#### Chapter 7

## Partially Balanced Incomplete Block Design (PBIBD)

The balanced incomplete block designs have several advantages. They are connected designs as well as the block sizes are also equal. A restriction on using the BIBD is that they are not available for all parameter combinations. They exist only for certain parameters. Sometimes, they require a large number of replications also. This hampers the utility of the BIBDs. For example, if there are v = 8 treatments and block size is k = 3 (i.e., 3 plots in each block) then the total number of required blocks

are 
$$b = \begin{pmatrix} 6 \\ 3 \end{pmatrix} = 56$$
 and so using the relationship  $bk = vr$ , the total number of required replicates is  
 $r = \frac{bk}{v} = 21.$ 

Another important property of the BIBD is that it is efficiency balanced. This means that all the treatment differences are estimated with the same accuracy. The partially balanced incomplete block designs (PBIBD) compromise on this property up to some extent and help in reducing the number of replications. In simple words, the pairs of treatments can be arranged in different sets such that the difference between the treatment effects of a pair, for all pairs in a set, is estimated with the same accuracy. The partially balanced incomplete block designs remain connected like BIBD but no more balanced. Rather they are partially balanced in the sense that some pairs of treatments have the same efficiency whereas some other pairs of treatments have the same efficiency but different from the efficiency of earlier pairs of treatments. This will be illustrated more clearly in the further discussion.

Before describing the set up of PBIBD, first, we need to understand the concept of "Association Scheme". Instead of explaining the theory related to the association schemes, we consider here some examples and then understand the concept of an association scheme. Let there be a set of v treatments. These treatments are denoted by the symbols 1, 2,..., v.

#### **Partially Balanced Association Schemes**

A relationship satisfying the following three conditions is called a partially balanced association scheme with *m*-associate classes.

(i) Any two symbols are either first, second,..., or  $m^{th}$  associates and the relation of associations is symmetrical, i.e., if the treatment A is the  $i^{th}$  associate of treatment B, then B is also the  $i^{th}$  associate of treatment A.

- (ii) Each treatment A in the set has exactly  $n_i$  treatments in the set which are the  $i^{th}$  associate and the number  $n_i$  (i = 1, 2, ..., m) does not depend on the treatment A.
- (iii) If any two treatments A and B are the  $i^{th}$  associates, then the number of treatments which are both  $j^{th}$  associate A and  $k^{th}$  associate of B is  $p_{jk}^{i}$  and is independent of the pair of  $i^{th}$  associates A and B.

The numbers  $v, n_1, n_2, ..., n_m, p_{jk}^i$  (i, j, k=1, 2, ..., m) are called the **parameters of** *m*-associate partially balanced scheme.

We consider now the examples based on rectangular and triangular association schemes to understand the conditions stated in the partially balanced association scheme.

# **Rectangular Association Scheme**

Consider an example of m = 3 associate classes. Let there be six treatments denoted as 1, 2, 3, 4, 5 and 6. Suppose these treatments are arranged as follows:

1	2	3
4	5	6

Under this arrangement, with respect to each symbol, the

- two other symbols in the same row are the first associates.
- One another symbol in the same column is the second associate and
- remaining two symbols are in the other row are the third associates.

For example, with respect to treatment 1,

- treatments 2 and 3 occur in the same row, so they are the first associates of treatment 1,
- treatment 4 occurs in the same column, so it is the second associate of treatment 1 and
- the remaining treatments 5 and 6 are the third associates of treatment 1 as they occur in the other (second) row.

Similarly, for treatment 5,

- treatments 4 and 6 occur in the same row, so they are the first associates of treatment 5,
- treatment 2 occurs in the same column, so it is the second associate of treatment 5 and
- remaining treatments 1 and 3 are in the other (second) row, so they are the third associates of treatment 5.

Treatment	First	Second	Third
number	associates	associates	associates
1	2, 3	4	5, 6
2	1, 3	5	4, 6
3	1, 2	6	4, 5
4	5, 6	1	2, 3
5	4, 6	2	1, 3
6	4, 5	3	1, 2

The table below describes the first, second and third associates of all the six treatments.

Further, we observe that for treatment 1, the

- number of first associates  $(n_1) = 2$ ,
- o number of second associates  $(n_2) = 1$ , and
- the number of third associates  $(n_3) = 2$ .

The same values of  $n_1, n_2$  and  $n_3$  hold true for other treatments also.

Now we understand the condition (iii) of the definition of partially balanced association schemes related to  $p_{ik}^{i}$ .

Consider treatments 1 and 2. They are the first associates (which means i = 1), i.e. treatments 1 and 2 are the first associate of each other; treatment 6 is the third associate (which means j = 3) of treatment 1 and also the third associate (which means k = 3) of treatment 2. Thus the number of treatments which are both, i.e., the  $j^{th}$  (j = 3) associate of treatment A (here  $A \equiv 1$ ) and  $k^{th}$  associate of treatment B (here  $B \equiv 2$ ) are  $i^{th}$  (i.e., i = 1) associate is  $p_{jk}^i = p_{33}^1 = 1$ .

Similarly, consider the treatments 2 and 3 which are the first associate (which means i=1); treatment 4 is the third (which means j=3) associate of treatment 2 and treatment 4 is also the third (which means k=3) associate of treatment 3. Thus  $p_{33}^1 = 1$ .

Other values of  $p_{jk}^{i}$  (*i*, *j*, *k* = 1, 2, 3) can also be obtained similarly.

