BIB DESIGNS WITH ONE TREATMENT MISSING

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1. Introduction

The object of this paper is to consider the analysis of BIB designs, when the yields in the plots containing a particular treatment are totally missing. A situation of this type occurs in practice when,

(i) after the experimental area has been prepared for a BIB design it may be found out that two of the v-treatments are identical in formulæ though not in brand, so that to avoid repetition and costs of laying out and harvesting, the experiment may be carried out with only $v - 1$ treatments, using the same experimental area, analyzing as a BIB with a missing treatment;

(ii) one of the treatments (generally the control) may happen to be not pest resistant, so that during the experiment the yields in the plots where this treatment is applied are affected to a large extent;

(iii) the number of treatments to be compared may be only s and the most useful and practicable BIBD may exist only with parameters v, b, r, k, λ where $v = s + 1$, so that the area is prepared for the above BIBD and removing at random one treatment and all its plots, the experiment is laid out.

Under the above conditions the design becomes one where all the blocks are not of the same size. The mode of analysis of variance is not simple for such a design in general as it depends on the structure of the actual design. However it has been shown in this paper that in some particular cases the analysis can be carried out quite easily and that this analysis comes out to be analogous to that of BIB, GD and PBIB designs, though the block sizes differ.

2. Analysis in the General Case

Consider a BIB with parameters v, b, r, k, λ. Let all the yields pertaining to the v-th treatment be deleted. Then we have a design with parameters

$$\left.\begin{array}{l} v' = v - 1, \;\; b' = b, \;\; r_j = r \;\text{ for } j = 1, 2, \cdots, \\ \quad v - 1\text{; and } k_i = k - 1 \text{ if } i\text{-th block con-} \\ \quad \text{tains } v\text{-th treatment} = k \text{ otherwise} \end{array}\right\} . \tag{1}$$

Let n_{ij} denote the number of times the j-th treatment occurs in the i-th block ($n_{ij} = 0$ or 1). Then

$$Q_j = T_j - \sum_i \frac{n_{ij} B_i}{k_i} \tag{2}$$

where T_j is the total of the j-th treatment and B_i is the total of the i-th block. Also under the usual notation we have

$$c_{jj} = r_j - \sum_i \frac{n_{ij}^2}{k_i} = \frac{r - \lambda}{(k - 1)} - \frac{(r - \lambda)}{k} \tag{3}$$

where $j = 1, 2, \ldots, v - 1$, since the j-th treatment occurs λ times in blocks where the v-th treatment occurs. Also

$$c_{jj'} = - \sum_i \frac{n_{ij} \cdot n_{ij'}}{k_i}, \tag{4}$$

Unless the actual structure of the BIBD is known the quantities c_{jj} cannot be evaluated in advance. Hence to proceed with the analysis, the normal equations

$$Q_j = \sum_{j'} c_{jj'} \hat{\tau}_{j'} \tag{5}$$

are to be actually constructed and solved. Thus a simple mode of analysis of variance does not exist in general. I shall now examine some particular cases where simple solutions exist for equations (5).

3. Balanced Designs

Suppose there exists a BIBD with parameters v, b, r, k, λ for which we can find an integer $\theta < \lambda$ such that any pair of treatments j, j' ($j, j' \neq v$) occur exactly θ times in the blocks where the v-th treatment occurs. Clearly if such an integer θ should exist, we should have

$$\theta (v - 2) = \lambda (k - 2) \tag{6}$$

In case of such a design, from (4) we have

$$c_{jj'} = - \frac{\theta}{(k - 1)} - \frac{(\lambda - \theta)}{k} \quad \text{for all } j, j' \neq v. \tag{7}$$

Also from (3) since $\lambda(v-1) = r(k-1)$,

$$c_{jj} = +\frac{\lambda v}{k} - \frac{\lambda}{k} - \frac{\lambda}{k(k-1)}. \tag{8}$$

