to have a Latin square for the whole-plot design (§ 20.3.8), whereas with the latter a Latin square may be impossible owing to the number of treatment combinations. In this event the greater efficiency of the Latin square design may contribute to a reduction of the difference between Error (a) and Error (b) and so cause the loss of efficiency on the main effect of A to be diminished, although, of course, the D.F. available for Error (a) will be reduced.

20.9 Usefulness of the split-plot design

20.9.1 The split-plot design tends to enjoy a popularity which it does not really deserve. It is a "lazy man's design" in the sense that it is the easiest thing in the world to introduce an additional factor into any design at the planning stage merely by splitting the plots of the existing design. There is also a tendency in these circumstances for the planner to delude himself into believing that the number of plots in the design is the number of whole-plots, and that somehow the work is going to be reduced in comparison with an ordinary factorial experiment, whereas, of course, the number of plots is the number of sub-plots.

20.9.2 *When an experiment is already in progress*, the split-plot design offers a method of bringing an additional factor into the design, provided there is no difficulty of the type mentioned in § 20.2.1. The additional factor may be applied by splitting the existing plots or by applying the treatments to whole blocks (if the original design is in randomized blocks). With the former method the number of levels will be limited by the size of the original plots, or else the sub-plots will be too small; hence, unless the original plots are over-large, it is unlikely that the number of levels of the added factor could be more than 2 or 3. A similar limitation applies to the latter method, since the number of blocks in the original experiment will usually be moderate. The choice of method will then depend on the importance of the added factor. The method of splitting the plots means that the additional factor becomes the sub-plot factor and so will be more precisely estimated than the original factor or factors; also the number of units in the experiment (though not the area) is multiplied by the number of levels of the added factor. If the extra factor is such that the interest lies not so much in its main effects but in its differential effects at the various levels of the original factor or factors, then the second method may be preferred; the whole-plot factor will be insufficiently replicated and there will be too few D.F. for Error (*a*), but this will be immaterial. In any case, except when some of the added treatments are so extreme as to cause failure or near-failure of the crop, little is lost from the original experiment either way, and it is obvious that there are limited possibilities, so that it is unlikely that a perfect arrangement can be achieved. The two methods given here do not exhaust all the possibilities as regards adding a factor, however.

20.9.3 *When the experiment is not actually in progress*, a calculated choice must be made between a split-plot design and a randomized blocks design, and in view of the facts of the efficiency comparison made in § 20.8, there should be some definite reason if a split-plot design is to be preferred. This applies even when the plan of an experiment has already been drawn up and the addition of an extra factor is suggested. Here physical difficulties caused by the size of the existing plots may no longer be a limitation, but even so the temptation to add the factor in the easy way by splitting plots should be resisted. It is rather unlikely that a last-minute factor of this sort would warrant the privilege of being applied as a sub-plot factor. Rather must the experiment as a whole be planned *de novo*, and a decision whether or not to use a split-plot design made on the basis of reasons given in the rest of this section.

20.9.4 The preference for a split-plot design should be based either on convenience or, bearing in mind the loss of information on the whole-plot factor, on a decision to sacrifice this information for the sake of added precision on the main effect of the sub-plot factor and on the interaction. These two considerations may apply singly, or, if both are applicable, they may both indicate a split-plot design or they may be incompatible.

20.9.5 Under the heading of *convenience* (not laziness!) the main point is that certain types of treatment are troublesome to apply to very small areas and may therefore be allocated to whole-plots. Cultivation treatments (especially when machinery is involved), irrigation treatments, burning treatments on pastures, etc. are examples of factors of this sort. In Example 20.1, which was a fictitious example artifically created from the data of Example 19.1 (itself partly fictitious), the cultivation methods were made the whole-plot factor for purposes of verisimilitude!

Sometimes a type of treatment requires plots of such large area that a split-plot design is not merely a convenience but the only possibility, e.g. irrigation treatments under the border-dyke system.