**Remark**: This method can be used to generate a 3-class association scheme in general for  $m \times n$  treatments (symbols) by arranging them in *m*-row and *n*-columns.

#### **Triangular Association Scheme**

The triangular association scheme gives rise to a 2-class association scheme. Let there be a set of v treatments which are denoted as  $1, 2, ..., v_{\perp}$ . The treatments in this scheme are arranged in q rows and q columns where.

$$v = \begin{pmatrix} q \\ 2 \end{pmatrix} = \frac{q(q-1)}{2}.$$

These symbols are arranged as follows:

- (a) Positions in the leading diagonals are left blank (or crossed).
- (b) The  $\left(\frac{q}{2}\right)$  positions are filled up in the positions above the principal diagonal by the treatment numbers 1, 2,..., v corresponding to the symbols.
- (c) Fill the positions below the principal diagonal symmetrically.

Rows $\rightarrow$	1	2	3	4		<i>q</i> - 1	q
Columns ↓							
1	×	1	2	3		<i>q</i> - 2	<i>q</i> - 1
2	1	×	q	q + 1		2 <i>q</i> - 2	2 <i>q</i> - 1
3	2	q	×				
4	3	<i>q</i> + 1					
:	•	:	:	•	·.	:	:
<i>q</i> - 1	<i>q</i> - 2	2 <i>q</i> - 2				×	<i>q</i> ( <i>q</i> - 1)/2
<i>q</i>	<i>q</i> - 1	2 <i>q</i> - 1				q(q-1)/2	×

This assignment is shown in the following table:

Now based on this arrangement, we define the first and second associates of the treatments as follows. The symbols entering in the same column i(i = 1, 2, ..., q) are the first associates of *i* and rest are the second associates. Thus two treatments in the same row or in the same column are the first associates of treatment *i*. Two treatments which do not occur in the same row or in the same column are the second associates of treatment *i*.

Now we illustrate this arrangement by the following example:

Let there be 10 treatments. Then q = 5 as  $v = \begin{pmatrix} 5 \\ 2 \end{pmatrix} = 10$ . The ten treatments denoted as 1, 2,..., 10 are

arranged under the triangular association scheme as follows:

$Rows \rightarrow$	1	2	3	4	5
Columns ↓					
1	×	1	2	3	4
2	1	×	5	6	7
3	2	5	×	8	9
4	3	6	8	×	10
5	4	7	9	10	×

For example,

- for treatment 1,
  - the treatments 2, 3 and 4 occur in the same row (or same column) and

• treatments 5, 6 and 7 occur in the same column (or same row).

So the treatments 2, 3, 4, 5, 6 and 7 are the first associates of treatment.

• Then rest of the treatments 8, 9 and 10 are the second associates of treatment 1.

Treatment number	First associa	ates	Second associates
1	2, 3, 4 5,	6, 7	8, 9, 10
2	1, 3, 4 5,	8,9	6, 7, 10
3	1, 2, 4 6,	8, 10	5, 7, 9
4	1, 2, 3 7,	9, 10	5, 6, 8
5	1, 6, 7 2,	8,9	3, 4, 10
6	1, 5, 7 3,	8, 10	2, 4, 9
7	1, 5, 6 4,	9, 10	2, 3, 8
8	2, 5, 9 3,	6, 10	1, 4, 7
9	2, 5, 8 4,	7, 10	1, 3, 6
10	3, 6, 8 4,	7,9	1, 2, 5

The first and second associates of the other treatments are stated in the following table.

We observe from this table that the number of first and second associates of each of the 10 treatments (v = 10) is same with  $n_1 = 6$ ,  $n_2 = 3$  and  $n_1 + n_2 = 9 = v - 1$ . For example, the treatment 2 in the column of first associates occurs six times, viz., in first, third, fourth, fifth, eighth and ninth rows. Similarly, the treatment 2 in the column of second associates occurs three times, viz., in the sixth, seventh and tenth rows. Similar conclusions can be verified for other treatments.

There are six parameters, viz.,  $p_{11}^1, p_{22}^1, p_{12}^1$  (or  $p_{21}^1$ ),  $p_{22}^2$  and  $p_{12}^2$  (or  $p_{21}^2$ ) which can be arranged in symmetric matrices  $P_1$  and  $P_2$  as follows:

$$P_{1} = \begin{bmatrix} p_{11}^{1} & p_{12}^{1} \\ p_{21}^{1} & p_{22}^{1} \end{bmatrix}, P_{2} = \begin{bmatrix} p_{11}^{1} & p_{12}^{1} \\ p_{21}^{2} & p_{22}^{2} \end{bmatrix}.$$

[Note: We would like to caution the reader not to read  $p_{11}^2$  as squares of  $p_{11}$  but 2 in  $p_{11}^2$  is only a superscript.]

$$P_1 = \begin{bmatrix} 3 & 2 \\ 2 & 1 \end{bmatrix}, \quad P_2 = \begin{bmatrix} 4 & 2 \\ 2 & 0 \end{bmatrix}.$$

In order to learn how to write these matrices  $P_1$  and  $P_2$ , we consider treatments 1, 2 and 8. Note that the treatment 8 is the second associate of treatment 1. Consider only the rows corresponding to treatments 1, 2 and 8 and obtain the elements of  $P_1$  and  $P_2$  as follows:

 $p_{11}^1$ : Treatments 1 and 2 are the first associates of each other. There are three common treatments (viz., 3, 4 and 5) between the first associates of treatment 1 and the first associates of treatment 2. So  $p_{11}^1 = 3$ .



