

## Split-Plot Design (Repeated Measures – Factorial Design with Block-Treatment Confounding).

We studied earlier the randomized block design (RBD). The goal of the RBD was to isolate the effect of subject heterogeneity when testing the treatment effects. This was done using repeated measurements of the same participant or through the process of matching. In the RBD, participants were blocked in such a way that the participants within each block are less than the variation between blocks. The split plot design (SPF) with repeated measures or matched participants is an extension of the randomized block to two or more treatment variables (independent variables). This design is appropriate for experiments that meet the following additional assumptions. That is, all of the assumptions of prior designs also apply here along with several others.

1. There are two or more independent variables (treatments). At least one is a nonrepeated measure treatment or between-block. There is also at least one repeated, or within-block treatment. The nonrepeated measure treatment is usually designated as A with p levels and B is used to represent the repeated measures treatment with q levels.
2. The number of combinations of treatment levels is greater than the desired number of observations within each block.
3. If repeated measurements are used on participants, then each block will consist of only one participant. If repeated measurements are not obtained then each block contains q participants.
4. When using repeated measurements, the p samples of n participants from a population of participants are randomly assigned to levels of the nonrepeated measure treatment (A). The sequence for administering the repeated measures levels in combination with each level of the nonrepeated measures treatment is randomized independently for each block.
5. When repeated measures is not used, the p samples of n blocks of q participants from the population are randomly assigned to levels of treatment (A). After this, levels of treatment (B) are randomly assigned to the q participants within each block.

Comparing the completely randomized factorial design to the randomized block factorial design and split plot design. In each case here, there are two treatments. The comparison is between the CRF-23, RBF-23 and SPF-23.

		a <sub>1</sub>	a <sub>1</sub>	a <sub>1</sub>	a <sub>2</sub>	a <sub>2</sub>	a <sub>2</sub>
		b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>
a <sub>1</sub>		s <sub>1</sub>	s <sub>2</sub>	s <sub>3</sub>			
a <sub>2</sub>		s <sub>4</sub>	s <sub>5</sub>	s <sub>6</sub>			

**CRF-23**

		a <sub>1</sub>	a <sub>1</sub>	a <sub>1</sub>	a <sub>2</sub>	a <sub>2</sub>	a <sub>2</sub>
		b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>
		s <sub>1</sub>	s <sub>1</sub>	s <sub>1</sub>	s <sub>1</sub>	s <sub>1</sub>	s <sub>1</sub>

**RBF-23**

			b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>
a <sub>1</sub>		s <sub>1</sub>	s <sub>1</sub>	s <sub>1</sub>	
a <sub>2</sub>		s <sub>2</sub>	s <sub>2</sub>	s <sub>2</sub>	

**SPF-23**

The split plot design is one where a participant receives all levels of some treatments but only one level of the other treatments. It is sometimes called a mixed design. When we look at the SPF-23 design, the comparison of a<sub>1</sub> and a<sub>2</sub> involves the comparison of s<sub>1</sub>

and  $s_2$  as well as the effect of treatment A. However, the difference between any two levels of treatment B do not involve differences between  $s_1$  and  $s_2$  since they both are observed under all levels of B. In this SPF-23 design, the main effect of treatment A is completely confounded with the differences between the blocks or sets of participants. The main effect of B and the interaction AB are free of this confounding. A treatment confounded with blocks does not effect the interpretation of the treatment effects. It only affects the precision of the estimate. The effects of A are called between-block (subjects) effect, B and AB are called within-blocks (subject) effects. The tests on B and AB are generally more powerful than tests on A.

In addition to its ability to handle the heterogeneity of participants, the split plot design is also useful in analyzing data from designs involving learning, transfer of learning, and fatigue. The SPF design does not include a source of variability for sequence or carry over effects. As such, repeated measurements on the same participant over time where one level affects performance on subsequent levels should be avoided. An exception is when the carryover effects are of primary importance.

The SPF designs require the error portion of the repeated measurements to be independent, uncorrelated of each other and the treatment effects. In many cases, this requirement is not met. The variance-covariance matrix for the scores must meet a certain form in order for this requirement to be met. That pattern is generally not present. The variances within the matrix (the diagonal element) must be equal and the covariances (off diagonal) must be equal.

