NATIONAL FELLOW SCHEME

EFFICIENT DESIGN OF EXPERIMENTS FOR QUALITY AGRICULTURAL RESEARCH

ANNUAL PROGRESS REPORT
2006-2007

Rajender Parsad

INDIAN AGRICULTURAL STATISTICS RESEARCH INSTITUTE
(ICAR)
LIBRARY AVENUE, PUSA, NEW DELHI- 110 012

Contents

Topic	Page Number
Introduction	**1**
Analytical Techniques for Multi-Response Experiments under Block Design Setup	**3**
Outliers in Multi-response Experiments	**33**
Minimally Connected Designs with Extra Observations	**46**
Designs for Crop Sequence Experiments	**47**
Nested Partially Balanced Incomplete Block Designs	**49**
Nested Block Designs under Correlated Error Structure	**55**
Doubly Nested Partially Balanced Incomplete Block Designs	**75**
Design Resources Server	**86**
Transfer of Technology / Advisory Services	**87**
Publications	**90**
Awards and Recognitions	**92**
Conferences/ Workshops Organized	**93**
Teaching and Research Guidance	**94**
Presentations in Conferences/ Symposia/ Workshop/ Seminar and Other fora	**96**
Summary	**99**

Introduction

Experimentation is an integrated component of every scientific endeavour. Designed experiments are conducted in the field of agricultural and other allied sciences. These experiments are being conducted under National Agricultural Research System (NARS) comprising of various ICAR Institutes, National Research Centres, Project Directorates, State Agricultural Universities, etc. It is through the data collected from designed experiments that the valid inferences are drawn. In any experiment, the total variability obtained in the data is broadly divided into two components (a) that part of variability to which a cause can be assigned and (b) that part of the variability to which no reason can be assigned, also called the experimental error. It is desirable that the experimental error is as small as possible otherwise the results emerging from the experimentation may be misleading. This part of the variability can be controlled either through designing or through analytical techniques, most common being the analysis of covariance. The first part of the variability has two major components: (i) treatments (ii) the experimental material. The variability arising because of the experimental material is taken care of by adopting the principle of local control like one-way blocking, two-way blocking, and so on. It is the variability among the treatments that is generally of interest to the experimenter.

The objectives of the experiment or the problems to be solved may be of some specified type of comparisons among the treatments. For instance, in varietal trials all the possible pairwise treatment comparisons could be of interest to the experimenter. In some other situations, when one particular treatment is on a special footing, also termed as control, as compared to other treatments, called the tests, the tests versus control comparisons are of interest to the experimenter. Similarly, when the treatment structure is factorial in nature, some special treatment contrasts known as factorial effects are of interest. But one design cannot be good for every problem. In other words, one has to pick up a design for the specific problem. This is the problem of designing an experiment. The data generated from a designed experiment is analyzed using the technique of analysis of variance. The proper choice of an experimental design reduces the per plot variance leading to a considerable reduction in error mean squares and hence the precision of the treatment comparisons. Further, contrast analysis can be used to answer further questions that cannot be answered by the usual analysis of variance. At present, the Indian Agriculture has steered from the era of chronic food deficits to that of self sufficiency and even exports. In fast changing scenario, to make agricultural research competitive, it is essential that sound statistical methodologies be used for the collection and analysis of experimental data.

This scheme aims at providing efficient design of experiments and sound analytical procedures so as to maintain high standards and good quality of agricultural research so as to make agricultural research globally competitive. The main emphasis is being laid on obtaining designs that simultaneously maximize the precision and economize on the experimental resources. These designs will be quite useful for the experiments with limited experimental material particularly the experiments for assessing the impact of soil erosion on crop productivity.

During the period under report, the emphasis was made on obtaining economic, efficient and robust designs for single reponse experiments and on the development of analytical procedures for the analysis of experimental data related to multi-response experiments with special emphasis on contrast analysis for identifying the best treatment.

Step wise procedure for the analysis of block designs for complete multi-response experiments including multivariate treatment contrast analysis has been developed. A criterion based on Euclidean distance of the treatment means from null vector has been developed for identification of

the best treatment in complete multi-response situations. A test statistic for detection of a single outlier vector in complete multi-response experiments conducted using block designs has been developed.

Minimally connected designs with extra observations, extended group divisible designs, nested partially balanced incomplete block designs, nested block designs for correlated observations, doubly nested partially balanced incomplete block designs have been obtained and catalogued.

To disseminate the knowledge available on the combinatorial aspects of designs and analytical procedures acquired to the scientists engaged in research in National Agricultural Research System, the advisory services are pursued rigorously. As a consequence, α-designs have been adopted by National Research Centre on Rapeseed and Mustard, Bharatpur. Three training programmes on (i) *Design and Analysis of Experiments for Rapeseed-Mustard Varietal Trials*; (ii) *Design and Analysis of Farmers Participatory Research Trials* and (iii) *Advances in Data Analytical Techniques* were organized as Course Director.

For the benefit of the experimenters and practicing statisticians, the beginning made last year in the development of DESIGN RESOURCES SERVER was strengthened. Efficient designs for making all possible pairwise treatment comparisons for $v \leq 35, b \leq 50, k \leq 34$ such that average replication number of treatments is not more than 20 and on-line software developed for generation of Hadamard matrices of order upto 1000 except the orders 668, 716 and 892 (for which no construction method is currently available) and 876 (yet to be implemented) have been posted on DESIGN RESOURCES SERVER. A brief description of the achievements made is given in the sequel.

A) Analytical Techniques for Multi-Response Experiments Under Block Design Setup

A.1 Introduction

Experiments in which data on several responses are measured from an experimental unit corresponding to the application of a treatment are known as multi-response experiments. There is a tendency to analyze data from these experiments as a single response experiment in the sense that each response variable is analyzed separately as if the responses were independent. As many analyses as the numbers of response variables are carried out. Another approach of analyzing data from multi-response experiments is to convert the data into univariate by defining an index. The index may be net returns, total calories, total energy, etc. or some weighted average of all the response variables, the weights being the relative importance of the response variables, decided in consultation with the subject matter specialist. Sometimes, the first principal component score is taken as an index. The first principal component may, however, not explain a significant part of the variability in the data. While observing several response variables in an experiment, the basic need is to exploit the correlations among the several response variables because these correlations contain a lot of information. On the contrary, if the data were analyzed, as if the variables were independent, then the advantage of the correlation structure is lost. It would, therefore, be advantageous to make treatment comparisons on the basis of several correlated responses observed on each experimental unit.

Therefore, to take advantage of correlation structure between several response variables in multi-response experiments the data should be analyzed using multivariate analysis of variance (MANOVA). The stepwise procedure for performing MANOVA of the data from RCB designs is available in the literature. A good account of analysis and designing for multi-response experiments are available in Roy (1957), Anderson (1958) and Johnson and Wichern (2002). There, however, exist situations, where the use of RCB design may not be possible and one has to use incomplete block design. It seems that a stepwise procedure of analysis of multi-response data from incomplete block designs is not available. In the present study an effort has been made to develop a stepwise procedure for the analysis of data of multi-response experiments conducted using an incomplete block design.

If the treatments are found to be significantly different for all the responses simultaneously, then the next question is "which treatments are significantly different?" To obtain the answer to this question, the procedure of performing multivariate treatment contrast analysis has been developed. Further, if the two treatments are found to be different, the procedure of identification of the better treatment among the two is required. Some procedures for identification of the best treatment have also been suggested.

The linear multi-response model for a complete multi-response experiments conducted using a block design is given in Section A.2. The information matrix for estimating the linear function of treatment effect vectors is also obtained in this section. Multivariate analysis of variance table for testing the equality of treatment and block effects is also given in Section A.2. A multivariate treatment contrast analysis along with the testing procedure is given in Section A.3. Some procedures for identification of the best treatment from multi-response experiments are described in Section A.4. The analytical procedures developed are illustrated with the help of real life examples in Section A.5.

A.2 Multivariate Analysis of Variance for Block Designs

Let there be v treatments laid out in a block design containing b blocks such that j^{th} block contains k_j experimental units; $j = 1,2,\ldots,b$ and treatment i is replicated r_i times, $\sum_{j=1}^{b} k_j = \sum_{i=1}^{v} r_i = n$, the total number of experimental units. From each experimental unit p responses are observed. Let $\mathbf{Y} = [\mathbf{y}_1\ \mathbf{y}_2\ \ldots\ \mathbf{y}_p]$ be $n \times p$ matrix of observations, where $\mathbf{y}_s$ is an $n \times 1$ vector of observations corresponding to the s^{th} response ($s = 1, 2, \ldots, p$). For s^{th} response the model is

$$\mathbf{y}_s = \mathbf{X}_s\boldsymbol{\theta}_s + \boldsymbol{\varepsilon}_s \qquad s = 1, 2, \ldots, p \tag{A.2.1}$$

where $\mathbf{X}_s = \left[\boldsymbol{\Delta}_s' \quad \mathbf{1} \quad \mathbf{D}_s'\right]$ is the design matrix for s^{th} response partitioned in conformity with the parameters, $\boldsymbol{\Delta}_s'$ is $(n \times v)$ design matrix of treatments for the s^{th} response, $\mathbf{1}$ is the n dimensional column vector of all elements unity and $\mathbf{D}_s'$ is the design matrix of blocks for the s^{th} response.

$\boldsymbol{\theta}_s = \begin{bmatrix} \boldsymbol{\tau}_s \\ \mu_s \\ \boldsymbol{\beta}_s \end{bmatrix}$ is a $(v + b + 1) \times 1$ vector of parameters, $\boldsymbol{\tau}_s$ is a $v \times 1$ vector of treatment effects, μ_s is general mean and $\boldsymbol{\beta}_s$ a $b \times 1$ vector of block effects for the s^{th} response, $\boldsymbol{\varepsilon}_S$ is the residual vector for s^{th} response variable distributed as N ($\mathbf{0}$, $\sigma_{ss}\,\mathbf{I}_n$).

The model for multi-response experiments in block design set up can be written as

$$\mathbf{Y} = \mathbf{Z}\boldsymbol{\theta} + \boldsymbol{\varepsilon} \tag{A.2.2}$$

Here $\mathbf{Y} = \left[\mathbf{y}_1 \quad \mathbf{y}_2 \quad \cdots \quad \mathbf{y}_p\right]$. (A.2.3)

Now one can roll out the matrix into vector form as follows

$$\mathbf{Y} = \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \vdots \\ \mathbf{y}_p \end{bmatrix}. \tag{A.2.4}$$

Assuming the usual Gauss-Markoff setup, the design matrix is

$$\mathbf{Z} = \left[\begin{array}{cccc|cccc|cccc} \boldsymbol{\Delta}_1' & \mathbf{0} & \cdots & \mathbf{0} & \mathbf{1} & \mathbf{0} & \cdots & \mathbf{0} & \mathbf{D}_1' & \mathbf{0} & \cdots & \mathbf{0} \\ \mathbf{0} & \boldsymbol{\Delta}_2' & \cdots & \mathbf{0} & \mathbf{0} & \mathbf{1} & \cdots & \mathbf{0} & \mathbf{0} & \mathbf{D}_2' & \cdots & \mathbf{0} \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\ \mathbf{0} & \mathbf{0} & \cdots & \boldsymbol{\Delta}_p' & \mathbf{0} & \mathbf{0} & \cdots & \mathbf{1} & \mathbf{0} & \mathbf{0} & \cdots & \mathbf{D}_p' \end{array}\right] = \bigoplus_{s=1}^{p} \mathbf{X}_s \tag{A.2.5}$$

where $\oplus$ denotes the direct sum of matrices.

The matrix of unknown parameters is given by

$$\boldsymbol{\theta} = \left[\boldsymbol{\theta}_1 \quad \boldsymbol{\theta}_2 \quad \cdots \quad \boldsymbol{\theta}_p\right] \tag{A.2.6}$$

which can also be written into vector form as

$$\boldsymbol{\theta} = \begin{bmatrix} \boldsymbol{\theta}_1 \\ \boldsymbol{\theta}_2 \\ \vdots \\ \boldsymbol{\theta}_p \end{bmatrix}. \tag{A.2.7}$$

We can write $\boldsymbol{\theta}$ as follows

$$\boldsymbol{\theta} = \begin{bmatrix} \boldsymbol{\tau} \\ \boldsymbol{\mu} \\ \boldsymbol{\beta} \end{bmatrix} \tag{A.2.8}$$

where treatment effect vectors, for all the response variables are appended one below the other to obtain a single treatment effect vector $\boldsymbol{\tau}$. Similarly general mean $\boldsymbol{\mu}$, block effect vector $\boldsymbol{\beta}$ are given by

$$\boldsymbol{\tau} = \begin{bmatrix} \boldsymbol{\tau}_1 \\ \boldsymbol{\tau}_2 \\ \vdots \\ \boldsymbol{\tau}_p \end{bmatrix}, \ \boldsymbol{\mu} = \begin{bmatrix} \mu_1 \\ \mu_2 \\ \vdots \\ \mu_p \end{bmatrix} \text{ and } \boldsymbol{\beta} = \begin{bmatrix} \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \\ \vdots \\ \boldsymbol{\beta}_p \end{bmatrix}.$$

The residual vector $\boldsymbol{\varepsilon}$ is given by

$$\boldsymbol{\varepsilon} = \begin{bmatrix} \boldsymbol{\varepsilon}_1 \\ \boldsymbol{\varepsilon}_2 \\ \vdots \\ \boldsymbol{\varepsilon}_p \end{bmatrix}. \tag{A.2.9}$$

It is assumed that $\boldsymbol{\varepsilon}$ have a p-variate normal distribution with response variables from same observation are correlated but there is no correlation between different observations. Therefore, one can say that $\boldsymbol{\varepsilon} \sim N_p(\mathbf{0}, \boldsymbol{\Omega})$, where $\boldsymbol{\Omega}$ is residual variance-covariance matrix and is

$$\boldsymbol{\Omega} = D(\boldsymbol{\varepsilon}) = \boldsymbol{\Sigma}_{pp} \otimes \mathbf{I}_n = \begin{bmatrix} \sigma_{11}\mathbf{I}_n & \sigma_{12}\mathbf{I}_n & \cdots & \sigma_{1p}\mathbf{I}_n \\ \sigma_{21}\mathbf{I}_n & \sigma_{22}\mathbf{I}_n & \cdots & \sigma_{2p}\mathbf{I}_n \\ \vdots & \vdots & & \vdots \\ \sigma_{p1}\mathbf{I}_n & \sigma_{p2}\mathbf{I}_n & \cdots & \sigma_{pp}\mathbf{I}_n \end{bmatrix}, \tag{A.2.10}$$

where σ_{ss} denotes variance of s^{th} variable and $\sigma_{ss'}$ is the covariance between s^{th} and s'^{th} variables, $s, s' = 1, 2, \ldots, p$. Here $\boldsymbol{\Sigma} = \left(\left(\sigma_{ss'}\right)\right)$ and $\boldsymbol{\Sigma}^{-1} = \left(\left(\sigma^{ss'}\right)\right)$ (say) $s, s' = 1, 2, \ldots, p$. $\boldsymbol{\Omega}$ is positive definite and

$$\boldsymbol{\Omega}^{-1} = \boldsymbol{\Sigma}_{pp}^{-1} \otimes \mathbf{I}_n = \begin{bmatrix} \sigma^{11}\mathbf{I}_n & \sigma^{12}\mathbf{I}_n & \cdots & \sigma^{1p}\mathbf{I}_n \\ \sigma^{21}\mathbf{I}_n & \sigma^{22}\mathbf{I}_n & \cdots & \sigma^{2p}\mathbf{I}_n \\ \vdots & \vdots & & \vdots \\ \sigma^{p1}\mathbf{I}_n & \sigma^{p2}\mathbf{I}_n & \cdots & \sigma^{pp}\mathbf{I}_n \end{bmatrix}.$$

In the sequel, we give some matrix results that are used in the development of the analytical procedure.

A.2.1 Some Results of Matrices

Let $\mathbf{A} = (a_{ij})$ and $\mathbf{B} = (b_{ij})$ be $m_1 \times n_1$ and $m_2 \times n_2$ matrices, respectively. Then the Kronecker product $\mathbf{A} \otimes \mathbf{B} = (a_{ij}\mathbf{B})$ is an $m_1 m_2 \times n_1 n_2$ matrix expressible as a partitioned matrix with $a_{ij}\mathbf{B}$ as the $(I, j)^{\text{th}}$ partition, $I = 1, 2, \ldots, m_1$ and $j = 1, 2, \ldots, n_1$.

Result A.2.1: Following holds as consequences of the above definition [Rao, 2002, p29].

i) $\mathbf{0} \otimes \mathbf{A} = \mathbf{A} \otimes \mathbf{0} = \mathbf{0}$, where $\mathbf{0}$ is a matrix of all elements 0.

ii) $(\mathbf{A}_1 + \mathbf{A}_2) \otimes \mathbf{B} = (\mathbf{A}_1 \otimes \mathbf{B}) + (\mathbf{A}_2 \otimes \mathbf{B})$

iii) $\mathbf{A}_1\mathbf{A}_2 \otimes \mathbf{B}_1\mathbf{B}_2 = (\mathbf{A}_1 \otimes \mathbf{B}_1)(\mathbf{A}_2 \otimes \mathbf{B}_2)$

iv) $[\mathbf{A}_1 \quad \mathbf{A}_2] \otimes \mathbf{B} = [\mathbf{A}_1 \otimes \mathbf{B} \quad \mathbf{A}_2 \otimes \mathbf{B}]$

v) $\mathbf{A} \otimes [\mathbf{B}_1 \quad \mathbf{B}_2] \neq [\mathbf{A} \oplus \mathbf{B}_1 \quad \mathbf{A} \oplus \mathbf{B}_2]$

vi) $(\mathbf{A} \otimes \mathbf{B})^{-1} = \mathbf{A}^{-1} \otimes \mathbf{B}^{-1}$, if the true inverses exist

vii) $(\mathbf{A} \otimes \mathbf{B})^{-} = \mathbf{A}^{-} \otimes \mathbf{B}^{-}$, using any g-inverses

viii) $(\mathbf{A} \otimes \mathbf{B})' = \mathbf{A}' \otimes \mathbf{B}'$

ix) $(\mathbf{A} \otimes \mathbf{B})(\mathbf{A}^{-1} \otimes \mathbf{B}^{-1}) = \mathbf{I}$

x) Eigenvalues of $\mathbf{A} \otimes \mathbf{B}$ are product of eigenvalues of $\mathbf{A}$ with those of $\mathbf{B}$

xi) Rank ($\mathbf{A} \otimes \mathbf{B}$) = Rank ($\mathbf{A}$).Rank ($\mathbf{B}$)

xii) trace ($\mathbf{A} \otimes \mathbf{B}$) = trace ($\mathbf{A}$). trace ($\mathbf{B}$). (A.2.11)

We know that the direct sum of w matrices, $\mathbf{A}_1, \mathbf{A}_2, \ldots, \mathbf{A}_w$ is represented as

$$\bigoplus_{i=1}^{w} \mathbf{A}_i = \begin{bmatrix} \mathbf{A}_1 & \mathbf{0} & \cdots & \mathbf{0} \\ \mathbf{0} & \mathbf{A}_2 & \cdots & \mathbf{0} \\ \vdots & \vdots & & \vdots \\ \mathbf{0} & \mathbf{0} & \cdots & \mathbf{A}_w \end{bmatrix} = \text{diag}(\mathbf{A}_i);\ i = 1,2,\ldots,w\,.$$

Result A.2.2: Following holds as consequences of the above definition [Rao, 2002, p29].

i) Transposing a direct sum gives the direct sum of transposes.

ii) The rank of a direct sum is the sum of the ranks

iii) $\mathbf{A} \oplus (-\mathbf{A}) \neq 0$ unless $\mathbf{A}$ is null

iv) $(\mathbf{A} \oplus \mathbf{B}) + (\mathbf{C} \oplus \mathbf{D}) = (\mathbf{A} + \mathbf{C}) \oplus (\mathbf{B} + \mathbf{D})$

v) $(\mathbf{A} \oplus \mathbf{B})\,(\mathbf{C} \oplus \mathbf{D}) = (\mathbf{AC} \oplus \mathbf{BD})$

vi) $(\mathbf{A} \oplus \mathbf{B})^{-1} = \mathbf{A}^{-1} \oplus \mathbf{B}^{-1}$ (A.2.12)

Using the Generalized Least Square (GLS) estimation procedure we can obtain the normal equations as follows,

$$(\mathbf{Z}'\boldsymbol{\Omega}^{-1}\mathbf{Z})\boldsymbol{\theta} = \mathbf{Z}'\boldsymbol{\Omega}^{-1}\mathbf{Y} \tag{A.2.13}$$

Now consider that from same block design from each experimental unit all responses are observed, i.e., we are in a complete multi-response experimental situation. Then we have,

$$\boldsymbol{\Delta}_s' = \boldsymbol{\Delta}',\ \mathbf{D}_s' = \mathbf{D}'\ \forall\, s = 1,2,\ldots,p$$

Therefore, all $\mathbf{X}_s$ become same, *i.e.*, $\mathbf{X}_s = \mathbf{X} = [\boldsymbol{\Delta}'\ \mathbf{1}\ \mathbf{D}']$ and $\mathbf{Z} = \oplus\mathbf{X}_s = \oplus\mathbf{X} = \mathbf{I}_p \otimes \mathbf{X}$. The design matrix $\mathbf{Z}$ can be written as $\mathbf{Z} = [\mathbf{I}_p \otimes \boldsymbol{\Delta}' \quad \mathbf{I}_p \otimes \mathbf{1} \quad \mathbf{I}_n \otimes \mathbf{D}']$.

Now

$$\mathbf{Z}'\boldsymbol{\Omega}^{-1}\mathbf{Z} = \begin{bmatrix} \mathbf{I}_p \otimes \boldsymbol{\Delta} \\ \mathbf{I}_p \otimes \mathbf{1}' \\ \mathbf{I}_p \otimes \mathbf{D} \end{bmatrix} \left[\boldsymbol{\Sigma}_{pp} \otimes \mathbf{I}_n\right]^{-1} \begin{bmatrix} \mathbf{I}_p \otimes \boldsymbol{\Delta}' & \mathbf{I}_p \otimes \mathbf{1} & \mathbf{I}_p \otimes \mathbf{D}' \end{bmatrix}$$

(using Result A.2.1 (vi))

$$= \begin{bmatrix} \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\boldsymbol{\Delta}' & \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\mathbf{D}' \\ \boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\boldsymbol{\Delta}' & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\mathbf{D}' \\ \boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\boldsymbol{\Delta}' & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\mathbf{D}' \end{bmatrix}$$

(using Result A.2.1(iii))

$$= \begin{bmatrix} \boldsymbol{\Sigma}^{-1} \otimes \mathbf{R} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{r} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{N} \\ \boldsymbol{\Sigma}^{-1} \otimes \mathbf{r}' & \boldsymbol{\Sigma}^{-1} \otimes n & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{k}' \\ \boldsymbol{\Sigma}^{-1} \otimes \mathbf{N}' & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{k} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{K} \end{bmatrix} \qquad \text{(A.2.14)}$$

where

$\mathbf{r} = (r_1, r_2, ..., r_v)'$, $v \times 1$ replication vector of treatments common to all responses.

$\mathbf{k} = (k_1, k_2, ..., k_b)'$, $b \times 1$ block size vector common to all the responses.

$\mathbf{R} = \text{diag}(r_1, r_2, ..., r_v)$.

$\mathbf{K} = \text{diag}(k_1, k_2, ..., k_b)$.

$\mathbf{N} = v \times b$ treatments vs blocks incidence matrix.

Let $\mathbf{T}_s$ = vector of treatment totals for s^{th} response

G_s = Grand total for s^{th} response and

$\mathbf{B}_s$ = vector of block totals for s^{th} response

Now we can have,

$$\mathbf{Z}'\boldsymbol{\Omega}^{-1}\mathbf{Y} = \begin{bmatrix} \mathbf{I}_p \otimes \boldsymbol{\Delta} \\ \mathbf{I}_p \otimes \mathbf{1}' \\ \mathbf{I}_p \otimes \mathbf{D} \end{bmatrix} \left[\boldsymbol{\Sigma}_{pp}^{-1} \otimes \mathbf{I}_n\right] \mathbf{Y}$$

$$= \begin{bmatrix} \left(\boldsymbol{\Sigma}_{pp}^{-1} \otimes \boldsymbol{\Delta}\right)\mathbf{Y} \\ \left(\boldsymbol{\Sigma}_{pp}^{-1} \otimes \mathbf{1}'\right)\mathbf{Y} \\ \left(\boldsymbol{\Sigma}_{pp}^{-1} \otimes \mathbf{D}\right)\mathbf{Y} \end{bmatrix} \qquad \text{(using Result A.2.1(iv))}$$

$$= \begin{bmatrix} \sigma^{11}\boldsymbol{\Delta}\mathbf{y_1} + .\cdots + \sigma^{1p}\boldsymbol{\Delta}\mathbf{y}_p \\ \sigma^{21}\boldsymbol{\Delta}\mathbf{y_1} + .\cdots + \sigma^{2p}\boldsymbol{\Delta}\mathbf{y}_p \\ \vdots \\ \sigma^{p11}\boldsymbol{\Delta}\mathbf{y_1} + .\cdots + \sigma^{pp}\boldsymbol{\Delta}\mathbf{y}_p \\ ---------- \\ \sigma^{11}\mathbf{1}'\mathbf{y_1} + .\cdots + \sigma^{1p}\mathbf{1}'\mathbf{y}_p \\ \sigma^{21}\mathbf{1}'\mathbf{y_1} + .\cdots + \sigma^{2p}\mathbf{1}'\mathbf{y}_p \\ \vdots \\ \sigma^{p1}\mathbf{1}'\mathbf{y_1} + .\cdots + \sigma^{pp}\mathbf{1}'\mathbf{y}_p \\ ---------- \\ \sigma^{11}\mathbf{D}\mathbf{y_1} + .\cdots + \sigma^{1p}\mathbf{D}\mathbf{y}_p \\ \sigma^{21}\mathbf{D}\mathbf{y_1} + .\cdots + \sigma^{2p}\mathbf{D}\mathbf{y}_p \\ \vdots \\ \sigma^{p1}\mathbf{D}\mathbf{y_1} + \cdots + \sigma^{pp}\mathbf{D}\mathbf{y}_p \end{bmatrix} = \begin{bmatrix} \sigma^{11}\mathbf{T}_1 + .\cdots + \sigma^{1p}\mathbf{T}_p \\ \sigma^{21}\mathbf{T}_1 + .\cdots + \sigma^{2p}\mathbf{T}_p \\ \cdots \\ \sigma^{p1}\mathbf{T}_1 + .\cdots + \sigma^{pp}\mathbf{T}_p \\ ---------- \\ \sigma^{11}\mathbf{G}_1 + .\cdots + \sigma^{1p}\mathbf{G}_p \\ \sigma^{21}\mathbf{G}_1 + .\cdots + \sigma^{2p}\mathbf{G}_p \\ \vdots \\ \sigma^{p1}\mathbf{G}_1 + .\cdots + \sigma^{pp}\mathbf{G}_p \\ ---------- \\ \sigma^{11}\mathbf{B}_1 + .\cdots + \sigma^{1p}\mathbf{B}_p \\ \sigma^{21}\mathbf{B}_1 + .\cdots + \sigma^{2p}\mathbf{B}_p \\ \vdots \\ \sigma^{p1}\mathbf{B}_1 + .\cdots + \sigma^{pp}\mathbf{B}_p \end{bmatrix} = \begin{bmatrix} \mathbf{a} \\ \mathbf{g} \\ \mathbf{b} \end{bmatrix} \text{ (say)} \qquad \text{(A.2.15)}$$

From the normal equations given in (A.2.13) one can obtain the reduced normal equations for linear function of treatment effects as

$$\mathbf{C}^*\boldsymbol{\tau} = \mathbf{Q}^* \qquad \text{(A.2.16)}$$

where

$$\mathbf{C}^* = \left(\boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\boldsymbol{\Delta}'\right) - \begin{bmatrix} \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\mathbf{D}' \end{bmatrix} \begin{bmatrix} \boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\mathbf{D}' \\ \boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\mathbf{D}' \end{bmatrix}^{-} \begin{bmatrix} \boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\boldsymbol{\Delta}' \\ \boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\boldsymbol{\Delta}' \end{bmatrix}$$

(using Result A.2.1(iii), (iv), (vi) and (ix))

$$= \boldsymbol{\Sigma}^{-1} \otimes \left(\boldsymbol{\Delta}\boldsymbol{\Delta}' - \boldsymbol{\Delta}\mathbf{D}'\left(\mathbf{D}\mathbf{D}'\right)^{-1}\mathbf{D}\boldsymbol{\Delta}'\right) \qquad \text{(A.2.17)}$$

and $\mathbf{Q}^* = \left(\boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\right)\mathbf{Y} - \begin{bmatrix} \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\mathbf{D}' \end{bmatrix} \begin{bmatrix} \boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\mathbf{D}' \\ \boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\mathbf{1} & \boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\mathbf{D}' \end{bmatrix}^{-} \begin{bmatrix} \left(\boldsymbol{\Sigma}^{-1} \otimes \mathbf{1}'\right)\mathbf{Y} \\ \left(\boldsymbol{\Sigma}^{-1} \otimes \mathbf{D}\right)\mathbf{Y} \end{bmatrix}$

(using Result A.2.1(iii), (iv), (vi) and (ix))

$$= \left[\boldsymbol{\Sigma}^{-1} \otimes \left(\boldsymbol{\Delta} - \boldsymbol{\Delta}\mathbf{D}'\left(\mathbf{D}\mathbf{D}'\right)^{-1}\mathbf{D}\right)\right]\mathbf{Y} \qquad \text{(A.2.18)}$$

Solving the reduced normal equations (A.2.16), one can obtain the estimate of linear function of treatment effects after eliminating the effect of nuisance parameters (general mean and block effects).

$$\hat{\boldsymbol{\tau}} = \mathbf{C}^{*-}\mathbf{Q}^* \qquad \text{(A.2.19)}$$

It is easy to verify that

$$\hat{\boldsymbol{\tau}} = \begin{bmatrix} \hat{\boldsymbol{\tau}}_1 \\ \hat{\boldsymbol{\tau}}_2 \\ \vdots \\ \hat{\boldsymbol{\tau}}_p \end{bmatrix} = \begin{bmatrix} \mathbf{C}^{-}\mathbf{Q}_1 \\ \mathbf{C}^{-}\mathbf{Q}_2 \\ \vdots \\ \mathbf{C}^{-}\mathbf{Q}_p \end{bmatrix} \quad \text{where } \mathbf{Q}_s = \mathbf{T}_s - \mathbf{N}\mathbf{K}^{-1}\mathbf{B}_s,\ s = 1, 2, \ldots, p. \tag{A.2.20}$$

Thus, a solution of $\hat{\boldsymbol{\tau}}$ is the same as the one obtained from the block designs separately for each of the responses. For a connected design Rank ($\mathbf{C}^{*}$) = $p(v-1)$.

Now to obtain residual sum of squares and cross products (Residual SSCP) matrix, we proceed as follows. In this case, we have,

$$\begin{aligned} R_0^{\,2} &= \left(\mathbf{Y} - \mathbf{Z}\hat{\boldsymbol{\theta}}\right)'\left(\mathbf{Y} - \mathbf{Z}\hat{\boldsymbol{\theta}}\right) = \mathbf{Y}'\mathbf{Y} - \mathbf{Y}'\mathbf{Z}\hat{\boldsymbol{\theta}} \\ &= \mathbf{Y}'\mathbf{Y} - \mathbf{Y}'\left[\mathbf{I}\otimes\boldsymbol{\Delta}' \quad \mathbf{I}\otimes\mathbf{1} \quad \mathbf{I}\otimes\mathbf{D}'\right]\begin{bmatrix} \hat{\boldsymbol{\tau}} \\ \hat{\boldsymbol{\mu}} \\ \hat{\boldsymbol{\beta}} \end{bmatrix} \\ &= \mathbf{Y}'\mathbf{Y} - \mathbf{Y}'\left(\mathbf{I}\otimes\boldsymbol{\Delta}'\right)\hat{\boldsymbol{\tau}} - \mathbf{Y}'\left(\mathbf{I}\otimes\mathbf{1}\right)\hat{\boldsymbol{\mu}} - \mathbf{Y}'\left(\mathbf{I}\otimes\mathbf{D}'\right)\hat{\boldsymbol{\beta}}. \end{aligned}$$

From normal equations, it can be easily seen that

$$\begin{aligned} \hat{\boldsymbol{\beta}} &= \left[\mathbf{I}\otimes\left(\mathbf{D}\mathbf{D}'\right)^{-1}\mathbf{D}\right]\mathbf{Y} - \left[\mathbf{I}\otimes\left(\mathbf{D}\mathbf{D}'\right)^{-1}\mathbf{D}\boldsymbol{\Delta}'\right]\hat{\boldsymbol{\tau}} - \left[\mathbf{I}\otimes\mathbf{1}\right]\hat{\boldsymbol{\mu}} \\ \therefore R_0^2 &= \left[\mathbf{y}_1'\ \mathbf{y}_2'\ \ldots\mathbf{y}_p'\right]\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \vdots \\ \mathbf{y}_p \end{bmatrix} - \left[\mathbf{y}_1'\ \mathbf{y}_2'\ \ldots\mathbf{y}_p'\right]\left[\mathbf{I}\otimes\left\{\mathbf{I} - \mathbf{D}'(\mathbf{D}\mathbf{D}')\mathbf{D}\right\}\boldsymbol{\Delta}'\right]\begin{bmatrix} \hat{\boldsymbol{\tau}}_1 \\ \hat{\boldsymbol{\tau}}_2 \\ \vdots \\ \hat{\boldsymbol{\tau}}_p \end{bmatrix} \\ &\qquad - \left[\mathbf{y}_1'\ \mathbf{y}_2'\ \ldots\ \mathbf{y}_p'\right]\left[\mathbf{I}\otimes\left\{\mathbf{D}'(\mathbf{D}\mathbf{D}')\mathbf{D}\right\}\right]\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \vdots \\ \mathbf{y}_p \end{bmatrix}. \end{aligned} \tag{A.2.21}$$

We can see that R_0^2 is the sum of individual residual sum of squares for all the responses and cross products for all possible pairs of responses. Following the results of Gauss Markoff setup for multi-response situations, we can obtain the $(s,s')^{\text{th}}$ element of residual SSCP matrix from R_0^2 considering that,

$$\mathbf{R_0}(s,s') = \mathbf{y}_s'\mathbf{y}_{s'} - \mathbf{y}_s'\left[\mathbf{I} - \mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D}\right]\boldsymbol{\Delta}'\hat{\boldsymbol{\tau}}_s - \mathbf{y}_s'\left[\mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D}\right]\mathbf{y}_{s'} \tag{A.2.22}$$

$\mathbf{R_0} = ((\mathrm{R}_0(s,s')))$ = **E**, is the $p\times p$ residual SSCP matrix. Now consider the null hypothesis as

$H_0 : \boldsymbol{\tau}_1 = \boldsymbol{\tau}_2 = \ldots = \boldsymbol{\tau}_v = \boldsymbol{\tau}^{*}(say)$ against the alternative hypothesis (A.2.23)

H_1 : At least two treatment effects vectors are not same.

Under null hypothesis, the model (A.2.2) reduces to

$$\mathbf{Y} = \mathbf{Z}_0\boldsymbol{\theta}_0 + \boldsymbol{\varepsilon}$$

where

$$\mathbf{Z}_0 = \left[\mathbf{I}\otimes\mathbf{1}\vdots\,\mathbf{I}\otimes\mathbf{1}\vdots\mathbf{I}\otimes\mathbf{D}'\right]$$

$$\boldsymbol{\theta}_0 = \begin{bmatrix}\boldsymbol{\tau}^* \\ \boldsymbol{\mu} \\ \boldsymbol{\beta}\end{bmatrix} \qquad \text{(A.2.24)}$$

$$\mathbf{Y} = (\mathbf{I}\otimes\mathbf{1})(\boldsymbol{\tau}^* + \boldsymbol{\mu}) + (\mathbf{I}\otimes\mathbf{D}')\boldsymbol{\beta} + \boldsymbol{\varepsilon}$$

$$\mathbf{Y} = (\mathbf{I}\otimes\mathbf{1})\boldsymbol{\alpha} + (\mathbf{I}\otimes\mathbf{D}')\boldsymbol{\beta} + \boldsymbol{\varepsilon} \qquad \text{(using Result A.2.1 (ii))}$$

$$\therefore \mathbf{Z}_0 = (\mathbf{I}\otimes\mathbf{1}):(\mathbf{I}\otimes\mathbf{D}') \text{ and } \boldsymbol{\theta}_0 = \begin{bmatrix}\boldsymbol{\alpha} \\ \boldsymbol{\beta}\end{bmatrix}.$$

So under H_0 residual sum of squares is

$$R_1^{\,2} = \left(\mathbf{Y} - \mathbf{Z}_0\hat{\boldsymbol{\theta}}_0\right)'\left(\mathbf{Y} - \mathbf{Z}_0\hat{\boldsymbol{\theta}}_0\right) = \mathbf{Y}'\mathbf{Y} - \mathbf{Y}'\mathbf{Z}_0\hat{\boldsymbol{\theta}}_0$$
$$= \mathbf{Y}'\mathbf{Y} - \mathbf{Y}'\left[\mathbf{I}\otimes\mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D}\right]\mathbf{Y}. \qquad \text{(A.2.25)}$$

Similarly we can obtain SSCP matrix for null hypothesis whose $(s,s')^{\text{th}}$ element can be given by

$$\mathbf{R}_1(s,s') = \mathbf{y}_s'\mathbf{y}_{s'} - \mathbf{y}_s'(\mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D})\mathbf{y}_{s'}$$
$$\mathbf{R}_1 = (R_1(s,s')), \quad s,s' = 1,2,\ldots,p \qquad \text{(A.2.26)}$$

Now we can obtain SSCP matrix due to treatments (adjusted for block effects) as follows,

$$\mathbf{R}_1 - \mathbf{R}_0 = (\mathbf{R}_1(s,s') - \mathbf{R}_0(s,s')) \qquad \text{(A.2.27)}$$

So $(s,s')^{\text{th}}$ element of treatment SSCP matrix is

$$= \mathbf{y}_s'\mathbf{y}_{s'} - \mathbf{y}_s'(\mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D})\mathbf{y}_{s'} - \mathbf{y}_s'\mathbf{y}_{s'} + \mathbf{y}_s'[\mathbf{I} - (\mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D})]\boldsymbol{\Delta}'\hat{\boldsymbol{\tau}}_{s'} + \mathbf{y}_s'(\mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D})\mathbf{y}_{s'}$$
$$= \mathbf{y}_s'\left[\mathbf{I} - (\mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D})\boldsymbol{\Delta}'\right]\hat{\boldsymbol{\tau}}_{s'}$$
$$= \mathbf{Q}_s'\boldsymbol{\tau}_{s'}' = \mathbf{Q}_s'\mathbf{C}^-\mathbf{Q}_{s'} \qquad \text{(A.2.28)}$$

This element is same as the treatment cross products for s^{th} and s'^{th} response variable. Therefore, the treatment SSCP matrix is

$$\mathbf{R_1} - \mathbf{R}_0 = \begin{bmatrix} \mathbf{Q}_1'\mathbf{C}^-\mathbf{Q}_1 & \mathbf{Q}_1'\mathbf{C}^-\mathbf{Q}_2 & \cdots & \mathbf{Q}_1'\mathbf{C}^-\mathbf{Q}_p \\ \mathbf{Q}_2'\mathbf{C}^-\mathbf{Q}_1 & \mathbf{Q}_2'\mathbf{C}^-\mathbf{Q}_2 & \cdots & \mathbf{Q}_2'\mathbf{C}^-\mathbf{Q}_p \\ \vdots & \vdots & & \vdots \\ \mathbf{Q}_p'\mathbf{C}^-\mathbf{Q}_1 & \mathbf{Q}_p'\mathbf{C}^-\mathbf{Q}_2 & \cdots & \mathbf{Q}_p'\mathbf{C}^-\mathbf{Q}_p \end{bmatrix} = \mathbf{H} \text{ (say).} \qquad \text{(A.2.29)}$$

The unadjusted block SSCP matrix obtained following the similar steps as for **H** is

$$\mathbf{B}\ (\text{UA}) = \left(\mathbf{B}(UA)(s,s')\right)$$

where, $\mathbf{B}(UA)(s,s') = \mathbf{y}_s'(\mathbf{D}'(\mathbf{D}\mathbf{D}')^{-1}\mathbf{D})\mathbf{y}_{s'} - \mathbf{y}_s'(\mathbf{D}'(\mathbf{1}'\mathbf{1})^{-1}\mathbf{D})\mathbf{y}_{s'}$ (A.2.30)

In nutshell, the procedure for analysis of multi-response experiments is summarized in Table A.2.1.