 $p_{12}^1$  and  $p_{21}^1$ : Treatments 1 and 2 are the first associates of each other. There are two treatments (viz., 6 and 7) which are common between the first associates of treatment 1 and the second associates of treatment 2. So  $p_{12}^1 = 2 = p_{21}^1$ .



 $p_{22}^1$ : Treatments 1 and 2 are the first associates of each other. There is only one treatment (viz., treatment 10) which is common between the second associates of treatment 1 and the second associates of treatment 2. So  $p_{22}^1 = 1$ .



 $p_{11}^2$ : Treatments 1 and 8 are the second associates of each other. There are four treatment (viz., 2,3,5 and 6) which are common between the first associates of treatment 1 and the first associates of treatment 8. So  $p_{11}^1 = 4$ .



 $p_{12}^2$  and  $p_{21}^2$ : Treatments 1 and 8 are the second associates of each other. There are two treatments (viz., 4 and 7) which are common between the first associates of treatment 1 and the second associates of treatment 8. So  $p_{12}^1 = 2 = p_{21}^1$ .



 $p_{22}^2$ : Treatments 1 and 8 are the second associates of each other. There is no treatment which is common between the second associates of treatment 1 and the second associates of treatment 8. So  $p_{22}^2 = 0$ .



In general, if q rows and q columns of a square are used, then for q > 3

$$v = {\binom{q}{2}} = \frac{q(q-1)}{2},$$

$$n_1 = 2q - 4,$$

$$n_2 = \frac{(q-2)(q-3)}{2},$$

$$P_1 = {\binom{q-2}{q-3}} \frac{(q-3)(q-4)}{2}$$

$$P_1 = {\binom{4}{2q-8}} \frac{(q-4)(q-5)}{2}.$$

For q = 3, there are no second associates. This is a degenerate case where second associates do not exist and hence  $P_2$  cannot be defined.

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The graph theory techniques can be used for counting  $p_{jk}^i$ .

Further, it is easy to see that all the parameters in  $P_1, P_2$ , etc. are not independent.

# **Construction of Blocks of PBIBD under Triangular Association Scheme**

The blocks of a PBIBD can be obtained in different ways through an association scheme. Even different block structure can be obtained using the same association scheme. We now illustrate this by obtaining different block structures using the same triangular scheme. Consider the earlier illustration

where  $v = \begin{pmatrix} q \\ 2 \end{pmatrix} = 10$  with q = 5 was considered and the first, second and third associates of treatments

were obtained.

**Approach 1**: One way to obtain the treatments in a block is to consider the treatments in each row. This constitutes the set of treatments to be assigned in a block. When q = 5, the blocks of PBIBD are constructed by considering the rows of the following table.

$Rows \rightarrow$	1	2	3	4	5
Columns $\downarrow$					
1	×	1	2	3	4
2	1	×	5	6	7
3	2	5	×	8	9
4	3	6	8	×	10
5	4	7	9	10	×

From this arrangement, the treatments are assigned in different blocks and following blocks are obtained.

Blocks	Treatments				
Block 1	1,	2,	3,	4	
Block 2	1,	5,	6,	7	
Block 3	2,	5,	8,	9	
Block 4	3,	6,	8,	10	
Block 5	4,	7,	9,	10	

The parameters of such a design are b = 5, v = 10, r = 2, k = 4,  $\lambda_1 = 1$  and  $\lambda_2 = 0$ .

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**Approach 2**: Another approach to obtain the blocks of PBIBD from a triangular association scheme is as follows:

- Consider the pair-wise columns of the triangular scheme.
- Then delete the common treatments between the chosen columns and retain others.
- The retained treatments will constitute the blocks.

Consider, e.g., the triangular association scheme for q = 5. Then the first block under this approach is obtained by deleting the common treatments between columns 1 and 2 which results in a block containing the treatments 2, 3, 4, 5, 6 and 7. Similarly, considering the other pairs of columns, the other blocks can be obtained which are presented in the following table:

Blocks	Columns of an association scheme	Treatments
Block 1	(1, 2)	2, 3, 4, 5, 6, 7
Block 2	(1, 3)	1, 3, 4, 5, 8, 9
Block 3	(1, 4)	1, 2, 4, 6, 8, 10
Block 4	(1, 5)	1, 2, 3, 7, 9, 10
Block 5	(2, 3)	1, 2, 6, 7, 8, 9
Block 6	(2, 4)	1, 3, 5, 7, 8, 10
Block 7	(2, 5)	1, 4, 5, 6, 9, 10
Block 8	(3, 4)	2, 3, 5, 6, 9, 10
Block 9	(3, 5)	2, 4, 5, 7, 8, 10
Block 10	(4, 5)	3, 4, 6, 7, 8, 9

The parameters of the PBIBD are b = 10, v = 10, r = 6, k = 6,  $\lambda_1 = 3$  and  $\lambda_2 = 4$ .

Since both these PBIBDs are arising from the same association scheme, so the values of  $n_1, n_2, P_1$  and  $P_2$  remains the same for both the designs. In this case, we have  $n_1 = 6, n_2 = 3$ ,

$$P_1 = \begin{bmatrix} 3 & 2 \\ 2 & 1 \end{bmatrix}, \qquad P_2 = \begin{bmatrix} 4 & 2 \\ 2 & 0 \end{bmatrix}.$$

**Approach 3**: Another approach to derive the blocks of PBIBD is to consider all the first associates of a given treatment in a block. For example, in the case of q = 5, the first associates of treatment 1 are the treatments 2, 3, 4, 5, 6 and 7. So these treatments constitute one block. Similarly, other blocks can also be found. This results in the same arrangement of treatments in blocks as considered by deleting the common treatments between the pair of columns.