*Then with very complex factorial experiments of a type not discussed in this book, suitable designs do not always exist for a given number of factors with the desired levels, and the answer may lie in a split-plot design for no other reason.

Some examples from experiments other than field experiments are given in § 20.11.

20.9.6 *As regards the sacrifice of information on the whole-plot factor*, this may be justifiable in the following instances, in which case the adoption of a split-plot design is indicated:

(1) There may be no real interest in the main effect of one of the factors, but only in its interactions with other factors. The factor concerned should, of course, be allocated to the whole-plots. An illustration is provided by the factor "witchweed infestation" in Example 19.3 (cf. Note W attached to the computation sheet). This experiment would have been well suited to a split-plot design. Another example is when "disease *versus* control" is introduced as a factor into an experiment by deliberately inoculating half the plots with the disease. In this case there is usually no interest in the main effect of the disease factor.

(2) One of the factors may be such that its main effects are expected to be relatively large. Such a factor can be allocated to whole-plots.

(3) There may be more interest in one factor than another, the less important factor being applied to whole-plots. Unfortunately, it is quite possible for the more interesting factor to be such that it can only be conveniently applied to whole-plots. Apart from a forced decision of this type, it is illogical to complain about obtaining large, but non-significant, main effects of the whole-plot factor.

20.9.7 Except when there is no interest in the main effect of the whole-plot factor, care must be taken that the design provides the minimum number of D.F. (12) for Error (*a*). In order to achieve this in an experiment of moderate size, the number of levels of the sub-plot factor is usually kept small.

20.10 Field lay-out

20.10.1 Since the whole-plots in the standard split-plot design act as blocks, the principles applied in determining a lay-out for a randomized blocks design (§ 13.9) apply here. Still more is it necessary to try and avoid excessive differences between blocks (whole-plots) since such differences contribute to Error (a).

20.10.2 Obviously there will be compromises in respect of size and shape of whole-plots and sub-plots, with the sub-plots from the nature of things being usually favoured. For example, in the presence of a known fertility gradient it will be impracticable to have long narrow whole-plots parallel to the gradient subdivided into shorter narrow or long narrower sub-plots. In such a case the whole-plot would usually be made fairly square. Where a fertility gradient of uncertain direction is expected, sub-plots may be made squarish and built up into fairly square whole-plots also, provided the number of levels of the sub-plot factor is small.

20.11 Generality of the split-plot design

The idea of splitting the experimental units into sub-units is a very common one in a wide variety of fields of application, apart from agricultural field experiments. It is sometimes called the "split-unit" design. An example is the subdivision of samples of butter prepared by different methods into sub-samples for testing various systems of storage. This illustrates the particular suitability of the split-plot design when the factors are applied in a natural sequence. Another example of treatments applied in sequence, but where the split-plot principle is differently applied, is when only a limited number of experimental units can be treated in one day (e.g. owing to limitations of apparatus) so that a complete replicate in a factorial experiment cannot be tested in a single day. If day-to-day variation contributes to error variation, days could be made whole-plots in the experiment and a less important factor applied to whole-plots, i.e. the levels of this factor would be changed daily according to some random design but kept constant for all treatments on a single day.

*20.12 The analysis of covariance with the split-plot design

20.12.1 Some difficulty arises because of the two error regressions. However, the tests of significance of the main effects and interactions of the adjusted treatment means are performed as usual in the manner explained in § 18.4.8, but for each section of the analysis separately. Thus, to test the main effect of the whole-plot factor (A), one forms a line "Main effect A + Error (a)", but for testing the main effect of the sub-plot factor (B) and interaction, one forms lines "Main effect B + Error (b)" and "Interaction AB + Error (b)".