Table A.2.1: Multivariate Analysis of Variance (MANOVA) Table for Simultaneous comparison of Treatment Effects

Sources of variation	d.f.	Matrix of SSCP
Block(Unadjusted)	$b-1=t$	**B** (UA)
Treatment (Adjusted)	$v-1=h$	$\mathbf{H}=\mathbf{R_1}-\mathbf{R}_0$
Residual	$n-b-v+1=s$	**E**
Total	$n-1$	**T**

To test the null hypothesis of equality of treatment effects vectors, we make use of the matrices **H** and **E** in the above table. In multi-response experiments, test statistic for testing the equality of treatment effects is based on the roots of

$$\left|\mathbf{H}-\boldsymbol{\tau}(\mathbf{H}+\mathbf{E})\right|=0. \qquad \text{(A.2.31)}$$

One of the most important statistic based on the roots of (A.2.31) is Wilk's likelihood ratio statistic (or Wilk's lambda) which is given by

$$\Lambda=\frac{\left|\mathbf{E}\right|}{\left|\mathbf{E}+\mathbf{H}\right|} \qquad \text{(A.2.32)}$$

The null hypothesis is tested using the F-statistic obtained as an approximation to Wilk's lambda by Rao(2002). Assuming the multivariate normal distribution of observation, Rao (2002) showed that under null hypothesis Λ is distributed as the product of independent beta variables. A better but more complicated approximation of the distribution of Λ is

$$\frac{1-\Lambda^{1/b}}{\Lambda^{1/b}}\frac{(ab-c)}{ph}\sim \mathrm{F}\,(ph,\ ab\text{-}c)$$

where $a=\left(s-\frac{p-h+1}{2}\right)$, $b=\sqrt{\left\{\left(p^2h^2-4\right)/\left(p^2+h^2-5\right)\right\}}$, $c=\frac{ph-2}{2}$.

For some particular values of *h* and *p*, it reduces to exact F-distribution. The special cases are given below:

For $h = 1$ and any *p*, this reduces to

$$\frac{(1-\Lambda)(s-p+1)}{\Lambda\qquad p}\sim \mathrm{F}\,(p,\ s-p+1)$$

For $h=2$ and any *p*, it reduces to

$$\frac{(1-\sqrt{\Lambda})(s-p+1)}{\sqrt{\Lambda}\qquad p}\sim \mathrm{F}\,(2p,\ 2(s-p+1))$$

For $p=2$ and any *h*

$$\frac{(1-\sqrt{\Lambda})(s-1)}{\sqrt{\Lambda}\qquad h}\sim \mathrm{F}\,(2h,\ 2(s-1)).$$

For $p = 1$, the statistic reduces to the usual variance ratio statistics.

There are three more multivariate test statistic available in literature viz. Pillai's trace, Hotellings-Lawley's trace and Roy's largest root. All these tests are made on eigenvalues of $\mathbf{A} = \mathbf{HE}^{-1}$. Each of the test statistic has its own associated *F*- ratio. In some cases all the four test statistic give an exact *F*- ratio for testing the null hypothesis and in other cases the *F*-ratio is approximated. The reason for different statistic and for approximations is that the algebra of MANOVA is quite complicated in

some cases and it is difficult to solve them. Here, all that is mentioned is their names and some properties. In terms of notations, assume that there are *p* dependent variables in the MANOVA, and let λ_i denote the i^{th} eigenvalue of matrix **A**. The three multivariate test statistic are then, given in the sequel. The first statistic is *Pillai's trace*. The formula for Pillai's trace is

$$\text{Pillai's trace} = \text{trace}\,[\mathbf{H}(\mathbf{H}\text{-}\mathbf{E})^{-1}] = \sum_{s=1}^{p} \frac{\lambda_s}{1+\lambda_s} \qquad \text{(A.2.33)}$$

The second test statistic is *Hotelling-Lawley's trace*.

$$\text{Hotelling-Lawley's trace} = \text{trace}\,(\mathbf{A}) = \text{trace}\,(\mathbf{H}\mathbf{E}^{-1}) = \sum_{s=1}^{p} \lambda_s \qquad \text{(A.2.34)}$$

The third and last statistic is *Roy's largest root*. This gives an upper bound for the *F*-statistic.

$$\text{Roy's largest root} = \max(\lambda_s). \qquad \text{(A.2.35)}$$

or the maximum eigenvalue of $\mathbf{A} = \mathbf{H}\mathbf{E}^{-1}$ (Recall that a "root" is another name for an eigenvalue). Hence, this statistic could also be called Roy's largest eigenvalue. This is the major reason why statistical softwares such as Statistical Analysis System (SAS) prints out the eigenvalues and eigenvectors of $\mathbf{A} = \mathbf{H}\mathbf{E}^{-1}$.

Once the statistics in (A.2.33.) through (A.2.35) are obtained, they are translated into *F*-statistic in order to test the null hypothesis. The reason for this translation is identical to the reason for converting Hotelling's T^2, the easy availability of published tables of the *F*-distribution. The important issue to recognize is that in some cases, the *F*-statistic is exact and in other cases it is approximate. In some cases, the four will generate identical *F*-statistic and identical probabilities. In others they will differ. In the present study, we have considered Wilk's lambda as the criterion for testing the significance of treatment effects.

The above description is for testing the equality of treatment effect vectors. If one is interested in testing the equality of block effects the null hypothesis is

$H_0 : \boldsymbol{\beta}_1 = \boldsymbol{\beta}_2 = \ldots = \boldsymbol{\beta}_b = \boldsymbol{\beta}^*(say)$ against the alternative hypothesis (A.2.36)

H_1 : At least two block effects vectors are not same.

The SSCP matrix for blocks adjusted for treatment effects is required to be obtained. Block SSCP matrix adjusted for treatment effects may be obtained by using the relationship

$$\mathbf{H} + \mathbf{B}(\text{UA}) = \mathbf{H}(\text{UA}) + \mathbf{B} \qquad \text{(A.2.37)}$$

where **H**(UA), **H**, **B**(UA) and **B** denote respectively the SSCP matrix for treatments unadjusted, treatments adjusted for block effects, block unadjusted and blocks adjusted for treatment effects. The treatment unadjusted SSCP matrix is

$$\mathbf{H}\,(\text{UA}) = \mathbf{H}(UA)(s,s')$$

where, $\mathbf{H}(UA)(s,s') = \mathbf{y}'_s(\boldsymbol{\Delta}'(\boldsymbol{\Delta}\boldsymbol{\Delta}')^{-1}\boldsymbol{\Delta})\mathbf{y}_{s'} - \mathbf{y}'_s(\boldsymbol{\Delta}'(\mathbf{1}'\mathbf{1})^{-1}\boldsymbol{\Delta})\mathbf{y}_{s'}$ (A.2.38)

The MANOVA table for testing the equality of block effects is given in Table A.2.2.

Table A.2.2: Multivariate Analysis of Variance (MANOVA) Table for Simultaneous Comparison of Block Effects

Sources of variation	d.f.	Matrix of SSCP
Block(Adjusted)	$b - 1 = t$	**B**
Treatment (Unadjusted)	$v - 1 = h$	**H** (UA)
Residual	$n - b - v + 1 = s$	**E**
Total	$n - 1$	**T**

To test the null hypothesis of equality of block effects vectors, we make use of the matrices **B** and **E** in the above table. The same test statistic (Wilk's Lambda) used for testing equality of block effects vectors by replacing **H** by **B** and is

$$\Lambda = \frac{|\mathbf{E}|}{|\mathbf{E}+\mathbf{B}|} \tag{A.2.39}$$

We reject the null hypothesis of equality of block effects if the ratio or Wilk's Lambda is too small using the exact Approximate F-distribution as discussed earlier.

Remark A.2.1: One complication of multivariate analysis of variance that does not arise in the univariate case is due to the ranks of the matrices. The rank of **E** should be greater than or equal to p or in other words error degrees of freedom s should be greater than or equal to p ($s \geq p$), the number of response variables.

A.3 Multivariate Treatment Contrast Analysis

If the treatments are found to be significantly different for all the response variables simultaneously, then the next question is "**which treatments are significantly different?**" This is achieved by making all possible pairwise treatment comparisons. Sometimes, one may be interested in making specific hypothesis. For example,

- A plant breeder may be interested in comparing exotic collections with indigenous cultivars.
- An agronomist may be interested in comparing the effects of biofertilisers and chemical fertilizers.
- A water technologist may be interested in studying the effect of nitrogen with farmyard manure over the nitrogen levels without farmyard manure in presence of irrigation.
- A medical experimenter might be concerned with the efficacy of each of several new drugs as compared to a standard drug.
- A nutrition experiment may be run to compare high fiber diets with low fiber diets.

Such questions can be answered through treatment contrasts analysis. In single response experiments, treatment contrast analysis can be performed for testing the significance of a treatment contrast {see e.g. Dean and Voss (1999)}. The procedure of treatment contrast analysis in multi-response experiments is developed in the present investigation and is given in the sequel. Let $\mathbf{P}'\boldsymbol{\tau}$ is a treatment contrast such that $\mathbf{P}' = \mathbf{I}_p \otimes \boldsymbol{\gamma}'$, where $\boldsymbol{\gamma}$ is a ($v \times 1$) vector and $\boldsymbol{\gamma}'\mathbf{1} = \mathbf{0}$. The interest is in testing the null hypothesis H_0: $\mathbf{P}'\boldsymbol{\tau} = \mathbf{0}$, against alternative hypothesis H_1: $\mathbf{P}'\boldsymbol{\tau} \neq \mathbf{0}$.

Following on the lines of procedure of obtaining SSCP matrix due to treatments, SSCP matrix for the treatment contrast is given by

$$\begin{bmatrix} (\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_1)'(\boldsymbol{\gamma}'\mathbf{C}^{-}\boldsymbol{\gamma})^{-1}(\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_1) & \cdots & (\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_1)'(\boldsymbol{\gamma}'\mathbf{C}^{-}\boldsymbol{\gamma})^{-1}(\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_p) \\ (\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_2)'(\boldsymbol{\gamma}'\mathbf{C}^{-}\boldsymbol{\gamma})^{-1}(\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_1) & \cdots & (\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_2)'(\boldsymbol{\gamma}'\mathbf{C}^{-}\boldsymbol{\gamma})^{-1}(\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_p) \\ \vdots & \ddots & \vdots \\ (\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_p)'(\boldsymbol{\gamma}'\mathbf{C}^{-}\boldsymbol{\gamma})^{-1}(\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_1) & \cdots & (\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_p)'(\boldsymbol{\gamma}'\mathbf{C}^{-}\boldsymbol{\gamma})^{-1}(\boldsymbol{\gamma}'\hat{\boldsymbol{\tau}}_p) \end{bmatrix} = \mathbf{M} \qquad \text{(A.3.1)}$$

Now the null hypothesis H_0: $\mathbf{P}'\boldsymbol{\tau} = \mathbf{0}$, against alternative hypothesis H_1: $\mathbf{P}'\boldsymbol{\tau} \neq \mathbf{0}$ can be tested using the test statistic, Wilks' Lambda (Λ^*).

$$\Lambda^* = \frac{|\mathbf{E}|}{|\mathbf{E}+\mathbf{M}|} \qquad \text{(A.3.2)}$$

where **E** is the residual SSCP matrix as obtained through MANOVA. The hypothesis is then tested using the following F-test statistic based on Wilk's Lambda for $h = 1$

$$\frac{1-\boldsymbol{\Lambda}^*}{\boldsymbol{\Lambda}^*}\frac{error\ df - p + 1}{p} \sim \mathrm{F}(p,\ s\text{-}p\text{+}1).$$

where s is the error degrees of freedom.

If the experimenter is interested in making all possible pairwise treatment comparisons, one has to write all possible $\binom{v}{2}$ pairwise treatment contrasts. For example, to test $H_0 : \tau_1 = \tau_2$ against $H_1 : \tau_1 \neq \tau_2$, $\mathbf{P}'\boldsymbol{\tau}$ can be written as $\boldsymbol{\gamma}'\boldsymbol{\tau}$, where $\boldsymbol{\gamma}'$ = (1 –1 0 0 . . . 0) and using the above procedure one can test the null hypothesis $H_0: \boldsymbol{\gamma}'\boldsymbol{\tau} = 0$ against the alternative hypothesis $H_1 : \boldsymbol{\gamma}'\boldsymbol{\tau} \neq 0$.

A.4 Identification of Best Treatment

From multivariate treatment contrast analysis if the two treatments are found to be significantly different, then the next question is "How to identify the better treatment from the two significantly different treatments?". In univariate case we take the mean of the observations pertaining to each treatment for the response variable of interest. Then for the identification of the best treatment, we take the treatment having highest/ lowest mean value based on the nature of response variable of interest. For example, if the response of interest is yield, then we take the treatment with highest mean yield as best whereas if the interest is in insect intensity after application of pesticides/ insecticides, then the treatment with lowest insect intensity is considered to be the best. In case of multi-response experiments this method can not be applied in general.

One way to resolve this problem in multi-response experiments is taking weighted average of the response variables and comparing the new averages over the treatments. The weights need to be given by subject matter experts depending upon the importance of variables in identification of treatments. Assigning proper weights is really tough and a challenging task. It needs thorough understanding of the system to assign proper weights to each of the response variables which may vary from person to person, situation to situation and objectives of the analysis. So it is not a robust procedure for identification of a best treatment. If we give equal weights to all the response variables, it amounts to saying that inferences are drawn on the average over all the responses.

One may think of using techniques of multidimensional scaling, one tailed tests, J-plot and Euclidean distance from null vector for identification of best treatment. In the present investigation, we have

suggested the procedures based on J-plot and Euclidean distance from null vector for identification of best treatment. While illustrating the procedures, we have also taken into consideration, the average over all responses as one of the criterion. Limitations of the procedure suggested and guidelines to overcome these limitations are also discussed in the Remark A.4.1. We begin with J-plot and Euclidean distance from null vector.

A.4.1 J-plot and Euclidean Distance from Null Vector

Let us consider the $v \times p$ matrix of treatment effects (treatment means/ adjusted treatment means) $\mathbf{E}_{v\times p}$ of rank r, where $r \le \min(v-1, p)$

$$\mathbf{E} = \left[\mathbf{T}_1\ \mathbf{T}_2 \cdots \mathbf{T}_p\right] \tag{A.4.1}$$

where $\mathbf{T}_s$ is $v \times 1$ vector of treatment means for s^{th} response variable, (s =1, 2, …, p).

It is possible to write $\mathbf{E}_{v\times p}$, using the singular value decomposition (SVD) (e.g. see Good 1969, Jackson 1991) as

$$\mathbf{E}_{v\times p} = \mathbf{P}_{v\times r}\mathbf{\Lambda}_{r\times r}\mathbf{Q}'_{r\times p}, \tag{A.4.2}$$

where columns of $\mathbf{P}$ denotes orthonormal eigenvectors of $\mathbf{EE}'$ and the columns of $\mathbf{Q}$ denotes orthonormal eigenvectors of $\mathbf{E}'\mathbf{E}$; that is, $\mathbf{P}'\mathbf{P} = \mathbf{Q}'\mathbf{Q} = \mathbf{I}_{r\times r}$. The matrix $\mathbf{\Lambda}$ denotes diagonal matrix of ordered singular values $l_1 \ge l_2 \ge \cdots \ge l_r > 0$, l_k's (k =1, 2, …, r) which are positive square root of the non-zero eigenvalues $\lambda_1, \lambda_2, \ldots, \lambda_r$ of $\mathbf{EE}'$ or $\mathbf{E}'\mathbf{E}$. On a per-element basis, each element e_{ij} of $\mathbf{E}_{v\times p}$ can be expressed as

$$e_{ij} = \sum_{k=1}^{r} l_k p_{ik} q_{jk}, \tag{A.4.3}$$

where p_{ik} and q_{jk} are the k^{th} element in the i^{th} row of $\mathbf{P}$ and the j^{th} column of $\mathbf{Q}'$, respectively.

According to Smith and Cornell (1993), the J-plot is a graphical display of a $v \times p$ data matrix by means of two dimensional markers $\mathbf{r}_1, \mathbf{r}_2, \ldots, \mathbf{r}_v$ for its rows and two dimensional markers $\mathbf{c}_1, \mathbf{c}_2, \ldots, \mathbf{c}_p$ for its columns. The J-plot is a method of displaying a lower rank (usually rank 2 approximation of a data matrix (Gabriel 1971, 1981). Because data matrices are usually of rank greater than 2 and we choose the display to be two-dimensional, first we shall approximate the data matrix (hereafter, when we refer to the data matrix we shall be talking about the effects matrix, $\mathbf{E}_{v\times p}$) by a matrix $\mathbf{E}^*_{v\times p}$ where rank of $\mathbf{E}^*_{v\times p}$ is 2.

The rank-two $\mathbf{E}^*_{v\times p}$, which approximates the matrix $\mathbf{E}_{v\times p}$, is now defined by letting r = 2 in (A.4.3), as

$$\begin{aligned}\mathbf{E}^*_{v\times p} &= \mathbf{l}_1\mathbf{p}_1\mathbf{q}'_1 + \mathbf{l}_2\mathbf{p}_2\mathbf{q}'_2 \\ &= \begin{bmatrix}\mathbf{p}_1 & \mathbf{p}_2\end{bmatrix}\begin{bmatrix}\mathbf{l}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{l}_2\end{bmatrix}\begin{bmatrix}\mathbf{q}'_1 \\ \mathbf{q}'_2\end{bmatrix}.\end{aligned} \tag{A.4.4}$$

In (A.4.4), $\mathbf{p}_1$ and $\mathbf{p}_2$ are the first two (leftmost two) columns of $\mathbf{P}$ in (A.4.2) and $\mathbf{q}'_1$ and $\mathbf{q}'_2$ are the top two rows of $\mathbf{Q}'$ in (A.4.2). Equation (A.4.4) is the best rank-two approximation of $\mathbf{E}_{v\times p}$ in the sense of minimizing the Euclidean norm of the matrix of residuals

$$\left\| \mathbf{E}_{v\times p} - \mathbf{E}^{*}_{v\times p} \right\|. \tag{A.4.5}$$

Gabriel (1981) and Jackson (1991) defined $\mathbf{JK}'$ factorization of $\mathbf{E}^{*}_{v\times p}$ such that $\mathbf{E}^{*}_{v\times p} = \mathbf{JK}'$.

where

$$\mathbf{J}_{v\times 2} = \left[\mathbf{l}_1\mathbf{p}_1 \quad \mathbf{l}_2\mathbf{p}_2\right] \tag{A.4.6}$$

$$\mathbf{K}_{p\times 2} = \left[\mathbf{q}_1 \quad \mathbf{q}_2\right]. \tag{A.4.7}$$

In this factorization, the columns of **K** are orthonormal, and therefore, $\mathbf{K}'_{2\times p}\mathbf{K}_{2\times p} = \mathbf{I}_2$, so that

$$\begin{aligned}\mathbf{E}^{*}_{v\times p}\mathbf{E}'^{*}_{v\times p} &= \mathbf{J}_{v\times 2}\mathbf{K}'_{2\times v}\mathbf{K}_{v\times 2}\mathbf{J}'_{2\times v} \\ &= \mathbf{J}_{v\times 2}\mathbf{J}'_{2\times v}\end{aligned} \tag{A.4.8}$$

The v diagonal elements of $\mathbf{E}^{*}_{v\times p}\mathbf{E}^{*'}_{p\times v}$ will approximate the v diagonal elements of $\mathbf{E}_{v\times p}\mathbf{E}'_{p\times v}$. In $\mathbf{JK}'$ factorization, the row markers for the J-plot are the v rows of $\mathbf{J}_{v\times 2}$, and the column markers are the p rows of $\mathbf{K}_{p\times 2}$.

From the J-plot inferences can be made about the relative directions as well as the approximate relative magnitudes of the treatment effects simultaneously for the multiple responses. Using J-plot one can identify the subgroup of treatments which are suitable for a set of response variables. J-plot for data of multi-response experiments can be obtained using the following steps.

Steps of Obtaining J-plot

The J-plot (Smith and Cornell, 1993) is a graphical display of a $v \times p$ data matrix of treatment effects (treatment means/ adjusted treatment means) in the form of a two-dimensional plot.

Step 1: Arrange the data on v treatment means/ adjusted treatment means for p response variables in the form of $v \times p$ data matrix **E**.

Step 2: It is possible to write $\mathbf{E}_{v\times p}$, using the singular value decomposition (SVD) as described above. SAS code will directly generate the matrices **P**, **Q** and **Λ**. SAS code for obtaining these matrices is given in Appendix 2.2.

Step 3: Obtain the two column vectors of the matrices **P** and **Q** obtained after SVD of **E**.

Step 4: Take first two columns of **P** and multiply first column by highest diagonal value of **Λ** and multiply second column by second highest diagonal value of **Λ**. Now we have $v \times 2$ vector which denotes v data points corresponding to treatments.

Step 5: Find the maximum absolute value from the two columns and divide each value by the maximum absolute values. This ensures that the values of these two columns are within the range of –1 to +1.

Step 6: Similarly taking first two columns of **Q** we can obtain $p \times 2$ vector corresponds to p data points for p response variables. Follow the step 5 to obtain the values of the two columns within the range of –1 to +1.

Step 7: Now take the columns obtained in Step 5 and append the columns obtained in Step 6. Now we have data points in two dimensions for v treatments and p response variables.

Step 8: Plot the two dimensional data in MS-Excel using Scatter Plot option choosing two columns as two series for X and Y axis. After plotting remove the Grid lines, clear the Area colour.

Step 9: After plotting all the data points, click each point and put a label by inserting a text box.

J-plot only helps in identification of best treatments for subset of responses separately. The ranking of treatments on the basis of all the responses simultaneously, can be done on the basis of square root

of diagonal elements of $\mathbf{E}^{*}_{v\times p}\mathbf{E}^{*'}_{p\times v}$. $\mathbf{E}^{*}_{v\times p}$ is an approximation to $\mathbf{E}_{v\times p}$. Therefore, one may take actual *v* diagonal elements of $\mathbf{E}_{v\times p}\mathbf{E}'_{p\times v}$ without approximating with rank-two matrix for ranking the treatments. The square root of diagonal elements of $\mathbf{E}_{v\times p}\mathbf{E}'_{p\times v}$ represents *Euclidean distance* of treatment effects means from the null vector (0, 0, …, 0). For single response experiments this is nothing but the treatment mean.

Remark A.4.1: The method proposed based on Euclidian distance from null vector has a drawback that it is valid only for the situations in which either maximization or minimization of response variables is desired. It may fail in those situations in which the experimenter is interested in maximum value of some of the response variables and minimum value of the other set. In these situations, one may think of weighted mean of the variables. As discussed earlier, assigning weights to different response variables is quite subjective in nature. Therefore, one may think of giving equal weight to all the response variables, i.e., + 1 to the variables whose maximum values is desired and −1 to the variables whose minimum value is desired. This procedure has a drawback that it involves adding response variables which are in different units. Another thought can be useful for identification of the best treatment out of two significantly different treatments by using the following one tailed test. Consider two *p*-component treatment effect vectors $\boldsymbol{\tau}_i$ and $\boldsymbol{\tau}_{i'}$ (i, i' = 1, 2, …, v) which are significantly different. Consider testing of the null hypothesis of the following form H_0: $\boldsymbol{\tau}_i > \boldsymbol{\tau}_{i'}$ against the alternative hypothesis H_1: $\boldsymbol{\tau}_i \leq \boldsymbol{\tau}_{i'}$. If null hypothesis is rejected then either treatment $\boldsymbol{\tau}_{i'}$ is better than treatment $\boldsymbol{\tau}_i$ or they are equal. On the other hand, if null hypothesis is accepted then one can infer that treatment $\boldsymbol{\tau}_i$ is better than treatment $\boldsymbol{\tau}_{i'}$ with specified level of significant. This is still an open area of research. Further efforts need to be made in this direction.

Alternatively, one may transform the variables in the following manner. If the original variables follow a *p*-variate normal distribution with mean vector $\boldsymbol{\mu}$ and dispersion matrix $\boldsymbol{\Sigma}$ then the transformed variables obtained after premultiplying the matrix of response variables by $\boldsymbol{\Sigma}^{-\frac{1}{2}}$ follows *p*-variate normal distribution with mean vector as $\mathbf{0}$ and dispersion matrix as $\mathbf{I}$. Now working with these standardized transformed variables, if through multivariate treatment contrast analysis one gets that treatments 1 and 2 are significantly different then one can take the estimate $\mathbf{P}'\boldsymbol{\tau}$ and take the sum of the estimates obtained. If the sum is positive, then treatment 1 is taken as better than treatment 2 and if sum is negative, then we can say that treatment 2 is better than treatment 1. Of course while estimating, care should be taken that the values of the response variables to be minimized are taken as negative of the original values. It ensures that maximization amounts to minimization. Now if a particular treatment is significantly different from every other treatment and the decision in each case is towards that treatment, then this can be taken as the best treatment. This method has a drawback that one needs to estimate of variance-covariance matrix of the residuals, from the same data set. Therefore, further refinements need to be made.

A.5 Illustrations

In this section we describe the analytical procedures described in the previous sections with the help of real life examples.

Example A.5.1: An experiment was conducted during 2004-05 at Department of Agronomy, Bidhan Chandra Krishi Viswavidyalaya on Integrated Nutrient Management on Rapeseed. Three different sources of sulphur were tested along with recommended dose of nitrogen (N), phosphorus (P) and potassium (K) and Farmyard Manure (FYM). Following 9-treatment combinations were tested:

T_1: $N_0 P_0 K_0$
T_2: N80 $P_{40} K_{40}$
T_3: T_2 + FYM (5t/ha)
T_4: T_2 + S_{40} (Aluminum Sulphate)
T_5 T_2 + S_{40} (Aluminum Sulphate) + FYM (5t/ha)
T_6: T_2 + S_{40} (Gypsum)
T_7: T_2 + S_{40} (Gypsum) + FYM (5t/ha)
T_8: T_2 + S_{40} (El S)
T_9: T_2 + S_{40} (El S) + FYM (5t/ha)

The experiment was laid out in Randomized Complete Block (RCB) design in 3 replications. Data on the following response variables were collected: Number of branches per plant, Number of siliqua per plant, Number of seed per siliqua, Seed yield (g/plant), Straw yield (g), HI (Harvest Index), Test weight (g), Leaf Area Index 45 DAS Leaf Area Index 90 DAS. The data obtained is given in Table A.5.1 (Appendix A.1).

At the first instance data were analyzed separately for each for the response variables. The best treatment is identified for each response variable separately. The results obtained are given in Table A.5.1a.

Table A.5.1a: Best Treatments for Individual Response Variables

Response variables	Character (or Response)	Prob>F (Treatments)	Best treatment	Prob>F (Blocks)
P1	Number of branches	0.0004	T6: NS with T3, T7 and T9	0.2460
P2	Siliqua per plant	< 0.0001	T7: NS with T6 and T9	0.9588
P3	Seed per siliqua	0.0041	T6: NS with T3	0.0123
P4	Seed yield	0.0076	T9: NS with T3, T6 and T7	0.5680
P5	Straw yield	0.0788	-	0.7252
P6	Harvest Index (HI)	0.2978	-	0.9591
P7	Test weight	0.0024	T9: NS with T7	0.0675
P8	Leaf Area Index @ 45	0.0035	T3: NS with T9	0.7530
P9	Leaf Area Index @ 90	0.8646	-	0.1055

* NS = Not Significant

From Table A.5.1a, it can be observed that treatment effects are significantly different for the response variables like P1, P2, P3, P4, P7 and P8. The treatments which are found to be best for different response variables are T3, T6, T7 and T9. For P1, T6 is the best treatment which is not significantly different from T3, T7 and T9. Therefore, for number of branches per plant (P1) one may recommend or select any one of the T3, T6, T7 and T9 treatments. Similarly, any one of the T3, T6, T7 and T9 may be selected as best for seed yield (P4). For leaf area index (P8) the best treatment is T3 which is not significantly different from T9. In this way, one can see that different treatments may be selected as best for different responses and it is not possible to find a single treatment as best for all the responses. In this kind of a situation we need a method which identifies a single treatment as the best treatment for all the response variables.

Keeping in view the above, the data were also analyzed by taking first principal component score as dependent variable. First Principal Component explained 85% of the total variation. ANOVA based on first principal component revealed that treatment effects are significantly different (Prob > F = 0.0452) and block effects are not significantly different (Prob > F = 0.6734). From all possible

pairwise treatment comparisons made using least significant difference, it is found that treatment 1 is significantly different from all other treatments. Therefore, any of the treatments T2 through T9 may be taken as best (Table A.5.1b).

Table A.5.1b: LSD Grouping of Treatments using First Principal Component

LSD grouping	Treatment
A	5
A	4
A	9
A	8
A	7
A	3
A	2
A	6
B	1

As first principal component only explained 85% of the variation and 15% of the variation remained unexplained therefore, there is need to perform multivariate analysis of variance. Therefore, the MANOVA was performed and given in Table A.5.1c.

Table A.5.1c: **Multivariate Analysis of Variance (MANOVA) Table for Simultaneous Comparison of Treatment Effects**

Sources of variation	d.f.	Matrix of SSCP	Wilk's Lambda	Prob>F
Block	2	**B**	0.13286	0.1917
Treatment	8	**H**	0.00017	0.0003
Residual	16	**E**		
Total	26	**T** = **B** + **H** + **E**		

From MANOVA, treatment effects are found to be significantly different and replication effects are not significantly different. Since the treatment effects are significantly different, therefore, the next question one needs to answer is, which treatments are significantly different? To answer this significance of all possible treatment comparisons $\binom{9}{2} = 36$ was tested using the procedure of multivariate treatment contrast analysis. The probability levels of the all possible pair-wise treatment comparisons are given in Table A.5.1d

Table A.5.1d: Probabilities of Significance of All Possible Pairwise Treatment Comparisons using Wilk's lambda (Λ)

Treatment	1	2	3	4	5	6	7	8	9
1	.								
2	**0.0130**	.							
3	**0.0007**	0.0963	.						
4	**0.0021**	0.1114	**0.0105**	.					
5	**0.0016**	0.0595	**0.0057**	0.9980	.				
6	**0.0008**	**0.0235**	**0.0112**	0.3326	0.2046	.			
7	**0.0004**	**0.0015**	**0.0003**	**0.0421**	0.0675	**0.0367**	.		
8	**0.0038**	0.1186	**0.0115**	0.7049	0.5194	0.4217	**0.0418**	.	
9	**0.0011**	**0.0094**	**0.0011**	0.3839	0.4710	0.1390	0.5117	0.2833	.

*Bold face indicates two treatments are significantly different.

From Table A.5.1d, one can observe that treatment T1 is significantly different from all the treatments. Treatment T2 is significantly different from T6, T7 and T9. T3 is significantly different from T4, T5, T6, T7, T8 and T9. Treatment T4 is significantly different from T1 and T7. T7 is significantly different from T1, T2, T4, T6 and T7. T8 is significantly different from T1, T3 and T7. However, ANOVA using first Principal Component scores shows that all the treatments except T1 are found to be not significantly different from the remaining treatments. Results based on multivariate treatment contrast analysis deviates from the results based on first Principal Component and provide more information about the significance of the treatment effects.

We have seen that treatment effects are significantly different and some of the pairs of treatments are significantly different. Therefore, to identify the best treatment for all the response variables simultaneously, Euclidean distance from null vector as well as the average over the response variables were computed and are given in Table A.5.1e.

Table A.5.1e: Identification of Best Treatment using J-plot and Euclidean Distance from Rapeseed Data

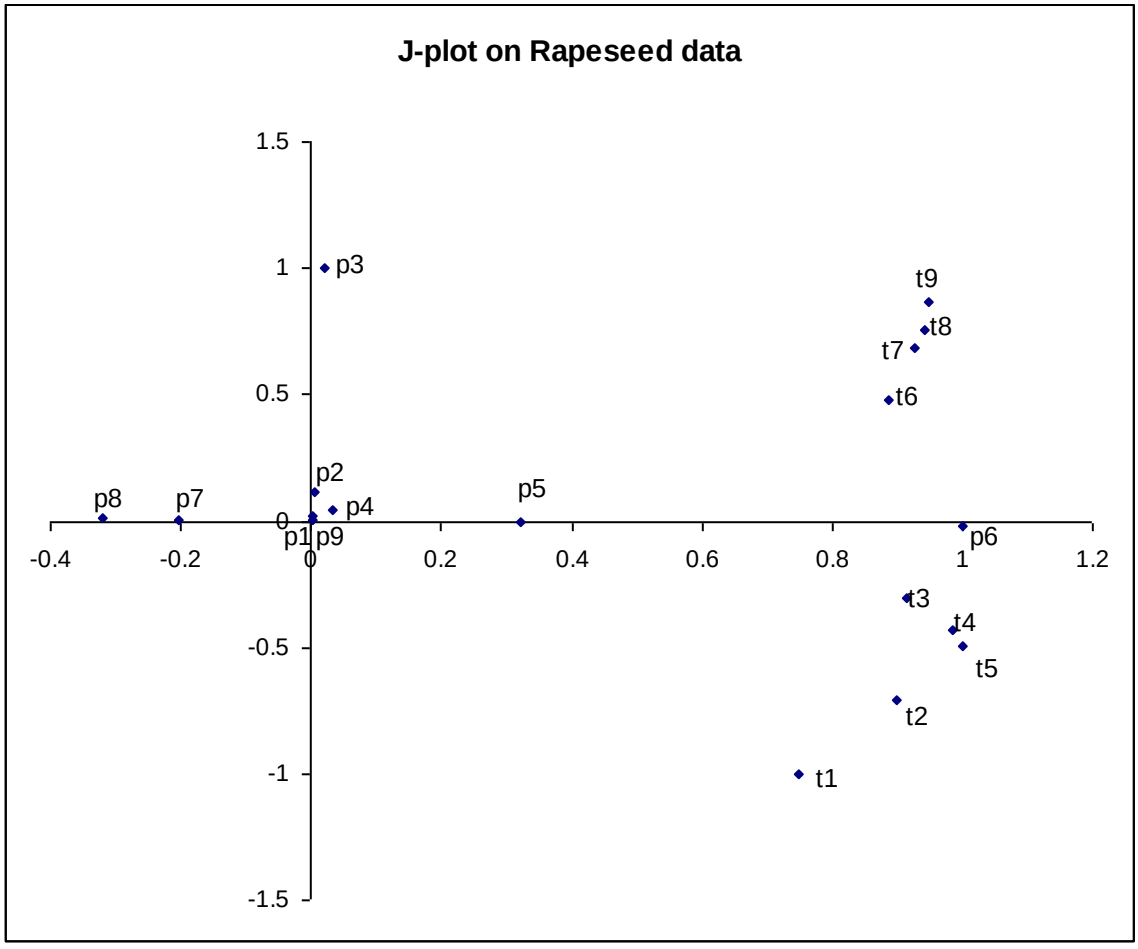
Euclidean distance from null vector	Treatment	Average over responses	Treatment
5534.5503	T9	779.5211	T9
5493.8795	T8	771.4838	T8
5403.5188	T7	760.2325	T7
5162.2849	T6	723.0665	T6
5828.7208	**T5**	796.8142	**T5**
5740.3873	T4	785.7149	T4
5321.7425	T3	730.0494	T3
5244.9685	T2	710.9152	T2
4371.7455	T1	584.4298	T1

According to Euclidean distance from null vector and average over all response variables T5 is the best treatment. Through multivariate treatment contrast analysis, T5 is significantly different only from T1 and T3. Therefore, one may recommend any of the T2, T4, T5, T6, T7, T8 or T9 treatments.

Using Euclidean distance from null vector and average of the response variables we can infer that treatment number 5 i.e. Sulphur through Ammonium Sulphate along with recommended level of N, P and K and FYM gives better result in Rapeseed for all the characters. Out of these two methods Euclidean distance from null vector is easily comprehensible and requires very less computational

effort, therefore we recommend Euclidean distance from null vector for identification of the best treatment.

The data were represented pictorially in the form of a two-dimensional plot, J-plot. Treatments which are close to any response variable are influenced by that response. For example, top right hand corner we have treatments T6, T7, T8 and T9 which influences response variables P2, P3, P4, P5. This results match with the results obtained from the analysis of response variables individually as given in Table A.5.1a. So using J-plot one can subgroup the treatments based on the response variables of interest. Now these subgroups can be used to pick up the desired treatment based on choice of subset of response variables.



-p9 represents 9 response variables and t1-t9 represents 9 treatments presented in Table A.5.1a.

A SAS code for the procedure of identification of best treatment has been developed and is given in Appndix A.2.

In the above example the experiment was conducted in RCB design. There are situations where multi-response experiments are conducted in incomplete block designs. The following example is considered for the illustration of analysis of data from a complete multi-response experiment conducted using an incomplete block design.

Example A.5.2: An experiment was conducted using a square lattice design with 49 treatments, in 28 blocks each of size 7 in 4 replications. The data are collected on 4 response variables. The data obtained is given in Table A.5.2 (Appendix A.1).

At the first instance the data were analyzed separately for each of the response variables. The best treatment is identified for each response variable separately. The results obtained are given in Table A.5.2a.