The PBIBD with two associate classes are popular in practical applications and can be classified into the following types depending on the association scheme,

(*Reference: Classification and analysis of partially balanced incomplete block designs with two associate classes, R. Bose and Shimamoto, 1952, Journal of American Statistical Association, 47, pp. 151-184*).

- 1. Triangular
- 2. Group divisible
- 3. Latin square with *i* constraints  $(L_i)$
- 4. Cyclic and
- 5. Singly-linked blocks.

The triangular association scheme has already been discussed. We now briefly present other types of association schemes.

### Group divisible association scheme:

Let there be v treatments which can be represented as v = pq. Now divide the v treatments into p groups with each group having q treatments such that any two treatments in the same group are the first associates and two treatments in the different groups are the second associates. This is called the group divisible type scheme. The scheme simply amounts to arrange the v = pq treatments in a  $(p \times q)$  rectangle and then the association scheme can be exhibited. The columns in the  $(p \times q)$  rectangle will form the groups.

Under this association scheme,

$$n_1 = q - 1$$
  
 $n_2 = q(p - 1),$ 

hence

$$(q-1)\lambda_1 + q(p-1)\lambda_2 = r(k-1)$$

and the parameters of the second kind are uniquely determined by p and q. In this case

$$P_{1} = \begin{pmatrix} q-2 & 0 \\ 0 & q(p-1) \end{pmatrix}, \qquad P_{2} = \begin{pmatrix} 0 & q-1 \\ q-1 & q(p-2) \end{pmatrix},$$

For every group divisible design,

$$r \ge \lambda_1,$$
$$rk - v\lambda_2 \ge 0.$$

If  $r = \lambda_1$ , then the group divisible design is said to be **singular**. Such a singular group divisible design can always be derived from a corresponding BIBD. To obtain this, just replace each treatment by a group of *q* treatments. In general, if a BIBD has the following parameters  $b^*, v^*, r^*, k^*, \lambda^*$ , then a group divisible design is obtained from this BIBD which has parameters

$$b = b^*$$
,  $v = qv^*$ ,  $r = r^*$ ,  $k = qk^*$ ,  $\lambda_1 = r$ ,  $\lambda_2 = \lambda^*$ ,  $n_1 = p$ ,  $n_2 = q$ .

A group divisible design is **nonsingular** if  $r \neq \lambda_1$ . Nonsingular group divisible designs can be divided into two classes – semi-regular and regular.

A group divisible design is said to be **semi-regular** if  $r > \lambda_1$  and  $rk - v\lambda_2 = 0$ . For this design

$$b \ge v - p + 1$$
.

Also, each block contains the same number of treatments from each group so that k must be divisible by p.

A group divisible design is said to be **regular** if  $r > \lambda_1$  and  $rk - v\lambda_2 > 0$ . For this design

$$b \geq v$$
.

## Latin Square Type Association Scheme

Let  $L_i$  denotes the Latin square type PBIBD with *i* constraints. In this PBIBD, the number of treatments are expressible as  $v=q^2$ . The treatments may be arranged in a  $(q \times q)$  square. For the case of i=2, two treatments are the first associates if they occur in the same row or the same column, and second associates otherwise. For the general case, we take a set of (i=2) mutually orthogonal Latin squares, provided it exists. Then two treatments are the first associates if they occur in the same row or the same column, or corresponding to the same letter of one of the Latin squares. Otherwise, they are second associates.

Under this association scheme,

$$\begin{split} &v = q^2, \\ &n_1 = i(q-1), \\ &n_2 = (q-1)(q-i+1) \\ &P_1 = \begin{pmatrix} (i-1)(i-2) + q - 2 & (q-i+1)(i-1) \\ & (q-i+1)(i-1) & (q-i+1)(q-i) \end{pmatrix}, \\ &P_2 = \begin{pmatrix} i(i-1) & i(q-i) \\ & i(q-i) & (q-i)(q-i-1) + q - 2 \end{pmatrix}. \end{split}$$

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### **Cyclic Type Association Scheme**

Let there be v treatments and they are denoted by integers 1, 2, ..., v. In a cyclic type PBIBD, the first associates of treatment *i* are

$$i+d_1, i+d_2, \dots, i+d_{n1} \pmod{\nu},$$

where the d's satisfy the following conditions:

- (i) the d's are all different and  $0 < d_j < v(j=1,2,...,n_1);$
- (ii) among the  $n_1(n_1-1)$  differences  $d_j d_{j'}$ ,  $(j, j'=1, 2, ..., n_1, j \neq j')$  reduced (mod v), each of numbers  $d_1, d_2, ..., d_n$  occurs  $\alpha$  times, whereas each of the numbers  $e_1, e_2, ..., e_{n_2}$  occurs  $\beta$ times, where  $d_1, d_2, ..., d_{n_1}, e_1, e_2, ..., e_{n_2}$  are all the different v-1 numbers 1, 2, ..., v-1.

[Note: To reduce an integer mod v, we have to subtract from it a suitable multiple of v, so that the reduced integer lies between 1 and v. For example, 17 when reduced *mod* 13 is 4.]