20.12.2 The difficulty arises with the calculation of the adjusted means themselves. Different procedures are followed according as the whole-plot and sub-plot error regressions are the same or not. One might expect these two regressions to be similar, since in field experiments, at least, only a difference of plot size would seem to be involved, but it is found surprisingly often that they differ significantly. The same applies to the blocks and error regressions in a randomized blocks design (cf. § 18.9.2). A test of significance of the two regressions may be made by the methods of § 20.7, the variance of the difference of the two regression coefficients being estimated as

$$\frac{\text{Reduced error}\,(a)\text{ M.S.}}{\text{S.S.}(x)\text{ for Error }(a)}+\frac{\text{Reduced error}\,(b)\text{ M.S.}}{\text{S.S.}(x)\text{ for Error }(b)}.$$

20.12.3 If the two regressions are not significantly different, the treatment means may be adjusted with the aid of the sub-plot regression coefficient. This ignores the information on the presumed common regression coefficient supplied by the whole-plot coefficient, but any alternative is too complicated.

20.12.4 If the two regressions differ significantly, and if adjustments to whole-plot treatment means are made by the whole-plot regression and adjustments to individual treatment means by the sub-plot regression, there will be the awkward situation that in the adjusted interaction table the whole-plot treatment means adjusted by the whole-plot regression will not be equal to the corresponding marginal means of the individual means adjusted by the sub-plot regression. This can be avoided by using the following formula for adjusted means,

$$y_{iok} - b_w(x_{ioo} - \bar{x}) - b(x_{iok} - x_{ioo}),$$

where the notation is that of § 20.5 and Chapter 18, and b_w and b are, respectively, the whole-plot and sub-plot error regression coefficients. With this formula b does not enter into comparisons of whole-plot main effects and b_w does not enter into comparisons of sub-plot main effects. There are, however, some awkward S.E.'s for comparisons of the type discussed in §§ 20.6.4 and 20.6.5, for example.

20.13 Some variants of the split-plot design

20.13.1 *The split-split-plot design.* Any split-plot design can have a further factor added by introducing an additional stage of splitting, i.e. the sub-plots are split into sub-sub-plots and the levels of the extra factor are randomized over the sub-sub-plots within each sub-plot. In theory there is nothing to prevent an extension of this process, so that after a third stage of splitting we would have a split-split-split-plot design with sub-sub-sub-plots as the ultimate experimental units, and so on. One may even write of a split^3-design with sub^3-plots! In practice designs with more than two stages of splitting would be very rarely appropriate, since each stage would have to be justified on the lines indicated in § 20.9.3 or § 20.11. The experimenter who lazily splits plots for every factor in his experiment will have a design with as many Error M.S.'s as there are splits, and a series of S.E.'s even more awkward than those discussed in § 20.6.

*20.13.2 *The split-plot design with sub-plot treatments in a Latin square.* In this design (which is, of course, entirely different from that illustrated by Table 20.4) there must be as many replications as there are levels of the sub-plot factor. Let us suppose as an example that there are 4 replications and that there are 4 levels of the sub-plot factor. Then for the four whole-plots which receive a particular level of the whole-plot factor, each level of the sub-plot factor must occupy the first, second, third, and fourth positions within a whole-plot once and once only. In other words, the arrangement of the levels of the sub-plot factor within any set of whole-plots receiving the same level of the whole-plot factor is a 4 × 4 Latin square. The whole-plot design can be of any sort provided the number of replications complies with the condition stated above. The whole-plot design is randomized in the normal way, and for any set of whole-plots with the same treatment the sub-plot treatments are allocated to sub-plots by a Latin-square randomization. In the analysis a number of D.F. equal to (No. of replications) × (D.F. for sub-plot main effect) must be set aside for elimination of variability due to position of sub-plot within whole-plots, the design being suitable in circumstances when a regular trend (e.g. fertility gradient) is anticipated within whole-plots. The analysis is somewhat similar to that for repeated Latin squares (§ 14.8.5). A further variant of the design is when the number of replications is some multiple of the number of levels of the sub-plot factor.

20.13.3 Putting together the design just discussed and the idea of applying treatments to whole blocks in a randomized blocks design (§ 20.2.3), the student may come up with the idea of applying treatments to whole rows or columns of a Latin square design. This is, however, something different again, and must in general be avoided because it results in non-orthogonality between the interaction of the two factors concerned and columns or rows, respectively.