Substituting these values in (5), and remembering that $\Sigma \hat{\tau}_j = 0$ and simplifying, we get

$$Q_j = \left[\frac{\lambda v}{k} - \frac{(\lambda - \theta)}{k(k-1)}\right] \hat{\tau}_j \qquad \text{for all } j \neq v. \tag{9}$$

From equations (9) we can readily obtain $\hat{\tau}_j$ and hence calculate the S.S. due to treatments adjusted for blocks. Also we can see that any pair of treatments is compared with a constant efficiency so that the design is a balanced one, though the blocks are not of the same size. Again, comparing the bracketted term on the R.H.S. of (9) with the corresponding term in the normal equations for the BIBD we see that since $\theta < \lambda$ this design is less efficient than the BIBD and the loss of efficiency can be at once obtained.

The series of BIB designs, $v = n = b$, $r = n - 1 = k$, $\lambda = n - 2$, for all integral values of n fall into this type. The value of θ will be $n - 3$. Given $n - 1$ treatments this design can be constructed as follows: allot all these treatments to a block of size $n - 1$; then take all possible combinations of $n - 2$ treatments from these and allot each of these combinations to a block of size $n - 2$; thus there will be one block of size $n - 1$ and $n - 1$ blocks of size $n - 2$, and any pair of treatments occur together once in the block of size $n - 1$ and $n - 3$ times in blocks of size $n - 2$.

Now consider the set of BIBD derivable from $EG(N, 2)$, taking all the points belonging to a m-flat and allotting these to a block. The parameters of this design are as follows:

$$v = 2^N, \quad k = 2^m,$$

$$\lambda = \frac{(1+2+2^2+\cdots+2^{N-2})\cdots(1+2+2^2+\cdots+2^{N-m+1})}{(1+2+2^2+\cdots+2^{m-2})\cdots 1} \tag{10}$$

the values of b and r being obtainable from the above parameters. From this it can be readily seen that,

$$\frac{\lambda(k-2)}{(v-2)}$$

is an integer θ equal to 1 if $m = 2$ and

$$\theta = \frac{(1+2+2^2+\cdots+2^{N-3})\cdots(1+2+2^2+\cdots+2^{N-m+1})}{(1+2+2^2+\cdots+2^{m-3})\cdots 1} \tag{11}$$

otherwise. Also it can be seen by actual construction (since every line contains exactly 2 points) that among the blocks where any pair of treatments occur (exactly λ in number) every other treatment is replicated θ times. Thus this set of designs also belongs to the balanced type of designs. The only practicable design ($r \leqslant 10$) of this series is given by

$$v = 8, \; b = 14, \; r = 7, \; k = 4, \; \lambda = 3 \qquad (12)$$

which gives rise, when a treatment and its plots are missing, to a balanced design with 7 blocks of size 4 and 7 of size 3 and $\theta = 1$.

Two other designs of this series are

$$\left.\begin{array}{l} v = 16, \; b = 30, \; r = 15, \; k = 8, \; \lambda = 7 \text{ and } \theta = 3 \\ v = 16, \; b = 140, \; r = 35, \; k = 4, \; \lambda = 7 \text{ and } \theta = 1 \end{array}\right\} \qquad (13)$$

4. *GD* Type Designs

Let a BIBD exist with parameters v, b, r, k, λ such that the first $v - 1$ treatments fall into m-classes of n-treatments each such that any pair of treatments belonging to the same class occurs θ_1 times and any two belonging to different classes occur θ_2 times among blocks where the v-th treatment occurs. Then we should have

$$nm = v - 1$$

and

$$\lambda (k - 2) = (n - 1)\, \theta_1 + (m - 1)\, n \cdot \theta_2$$

and

$$\left.\begin{array}{ll} c_{jj'} = -\dfrac{\theta_1}{(k-1)} - \dfrac{(\lambda - \theta_1)}{k} & \text{if } j \text{ and } j' \text{ belong to the same set} \\ \quad\; = -\dfrac{\theta_2}{(k-1)} - \dfrac{(\lambda - \theta_2)}{k}. & \text{otherwise.} \end{array}\right\} \qquad (14)$$

Putting these values in (5), summing them over the treatments belonging to the same class as j and simplifying we see that

$$S_1(Q_j) = \frac{(v-1)}{k(k-1)} \cdot \{\lambda (k - 1) + \theta_2\} \cdot S_1(\hat{\tau}_j) \qquad (15)$$

where $S_1(Q_j)$ denotes the sum of all the Q_j's pertaining to the treatments which belong to the same class as the j-th treatment.