For this scheme,

$$n_{1}\alpha + n_{2}\beta = n_{1}(n_{1} - 1),$$

$$P_{1} = \begin{pmatrix} \alpha & n_{1} - \alpha - 1 \\ n_{1} - \alpha - 1 & n_{2} - n_{1} + \alpha + 1 \end{pmatrix},$$

$$P_{2} = \begin{pmatrix} \beta & n_{1} - \beta \\ n_{1} - \beta & n_{2} - n_{1} + \beta - 1 \end{pmatrix}.$$

#### Singly Linked Block Association Scheme

Consider a BIBD D with parameters  $b^{**}, v^{**}, r^{**}, k^{**}, \lambda^{**}=1$  and  $b^{**}>v^{**}$ .

Let the block numbers of this design be treated as treatments, i.e.,  $v = b^{**}$ . The first and second associates in the singly linked block association scheme with two classes are determined as follows: Define two block numbers of D to be the first associates if they have exactly one treatment in common and second associates otherwise.

Under this association scheme,

$$\begin{split} &v = b^{**}, \\ &n_1 = k^{**}(r^{**} - 1), \\ &n_2 = b^{**} - 1 - n_1, \\ &P_1 = \begin{pmatrix} r^{**} - 2 + (k^{**} - 1)^2 & n_1 - r^{**} - (k^{**} - 1)^2 + 1 \\ n_1 - r^{**} - (k^{**} - 1)^2 + 1 & n_2 - n_1 + r^{**} + (k^{**} - 1)^2 - 1 \end{pmatrix}, \\ &P_2 = \begin{pmatrix} k^{**2} & n_1 - k^{**2} \\ n_1 - k^{**2} & n_2 - n_1 + k^{**2} - 1 \end{pmatrix}. \end{split}$$

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## **General Theory of PBIBD**

A PBIBD with m-associate classes is defined as follows. Let there be v treatments. Let there are b blocks and the size of each block is k, i.e., there are k plots in each block. Then the v treatments are arranged in b blocks according to an m-associate partially balanced association scheme such that

- (a) every treatment occurs at most once in a block,
- (b) every treatment occurs exactly in *r* blocks and
- (c) if two treatments are the *i*<sup>th</sup> associates of each other then they occur together exactly in  $\lambda_i (i = 1, 2, ..., m)$  blocks.

The number  $\lambda_i$  is independent of the particular pair of  $i^{th}$  associate chosen. It is not necessary that  $\lambda_i$  should all be different and some of them  $\lambda_i$ 's may be zero.

If v treatments can be arranged in such a scheme then we have a PBIBD. Note that here two treatments which are the *i*<sup>th</sup> associates, occur together in  $\lambda_i$  blocks.

The parameters  $b, v, r, k, \lambda_1, \lambda_2, ..., \lambda_m, n_1, n_2, ..., n_m$  are termed as the **parameters of the first kind** and  $p_{jk}^i$  are termed as the **parameters of the second kind**. It may be noted that  $n_1, n_2, ..., n_m$  and all  $p_{jk}^i$  of the design is obtained from the association scheme under consideration. Only  $\lambda_1, \lambda_2, ..., \lambda_m$ , occur in the definition of PBIBD.

If  $\lambda_i = \lambda$  for all i = 1, 2, ..., m then PBIBD reduces to BIBD. So BIBD is essentially a PBIBD with one associate class.

# **Conditions for PBIBD**

The parameters of a PBIBD are chosen such that they satisfy the following relations:

(i) bk = vr(ii)  $\sum_{i=1}^{m} n_i = v - 1$ (iii)  $\sum_{i=1}^{m} n_i \lambda_i = r(k - 1)$ (iv)  $n_k p_{ij}^k = n_i p_{jk}^i = n_j p_{ki}^j$ (v)  $\sum_{k=1}^{m} p_{jk}^i = \begin{cases} n_j - 1 & \text{if } i = j \\ n_j & \text{if } i \neq j. \end{cases}$ 

It follows from these conditions that there are only  $m(m^2-1)/6$  independent parameters of the second kind.

## **Interpretations of Conditions of PBIBD**

The interpretations of conditions (i)-(v) are as follows.

# (i) bk = vr

This condition is related to the total number of plots in an experiment. In our settings, there are k plots in each block and there are b blocks. So the total number of plots are bk. Further, there are v treatments and each treatment is replicated r times such that each treatment occurs atmost in one block. So the total number of plots containing all the treatments is vr. Since both, the statements counts the total number of blocks, hence bk = vr.

(ii) 
$$\sum_{i=1}^{m} n_i = v - 1$$

This condition interprets as follows:

Since with respect to each treatment, the remaining (v-1) treatments are classified as first, second,..., or  $m^{th}$  associates and each treatment has  $n_i$  associates, so the sum of all  $n_i$ 's is the same as the total number of treatments except the treatment under consideration.

(iii) 
$$\sum_{i=1}^{m} n_i \lambda_i = r(k-1)$$

Consider *r* blocks in which a particular treatment *A* occurs. In these *r* blocks, r(k-1) pairs of treatments can be found, each having *A* as one of its members. Among these pairs, the *i*<sup>th</sup> associate of *A* must occur  $\lambda_i$  times and there are  $n_i$  associates, so  $\sum_i n_i \lambda_i = r(k-1)$ .

# (iv) $n_i p_{jk}^i = n_j p_{ki}^j = n_k p_{ij}^k$

Let  $G_i$  be the set of  $i^{th}$  associates, i = 1, 2, ..., m of a treatment A. For  $i \neq j$ , each treatment in  $G_i$ has exactly  $p_{jk}^i$  numbers of  $k^{th}$  associates in  $G_i$ . Thus the number of pairs of  $k^{th}$  associates that can be obtained by taking one treatment from  $G_i$  and another treatment from  $G_j$  on the one hand is  $n_i p_{jk}^i$ and  $n_j p_{jk}^i$ , respectively.