Table A.5.2a Best Treatments for Individual Characters

Characters or Response variable	Prob > F (Treatments)	Best treatment	Prob > F (Blocks)
P1	0.0247	T41	0.0003
P2	0.0141	T44	0.0117
P3	< 0.0001	T27	0.0192
P4	0.5101	-	0.1203

From Table A.5.2a, it can be observed that treatment effects are significantly different for the response variables like P1, P2 and P3. The treatments which are found to be best for different response variables P1, P2 and P3 are respectively T41, T44 and T27. Therefore, different treatments may be selected as best for different responses and it is not possible to find a single treatment as best for all the responses. In this kind of situation, a method which identifies a single treatment as the best treatment for all the response variables is required. Therefore, there is need to perform multivariate analysis of variance and is given in Table A.5.2b.

Table A.5.2b: **Multivariate Analysis of Variance (MANOVA) Table for Simultaneous Comparison of Treatment Effects**

Sources of variation	d.f.	Wilk's Lambda	Prob>F
Treatment	48	0.0593	<0.0001
Block (replication)	24	0.2767	<0.0001
Replication	3	0.3172	<0.0001
Residual	120		
Total	195		

From MANOVA, treatment effects are found to be significantly different and block within replication effects and replication effects are also significantly different.

Since the treatment effects are significantly different, therefore, the next question one needs to answer is, which treatments are significantly different? To answer this significance of all possible treatment comparisons $\binom{49}{2}$ = 1176 was tested using the procedure of multivariate treatment contrast analysis. The treatment pairs which are significantly different at 5% level of significance are given in Table A.5.2c in the form of treatment number in column (1) and corresponding treatments in column (2) which are significant at 5% level of significance.

Table A.5.2c: Multivariate Treatment Contrast Analysis Results Based on Wilk's Lambda Criterion

Treatment Number (1)	**Significant treatments at 5% level of significance** (2)
1	4, 5, 9, 10, 15, 16, 18, 20, 21, 24, 26, 27, 29, 30, 31, 35, 40, 44, 48
2	5, 7, 8, 9, 16, 24, 26, 26, 27, 29, 30, 31, 38, 40, 42, 44
3	4, 5, 8, 9, 10, 11, 12, 15, 16, 18, 20, 21, 23, 24, 26, 27, 28, 29, 30, 31, 34, 35, 44, 45, 46, 48, 49
4	6, 5, 7, 8, 9, 15, 16, 21, 22, 27, 29, 31, 32, 33, 36, 37, 38, 39, 40, 42, 44, 45, 46, 47, 49
5	6, 7, 9, 22, 27, 31, 33, 35, 38, 40, 41, 42, 47, 49
6	8, 9, 10, 16, 18, 20, 24, 26, 27, 29, 30, 31, 32, 34, 35, 44, 48
7	8, 9, 10, 11, 16, 17, 18, 20, 24, 26, 27, 29, 30, 31, 32, 34, 35, 44, 48
8	9, 15, 16, 22, 24, 24, 26, 28, 29, 30, 31, 32, 34, 35, 44, 48
9	10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 , 21, 22, 23, 25, 26, 27, 28, 29, 30, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49
10	22, 27, 31, 37, 38, 40, 41, 42, 47, 49
11	16, 27, 31, 38, 40, 42, 44,
12	27, 30, 31, 38, 40
13	16, 24, 26, 27, 30, 31, 44
14	16, 24, 26, 27, 30, 31, 38, 44
15	16, 24, 26, 27, 30, 31, 32, 44
16	18, 19, 20 , 21, 22, 23, 27, 28, 31, 32, 33, 35, 36, 37, 38, 39, 40, 41, 42, 43, 47, 49
17	27, 30, 31, 38, 40
18	27, 31, 38, 40, 42, 47, 49
19	24, 26, 27, 30, 31, 38, 40, 44
20	22, 27, 31, 33, 37, 38, 40, 41, 42, 47, 49
21	27, 30, 31, 32, 38, 41, 42
22	24, 26, 27, 29, 30, 31, 32, 34, 35, 36, 40, 44, 45
23	24, 27, 30, 31, 38, 40
24	27, 28, 31, 32, 33, 36, 37, 38, 39, 40, 41, 42, 43, 47, 49
25	27, 31, 38
26	27, 31, 32, 33, 37, 38, 39, 40, 41, 42, 43, 47, 49
27	28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48
28	31, 38, 40, 42, 44, 47, 49
29	30, 31, 32, 35, 37, 38, 40, 41, 47

…

30	31, 32, 33, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49
31	32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49
32	38, 40, 41, 44, 48, 49
33	35, 40, 44
34	38, 40, 41, 42, 47, 49
35	38, 40, 42, 44, 47, 49
36	38, 41, 44
37	44, 48
38	40, 44, 45, 46, 48
39	44
40	41, 43, 44, 45, 48
41	42, 44, 45, 47, 48
42	44, 48
43	44
44	47, 49
47	48

From Table A.5.2c, it can easily be seen that some of the pairs of treatments are significantly different. Therefore, to obtain the best treatment for all the response variables simultaneously, Euclidean distance as well as the average (adjusted treatment means) over the response variables were computed and are given in Table A.5.2d. As the experimental design considered in this example is incomplete block design (square lattice design), we have taken adjusted treatment means over the response variables instead of simple averages.

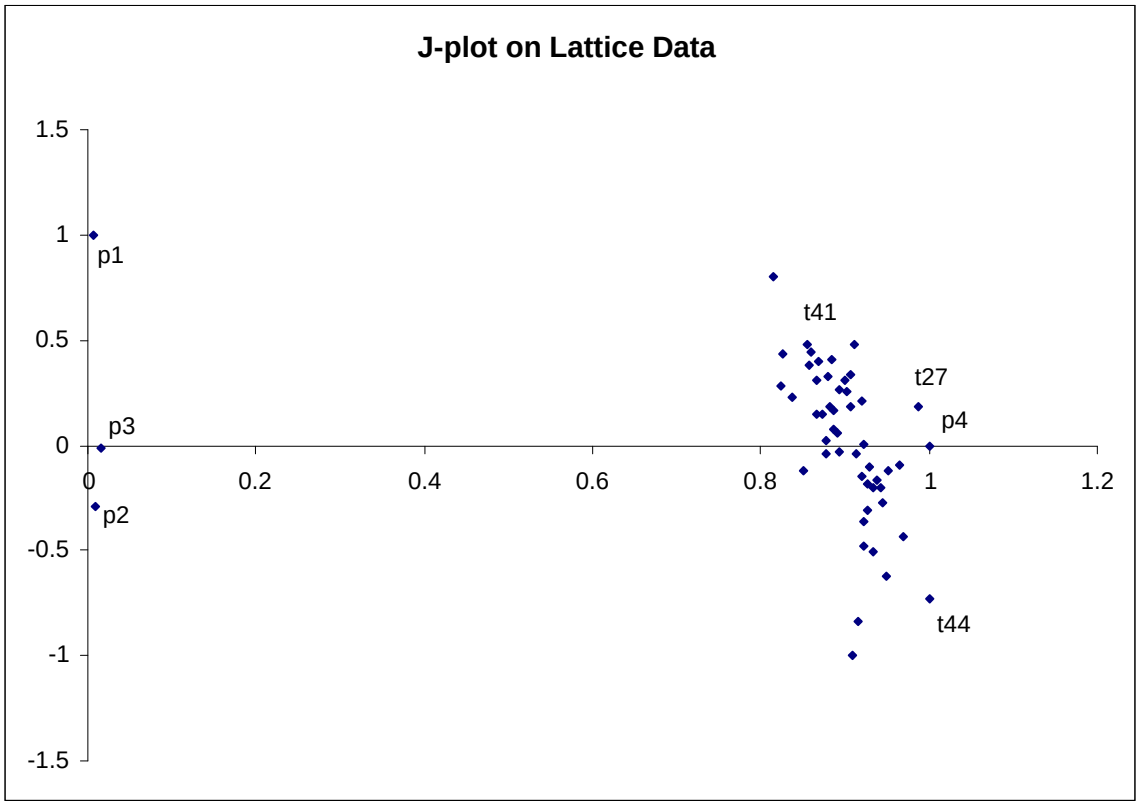
Table A.5.2d: Identification of Best Treatment Using Euclidean Distance from Null Vector from Rapeseed Data

Euclidean distance from null vector	**Treatment**	**Average over responses**	**Treatment**
(1)	(2)	(3)	(4)
297.635	1	95.746	1
289.402	2	93.255	2
275.610	3	90.080	3
278.641	4	89.491	4
311.987	5	97.944	5
299.168	6	96.096	6
306.337	7	98.056	7
311.226	8	98.559	8
310.010	9	95.888	9
296.430	10	93.963	10
292.941	11	93.554	11
316.971	12	100.145	12
292.802	13	93.972	13
297.865	14	95.076	14
321.188	15	101.460	15
321.040	16	99.763	16

…

315.126	17	99.445	17
302.143	18	95.974	18
299.587	19	95.802	19
312.802	20	98.386	20
318.311	21	100.177	21
304.715	22	97.596	22
313.716	23	99.324	23
312.078	24	97.474	24
299.167	25	95.197	25
315.194	26	98.419	26
333.339	27	**106.165**	**27**
295.153	28	94.256	28
327.846	29	102.606	29
287.550	30	91.029	30
307.736	31	94.354	31
278.873	32	90.114	32
306.014	33	97.842	33
296.530	34	94.426	34
283.053	35	90.573	35
300.651	36	95.716	36
293.676	37	94.601	37
307.570	38	99.038	38
301.739	39	96.612	39
290.773	40	93.308	40
289.132	41	93.379	41
310.644	42	99.239	42
311.981	43	99.149	43
338.056	**44**	104.896	44
313.437	45	98.915	45
308.898	46	97.926	46
304.297	47	97.447	47
319.529	48	100.394	48
325.879	49	102.916	49

According to Euclidean distance from null vector T44 is found to be the best treatment. On the other hand, average (adjusted treatment means) over all response variables suggests that T27 is the best. Again from multivariate treatment contrast analysis it is clear that these two treatments (T27 and T44) are not significantly different. Therefore, one may recommend any of the treatments, T27 or T44.



*p1-p4 represents 4 response variables and t27, t41 and t44 represents the treatments (for clarity of the chart all the treatment labels are not shown)

The data were represented pictorially in the form of a two-dimensional plot, J-plot. Treatments which are close to any response variable are influenced by that response. For example, top right hand corner we have treatment T41 which influences response variable P1, T44 influences response variable P2 and T27 influences P1. Treatment effects are not significant for P4, so we don't consider this response variable for making inference. This results match with the results obtained from the analysis of response variables individually as given in Table A.5.2a. So using J-plot one can subgroup the treatments based on the response variables of interest. Now these subgroups can be used to select the desired treatment based on choice of subset of response variables.

References

Anderson, T.W. (1958). *Introduction to Multivariate Analysis*. John Wiley, New York.

Dean, A. and Voss, D. (1999). *Design and Analysis of Experiments*. Springer Texts in Statistics, New York.

Gabriel, K.R (1971). The biplot-graphic display of matrices with application to principal component analysis. *Biometrika*, **58**, 453-467.

Gabriel, K.R (1981). *Biplot Display of Multivariate Matrices for Inspection of Data and Diagnosis in Interpreting Multivariate Data*, Edition. V. Barnett, New York: John Wiley, 147-173.

Good, I.J. (1969). Some applications of the singular value decomposition of a matrix. *Technometrics*, **11**, 823-831; Erata (1970) **12**, 722.

Jackson, J.E. (1991). *Biplots, A User Guide to Principal Components.* John Wiley, New York.

Johnson, R.A. and Wichern, D.W. (2002). *Applied Multivariate Statistical Analysis*. John Wiley, New York.

Rao, C.R. (2002). *Linear Statistical Inference and its Applications*. 2nd Edition, John Wiley & Sons, New York.

Roy, S. N. (1957). *Some Aspects of Multivariate Analysis.* John Wiley, New York.
Smith, W.F. and Cornell, J.A. (1993). Biplot displays for looking at multiple response data in mixture experiments. *Technometrics*, **35**(**4**), 337-350.

Appendix A.1

Table A.5.1: Experimental Data on Integrated Nutrient Management on Rapeseed (Example A.5.1)

Treat	Rep	No.of branches	Siliqua/ Plant	Seed/ Siliqua	Seed yield	Straw yield	HI	Test weight	LAI @45	LAI @90
1	1	4.1	46.0	21.0	975.0	5000.0	0.16	2.65	2.76	1.20
2	1	7.8	71.8	22.5	1241.7	5000.0	0.20	3.13	7.31	2.52
3	1	7.7	106.5	22.8	1383.3	5166.6	0.21	2.26	7.69	0.67
4	1	7.3	93.0	23.3	1141.7	5333.3	0.18	3.18	6.65	1.67
5	1	8.2	98.0	22.3	1191.7	4916.6	0.20	3.19	6.25	1.63
6	1	8.9	107.3	24.2	1216.7	5083.3	0.19	2.94	3.94	1.45
7	1	7.3	116.0	22.8	1366.7	4916.6	0.22	3.22	4.72	1.32
8	1	8.0	113.2	22.5	1458.3	5166.6	0.22	3.00	5.60	1.08
9	1	8.3	95.7	22.8	1583.3	5100.0	0.24	3.43	6.40	1.32
1	2	6.1	50.5	22.2	833.3	3833.3	0.18	3.16	3.22	0.40
2	2	7.6	66.6	23.3	966.7	5333.3	0.15	3.01	4.91	0.40
3	2	8.0	79.5	24.8	1433.3	4750.0	0.23	3.15	8.08	1.54
4	2	7.4	97.0	23.5	1350.0	5500.0	0.20	3.17	6.30	0.71
5	2	7.8	106.3	23.7	1325.0	6416.6	0.17	3.28	7.20	0.72
6	2	8.4	104.7	24.0	1558.3	4500.0	0.26	3.14	3.85	0.62
7	2	9.6	125.3	23.0	1416.7	5583.3	0.20	3.52	3.63	1.55
8	2	8.9	103.4	23.0	1575.0	5666.6	0.22	3.02	5.28	1.45
9	2	8.5	126.0	24.2	1675.0	5166.6	0.24	3.32	6.70	1.05
1	3	4.8	49.8	22.3	891.6	4000.0	0.18	2.90	2.09	0.70
2	3	7.4	74.3	22.8	1316.7	5000.0	0.21	3.07	6.04	1.26
3	3	7.8	78.2	24.5	999.9	5583.3	0.15	2.70	7.04	1.41
4	3	9.1	107.2	22.3	1566.7	5900.0	0.21	3.17	6.38	0.69
5	3	7.8	100.4	22.4	1566.7	5666.6	0.22	3.23	6.62	1.18
6	3	7.9	118.3	24.1	1375.0	5333.3	0.20	3.04	7.72	1.04
7	3	8.2	128.7	22.6	1666.7	5083.3	0.25	3.37	6.48	1.00
8	3	7.6	91.8	22.4	1533.3	5000.0	0.23	3.01	5.09	1.26
9	3	7.9	107.5	22.0	1400.0	5666.6	0.20	3.37	5.21	1.19
1	1	4.1	46.0	21.0	975.0	5000.0	0.16	2.65	2.76	1.20
2	1	7.8	71.8	22.5	1241.7	5000.0	0.20	3.13	7.31	2.52

Treat: treatments and Rep: Replication

Table A.5.2: Experimental Data on Square Lattice Design (Example A.5.2)

Replication	Block	Treatment	Response 1	Response 2	Response 3	Response 4
1	1	45	1.3	292	79.9	8.6
1	1	31	1.2	284	66.4	7.4
1	1	38	1.4	261	89.8	8.3
1	1	24	1.3	299	75.9	7.7
1	1	10	1.3	267	79.3	7.8
1	1	3	1.5	230	86.0	8.7
1	1	17	1.8	302	83.2	8.6
1	2	40	1.4	270	84.8	0.0
1	2	12	1.5	342	86.3	7.9
1	2	33	1.5	295	88.8	8.4
1	2	47	1.8	309	87.3	7.0
1	2	26	1.9	335	74.6	7.4
1	2	5	1.8	286	79.5	7.1
1	2	19	1.5	283	82.2	8.3
1	3	21	1.6	348	83.8	7.5
1	3	7	1.4	332	90.1	9.9
1	3	35	1.4	312	82.7	7.3
1	3	28	1.6	312	81.9	8.4
1	3	42	1.3	284	89.5	8.3
1	3	14	1.3	295	83.1	8.4
1	3	49	1.4	336	88.6	7.9
1	4	22	2.2	285	90.4	8.0
1	4	15	1.7	326	82.8	7.7
1	4	29	1.6	337	82.2	8.0
1	4	36	1.7	343	83.9	9.4
1	4	43	1.7	341	87.8	8.7
1	4	1	1.6	323	89.8	9.3
1	4	8	1.5	311	81.9	9.4
1	5	34	1.7	264	85.9	9.6
1	5	27	1.6	325	99.6	7.8
1	5	41	1.7	255	83.8	8.5
1	5	13	1.8	251	84.6	7.6
1	5	20	1.9	296	80.1	7.8
1	5	48	1.8	310	84.6	7.3
1	5	6	1.6	264	89.4	7.4
1	6	9	1.6	327	69.6	8.7
1	6	2	1.8	309	86.2	8.6
1	6	37	1.6	290	82.3	9.0
1	6	30	1.7	328	75.3	6.9
1	6	16	1.5	333	78.4	7.4
1	6	44	1.6	341	81.8	7.6
1	6	23	1.5	347	85.8	8.2
1	7	46	1.5	332	79.7	7.8
1	7	39	1.5	364	86.8	8.4
1	7	32	1.4	306	80.7	9.2
1	7	11	1.8	342	82.3	7.8
1	7	18	1.8	319	83.8	7.3
						…

1	7	4	2.0	293	82.5	7.5
1	7	25	1.6	307	85.9	7.9
2	1	43	1.8	307	86.6	8.5
2	1	45	1.6	289	83.5	7.9
2	1	46	1.7	262	85.9	8.2
2	1	48	1.8	300	83.3	7.3
2	1	44	1.8	302	83.4	7.3
2	1	47	1.8	290	90.2	7.5
2	1	49	1.9	347	90.1	7.5
2	2	26	1.7	280	80.6	7.2
2	2	22	2.2	319	92.8	7.5
2	2	23	2.1	312	84.7	7.6
2	2	25	1.6	286	81.8	7.3
2	2	28	1.9	281	79.8	8.3
2	2	27	1.8	316	96.0	7.3
2	2	24	1.9	299	81.0	7.2
2	3	40	1.2	253	84.3	8.8
2	3	38	2.1	290	94.5	7.7
2	3	36	1.5	265	84.4	6.6
2	3	42	1.6	310	88.9	8.9
2	3	37	1.6	308	90.8	8.8
2	3	39	1.9	272	87.3	8.7
2	3	41	1.9	265	91.8	7.8
2	4	6	1.8	292	90.8	6.8
2	4	4	1.7	278	81.1	6.7
2	4	2	1.9	258	85.2	8.1
2	4	7	1.8	294	90.6	0.0
2	4	1	1.5	258	90.8	8.9
2	4	3	1.4	246	85.1	7.7
2	4	5	1.6	292	81.4	6.8
2	5	14	1.8	315	91.2	7.7
2	5	9	1.5	317	74.8	7.9
2	5	8	1.7	293	79.2	8.6
2	5	11	1.6	297	88.0	7.6
2	5	13	1.7	264	88.4	8.2
2	5	10	1.5	274	82.7	6.8
2	5	12	2.0	275	83.1	7.7
2	6	33	1.6	264	89.3	8.5
2	6	31	1.6	292	69.4	7.3
2	6	32	1.7	268	90.2	8.2
2	6	29	1.5	306	82.9	8.0
2	6	30	1.8	272	82.4	7.5
2	6	34	1.6	280	80.9	8.4
2	6	35	1.9	271	82.1	8.1
2	7	18	2.0	310	86.2	9.0
2	7	15	1.8	292	88.7	7.8
2	7	19	1.6	277	90.8	8.9
2	7	16	1.4	317	82.7	7.8
2	7	21	1.6	288	86.9	8.0
						…

2	7	17	1.5	280	89.2	8.9
2	7	20	1.8	310	84.8	8.3
3	1	21	1.6	290	81.9	7.1
3	1	20	1.9	280	82.8	8.1
3	1	16	1.6	308	73.8	6.9
3	1	17	2.0	294	80.5	7.6
3	1	15	1.9	310	84.3	7.6
3	1	19	2.0	300	84.2	8.1
3	1	18	1.8	280	78.9	8.6
3	2	49	1.9	280	86.8	7.7
3	2	43	2.1	258	89.9	8.3
3	2	44	2.3	332	81.7	8.4
3	2	46	2.1	310	87.5	7.6
3	2	47	1.3	280	91.1	7.2
3	2	45	1.9	300	87.3	7.8
3	2	48	2.0	280	84.9	7.0
3	3	5	1.6	310	81.9	7.9
3	3	4	1.9	265	82.9	8.0
3	3	7	1.5	268	93.7	9.8
3	3	6	1.5	276	93.7	6.9
3	3	2	2.0	287	88.8	7.8
3	3	1	1.6	270	93.5	9.3
3	3	3	1.6	272	90.8	8.1
3	4	23	1.3	280	86.1	7.7
3	4	24	1.6	282	78.8	7.2
3	4	28	1.5	260	92.5	8.0
3	4	22	1.3	300	83.9	8.6
3	4	27	2.0	332	91.4	8.0
3	4	26	1.5	322	79.5	6.8
3	4	25	1.4	300	82.9	7.5
3	5	29	1.6	315	87.9	7.4
3	5	33	1.6	282	87.5	7.4
3	5	32	1.3	245	87.1	8.1
3	5	35	1.5	252	84.7	7.0
3	5	30	1.5	220	78.8	8.1
3	5	31	1.2	300	69.9	6.8
3	5	34	1.6	258	84.2	7.8
3	6	12	1.9	312	88.6	8.0
3	6	9	1.9	302	73.2	8.3
3	6	14	1.8	270	86.8	7.1
3	6	8	1.7	322	89.7	9.2
3	6	10	1.8	290	83.4	7.4
3	6	13	1.8	304	87.2	7.9
3	6	11	1.7	238	84.7	8.1
3	7	39	1.7	258	91.0	6.9
3	7	41	2.1	270	90.7	7.7
3	7	37	1.5	254	88.4	8.0
3	7	38	1.6	302	98.3	8.2
3	7	42	1.5	290	91.1	8.4
3	7	40	1.6	300	94.7	7.4

...

3	7	36	1.3	282	84.9	8.5
4	1	8	1.6	280	85.4	8.6
4	1	1	1.8	284	77.4	7.2
4	1	29	2.1	290	82.7	7.6
4	1	15	2.3	304	90.7	7.5
4	1	43	2.1	280	81.4	7.7
4	1	36	1.9	260	84.9	8.7
4	1	22	2.2	268	84.9	7.9
4	2	45	2.0	280	86.6	7.9
4	2	3	2.0	258	98.5	8.1
4	2	17	1.8	300	83.8	8.1
4	2	10	2.4	282	84.2	7.8
4	2	31	2.1	270	72.0	6.6
4	2	24	2.0	300	78.2	7.6
4	2	38	2.3	281	93.1	8.0
4	3	12	2.0	298	86.8	7.4
4	3	40	1.9	280	91.8	8.6
4	3	19	1.8	282	87.0	8.2
4	3	26	1.9	288	82.3	7.0
4	3	47	1.9	270	92.0	7.6
4	3	5	1.8	314	82.4	7.4
4	3	33	2.1	310	89.8	8.1
4	4	2	1.6	266	86.4	7.5
4	4	16	1.7	300	79.2	7.3
4	4	37	1.6	282	92.0	8.3
4	4	44	2.0	342	80.3	7.4
4	4	9	1.8	285	72.3	7.2
4	4	30	1.9	285	76.3	7.1
4	4	23	2.2	292	83.4	8.0
4	5	32	1.7	278	80.8	8.2
4	5	18	2.0	302	82.8	7.8
4	5	4	2.0	281	81.4	6.9
4	5	39	2.1	310	88.6	7.1
4	5	25	1.9	315	84.7	7.0
4	5	11	2.1	307	81.3	7.4
4	5	46	1.6	325	86.7	7.7
4	6	42	1.7	315	92.0	8.7
4	6	7	1.9	288	89.8	9.0
4	6	14	1.9	282	84.4	8.1
4	6	35	2.0	242	82.4	7.7
4	6	49	2.2	292	91.3	7.4
4	6	21	2.3	310	87.9	6.9
4	6	28	2.3	298	82.3	7.8
4	7	13	2.2	282	92.1	7.6
4	7	34	1.9	292	85.6	8.4
4	7	48	2.2	305	89.1	7.2
4	7	6	2.2	282	91.1	7.1
4	7	27	2.3	285	98.9	7.3
4	7	41	2.4	282	92.5	8.4
4	7	20	2.1	292	82.7	8.3

Appendix A.2

SAS Code for the Identification of Best Treatment

```
proc iml;
/* Input v × p matrix of treatment means for all the response variables */
 indat = {
40.28   8.71    111.40  5.00    48.77   21.83   899.97  4277.770.17     41.67   295.27  3.39
        3.69    2.69    0.77,
46.33   9.21    120.37  7.60    70.90   22.87   1175.035111.100.19      65.23   368.43  5.65
        6.26    6.09    1.39,
46.17   8.11    122.70  7.83    88.07   24.03   1272.175166.630.20      65.97   405.67  5.84
        6.33    7.60    1.21,
…                       …                       …                       …
45.93   10.11   115.37  8.37    123.33  22.80   1483.375194.400.22      80.43   396.03  6.54
        4.82    4.94    1.29,
46.87   9.03    121.17  8.17    102.80  22.63   1522.205277.730.22      84.10   349.30  6.09
        3.29    5.32    1.26,
47.27   10.12   122.30  8.23    109.73  23.00   1552.775311.070.23      84.90   386.03  6.13
        3.55    6.10    1.19
};
run;

%macro jplot(vp);
call svd(u,v,q,&vp);        /* performing singular value decomposition */
*print u v q;
g=u[,1:2];                  /* take first two columns of U which are p1 and p2 as referred in theory */
h = diag(v[1:2,])*q[1:2,];
j = u[,1:2]*diag(v[1:2,]);          /* obtaining J */
jj = j*j`;                          /* obtaining  the values of JJ` */
jjj = diag(sqrt(jj));
mx=max(jjj);
do i= 1 to nrow(jjj);
        if jjj[i,i] = mx
        then best= i;
end;
res = j(1,2,0);
do i = 1 to nrow(jjj);
        res1= jjj[i,i]||i;
        res=res//res1;
end;
res=res[2:nrow(res),];
title ' J - plot ';
print mx best / res;
run;
%mend;

/* invoke the SAS macro with the name of the data matrix (INDAT here) as the input parameter */
%jplot(indat);
```

B) Outliers in Multi-response Experiments

B.1 Introduction

An outlier in a set of data is an observation (or an observation vector) that appears to be inconsistent with the remainder of the observations in that data set. Occurrence of outlier(s) is common in every field in which data collection is involved. In many experimental situations, data on more than one response variable is recorded from the same experimental unit through application of same treatment. Such experiments are known as multi-response experiments. Outlier(s) in multi-response experiments is/ are likely to appear. If an experimental plot is heavily infested with pests, disease and/or weeds then all the responses observed from that plot may be outlier(s). It may also be due to heavy irrigation by mistake on some experimental plot(s) or mistake in recording/ transcription of observations etc. The presence of outlier(s) in the data generated from multi-response experiments may cause departures from the assumptions of parameter estimation. The analysis of data in presence of outlier(s) may give misleading results. Therefore, before analysis of multi-response data, detection of outlier is required. Barrett and Ling (1992) proposed a measure of influence for multivariate regression as an extension of measure given by Cook and Weisberg (1980) for univariate regression. Test statistic, available in literature for detecting outlier(s) in multivariate regression cannot directly be applied to the multi-response experimental settings because

i) design matrix of multi-response experiments is not of full column rank as in multivariate regression
ii) in multi-response experiments, interest is in a sub set of parameters (linear function of treatment effects) rather than whole vector of parameters.

Most of the literature available for detection of outlier(s) in the experimental data and obtaining robust experimental designs in presence of outlier(s) is for single response situations see e.g. Box and Draper (1975), John (1978), Gopalan and Dey (1976), Ghosh (1983, 1989), Singh *et al*. (1987), Ben and Yohai (1992), Bhar (1997), Bhar and Gupta (2001, 2003), Sarker (2002) and Sarker *et al*. (2003, 2005).

John (1978) studied the problems that arise in detecting the presence of outliers in the results from factorial experiments by applying the Q_k-statistic of Gentleman and Wilk (1975). Ben and Yohai (1992) studied the asymptotic theory of M-estimates and their associated test for a one-factor experiment in randomized complete block (RCB) design. Gopalan and Dey (1976) studied the robustness of general block designs in the presence of a single outlier by minimizing the variance of discrepancy or bias in the measurement of error variance (σ^2). Singh *et al*. (1987) showed that the variance balanced row-column designs satisfying the property of adjusted orthogonality are robust against the presence of a single outlier. Bhar (1997) have investigated the problem of outlier(s) in the experimental data for the block designs and modified Cook-statistic, Q_k-statistic and AP- statistic for detection of single outlier in experimental data for both mean shift and variance inflation models. Bhar and Gupta (2001) studied the robustness of block designs by minimizing the value of Cook-statistic. Bhar and Gupta (2003) made a study of outliers under variance-inflation model in experimental designs. Sarker *et al*. (2003) extended these results to the experimental situations where the interest of the experimenter is only in a subset of all possible elementary treatment contrasts (test treatments-control treatment comparisons) rather than the complete set of all the possible elementary contrasts. Sarker *et al.* (2005) formulated a test statistic for detection of a single outlier in block designs for diallel crosses. They also established a correspondence between two existing criteria of robustness *i.e.* minimization of average Cook-statistic and minimization of variance of discrepancy or bias in estimation of error variance. It has been shown that a proper binary balanced block design for diallel crosses is robust against the presence of a single outlier. Block

designs for diallel crosses in which every line appears an equal number of times in each block are also found to be robust against the presence of a single outlier.

In multi-response experiments, for taking the advantage of correlation structure among the response variables, multivariate analysis of variance (MANOVA) of data should be performed for testing the equality of treatment effects,. The inference(s) drawn from MANOVA may be misleading if outlier(s) are present in the data. Very little work seems to have been done on detection of outlier(s) in data from multi-response experiments. Therefore, in the present investigation an attempt has been made to develop a test statistic for detection of an outlier observation from multi-response data generated through block design. The test statistic is given in Section B.3. We begin with some preliminaries in Section B.2.

B.2 Preliminaries

Let there be v treatments laid out in a block design containing b blocks such that j^{th} block contains k_j experimental units; $j = 1,2,\ldots,b$ and treatment i is replicated r_i times, $\sum_{j=1}^{b} k_j = \sum_{i=1}^{v} r_i = n$, the total number of experimental units. From each experimental unit p responses are observed. Let $\mathbf{Y} = [\mathbf{y}_1\ \mathbf{y}_2\ \ldots\ \mathbf{y}_p]$ be $n \times p$ matrix of observations, where $\mathbf{y}_s$ is an $n \times 1$ vector of observations corresponding to the s^{th} response ($s = 1,2, \ldots, p$). For s^{th} response the model is given by

$$\mathbf{y}_s = \mathbf{X}\boldsymbol{\theta}_s + \boldsymbol{\varepsilon}_s \quad s = 1, 2, \ldots, p \tag{B.2.1}$$

where $\mathbf{X} = \lfloor \boldsymbol{\Delta}' \quad \mathbf{1} \quad \mathbf{D}' \rfloor$ is the design matrix for s^{th} response partitioned in conformity with the parameters, $\boldsymbol{\Delta}'$ is $(n \times v)$ design matrix of treatments, $\mathbf{1}$ is the n dimensional column vector of all elements unity and $\mathbf{D}'$ is the design matrix of blocks.

$\boldsymbol{\theta}_s = \left[\boldsymbol{\tau}_s' \quad \mu_s \quad \boldsymbol{\beta}_s'\right]'$ is a $(v + b + 1)$ component vector, $\boldsymbol{\tau}_S$ being v-component vector of treatment effects, μ_S the general mean and $\boldsymbol{\beta}_S$ the b-component vector of block effects for the s^{th} response. $\boldsymbol{\varepsilon}_S$ is the residual vector for s^{th} response variable distributed as N ($\mathbf{0}$, $\sigma_{SS}\mathbf{I}_n$).

So the model for multi-response experiments in block design set up is

$$\mathbf{Y} = \mathbf{Z}\boldsymbol{\theta} + \boldsymbol{\varepsilon} \tag{B.2.2}$$

where $\mathbf{Y} = \left(\mathbf{y}_1' \quad \mathbf{y}_2' \quad \cdots \quad \mathbf{y}_p'\right)'$.

Now we can roll out the matrix into vector form as

$$\mathbf{Z} = \lfloor \mathbf{I}_p \otimes \boldsymbol{\Delta}' \quad \mathbf{I}_p \otimes \mathbf{1} \quad \mathbf{I}_p \otimes \mathbf{D}' \rfloor = \mathbf{I}_p \otimes \mathbf{X} \text{ and } \boldsymbol{\theta} = \begin{bmatrix} \boldsymbol{\tau} \\ \boldsymbol{\mu} \\ \boldsymbol{\beta} \end{bmatrix}, \tag{B.2.3}$$

where treatment effect vectors, general mean and block effect vectors for all the response variables are appended one below the other to obtain a single treatment effect vector $\boldsymbol{\tau}$, general mean vector $\boldsymbol{\mu}$ and block effect vector $\boldsymbol{\beta}$, $\boldsymbol{\varepsilon}$ is p-variate normal with response variables from same observation are correlated but there is no correlation between different observations and $\oplus$ denotes the direct sum of matrices. As a consequence $\boldsymbol{\varepsilon}$ is now $\boldsymbol{\varepsilon} \sim N_p(\mathbf{0}, \boldsymbol{\Omega})$,

where $\boldsymbol{\Omega} = D(\boldsymbol{\varepsilon}) = \begin{bmatrix} \sigma_{11}\mathbf{I}_n & \sigma_{12}\mathbf{I}_n & \cdots & \sigma_{1p}\mathbf{I}_n \\ \sigma_{21}\mathbf{I}_n & \sigma_{22}\mathbf{I}_n & \cdots & \sigma_{2p}\mathbf{I}_n \\ \vdots & \vdots & \ddots & \vdots \\ \sigma_{p1}\mathbf{I}_n & \sigma_{p2}\mathbf{I}_n & \cdots & \sigma_{pp}\mathbf{I}_n \end{bmatrix} = \boldsymbol{\Sigma}_{pp} \otimes \mathbf{I}_n$, (B.2.4)

where $\sigma_{ss'}$ is the variance between s^{th} and s'^{th} response variables when s=s, $s, s' = 1, 2, \ldots, p$; $\otimes$ denotes Kronecker product of matrices and D(.) denotes the dispersion matrices. Using the Generalized Least Square (GLS) estimation procedure, the normal equations are

$$\left(\mathbf{Z}'\boldsymbol{\Omega}^{-1}\mathbf{Z}\right)\boldsymbol{\theta} = \mathbf{Z}'\boldsymbol{\Omega}^{-1}\mathbf{Y} \tag{B.2.5}$$

The reduced normal equations for estimating the linear functions of treatment effects are

$$\mathbf{C}^*\boldsymbol{\tau} = \mathbf{Q}^* \tag{B.2.6}$$

where

$$\mathbf{C}^* = \boldsymbol{\Sigma}^{-1} \otimes \left(\boldsymbol{\Delta}\boldsymbol{\Delta}' - \boldsymbol{\Delta}\mathbf{D}'\left(\mathbf{D}\mathbf{D}'\right)^{-1}\mathbf{D}\boldsymbol{\Delta}'\right) = \boldsymbol{\Sigma}^{-1} \otimes \left(\boldsymbol{\Delta}\mathbf{S}\boldsymbol{\Delta}'\right) = \boldsymbol{\Sigma}^{-1} \otimes \mathbf{C} \tag{B.2.7}$$

$$\mathbf{Q}^* = \left[\boldsymbol{\Sigma}^{-1} \otimes \left(\boldsymbol{\Delta} - \boldsymbol{\Delta}\mathbf{D}'\left(\mathbf{D}\mathbf{D}'\right)^{-1}\mathbf{D}\right)\right]\mathbf{Y} = \boldsymbol{\Sigma}^{-1} \otimes \left(\boldsymbol{\Delta}\mathbf{S}\mathbf{Y}\right) = \boldsymbol{\Sigma}^{-1} \otimes \mathbf{Q} \tag{B.2.8}$$

and $\mathbf{S} = \mathbf{I} - \mathbf{D}'\left(\mathbf{D}\mathbf{D}'\right)^{-1}\mathbf{D}$.

Here **C** is the information matrix and **Q** is the vector of adjusted treatment totals in the usual setup for the univariate case. A solution of the reduced normal equations (B.2.6) is

$$\hat{\boldsymbol{\tau}} = \mathbf{C}^{*-}\mathbf{Q}^* \tag{B.2.9}$$

Following theorem can be given for multi-response experiments:

Theorem 2.1:

(i) $E\left(\mathbf{Q}^*\right) = \mathbf{C}^*\boldsymbol{\tau}$

(ii) $D\left(\mathbf{Q}^*\right) = \boldsymbol{\Sigma}^{-1} \otimes \mathbf{C} = \mathbf{C}^*$ (B.2.10)

(iii) A design for multi-response experiment is connected for parameters $\boldsymbol{\tau}$ iff Rank($\mathbf{C}^*$) = $p(v-1)$. In a connected design all contrasts of $\boldsymbol{\tau}$ are estimable.

Here we assume that the design is connected *i.e.* all $p(v-1)$ orthonormalized treatment contrasts are estimable or equivalently Rank ($\mathbf{C}^*$) = $p(v-1)$. Let the set of all $p(v-1)$ orthonormalized treatment contrasts for the parameters $\boldsymbol{\tau}$ be given by $\mathbf{P}\boldsymbol{\tau}$, where $\mathbf{P} = \mathbf{I}_p \otimes \mathbf{L}$ and **L** is such that $\mathbf{L}\mathbf{L}' = \mathbf{I}_{v-1}$ and $\mathbf{L}'\mathbf{L} = \mathbf{I}_v - \frac{1}{v}\mathbf{1}\mathbf{1}'$, $\mathbf{P}\mathbf{P}' = \mathbf{I} \otimes \mathbf{L}\mathbf{L}' = \mathbf{I}_p \otimes \mathbf{I}_{v-1}$ and $\mathbf{P}'\mathbf{P} = \mathbf{I} \otimes \mathbf{L}'\mathbf{L} = \mathbf{I} \otimes \left(\mathbf{I}_v - \frac{1}{v}\mathbf{1}_v\mathbf{1}_v'\right)$. The best linear unbiased estimator (BLUE) of $\mathbf{P}\boldsymbol{\tau}$ is given by $\mathbf{P}\hat{\boldsymbol{\tau}}$, where $\hat{\boldsymbol{\tau}}$ is any solution of the reduced normal equation in (B.2.6).