20.13.4 *The strip design.* If in a split-plot design the sub-plot treatments are not separately randomized for each whole-plot, but are randomly allocated to strips of sub-plots cutting across each replication, we have what is called a **strip design**, variously called the "strip-plot", "criss-cross", or "split-block" design. The first is to be preferred, the levels of each factor forming strips at right-angles across each block. This is illustrated in the diagram:

*B*1	*E*1	*A*1	*D*1	C1
*B*2	*E*2	*A*2	*D*2	*C*2
*B*3	*E*3	*A*3	*D*3	*C*3

*A*3	*C*3	*E*3	*B*3	*D*3
*A*1	*C*1	*E*1	*B*1	*D*1
*A*2	*C*2	*E*2	*B*2	*D*2

Figure 20.1: Two replications of a strip design with two factors in randomized blocks.

There are here two types of whole-plot corresponding to the two factors, the levels of each factor being separately randomized in each block. This is a valid design and has a use when it is convenient to apply both factors to large areas. However, corresponding to the three types of unit (2 types of whole-plot and sub-plots) there are three error terms, one for each main effect and one for the interaction, and these three errors can give rise to some awkward S.E.'s in some types of comparison.

EXERCISES

20.1 The following yields of hay (dry weight in lb.) are from an experiment on permanent grass plots. The treatments were P_0 = no phosphate, P_1 = superphosphate, P_2 = mineral phosphate, P_3 = low soluble slag, P_4 = high soluble slag (P_1, P_2, P_3, P_4 in equivalent quantities), K = muriate of potash. Analyse and express results in cwt. per acre. The size of a whole-plot = 1/15 acre; 1 cwt. = 112 lb. (Data from Rothamsted Report, 1931, page 166)

P_4K 117·2	P_3K 104·7	P_2 86·3	P_0 76·7	P_1 94·4
P_4 104·7	P_3 102·5	P_2K 98·8	P_0K 88·5	P_1K 106·9
P_2K 123·1	P_4K 120·9	P_0 97·3	P_1K 112·6	P_3K 101·0
P_2 117·2	P_4 107·6	P_0K 99·5	P_1 108·4	P_3 97·3
P_1K 126·2	P_0K 117·2	P_3 115·6	P_2K 120·9	P_4 107·6
P_1 111·7	P_0 113·9	P_3K 116·1	P_2 112·1	P_4K 120·9
P_3 100·5	P_2 101·6	P_1 107·2	P_4K 110·0	P_0K 100·5
P_3K 112·7	P_2K 120·3	P_1K 115·0	P_4 108·0	P_0 97·4
P_0K 108·7	P_1K 132·4	P_4 108·7	P_3 91·8	P_2 102·0
P_0 110·1	P_1 104·0	P_4K 105·3	P_3K 82·4	P_2K 105·3

20.2 In a varietal and manurial trial with oats, three varieties (M, G, and V) were tested in a randomized blocks design with four replications. Each plot was split into four sub-plots for the comparison of four levels of Sulphate of Ammonia (n_0 = nil, n_1 = 0·2 cwt. N per acre, n_2 = 0·4 cwt. N per acre, n_3 = 0·6 cwt. N per acre).

Yields of grain are given in lb. per $\frac{1}{80}$ acre sub-plot. Analyse the data and present the results in bags per acre given that 1 bag = 200 lb. (Data from Rothamsted Report, 1931, page 143)

Treatment		Block 1	2	3	4
M	n_0	15·75	22·25	24·25	26·25
	n_1	17·50	32·25	24·75	35·00
	n_2	27·25	33·00	29·75	29·50
	n_3	24·75	31·00	30·25	39·00
G	n_0	20·00	15·00	22·25	29·25
	n_1	20·50	25·50	20·50	28·50
	n_2	23·50	22·25	21·50	40·25
	n_3	31·50	24·00	26·00	35·25
V	n_0	15·50	17·00	13·25	27·75
	n_1	22·50	16·00	18·50	32·50
	n_2	25·00	28·00	29·50	39·25
	n_3	29·00	21·50	28·25	43·50