(v) 
$$\sum_{k=1}^{m} p_{jk}^{i} = n_{j} - 1$$
 if  $i = j$  and  $\sum_{k=1}^{m} p_{jk}^{i} = n_{j}$  if  $i \neq j$ .

Let the treatments A and B be  $i^{th}$  associates. The  $k^{th}$  associate of A(k = 1, 2, ..., m) should contain all the  $n_j$  number of  $j^{th}$  associates of  $B(j \neq i)$ . When j = i, A itself will be one of the  $j^{th}$  associates of B. Hence  $k^{th}$  associate of A, (k = 1, 2, ..., m) should contain all the  $(n_j - 1)$  numbers of  $j^{th}$  associate of B. Thus the condition holds.

#### Intrablock Analysis of PBIBD With Two Associates

Consider a PBIBD under two associates scheme. The parameters of this scheme are  $b, v, r, k, \lambda_1, \lambda_2, n_1, n_2, p_{11}^1, p_{22}^1, p_{12}^1, p_{22}^2$  and  $p_{12}^2$ . The linear model involving block and treatment effects is

$$y_{ij} = \mu + \beta_i + \tau_j + \varepsilon_{ij}; i = 1, 2, ..., b, j = 1, 2, ..., v,$$

where

 $\mu$  is the general mean effect;

 $\beta_i$  is the fixed additive  $i^{th}$  block effect satisfying  $\sum_i \beta_i = 0$ ;

 $\tau_j$  is the fixed additive  $j^{th}$  treatment effect satisfying  $\sum_{i=1}^{r} \tau_j = 0$  and

 $\varepsilon_{ijm}$  is the i.i.d. random error with  $\varepsilon_{ijm} \sim N(0, \sigma^2)$ .

The PBIBD is a binary, proper and equi-replicate design. So in this case, the values of the parameters become  $n_{ij} = 0$  or 1,  $k_i = k$  for all i = 1, 2, ..., b and  $r_j = r$  for all j = 1, 2, ..., v. There can be two types of null hypothesis which can be considered – one for the equality of treatment effects and another for the equality of block effects. We are considering here the intrablock analysis, so we consider the null hypothesis related to the treatment effects only. As done earlier in the case of BIBD, the block effects can be considered under the interblock analysis of PBIBD and the recovery of interblock information.

The null hypothesis of interest is  $H_0: \tau_1 = \tau_2 = ... = \tau_v$  against alternative hypothesis  $H_1:$  at least one pair of  $\tau_j$  is different. The null hypothesis related to the block effects is of not much practical relevance and can be treated similarly. This was illustrated earlier in case of BIBD. In order to obtain the least-squares estimates of  $\mu$ ,  $\beta_i$  and  $\rho_j$ , we minimize of the sum of squares due to residuals

$$\sum_{i=1}^{b} \sum_{j=1}^{v} (y_{ij} - \mu - \beta_i - \tau_j)^2$$

with respect to  $\mu$ ,  $\beta_i$  and  $\tau_j$  This results in the three normal equations which can be unified using the matrix notations. The set of reduced normal equations in matrix notation after eliminating the block effects are expressed as

$$Q = C \imath$$

where

$$C = R - N' K^{-1}N,$$
  

$$Q = V - N' K^{-1}B,$$
  

$$R = rI_{v},$$
  

$$K = kI_{b}.$$

Then the diagonal elements of C are

$$c_{jj} = r - \frac{\sum_{i=1}^{b} n_{ij}^2}{k} = \frac{r(k-1)}{k}, \quad (j = 1, 2, ..., v),$$

the off-diagonal elements of C are obtained as

$$c_{jj'} = -\frac{1}{k} \sum_{i=1}^{b} n_{ij} n_{ij'} = \begin{cases} -\frac{\lambda_1}{k} & \text{if treatment } j \text{ and } j' \text{ are the first associates} \\ -\frac{\lambda_2}{k} & \text{if treatment } j \text{ and } j' \text{ are the second associates} \quad (j \neq j'=1, 2, ..., v) \end{cases}$$

and the  $j^{th}$  value in Q is

$$Q_{j} = V_{j} - \frac{1}{k} [\text{Sum of block totals in which } j^{th} \text{ treatment occurs}]$$
$$= \frac{1}{k} \left[ r(k-1)\tau_{j} - \sum_{i} \sum_{j'(j \neq j')} n_{ij} n_{ij'} \tau_{j} \right].$$

Next, we attempt to simplify the expression of  $Q_i$ .

Let  $S_{j1}$  be the sum of all treatments which are the first associates of  $j^{th}$  treatment and  $S_{j2}$  be the sum of all treatments which are the second associates of  $j^{th}$  treatment. Then

$$\tau_j + S_{j1} + S_{j2} = \sum_{j=1}^{\nu} \tau_j.$$

Thus the equation in  $Q_j$  using this relationship for j = 1, 2, ..., v, becomes

$$kQ_{j} = \left[r(k-1)\tau_{j} - (\lambda_{1}S_{j1} + \lambda_{2}S_{j2})\right]$$
  
=  $r(k-1)\tau_{j} - \lambda_{1}S_{j1} - \lambda_{2}\left[\sum_{j=1}^{\nu}\tau_{j} - \tau_{j} - S_{j1}\right]$   
=  $\left[r(k-1) + \lambda_{2}\right]\tau_{j} + (\lambda_{2} - \lambda_{1})S_{j1} - \lambda_{2}\sum_{j=1}^{\nu}\tau_{j}.$ 

Imposing the side condition  $\sum_{j=1}^{\nu} \tau_j = 0$ , we have

$$kQ_{j} = \left[r(k-1)\tau_{j} + \lambda_{2}\right]\tau_{j} + (\lambda_{2} - \lambda_{1})S_{j1}$$
$$= a_{12}^{*}\tau_{j} + b_{12}^{*}S_{j1}, \quad j = 1, 2, ..., v$$

where  $a_{12}^* = r(k-1) + \lambda_2$  and  $a_{12}^* = \lambda_2 - \lambda_1$ .