We have the following lemma:

Lemma 2.1: For a connected design for multi-response experiments, the dispersion matrix of $\mathbf{P}\hat{\boldsymbol{\tau}}$ can be written as

$$D\left(\mathbf{P}\hat{\boldsymbol{\tau}}\right) = \boldsymbol{\Sigma} \otimes \left(\mathbf{L}\mathbf{C}\mathbf{L}'\right)^{-1} = \left(\mathbf{P}\mathbf{C}^*\mathbf{P}'\right)^{-1}. \tag{B.2.11}$$

Proof: We know that the information matrix for estimation of a linear function of treatment effects for multi-response experiments run in a block design is given by $\mathbf{C}^* = \boldsymbol{\Sigma}^{-1} \otimes \mathbf{C}$. Therefore,

$$\mathbf{P}'\mathbf{P}\mathbf{C}^* = \boldsymbol{\Sigma}^{-1} \otimes \left(\mathbf{I}_v - \frac{1}{v}\mathbf{1}_v\mathbf{1}_v' \right) \mathbf{C} = \boldsymbol{\Sigma}^{-1} \otimes \mathbf{C}.$$

Also $\mathbf{C}^*\mathbf{P}'\mathbf{P} = \boldsymbol{\Sigma}^{-1} \otimes \mathbf{C}$, so we can write $\mathbf{C}^*\mathbf{P}'\mathbf{P} = \mathbf{P}'\mathbf{P}\mathbf{C}^*$.
Premultiplying **P** we get,

$$\mathbf{P}\mathbf{C}^*\mathbf{P}'\mathbf{P} = \mathbf{P}\mathbf{P}'\mathbf{P}\mathbf{C}^* = \mathbf{P}\mathbf{C}^*$$

$$\Rightarrow \mathbf{P} = \left(\mathbf{P}\mathbf{C}^*\mathbf{P}'\right)^{-1}\mathbf{P}\mathbf{C}^*.$$

This follows from the fact that $\mathbf{P}\mathbf{C}^*\mathbf{P}' = \boldsymbol{\Sigma}^{-1} \otimes \mathbf{L}\mathbf{C}\mathbf{L}'$ and $\mathbf{L}\mathbf{C}\mathbf{L}'$ is positive definite using Lemma 2.1 of Bhar and Gupta (2001). Therefore, $\mathbf{P}\mathbf{C}^*\mathbf{P}'$ is positive definite.

Post multiplying $\hat{\boldsymbol{\tau}}$ we get,

$$\mathbf{P}\hat{\boldsymbol{\tau}} = \left(\mathbf{P}\mathbf{C}^*\mathbf{P}'\right)^{-1}\mathbf{P}\mathbf{C}^*\hat{\boldsymbol{\tau}}$$

$$= \left(\mathbf{P}\mathbf{C}^*\mathbf{P}'\right)^{-1}\mathbf{P}\mathbf{C}^*\left(\mathbf{C}^{*^-}\mathbf{Q}^*\right)$$

The dispersion matrix of $\mathbf{P}\hat{\boldsymbol{\tau}}$ is given by

$$D\left(\mathbf{P}\hat{\boldsymbol{\tau}}\right) = \left(\mathbf{P}\mathbf{C}^*\mathbf{P}'\right)^{-1}\mathbf{P}\mathbf{C}^*\mathbf{C}^{*^-}\mathbf{C}^*\mathbf{C}^{*^-}\mathbf{C}^*\mathbf{P}'\left(\mathbf{P}\mathbf{C}^*\mathbf{P}'\right)^{-1}$$

$$= \left[\mathbf{P}\mathbf{C}^*\mathbf{P}'\right]^{-1}. \qquad \text{(B.2.12)}$$

B.3 Detection of Outlier in Multi-Response Experiments

Let us assume that a single observation vector is suspected to be an outlier in the sense that its expected value is shifted from the expected value of other observations. We consider the *mean-shift* model of the form,

$$\mathbf{Y} = \mathbf{Z}\boldsymbol{\theta} + \mathbf{U}\boldsymbol{\gamma} + \boldsymbol{\varepsilon} \qquad \text{(B.3.1)}$$

where $\mathbf{U} = \left(\mathbf{I}_p \otimes \mathbf{u}\right)$, $\mathbf{u} = \left(0 \quad \cdots \quad 0 \quad 1\left(t^{\text{th}}\right) \quad 0 \quad \cdots \quad 0\right)'$, if t^{th} observation vector is suspected as an outlier and **Y** and **Z** are as given in (B.2.2).The dispersion matrix of $\boldsymbol{\varepsilon}$ from (B.2.4) is $\boldsymbol{\Omega}^* = D\left(\boldsymbol{\varepsilon}\right) = \boldsymbol{\Sigma} \otimes \mathbf{I}$.

Now making use of **Z** as given in (B.2.2) reduced normal equations for estimating the linear function of treatment effects under model (B.3.1) are obtained as

$$\mathbf{C}^*_{(t)}\,\boldsymbol{\tau}_{(t)} = \mathbf{Q}^*_{(t)} \qquad \text{(B.3.2)}$$

where $\mathbf{C}^*_{(t)} = \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\mathbf{S}\left[\mathbf{I} - \mathbf{u}\left(\mathbf{u}'\mathbf{S}\mathbf{u}\right)^{-1}\mathbf{u}'\right]\mathbf{S}\boldsymbol{\Delta}'$,

$$= \boldsymbol{\Sigma}^{-1} \otimes \left[\mathbf{C} - \mathbf{f}\mathbf{f}'\right]. \qquad \text{(B.3.3)}$$

$$\mathbf{Q}^*_{(t)} = \boldsymbol{\Sigma}^{-1} \otimes \boldsymbol{\Delta}\mathbf{S}\left[\mathbf{I} - \mathbf{u}\left(\mathbf{u}'\mathbf{S}\mathbf{u}\right)^{-1}\mathbf{u}'\right]\mathbf{S}\,\mathbf{Y}$$

$$= \boldsymbol{\Sigma}^{-1} \otimes \left[\mathbf{Q} - w^{1/2}\mathbf{f}\mathbf{u}'\mathbf{S}\,\mathbf{Y}\right] \qquad \text{(B.3.4)}$$

where $w = (\mathbf{u}'\mathbf{S}\mathbf{u})^{-1}$ and $\mathbf{f} = w^{1/2}\boldsymbol{\Delta}\mathbf{S}\mathbf{u}$.

Following the definition of Cook-statistic for univariate case (Bhar 1997) we give the Cook-statistic for the set of contrasts $\mathbf{P}\boldsymbol{\tau}$ of $\boldsymbol{\tau}$ in multi-response experiment as:

$$(\mathbf{CD})_t = \frac{\left[\mathbf{P}\left(\hat{\boldsymbol{\tau}} - \hat{\boldsymbol{\tau}}_{(t)}\right)\right]\left[\mathbf{D}\left(\mathbf{P}\hat{\boldsymbol{\tau}}\right)\right]^{-1}\left[\mathbf{P}\left(\hat{\boldsymbol{\tau}} - \hat{\boldsymbol{\tau}}_{(t)}\right)\right]}{\text{Rank}\left(\mathbf{D}\left(\mathbf{P}\hat{\boldsymbol{\tau}}\right)\right)} \qquad \text{for } t = 1, 2, \ldots, n. \tag{B.3.5}$$

Lemma B.3.2: The difference between the estimators of the contrasts of $\boldsymbol{\tau}$ under the model (B.2.2) and (B.3.1) can be expressed as

$$\mathbf{P}\left(\hat{\boldsymbol{\tau}} - \hat{\boldsymbol{\tau}}_{(t)}\right) = \left(\mathbf{I} \otimes \mathbf{L}\mathbf{C}^{-}\mathbf{M}\right)\mathbf{Y}, \tag{B.3.6}$$

where $\mathbf{M} = \mathbf{E}\mathbf{C}^{-}\mathbf{F} + \mathbf{F} - \mathbf{E}\mathbf{C}^{-}\boldsymbol{\Delta}\mathbf{S}$, $\mathbf{E} = \dfrac{\mathbf{f}\mathbf{f}'}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}$, $\mathbf{F} = w^{1/2}\mathbf{f}\mathbf{u}'\mathbf{S}$.

Proof: From (B.3.3) we have

$$\mathbf{C}^{*}_{(t)} = \boldsymbol{\Sigma}^{-1} \otimes \left[\mathbf{C} - \mathbf{f}\mathbf{f}'\right]$$

And a g-inverse of $\mathbf{C}^{*}_{(t)}$ is obtained as [Pringle and Rayner (1971, p.32) and Dey (1993, Theorem 2)]

$$\mathbf{C}^{*-}_{(t)} = \boldsymbol{\Sigma} \otimes \left[\mathbf{C}^{-} + \frac{\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\right].$$

Thus

$$\mathbf{C}^{*-}_{(t)}\mathbf{Q}^{*}_{(t)} =$$

$$(\boldsymbol{\Sigma} \otimes \mathbf{C}^{-}).(\boldsymbol{\Sigma}^{-1} \otimes \mathbf{Q}) - (\boldsymbol{\Sigma} \otimes \mathbf{C}^{-}).(\boldsymbol{\Sigma}^{-1} \otimes w^{1/2}\mathbf{f}\mathbf{u}'\mathbf{S}\mathbf{Y})$$
$$+ \left(\boldsymbol{\Sigma} \otimes \frac{\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\right).(\boldsymbol{\Sigma}^{-1} \otimes \mathbf{Q}) - \left(\boldsymbol{\Sigma} \otimes \frac{\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\right).(\boldsymbol{\Sigma}^{-1} \otimes w^{1/2}\mathbf{f}\mathbf{u}'\mathbf{S}\mathbf{Y})$$

Then

$$\mathbf{C}^{*-}\mathbf{Q}^{*} - \mathbf{C}^{*-}_{(t)}\mathbf{Q}^{*}_{(t)} = \mathbf{I}_p \otimes w^{1/2}\mathbf{C}^{-}\mathbf{f}\mathbf{u}'\mathbf{S}\mathbf{Y} - \mathbf{I}_p \otimes \frac{\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\mathbf{Q} + \mathbf{I}_p \otimes w^{1/2}\frac{\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\mathbf{f}\mathbf{u}'\mathbf{S}\mathbf{Y}$$

Then it follows

$$\mathbf{P}\left(\hat{\boldsymbol{\tau}} - \hat{\boldsymbol{\tau}}_{(t)}\right) = \left(\mathbf{I}_p \otimes \mathbf{L}\right)\left(\mathbf{I}_p \otimes w^{1/2}\mathbf{C}^{-}\mathbf{f}\mathbf{u}'\mathbf{S}\mathbf{Y} - \mathbf{I}_p \otimes \frac{\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\mathbf{Q} + \mathbf{I}_p \otimes w^{1/2}\frac{\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\mathbf{f}\mathbf{u}'\mathbf{S}\mathbf{Y}\right)$$

$$= \mathbf{I}_p \otimes w^{1/2}\mathbf{L}\mathbf{C}^{-}\mathbf{f}\mathbf{u}'\mathbf{S}\mathbf{Y} - \mathbf{I}_p \otimes \frac{\mathbf{L}\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\mathbf{Q} + \mathbf{I}_p \otimes w^{1/2}\frac{\mathbf{L}\mathbf{C}^{-}\mathbf{f}\mathbf{f}'\mathbf{C}^{-}}{1 - \mathbf{f}'\mathbf{C}^{-}\mathbf{f}}\mathbf{f}\mathbf{u}'\mathbf{S}\mathbf{Y}$$

$$= \mathbf{I}_p \otimes \mathbf{L}\mathbf{C}^{-}\mathbf{F}\mathbf{Y} - \mathbf{I}_p \otimes \mathbf{L}\mathbf{C}^{-}\mathbf{E}\mathbf{C}^{-}\mathbf{Q} + \mathbf{I}_p \otimes \mathbf{L}\mathbf{C}^{-}\mathbf{E}\mathbf{C}^{-}\mathbf{F}\mathbf{Y}$$

$$= (\mathbf{I}_p \otimes \mathbf{L}\mathbf{C}^{-}\mathbf{M})\mathbf{Y}$$

Now from (B.3.5) and (B.3.6) Cook-statistic for multi-response experiments can be written as

$$(\mathbf{CD})_t = \frac{1}{p(v-1)}\mathbf{Y}'\left(\mathbf{I}\otimes\mathbf{M}'\mathbf{C}^{-}\mathbf{L}'\right)\left[\mathbf{P}\left(\boldsymbol{\Sigma}^{-1}\otimes\mathbf{C}\right)\mathbf{P}'\right]\left(\mathbf{I}\otimes\mathbf{L}\mathbf{C}^{-}\mathbf{M}\right)\mathbf{Y}$$
$$= \frac{1}{p(v-1)}\left[\mathbf{Y}'\left(\boldsymbol{\Sigma}^{-1}\otimes\mathbf{M}'\mathbf{C}^{-}\mathbf{M}\right)\mathbf{Y}\right]. \qquad \text{(B.3.7)}$$

Remark: For a Randomized Complete Block (RCB) design the matrix **S** can be written as $\mathbf{S} = \text{diag}\left[(\mathbf{I}_v - \frac{1}{v}\mathbf{1}_v\mathbf{1}_v'), (\mathbf{I}_v - \frac{1}{v}\mathbf{1}_v\mathbf{1}_v'), ..., (\mathbf{I}_v - \frac{1}{v}\mathbf{1}_v\mathbf{1}_v')\right]$. Thus the matrices **E** and **F** simplified as

$\mathbf{E} = \frac{r}{r-1}\mathbf{f}\mathbf{f}'$ and $\mathbf{F} = \frac{v-1}{v}\mathbf{f}\,\mathbf{u}'\mathbf{S}$, where $\mathbf{f} = \left(1 - \frac{1}{v} \quad -\frac{1}{v} \quad \ldots \quad -\frac{1}{v}\right)'$. Using these simplifications, one can obtain a $(CD)_t$ for t^{th} observation in a RCB design.

Belsely et al. (2004) have given a cut off point for $(CD)_t$ in case of a multiple linear regression as $4/n$. For any observation vector if calculated value of $(\mathbf{CD})_t$ (t = 1, 2, …, n) is more than $4/n$, then we may conclude that the observation vector from the t^{th} experimental unit is an outlier. Approximate distribution of $(\mathbf{CD})_t$ (t = 1, 2, …, n) is unknown and is an open problem. A SAS code has been written for obtaining the test statistic for detection of outlier observation vector and is given in the Appendix B.1.

The above test statistic helps in detection of a single outlier vector. Once the outlier vector is detected, the next question arises as to what to do with this observation vector? First and foremost step we have to do is whether there are any recording or tabulation errors? If there are recording or tabulation errors, correct them and perform the analysis. If one finds that outlying observation is not due to recording or tabulation errors, then one simple way is delete the observation vector that is identified as an outlier or perform multivariate analysis of covariance by defining a covariate for each outlier. The above procedure is illustrated with the help of an example in Section B.4.

B.4 Illustration

Example B.4.1: Consider an experiment conducted during winter season of 2003-04 in Terai region of West Bengal to study the effect of integrated nutrient management on growth and yield of late-sown wheat. The experiment was laid out in RCB design with 14 treatments in 3 replications. The data on following 9 characters were observed: plant height at harvest (cm), dry matter (DM) accumulation at 90 days after sowing (DAS), leaf area index (LAI) at 75 DAS, number of spikes/ sq cm, number of grains per spike, test weight (g), grain yield (q/ha), straw yield (q/ha) and harvest index (%).

The data were analyzed for detection of single outlier vector using the test statistic developed in Section B.3. The results obtained are given in Table B.4.1 (Appendix B.1). From Table B.4.1, it can be observed that the observation corresponding to treatment number 1 and replication 3 has value of $(CD)_t$-statistic (0.1043) which is more than the cut off value of ($4/n$ =0.09524). Therefore, we can say that the observation vector pertaining to treatment number 1 in replication 3 is an outlier.

Multivariate analysis of variance for testing the equality of treatment effect vectors was performed on original data and after deleting the observation outlier vector. The significance of treatment and replication effects were tested using Wilk's Lamda criterion. Multivariate analysis of covariance was also performed by defining a covariate for the outlier observation vector as defined in (B.3.3). The results obtained are given in Table B.4.2 (Appendix B.1). From the analysis of original data given in Table B.4.2, we can see that replication effects are not significantly different at 5% level of significance whereas from the analysis after deleting the outlying observation (observation number 3) showed that replication effects are significantly different at 5% level of significance. Though there is no change in the results pertaining to treatment effects. It has been observed that deleting any other observation does not change the result of original data.

One can also observe that the results with analysis of covariance and by deleting the outlying observation are same. Therefore, these approaches may be able to take care of presence of outlier(s) in the experimental data. However, it is necessary that the outlier(s) is (are) detected at the first instance. The statistic developed for the detection of outlier(s) in the experimental data may be very helpful

B.5 Discussion

In the present investigation, a test statistic has been developed for detection of a single outlying observation vector in multi-response experiments conducted in block designs. It may happen that all the components of the observation vector obtained from an experimental unit may not be outlier. Therefore, further efforts need to be made for developing a test statistic for detection of a p_1-component sub-vector of a p-component observation vector as outlier. Further, outlier(s) may exist in more than one observation vector. Therefore, a test statistic for detection of outlier(s) in more than one observation vector needs to be developed. Once an outlier is detected, one may think of either deleting the observation(s) identified as outlier(s) or carrying out the analysis of covariance. This procedure may be subjected to criticism. Therefore, one way to deal with such a situation is to develop robust procedure of estimation of treatment contrasts. Therefore, research efforts need to be made for developing a procedure of robust estimation in presence of outlier(s) in multi-response experiments.

A lot of literature is available on designs that are robust in presence of a single outlier in single response situations {see *e.g.* Gopalan and Dey (1976), Singh *et al*. (1987), Ben and Yohai (1992), Bhar (1997), Bhar and Gupta (2001, 2003), Sarker (2002) and Sarker *et al.* (2003, 2005)}. A criteria of robustness of multi-response designs in presence of a single outlying observation vector needs to be developed.

References

Barrett, B. E. and Ling, R. F. (1992) General classes of influence measure for multivariate regression, *Journal of American Statistical Association*, 87(417), 184-191.

Belsley, D.A., Kuh, E. and Welsch, R.E. (2004). *Regression Diagnostics-Identifying Influential Data and Sources of Collinearity*. John Wiley and Sons, New York.

Ben, M.G. and Yohai, V.J. (1992) Robust analysis of variance for a randomized block design, *Commun. Statist.-Theory & Meth.*, 21 (7), 1779-1798.

Bhar, L. (1997) *Outliers in experimental designs*, Unpublished Ph.D. Thesis. I.A.R.I. New delhi.

Bhar, L. and Gupta, V. K. (2001) A useful statistic for studying outliers in experimental designs, *Sankhya*, B63 (4), 338-350.

Bhar, L. and Gupta, V. K. (2003) Study of outliers under variance-inflation model in experimental designs. *J. Indian. Soc. Agril. Statist*. 56(2), 142-154.

Box, G.E.P. and Draper, N.R. (1975). Robust designs. *Biometrika*, 62(2), 347-352.

Cook, R. D. (1977) Detection of influential observations in linear regression, *Technometrics*, 19, 15-18.

Cook, R. D. and Weisberg, S. (1980) Characterizations of an empirical influence function for detecting influential cases in regression, *Technometrics*, 22, 495-508.

Dey, A. (1993). Robustness of block designs against missing data. *Statistica Sinica,* 3, 219-231.

Gnanadesikan, R. and Kettenting, J.R. (1972). Robust estimates, residuals, and outlier detection with multiresponse data. *Biometrics*, **28**, 81-124.

Gnanadesikan, R. and Lee, E.T. (1970). Graphical techniques for internal comparisons amongst equal degree of freedom groupings in multiresponse experiments. *Biometrika*, **57**, 229-237.

Gentleman, J.E. and Wilk, M.B. (1975). Detecting outliers in two-way table: 1. Statistical behavior of residuals. *Technometrics* 17, 1-14.

Ghosh, S. (1983). Influential observations in view of design and inference. *Commu. Stat.-Theory and Methods*, **12**(**14**), 1675-1683.

Ghosh, S. (1989). On two methods of identifying influential sets of observations. *Statist. Prob. Letters*, **7**, 241-245.

Gopalan, R. and Dey, A. (1976) On robust experimental designs, *Sankhya*, B38, 297-299.

John, J.A. (1978). Outliers in factorial experiments. *Appl. Statist.*, 27, 111-119.

Kang, G. and Bates, D.M. (1990). Approximate inferences in multiresponse regression analysis. *Biometrika,* **77**, 321-332.

Pringle, R.M. and Rayner, A.A. (1971). *Generalized Inverse Matrices with Applications in Statistics.* Griffin's Statistical Monographs and Courses, No. 28. *Hafner Publishing Co., New York.*

Singh, G., Gupta, S. and Singh, M. (1987) Robustness of row column designs, *Statistics and probability letters*, 5, 421-424

Sarker, S. (2002) *Studies on outlier(s) in designed experiments*. Unpublished Ph. D. Thesis, I.A.R.I.

Sarker, S., Gupta, V. K. and Parsad, R. (2003) Robust block designs for making test treatment-control treatment comparisons against the presence of an outlier. *J. Indian. Soc. Agril. Statist.* 56(1), 7-18.

Sarker, S., Parsad, R. and Gupta, V.K. (2005) Outliers in block designs for diallel crosses. *Metron-International Journal of Statistics*, 63(2), 177-191.

Appendix B.1

Table B.4.1: Detection of Outlier Using the Test-statistic Developed on the Line of Cook Statistic

Treat	Rep	Plant Height at harvest(cm)	DM accumulation at 90 DAS	LAI at 75 DAS	No. of spikes/ sq m	No. of grains/ spike	Test weight(g)	Grain yield (q/ha)	Straw yield (q/ha)	Harvest index (%)	$(CD)_t$
1	1	112.0	723.1	3.3	343.2	34.1	40.7	27.3	44.3	38.1	0.076812
1	2	133.0	729.0	4.2	325.0	37.0	49.0	32.0	36.0	37.0	0.078462
1	3	124.0	745.0	3.2	356.0	36.0	78.0	25.0	37.0	26.0	**0.104318**
2	1	111.1	784.6	3.7	372.2	38.2	41.4	29.0	47.0	40.3	0.040911
2	2	123.0	765.0	3.8	354.0	35.0	47.0	27.0	45.0	41.0	0.034252
2	3	112.0	734.0	3.2	345.0	32.0	43.0	29.0	48.0	43.0	0.063704
3	1	105.1	722.5	3.1	330.3	33.0	40.4	26.3	43.2	37.9	0.015557
3	2	110.0	734.0	3.4	323.0	32.0	46.0	27.0	46.0	38.0	0.0346
3	3	109.0	720.0	3.2	354.0	36.0	42.0	26.0	43.0	39.0	0.049034
4	1	104.4	715.3	3.1	325.3	33.2	40.4	25.9	54.0	37.8	0.014674
4	2	109.0	726.0	3.5	342.0	34.0	46.0	25.0	52.0	36.0	0.026203
4	3	107.0	745.0	3.4	325.0	37.0	43.0	26.0	51.0	39.0	0.032702
5	1	106.8	729.2	3.2	337.2	45.0	40.5	26.9	43.9	38.0	0.014317
5	2	110.0	765.0	3.5	335.0	46.0	39.0	27.0	41.0	36.0	0.028023
5	3	107.0	754.0	3.2	342.0	41.0	42.0	25.0	42.0	41.0	0.035353
6	1	103.1	704.2	3.0	319.8	32.0	40.0	25.5	42.4	37.5	0.016434
6	2	109.0	765.0	3.1	323.0	29.0	43.0	25.0	43.0	38.0	0.060864
6	3	111.0	702.0	3.4	312.0	32.0	47.0	26.0	41.0	36.0	0.04558
7	1	102.6	696.9	2.9	315.3	32.1	40.0	34.0	41.8	37.4	0.03537
7	2	103.0	692.0	3.2	312.0	33.0	46.0	32.0	45.0	35.0	0.032348
7	3	109.0	723.0	3.0	321.0	35.0	42.0	29.0	43.0	36.0	0.046583

…

8	1	105.8	718.8	3.1	331.2	33.1	40.4	26.0	43.1	37.6	0.037268
8	2	105.0	726.0	3.2	335.0	31.0	46.0	27.0	42.0	39.0	0.021785
8	3	106.0	765.0	3.1	345.0	36.0	48.0	26.0	45.0	41.0	0.042323
9	1	109.0	761.9	3.5	362.5	37.0	41.0	28.7	46.4	38.2	0.030287
9	2	101.0	765.0	3.6	365.0	36.0	41.0	28.0	43.0	37.0	0.032326
9	3	109.0	786.0	3.4	356.0	38.0	46.0	29.0	42.0	38.0	0.018721
10	1	107.2	757.0	3.4	357.8	36.0	40.9	27.2	45.7	38.2	0.019468
10	2	110.0	725.0	3.5	357.0	40.0	42.0	25.0	48.0	39.0	0.062378
10	3	105.0	754.0	3.4	376.0	35.0	41.0	25.0	45.0	34.0	0.057845
11	1	110.7	769.5	3.6	363.0	37.5	41.2	29.6	46.9	38.7	0.049584
11	2	105.0	754.0	3.4	387.0	38.0	43.0	25.0	43.0	36.0	0.040707
11	3	113.0	767.0	3.4	367.0	36.0	41.0	28.0	39.0	37.0	0.029235
12	1	106.0	744.3	3.4	353.8	36.0	40.6	28.0	45.3	38.2	0.007566
12	2	106.0	765.0	3.3	356.0	35.0	42.0	29.0	45.0	35.0	0.036392
12	3	109.0	723.0	3.2	354.0	32.0	43.0	24.0	47.0	41.0	0.040477
13	1	105.0	738.9	3.3	350.5	34.9	40.6	27.7	44.9	38.2	0.047424
13	2	109.0	734.0	3.2	356.0	33.0	43.0	26.0	51.0	34.0	0.028278
13	3	110.0	743.0	3.2	354.0	35.0	40.0	28.0	48.0	37.0	0.012904
14	1	107.8	755.2	3.5	358.2	36.9	41.0	29.0	46.0	38.7	0.033924
14	2	112.0	765.0	3.4	343.0	36.0	40.0	28.0	46.0	39.0	0.024054
14	3	113.0	734.0	3.5	323.0	31.0	41.0	25.0	42.0	41.0	0.056339

***4**/*n*=0.095238

Table B.4.2: **Multivariate Analysis of Variance/ Covariance for Simultaneous Comparison of Treatment Effects from Original Data, after Removing Outlier Observation Vector and by Defining a Covariate Corresponding to Outlier Observation Vector**

Source	Original Data		After removing the outlying observation vector		Defining a covariate corresponding to Outlying observation vector	
	Wilk's Lambda	**Prob > F**	**Wilk's Lambda**	**Prob > F**	**Wilk's Lambda**	**Prob > F**
Treatment	0.0001	< 0.0001	0.0001	< 0.0001	0.0001	< 0.0001
Replication	0.2684	0.0556	0.2406	0.0443	0.2406	0.0443
Covariate	-	-	-	-	0.2058	0.0002

SAS code for Detecting Outlier Observation Vector from Multi-response Experiments:

```
options ps=2000 ls=100;
data outlier;
input trt blk y1-y9;
cards;
1   1   112.0  723.1  3.3  343.2  34.1  40.7  27.3  44.3  38.1
1   2   133.0  729.0  4.2  325.0  37.0  49.0  32.0  36.0  37.0
1   3   124.0  745.0  3.2  356.0  36.0  78.0  25.0  37.0  26.0
⋮   ⋮   ⋮      ⋮      ⋮    ⋮      ⋮     ⋮     ⋮     ⋮     ⋮
14  1   107.8  755.2  3.5  358.2  36.9  41.0  29.0  46.0  38.7
14  2   112.0  765.0  3.4  343.0  36.0  40.0  28.0  46.0  39.0
14  3   113.0  734.0  3.5  323.0  31.0  41.0  25.0  42.0  41.0
;
run;

proc iml;
use outlier;
read all into d;
run;
n = nrow(d); *number of observations;
v = max(d[,1]); *number of treatments;
b = max(d[,2]); *number of blocks;
x1 = J(n,v,0); *x1 is del prime;
x2 = j(n,b,0); *x2 is d prime;
y = d[,3:ncol(d)];
p = ncol(y); *p is number of response variables;

do i = 1 to n;
        do j = 1 to v;
                if d[i,1] = j then x1[i,j] = 1;
        end;
end;
do i = 1 to n;
        do j = 1 to b;
                if d[i,2] = j then x2[i,j] = 1;
        end;
end;
x21 = j(nrow(y),1,1);
```

```
x = x1||x2||x21;
beta = ginv(x`*x)*x`*y;
yv0 = j(1,1,0);
do i = 1 to ncol(y);
        yv0 = yv0//y[,i];
end;
print yv0;
yv = yv0[2:nrow(yv0),];
c0 = x1`*x1-x1`*x2*ginv(x2`*x2)*x2`*x1;
print c0;
q0 = (x1`-x1`*x2*ginv(x2`*x2)*x2`)*y;
print q0;
run;

b0 = x2`*y;
b01 = b0[,1];
b02 = b0[,2];

tau0 = ginv(c0)*q0;

c01 = ginv(c0);

trssp = q0`*c01*q0;

tssp = j(ncol(y),ncol(y),0);

do i = 1 to ncol(y);
        do j = 1 to ncol(y);
        tssp[i,j] = y[,i]`*y[,j]-(y[+,i]*y[+,j])/(nrow(y));
        end;
end;

Repssp=j(ncol(y),ncol(y),0);
do i=1 to ncol(y);
        do j=1 to ncol(y);
                Repssp[i,j]=b0[,i]`*inv(x2`*x2)*b0[,j]-(y[+,i]*y[+,j])/(nrow(y));
        end;
end;

ressp = tssp - repssp - trssp;
wl_trt = det(ressp)/det(trssp + ressp);
wl_blk = det(ressp)/det(repssp + ressp);

print trssp;
print repssp;
print ressp;
sig_est = ressp/(nrow(y) - v - b + 1);
print sig_est;
c =  inv(sig_est) @ c0;
q =  (inv(sig_est) @ (x1`-x1`*x2*ginv(x2`*x2)*x2`))*yv;
tau = ginv(c)*q;

/*Finding out Cook's Distance for outlier detection */

S = i(nrow(y))-x2*inv(x2`*x2)*x2`;
u = i(nrow(y));
```

```
c_d = j(1,1,0);

dd = j(1,2,0);
d = j(1,1,0);


do i = 1 to nrow(y);
w=inv(u[,i]`*S*u[,i]);
f1=sqrt(w)*x1`*S*u[,i];
F=sqrt(w)*f1*u[,i]`*S;
E=f1*f1`*inv(1-f1`*ginv(c0)*f1);
M=E*ginv(c0)*F+F-E*ginv(c0)*x1`*S;

C_Dt=(yv`*(inv(sig_est)@(M`*ginv(c0)*M))*yv)/(p*(v-1));
            c_d=c_d//c_d1;
            dd=dd//(i||c_d1);

end;
dd1= dd[2:nrow(dd),];
print dd1;
cut = 4/n;
print the cut off point is=' cut;
run;
```

C) Minimally Connected Designs with Extra Observations

In NARS some experiments are conducted to study the effect of soil erosion on crop yield. In such experiments, the soil erosion is done artificially at different levels in different experimental plots and their effect is seen on the yield. Artificial creation of soil erosion is quite difficult to be made. Moreover, this also amounts to destroying some of the upper layers of the soil from a part of the land. Therefore, it is always better to plan such experiments in the minimum possible number of experimental units. To ensure that all pairwise treatment comparisons are possible in a block design, the minimum number of experimental units required is equal to one less than the sum of the number of blocks and treatments. A design in minimal number of experimental units that provides all possible pairwise treatment comparisons is called a minimally connected design. For such experimental situations, the minimally connected designs, minimally connected designs with some extra observations may be useful. The basic objection to this kind of designs with minimum number of observations in agricultural experimentation is that they do not provide an estimate of error. Therefore, to get an estimate of error, some modifications in these designs are required to be made, possibly by adding some more experimental units.

Keeping these problems in mind, last year we had prepared a catalogue of block designs with $n = v+b-1+i$, $i=1, 2, 3$ observations, where v is the number of treatments; b the block size; k is the block size and n is the total number of experimental units. Block contents along with lower bounds to A- and D-efficiencies were also given. This year we have prepared catalogues of block designs with $n = v+b-1+i$, $i=4, 5, 6, 7$ and 8 observations. Block contents along with lower bounds to A- and D-efficiencies are also given. These catalogues alongwith block contents and lower bounds to A- and D-efficiencies are available with the author and can be obtained by sending an E-mail to rajender@iasri.res.in.

D) Designs for Crop Sequence Experiments

In crop sequence experiments, instead of a mono crop, crop sequences comprising of two or more crops are grown in the respective cropping seasons. The two cropping seasons considered here are Kharif followed by Rabi. Generally there are two major crops grown, one in each of the Kharif and Rabi seasons. Two different sets of treatments are applied; the treatments belonging to one set are applied to the Kharif crop and the other set of treatments are applied to the Rabi crop. In these experiments, the interest of the experimenter is in direct effects of treatments applied in Kharif and Rabi season, residual effects of Kharif treatments and the interaction between the residual effects of Kharif treatments and direct effects of Rabi treatments. The nature of the experiment and the questions to be answered from the experiment suggests that block designs with factorial structure of treatments may be an appropriate alternative for such experiments. In the class of block designs with factorial structure, extended group divisible (EGD) designs are very important because these designs have orthogonal factorial structure. In this design the experimenter can complete the randomization for both the seasons in the beginning because the treatments on every experimental unit would be the treatment combinations pertaining to both the seasons. This equivalence between EGD designs and designs for crop sequence experiments has encouraged the experimenters to conduct their experiments using EGD designs. EGD designs are obtained as the Kronecker Product of incidence matrices of two or more block designs with specified parameters. It is also seen that there is a loss of information on the main effects, the direct effects of Kharif and Rabi treatments and the residual effects of Kharif treatments, as well as the interaction of the residual effects of Kharif treatments and the direct effects of Rabi treatments. Indeed it may be possible to obtain designs with desired efficiency of the main effects and interactions, but it is not always possible to obtain designs with no loss of information on all the main effects. From experimenters' interest, it is desirable to generate designs that permit estimation of the main effects with full efficiency. In view the above, EGD designs for three factors that permit the estimation of all main effects with no loss of information have been obtained using self-complementary GD designs with $r, k \leq 10$ and a catalogue of such designs along with efficiencies for main effects and interactions have been prepared. In all these designs, first factor is at 2 levels. The designs obtained are given in Table D.1.

Table D.1: EGD designs with r ≤ 5 and k ≤ 10 Obtained through Self Complementary GD Designs

m_1	m_2	m_3	b	r	k	λ_{001}	λ_{010}	λ_{011}	λ_{100}	λ_{101}	λ_{110}	λ_{111}	E(100)	E(010)	E(001)	E(110)	E(101)	E(011)	E(111)
4	2	2	6	3	8	0	0	3	1	2	2	1	1.000	1.000	1.000	1.000	1.000	1.000	0.667
2	4	3	9	3	8	0	1	1	3	0	1	1	1.000	1.000	0.750	1.000	1.000	0.750	1.000
2	4	3	6	3	6	3	1	1	3	3	1	1	1.000	0.333	1.000	1.000	1.000	1.000	1.000
2	2	2	4	2	4	0	1	1	0	2	1	1	1.000	1.000	1.000	1.000	0.500	1.000	0.500
2	2	2	8	4	4	0	2	2	0	4	2	2	1.000	1.000	1.000	1.000	0.500	1.000	0.500
2	2	2	8	4	4	2	1	1	0	2	3	3	1.000	1.000	1.000	0.500	0.750	1.000	0.750
2	2	2	10	5	4	3	1	1	0	2	4	4	1.000	1.000	1.000	0.400	0.800	1.000	0.800
2	2	2	10	5	4	1	2	2	0	4	3	3	1.000	1.000	1.000	0.800	0.600	1.000	0.600
2	3	2	4	2	6	0	1	1	0	2	1	1	1.000	1.000	1.000	1.000	0.667	1.000	0.667
2	3	2	6	3	6	2	1	1	0	1	2	2	1.000	1.000	1.000	0.667	0.889	1.000	0.889
2	3	2	8	4	6	0	2	2	0	4	2	2	1.000	1.000	1.000	1.000	0.667	1.000	0.667
2	4	2	6	3	8	3	1	1	0	0	2	2	1.000	1.000	1.000	0.667	1.000	1.000	1.000
2	2	4	6	3	8	1	0	2	0	2	3	1	1.000	1.000	1.000	1.000	1.000	1.000	0.667
2	4	2	8	4	8	0	2	2	0	4	2	2	1.000	1.000	1.000	1.000	0.750	1.000	0.750
2	4	2	10	5	8	3	2	2	0	2	3	3	1.000	1.000	1.000	0.800	0.900	1.000	0.900
2	5	2	8	4	10	0	2	2	0	4	2	2	1.000	1.000	1.000	1.000	0.800	1.000	0.800
2	5	2	10	5	10	4	2	2	0	1	3	3	1.000	1.000	1.000	0.800	0.960	1.000	0.960

Here m_1, m_2, m_3 are the levels of the three factors, b is the number of blocks, r is the number of replications, k is the block size, λ_{stu} denotes the concurrences of stuth associates and E(stu) denotes the efficiency of the factorial effect, for eg. If s = 1, t = 0 and u = 1 then it denotes the efficiency of two factor interaction between first and third factor.

E) Nested Partially Balanced Incomplete Block Designs

E.1 Introduction

Nested block designs are the designs in which one system of blocks is nested within another system of blocks. Here the blocks with larger size are called bigger blocks and sub-blocks are nested within these bigger blocks. Nested block designs are useful in many situations. For example, consider a field experiment conducted using a block design where harvesting is done block-wise. The harvested samples are to be analyzed for their contents (quality indicators viz. protein content, etc.) in the laboratory by different technicians at same time or by a technician over different periods of time. The variation due to technicians or time periods may be controlled by another blocking system. Technicians or time periods form a system of blocks called sub-blocks that are nested within blocks. Preece (1967) introduced nested balanced incomplete block (NBIB) designs and gave methods of construction of NBIB designs. Jimbo and Kuriki (1983), Dey *et al.* (1986), Saha *et al.* (1998) and Morgan *et al.* (2001) gave some systematic methods of construction of NBIB designs. All NBIB designs for v (number of treatments) ≤ 16, r (replication number) ≤ 30 are catalogued by Morgan *et al.* (2001). An NBIB design may not always exist or even if it exists may require a large number of replications, which the experimenter may not be able to afford. To deal with such situations, Homel and Robinson (1975) defined nested partially balanced incomplete block (NPBIB) designs. Banerjee and Kageyama (1993), Kageyama *et al.* (1995) and Satpati and Parsad (2004) obtained some methods of construction of NPBIB designs. Satpati and Parsad (2004) presented a comprehensive catalogue of NPBIB designs for $v \le 30,\ r \le 15.$ For completeness, we define NPBIB designs.