20.3 In a trial with 4 varieties of green beans in a randomized blocks design conducted at Cedara in 1961, an additional factor (spraying treatments) was applied to whole blocks. The following are the field plan and plot yields (in lb.):

Replication 1	*M*3 14·3	*M*2 15·8	*B*2 11·8	*B*1 10·9	*C*2 10·9	*C*1 9·1
	*M*1 12·8	*M*4 10·8	*B*4 8·7	*B*3 13·4	*C*4 4·2	*C*3 10·7
Replication 2	*B*2 11·8	*B*3 10·7	*C*2 12·2	*C*4 6·1	*M*1 12·9	*M*4 12·6
	*B*4 10·1	*B*1 9·9	*C*1 9·5	*C*3 12·1	*M*3 11·8	*M*2 15·8
Replication 3	*B*4 7·3	*B*3 10·5	*C*3 9·6	*C*1 9·5	*M*2 13·7	*M*4 12·9
	*B*1 7·4	*B*2 9·8	*C*4 6·8	*C*2 11·1	*M*3 15·1	*M*1 15·2
Replication 4	*C*1 6·2	*C*4 5·5	*M*3 11·2	*M*1 13·0	*B*2 11·2	*B*4 8·0
	*C*3 8·0	*C*2 8·9	*M*2 13·2	*M*4 11·8	*B*3 13·2	*B*1 13·6
Replication 5	*M*2 10·7	*M*1 11·8	*C*1 8·6	*C*4 6·6	*B*3 11·8	*B*1 12·5
	*M*4 11·3	*M*3 11·9	*C*3 10·5	*C*2 12·2	*B*4 7·6	*B*2 11·4
Replication 6	*M*2 13·7	*M*3 14·8	*B*4 10·2	*B*3 17·2	*C*4 7·2	*C*1 11·6
	*M*4 11·4	*M*1 16·3	*B*2 13·1	*B*1 14·5	*C*2 11·7	*C*3 13·2

The factors were:

Sprays	Varieties
M = Maneb	1 = Seminole
B = Bordeaux mixture	2 = Streamliner
C = Control	3 = Contender
	4 = Topcrop

The variety "Contender" may be regarded as a standard one for the area.

Analyse the data presenting results in lb. per morgen, given that each individual yield is from two rows 10 ft. long and 3 ft. apart and that 1 morgen = 10,244 sq. yds.

(Adapted from data supplied by the Department of Horticultural Science, Natal Region, Department of Agricultural Technical Services)

A First Course in Biometry for Agriculture Students

ERRATA

Title page and following page: The date of publication should be 1969, not 1967.

Page 6 (4 lines from foot of page): For "preceeding" read "preceding".

Page 11: The two diagrams in § 1.9.6. should be labelled (1) and (2).

Page 62: Formula 5.3 should read:

$$\bar{x} = \sum_{j} x_j \left(\frac{n_j}{n}\right)$$

Page 344, second line of Note K: For $\Sigma\xi_1 n$ * read $\Sigma\xi_1 n_1$*.

Page 376, Table 17.2: The last M.S. should be $s^2_{y,x}$.

Page 408: Value of x for Treatment D, Block 4, should be 62.2, not 62.3.

Page 486, line 13: For "D.F. of s^2" read "D.F. of s_a^2".

Page 507, end of first line of Note B: For "works" read "work-"; end of line 4 of same paragraph: "analysi-" to read "analysis".

Page 537: Data acknowledgement at end of Exercise 22.2 should read "Department of Agricultural Technical Services".

Page 570, line 11 of § 25.2.1: For "hervesting" read "harvesting".

Page 577, Table 25.6: Heading of last column should read "Estimated C.V.".