These equations are used to obtain the adjusted treatment sum of squares.

Let  $Q_{j1}$  denotes the adjusted sum of  $Q_j$ 's over the set of those treatments which are the first associate of  $j^{th}$  treatment. We note that when we add the terms  $S_{j1}$  for all j, then j occurs  $n_1$  times in the sum, every first associate of j occurs  $p_{11}^1$  times in the sum and every second associate of joccurs  $p_{11}^2$  times in the sum with  $p_{11}^2 + p_{12}^2 = n_1$ . Then using  $K = kI_h$  and  $\sum_{i=1}^{v} \tau_i = 0$ , we have

ccurs 
$$p_{11}^2$$
 times in the sum with  $p_{11}^2 + p_{12}^2 = n_1$ . Then using  $K = kI_b$  and  $\sum_{j=1}^{\nu} \tau_j = 0$ , we have

$$kQ_{j1} = k \sum_{j \in S_{j1}} Q_j = \text{Sum of } Q_j \text{'s which are the first associates of treatment } j$$
  
=  $[r(k-1) + \lambda_2] S_{j1} + (\lambda_2 - \lambda_1) [n_1 \tau_j + p_{11}^1 S_{j1} + p_{11}^2 S_{j2}]$   
=  $[r(k-1) + \lambda_2 + (\lambda_2 - \lambda_1)(p_{11}^1 - p_{11}^2] S_{j1} + (\lambda_2 - \lambda_1) p_{12}^2 \tau_j$   
=  $b_{22}^* S_{j1} + a_{22}^* \tau_j$ 

where

$$a_{22}^* = (\lambda_2 - \lambda_1) p_{12}^2$$
  

$$b_{22}^* = r(k-1) + \lambda_2 + (\lambda_2 - \lambda_1) (p_{11}^1 - p_{11}^2).$$

Now we have following two equations in  $kQ_j$  and  $kQ_{j1}$ :

$$kQ_{j} = a_{12}^{*}\tau_{j} + b_{12}^{*}S_{j1}$$
$$kQ_{j1} = a_{22}^{*}\tau_{j} + b_{22}^{*}S_{j1}$$

Now solving these two equations, the estimate of  $\tau_j$  is obtained as

$$\hat{\tau}_{j} = \frac{k[b_{22}^{*}Q_{j} - b_{12}^{*}Q_{j1}]}{a_{12}^{*}b_{12}^{*} - a_{22}^{*}b_{12}^{*}}, \quad (j = 1, ..., v).$$

We see that

$$\sum_{j=1}^{\nu} Q_j = \sum_{j=1}^{\nu} Q_{j1} = 0,$$

so

$$\sum_{j=1}^{\nu} \hat{\tau}_j = 0.$$

Thus  $\hat{\tau}_j$  is a solution of the reduced normal equation.

The analysis of variance can be carried out by obtaining the unadjusted block sum of squares as

$$SS_{Block(unadj)} = \sum_{i=1}^{b} \frac{B_i^2}{k} - \frac{G^2}{bk},$$

the adjusted sum of squares due to treatment as

$$SS_{Treat(adj)} = \sum_{j=1}^{\nu} \hat{\tau}_j Q_j$$

where  $G = \sum_{i=1}^{b} \sum_{j=1}^{v} y_{ij}$ . The sum of squares due to error as

$$SS_{Error(t)} = SS_{Total} - SS_{Block(unadj)} - SS_{Treat(adj)}$$

where

$$SS_{Total} = \sum_{i=1}^{b} \sum_{j=1}^{v} y_{ij}^2 - \frac{G^2}{bk}.$$

A test for  $H_0: \tau_1 = \tau_2 = ... = \tau_v$  is then based on the statistic

$$F_{Tr} = \frac{SS_{Treat(adj)} / (v-1)}{SS_{Error(unadj)} / (bk - b - v + 1)}.$$

If  $F_{Tr} > F_{1-\alpha;\nu-1,bk-\nu-b+1}$  then  $H_0$  is rejected.