Thus we have

$$Q_j = \left[\frac{\lambda v}{k} - \frac{(\lambda - \theta_1)}{k(k-1)}\right] \hat{\tau}_j$$

$$- \frac{\theta_1 - \theta_2}{v - 1} [\lambda (k-1) + \theta_2] S_1 (Q_j). \qquad (16)$$

From the above equations the values of $\hat{\tau}_j$ and hence the S.S. due to treatments, etc., can be calculated.

From the above steps it can be readily seen that this procedure is analogous to the analysis of *GD* designs and that the variances of treatment-comparisons fall into two classes. The actual values can be obtained from (16).

All the BIBD with $\lambda = 1$ fall into this type, because with respect to any treatment the rest of the $v - 1$ treatments fall into r classes of $k - 1$ each such that any two belonging to the same class occur together once among the blocks occupied by it and any two belonging to different classes do not occur together in these blocks at all. Thus when one treatment and all its plots are missing we have a design with $v - 1$ treatments each replicated r times in b blocks, r of which contain $k - 1$ plots each and the rest contain k plots each. Here $\theta_1 = 1$, $\theta_2 = 0$, $n = k - 1$ and $m = r$.

Again consider the BIBD given by

$$v = b = 7, \ r = k = 4, \ \lambda = 2.$$

In the next section we shall see that any SBIBD with $\lambda = 2$ will give rise to a PBIB in two associate classes, when all blocks containing a particular treatment are considered, *deleting* that treatment. In the case of this particular design, this PBIB reduces itself to *GD* type. Thus when a treatment and all its plots are missing from this design we get a *GD* type design discussed above. Constructing this design from the initial block (0, 1, 3, 6) and deleting 0 we see that the remaining six treatments fall into three classes, *viz.*, (1, 5); (2, 3); (4, 6), of two each such that the treatments in the same class do not occur together in the blocks occupied by 0 and treatments belonging to different classes occur together once among these. Hence here we have

$$\theta_1 = 0, \ \theta_2 = 1, \ n = 2, \ m = 3.$$

5. PBIB Type Designs

Let us suppose that there exists a BIBD with parameters v, b, r, k, λ such that with respect to any treatment $j \neq v$ the rest of the $v - 2$

treatments (not equal to v) fall into s classes of sizes $n_1, n_2, \cdots, n_s$ such that any treatment j' $(\neq j, v)$ which is an i-associate of j occurs with it in θ_i blocks where the treatment v occurs. Let us further suppose that the numbers p_{jk}^i which denote the number of treatments which are j-associates of one and k-associates of other of two treatments which are themselves i-associates, are independent of the particular treatments considered (as in the case of usual PBIBD). Then we can readily see that

$$\left.\begin{aligned} n_1 + n_2 + \cdots + n_s &= v - 2 \\ n_1\theta + n_2\theta_2 + \cdots + n_s\theta_s &= \lambda (k - 2) \end{aligned}\right\} \tag{18}$$

and the equations among p_{jki}'s are the same as in the case of PBIBD.

Thus from (4) we have

$$c_{jj'} = -\frac{\theta_i}{k-1} - \frac{(\lambda - \theta_i)}{k} \tag{19}$$

if j and j' are i-associates. Substituting these values in (5) we see that these can be solved in the same way as in the case of PBIBD. Thus we have a design analogous to the PBIBD, with unequal block sizes and here also there will be s different sets of comparisons with respect to every treatment having corresponding variances. The normal equations in this case will be in general more complicated than those for the PBIBD.