Definition E.1: An NPBIB design based on m (≥ 2)-class association scheme defined in v symbols, is an arrangement of v symbols into b_2 sub-blocks of size k_2 nested within b_1 (= b_2 / q, q is an integer) blocks of size k_1 (= $qk_2 < v$) such that

(i) every symbol occurs at most once in a block;

(ii) every symbol appears at most r times in the design;

(iii) if two symbols, say α and β, are i^{th} associates, then they occur together in λ_{1i} blocks and λ_{2i} sub-blocks, the numbers λ_{1i}, λ_{2i} being independent of the particular pair of i^{th} associates α and β, i = 1, 2, ..., m.

The numbers $v, b_1, b_2, r, k_1, k_2, \lambda_{1i}, \lambda_{2i}$ (i = 1, 2, ..., m) are called parameters of the design. If $\lambda_{1i} = \lambda_1$ and $\lambda_{2i} = \lambda_2$; $\forall\ i$ = 1, 2, ..., m, then an NPBIB design reduces to NBIB design.

We have obtained some conditions of non-existence of NPBIB designs and two new methods of construction of NPBIB designs. These are described in the sequel.

E.2 Non-Existence of NPBIB Designs Based on Group Divisible Association Scheme

Consider a NPBIB design based on group divisible (GD) association scheme with parameters v = mn, b_1, b_2, $r, k_1, k_2, \lambda_{11}, \lambda_{12}, \lambda_{21}, \lambda_{22}, n_1 = n-1, n_2 = n(m-1)$. Here symbols have their usual meaning. Let there are q sub-blocks within a bigger block. Therefore, $vr = b_1k_1 = b_2k_2$, $b_2 / b_1 = k_1 / k_2 = q$, $n_1\lambda_{11} + n_2\lambda_{12} = r(k_1 - 1)$, $n_1\lambda_{21} + n_2\lambda_{22} = r(k_2 - 1)$. Now consider λ_{21} = 0, i.e., no two treatments that are mutually 1st associates occur together in a sub-block, therefore, among the 1st associates a treatment that occur in a sub-block will occur in any of the remaining (q – 1) sub-blocks nested within a bigger-block. It is clear that possibility of the concurrences of any two mutually 1st associates in bigger block is (q – 1). A treatment i that appears in r blocks

may have at most $r(q-1)$ concurrences with its 1st associates. Treatment *i* appear with anyone of its 1st associates in λ_{11} bigger blocks. The number of 1st associates of treatment *i* is n_1, therefore, treatment *i* can appear with its 1st associates in $n_1\lambda_{11}$ in bigger blocks. Therefore, the NPBIB designs with $\lambda_{21} = 0$, can exist if $n_1\lambda_{11} \le r(q-1)$. Hence we have the following theorem:

Theorem E.2.1: A NPBIB design based on GD association scheme with parameters $v = mn$, b_1, b_2, $r, k_1, k_2, \lambda_{11}, \lambda_{12}, \lambda_{21} = 0, \lambda_{22}, n_1 = n-1, n_2 = n(m-1)$ cannot be constructed if $n_1\lambda_{11} > r(q-1)$.

Example E.2.1: Consider a NPBIB design based on GD association scheme with $m = 2$, $n = 4$, v=8, $b_1 = 16$, $b_2 = 32$, $r = 8$, $k_1 = 4$, $k_2 = 2$, $\lambda_{11} = 4, \lambda_{12} = 3, \lambda_{21} = 0, \lambda_{22} = 2$, $q = 32/16 = 2$, $n_1 = 3$, $n_2 = 4$ is non-existent because $n_1\lambda_{11} = 3\times 4 = 12 > r(q-1) = 8$.

Theorem E.2.2: If $b_1 - 2r + \lambda_{12} = 0$, then b_1 should be a multiple of *m* provided $v - k_1 \le n$ and/or $b_2 - 2r + \lambda_{22} = 0$, then b_2 should be a multiple of *m* provided $v - k_2 \le n$. Otherwise design is non-existent. { $b_1 - 2r + \lambda_{12} = 0$ or $b_2 - 2r + \lambda_{22} = 0$ implies that the corresponding complementary design is disconnected and for a disconnected design number of blocks has to be multiple of number of rows in the association scheme).

E.3 Methods of Construction

In this section, we give some methods of constructions of NPBIB designs based on 2- and 3- class association schemes.

Method E.3.1: This is a generalization of Method 2.1 given by Satpati and Parsad (2004). Let $v = s^2$ symbols are defined on an L_p-association scheme. Take all possible combinations of *m* ($\le s-1$) rows of the association scheme. Consider the treatments in *m* rows to form a block and the treatments from the same row within the block as sub-blocks. This process yields $\binom{s}{m}$ blocks each of size *ms*, their being *m* sub-blocks each of size *s* nested within each block. Repeating the same procedure for columns, we get another set of $\binom{s}{m}$ blocks. Consider the treatments appearing in the positions of the same alphabet in one of the $(p-2)$ Latin squares as rows or columns. Repeat this process for each of the $(p-2)$ Latin squares. Union of all the blocks so obtained gives an NPBIB design based on L_p-association scheme with parameters $v = s^2$, $b_1 = p\binom{s}{m}$, $b_2 = pm\binom{s}{m}$, $r = p\binom{s-1}{m-1}$, $k_1 = ms$, $k_2 = s$, $\lambda_{11} = \binom{s-1}{m-1} + (p-1)\binom{s-2}{m-2}$, $\lambda_{12} = p\binom{s-2}{m-2}$, $\lambda_{21} = \binom{s-1}{m-1}$, $\lambda_{22} = 0$.

Example E.3.1: Consider $v = 16$ treatments defined on L_3-association scheme. First associates of a particular treatment are the treatments appearing in the same rows, same columns and with the same symbols on one of the 3 (4×4) mutually orthogonal Latin squares. For example,

$$\begin{bmatrix} 1A & 2B & 3C & 4D \\ 5B & 6C & 7D & 8A \\ 9C & 10D & 11A & 12B \\ 13D & 14A & 15B & 16C \end{bmatrix}.$$

Following the procedure of Method E.3.1 for $m = 3$, we get a NPBIB design based on L_3-association scheme with the blocks

[(1,2,3,4); (5,6,7,8); (9,10,11,12)]; [(1,2,3,4); (5,6,7,8); (13,14,15,16)];
[(1,2,3,4); (9,10,11,12); (13,14,15,16)]; [(5,6,7,8); (9,10,11,12); (13,14,15,16)];
[(1,5,9,13); (2,6,10,14); (3,7,11,15)]; [(1,5,9,13); (2,6,10,14); (4,8,12,16)];
[(1,5,9,13); (3,7,11,15); (4,8,12,16)]; [(2,6,10,14); (3,7,11,15); (4,8,12,16)];
[(1,8,11,14); (2,5,12,15); (3,6,9,16)]; [(1,8,11,14); (2,5,12,15); (4,7,10,13)];
[(1,8,11,14); (3,6,9,16); (4,7,10,13)]; [(2,5,12,15); (3,6,9,16); (4,7,10,13)].

The parameters of the above design are $v = s^2 = 16$, $b_1 = 12$, $b_2 = 36$, $r = 9$, $k_1 = 12$, $k_2 = 4$, $\lambda_{11} = 7$, $\lambda_{12} = 6$, $\lambda_{21} = 3$, $\lambda_{22} = 0$.

The designs generated by Method E.3.1 for $v \le 30$, $r \le 15$ are catalogued in the Appendix E.1. The designs which are marked with aestriks (*) are nested complete block partially balanced incomplete sub-block designs and the remaining are NPBIB designs.

Method E.3.2: Let $v = mn$ symbols are defined on GD association scheme on an array of $m \times n$. Consider the symbols come from the same row are 1st associate to each other and are 2nd associates otherwise. Taking the rows as sub-blocks and putting a set of x disjoint sub-blocks to form a block of size nx. Repeat this procedure and form $\binom{m}{x}$ blocks from the complete set of such sub-blocks. Now correspondence of each symbol to v different treatments, we get an NPBIB design with the following parameters:

$v = mn$, $b_1 = \binom{m}{x}$, $b_2 = x\binom{m}{x}$, $k_1 = nx$, $k_2 = n$, $r = \binom{m-1}{x-1}$, $\lambda_{11} = r$, $\lambda_{12} = \binom{m-2}{x-2}$, $\lambda_{21} = r$, $\lambda_{22} = 0$.

Example E.3.2: Let $v = 12$ treatments are arranged in $m = 3$ rows and $n = 4$ columns as given below:

1 5 9
2 6 10
3 7 11
4 8 12

Consider that the GD association scheme is defined on these 12 treatments. Then applying the procedure of Method E.3.2 by taking $x = 3$, we get a NPBIB design based on rectangular association scheme with blocks as

[(1, 5, 9); (2, 6, 10); (3, 7, 11)]; [(1, 5, 9); (2, 6,10); (4, 8, 12)];
[(1, 5, 9); (3, 7, 11); (4, 8, 12)]; [(2, 6,10); (3,7,11); (4, 8, 12)].

The parameters of the above NPBIB design are $v = 12$, $b_1 = 4$, $b_2 = 12$, $r = 3$, $k_1 = 9$, $k_2 = 3$, $\lambda_{11} = 3$, $\lambda_{12} = 2$, $\lambda_{21} = 3$, $\lambda_{22} = 0$.

The design generated by this procedure is disconnected in the sub-blocks, therefore, they are not catalogued.

Method E.3.3: This method is also a generalization of Method 2.3 of Satpati and Parsad (2004). Consider a rectangular association scheme with $v = mn$. The mn treatments are arranged in a rectangular array of m rows and n columns. Let the treatment symbols, in the same row, are 1st associates, treatment symbols in the same column are 2nd associates and the remaining are 3rd associates. If $m = n + 1$, then an NPBIB design based on rectangular association scheme may be constructed using the following procedure.

Step 1: Take all the treatments appearing in the i^{th} row of the association scheme into one block, say B_{1i}.

Step 2: Write n-sub-blocks each of size $n = (m - 1)$ by taking treatment symbols in the columns (except the treatment symbols in i^{th} row) as sub-blocks. Number these sub-blocks as B_{21i}, B_{22i}, ..., B_{2ni}.

Step 3: Take all possible combination of α $(2 \le \alpha \le n)$ blocks from such n-blocks to form $\binom{n}{\alpha}$-blocks like the following manner

$$\left[(\mathbf{B}_{1i});(\mathbf{B}_{21i});(\mathbf{B}_{22i});\cdots;(\mathbf{B}_{2\alpha i})\right];\cdots;\left[(\mathbf{B}_{1i});(\mathbf{B}_{2(n-\alpha+1)i});\cdots;(\mathbf{B}_{2ni})\right]$$

Step 4: Repeat Steps 1 to 3 for all the rows $i = 1, 2, ..., m$.

This procedure yields a NPBIB design with rectangular association scheme with parameters as

$v = mn$, $b_1 = m\binom{n}{\alpha}$, $b_2 = m(\alpha+1)\binom{n}{\alpha}$, $r = \left(\frac{n}{\alpha}+n\right)\binom{n-1}{\alpha-1}$, $k_1 = n(\alpha+1)$, $k_2 = n$, $\lambda_{11} = n\binom{n-2}{\alpha-2} + \binom{n}{\alpha}$, $\lambda_{12} = m\binom{n-1}{\alpha-1}$, $\lambda_{13} = (\alpha+1)\binom{n-1}{\alpha-1}$, $\lambda_{21} = \binom{n}{\alpha}$, $\lambda_{22} = (n-1)\binom{n-1}{\alpha-1}$, $\lambda_{23} = 0$.

Example E.3.3: Let $v = 12$ treatments are arranged in $m = 4$ rows and $n = 3$ columns as given below

1	5	9
2	6	10
3	7	11
4	8	12

Consider that the rectangular association scheme is defined on these 12 treatments. Then applying the procedure of Method E.3.3 by taking $\alpha = 2$, we get a NPBIB design based on rectangular association scheme with blocks as

[(1, 5, 9); (2,3,4); (6,7,8)];	[(1,5,9); (2,3,4); (10,11,12)];	[(1,5,9); (6,7,8); (10,11,12)];
[(2,6,10); (1,3,4); (5,7,8)];	[(2,6,10); (1,3,4); (9,11,12)];	[(2,6,10); (5,7,8); (9,11,12)];
[(3,7,11); (1,2,4); (5,6,8)];	[(3,7,11); (1,2,4); (9,10,12)];	[(3,7,11); (5,6,8); (9,10,12)];
[(4,8,12); (1,2,3); (5,6,7)];	[(4,8,12); (1,2,3); (9,10,11)];	[(4,8,12); (5,6,7); (9,10,11)].

The parameters of the above NPBIB design are $v = 12$, $b_1 = 12$, $b_2 = 36$, $r = 9$, $k_1 = 9$, $k_2 = 3$, $\lambda_{11} = 6$, $\lambda_{12} = 8$, $\lambda_{13} = 6$, $\lambda_{21} = 3$, $\lambda_{22} = 4$, $\lambda_{23} = 0$.

The designs generated by this procedure are catalogued in the Appendix E.1 for $v \le 30, r \le 15$.

References

Banerjee, S. and Kageyama, S. (1990). Existence of α-resolvable nested balanced incomplete block designs. *Utilitas Mathematica*, **38**, 237-243.

Banerjee, S. and Kageyama, S. (1993). Methods of constructing nested partially balanced incomplete block designs. *Utilitas Mathematica*, **43**, 3-6.

Dey, A., Das, U.S. and Banerjee, A.K. (1986). On nested balanced incomplete block designs. *Calcutta Statist. Assoc. Bull.*, **35** , 161-167.

Gupta,V.K. (1993). Optimal nested block designs. *Jour. Ind. Soc. Agri. Stat*., **45(2)**, 187-194.

Homel, R.J. and Robinson, J. (1975). Nested partially balanced incomplete block designs. *Sankhy* $\bar{a}$, **B37**, 201-210.

Jimbo, M. and Kuriki, S. (1983). Constructions of nested designs. *Ars Comb.*, **16**, 275-285.

Kageyama, S., Philip, J. and Banerjee, S. (1995). Some constructions of nested BIB and 2-associate PBIB designs under restricted dualization. *Bull. Fac. Sch. Educ. Hiroshima Univ., Part-II,* **17**, 33-39.

Morgan, J.P., Preece, D.A. and Rees, D.H. (2001). Nested balanced incomplete block designs. *Discrete Mathematics*, **231**, 351-389.

Parsad, R., Gupta, V.K. and Srivastava, R. (1999). Universally optimal block designs for diallel crosses. *Statistics and Applications*, **1**, 35-52.

Philip, J., Banerjee, S. and Kageyama, S. (1997). Construction of nested t-associate class PBIB designs under restricted dualization. *Utilitas Mathematica*, **51**, 27-32.

Preece, D.A.(1967).Nested balanced incomplete block designs. *Biometrika*, **54**, 479-486.

Saha, G.M., Dey, A. and Midha, C.K. (1998). Construction of nested incomplete block designs. *Calcutta Statist. Assoc. Bull*., **48**, 195-205.

Satpati, S.K. and Parsad, R. (2004). Constructions and cataloguing of the Nested partially balanced incomplete block designs. *Ars Combinatoria*, **73**, 299-309.

Appendix E.1

Table E.3.1: Latin-squares Association Scheme Designs Obtained by Method E.3.1

Sl. No.	v	b_1	b_2	r	k_1	k_2	λ_{11}	λ_{12}	λ_{21}	λ_{22}	m	Association Scheme
*1	9	2	6	2	9	3	2	2	1	0	3	L_2
*2	9	3	9	3	9	3	3	3	1	0	3	L_3
*3	16	2	8	2	16	4	2	2	1	0	4	L_2
*4	16	2	8	2	16	4	2	2	1	0	4	L_2
*5	16	3	12	3	16	4	3	3	1	0	4	L_3
*6	16	4	16	4	16	4	4	4	1	0	4	L_4
7	16	8	24	6	12	4	5	4	3	0	3	L_2
8	16	12	36	9	12	4	7	6	3	0	3	L_3
9	16	16	48	12	12	4	9	8	3	0	3	L_4
*10	25	3	15	3	25	5	3	3	1	0	5	L_3
*11	25	4	20	4	25	5	4	4	1	0	5	L_4
*12	25	5	25	5	25	5	5	5	1	0	5	L_5
13	25	10	40	8	20	5	7	6	4	0	4	L_5
14	25	20	60	12	15	5	9	6	6	0	3	L_2
15	25	20	60	12	15	5	9	6	6	0	3	L_2
16	25	15	60	12	20	5	10	9	4	0	4	L_3

* denotes that the design is nested complete block partially balanced incomplete sub-block designs.

Table E.3.2: Designs of Rectangular Association scheme Obtained by Method E.3.3

Sl. No.	v	b_1	b_2	r	k_1	k_2	λ_{11}	λ_{12}	λ_{13}	λ_{21}	λ_{22}	λ_{23}
1	6	3	9	3	6	2	3	3	3	1	1	0
2	12	12	36	9	9	3	6	8	6	3	4	0
3	12	4	16	4	12	3	4	4	4	1	2	0
4	20	5	25	5	20	4	5	5	5	1	3	0
5	30	6	36	6	30	5	6	6	6	1	4	0

F) Nested Block Designs under Correlated Error Structure

F.1 Introduction

Section E deals with the situations where errors within sub-blocks and between sub-blocks within blocks are independent. There, however, do occur experimental situations in which the assumption of independence of observations gets violated; observations within sub-blocks or between sub-blocks within blocks or both may be correlated. The observations between any two blocks are generally assumed as independent. To make the exposition clear about the correlation structure for nested block designs: consider an experimental situation, where v treatments are to be compared via n experimental units, arranged in a nested block set up involving b_1 blocks; there are q mutually exclusive sub-blocks nested within each block, so that $qb_1 = b_2$ is the total number of sub-blocks. Let k_1 be the bigger-block size and $k_2 = k_1/q$ be the sub-block size so that total number of observations is $n = b_1k_1 = b_2k_2$. Let the observations be arranged in such a way that the first k_2 observations come from first sub-block nested within first bigger block, second k_2 observations come from second sub-block nested within the first bigger block, likewise last k_2 observations come from the last sub-block of the last bigger block. All the observations are arranged according to the positions of occurrences within a sub-block. The correlation structure that may exist among the observations is of Kronecker product type and is of the following form $\mathbf{I}_{b_1} \otimes \mathbf{\Phi}_q \otimes \mathbf{\Omega}_{k_2}$, the first part denotes that observations from any two different bigger blocks are independent, second part denotes the correlation structure of the observations between sub-blocks nested within a bigger block and the last part represents the correlation structure among the observations within a sub-block. Further, it is assumed that the correlation structure along with correlation values is same for all the sub-blocks and blocks. $\mathbf{\Phi}_q$ and $\mathbf{\Omega}_{k_2}$ may be any one of the nearest neighbour (NN), autoregressive of order 1 (AR(1)), equi-correlated or no correlation structures. When $\mathbf{\Phi}_q = \mathbf{I}_q$ and $\mathbf{\Omega}_{k_2} = \mathbf{I}_{k_2}$ then it reduces to the set up with uncorrelated error structure. Let $y_{tl(j)}$ be the observation pertaining to the t^{th} position within l^{th} sub-block nested within the j^{th} block, then the different types of correlation structures can be summarized as follows

The correlation between $y_{tl(j)}$ and $y_{t'l'(j')}$ is of the following form:

$$\text{Corr}(y_{tl(j)}, y_{t'l'(j')}) = \begin{cases} \rho_1^{f_1(h)} \rho_2^{f_2(g)} & \text{if } |t-t'| = g, |l-l'| = h \text{ and } j = j' \\ 0 & \text{elsewhere} \end{cases} \qquad \text{(F.1.1)}$$

where $|\rho_1| \le 1$ and $|\rho_2| \le 1$ and ρ_1 is the correlation between observations coming from the experimental units of two neighbouring sub-blocks and ρ_2 is the correlation between two experimental units that are neighbour within a sub-block ignoring other types of correlations and Corr(.) denotes correlation coefficient. Different choices of functions $f_2(g)$ and $f_1(h)$ defined give rise to different types of Kronecker Product type correlation structure $\mathbf{I}_{b_1} \otimes \mathbf{\Phi}_q \otimes \mathbf{\Omega}_{k_2}$. If

$$f_1(h) = \begin{cases} 0 & \text{for } h = 0 \\ 1 & \text{for } h = 1 \\ -\infty & \text{for } h > 1 \end{cases} \quad \text{and } \rho_1 \neq 0$$

then the correlation structure between the sub-blocks nested within a bigger-block is of NN type. If $f_1(h) = h$, $\forall\ h = 0, 1, 2, \ldots, q-1$ and $\rho_1 \neq 0$, then this correlation structure is of AR(1) type. The correlation structure is called equi-correlated structure if

$$f_1(h) = \begin{cases} 0 & \text{for } h = 0 \\ 1 & \text{for } h > 0 \end{cases} \qquad \text{and } \rho_1 \neq 0$$

Defining the identical function $f_2(g)$ as $f_1(h)$, we get similar correlation structure between the observations pertaining to the same sub-block. If

$$f_1(g) = \begin{cases} 0 & \text{for } g = 0 \\ 1 & \text{for } g = 1 \\ -\infty & \text{for } g > 1 \end{cases} \qquad \text{and } \rho_2 \neq 0$$

then the correlation structure between the observations within a sub-block is of NN type. If $f_2(g) = g$, $\forall\ g = 1, 2, \ldots, k_2 - 1$ and $\rho_2 \neq 0$, then this correlation structure is of AR(1) type. The correlation structure is called equi-correlated structure if

$$f_1(g) = \begin{cases} 0 & \text{for } g = 0 \\ 1 & \text{for } g > 0 \end{cases} \qquad \text{and } \rho_2 \neq 0.$$

The generalized Kronecker product type of correlation structure defined above can produce $\mathbf{NN} \otimes \mathbf{NN}$, $\mathbf{AR(1)} \otimes \mathbf{AR(1)}$, $\mathbf{NN} \otimes \mathbf{AR(1)}$, $\mathbf{AR(1)} \otimes \mathbf{NN}$, $\mathbf{I}_q \otimes \mathbf{AR(1)}$, $\mathbf{I}_q \otimes \mathbf{NN}$, $\mathbf{AR(1)} \otimes \mathbf{I}_{k_2}$, $\mathbf{NN} \otimes \mathbf{I}_{k_2}$ and $\mathbf{I}_q \otimes \mathbf{I}_{k_2} = \mathbf{I}_{k_1}$.

For these experimental situations with correlated observations, it is useful to have efficient nested block designs that provide protection against the effects of correlated observations or potentially unknown trends, which are highly correlated with positions of experimental units within blocks. In the example described earlier, nested block designs are used for laboratory analysis whereas the field experiment is conducted using a block design and harvested samples are to be analyzed for their contents in the laboratory by different technicians at the same time. The variation due to technicians or time periods is controlled through forming sub-blocks within blocks. In this experiment, experimenter also records yield in the field besides the characters based on laboratory analysis. The experimenter may want to compare the treatments based on their yield performance and as well as on the character like protein contents recorded in the laboratory based on the analysis of harvested samples. The yield is obtained from the field itself and has not been subjected to the laboratory analysis. Therefore, the analysis of experimental data has to be carried out as per design adopted for field experimentation *i.e.* a block design. Therefore, we have to choose a design which is efficient both under nested block design setup and block design setup ignoring sub-block classification.

The available methods can be used for obtaining efficient nested block designs for independent observations. However, using these methods of construction one may not be able to obtain designs for all parametric combinations. It seems that very little attention has been paid to obtain efficient nested block designs when observations are correlated. In the present investigation, therefore, a computer-aided search has been made of efficient nested block designs for given parametric combinations both under uncorrelated/ correlated error structure. The algorithm for obtaining efficient nested block designs for dependent and independent observations has been developed and presented in Section F.3. Implementation of the algorithm and the designs obtained through the computer aided search have been summarized in Section F.4. Although the algorithm is general in nature and can give designs for any of the correlation structures defined earlier, in the present investigation, the main emphasis on the computer aided search has been made for $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure for nested block design and block designs ignoring sub-

block classification. An attempt has also been made for computer aided search of efficient nested block designs with $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure that are simultaneously efficient for zero correlation structure in block designs ignoring sub-block classification. Some designs have also been obtained for $\mathbf{NN} \otimes \mathbf{NN}$ correlation structure at both stages. Efficient nested block designs have also been obtained for uncorrelated error structures. Resolvable block designs are also a type of nested complete block designs wherein the resolvable group (bigger blocks) are the complete replicates and the blocks of the resolvable groups are small or sub-blocks. The computer algorithm developed in the present investigation can also be used for generating resolvable block designs by defining the bigger block size equal to the number of treatments. Resolvable balanced incomplete block (BIB) designs are also described in Section F.4. We begin with the usual model of nested block designs and estimates of the linear function of treatment effects when observations are correlated.

F.2 Model for Nested Block Designs

The usual model for nested block designs in matrix notations is

$$y = \mu \mathbf{1}_n + \boldsymbol{\Delta}'\tau + \mathbf{D}_1'\boldsymbol{\beta}_1 + \mathbf{D}_2'\boldsymbol{\eta} + \mathbf{e} \tag{F.2.1}$$

where $\boldsymbol{y}$ is n-component vector of the observations, μ is the general mean, $\mathbf{1}_n$ is a n component vector of 1's, $\boldsymbol{\tau} = (\tau_1, \tau_2, \ldots, \tau_v)'$ is v-component vector of treatment effects, $\boldsymbol{\Delta}'$ is the observations *versus* treatments incidence matrix, $\boldsymbol{\beta}_1 = (\beta_1, \beta_2, \ldots, \beta_{b_1})'$ is b_1-component vector of block effects and $\mathbf{D}_1' = \mathbf{I}_{b_1} \otimes 1_{k_1}$ is the observations *versus* blocks incidence matrix, and $\boldsymbol{\eta} = \left(\eta_{1(1)}, \eta_{2(1)}, \cdots, \eta_{q(1)}, \eta_{1(2)}, \cdots, \eta_{q(b_1)}\right)'$ is b_2-component vector of nested-block effects, $\mathbf{D}_2' = \mathbf{I}_{b_2} \otimes 1_{k_2}$ is the observations *versus* sub-blocks incidence matrix and $\mathbf{e}$ is the vector of random error associated with the observation vector $\boldsymbol{y}$. Assuming all the parameters in (F.2.1) have fixed effects and errors are distributed as multivariate normal with mean $\mathbf{0}$ and

$$\text{Cov}(\mathbf{e}) = \sigma^2 \left(\mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}_q \otimes \boldsymbol{\Omega}_{k_2}\right) = \sigma^2 \boldsymbol{\Sigma}. \tag{F.2.2}$$

For obtaining the best linear unbiased estimate of estimable linear functions of treatment effects, the usual coefficient matrix $\mathbf{C}$ is given by

$$\mathbf{C}_{B_2(GLS)} = \mathbf{X}_1'\boldsymbol{\Sigma}^{-\frac{1}{2}}\left(\mathbf{I} - \boldsymbol{\Sigma}^{-\frac{1}{2}}\mathbf{X}_2\left(\mathbf{X}_2'\boldsymbol{\Sigma}^{-1}\mathbf{X}_2\right)^{-}\mathbf{X}_2'\boldsymbol{\Sigma}^{-\frac{1}{2}}\right)\boldsymbol{\Sigma}^{-\frac{1}{2}}\mathbf{X}_1 \tag{F.2.3}$$

where $\mathbf{X}_1 = [\boldsymbol{\Delta}']$ and $\mathbf{X}_2 = [\mathbf{D}_2' \quad \mathbf{1}_n \quad \mathbf{D}_1'] = \left[\mathbf{I}_{b_1} \otimes \mathbf{I}_q \otimes \mathbf{1}_{k_2} \quad \mathbf{1}_{b_1} \otimes \mathbf{I}_q \otimes \mathbf{1}_{k_2} \quad \mathbf{I}_{b_1} \otimes \mathbf{1}_q \otimes \mathbf{1}_{k_2}\right]$

$\boldsymbol{\Sigma}^{-\frac{1}{2}} = \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}}$ is the Grammian root of $\boldsymbol{\Sigma}^{-1}$. Now taking

$$\mathbf{W} = \boldsymbol{\Sigma}^{-\frac{1}{2}}\mathbf{X}_2 = \left[\mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}}\right]\left[\mathbf{I}_{b_1} \otimes \mathbf{I}_q \otimes \mathbf{1}_{k_2} \quad \mathbf{1}_{b_1} \otimes \mathbf{1}_q \otimes \mathbf{1}_{k_2} \quad \mathbf{I}_{b_1} \otimes \mathbf{1}_q \otimes \mathbf{1}_{k_2}\right]$$

$$= \left[\mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}}\mathbf{1}_{k_2} \quad \mathbf{1}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}}\mathbf{1}_q \otimes \boldsymbol{\Omega}^{-\frac{1}{2}}\mathbf{1}_{k_2} \quad \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}}\mathbf{1}_q \otimes \boldsymbol{\Omega}^{-\frac{1}{2}}\mathbf{1}_{k_2}\right].$$

$$\mathbf{W}'\mathbf{W}$$

$$= \begin{bmatrix} \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-1} \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} & \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-1} \mathbf{1}_q \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} & \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-1} \mathbf{1}_q \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} \\ \mathbf{1}'_{b_1} \otimes \mathbf{1}'_q \boldsymbol{\Phi}^{-1} \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} & \mathbf{I}'_{b_1} \otimes \mathbf{1}'_q \boldsymbol{\Phi}^{-1} \mathbf{1}_q \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} & \mathbf{I}'_{b_1} \otimes \mathbf{1}'_q \boldsymbol{\Phi}^{-1} \mathbf{1}_q \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} \\ \mathbf{I}_{b_1} \otimes \mathbf{1}'_q \boldsymbol{\Phi}^{-1} \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} & \mathbf{I}_{b_1} \otimes \mathbf{1}'_q \boldsymbol{\Phi}^{-1} \mathbf{1}_q \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} & \mathbf{I}_{b_1} \otimes \mathbf{1}'_q \boldsymbol{\Phi}^{-1} \mathbf{1}_q \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-1} \mathbf{1}_{k_2} \end{bmatrix}$$

Taking the scalars $\mathbf{1}'\boldsymbol{\Omega}^{-1}\mathbf{1} = \mathrm{S_S}$ and $\mathbf{1}'\boldsymbol{\Phi}^{-1}\mathbf{1} = \mathrm{S_B}$, we get,

$$\mathbf{W}'\mathbf{W} = \mathrm{S_S} \begin{bmatrix} \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-1} & \mathbf{1}_{b_1} \otimes \boldsymbol{\Phi}^{-1} \mathbf{1}_q & \mathbf{I}_{b_1} \boldsymbol{\Phi}^{-1} \mathbf{1}_q \\ \mathbf{1}'_{b_1} \otimes \mathbf{1}'_q \boldsymbol{\Phi}^{-1} & b_1 \mathrm{S_B} & \mathbf{S_B} \mathbf{1}'_{b_1} \\ \mathbf{I}_{b_1} \otimes \mathbf{1}'_q \boldsymbol{\Phi}^{-1} & \mathrm{S_B} \mathbf{1}_{b_1} & \mathbf{S_B} \mathbf{I}_{b_1} \end{bmatrix}$$

A g-inverse of $\mathbf{W}'\mathbf{W}$ is $\left[\mathbf{W}'\mathbf{W}\right]^- = \mathrm{S_S} \begin{bmatrix} \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi} & \mathbf{0}_{b_1 \times b_1} & \mathbf{0}_{b_1 \times 1} \\ \mathbf{0}_{b_1 \times b_1} & 0 & \mathbf{0}_{b_1 \times 1} \\ \mathbf{0}_{1 \times b_1} & \mathbf{0}_{1 \times b_1} & \mathbf{0}_{b_1 \times b_1} \end{bmatrix}$.

As, $\mathbf{W} = \begin{bmatrix} \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}_{k_2} & \mathbf{1}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \mathbf{1}_q \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}_{k_2} & \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \mathbf{1}_q \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}_{k_2} \end{bmatrix}$.

Then, $\mathbf{W}\left[\mathbf{W}'\mathbf{W}\right]^- \mathbf{W}'$

$$= (\mathrm{S_S}) \left\{ \left(\mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}_{k_2} \right) \left(\mathbf{1}_{b_1} \otimes \boldsymbol{\Phi} \right) \left(\mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-\frac{1}{2}} \right) + \mathbf{0} \right\}$$

$$= (\mathrm{S_S})^{-1} \left\{ \mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} . \boldsymbol{\Phi} . \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}_{k_2} . 1 . \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-\frac{1}{2}} \right\}$$

$$= (\mathrm{S_S})^{-1} \left\{ \mathbf{I}_{b_1} \otimes \mathbf{1}_q \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}_{k_2} \mathbf{1}'_{k_2} \boldsymbol{\Omega}^{-\frac{1}{2}} \right\}.$$

$$\Rightarrow \mathbf{W}\left[\mathbf{W}'\mathbf{W}\right]^- \mathbf{W}' = \left[(\mathrm{S_S})^{-1} \mathbf{I}_{b_2} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}\mathbf{1}' \boldsymbol{\Omega}^{-\frac{1}{2}} \right].$$

Now, $\mathbf{I}_n - \mathbf{W}\left[\mathbf{W}'\mathbf{W}\right]^- \mathbf{W}' = \left[\mathbf{I}_{b_1} \otimes \mathbf{I}_q \otimes \left(\mathbf{I}_{k_2} - (\mathrm{S_S})^{-1} \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}\mathbf{1}' \boldsymbol{\Omega}^{-\frac{1}{2}} \right) \right]$, then

$$\mathbf{C}_{\mathrm{B}_2(GLS)} = \boldsymbol{\Delta} \left[\left(\mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \right) \left[\mathbf{1}_{b_1} \otimes \mathbf{I}_q \otimes \left(\mathbf{1}_{k_2} - (\mathrm{S_S})^{-1} \boldsymbol{\Omega}^{-\frac{1}{2}} \mathbf{1}\mathbf{1}' \boldsymbol{\Omega}^{-\frac{1}{2}} \right) \right] \left(\mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-\frac{1}{2}} \otimes \boldsymbol{\Omega}^{-\frac{1}{2}} \right) \right] \boldsymbol{\Delta}'$$

Therefore,

$$\mathbf{C}_{\mathrm{B}_2(GLS)} = \boldsymbol{\Delta} \left[\mathbf{I}_{b_1} \otimes \boldsymbol{\Phi}^{-1} \otimes \left(\boldsymbol{\Omega}^{-1} - (\mathrm{S_S})^{-1} \boldsymbol{\Omega}^{-1} \mathbf{1}\mathbf{1}' \boldsymbol{\Omega}^{-1} \right) \right] \boldsymbol{\Delta}' \qquad \text{(F.2.4)}$$

Taking, $\boldsymbol{\Gamma} = \boldsymbol{\Phi}^{-1} \otimes \left(\boldsymbol{\Omega}^{-1} - (\mathrm{S_S})^{-1} \boldsymbol{\Omega}^{-1} \mathbf{1}\mathbf{1}' \boldsymbol{\Omega}^{-1} \right)$ $\boldsymbol{\Gamma}$, for Kronecker product correlation structure

$$\mathbf{C}_{\mathrm{B}_2(GLS)} = \boldsymbol{\Delta} \left(\mathbf{I}_{b_1} \otimes \boldsymbol{\Gamma} \right) \boldsymbol{\Delta}' \qquad \text{(F.2.5)}$$

We know that $\text{trace}(\mathbf{AB}) = \text{trace}(\mathbf{BA})$ and as $\mathbf{\Delta}'\mathbf{\Delta} = \mathbf{I}_n$ (for a binary block design)

$$\text{trace}\,(\mathbf{C}_{\mathrm{B}_2(GLS)}) = \text{trace}\left(\mathbf{I}_n(\mathbf{I}_{b_1} \otimes \mathbf{\Gamma})\right) = b_1\ \text{trace}(\mathbf{\Gamma}) \tag{F.2.6}$$

which is independent of design matrix or treatments *versus* observations matrix $\mathbf{\Delta}$. Therefore, $\text{trace}\,(\mathbf{C}_{\mathrm{B}_2(GLS)})$ is constant for a choice of v, b_1, k_1, q, $\mathbf{\Phi}$ and $\mathbf{\Omega}$.

It is well known that the problem of obtaining A- [D-] optimal nested block designs for making all possible pairwise treatment comparisons is equivalent to the problem of obtaining an A- [D-] optimal design for a complete set of orthonormal treatment contrasts $\mathbf{P}'\boldsymbol{\tau}$; $\mathbf{P}'\mathbf{P} = \mathbf{I}_{v-1}, \mathbf{PP}' = \mathbf{I}_v - \mathbf{11}'/v$. Let $\mathfrak{D} = \mathbf{D}\left(v, b_1, b_2, k_1, k_2, \mathbf{I}_{b_1} \otimes \mathbf{\Phi}_q \otimes \mathbf{\Omega}_{k_2}\right)$ be the class of connected nested block designs in which v treatments are arranged in b_1 blocks of size k_1 each such that there are $b_2 = b_1 q$ sub-blocks of size $k_2 = k_1/q$ each and correlation between the observation is of the form $\mathbf{I}_{b_1} \otimes \mathbf{\Phi}_q \otimes \mathbf{\Omega}_{k_2}$. For inferring on complete set of orthonormal treatment contrasts, a design $d \in \mathfrak{D}$ is said to be A-optimal if it minimizes the sum of reciprocals of the non-zero eigenvalues of the $\mathbf{C}_{d\,\mathrm{B}_2(GLS)}$-matrix over $\mathfrak{D}$ and is said to be D-optimal if it minimizes the inverse of the product of the nonzero eigenvalues of $\mathbf{C}_{d\,\mathrm{B}_2(GLS)}$-matrix over $\mathfrak{D}$. For a nested block design $d \in \mathfrak{D}$, let $\theta_1, \theta_2, \cdots, \theta_{v-1}$ be the non-zero eigenvalues of $\mathbf{C}_{d\,\mathrm{B}_2(GLS)}$. Now define $\phi_{\mathrm{A}}(d) = \sum_{i=1}^{v-1} \theta_i^{-1}$ and $\phi_{\mathrm{A}}(d) = \prod_{i=1}^{v-1} \theta_i^{-1}$. Then, a design is A- [D-] optimal if it minimizes $\phi_{\mathrm{A}}(d)\left[\phi_{\mathrm{D}}(d)\right]$ over $\mathfrak{D}$.

The *A*-efficiency $\{e_{\mathrm{A}}(d)\}$ and D-efficiency $\{e_{\mathrm{D}}(d)\}$ of any design d over $\mathfrak{D}$ is defined as

$$e_{\mathrm{A}}(d) = \frac{\phi_{\mathrm{A}}(d_{\mathrm{A}}^*)}{\phi_{\mathrm{A}}(d)} \text{ and } e_{\mathrm{D}}(d) = \left[\frac{\phi_{\mathrm{D}}(d_{\mathrm{D}}^*)}{\phi_{\mathrm{D}}(d)}\right]^{1/(v-1)}$$

where, d_{A}^* and d_{D}^* are the A-optimal and D-optimal designs over $\mathfrak{D}$, respectively.

