



BIOMETRICS INFORMATION

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PAMPHLET NO. # 54

DATE: January 10, 1996

SUBJECT: Incomplete Block Designs: Connected designs can be analysed

The previous pamphlet (#53) discussed how complete Randomized Block Designs are sometimes not suitable because the large block size required would be impossible and/or the plots within the large blocks would be too heterogeneous. While Balanced Incomplete Block designs (BIBD) have many desirable properties, particularly in the days of hand calculations, we need not restrict ourselves to the limited set of BIBDs that are available. For instance, there are many variations of incomplete block designs, such as Partially Balanced Incomplete Block Design (PBIBD), Lattice Designs, and Youden Squares. Still, these are very specialized designs which would take some time to learn about and which, after that effort, may not be suitable for the situation at hand. It may be preferable to consider how to design incomplete studies regardless of whether they fit into any particular category. Mead (1988) clearly describes how to design these sorts of studies and his methods naturally lead to the creation of suitable designs. For instance, if a study lent itself to a balanced incomplete block design you would most likely end up with just that design by following his methods, even if you did not know what such a design was. An essential feature of any such design is that it be **connected** (Searle, 1987).

The missing cells of an incomplete design result in a loss of information about at least some of the interactions in the design. Thus, these interactions should be carefully considered before proceeding with an incomplete design. Analysis will be possible, and simpler, if these interactions can be considered negligible. For incomplete block designs, the interaction of concern is that between blocks and treatments. This may be reasonably considered negligible if blocks are groups of similar experimental units regardless of whether the blocks are quite different from each other. Explaining possible differences in treatment responses between blocks should not be of interest nor should it be the objective of a randomized block design¹.

Identification of connectedness is easiest if the factorial structure of the design can be displayed in a two-dimensional grid or map. For instance, the designs of the Balanced Incomplete Block Designs of the previous pamphlet were represented by boxes forming a grid. This grid representation can be used to determine if the design is connected by noting if the filled cells of the grid can be joined by a continuous line, consisting solely of horizontal and vertical segments,

¹ Blocks may be the experimental units for some other factor, such as site series or aspect. In this case, these other factors must be properly replicated by inclusion of two or more blocks per level of the factor(s). But then, this design would be a split-plot and not a randomized block design. See BI #34 for more discussion.

that has changes of direction only in filled cells' (Searle, 1987, pg 140). Two examples from the previous pamphlet are shown below with the addition of the continuous line between filled cells.

BIBD(4,4,3,3;2):

Df / Dr	Block			
	1	2	3	4
100/0	✓	✓	✓	
70/30	✓	✓		✓
40/60	✓		✓	✓
0/100		✓	✓	✓

BIBD(4,6,2,3;1):

Df / Dr	Block					
	1	2	3	4	5	6
100/0	✓		✓		✓	
70/30	✓			✓		✓
40/60		✓	✓			✓
0/100		✓		✓	✓	

The following two designs are not connected. The design on the right is really two separate randomized block designs, which would require a separate analysis for each block. Thus this one set of data would have to be analyzed as if it were two sets of data.

Treatment	Block				
	1	2	3	4	5
Trmt 1	✓		✓		
Trmt 2		✓		✓	✓
Trmt 3			✓		
Trmt 4		✓		✓	

Treatment	Block					
	1	2	3	4	5	6
Trmt 1	✓	✓	✓			
Trmt 2	✓	✓	✓			
Trmt 3				✓	✓	✓
Trmt 4				✓	✓	✓

As shown below small changes can make them connected. While the design on the right is now connected it is not balanced like the six block BIB design shown at the top of the page.

Treatment	Block				
	1	2	3	4	5
Trmt 1	✓		✓		
Trmt 2		✓		✓	
Trmt 3			✓		✓
Trmt 4	✓			✓	

Treatment	Block					
	1	2	3	4	5	6
Trmt 1	✓	✓	✓			
Trmt 2	✓	✓	✓			
Trmt 3			✓		✓	✓
Trmt 4				✓	✓	✓

Next, let's look at some simple incomplete block designs that might be suitable for operational trials. Each block would be a different site or location. In the first case, each site would contain two plots: a control plot and a plot assigned one of two treatments. It is desirable that the sites used in the study be randomly selected from a clearly defined population and that the two plots be randomly assigned either the control or the treatment. The treatment to use in a block should also be randomly selected. This design is connected as shown by its grid representation:

	Block							
<u>Treatment</u>	1	2	3	4	5	6	7	8
Control	✓	✓	✓	✓	✓	✓	✓	✓
Trmt 1	✓	✓	✓	✓	✓			
Trmt 2						✓	✓	✓

A variation on this design would be to randomly choose which of the three treatments (control, treatment 1 and treatment 2) to randomly assign to each of two plots at each location. This would reduce the number of control plots so that the active treatments can be replicated more times. A grid representation for this design is:

	Block							
<u>Treatment</u>	1	2	3	4	5	6	7	8
Control	✓	✓	✓				✓	✓
Trmt 1	✓	✓	✓	✓	✓	✓		
Trmt 2				✓	✓	✓	✓	✓

A third variation might be to have many treatments, say, five including the control. Depending upon the size of block, each block will contain from two to five of the treatments. Blocks with the same treatments should be grouped in the grid representation. Such a design might look like:

Treatment	Block											
	1	2	3	4	5	6	7	8	9	10	11	12
Control	✓	✓	✓	✓						✓	✓	✓
Trmt 1	✓	✓	✓									
Trmt 2			✓	✓	✓	✓			✓	✓		
Trmt 3				✓	✓	✓	✓	✓	✓	✓	✓	✓
Trmt 4						✓	✓	✓		✓	✓	✓

An incomplete block design should meet several criteria. As already discussed, the design should be connected². The main effects of a connected design can be analyzed if the interaction between the two dimensions of the grid representation can be considered negligible³. Contrasts between the main effect means, including differences between pairs of treatments can be estimated and tested. The other requirements include symmetry and balance, so that each treatment is applied to almost the same number of plots (denoted by r for BIBD's) and that each pair of treatments occur together in a block almost the same number of times (denoted by λ for BIBD's). Meeting these conditions means that the standard error of the difference between any pair of treatments will be of similar size. For instance, BIB Designs provide equal precision (constant standard error) for all pair-wise treatment comparisons. If all treatments are not of equal interest then these criteria may need some modification. See Mead (1988) for a thorough discussion.

Before implementing your own incomplete design, consultation with a statistician and/or thorough reading of the references is strongly recommended.

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References:

- Cox, D. R., 1958, *Planning of Experiments*, John Wiley.
 Kuehl, R. O., 1994, *Statistical Principles of Research Design and Analysis*, Duxbury Press.
 Mead, R., 1988, *The Design of Experiments: Statistical principles for practical application*.
 Cambridge, U.K.: Cambridge University Press. See Chapters 2, 7 and 15.
 Searle, S., 1987, *Linear Models for Unbalanced Data*, John Wiley.

² For the technical minded, connectedness is a sufficient but not a necessary condition for analysis of a study design to be possible. Connectedness allows the data to be analyzed as one set of data instead of as 2 or more sets.

³ If this interaction cannot be considered negligible it may be possible to examine suitable subsets of the design for interaction and main effects (Searle, 1987).