Let us consider a SBIBD with parameters $v = b$, $r = k$, λ. It is known for such designs that any pair of blocks contain λ treatments commonly. Thus if we take all the blocks where any treatment j $(j \neq v)$ occurs with the treatment v, any pair from these blocks should contain $\lambda = 2$ more treatments other than j and v as common.

Now consider all SBIBD for which $\lambda = 2$. From the above argument it follows that any pair of blocks containing j and v together cannot have any other treatment in common. There are exactly $2(k-2)$ such treatments and all these must be distinct. Thus in a SBIBD with $\lambda = 2$, with respect to any treatment $j \neq v$ the rest of the $v - 2$ treatments (other than j and v) fall into two classes, the first containing $2(k-2)$ treatments which occur once and the second containing $v - 2 - 2(k-2) = (k-2)(k-3)/2$ treatments which do not occur at all among the blocks where j and v occur together. Thus if we consider the k blocks where v occurs and delete v we have a PBIBD in two associate classes with first kind of parameters as

$$v^* = v - 1,\ b^* = k,\ r^* = 2,\ k^* = k - 1,\ \lambda_1 = 1,\ \lambda_2 = 0,$$
$$n_1 = 2(k-2),\ n_1 = \frac{(k-2)(k-3)}{2}. \tag{20}$$

Now let us consider the second kind of parameters. Let j and j' be first associates. Then they occur together in one block with v. In this block there are $k-3$ more treatments all of which must be first associates of both j and j'. Also v occurs with j in one more block not containing j' and with j' in another block not containing j and these two blocks must have another common treatment different from v, j and j'. This treatment also will be a first associate of both j and j'. This property is independent of the choice of j and j'. Thus we should have

$$p_{11}{}^1 = k - 2. \tag{21}$$

From this it follows that

$$p_{12}{}^1 = k - 3 \quad \text{and} \quad p_{22}{}^1 = \frac{(k-3)(k-4)}{2}.$$

Also the values of other second kind of parameters can be at once evaluated and we see that

$$p_{11}{}^2 = 4,\ p_{12}{}^2 = 2(k-4),\ p_{22}{}^2 = \frac{(k-4)(k-5)}{2}. \tag{22}$$

Thus if from a SBIBD with $\lambda = 2$ a treatment and all its plots are missing we have a PBIB type design in two associate classes, with k blocks containing $k-1$ plots each and the rest containing k plot, each, with first kind of parameters

$$\theta_1 = 1,\ \theta_2 = 0,\ n_1 = 2(k-2),\ n_2 = \frac{(k-2)(k-3)}{2} \tag{23}$$

and second kind of parameters as given above.

Also the above discussion gives us the methods of constructing the following PBIBD in two associate classes.

$$v^* = v - 1,\ b^* = k,\ r^* = 2,\ k^* = k - 1,\ \lambda_1 = 1,\ \lambda_2 = 0s$$
$$n_1 = 2(k-2),\ n_2 = \frac{(k-2)(k-3)}{2} \tag{24}$$

and

$$v^* = v - 1,\ b^* = v - k,\ r^* = k - 2,\ k^* = k,\ \lambda_1 = 0,$$
$$\lambda_2 = 1,\ n_1 = 2(k-2),\ n_2 = \frac{(k-2)(k-3)}{2} \tag{25}$$

and the values of p_{jk}^i as given above, where v and k are the parameters of an existing SBIBD with $\lambda = 2$. (The second series are obtained by deleting a treatment and all the blocks containing it from the SBIBD.)