It is not always possible to obtain a design that is A-optimal or D-optimal over $\mathfrak{D}$. Therefore, it is required to see the performance of a given design with respect to an hypothetical optimal design. To deal with such situations, Cheng and Wu (1981) and Rathore *et al.* (2006) provided expressions of lower bounds to A-efficiency and D-efficiency of a given binary proper block design for zero correlation structure for making all possible pairwise treatment comparisons which is equivalent to obtaining lower bounds to A-efficiency and D-efficiency of a connected block design for a specific correlation structure for inferring on a complete set of orthonormalized treatment contrasts. On similar lines, we have obtained lower bounds to A- and D-efficiencies for $\mathfrak{D}$. The lower bounds to $\phi_{\mathrm{A}}(d)$ and $\phi_{\mathrm{D}}(d)$ are used instead of $\phi_{\mathrm{A}}(d_{\mathrm{A}}^*)$ and $\phi_{\mathrm{D}}(d_{\mathrm{D}}^*)$ in the computation of $e_{\mathrm{A}}(d)$ and $e_{\mathrm{D}}(d)$.

The lower bounds to A- and D-efficiencies of a nested block design d compared to the hypothetical optimal design belong to the class that contains design d are

$$\text{A-efficiency} = \frac{(v-1)^2}{b_1 \times \text{trace}(\mathbf{\Gamma}) \times (\phi_{\mathrm{A}_2}(d))} \tag{F.2.7}$$

and

$$\text{D-efficiency} = \frac{(v-1)}{b_1 \times \text{trace}(\boldsymbol{\Gamma}) \times (\phi_{\text{D}_2}(d))^{1/(v-1)}} \tag{F.2.8}$$

where, $\boldsymbol{\Gamma} = \boldsymbol{\Phi}^{-1} \otimes \left(\boldsymbol{\Omega}^{-1} - (\text{S}_\text{S})^{-1} \boldsymbol{\Omega}^{-1} \mathbf{1}\mathbf{1}' \boldsymbol{\Omega}^{-1} \right)$.

As mentioned in Section F.1, we are searching for efficient nested block designs that are efficient for bigger block set up ignoring the sub-block classification as well. Hence, we define the lower bounds to A- and D-efficiencies of the block designs ignoring sub-block classification. We know that ignoring the sub-block classifications, a nested block design becomes a block design $d \in \mathbf{D}(v, b_1, k_1, \boldsymbol{\Phi} \otimes \boldsymbol{\Omega})$ for correlated observations if the correlation structure is same in the bigger-block design as in the nested-block design set up. We know that the coefficient matrix of reduced normal equations for estimating linear function of treatment effects for a block design $d \in (v, b, k, \boldsymbol{\Omega})$ is $\mathbf{C} = \boldsymbol{\Delta}(\mathbf{I}_b \otimes \boldsymbol{\Omega}^*)\boldsymbol{\Delta}'$, where $\boldsymbol{\Omega}^* = \boldsymbol{\Omega}^{-1} - \frac{\boldsymbol{\Omega}^{-1}\mathbf{1}_k\mathbf{1}_k'\boldsymbol{\Omega}^{-1}}{\mathbf{1}_k'\boldsymbol{\Omega}^{-1}\mathbf{1}_k}$. Then **C**-matrix of bigger block design ignoring sub-block classification is

$$\mathbf{C}_{\text{B}_1(GLS)=}\boldsymbol{\Delta}\left[\mathbf{I}_{b_1} \otimes \left\{ \left(\boldsymbol{\Phi}^{-1} \otimes \boldsymbol{\Omega}^{-1} \right) - \frac{1}{(\text{S}_\text{B}\text{S}_\text{S})} \left(\boldsymbol{\Phi}^{-1}\mathbf{1}\mathbf{1}'\boldsymbol{\Phi}^{-1} \right) \otimes \left(\boldsymbol{\Omega}^{-1}\mathbf{1}\mathbf{1}'\boldsymbol{\Omega}^{-1} \right) \right\} \right] \boldsymbol{\Delta}'. \tag{F.2.9}$$

As $\boldsymbol{\Omega}^* = \boldsymbol{\Omega}^{-1} - \frac{\boldsymbol{\Omega}^{-1}\mathbf{1}_k\mathbf{1}_k'\boldsymbol{\Omega}^{-1}}{\mathbf{1}_k'\boldsymbol{\Omega}^{-1}\mathbf{1}_k}$, we get $\left[\boldsymbol{\Phi} \otimes \boldsymbol{\Omega}\right]^{-1} = \boldsymbol{\Phi}^{-1} \otimes \boldsymbol{\Omega}^{-1}$, $\mathbf{1}'\left[\boldsymbol{\Phi} \otimes \boldsymbol{\Omega}\right]^{-1}\mathbf{1} = \frac{1}{(\text{S}_\text{B}\text{S}_\text{S})}$, and $\left[\boldsymbol{\Phi} \otimes \boldsymbol{\Omega}\right]^{-1}\mathbf{1}_{k_1}\mathbf{1}_{k_1}'\left[\boldsymbol{\Phi} \otimes \boldsymbol{\Omega}\right]^{-1} = \left(\boldsymbol{\Phi}^{-1}\mathbf{1}\mathbf{1}'\boldsymbol{\Phi}^{-1} \right) \otimes \left(\boldsymbol{\Omega}^{-1}\mathbf{1}\mathbf{1}'\boldsymbol{\Omega}^{-1} \right)$.

Now the lower bounds to A-efficiency and D-efficiency of the bigger-block design ignoring sub-block classification are

$$\text{A-efficiency} = \frac{(v-1)^2}{b_1 \times \text{trace}\left(\left\{ \boldsymbol{\Phi}^{-1} \otimes \boldsymbol{\Omega}^{-1} \right\} - \frac{1}{\text{S}_\text{B}\text{S}_\text{S}} \left\{ \boldsymbol{\Phi}^{-1}\mathbf{1}\mathbf{1}'\boldsymbol{\Phi}^{-1} \right\} \otimes \left\{ \boldsymbol{\Omega}^{-1}\mathbf{1}\mathbf{1}'\boldsymbol{\Omega}^{-1} \right\} \right) \times (\phi_{\text{A}_1}(d))} \tag{F.2.10}$$

and

$$\text{D-efficiency} = \frac{(v-1)}{b_1 \times \text{trace}\left(\left\{ \boldsymbol{\Phi}^{-1} \otimes \boldsymbol{\Omega}^{-1} \right\} - \frac{1}{\text{S}_\text{B}\text{S}_\text{S}} \left\{ \boldsymbol{\Phi}^{-1}\mathbf{1}\mathbf{1}'\boldsymbol{\Phi}^{-1} \right\} \otimes \left\{ \boldsymbol{\Omega}^{-1}\mathbf{1}\mathbf{1}'\boldsymbol{\Omega}^{-1} \right\} \right) \times (\phi_{\text{D}_1}(d))^{1/(v-1)}} \tag{F.2.11}$$

For zero correlation structure, the coefficient matrix of the reduced normal equations of bigger-block design ignoring the sub-block classifications can be obtained by replacing $\mathbf{I}_{k_1}$ in the place of $\boldsymbol{\Phi}_q \otimes \boldsymbol{\Omega}_{k_2}$ and is same as the **C**-matrix of block design set-up under zero correlation structure.

$$\mathbf{C}_{\text{B}_1(OLS)} = \boldsymbol{\Delta}\left[\mathbf{I}_{b_1} \otimes \left\{ \mathbf{I}_{k_1} - \frac{1}{k_1}\mathbf{1}_{k_1}\mathbf{1}_{k_1}' \right\} \right] \boldsymbol{\Delta}' \tag{F.2.12}$$

Now we describe the cases of different choices of $\boldsymbol{\Phi}$, $\boldsymbol{\Omega}$ and on their effect on **C**-matrix:

Case I: If $\mathbf{\Phi} = \mathbf{I}$, then $\mathbf{C}_{\mathrm{B}_2(GLS)} = \mathbf{\Delta}\left[\mathbf{I}_{b_1} \otimes \left\{\mathbf{\Omega}^{-1} - (\mathrm{S}_{\mathrm{S}})^{-1}\mathbf{\Omega}^{-1}\mathbf{1}\mathbf{1}'\mathbf{\Omega}^{-1}\right\}\right]\mathbf{\Delta}'$, , this is the **C**-matrix for correlated observations for sub-block classification ignoring the block classification.

Case II: If $\mathbf{\Phi} = \mathbf{I}$, and $\mathbf{\Omega} = \mathbf{I}$, then $\mathbf{C}_{\mathrm{B}_2(GLS)} = \mathbf{\Delta}\left[\mathbf{I}_{b_2} \otimes \left\{\mathbf{I} - (k_2)^{-1}\mathbf{1}\mathbf{1}'\right\}\right]\mathbf{\Delta}' = \mathbf{R} - (k_2)^{-1}\mathbf{H}\mathbf{H}'$ = $\mathbf{C}_{\mathrm{B}_2(OLS)}$, we can get this expression by solving (F.2.4), where, **R** is the diagonal matrix of replications and **H** is the treatments versus nested-blocks incidence matrix *i.e.* usual **C**-matrix for independent correlation structure.

Case III: If $\mathbf{\Phi} = \mathbf{I}$, and k_2 = 2, then $\mathbf{\Omega} = \begin{bmatrix} 1 & \rho \\ \rho & 1 \end{bmatrix}$. Doing simple algebra we get $\mathbf{\Omega}^{-1} = \frac{1}{1-\rho^2}\begin{bmatrix} 1 & -\rho \\ -\rho & 1 \end{bmatrix}$ and $\mathbf{\Omega}^{-1} - (\mathrm{S}_{\mathrm{S}})^{-1}\mathbf{\Omega}^{-1}\mathbf{1}\mathbf{1}'\mathbf{\Omega}^{-1} = \frac{1}{1-\rho}\left(\mathbf{I}_{k_2} - \frac{1}{k_2}\mathbf{1}\mathbf{1}'\right)$. Therefore, $\mathbf{C}_{\mathrm{B}_2(GLS)} = (1-\rho)^{-1}\mathbf{\Delta}\left[\mathbf{I}_{b_2} \otimes \left\{\mathbf{I}_{k_2} - (k_2)^{-1}\mathbf{1}\mathbf{1}'\right\}\right]\mathbf{\Delta}' = (1-\rho)^{-1}\left(\mathbf{R} - (k_2)^{-1}\mathbf{H}\mathbf{H}'\right)$ = $(1-\rho)^{-1}\mathbf{C}_{\mathrm{B}_2(OLS)}$. This is proportional to the **C**-matrix for independent observations for nested block design.

Remark F.2.1: If we ignore nested-block structure and consider only bigger-block structure, then the problem reduces as block design for dependent observations. Further assuming the correlation structure in the bigger-block part of the design same as that of the nested-block design, we can compute the efficiencies of the bigger-block design by usual way of obtaining lower bounds to A- and D-efficiencies for the block design $d \in \mathcal{D}$ using (F.2.10) and (F.2.11) respectively. In the present investigation, we consider the correlation structure in the bigger block design is same as that of the nested-block designs. This is useful for the situations, where it is known in advance that a particular sub-set of treatments will be allocated to a given sub-block and even the position of sub-blocks nested within bigger-blocks are known in advance. In some situations, however, the design is conducted using the bigger block structures where there may be zero correlation structure. While sub-dividing the treatments allocated to a given bigger block to sub-blocks, there may be correlation within sub-blocks and/ or sub-blocks within blocks. Therefore, we have obtained some designs for these experimental situations as well.

In the following section, we describe the computer-aided search of efficient nested block designs for correlated observations. The algorithm developed is general in nature and can produce the design for different types of correlation structures. This has been illustrated by generating designs for different combinations of correlation structure. The designs obtained are presented in Appendix F.1. In the present investigation, however, main emphasis has been given on obtaining block designs when the observations between sub-blocks within a bigger block are uncorrelated and the experimental units within a sub-block are correlated, *i.e.*, for Case I. Some designs also have been obtained for $\mathbf{NN} \otimes \mathbf{NN}$, $\mathbf{NN} \otimes \mathbf{AR(1)}$, $\mathbf{AR(1)} \otimes \mathbf{NN}$ and $\mathbf{AR(1)} \otimes \mathbf{AR(1)}$ correlation structure at both systems of blocks. Nested block designs have also been obtained for zero correlation structure as well. An attempt has also been made for computer aided search of efficient nested block designs with $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure that are simultaneously efficient for zero correlation structure in bigger blocks ignoring the sub-block classification. Lower bounds to A- and D-efficiencies of the generated nested block designs are obtained using (F.2.7) and (F.2.8) respectively and Remark F.2.1 and the lower bounds to A- and D-efficiencies of the bigger block designs are obtained using (F.2.10) and (F.2.11) respectively.

Martin and Eccleston (1991) derived that $\mathbf{\Omega}_q$ is positive definite under **NN** correlation structure if $|\rho_2| < \left[2\cos\{\Pi/(k_2+1)\}\right]^{-1}$. This bound depends upon k_2. Pooladsaz and Martin (2005)

investigated for more restrictive nearest neighbour correlation structure $|\rho_2| \leq 0.50$. In present investigation we consider $|\rho_2| \leq 0.50$ for **NN** correlation structure between the observations within sub-blocks and taking $\rho_1 = 0$. The computer aided search of designs was made starting from –0.50 to 0.50 by taking the step of the correlation as 0.05, and the efficiencies of the designs are recorded. We computed the percent coefficient of variation (CV) of A-efficiencies and D-efficiencies for each of the four ranges: (i) $-0.50 \leq \rho_2 < 0.00$ (ii) $0.00 < \rho_2 \leq 0.50$ (iii) $0.20 \leq \rho_2 \leq 0.20$ and (iv) $-0.50 \leq \rho_2 \leq 0.50$ (except zero).

F.3 Computer Algorithm to Construct Efficient Nested Block Designs

In this section we describe the algorithm to construct efficient nested incomplete block designs. The algorithm is dynamic and general in nature and is capable of producing efficient designs for dependent observations as well as independent observations. Jones and Eccleston (1980), Zergaw (1989), Martin and Eccleston (1992), Rathore *et al.* (2006) gave exchange and interchange algorithm to develop computer-aided search for efficient block designs. We make use of exchange and interchange procedures after random start in the bigger blocks taking care of binarity and connectedness in the sub-blocks. For application of exchange and interchange steps, we have redefined the weakest observations, the strongest observations and the strongest treatment interchange with respect to the nested block design setup. The random start and exchange and interchange steps are described in the sequel. The algorithm starts with a random selection of initial design.

Step 1: Random Start

Initialize a $b_1 \times k_1$ array with all elements as zero. Now generate $n = b_1 k_1$ random numbers of modulo v one by one and put into this array. If any random number gets repeated in k_1 runs, it is rejected. In other words, choose one set of k_1 distinct random numbers. Put the random numbers into one row of that array. Likewise, search for b_1 such distinct set of random numbers to put into $b_1 \times k_1$ array. This yields the random initial design for the bigger blocks. Sub-blocks are created by making q groups from each set of k_1 elements in a particular run by making q sets of k_2 elements, randomly. From each set of k_1 elements first k_2 random elements form first sub-block, next k_2 random elements form next sub-block, likewise remaining k_2 elements are used to form last sub-block in the last block. This random start is selected for further processing if the design is connected in nested block set up and also in bigger blocks classification ignoring the sub-blocks. Otherwise, repeat the process.

Once the connected design is obtained through random start the process enters into exchange step.

Step 2: Exchange Steps

Exchange refers to replacement of the weakest observation from the design by the strongest observation. The strongest observation is chosen so that design remains binary with respect to sub-blocks and hence blocks. Exchange step is implemented for improving the criterion considered by changing replication vector of the treatments. Here we are interested in obtaining an efficient nested block design which is efficient for block classification as well. Therefore, through the exchange of treatments, it may sometimes happen that the exchange improves the criterion value for nested block design set up and efficiency for block design ignoring sub-block classification may decrease or vice versa. Therefore, we redefine the concept of weakest and strongest observations. Let $\mathbf{C}_{\mathrm{B}_2(GLS)_{n(o)}}$ be the coefficient matrix of reduced normal equations for estimating the treatment effects using GLS for nested-block design with original n observations, $\mathbf{C}_{\mathrm{B}_2(GLS)_{n-1}}$ is same for $n - 1$ observations after 1 observation is deleted, and

$\mathbf{C}_{\mathrm{B}_2(GLS)_{n(n)}}$ is the new **C**-matrix of nested-block design when a new observation is added to the design with deleted observation. $\mathbf{C}_{\mathrm{B}_1(GLS)_{n(o)}}$ is the coefficient matrix of reduced normal equations for estimating the treatment effects using GLS for bigger-block design ignoring the sub-block classification with original *n* observations, $\mathbf{C}_{\mathrm{B}_1(GLS)_{n-1}}$ is same for $n-1$ observations after the observation has been deleted and $\mathbf{C}_{\mathrm{B}_1(GLS)_{n(n)}}$ is new **C**-matrix for bigger block design when the new observation is added to the design in place of deleted observation. In exchange step we first find the weakest observation from the design.

Weakest Observation: An observation is said to be weakest if trace $(\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_{n-1}}\mathbf{PP}')$ − trace $(\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_{n(o)}}\mathbf{PP}')$ is minimum subject to trace $(\mathbf{C}^{-}_{\mathrm{B}_2(GLS)_{n-1}}\mathbf{PP}')$ is minimum for all possible $\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_{n-1}}$ and $\mathbf{C}^{-}_{\mathrm{B}_2(GLS)_{n-1}}$; in other words trace $(\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_{n-1}}\mathbf{PP}')$ and trace $(\mathbf{C}^{-}_{\mathrm{B}_2(GLS)_{n-1}}\mathbf{PP}')$ is jointly minimum.

We delete the weakest observation from the design. This weakest observation is to be replaced by the strongest observation.

Strongest Observation: An observation for which trace $(\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_{n-1}}\mathbf{PP}')$ − trace $(\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_{n(n)}}\mathbf{PP}')$ is maximum subject to trace $(\mathbf{C}^{-}_{\mathrm{B}_2(GLS)_{n(n)}}\mathbf{PP}') \leq$ trace $(\mathbf{C}^{-}_{\mathrm{B}_2(GLS)_{n(o)}}\mathbf{PP}')$ for all possible $\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_{n(n)}}$ is called the strongest observation.

The strongest observation is added at the position of the deleted treatment. The algorithm continues with the exchange steps till the weakest and the strongest observation pertains to the same treatment. After this there is no further scope of improvement on continuing the exchange steps, therefore, the exchange step gets terminated.

Step 3: Interchange Steps

After the termination of exchange step, the interchange process is implemented. Interchange means, the mutually swapping of the positions between a pair of observations to improve the criterion under consideration. The positions of treatments are swapped by putting a restriction that the design remains binary with respect to sub-blocks and blocks. While trying to improve the criterion for any of the blocking systems by interchanging the position of two treatments may adversely affect the criterion in other blocking system. Therefore, care should be taken. If the improved design is one that minimizes the criterion value in one blocking system, then change in the criterion value in the other system must be non-positive. To deal with this situation, we define the strongest treatment interchange as follows:

Let $\mathbf{C}_{\mathrm{B}_1(GLS)_I}$ be the new **C**-matrix after swapping the positions between two observations in the bigger block and $\mathbf{C}_{\mathrm{B}_2(GLS)_I}$ be the same for the nested-block design set up.

The positions of two treatments are swapped which favours the criterion most *i.e.* for which trace $(\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_O}\mathbf{PP}')$ −trace $(\mathbf{C}^{-}_{\mathrm{B}_1(GLS)_I}\mathbf{PP}')$ is maximum subject to trace $(\mathbf{C}^{-}_{\mathrm{B}_2(GLS)_O}\mathbf{PP}') \geq$

trace $(\mathbf{C}^{-}_{\mathrm{B}_{2(GLS)_I}}\mathbf{PP}')$ is called Strongest treatment interchange for bigger-blocks and the swapping of the positions of two observations which favours the nested-block criterion most *i.e.* for which the trace $(\mathbf{C}^{-}_{\mathrm{B}_{2(GLS)_O}}\mathbf{PP}')$ – trace $(\mathbf{C}^{-}_{\mathrm{B}_{2(GLS)_I}}\mathbf{PP}')$ is maximum subject to trace $(\mathbf{C}^{-}_{\mathrm{B}_{1(GLS)_O}}\mathbf{PP}') \geq$ trace $(\mathbf{C}^{-}_{\mathrm{B}_{1(GLS)_I}}\mathbf{PP}')$ is called **S**trongest treatment interchange for sub-block structure.

The strongest treatment interchange procedure is implemented for the bigger-blocks first *i.e.*, swapping the positions between/ within bigger blocks. Once the procedure of strongest treatment interchange is implemented for bigger blocks gets terminated we follow the process of the strongest treatment interchange for sub-blocks. We go on swapping the positions of treatments between and within sub-blocks of a given bigger block by the strongest treatment interchange for the sub-block structure procedure. This process terminates when there is no further improvement in the nested-block criterion. With this interchange step gets terminated.

Step 4: Computation of Lower Bounds to A- and D-Efficiency
After termination of the interchange steps, we compute the lower bounds to A- and D-efficiencies for the nested block designs using (F.2.7) and (F.2.8), respectively and for bigger-block structure ignoring the sub-block classification using (F.2.10) and (F.2.11).

If the efficiency of the design is not satisfactory, then the whole procedure is repeated by selecting a new starting design. This procedure is continued till a design with satisfactory efficiency is obtained. In the present investigation, all the designs are obtained with maximum of 3 to 4 random starts.

F.4 Implementation of Algorithm and Generated Designs

The algorithm developed was used for computer aided search of efficient nested block designs for dependent/independent observations. For this, the algorithm was converted into an efficient VC++ code. In this code user is asked to enter the parameters as v, b_1, k_1, q, and ρ_1 and ρ_2 for a specified correlation structure, in the front end. These are sufficient as we incorporate the equal numbers of sub-blocks to be nested within the bigger-blocks and the given correlation structure is dependent on ρ_1 and ρ_2. The algorithm can be implemented for any type of Kronecker product correlation structure; however, the rigorous search of designs has been attempted for the correlation structure $\mathbf{I}_q \otimes \mathbf{NN}$ *i.e.* the observations have a nearest neighbour correlation structure in sub-blocks and observations between sub-blocks within blocks and between blocks are independent. Some designs have also been generated for the general correlation structures and are presented in Appendix F.3. Within the parametric restrictions v (number of treatments) ≤ 10, n (total number of experimental units) ≤ 100, k_1 (bigger block size) $< v$, b_1 (number of blocks) = n/k_1, k_2 (sub-block size) is a factor of k_1 and b_2 (number of sub-blocks) = $b_1(k_1/k_2)$, for $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure, the generated designs have the frequency distribution as given in Table F.1.

Table F.1: Summary of generated Nested block designs.

Nested-block design A-efficiency	Bigger-block design A-efficiency	Designs
0.95-0.98 (639)	0.95-0.98	229
	0.98-0.99	270
	Above 0.99	140
0.98-0.99 (1074)	0.95-0.98	139
	0.98-0.99	296
	Above 0.99	639
Above 0.99 (1182)	0.95-0.98	153
	0.98-0.99	208
	Above 0.99	821

From the designs summarized in Table F.1, 38 designs are A-optimal in both blocking systems, 96 designs are optimal in nested block set-up and not in bigger blocks and 4 designs are optimal in bigger-block set-up and not in the nested-block set up for **NN** correlation structure in sub-blocks.

The design from the algorithm is generated by using a particular value of correlation coefficient ρ_2 in $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure. The value of correlation coefficient may not be known exactly. A design which is efficient for given values of ρ_2 may not be efficient for other values of ρ_2. We have to study the behaviour of the designs that are efficient for a particular value of ρ_2, for any other value of ρ_2 in $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure. A design is said to be robust for a specific correlation structure if the percent coefficient of variation (CV) of efficiencies for different correlation values is less than 1% for both the blocking systems. However, only those designs whose lower bound to the A-efficiencies is at least 0.95 and have minimum CV of A- and D-efficiencies for other value of ρ_2 for both systems of block designs are catalogued.

We could obtain 91 such designs for $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure. Out of these 91 designs, 25 designs are equireplicated and 66 designs are un-equireplicated. In most of the unequireplicated designs, replications of the treatments differ at most by one, except in two cases where these differ by 2. All equireplicated designs are catalogued in Table F.2 of Appendix F.1 and all unequireplicated designs are catalogued in Table F.3 of Appendix F.1. The tables contain the parameters of the designs v, b_1, b_2, k_1, k_2, r or the average replication number ($\bar{r}$), ρ_2, AE_0 denotes the A-efficiency in the bigger-block and DE_0 denotes the D-efficiency in the bigger-block assuming zero correlation structure for the bigger blocks ignoring sub-block classification, AE_1 denotes the A-efficiency in the bigger-block and DE_1 denotes the D-efficiency in the bigger-block assuming $\mathbf{I}_q \otimes \mathbf{NN}$ for the bigger blocks ignoring sub-block classification, AE_2 denotes the A-efficiency in the nested-block, DE_2 denotes the D-efficiency for the nested-block design for $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure, CAN_1 denotes CVs of A-efficiencies in bigger-block design for negative ρ_2 ($-0.50 \leq \rho_2 < 0$), CAP_1 denotes CVs of A-efficiencies in bigger-block design for positive ρ_2 ($0 < \rho_2 \leq 0.50$), CAL_1 denotes CVs of A-efficiencies in bigger-block design for low ρ_2 ($-0.20 \leq \rho_2 \leq 0.20$), CA_1 denotes CVs of A-efficiencies in bigger-block design for whole range of ρ_2 except 0, and CDN_1, CDP_1, CDL_1, CD_1 denotes the same description but for D-efficiencies in bigger-block design, and CAN_2, CAP_2, CAL_2, CA_2, CDN_2, CDP_2, CDL_2, and CD_2 have the same description as earlier for nested-block design set up.

With $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure, the **C**-matrix of nested block design is same as that of a design considering sub-blocks as blocks ignoring bigger block classification with **NN** correlation structure. In this case when k_2 (sub-block size) is 2, then the **C**-matrix becomes proportional to **C**-matrix of an uncorrelated error structure (Case III, Section F.2). Therefore, for sub-block size 2, the efficiencies of all the correlation values will be same. However, when we compute efficiencies for bigger blocks ignoring sub-block classification with this correlation structure, then the efficiencies may change for different values of correlation. Therefore, such designs have also been included in Tables F.2 and F.3, respectively.

An attempt has also been made for computer aided search of efficient nested block designs with $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure that are simultaneously efficient for zero correlation structure in bigger blocks ignoring the sub-block classification. The designs obtained for this are catalogued in Table F.4 of Appendix F.2.

To illustrate that the algorithm is general in nature, we have obtained some designs for $\mathbf{NN} \otimes \mathbf{NN}$, $\mathbf{NN} \otimes \mathbf{AR(1)}$, $\mathbf{AR(1)} \otimes \mathbf{NN}$ and $\mathbf{AR(1)} \otimes \mathbf{AR(1)}$ correlation structure as well. These are presented in Tables 5, 6, 7 and 8 of Appendix 3. Efficiencies of these designs are more than 0.96 in both systems of blocks.

Nested Block Designs for Uncorrelated Error Structure

If we take $\mathbf{\Phi} = \mathbf{I}$, and $\mathbf{\Omega} = \mathbf{I}$ in the algorithm described in Section F.3, we get efficient nested block designs for independent observations. In the present investigation, this has been used for generation of nested incomplete block designs for independent observations. Within the parametric range tried, there are 13 existent NBIB designs. NBIB design with parameters v = 10, b_1 = 15, b_2 = 30, r = 9, k_1 = 6, k_2 = 3 is non-existent within the restricted parametric range. Applying the algorithm, we got 7 out of these 13 NBIB designs. These are presented in Table F.9 in Appendix F.4. For the rest 6 existent NBIB designs and 1 non-existent NBIB design, we got designs which are BIB designs in bigger-blocks and have efficiencies greater than 0.98 for the other block structure. These designs are given in Table F.10 of Appendix F.4. While emphasis was laid on sub-blocks, 4 designs are obtained which are BIB designs in sub-blocks ignoring block classification and have efficiencies more than 0.99 for block designs obtained by ignoring the sub-block classification. These designs are given in Table F.11 of Appendix F.4.

Resolvable Block Designs

Resolvable block designs are also a kind of nested block designs with set of blocks forming a complete replicate as bigger block and blocks of the resolvable block designs as sub-blocks. The algorithm has also been used for obtaining efficient resolvable BIB designs. Of course it can usefully be employed for generation of efficient resolvable block designs by taking $k_1 = v$. All resolvable BIB designs for $v \leq 10$ and $n \leq 100$ have been obtained using the algorithm.

All the nested block designs generated are available with the authors and can be available by writing a mail to rajender@iasri.res.in.

References

Banerjee, S. and Kageyama, S. (1993). Methods of constructing nested partially balanced incomplete block designs. *Utilitas Mathematica*, **43**, 3-6.

Cheng, C.S. and Wu, C.F. (1981). Nearly balanced incomplete block designs. *Biometrika*, **68**, 493-500.

Dey, A., Das, U.S. and Banerjee, A.K. (1986). On nested balanced incomplete block designs. *Cal. Statist. Assoc. Bull.*, **35** , 161-167.

Homel, R.J. and Robinson, J. (1975). Nested partially balanced incomplete block designs. *Sankhy$\bar{a}$* , **B37**, 201-210.

Jimbo, M. and Kuriki, S. (1983). Constructions of nested designs. *Ars Comb.*, **16**, 275-285.

Jones, B. and Eccleston, J.A.(1980). Exchange and interchange procedure to search for optimal design. *J. Roy. Statist. Soc.*, **B42**, 291-297.

Kageyama, S., Phillip, J. and Banerjee, S. (1995). Some constructions of nested BIB and 2-associate PBIB designs under restricted dualization. *Bull. Fac. Sch. Educ. Hiroshima Univ., Part-II*, 17, 33-39.

Martin, R.J. (1996). Spatial experimental design. *Handbook of Statistics*, **13**, S. Ghosh and C. R. Rao (Eds), 477-514. Amsterdam: North Holland.

Martin, R.J. and Eccleston, J.A. (1991). Optimal incomplete block designs for general dependence structures. *J. Statist. Plann. Inf.*, **28**, 67-81.

Martin, R.J. and Eccleston, J.A. (1992). Recursive formulae for constructing block designs with dependent errors. *Biometrika*, **76**, 426-430.

Morgan, J.P., Preece, D.A. and Rees, D.H. (2001). Nested balanced incomplete block designs. *Discrete Mathematics*, **231,** 351-389.

Preece, D.A.(1967).Nested balanced incomplete block designs. *Biometrika*, **54**, 479-486.

Pooladsaz, S. and Martin, R.J. (2005). Optimal extended complete block designs for dependent observations. *Metrika*, **61**, 185-197.

Rathore, A., Parsad, R. and Gupta, V.K. (2006). Computer aided search of efficient block designs for making all possible pairwise treatment comparisons. *Journal of Statistics and Applications*: *The Journal of the Forum of Interdisciplinary Mathematics*, **1(1),** 15-33..

Saha, G.M., Dey, A. and Midha, C.K.(1998). Construction of nested incomplete block designs. *Cal. Statist. Assoc. Bull.*, **48**, 195-205.

Satpati, S.K. and Parsad, R. (2004). Constructions and cataloguing of the Nested partially balanced incomplete block designs. *Ars Comb.*, **73**, 299-309.

Zergaw, G. (1989). A sequential method of constructing optimal block designs. *Austral. J. Statist.*, **31**, 333-342.

Appendix F.1

Table F.2: Catalogue of Robust and Efficient Equireplicated Nested Block Designs (all the designs are generated for $\rho = -0.50$)

SN	v	b_1	b_2	K_1	k_2	r	AE_0	DE_0	AE_1	DE_1	AE_2	DE_2	CAN_1	CAP_1	CAL_1	CA_1	CDN_1	CDP_1	CDL_1	CD_1	CAN_2	CAP_2	CAL_2	CA_2	CDN_2	CDP_2	CDL_2	CD_2
1	5	5	10	4	2	4	1.000	1.000	1.000	1.000	1.000	1.000	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	6	9	18	4	2	6	0.995	0.998	0.972	0.986	0.980	0.990	0.73	0.11	0.20	0.69	0.35	0.00	0.00	0.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
3	6	12	24	4	2	8	0.996	0.998	0.969	0.985	0.987	0.993	0.84	0.00	0.24	0.82	0.40	0.00	0.12	0.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
4	6	15	30	4	2	10	0.997	0.999	0.992	0.996	1.000	1.000	0.18	0.00	0.00	0.24	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
5	7	7	14	6	3	6	1.000	1.000	0.960	0.981	0.996	0.998	1.28	1.55	0.17	1.43	0.61	0.77	0.00	0.70	0.00	1.35	0.36	1.32	0.00	0.66	0.18	0.65
6	7	7	21	6	2	6	1.000	1.000	1.000	1.000	1.000	1.000	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
7	8	8	24	6	2	6	0.999	0.999	0.987	0.993	0.980	0.990	0.38	0.17	0.00	0.33	0.19	0.00	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
8	8	12	24	4	2	6	0.988	0.994	0.958	0.980	0.980	0.990	0.97	0.00	0.31	0.99	0.45	0.00	0.15	0.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
9	8	14	28	4	2	7	0.990	0.995	0.966	0.983	1.000	1.000	0.72	0.22	0.39	0.96	0.35	0.11	0.19	0.47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
10	8	16	32	4	2	8	0.995	0.998	0.983	0.992	0.988	0.994	0.45	0.00	0.14	0.45	0.22	0.00	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
11	8	18	36	4	2	9	0.996	0.998	0.980	0.990	0.984	0.992	0.52	0.00	0.13	0.48	0.26	0.00	0.00	0.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
12	8	20	40	4	2	10	0.996	0.998	0.980	0.990	0.986	0.993	0.50	0.00	0.13	0.47	0.25	0.00	0.00	0.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
13	8	22	44	4	2	11	0.992	0.996	0.978	0.989	0.990	0.995	0.69	0.00	0.25	0.74	0.33	0.00	0.12	0.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
14	8	16	32	6	3	12	0.999	1.000	0.972	0.985	0.999	0.999	0.86	0.71	0.14	0.81	0.44	0.35	0.00	0.41	0.00	0.55	0.15	0.55	0.00	0.26	0.00	0.27
15	8	16	48	6	2	12	0.999	1.000	0.995	0.997	0.992	0.996	0.15	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
16	8	24	48	4	2	12	0.996	0.998	0.977	0.989	0.992	0.996	0.58	0.00	0.20	0.61	0.28	0.00	0.00	0.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
17	9	9	27	6	2	6	0.998	0.999	0.983	0.992	0.970	0.984	0.49	0.30	0.00	0.41	0.24	0.16	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
18	9	12	36	6	2	8	0.998	0.999	0.995	0.998	1.000	1.000	0.00	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
19	9	18	36	4	2	8	0.992	0.996	0.974	0.987	1.000	1.000	0.56	0.17	0.30	0.75	0.27	0.00	0.15	0.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
20	9	15	30	6	3	10	0.998	0.999	0.967	0.983	0.998	0.999	1.01	1.54	0.16	1.32	0.50	0.78	0.00	0.67	0.00	1.25	0.33	1.22	0.00	0.63	0.17	0.62
21	9	15	45	6	2	10	0.998	0.999	0.990	0.995	0.986	0.993	0.25	0.00	0.00	0.22	0.12	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
22	10	10	20	6	3	6	0.994	0.997	0.893	0.949	0.992	0.996	3.29	2.65	0.36	3.00	1.55	1.40	0.18	1.48	0.13	2.22	0.65	2.23	0.00	1.16	0.33	1.16
23	10	10	30	6	2	6	0.995	0.998	0.960	0.980	0.954	0.976	1.11	0.34	0.24	0.98	0.54	0.18	0.12	0.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
24	10	10	40	8	2	8	1.000	1.000	0.995	0.997	0.988	0.994	0.15	0.11	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
25	10	10	30	9	3	9	1.000	1.000	0.967	0.984	0.995	0.998	1.06	1.60	0.16	1.37	0.52	0.80	0.00	0.69	0.00	1.33	0.36	1.32	0.00	0.66	0.18	0.66
26	10	15	45	6	2	9	0.997	0.998	0.991	0.996	1.000	1.000	0.17	0.00	0.11	0.25	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

*Subscript 0 is for the bigger block design for zero correlation structure, and Subscript 1 is for bigger-block designs, and Subscript 2 is for NIB designs with. $\mathbf{I}_q \otimes \mathbf{NN}$ correlation structure; **AE** is the A-efficiency, **DE** is for D-efficiency, **CAN** denotes CV of **AE** for (−)ve correlations, **CAP** denotes CV of **AE** for (+)ve correlations, **CAL** denotes CV of **AE** for low-correlations [−0.20, 0.20], **CA** denotes CV of **AE**, **CDN** denotes CV of **DE** for (−)ve correlations, **CDP** denotes CV of **DE** for (+)ve correlations, **CDL** denotes CV of **DE** for low-correlations [−0.20, 0.20], **CD** denotes CV of **DE**.