The Linear Model:

$$Y_{ijm} = \mu + \alpha_i + \pi_{m(i)} + \beta_j + \alpha\beta_{ij} + \beta\pi_{jm(i)} + \varepsilon_{o(ijm)}$$

$Y_{ijm}$  is the dependent variable measure for a randomly selected participant  $m$  in treatment population  $ab_{ij}$ .

$\mu$  = grand mean of treatment populations

$\alpha_i$  = effect of treatment  $i$ , which is constant for all subjects within treatment population  $i$

$\beta_j$  = effect of treatment  $j$ , which is constant for all subjects within treatment population  $j$ .

$\pi_{m(i)}$  = constant associated with person  $m$ , who is nested under level  $\alpha_i$

$\alpha\beta_{ij}$  = effect that represents nonadditivity of effects  $\alpha_i$  and  $\beta_j$ .

$\beta\pi_{jm(i)}$  = effect that represents nonadditivity of effects  $\pi_{m(i)}$  and  $\beta_j$ .

$\varepsilon_{o(ijm)}$  = experimental error that is independent of the other  $\varepsilon$ 's. It is normally distributed with mean = 0 and constant variance.  $\varepsilon_{o(ijm)}$  cannot be estimated separately from  $\beta\pi_{jm(i)}$ .

The null and alternative hypotheses:

$H_0: \alpha_i = 0$  for all  $i$       $H_1: \alpha_i \neq 0$  for some  $i$ .

$H_0: \beta_j = 0$  for all  $j$ ,      $H_1: \beta_j \neq 0$  for some  $j$ .

$H_0: \alpha\beta_{ij} = 0$  for all  $ij$ ,  $H_1: \alpha\beta_{ij} \neq 0$  for some  $ij$ .

### ANOVA SUMMARY TABLE for SPF

Source	SS	df	MS	F
Between Subjects				
A	SSA	$p - 1$	$SSA/(p - 1)$	$MSA/[X]$
Subj w.group	$SS_{\text{subj w.group}}$	$p(n - 1)$	$SS_{\text{subj w.group}}/p(n - 1)$ [X]	
Within Subjects				
B	SSB	$q - 1$	$SSB/(q - 1)$	$SSB/[V]$
AB	SSAB	$(p - 1)(q - 1)$	$SSAB/dfAB$	$SSAB/[V]$
B x subj w.group	$SS_{B \times \text{subj w.group}}$	$p(n - 1)(q - 1)$	$SS_{B \times \text{subj w.group}}/p(n - 1)(q - 1)$ {V}	
TOTAL		$npq - 1$		

The SPF design has two error terms. One corresponds to the pooled variation between participants within  $p$  groups and the other is the pooled interaction of treatment B with participants in each block.

The  $MS_A/MS_{\text{subj w.group}}$  is the same as the  $MS_{BG}/MS_W$  in the CRD. The  $MS_B/MS_{B \times \text{sub w.groups}}$  is the same as  $MS_B/MS_{\text{res}}$  in the RBD.

If the variance-covariance matrices have equality and symmetry, the univariate procedures provide an exact test of the hypothesis of equal means. This was true when we discussed the randomized block design. When the variance-covariance matrices do not meet the pattern expected, we can use the Geisser-Greenhouse Conservative test. This is a negatively biased test. It is conservative in that it is more likely to commit an error of not rejecting the null hypothesis when it should have. The conservative F test is identical to the traditional F test except that different degrees of freedom are used. If the F-value for MSB and MSAB are significant, the exact test would also be significant. If the conservative test is not significant but the conventional F test is significant, the analysis would proceed with a multivariate test instead of a univariate.

The adjusted degrees of freedom are

Numerator of F	Conventional F df	Conservative F df
MSB	$(q - 1), p(n - 1)(q - 1)$	$1, p(n - 1)$
MSAB	$(p - 1)(q - 1), p(n - 1)(q - 1)$	$(p - 1), p(n - 1)$