The SBIBD with $k = 4$ was already discussed and the other practicable SBIBD with $\lambda = 2$ are as follows:

$$v = b = 11, \quad r = k = 5, \quad \lambda = 2, \quad \theta_1 = 1, \quad \theta_2 = 0,$$
$$n_1 = 6, \quad n_2 = 3. \tag{26}$$

$$v = b = 16, \quad r = k = 6, \quad \lambda = 2, \quad \theta_1 = 1, \quad \theta_2 = 0,$$
$$n_1 = 8, \quad n_2 = 6. \tag{27}$$

$$v = b = 37, \quad r = k = 9, \quad \lambda = 2, \quad \theta_1 = 1, \quad \theta_2 = 0,$$
$$n_1 = 14, \quad n_2 = 21. \tag{28}$$

Now let us turn to two SBIBD with $\lambda = 3$ which also give rise to PBIB type designs with two associate classes when a treatment is deleted. Firstly consider

$$v = b = 11, \quad r = k = 6, \quad \lambda = 3. \tag{29}$$

Taking all the blocks containing any particular treatment j say and using the argument that any two of these must contain exactly two treatments $(\neq j)$ as common, it can be easily deduced that with respect to any treatment $(\neq j)$, the remaining 9 treatments fall into two classes, the first containing six treatments which occur once and the second three treatments which occur twice with that treatment among these six blocks. The values for the parameters of the second kind can also be easily computed and thus by the deletion of j we have the PBIB type design with parameters:

$$v = 10, \quad b = 11, \quad r = 6, \quad k = 6 \text{ or } 5, \quad \lambda = 3, \quad \theta_1 = 1, \quad \theta_2 = 2,$$
$$n_1 = 6, \quad n_2 = 3, \quad p_{11}^1 = 0, \quad p_{12}^1 = p_{12}^2 = 2, \quad p_{11}^2 = 1,$$
$$p_{22}^2 = 3, \quad p_{22}^1 = 4. \tag{30}$$

Also from arguments already given the above design can be broken up into two PBIBD in two associate classes, one with block-size 5 and the other with 6.

Now consider the SBIB given by

$$v = b = 15, \quad r = k = 7, \quad \lambda = 3. \tag{31}$$

The above design can be constructed from $PG(2, 3)$, by taking the planes as blocks. Since in this PG every line contains exactly 3 points, it follows that if 0, 1, 2 are coplanar then 2 must always occur in every plane where 0 and 1 occur together! Thus since any two blocks containing 0 must have just two more treatments in common it follows that the totality of the remaining 14 treatments is divisible into seven pairs such that in a block where 0 occurs both or none of the treatments belonging to a pair can occur. From this we see that when 0 is deleted we get a PBIB-type in two associate classes (actually a *GD*-type) with parameters

$$v = 14, \quad b = 15, \quad r = 7, \quad k = 7 \text{ or } 6, \quad \lambda = 3, \quad \theta_1 = 3,$$
$$\theta_2 = 1, \quad n_1 = 1, \quad n_2 = 12. \tag{32}$$

[The above argument followed from the actual mode of construction for the SBIBD. But it can be rigorously shown that whatever be the mode of construction the design (31) always gives rise to (32) when one treatment is deleted. I am leaving the proof as it is not essential for the practical aspects of this paper.]

6. Conclusions

The analysis of many types of BIBD of common occurrence with one treatment missing has been discussed in this paper and it has been shown that this analysis is analogous to that of BIB, GD and PBIB designs. The solution of the normal equations however will be more complicated. One interesting feature is the existence of balanced, GD and PBIB type designs with all blocks not having the same number of plots. However these designs are of practical utility only when the intra-block error variance between blocks of different sizes does not differ much. Since there are only two possible block sizes k and $k-1$, and we are mainly concerned with agricultural field experiments where the area is prepared in advance we may assume that this difficulty can be eliminated.

The construction of GDD from BIBD by deleting a treatment and all blocks containing it had already been discussed by others but GD type designs as defined by me are more efficient since the number of replications for the treatments is more. Also this paper throws more light on the construction of GD and PBIB designs in two associate classes starting from a BIBD and deleting a treatment from all the blocks containing it or its compliment.

7. Acknowledgements

My sincerest thanks are to Dr. S. S. Shrikhande and Prof. M. C. Chakrabarti who kindly read the paper and gave some valuable suggestions for improvement.

8. References

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