Table F.3: Catalogue of Robust and Efficient Unequireplicated Nested Block Designs (all the designs are generated for ρ = – 0.50)

SN	v	b_1	b_2	k_1	k_2	$\bar{r}$	AE_0	DE_0	AE_1	DE_1	AE_2	DE_2	CAN_1	CAP_1	CAL_1	CA_1	CDN_1	CDP_1	CDL_1	CD_1	CAN_2	CAP_2	CAL_2	CA_2	CDN_2	CDP_2	CDL_2	CD_2
1	5	6	12	4	2	4.8	0.990	0.995	0.980	0.990	0.972	0.986	0.30	0.18	0.00	0.25	0.16	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	5	7	14	4	2	5.6	0.989	0.995	0.977	0.988	0.969	0.984	0.40	0.22	0.00	0.34	0.21	0.11	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
3	6	8	16	4	2	5.3	0.985	0.992	0.974	0.987	0.987	0.993	0.35	0.00	0.17	0.43	0.17	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
4	6	10	20	4	2	6.7	0.989	0.994	0.956	0.979	0.975	0.987	1.03	0.00	0.30	1.02	0.49	0.00	0.15	0.49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
5	6	11	22	4	2	7.3	0.994	0.997	0.985	0.992	0.978	0.989	0.28	0.17	0.00	0.23	0.14	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
6	6	13	26	4	2	8.7	0.994	0.997	0.989	0.994	0.986	0.993	0.17	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
7	6	14	28	4	2	9.3	0.995	0.998	0.992	0.996	0.992	0.996	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
8	6	16	32	4	2	10.7	0.995	0.998	0.988	0.994	0.994	0.997	0.21	0.00	0.00	0.24	0.11	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
9	6	17	34	4	2	11.3	0.997	0.998	0.994	0.997	0.992	0.996	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
10	7	6	18	6	2	5.1	0.995	0.997	0.991	0.996	0.972	0.986	0.37	0.23	0.00	0.32	0.18	0.11	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
11	7	8	24	6	2	6.9	0.997	0.998	0.992	0.996	0.984	0.992	0.16	0.11	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
12	7	9	18	4	2	5.1	0.989	0.994	0.961	0.981	0.972	0.986	0.88	0.13	0.22	0.82	0.43	0.00	0.11	0.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
13	7	9	18	6	3	7.7	0.996	0.998	0.953	0.975	0.996	0.998	1.40	2.05	0.24	1.79	0.72	1.04	0.12	0.91	0.23	2.11	0.69	2.22	0.11	1.05	0.34	1.11
14	7	9	27	6	2	7.7	0.996	0.998	0.989	0.994	0.979	0.990	0.23	0.16	0.00	0.20	0.12	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
15	7	10	20	6	3	8.6	0.996	0.998	0.951	0.975	0.998	0.999	1.46	2.21	0.25	1.92	0.73	1.07	0.12	0.94	0.25	2.54	0.76	2.60	0.13	1.21	0.37	1.26
16	7	10	30	6	2	8.6	0.996	0.998	0.989	0.994	0.981	0.990	0.23	0.15	0.00	0.20	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
17	7	11	22	4	2	6.3	0.997	0.998	0.970	0.985	0.991	0.995	0.46	0.14	0.25	0.61	0.21	0.00	0.12	0.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
18	7	11	33	6	2	9.4	0.997	0.998	0.990	0.995	0.985	0.992	0.21	0.12	0.00	0.17	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
19	8	7	21	6	2	5.3	0.991	0.995	0.958	0.981	0.955	0.977	1.06	0.34	0.19	0.91	0.47	0.17	0.00	0.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
20	8	9	18	4	2	4.5	0.967	0.984	0.900	0.952	0.927	0.962	2.22	0.37	0.45	1.96	1.02	0.20	0.21	0.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
21	8	9	27	6	2	6.8	0.994	0.997	0.989	0.995	0.981	0.991	0.16	0.12	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
22	8	10	30	6	2	7.5	0.994	0.997	0.990	0.995	0.990	0.995	0.11	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
23	8	11	33	6	2	8.3	0.996	0.998	0.991	0.995	0.985	0.992	0.17	0.10	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
24	8	12	36	6	2	9.0	0.996	0.998	0.989	0.995	0.982	0.991	0.20	0.13	0.00	0.17	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
25	8	13	39	6	2	9.8	0.997	0.998	0.989	0.995	0.983	0.992	0.24	0.12	0.00	0.20	0.12	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
26	8	14	28	6	3	10.5	0.997	0.998	0.958	0.978	0.999	0.999	1.26	1.47	0.18	1.38	0.63	0.75	0.00	0.70	0.19	1.54	0.53	1.66	0.00	0.79	0.27	0.85
27	8	14	42	6	2	10.5	0.997	0.998	0.990	0.995	0.986	0.993	0.21	0.11	0.00	0.18	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
28	8	15	30	4	2	7.5	0.984	0.992	0.957	0.979	0.990	0.995	0.86	0.18	0.40	1.05	0.41	0.00	0.19	0.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
29	8	15	30	6	3	11.3	0.997	0.999	0.970	0.985	0.999	0.999	0.85	1.06	0.11	0.97	0.43	0.53	0.00	0.48	0.00	1.14	0.35	1.17	0.00	0.57	0.17	0.58
30	8	15	45	6	2	11.3	0.997	0.999	0.989	0.995	0.988	0.994	0.25	0.00	0.00	0.22	0.12	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
31	8	17	34	4	2	8.5	0.986	0.993	0.953	0.977	0.983	0.991	1.04	0.10	0.41	1.16	0.50	0.00	0.20	0.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
32	8	19	38	4	2	9.5	0.988	0.994	0.954	0.977	0.983	0.991	1.07	0.00	0.39	1.14	0.52	0.00	0.19	0.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
33	8	21	42	4	2	10.5	0.992	0.996	0.972	0.986	0.985	0.992	0.63	0.00	0.20	0.64	0.31	0.00	0.00	0.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
34	8	23	46	4	2	11.5	0.992	0.996	0.975	0.988	0.988	0.994	0.63	0.00	0.22	0.67	0.31	0.00	0.11	0.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

SN	v	b_1	b_2	k_1	k_2	$\bar{r}$	AE_0	DE_0	AE_1	DE_1	AE_2	DE_2	CAN_1	CAP_1	CAL_1	CA_1	CDN_1	CDP_1	CDL_1	CD_1	CAN_2	CAP_2	CAL_2	CA_2	CDN_2	CDP_2	CDL_2	CD_2
35	9	8	24	6	2	5.3	0.985	0.992	0.959	0.980	0.945	0.971	0.86	0.40	0.12	0.72	0.41	0.21	0.00	0.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
36	9	10	30	6	2	6.7	0.990	0.995	0.976	0.989	0.972	0.986	0.45	0.16	0.00	0.40	0.21	0.00	0.00	0.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
37	9	11	22	6	3	7.3	0.992	0.996	0.944	0.972	0.994	0.997	1.55	1.96	0.21	1.78	0.76	0.98	0.11	0.89	0.11	2.24	0.61	2.20	0.00	1.11	0.30	1.10
38	9	11	33	6	2	7.3	0.985	0.993	0.997	0.992	0.985	0.993	0.26	0.00	0.00	0.25	0.13	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
39	9	11	44	8	2	9.8	0.993	0.998	0.999	0.997	0.985	0.993	0.15	0.11	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
40	9	12	48	8	2	10.7	0.998	0.999	0.993	0.996	0.985	0.992	0.16	0.12	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
41	9	13	39	6	2	8.7	0.994	0.997	0.987	0.993	0.991	0.995	0.24	0.00	0.00	0.26	0.12	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
42	9	14	28	6	3	9.3	0.996	0.998	0.960	0.979	0.998	0.999	1.17	1.88	0.20	1.61	0.60	0.95	0.10	0.81	0.18	1.90	0.60	1.98	0.00	0.96	0.30	1.01
43	9	14	42	6	2	9.3	0.996	0.998	0.989	0.994	0.987	0.993	0.23	0.00	0.00	0.21	0.12	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
44	9	15	30	4	2	6.7	0.985	0.993	0.971	0.985	0.972	0.986	0.47	0.12	0.10	0.42	0.24	0.00	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
45	9	16	32	4	2	7.1	0.986	0.993	0.971	0.985	0.984	0.992	0.70	0.00	0.28	0.79	0.35	0.00	0.14	0.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
46	9	16	32	6	3	10.7	0.995	0.998	0.954	0.977	0.998	0.999	1.34	1.93	0.22	1.70	0.67	0.95	0.11	0.84	0.14	1.94	0.55	1.95	0.00	0.95	0.28	0.97
47	9	16	48	6	2	10.7	0.996	0.998	0.992	0.996	0.985	0.992	0.14	0.11	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
48	9	17	34	4	2	7.6	0.985	0.992	0.963	0.982	0.988	0.994	0.67	0.13	0.31	0.81	0.31	0.00	0.15	0.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
49	9	19	38	4	2	8.4	0.989	0.995	0.975	0.988	0.992	0.996	0.43	0.10	0.21	0.55	0.21	0.00	0.10	0.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
50	9	20	40	4	2	8.9	0.990	0.995	0.97	0.986	0.990	0.995	0.59	0.00	0.26	0.70	0.29	0.00	0.13	0.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
51	9	21	42	4	2	9.3	0.991	0.995	0.967	0.983	0.987	0.993	0.75	0.00	0.28	0.82	0.37	0.00	0.14	0.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
52	9	22	44	4	2	9.8	0.991	0.995	0.975	0.988	0.985	0.993	0.49	0.00	0.17	0.51	0.24	0.00	0.00	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
53	9	23	46	4	2	10.2	0.991	0.996	0.968	0.984	0.985	0.992	0.72	0.00	0.26	0.77	0.36	0.00	0.13	0.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
54	9	24	48	4	2	10.7	0.990	0.995	0.96	0.981	0.985	0.992	0.93	0.00	0.33	0.99	0.44	0.00	0.16	0.47	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
55	9	25	50	4	2	11.1	0.995	0.997	0.976	0.988	0.986	0.993	0.60	0.00	0.18	0.59	0.29	0.00	0.00	0.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
56	10	8	32	8	2	6.4	0.993	0.996	0.975	0.988	0.958	0.978	0.58	0.34	0.00	0.49	0.27	0.17	0.00	0.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
57	10	9	36	8	2	7.2	0.996	0.998	0.988	0.994	0.973	0.986	0.28	0.22	0.00	0.25	0.14	0.11	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
58	10	9	27	9	3	8.1	0.999	0.999	0.966	0.983	0.995	0.998	1.06	1.78	0.18	1.49	0.52	0.89	0.00	0.75	0.10	1.58	0.45	1.58	0.00	0.80	0.23	0.81
59	10	11	33	6	2	6.6	0.989	0.995	0.975	0.988	0.962	0.980	0.55	0.26	0.00	0.46	0.26	0.14	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
60	10	11	44	8	2	8.8	0.997	0.998	0.993	0.997	0.991	0.995	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
61	10	11	33	9	3	9.9	0.999	0.999	0.963	0.982	0.996	0.998	1.15	1.82	0.18	1.55	0.56	0.89	0.00	0.76	0.14	1.70	0.49	1.72	0.00	0.81	0.24	0.83
62	10	12	36	6	2	7.2	0.991	0.996	0.979	0.989	0.974	0.987	0.40	0.15	0.00	0.35	0.20	0.00	0.00	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
63	10	12	48	8	2	9.6	0.997	0.998	0.995	0.998	0.993	0.996	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
64	10	13	39	6	2	7.8	0.993	0.997	0.983	0.992	0.982	0.991	0.32	0.00	0.00	0.29	0.15	0.00	0.00	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
65	10	14	42	6	2	8.4	0.994	0.997	0.988	0.994	0.989	0.995	0.21	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
66	10	16	32	6	3	9.6	0.994	0.997	0.959	0.979	0.998	0.999	1.15	1.47	0.17	1.33	0.59	0.75	0.00	0.68	0.16	1.68	0.54	1.76	0.00	0.85	0.27	0.89

*Subscript 0 is for the bigger block design for zero correlation structure, and Subscript 1 is for bigger-block designs, and Subscript 2 is for NIB designs with. $\mathbf{I}_q \otimes$ **NN** correlation structure; **AE** is the A-efficiency, **DE** is for D-efficiency, **CAN** denotes CV of **AE** for (−)ve correlations, **CAP** denotes CV of **AE** for (+)ve correlations, **CAL** denotes CV of **AE** for low-correlations [−0.20, 0.20], **CA** denotes CV of **AE**, **CDN** denotes CV of **DE** for (−)ve correlations, **CDP** denotes CV of **DE** for (+)ve correlations, **CDL** denotes CV of **DE** for low-correlations [−0.20, 0.20], **CD** denotes CV of **DE**.

Appendix F.2

Table F.4: Catalogue of Robust and Equireplicated Efficient Nested Block Designs for Correlation Structure of type $I_q \otimes NN$ for Sub-Blocks and Zero Correlation Structure for the Bigger-Block (all the designs are generated for $\rho = -0.50$)

SN	v	b_1	b_2	k_1	k_2	r	AE_0	DE_0	AE_2	DE_2	CAN_2	CAP_2	CAL_2	CA_2	CDN_2	CDP_2	CDL_2	CD_2
1	7	7	14	6	3	6	0.990	0.995	0.986	0.993	0.14	3.31	0.86	3.20	0.00	1.67	0.44	1.63
2	7	9	18	6	3	7.8	0.996	0.998	0.995	0.997	0.23	1.77	0.63	1.93	0.12	0.91	0.32	0.99
3	8	14	28	6	3	10.5	0.997	0.998	0.996	0.998	0.13	1.44	0.43	1.47	0.00	0.71	0.22	0.74
4	8	15	30	6	3	11.2	0.998	0.999	0.997	0.999	0.00	1.23	0.36	1.24	0.00	0.62	0.18	0.63
5	8	16	32	6	3	12.0	0.998	0.999	0.998	0.999	0.12	1.48	0.45	1.52	0.00	0.75	0.23	0.77
6	9	11	22	6	3	7.3	0.995	0.997	0.992	0.996	0.19	2.19	0.66	2.24	0.00	1.07	0.33	1.11
7	9	14	28	6	3	9.3	0.997	0.998	0.994	0.997	0.20	1.84	0.60	1.94	0.00	0.93	0.30	0.98
8	9	15	30	6	3	10.0	0.997	0.998	0.996	0.998	0.17	2.26	0.64	2.27	0.00	1.10	0.32	1.12
9	10	9	27	9	3	8.1	0.999	0.999	0.990	0.995	0.12	1.96	0.55	1.96	0.00	0.97	0.28	0.98
10	10	10	20	6	3	6	0.997	0.998	0.985	0.993	0.00	2.26	0.57	2.17	0.00	1.12	0.28	1.09

Appendix F.3

Table F.5: Designs for NN between Sub-Blocks and NN within Sub-Blocks

SN	v	b_1	b_2	k_1	k_2	$\bar{r}$	ρ_1	ρ_2	AE_1	DE_1	AE_2	DE_2
1	7	7	14	6	3	6	0.25	0.25	0.9627	0.9817	0.9978	0.9989
[(6,0,2);(1,4,5)]; [(0,5,6);(3,2,4)]; [(5,0,2);(3,1,4)]; [(6,5,1);(2,4,3)]; [(2,3,0);(1,4,6)]; [(1,3,5);(2,6,0)]; [(3,6,4);(5,1,0)].												
2	8	8	16	6	3	6	0.25	0.25	0.9645	0.9832	0.9987	0.9994
[(3,2,4);(0,1,7)]; [(2,7,6);(4,0,5)]; [(1,6,2);(5,3,0)]; [(2,1,3);(0,6,7)]; [(4,6,2);(1,0,5)]; [(4,5,7);(6,3,1)]; [(5,4,0);(6,3,7)]; [(5,7,2);(1,4,3)].												
3	9	9	18	8	4	8	0.50	0.50	0.9841	0.9920	0.9981	0.9940
[(5,8,2,4);(3,6,7,1)]; [(4,5,1,8);(3,0,2,6)]; [(8,4,0,2);(5,3,7,6)]; [(6,4,3,2);(5,1,0,7)]; [(0,6,8,4);(3,1,7,2)]; [(6,1,4,7);(5,8,0,3)]; [(3,1,0,4);(8,7,5,2)]; [(6,0,5,4);(3,8,2,7)]; [(2,5,7,4);(1,6,3,8)].												
4	10	15	30	6	3	9	0.50	0.50	0.9755	0.9883	0.9955	0.9977
[(7,9,2);(6,4,1)]; [(8,2,4);(0,9,3)]; [(8,1,5);(9,6,7)]; [(4,3,6);(8,2,5)]; [(4,9,1);(7,3,5)]; [(5,8,9);(0,2,4)]; [(3,7,9);(1,6,5)]; [(3,9,6);(0,1,4)]; [(4,0,3);(5,9,8)]; [(0,2,3);(5,7,4)]; [(1,7,8);(6,2,5)]; [(7,0,4);(8,6,2)]; [(6,0,1);(4,8,3)]; [(8,5,2);(0,7,1)]; [(8,6,5);(1,3,0)].												

*Subscript 1 is for bigger-block designs, and Subscript 2 is for nested block designs.

Table F.6: Designs for NN between Sub-Blocks and AR(1) within Sub-Blocks

SN	v	b_1	b_2	k_1	k_2	$\bar{r}$	ρ_1	ρ_2	AE_1	DE_1	AE_2	DE_2
1	7	7	14	6	3	6	0.25	0.25	0.9835	0.9916	0.9877	0.9833
	[(4,3,6);(0,5,2)]; [(0,2,4);(1,5,6)]; [(6,5,4);(0,3,1)]; [(6,1,2);(0,5,4)]; [(1,3,0);(2,6,4)]; [(4,5,1);(3,2,0)]; [(2,3,4);(0,6,1)].											
2	8	8	16	6	3	6	0.25	0.25	0.9640	0.9825	0.9946	0.9973
	[(0,5,7);(2,6,4)]; [(5,2,7);(1,3,0)]; [(6,7,2);(0,3,1)] [(4,2,3);(0,1,5)]; [(0,6,3);(7,1,4)]; [(5,4,0);(3,6,1)]; [(5,7,1);(2,3,4)]; [(4,5,0);(7,6,2)].											
3	9	9	18	8	4	8	0.50	0.50	0.9924	0.9962	0.9957	0.9978
	[(3,1,5,8);(7,4,0,2)]; [(4,6,0,2);(5,1,3,7)]; [(8,5,3,0);(2,6,7,1)]; [(0,8,7,1);(5,6,4,3)]; [(3,5,7,2);(6,4,8,1)]; [(4,2,1,6);(8,3,0,7)]; [(0,4,5,2);(7,1,8,6)]; [(8,3,4,2);(0,6,7,5)]; [(3,2,5,1);(4,8,6,0)].											
4	10	15	30	6	3	9	0.50	0.50	0.9925	0.9962	0.9950	0.9975
	[(3,9,5);(7,6,1)]; [(7,8,4);(2,3,9)]; [(7,1,9);(5,4,3)]; [(5,9,4);(1,2,3)]; [(2,9,8);(4,0,6)]; [(5,6,2);(7,0,8)]; [(4,1,6);(3,0,2)]; [(0,1,3);(7,9,6)]; [(3,8,2);(6,5,0)]; [(6,5,3);(4,2,1)]; [(2,5,1);(8,4,9)]; [(8,5,7);(6,2,4)]; [(8,9,0);(1,7,4)]; [(6,7,3);(8,0,5)]; [(7,8,1);(2,0,3)].											

Table F.7: Designs for AR(1) between Sub-Blocks and AR(1) within Sub-Blocks

SN	v	b_1	b_2	k_1	k_2	$\bar{r}$	ρ_1	ρ_2	AE_1	DE_1	AE_2	DE_2
1	7	7	14	6	3	6	0.25	0.25	0.9828	0.9914	0.9828	0.9864
	[(2,5,0);(4,6,3)]; [(3,5,1);(4,0,6)]; [(6,5,2);(3,1,0)]; [(2,3,1);(4,5,6)]; [(3,5,0);(2,4,1)]; [(6,2,1);(4,0,3)]; [(3,2,6);(4,1,0)].											
2	8	8	16	6	3	6	0.25	0.25	0.9696	0.9852	0.9940	0.9970
	[(3,4,5);(0,2,7)]; [(3,2,5);(7,0,1)]; [(3,7,2);(6,4,1)]; [(6,2,5);(1,7,0)]; [(1,4,2);(0,5,6)]; [(6,7,1);(0,4,3)]; [(3,1,5);(0,4,6)]; [(7,6,1);(5,3,2)].											
3	9	9	18	8	4	8	0.50	0.50	0.9827	0.9915	0.9926	0.9963
	[(4,5,8,3);(6,0,7,1)]; [(5,6,3,7);(1,2,0,4)]; [(6,8,7,3);(2,5,1,4)]; [(5,2,0,6);(4,8,1,3)]; [(3,4,8,1);(2,7,0,6)]; [(6,7,5,8);(1,0,3,4)]; [(0,2,4,1);(5,7,6,8)]; [(4,7,5,6);(0,3,2,1)]; [(1,0,4,5);(3,8,2,6)].											
4	10	15	30	6	3	9	0.50	0.50	0.9901	0.9951	0.9948	0.9974
	[(4,8,1);(7,2,6)]; [(1,3,0);(9,7,8)]; [(4,2,0);(3,8,5)]; [(5,9,7);(4,3,6)]; [(1,2,9);(4,8,6)]; [(7,1,9);(0,3,5)]; [(2,9,4);(3,8,6)]; [(0,8,4);(2,5,1)]; [(7,4,0);(1,5,6)]; [(8,1,2);(9,6,3)]; [(5,3,7);(0,9,6)]; [(5,6,2);(7,8,0)]; [(5,9,0);(7,3,1)]; [(2,6,4);(5,0,1)]; [(7,2,1);(0,4,9)].											

Table F.8: Designs for AR(1) between Sub-Blocks and NN within Sub-Blocks

SN	v	b_1	b_2	k_1	k_2	$\bar{r}$	ρ_1	ρ_2	AE_1	DE_1	AE_2	DE_2
1	7	7	14	6	3	6	0.25	0.25	0.9861	0.9880	0.9941	0.9971
	[(2,0,3);(4,6,5)]; [(2,1,0);(3,4,5)]; [(2,6,4);(5,1,0)]; [(0,3,5);(4,1,6)]; [(5,1,6);(4,2,3)]; [(3,4,2);(6,0,5)]; [(5,1,3);(0,2,6)].											
2	8	8	16	6	3	6	0.25	0.25	0.9769	0.9883	0.9814	0.9903
	[(7,5,1);(4,0,2)]; [(2,6,4);(7,3,1)]; [(2,0,7);(4,6,1)]; [(2,6,1);(7,5,4)]; [(5,6,7);(3,0,1)]; [(6,3,5);(7,0,1)]; [(2,4,3);(5,0,1)]; [(4,3,7);(5,2,1)].											
3	9	9	18	8	4	8	0.50	0.50	0.9845	0.9924	0.9873	0.9937
	[(0,7,3,8);(2,5,1,6)]; [(7,6,5,0);(8,4,2,1)]; [(8,6,4,7);(1,0,5,3)]; [(1,4,3,6);(5,8,0,7)]; [(7,2,0,3);(8,1,5,6)]; [(2,4,0,6);(3,7,1,8)]; [(6,2,5,4);(3,8,7,1)]; [(7,1,6,5);(0,3,2,8)]; [(8,3,4,1);(7,2,0,6)].											
4	10	15	30	6	3	9	0.50	0.50	0.9773	0.9889	0.9948	0.9974
	[(0,1,9);(6,7,5)]; [(1,7,8);(4,9,0)]; [(5,4,6);(1,7,0)]; [(2,7,0);(3,8,1)]; [(0,3,6);(2,8,1)]; [(6,9,8);(4,3,2)]; [(4,9,5);(0,8,6)]; [(4,8,1);(2,6,3)]; [(0,3,1);(2,7,9)]; [(4,5,6);(2,3,7)]; [(3,5,4);(1,2,9)]; [(9,5,1);(2,8,6)]; [(2,5,6);(9,0,4)]; [(0,7,4);(8,5,2)]; [(0,4,1);(6,3,9)]											

*Subscript 1 is for bigger-block designs, and Subscript 2 is for nested block designs.

Appendix F.4

Table F.9: NBIB Designs Generated from the Computer Algorithm for $v \leq 10$, $b_1 \leq 33$ and $k_1 < \min(10, v)$

SN	v	b_1	b_2	k_1	k_2	r	Block Diagram
1	5	5	10	4	2	4	[(4,0);(3,1)]; [(0,3);(1,2)]; [(4,2);(0,1)];[(2,3);(1,4)]; [(2,0);(3,4)].
2	6	15	30	4	2	10	[(0,3);(5,4)]; [(2,4);(5,0)]; [(5,4);(2,3)]; [(4,3);(1,0)]; [(4,2);(5,1)]; [(2,5);(0,3)]; [(4,3);(0,2)]; [(0,4);(1,5)]; [(1,3);(0,5)]; [(2,5);(1,0)]; [(2,1);(5,3)]; [(3,5);(1,4)]; [(2,3);(1,4)]; [(4,0);(2,1)]; [(2,0);(1,3)].
3	7	7	14	6	3	6	[(6,3,4);(2,1,0)]; [(3,1,5);(6,2,0)]; [(3,1,2);(0,4,5)]; [(5,1,6);(4,3,2)]; [(2,6,5);(1,4,0)]; [(6,4,1);(3,5,0)]; [(4,5,2);(0,6,3)].
4	7	7	21	6	2	6	[(3,1);(0,6);(2,4)]; [(3,5);(2,0);(4,6)]; [(3,0);(5,6);(1,4)]; [(0,1);(4,3);(2,5)]; [(4,5);(1,2);(6,3)]; [(0,4);(5,1);(2,6)]; [(2,3);(1,6);(5,0)].
5	7	21	42	4	2	12	[(1,3);(2,4)]; [(3,2);(5,6)]; [(5,1);(4,6)]; [(1,0);(2,5)]; [(4,1);(2,0)]; [(4,5);(6,0)]; [(5,1);(0,4)]; [(1,4);(3,5)]; [(4,5);(0,3)]; [(0,2);(4,6)]; [(2,1);(0,3)]; [(2,6);(3,4)]; [(1,6);(3,4)]; [(4,2);(3,5)]; [(3,6);(0,5)]; [(2,3);(5,0)]; [(6,2);(4,0)]; [(3,1);(0,6)]; [(1,0);(3,6)]; [(5,6);(2,1)]; [(2,5);(6,1)].
6	9	9	36	8	2	8	[(5,4);(3,8);(6,1);(2,7)]; [(4,0);(5,7);(1,2);(6,8)]; [(5,6);(7,1);(8,0);(2,3)]; [(5,3);(8,7);(6,0);(4,1)]; [(2,5);(4,6);(3,1);(7,0)]; [(3,6);(8,2);(7,4);(5,0)]; [(1,0);(2,4);(8,5);(3,7)]; [(6,2);(0,3);(8,4);(1,5)]; [(3,4);(0,2);(8,1);(7,6)].
7	9	12	36	6	2	8	[(1,0);(4,5);(2,6)]; [(6,4);(3,1);(2,7)]; [(4,3);(6,5);(0,7)]; [(3,5);(6,8);(2,4)]; [(7,5);(8,4);(0,2)]; [(4,1);(7,3);(5,8)]; [(8,0);(3,6);(5,1)]; [(0,6);(4,7);(1,8)]; [(7,1);(3,2);(5,0)]; [(6,7);(8,2);(3,0)]; [(7,8);(2,5);(6,1)]; [(0,4);(8,3);(1,2)].

Table F.10: Nested Block Designs Generated that are BIB Designs in Bigger-blocks and Their A-Efficiencies (AE) and D-Efficiencies (DE) in Sub-blocks

SN	v	b_1	b_2	k_1	k_2	r	AE	DE	Block Diagram
1	8	14	28	4	2	7	0.9813	0.9908	[(3,7);(2,1)]; [(5,4);(7,0)]; [(5,3);(4,2)]; [(4,0);(3,6)]; [(2,6);(7,4)]; [(1,4);(2,0)][(5,3);(6,7)]; [(4,3);(7,1)]; [(1,0);(7,5)]; [(5,0);(2,3)]; [(2,5);(1,6)]; [(5,1);(6,4)];[(0,6);(2,7)]; [(1,6);(0,3)].
2	9	9	18	8	4	8	0.9961	0.9980	[(1,0,7,3);(4,5,8,2)]; [(0,8,7,3);(5,4,1,6)]; [(3,5,0,4);(1,6,2,7)]; [(1,8,3,6);(0,2,7,4)]; [(5,3,6,7);(0,2,1,8)]; [(3,2,5,1);(6,7,4,8)]; [(6,8,0,5);(7,3,4,2)]; [(1,4,3,8);(6,0,5,2)]; [(7,8,5,2);(0,4,1,6)].
3	9	12	24	6	3	8	0.9953	0.9977	[(2,5,4);(3,1,6)]; [(7,6,3);(4,1,8)]; [(0,2,7);(3,5,1)]; [(2,8,3);(4,7,5)]; [(3,0,4);(1,8,2)]; [(7,1,0);(4,6,2)]; [(1,7,2);(5,8,6)]; [(8,0,5);(6,2,4)]; [(6,5,0);(3,4,7)]; [(0,4,8);(7,1,5)]; [(8,7,6);(0,3,2)]; [(8,3,5);(1,0,6)].
4	9	18	36	4	2	8	0.9811	0.9906	[(3,0);(5,1)]; [(0,6);(7,3)]; [(8,1);(7,0)]; [(4,6);(5,8)]; [(2,6);(0,8)]; [(7,4);(6,3)]; [(2,4);(0,1)]; [(1,3);(4,8)]; [(7,6);(1,2)]; [(6,8);(1,3)]; [(5,3);(2,7)]; [(2,5);(3,8)]; [(7,8);(5,0)]; [(4,0);(6,5)]; [(7,1);(4,5)]; [(2,5);(1,6)]; [(0,2);(4,3)]; [(2,8);(7,4)].
5	10	10	30	9	3	9	0.9967	0.9983	[(1,7,3);(5,4,0);(8,6,2)]; [(3,2,7);(0,4,1);(9,6,8)]; [(7,6,0);(3,2,9);(1,5,8)]; [(6,3,5);(2,4,1);(7,9,8)]; [(2,6,5);(9,3,0);(7,8,4)]; [(1,0,6);(7,5,9);(3,4,8)]; [(4,6,3);(7,5,0);(9,1,2)]; [(8,0,3);(4,2,7);(9,1,5)]; [(6,4,9);(8,0,2);(3,5,1)]; [(7,1,6);(4,5,8);(9,2,0)].
*6	10	15	30	6	3	9	0.9956	0.9978	[(7,5,4);(1,6,2)]; [(2,7,4);(0,1,9)]; [(6,3,5);(9,7,2)]; [(1,6,2);(9,4,8)]; [(8,4,0);(9,7,5)]; [(2,8,0);(1,3,7)]; [(0,3,2);(6,8,4)]; [(5,0,1);(9,6,8)]; [(6,5,3);(1,4,0)]; [(4,6,9);(3,8,7)]; [(8,2,5);(7,6,0)]; [(0,9,5);(4,3,2)]; [(4,3,5);(8,7,1)]; [(3,9,2);(1,8,5)]; [(6,7,0);(9,1,3)].
7	10	15	45	6	2	9	0.9908	0.9955	[(0,5);(4,9);(8,3)]; [(0,7);(8,9);(2,6)]; [(6,3);(0,1);(4,9)]; [(1,5);(0,2);(6,4)]; [(9,7);(4,8);(6,1)]; [(3,5);(6,8);(1,2)]; [(6,0);(2,7);(3,4)]; [(8,2);(4,1);(7,3)]; [(7,6);(1,3);(9,5)]; [(9,0);(1,8);(2,3)]; [(7,4);(5,2);(3,9)]; [(2,9);(0,1);(7,5)]; [(8,0);(7,1);(5,4)]; [(9,6);(8,5);(2,4)]; [(5,6);(3,0);(7,8)].

*denotes the non-existent NBIB design

Table F.11: Nested Block Designs that are BIB Designs in Sub-blocks and their Efficiencies in Bigger-blocks

SN	v	b_1	b_2	k_1	k_2	r	AE	DE	Block Diagram
1	8	14	28	4	2	7	0.9980	0.9990	[(1,0);(4,6)]; [(6,7);(4,5)]; [(5,3);(0,4)]; [(2,5);(1,4)]; [(3,1);(5,0)]; [(3,4);(1,2)]; [(3,2);(6,1)]; [(7,4);(6,3)]; [(5,6);(2,0)]; [(3,7);(5,1)]; [(2,4);(0,7)]; [(6,0);(1,7)]; [(7,5);(6,2)]; [(0,3);(7,2)].
2	9	18	36	4	2	8	0.9966	0.9983	[(5,3);(4,6)]; [(7,1);(5,6)]; [(2,8);(0,4)]; [(5,8);(1,0)]; [(0,6);(3,7)]; [(2,1);(8,7)]; [(7,5);(8,3)]; [(7,2);(5,4)]; [(2,4);(3,1)]; [(8,0);(6,2)]; [(1,8);(4,3)]; [(6,1);(3,0)]; [(0,5);(7,4)]; [(8,6);(1,4)]; [(3,2);(0,7)]; [(0,2);(5,1)]; [(6,7);(8,4)]; [(3,6);(5,2)].
*3	10	15	30	6	3	9	0.9959	0.9980	[(9,0,5);(2,8,6)]; [(0,3,6);(8,5,7)]; [(7,3,9);(4,0,2)]; [(2,8,9);(0,5,1)]; [(9,8,1);(3,4,7)]; [(9,5,3);(8,4,1)]; [(6,1,3);(5,7,4)]; [(2,9,0);(4,3,8)]; [(6,0,7);(5,2,4)]; [(9,1,7);(3,5,2)]; [(1,6,5);(7,8,0)]; [(1,2,7);(8,6,5)]; [(1,2,3);(6,4,9)]; [(8,3,0);(6,4,9)]; [(7,2,6);(0,4,1)].
4	10	15	45	6	2	9	0.9986	0.9993	[(8,2);(0,9);(4,6)]; [(2,6);(7,8);(5,0)]; [(0,8);(1,2);(7,4)]; [(7,1);(6,3);(2,0)]; [(8,4);(6,9);(3,7)]; [(2,5);(4,9);(1,6)]; [(9,7);(6,5);(0,3)]; [(8,6);(0,1);(9,3)]; [(0,7);(5,9);(1,8)]; [(9,8);(7,2);(1,3)]; [(5,8);(7,6);(1,4)]; [(4,2);(5,3);(6,0)]; [(7,5);(4,3);(2,9)]; [(2,3);(5,1);(0,4)]; [(1,9);(4,5);(8,3)].

*denotes the non-existent NBIB design

G) Doubly Nested Partially Balanced Incomplete Block Designs

G.1 Introduction

Nested block designs are useful for the experimental situations, where there are two sources of variation in the experimental units and one is nested within another. For such experimental situations, Preece (1967) introduced nested balanced incomplete block (NBIB) designs. Some methods of construction of NBIB designs have been given by Preece (1967), Jimbo and Kuriki (1983) and Dey *et al*. [3]. For a complete catalogue of NBIB designs for $v \le 16, r \le 30$, a reference may be made to Morgan *et al*. (1999). An NBIB design may not exist for all parametric combinations or even if it exists, it may require a large number of replications which the experimenter may not be able to afford. Hence, Homel and Robinson (1975) introduced nested partially balanced incomplete block (NPBIB) designs. Construction of NPBIB designs can be found in Homel and Robinson (1975), Banerjee and Kageyama (1993), Phillip *et al*. (1997) and Satpati and Parsad (2004). Kageyama *et al.* (1995) and Saha *et al*. (1998) cover some methods of constructions of both NBIB and NPBIB designs. Satpati and Parsad (2004) gave a catalogue of 2-associate NPBIB designs and 3-associate NPBIB designs for $v \le 30, r \le 15.$

There may arise situations when there exists another source of variation among the units in sub-blocks of a nested incomplete block design. To be clearer, consider the following experimental situation. Consider a field experiment which is conducted at several locations using a nested block design. The harvesting is done sub-block wise and the harvested samples from each sub-block are to be analyzed for their content in laboratory by different technicians. To control variation due to technicians, this may be taken as another blocking factor. Hence, nesting of units within sub-blocks may be required. To deal with the experimental situations where there are three sources of variation; third source of variation is nested within the second and the second source is nested within the first, doubly nested balanced incomplete block (DNBIB) designs are introduced by Preece *et al.* (1999). In these designs, there are *n* experimental units that can be arranged in *b* blocks such that there are m_1 sub-blocks within each block and m_2 sub-sub-blocks within each sub-block. In general, in a proper block design set up, a DNBIB design with parameters $(v, r, b_1, k_1, \lambda_1, b_2, k_2, \lambda_2, m_1, b_3, k_3, \lambda_3, m_2)$ may be defined as an arrangement of *v* treatments each replicated *r* times in three systems of blocks if

a) each block of the first system contains m_1 blocks of the second system and each block of the second system contains m_2 blocks of the third system.
b) ignoring the first and second system of blocks, it leaves a BIB design with $b_3 = m_1 m_2 b_1$ blocks each of size $k_3 = \frac{k_2}{m_2} = \frac{k_1}{m_1 m_2}$ units with λ_3 concurrences.
c) ignoring the first and third system of blocks, it leaves a BIB design with $b_2 = m_1 b_1$ blocks each of size $k_2 = \frac{k_1}{m_1}$ units with λ_2 concurrences.
d) ignoring the second and third system of blocks, it leaves a BIB design with b_1 blocks each of size k_1 units with λ_1 concurrences.

The parameters of the design satisfy the following necessary conditions:
$vr = b_1 k_1 = b_2 k_2 = b_3 k_3,\ \lambda_1(v-1) = r(k_1 - 1), \lambda_2(v-1) = r(k_2 - 1),\ \lambda_3(v-1) = r(k_3 - 1)$.

Preece *et al*. (1999) also gave a catalogue of DNBIB designs for $v \le 20$ and $r \le 30$. A DNBIB design may not exist for all parametric combinations or even if it exists it may require large

number of replications which the experimenter may not be able to afford. To deal with such situations, one can use doubly nested partially balanced incomplete block (DNPBIB) designs. In these designs, there are n experimental units that can be arranged in b blocks such that there are m_1 sub-blocks within each block and m_2 sub-sub-blocks within each sub-block. In general, in a proper block design set up, a DNPBIB design based on m-class association scheme with parameters $(v, r, b_1, k_1, \lambda_{1i}, b_2, k_2, \lambda_{2i}, m_1, b_3, k_3, \lambda_{3i}, m_2,\ i = 1, 2, \ldots, m)$ may be defined as an arrangement of v treatments each replicated r times in three systems of blocks if

a) Each block of the first system contains m_1 blocks of the second system and each block of the second system contains m_2 blocks of the third system.
b) Ignoring the first and second system of blocks, it leaves a PBIB design with $b_3 = m_1 m_2 b_1$ blocks each of size $k_3 = \frac{k_2}{m_2} = \frac{k_1}{m_1 m_2}$ units with λ_{3i} concurrences of any pair of treatments which are i^{th} associates of each other ($i = 1, 2, \ldots, m$).
c) Ignoring the first and third system of blocks, it leaves a PBIB design with $b_2 = m_1 b_1$ blocks each of size $k_2 = \frac{k_1}{m_1}$ units with λ_{2i} concurrences of two treatments which are i^{th} associates of each other ($i = 1, 2, \ldots, m$).
d) Ignoring the second and third system of blocks, it leaves a PBIB design with b_1 blocks each of size k_1 units with λ_{1i} concurrences of two treatments which are ith associates of each other ($i = 1, 2, \ldots, m$).

Here, the three PBIB designs obtained from a DNPBIB design share the same association scheme. But it may be mentioned that it is always not necessary that all the three PBIB designs in a DNPBIB design are based on same association scheme. Some methods of constructions of DNPBIB designs sharing same association scheme are given in Section G.2. A Catalogue of all DNPBIB designs for $v \le 20, r \le 20$ obtainable from these methods of construction is given in the Appendix G.1.

G.2 Methods of Construction of DNPBIB Designs

Method G.2.1: Let a DNBIB design D with parameters $v^* = m, r^*, b_1^*, k_1^*, \lambda_1^*, b_2^*, k_2^*, \lambda_2^*, b_3^*, k_3^*, \lambda_3^*$ exists. Replace treatment i in design D by the set of n new treatments, $i,\ i + v^*, i + 2v^*, \ldots, i + (n-1)v^*$. Repeating this procedure for all v^* treatments, we get a 2-associate DNPBIB design based on group divisible association scheme in which super blocks, sub-blocks and sub-sub-blocks form a singular group divisible design. The parameters of DNPBIB so obtained are

$v = nv^*, r = r^*, b_1 = b_{1*}^*, k_1 = nk_1^*, b_2 = b_2^*, k_2 = nk_2^*, b_3 = b_3^*, k_3 = nk_3^*, \lambda_{11} = r^*, \lambda_{12} = \lambda_1^*,\ \lambda_{21} = r^*$

$\lambda_{22} = \lambda_2^*, \lambda_{31} = r^*, \lambda_{32} = \lambda_3^*$, $m = v^*$, $n = n$.

Here n new set of treatments which replace a particular treatment will be first associate to each other and treatments from the different sets will be second associates.