Sum of squares	Degrees of	Mean squares	F
	freedom		
$SS_{Treat(adj)} =$	$df_{Treat} = v - 1$	$MS_{T} = \frac{SS_{Treat(adj)}}{S_{T}}$	<u>MS<sub>Treat</sub></u>
$\sum_{\nu}^{\nu} \hat{\tau} O$		$df_{\rm Treat}$	MSE
$\sum_{j=1}^{j \in j} j \in j$			
$SS_{Block(unadj)}$			
$\sum_{b}^{b} B^{2} G^{2}$	df - h - 1		
$\sum_{i=1}^{k} \overline{k}^{-} \overline{bk}$	$u_{Block} - v - 1$		
$SS_{Frror(t)}$		SS-	
(By substraction)	$df_{ET} =$	$MSE = \frac{SSE_{Error}}{df_{ET}}$	
ו /	bk-b-v+1	5 E1	
$SS_{Total} =$	$df_T = bk - 1$		
$\sum_{\nu}^{b} \sum_{\nu}^{\nu} v^2 - \frac{G^2}{G^2}$			
$\sum_{i=1}^{j} \sum_{j=1}^{j} y_{ij} bk$			
	Sum of squares $SS_{Treat(adj)} =$ $\sum_{j=1}^{v} \hat{\tau}_{j} Q_{j}$ $SS_{Block(unadj)}$ $\sum_{i=1}^{b} \frac{B^{2}}{k} - \frac{G^{2}}{bk}$ $SS_{Error(t)}$ (By substraction) $SS_{Total} =$ $\sum_{i=1}^{b} \sum_{j=1}^{v} y_{ij}^{2} - \frac{G^{2}}{bk}$	Sum of squaresDegreesof $SS_{Treat(adj)} =$ $df_{Treat} = v - 1$ $\sum_{j=1}^{v} \hat{\tau}_{j} Q_{j}$ $df_{Treat} = v - 1$ $SS_{Block(unadj)}$ $df_{Block} = b - 1$ $\sum_{i=1}^{b} \frac{B^{2}}{k} - \frac{G^{2}}{bk}$ $df_{Block} = b - 1$ $SS_{Error(t)}$ $df_{ET} =$ $(By substraction)$ $df_{ET} =$ $SS_{Total} =$ $df_{T} = bk - 1$ $\sum_{i=1}^{b} \sum_{j=1}^{v} y_{ij}^{2} - \frac{G^{2}}{bk}$ $df_{T} = bk - 1$	Sum of squaresDegreesofMean squares $SS_{Treat(adj)} =$ $df_{Treat} = v - 1$ $MS_{Treat} = \frac{SS_{Treat(adj)}}{df_{Treat}}$ $\sum_{j=1}^{v} \hat{\tau}_{j} Q_{j}$ $df_{Ireat} = v - 1$ $MS_{Treat} = \frac{SS_{Treat(adj)}}{df_{Treat}}$ $SS_{Block(unadj)}$ $df_{Block} = b - 1$ $MSE = \frac{SS_{Error}}{df_{ET}}$ $SS_{Error(t)}$ $df_{ET} =$ $MSE = \frac{SS_{Error}}{df_{ET}}$ $SS_{Total} =$ $df_T = bk - 1$ $MSE = \frac{SS_{Error}}{df_{ET}}$

The intrablock analysis of variance for testing the significance of treatment effects is given in the following table:

Note that in the intrablock analysis of PBIBD analysis, at the step where we obtained  $S_{j1}$  and eliminated  $S_{j2}$  to obtain the following equation

$$kQ_j = \left[r(k-1) + \lambda_2\right]\tau_j + (\lambda_2 - \lambda_1)S_{j1} - \lambda_2\sum_{j=1}^{\nu}\tau_j,$$

another possibility is to eliminate  $S_{j1}$  instead of  $S_{j2}$ . If we eliminate  $S_{j2}$  instead of  $S_{j1}$  (as we approached), then the solution has less work involved in the summing of  $Q_{j1}$  if  $n_1 < n_2$ . If  $n_1 > n_2$ , then eliminating  $S_{j1}$  will involve less work in obtaining  $Q_{j2}$  where  $Q_{j2}$  denotes the adjusted sum of  $Q_j$ 's is over the set of those treatments which are the second associate of  $j^{th}$  treatment. When we do so, obtain the following estimate of the treatment effect is obtained as:

$$\hat{\tau}_{j}^{*} = \frac{k \left[ b_{21}^{*} Q_{j} - b_{11}^{*} Q_{j2} \right]}{a_{11}^{*} b_{21}^{*} - a_{21}^{*} b_{11}^{*}}$$

where

$$a_{11}^* = r(k-1) + \lambda_1$$
  

$$b_{11}^* = \lambda_1 - \lambda_2$$
  

$$a_{21}^* = (\lambda_1 - \lambda_2) p_{12}^1$$
  

$$b_{21}^* = r(k-1) + \lambda_1 + (\lambda_1 - \lambda_2) (p_{22}^2 - p_{22}^1)$$

The analysis of variance is then based on  $\hat{\tau}_{j}^{*}$  and can be carried out similarly.

The variance of the elementary contrasts of estimates of treatments (in case of  $n_1 < n_2$ )

$$\hat{\tau}_{j} - \hat{\tau}_{j'} = \frac{b_{22}^{*}(kQ_{j} - kQ_{j'}) - b_{12}^{*}(kQ_{j1} - kQ_{j'1})}{a_{12}^{*}b_{22}^{*} - a_{22}^{*}b_{12}^{*}}$$

is

$$Var(\hat{\tau}_{j} - \hat{\tau}_{j'}) = \begin{pmatrix} \frac{2k(b_{22}^{*} + b_{12}^{*})}{a_{12}^{*}b_{22}^{*} - a_{22}^{*}b_{12}^{*}} & \text{if treatment } j \text{ and } j' \text{ are the first associates} \\ \frac{2kb_{12}^{*}}{a_{12}^{*}b_{22}^{*} - a_{22}^{*}b_{12}^{*}} & \text{if treatment } j \text{ and } j' \text{ are the second associates.} \end{cases}$$

We observe that the variance of  $\hat{\tau}_j - \hat{\tau}_{j'}$  depends on the nature of j and j' in the sense that whether they are the first or second associates. So design is not (variance) balanced. But variance of any elementary contrast are equal under a given order of association, viz., first or second. That is why the design is said to be partially balanced in this sense.