Example G.2.1: Consider a DNBIB design {Serial number 1 in Preece *et al.* (1999)} with parameters $v = 9, r = 8, b_1 = 9, k_1 = 8,\ \lambda_1 = 7, b_2 = 18, k_2 = 4, \lambda_2 = 3, b_3 = 36, k_3 = 2, \lambda_3 = 1$ with block contents as

[{(1	5)	(3	7)}	{(2	6)	(4	8)}]
[{(5	9)	(4	2)}	{(8	3)	(6	7)}]
[{(8	7)	(1	4)}	{(6	9)	(5	3)}]
[{(4	6)	(7	9)}	{(1	8)	(2	5)}]
[{(6	3)	(2	1)}	{(5	7)	(8	9)}]
[{(9	1)	(6	8)}	{(7	4)	(3	2)}]
[{(3	4)	(8	5)}	{(9	2)	(7	1)}]
[{(2	8)	(9	3)}	{(4	5)	(1	6)}]
[{(7	2)	(5	6)}	{(3	1)	(9	4)}]

Replacing each treatments by n = 2 new treatments as per procedure of Method G.2.1 we get a DNPBIB design based on group divisible association scheme. The parameters of the design are $v=18, r=8, b_1=9, k_1=16, b_2=18, k_2=8, b_3=36, k_3=4, \lambda_{11}=8, \lambda_{12}=7, \lambda_{21}=8, \lambda_{22}=3, \lambda_{31}=8,\ \lambda_{12}=1.$ The blocks of the design are

[{(1	10	5	14)	(3	12	7	16)}	{(2	11	6	15)	(4	13	8	17)}]
[{(5	14	9	18)	(4	13	2	11)}	{(8	17	3	12)	(6	15	7	16)}]
[{(8	17	7	16)	(1	10	4	13)}	{(6	15	9	18)	(5	14	3	12)}]
[{(4	13	6	15)	(7	16	9	18)}	{(1	10	8	17)	(2	11	5	14)}]
[{(6	15	3	12)	(2	11	1	10)}	{(5	14	7	16)	(8	17	9	18)}]
[{(9	18	1	10)	(6	15	8	17)}	{(7	16	4	13)	(3	12	2	11)}]
[{(3	12	4	13)	(8	17	5	16)}	{(9	18	2	11)	(7	16	1	10)}]
[{(2	11	8	17)	(9	18	3	12)}	{(4	13	5	14)	(1	10	6	15)}]
[{(7	16	2	11)	(5	14	6	15)}	{(3	12	1	10)	(9	18	4	13)}]

Method G.2.2: Let there exists an m-class associate class PBIB design with parameters $v', b', r', k', \lambda_i', i=1,2,...,m$ and also there exists a DNBIB design with parameters $v^*=k', r^*, b_1^*, k_1^*, \lambda_1^*, b_2^*, k_2^*, \lambda_2^*, b_3^*, k_3^*, \lambda_3^*$. Then writing each block contents of PBIB design as DNBIB design, we get a DNPBIB design with parameters $v=v', r=r'r^*, b_1=b'b_1^*, k_1=k_1^*, b_2=b'b_2^*, k_2=k_2^*, b_3=b'b_3^*, k_3=k_3^*, \lambda_{1i}=\lambda_i'\lambda_1^*$ $\lambda_{2i}=\lambda_i'\lambda_2^*, \lambda_{3i}=\lambda_i'\lambda_3^*, i=1,2,...,m$ with common association scheme for blocks, sub-blocks and sub-sub-blocks.

Example G.2.2: Consider the following 2-associate class PBIB design based on group divisible association scheme {S82 in Clatworthy (1973)} with parameters v = 12, b = 4, r = 3, k = 9, $\lambda_1=3$ and $\lambda_2=2$.

(1	5	9	2	6	10	3	7	11)
(2	6	10	3	7	11	4	8	12)
(3	7	11	4	8	12	1	5	9)
(4	8	12	1	5	9	2	6	10)

There also exists a DNBIB design {at serial number 1 in Preece *et al.* (1999)} with parameters $v=9, r=8, b_1=9, k_1=8,\ \lambda_1=7, b_2=18,\ k_2=4, \lambda_2=3, b_3=36, k_3=2, \lambda_3=1$ with block contents as ((.) represents the sub-sub-blocks, {.} represents the sub-blocks and [.] represents the blocks of the design)

[{(1 5) (3 7)} {(2 6) (4 8)}]
[{(5 9) (4 2)} {(8 3) (6 7)}]
[{(8 7) (1 4)} {(6 9) (5 3)}]
[{(4 6) (7 9)} {(1 8) (2 5)}]
[{(6 3) (2 1)} {(5 7) (8 9)}]
[{(9 1) (6 8)} {(7 4) (3 2)}]
[{(3 4) (8 5)} {(9 2) (7 1)}]
[{(2 8) (9 3)} {(4 5) (1 6)}]
[{(7 2) (5 6)} {(3 1) (9 4)}]

Writing each of the block contents of PBIB design as DNBIB design, we get the following DNPBIB design with parameters $v = 12,\ r = 24,\ b_1 = 36,\ k_1 = 8,\ b_2 = 72,\ k_2 = 4, b_3 = 144,$ $k_3 = 2, \lambda_{11} = 21,\ \lambda_{12} = 14, \lambda_{21} = 9, \lambda_{22} = 6\ \lambda_{31} = 3$ and $\lambda_{32} = 2.$

[{(1 6) (9 3)} {(5 10) (2 7)}]
[{(6 11) (2 5)} {(7 9) (10 3)}]
[{(7 3) (1 2)} {(10 11) (6 9)}]
[{(2 10) (3 11)} {(1 7) (5 6)}]
[{(10 9) (5 1)} {(6 3) (7 11)}]
[{(11 1) (10 7)} {(3 2) (9 5)}]
[{(9 2) (7 6)} {(11 5) (3 1)}]
[{(5 7) (11 9)} {(2 6) (1 10)}]
[{(3 5) (6 10)} {(9 1) (11 2)}]
[{(2 7) (10 4)} {(6 11) (3 8)}]
[{(7 12) (3 6)} {(8 10) (11 4)}]
[{(8 4) (2 3)} {(11 12) (7 10)}]
[{(3 11) (4 12)} {(2 8) (6 7)}]
[{(11 10) (6 2)} {(7 4) (8 12)}]
[{(12 2) (11 8)} {(4 3) (10 6)}]
[{(10 3) (8 7)} {(12 6) (4 2)}]
[{(6 8) (12 10)} {(3 7) (2 11)}]
[{(4 6) (7 11)} {(10 2) (12 3)}]
[{(3 8) (11 1)} {(7 12) (4 5)}]
[{(8 9) (4 7)} {(5 11) (12 1)}]
[{(5 1) (3 4)} {(12 9) (8 11)}]
[{(4 12) (1 9)} {(3 5) (7 8)}]
[{(12 11) (7 3)} {(8 1) (5 9)}]
[{(9 3) (12 5)} {(1 4) (11 7)}]
[{(11 4) (5 8)} {(9 7) (1 3)}]
[{(7 5) (9 11)} {(4 8) (3 12)}]
[{(1 7) (8 12)} {(11 3) (9 4)}]
[{(4 5) (12 2)} {(8 9) (1 6)}]
[{(5 10) (1 8)} {(6 12) (9 2)}]
[{(6 2) (4 1)} {(9 10) (5 12)}]
[{(1 9) (2 10)} {(4 6) (8 5)}]
[{(9 12) (8 4)} {(5 2) (6 10)}]
[{(10 4) (9 6)} {(2 1) (12 8)}]
[{(12 1) (6 5)} {(10 8) (2 4)}]
[{(8 6) (10 12)} {(1 5) (4 9)}]
[{(2 8) (5 9)} {(12 4) (10 1)}]

Remark G.2.1: This method of construction is quite general in nature. Depending on the existence of families of DNBIB designs and corresponding PBIB design, one can develop a large number of DNPBIB designs.

Method G.2.3: Let there exists a NBIB design, D, with parameters $v^*=m, r^*, b_1^*, k_1^*, \lambda_1^*, b_2^*, k_2^*, \lambda_2^*$. Replace each treatment *i* in design D by the group of *n* new treatments, *i*, *i* + *v**, *i* + *2v*,..., i* + (*n* – 1)*v**. Repeating this procedure for all *v** treatments and considering the replaced treatments as sub-sub-blocks, we get a DNPBIB design with $v=nv^*, r=r^*, b_1=b_1^*, k_1=nk_1^*, b_2=b_2^*, \quad k_2=nk_2^*, b_3=k_2^*b_2^*, k_3=n, \lambda_{11}=r^*, \quad \lambda_{12}=\lambda_1^*, \lambda_{21}=r^*, \quad \lambda_{22}=\lambda_2^*, \lambda_{31}=r^*, \lambda_{32}=0.$

Example G.2.3: Consider the same NBIB design {serial number 5 in Morgan *et al*. (1999)} with parameters $v^*=9, r^*=8, b_1^*=18, k_1^*=4, \lambda_1^*=3, b_2^*=36, k_2^*=2, \lambda_2^*=1$. The block contents are given by

{(1	5)	(3	7)}	{(2	6)	(4	8)}
{(5	9)	(4	2)}	{(8	3)	(6	7)}
{(8	7)	(1	4)}	{(6	9)	(5	3)}
{(4	6)	(7	9)}	{(1	8)	(2	5)}
{(6	3)	(2	1)}	{(5	7)	(8	9)}
{(9	1)	(6	8)}	{(7	4)	(3	2)}
{(3	4)	(8	5)}	{(9	2)	(7	1)}
{(2	8)	(9	3)}	{(4	5)	(1	6)}
{(7	2)	(5	6)}	{(3	1)	(9	4)}

Replacing each treatments by *n* = 2 new treatments as per procedure of Method G.2.3, we get the following design with parameters $v=18, r=8, b_1=18, k_1=8, b_2=36, \quad k_2=4, b_3=72, k_3=2, \lambda_{11}=8, \quad \lambda_{12}=3, \lambda_{21}=8, \lambda_{22}=1, \lambda_{31}=8, \lambda_{32}=0.$

[{(1	10)	(5	14)}	{(3	12)	(7	16)}]	[{(2	11)	(6	15)}	{(4	13)	(8	17)}]
[{(5	14)	(9	18)}	{(4	13)	(2	11)}]	[{(8	17)	(3	12)}	{(6	15)	(7	14)}]
[{(8	17)	(7	16)}	{(1	10)	(4	13)}]	[{(6	15)	(9	18)}	{(5	14)	(3	12)}]
[{(4	13)	(6	15)}	{(7	16)	(9	18)}]	[{(1	10)	(8	17)}	{(2	11)	(5	14)}]
[{(6	15)	(3	12)}	{(2	11)	(1	10)}]	[{(5	14)	(7	16)}	{(8	17)	(9	18)}]
[{(9	18)	(1	10)}	{(6	15)	(8	17)}]	[{(7	16)	(4	13)}	{(3	12)	(2	11)}]
[{(3	12)	(4	13)}	{(8	17)	(5	14)}]	[{(9	18)	(2	11)}	{(7	16)	(1	10)}]
[{(2	11)	(8	17)}	{(9	18)	(3	12)}]	[{(4	13)	(5	14)}	{(1	10)	(6	15)}]
[{(7	16)	(2	11)}	{(5	14)	(6	15)}]	[{(3	12)	(1	10)}	{(9	18)	(4	13)}]

Here *m* = *v* = 9 and *n* = 2.

Remark G.2.2: The DNPBIB designs obtained through this method are disconnected at sub-sub-block level.

Method G.2.4: Let there exists a 2-associate class NPBIB design with parameters $v^*, r^*, b_1^*, k_1^*, b_2^*, k_2^*, \lambda_{11}^*, \lambda_{12}^*, \lambda_{21}^*, \lambda_{22}^*$. Also let there exists a resolvable BIB design with parameters $v'=k_2^*, r'=t, b'=t\beta, k', \lambda'$ where within each of *t* complete replications there are β blocks. Writing the sub-blocks of NPBIB design as BIB design one gets a DNPBIB design

with parameters $v = v^*, r = r^* r', b_1 = tb_1^*, k_1 = k_1^*, b_2 = tb_2^*, b_3 = b_2^* b', k_2 = k_2^*, \quad k_3 = k', \lambda_{11} = r'\lambda_{11}^*,$ $\lambda_{12} = r'\lambda_{12}^*, \lambda_{21} = r'\lambda_{21}^*, \lambda_{22} = r'\lambda_{22}^*, \lambda_{31} = \lambda'\lambda_{21}^*, \lambda_{32} = \lambda'\lambda_{22}^*$.

Example G.2.4: Consider the following 2-associate class NPBIB design {serial number 16 in Satpati and Parsad (2004)} based on GD association scheme {GD(5,2)} with parameters $v = 10, r = 4, b_1 = 5, k_1 = 8, b_2 = 10, k_2 = 4, \lambda_{11} = 4, \lambda_{12} = 3, \lambda_{21} = 4, \lambda_{22} = 1$.

{(	1	6	4	9	)	(	2	7	3	8	)}
{(	2	7	5	10	)	(	3	8	4	9	)}
{(	3	8	1	6	)	(	4	9	5	10	)}
{(	4	9	2	7	)	(	5	10	1	6	)}
{(	5	10	3	8	)	(	1	6	2	7	)}

The association scheme is

1	6
2	7
3	8
4	9
5	10

There exists a resolvable BIB design with parameters v = 4, b = 6, r = 3, k = 2, $\lambda = 1$ with block contents as (1,2), (3, 4), (1,3) ,(2, 4), (1, 4) , (2, 3). Following the Method G.2.4, we get the following DNPBIB design with parameters $v = 10, r = 12, b_1 = 15, k_1 = 8,$ $b_2 = 30, k_2 = 4, b_3 = 60, k_3 = 2, \lambda_{11} = 12, \lambda_{12} = 9, \lambda_{21} = 12, \lambda_{22} = 3, \lambda_{31} = 4, \lambda_{32} = 1$.

[{(1	6)	(4	9)}	{(2	7)	(3	8)}]
[{(2	7)	(5	10)}	{(3	8)	(4	9)}]
[{(3	8)	(1	6)}	{(4	9)	(5	10)}]
[{(4	9)	(2	7)}	{(5	10)	(1	6)}]
[{(5	10)	(3	8)}	{(1	6)	(2	7)}]
[{(1	4)	(6	9)}	{(2	3)	(7	8)}]
[{(2	5)	(7	10)}	{(3	4)	(8	9)}]
[{(3	1)	(8	6)}	{(4	5)	(9	10)}]
[{(4	2)	(9	7)}	{(5	1)	(10	6)}]
[{(5	3)	(10	8)}	{(1	2)	(6	7)}]
[{(1	9)	(6	4)}	{(2	8)	(7	3)}]
[{(2	10)	(7	5)}	{(3	9)	(8	4)}]
[{(3	6)	(8	1)}	{(4	10)	(9	5)}]
[{(4	7)	(9	2)}	{(5	6)	(10	1)}]
[{(5	8)	(10	3)}	{(1	7)	(6	2)}]

Method G.2.5: Let there exists a resolvable NPBIB design with parameters $v^*, r^* = t, b_1^* = t\beta, b_2^*, k_1^*, k_2^*, \lambda_{11}^*, \lambda_{12}^*, \lambda_{21}^*, \lambda_{22}^*$ where b_1^* blocks can be grouped into t sets such that there are β blocks in each set and every treatment appears once in each set. Taking all the β blocks of a complete replication of NPBIB design into one bigger block and repeating this procedure for all the t sets, a DNPBIB design can be constructed where sub-sub-blocks and sub-blocks form a PBIB but at block level, it is a complete block design. The parameters of the design

so constructed are $v = v^*,\ r = r^*, b_1 = t, b_2 = b_1^*,\quad b_3 = b_2^*, k_1 = \beta k_1^*, k_2 = k_1^*, k_3 = k_2^*,$ $\lambda_{11} = t, \lambda_{12} = t,\ \lambda_{21} = \lambda_{11}^*,\ \lambda_{22} = \lambda_{12}^*, \lambda_{31} = \lambda_{21}^*, \lambda_{32} = \lambda_{22}^*$

Example G.2.5: Consider the following resolvable NPBIB design {serial number 5 in Satpati and Parsad (2004)} based on group divisible association scheme {GD(4,2)} with parameters $v = 8, b_1 = 18, b_2 = 36, r = 9, k_1 = 4,\ k_2 = 2, \lambda_{11} = 9, \lambda_{12} = 3, \lambda_{21} = 3, \lambda_{22} = 1.$

[(1	2)	(5	6)]	[(3	4)	(7	8)]
[(1	5)	(2	6)]	[(3	7)	(4	8)]
[(1	6)	(2	5)]	[(3	8)	(4	7)]
[(1	3)	(5	7)]	[(2	4)	(6	8)]
[(1	5)	(3	7)]	[(2	6)	(4	8)]
[(1	7)	(3	5)]	[(2	8)	(4	6)]
[(1	3)	(5	8)]	[(2	4)	(6	7)]
[(1	5)	(3	8)]	[(2	6)	(4	7)]
[(1	8)	(3	5)]	[(2	7)	(4	6)]

Following the Method G.2.5, we get a DNPBIB design with parameters $v = 8,$ $b_1 = 9, b_2 = 18, b_3 = 36, r = 9, k_1 = 8, k_2 = 4, k_3 = 2, \lambda_{21} = 9, \lambda_{22} = 3, \lambda_{31} = 3, \lambda_2 = 1.$ with block contents as

[{(1	2)	(5	6)}	{(3	4)	(7	8)}]
[{(1	5)	(2	6)}	{(3	7)	(4	8)}]
[{(1	6)	(2	5)}	{(3	8)	(4	7)}]
[{(1	3)	(5	7)}	{(2	4)	(6	8)}]
[{(1	5)	(3	7)}	{(2	6)	(4	8)}]
[{(1	7)	(3	5)}	{(2	8)	(4	6)}]
[{(1	3)	(5	8)}	{(2	4)	(6	7)}]
[{(1	5)	(3	8)}	{(2	6)	(4	7)}]
[{(1	8)	(3	5)}	{(2	7)	(4	6)}]

A catalogue of the obtained DNPBIB designs through the above methods of constructions in the range $v \le 25, r \le 30$ is presented in the Appendix G.1.

G.3 Application of Doubly Nested Block Designs in Tetrallel Crosses

Tetrallel crosses involving four lines provide a useful method of conducting plant breeding experiments. It is a type of mating design used to study the genetic properties of a set of inbred lines. A four line cross is obtained by crossing two unrelated F_1 hybrids symbolized as $(l_1 \times l_2) \times l(_3 \times l_4)$ where l_i denotes the ith line {See Rawlings and Cockerham (1962), Hinkelman ((1967, 1968) and Parsad *et al*. (2005)}.

A doubly nested incomplete block design with sub-sub-block size 2 and sub-block size 4 has a one-to-one correspondence with the block designs for tetrallel crosses. Consider the treatments of doubly nested incomplete designs as lines of a tetrallel cross experiment. Performing crosses among the lines appearing in the same sub-sub-block of doubly nested incomplete design and then crossing the crosses so obtained in a sub-block gives a required tetrallel cross. If v, b_1, b_2, $b_3, r, k_1, k_2 = 4, k_3 = 2, \lambda_1, \lambda_2, \lambda_3$ are the parameters of a DNBIB design, then the parameters of block design for tetrallel crosses are $v, b = b_1, k = \frac{k_1}{4}$. Parsad *et al*. (2005) have shown that the

designs for tetrallel crosses obtained from DNBIB design are universally optimal in the D (*v*, *b*, *k*), the class of block designs in which tetrallel crosses of *v* inbred lines are arranged in *b* blocks of size *k*. Morgan et al. (2001) gave a comprehensive catalogue of DNBIB designs. Using their designs at serial number 1, 2, 5, 6, 9, 10, 16, 17 and 18 one can easily obtain efficient designs for number of inbred lines, $v = 9, 13, 16, 16, 17, 12, 13,$ and 15 respectively.

Often a design for tetrallel crosses may be required for some parametric combinations for which a corresponding DNBIB design may not exist. In such situations, designs for tetra-allel crosses can be obtained using DNPBIB designs. To be clearer, consider the following example.

Example G.3.1: Consider the DNPBIB design in Example G.2.5. Corresponding design for tetrallel cross is given by

[{(1	×	5)	×	(3	×	7)}	{(2	×	6)	×	(4	×	8)}]
[{(5	×	9)	×	(4	×	2)}	{(8	×	3)	×	(6	×	7)}]
[{(8	×	7)	×	(1	×	4)}	{(6	×	9)	×	(5	×	3)}]
[{(4	×	6)	×	(7	×	9)}	{(1	×	8)	×	(2	×	5)}]
[{(6	×	3)	×	(2	×	1)}	{(5	×	7)	×	(8	×	9)}]
[{(9	×	1)	×	(6	×	8)}	{(7	×	4)	×	(3	×	2)}]
[{(3	×	4)	×	(8	×	5)}	{(9	×	2)	×	(7	×	1)}]
[{(2	×	8)	×	(9	×	3)}	{(4	×	5)	×	(1	×	6)}]
[{(7	×	2)	×	(5	×	6)}	{(3	×	1)	×	(9	×	4)}]
[{(1	×	7)	×	(5	×	3)}	{(2	×	8)	×	(6	×	4)}]
[{(5	×	2)	×	(9	×	4)}	{(8	×	7)	×	(3	×	6)}]
[{(8	×	4)	×	(7	×	1)}	{(6	×	3)	×	(9	×	5)}]
[{(4	×	9)	×	(6	×	7)}	{(1	×	5)	×	(8	×	2)}]
[{(6	×	1)	×	(3	×	2)}	{(5	×	9)	×	(7	×	8)}]
[{(9	×	8)	×	(1	×	6)}	{(7	×	2)	×	(4	×	3)}]
[{(3	×	5)	×	(4	×	8)}	{(9	×	1)	×	(2	×	7)}]
[{(2	×	3)	×	(8	×	9)}	{(4	×	6)	×	(5	×	1)}]
[{(7	×	6)	×	(2	×	5)}	{(3	×	4)	×	(1	×	9)}]

Some connected block designs for tetrallel crosses are designs obtained through Method G.2.4 given at serial no. 2, 26, 30-35, 37, 40 in Table G.1 (Appendix G.1). Designs for tetrallel crosses can also be obtained using resolvable NPBIB designs. The NPBIB designs with sub-block size as 2 at serial number 5, 6, 8, 20, 28 and 43 given by Satpati and Parsad (2004) are resolvable and Now using Method G.2.5, one can obtain a DNPBIB design whose super blocks are complete blocks. Now following the above procedure, one can obtain designs for tetrallel crosses with following parameters:

$v = 8, b = 9, k = 2$; $v = 8, b = 12, k = 2$; $v = 8, b = 12, k = 2$; $v = 12, b = 15, k = 3$; $v = 16, b = 12, k = 4$; $v = 20, b = 15, k = 5$ respectively.

More efforts to obtain efficient designs for tetrallel crosses are required to be made.

References

Banerjee, S. and Kageyama, S. (1993). Methods of constructing nested partially balanced incomplete block designs. *Utilitas Mathematica*, **43**, 3-6.

Clatworthy, W. H. (1973). *Tables of two-associate class partially balanced designs*. Washington D.C.: National Bureau of Standards.

Dey, A., Das, U.S. and Banerjee, A. K. (1986). Construction of nested balanced incomplete block designs. *Calcutta Statist. Assoc. Bull.*, **35**,161-167.

Hinkelman, K. (1967). Circulant partial triallel crosses. *Biom. Zeit*, **9**, 242-265.

Hinkelman, K. (1968). Partial tetrallel crosses. *Theor. Appl. Genetics*, **38**, 85-89.

Homel, R.J. and Robinson (1975). J. Nested partially balanced incomplete block designs. S*ankhya*, **37B**, 201-210.

Jimbo, M. and Kuriki, S.(1983). Construction of nested designs. *Ars Combin.*, **16**, 275-285.

Kageyama, S., Philip, J. and Banerjee, S. (1995). Some constructions of nested BIB and 2-associate PBIB designs under restricted dualization. *Bull. Fac. Sch. Educ. Hiroshima Univ., Part II*, **17**, 33-39.

Morgan, J.P., Preece, D. A. and Rees, D.H. (2001). Nested balanced incomplete block designs. *Discrete Math.*, **231**, 351-389.

Parsad, R., Gupta, V. K. and Gupta, S. (2005). Optimal designs for experiments on two-line and four line crosses. *Utilitas Math.*, **68**, 11-32.

Philip, J., Banerjee, S. and Kageyama, S.((1997). Construction of nested *t*-associate class PBIB designs under restricted dualization, *Utilitas Math.*, **51**, 27-32.

Preece, D.A. (1967). Nested balanced incomplete block designs, *Biometrika*, **54**, 479-486.

Preece, D.A. and Rees, D.H. and Morgan, J.P. (1999). Doubly nested balanced incomplete block designs, *Congressus Numerantium*, **137**, 5-18.

Rawlings, J.O. and Cockerham, C.C. (1962). Analysis of double cross hybrid populations. *Biometrics*, **18**, 229-244.

Saha, G.M., Dey, A., and Midha, C.K. (1998). Construction of nested incomplete block designs, *Calcutta Statist. Assoc. Bull.*, **48**,195-205.

Satpati, S.K. and Parsad, R. (2004). Construction and cataloguing of nested partially balanced incomplete block designs. *Ars Combin.*, **73**, 299-309.

Appendix G.1

Table G.1: 2-associate class DNPBIB design with $v \leq 20, r \leq 30$

v	b_1	b_2	b_3	r	k_1	k_2	k_3	λ_{11}	λ_{12}	λ_{21}	λ_{22}	λ_{31}	λ_{32}	Method	Source Design	Association Scheme
18	9	18	36	8	16	8	4	8	7	8	3	8	1	2.1	PRM1	GD(9, 2)
12	36	72	144	24	8	4	2	21	14	9	6	3	2	2.2	S82, MPR1	GD(4, 3)
10	5	10	20	4	8	4	2	4	3	4	1	4	0	2.3	MPR1	GD(5, 2)
12	15	30	60	10	8	4	2	10	6	10	2	10	0	2.3	MPR13	GD(6, 2)
14	7	21	42	6	12	4	2	6	5	6	1	6	0	2.3	MPR2	GD(7, 2)
14	21	42	84	12	8	4	2	12	6	12	2	12	0	2.3	MPR19	GD(7, 2)
14	7	14	42	6	12	6	2	6	5	6	2	6	0	2.3	MPR3	GD(7, 2)
16	14	28	56	7	8	4	2	7	3	7	1	7	0	2.3	MPR4	GD(8, 2)
16	28	84	168	21	12	4	2	21	15	21	3	21	0	2.3	MPR50	GD(8, 2)
16	28	56	168	21	12	6	2	21	15	21	6	21	0	2.3	MPR51	GD(8, 2)
18	9	36	72	8	16	4	2	8	7	8	1	8	0	2.3	MPR8	GD(9, 2)
18	9	18	72	8	16	8	2	8	7	8	3	8	0	2.3	MPR9	GD(9, 2)
18	12	36	72	8	12	4	2	8	5	8	1	8	0	2.3	MPR6	GD(9, 2)
18	12	24	72	8	12	6	2	8	5	8	2	8	0	2.3	MPR7	GD(9, 2)
18	18	36	72	8	8	4	2	8	3	8	1	8	0	2.3	MPR5	GD(9, 2)
20	10	30	90	9	18	6	2	9	8	9	2	9	0	2.3	MPR12	GD(10, 2)
20	15	45	90	9	12	4	2	9	5	9	1	9	0	2.3	MPR10	GD(10, 2)
20	15	30	90	9	12	6	2	9	5	9	2	9	0	2.3	MPR11	GD(10,2)
20	30	60	180	18	12	6	2	18	10	18	4	18	0	2.3	MPR47	GD(10,2)
20	45	90	270	27	12	6	2	27	15	27	6	27	0	2.3	MPR58	GD(10,2)
20	45	90	180	18	8	4	2	18	6	18	2	18	0	2.3	MPR46	GD(10,2)
15	5	10	20	4	12	6	3	4	3	4	1	4	0	2.3	MPR1	GD(5,3)
18	15	30	60	10	12	6	3	10	6	10	2	10	0	2.3	MPR13	GD(6,3)
20	5	10	20	4	16	8	4	4	3	4	1	4	0	2.3	MPR1	GD(5,4)
10	15	30	60	12	8	4	2	12	9	12	3	4	1	2.4	SP16	Gd(5,2)
12	45	90	180	30	8	4	2	30	18	30	6	10	2	2.4	SP18	GD(6, 2)
14	21	63	126	18	12	4	2	18	15	18	3	6	1	2.4	SP23	GD(7, 2)
15	45	90	180	24	8	4	2	12	12	9	0	3	0	2.4	SP25	Triangular
16	36	72	144	18	8	4	2	12	6	9	0	3	0	2.4	SP30	L_2
16	54	108	216	27	8	4	2	15	9	9	0	3	0	2.4	SP31	L_2
16	72	84	168	21	8	4	2	21	9	21	3	7	1	2.4	SP33	GD(8, 2)
18	54	108	216	24	8	4	2	24	9	24	3	8	1	2.4	SP34	GD(9, 2)
18	36	108	216	24	12	4	2	24	15	24	3	8	1	2.4	SP35	GD(9, 2)
18	27	108	216	24	16	4	2	24	21	24	3	8	1	2.4	SP38	GD(9, 2)
20	45	135	270	27	12	4	2	27	15	27	3	9	1	2.4	SP40	GD(10, 2)
22	33	165	330	30	20	4	2	30	27	30	3	10	1	2.4	SP48	GD(11, 2)
25	75	150	300	24	8	4	2	9	6	9	0	3	0	2.4	SP54	L_2
8	9	18	36	9	8	4	2	9	9	9	3	3	1	2.5	SP5	GD(4, 2)
8	12	24	48	12	8	4	2	12	12	12	4	0	2	2.5	SP6	GD(4, 2)
8	12	24	48	12	8	4	2	12	12	0	6	0	2	2.5	SP8	GD(4, 2)
12	15	45	90	15	12	4	2	15	15	15	3	5	1	2.5	SP20	GD(6, 2)
16	12	48	96	12	16	4	2	12	12	0	3	0	1	2.5	SP28	GD(4, 4)
16	7	14	28	7	16	8	4	7	7	7	3	7	1	2.5	SP33	GD(8, 2)

…

20	15	75	150	15	20	4	2	15	15	0	3	0	1	2.5	SP43	GD(4,5)
24	11	33	66	11	24	8	4	11	11	11	3	11	1	2.5	SP50	GD(12,2)
24	7	14	28	7	24	12	6	7	7	7	3	7	1	2.5	SP51	GD(8,3)
24	11	22	66	11	24	12	4	11	11	11	5	11	1	2.5	SP52	GD(12,2)
24	11	22	44	11	24	12	6	11	11	11	5	11	2	2.5	SP53	GD(12,2)

PRM# denotes the design at serial number # in Preece, Rees and Morgan (1999).
MPR # denotes the design at serial number # in Morgan, Preece and Rees (2001).
SP# denotes the design at serial number # in Satpati and Parsad (2004).
S82 denotes the PBIB design S82 in Clatworthy (1973).

H) Design Resources Server

"Design Resources Server" (www.iasri.res.in/design) was launched on the website of Indian Agricultural Statistics Research Institute (I.A.S.R.I.), New Delhi in the year 2005 under the National Fellow Scheme. One of the main goals of the server is to help the experimenters in agricultural sciences, biological sciences, social sciences and industry in planning and designing their experiments. The site makes available design theory and the actual layout of the designs through web. The server also aims to spread the advances in theoretical, computational, and statistical aspects of Design of Experiments among the mathematicians and statisticians in academia and among the practicing statisticians involved in advisory and consultancy services.

During this year efforts have been made to strengthen the Design Resources Server in collaboration with National Professor at I.A.S.R.I., New Delhi

- Design Resources Server has been strengthened by uploading 6574 block designs for making all possible pair wise treatment comparisons for $v \leq 35, b \leq 50, k \leq 34$ such that average replication number of treatments is not more than 20 and $v > k$ have been added on the DESIGN RESOURCES SERVER linked with the website of the Institute. For given *v, b, k* user can generate the layout of these designs. A snapshot of the link and design generated is given on the left page.
- On-line software developed for generation of Hadamard matrices of order up to 1000 except the orders 668, 716 and 892 (for which no construction method is currently available) and 876 (yet to be implemented) has been posted on the Design Resources Server.
- Dissemination workshop proceedings and links to other URL where the literature on Designs of Experiments is available have been placed at the Design Resources Server. A snapshot of the link is given on left side of the next page.
- An electronic book on **Advances in Data Analytical Techniques** has been compiled, edited and developed by **Rajender Parsad**, V.K. Gupta, Lal Mohan Bhar and V.K. Bhatia. The E-book consists of chapters on 66 topics described in more than 920 pages. The topics covered in this electronic book have been categorized into six modules namely Computer Usage and Statistical Software Packages, Basic Statistical Techniques consisting of Statistical methods and Inference, Design of Experiments and Sample Surveys, Diagnostics and Remedial Measures, Applications of Multivariate Techniques, Modelling and Forecasting Techniques in Agriculture and Other Useful Techniques such as Bio-informatics, Geoinformatics, Microarrays, DNA Fingerprinting, nanotechnology in agriculture etc. This book is available at IASRI website (www.iasri.res.in/design).an electronic book on **Advances in Data Analytical Techniques.** A snap shot of the link of Electronic book and the text material available in the Electronic book is given on the next page.

I) Transfer of Technology/ Advisory services

Advisory services were pursued rigorously. Details of some of them are given below:

National Research Centre on Rapeseed and Mustard

- α-designs have been suggested for initial varietal trials conducted by National Research Centre on Rapeseed and Mustard, Bharatpur. These designs are resolvable incomplete block designs and a monograph has been published for the benefit of the experimenters. The parameters for which the α-designs recommended are: (i) v = 12, b = 6, r = 3, k =6; (ii) v = 15, b = 9, r = 3, k =5 ; (iii) v = 18, b = 9, r = 3, k = 6; (iv) v = 21, b = 9, r = 3, k = 7; (v) v = 24, b = 12, r = 3, k = 6 and (vi) v = 28, b = 12, r = 3, k = 7. These designs were developed during the preparation of Monograph on α-designs. Finally the following α-designs were adopted for 29 trials

v	b	r	k	Efficiency	Trial Name	Centres
12	12	3	3	0.9241	Mustard Saline	Faizabad
15	15	3	3	0.9067	Yellow Sarson	Faizabad, Pantnagar, Bharatpur, Shillongini
					Gobhi Sarson	Ludhiana
					Mustard Quality	Ludhiana, Faizabad, Morena, Pantangar
18	18	3	3	0.8915	IHT	Faizabad, Ludhiana, Morena, Varansi, Pantnagar
24	12	3	6	0.9699	Toria	Ludhiana, Faizabad, Jagdalpur, Morena, Kanke, Pantnagar, Shillongini
28	12	3	7	0.9603	Late Sown	Faizabad, Jalgaon, Pantnagar, Morena, Varans
36	12	2	6	0.9074	Mustard Timely Sown	Faizabad, Pantnagar

Rice-Wheat Consortium for Indo-Gangetic Plains

- Farmers' participatory Research Trials in Indo-Gangetic plains for conservation agriculture are designed and managed by farmers, the researchers have only advisory role in the selection of the resource conservation technologies (treatments). Farmer has full control over the selection of treatments to be tested on his/her field(s). The main objective of these trials is to establish and demonstrate the benefits of resource conservation technologies such as zero tillage, furrow irrigated raised bed planting system, fresh beds, reduced tillage, etc. over the conventional tillage practices. In these trials, farmers are briefed about new practices. The participating farmers are given full control over the selection of subset of resource conservation technologies to be tested on their fields with a view to assess farmer innovation and acceptability. They are also given the freedom to modify the treatments such as number of ploughings in reduced tillage, number of ploughings in conventional tillage, number of irrigation, leaving residue in the field, complete burning of the residue, zero tillage with different machines such as double disc, happy seeder, etc. as per their choice and availability of equipments. Further, date of sowing vary widely over years from treatment to treatment. Often as many treatments will arise as there are farmers.
- Further, Farmers' Participatory Research Trials are conducted over different regions and over years. The RCT options may have an interaction with regions and/ or years. It is desired to identify the RCT options that are suitable over regions/ years. It is desired to identify the varieties that are most suitable for zero tillage, bed planting systems, etc. Therefore, different

varieties are included in Farmers' Participatory Research Trials. Generally, the variety to be used is the prerogative of the participatory farmer. Farmers' Participatory Research Trials may have different soil types or land leveling. The aim is to study the interaction between treatments and varieties/ soil types/ land leveling. If we consider varieties, soil types, years, regions, land leveling, etc. as environments and RCT options as treatments then it amounts to studying the treatment × environment interactions. If there is no treatment × environment interaction then the best RCT option may be identified by averaging over the environments. If treatment × environment interaction is present then first we have to identify whether the interaction is a cross-over (treatment ranks change from one environment to another) or non-cross-over type where treatment difference change in magnitude but not in direction among environments. In non-cross-over interaction the treatments with superior mean can be used in all the environments. If there is cross-over interaction, then the subsets of treatments are to be recommended only for certain environments. Therefore, it is important to test for crossover interactions. In case of cross over interactions, one-way to identify the sub-sets of treatments for certain environments is to use the technique of biplots. Analytical techniques using linear mixed effects models and biplots have been developed for the analysis of data from these trials. These techniques have been passed on to the research personnel involved in conduct of Farmers' Participatory Research Trials in association with Rice-Wheat Consortium for Indo-Gangetic Plains.

Indian Agricultural Research Institure, New Delhi

- Dr. Dinesh Kumar, Senior Scientist from Division of Agronomy was advised on the analysis of experimental data conducted for standardization of nitrification inhibiting property of neem oil coated urea for Kharif Rice, 2005. In one experiment, 16 treatments tried were all possible combinations of 5 sources of nitrogen viz. prilled urea, 500 ppm oil coated urea, 1000 ppm oil coated urea, 2000 ppm oil coated urea, 5000 ppm oil coated urea and three doses viz. 50, 100, 150 kg/ha and one absolute control. In the another experiment, 16 treatments tried were all possible combinations of 5 sources of oil viz. FFA, pure oil, meliacins, saturated and unsaturated and three doses of oil viz. 500 ppm, 1000 ppm and 5000 ppm and one absolute control. The experiments were conducted using a randomized complete block design. The analysis was carried out using the concept of contrast analysis.
- Sh. Abdullah Altaher, Ph. D. student of Molecular Biology and Biotechnology was advised on the analysis of data pertaining to an experiment related to study of wheat transformation for tolerance to dehydration stress. 30 wheat genotypes were grown in the field in a randomized complete block design with 3 replications. Samples for each plot were taken and studied for callus formation in the laboratory. Samples from these 90 plots were also investigated in 2 regeneration media and the characters observed were G-spot, shoots per callus and number of shoots. The analysis was performed using PROC GLM of SAS.
- Dr U.K. Behera, Senior Scientist from Division of Agronomy was advised on the contrast analysis for comparison between durum, timely sown aestivum and late sown aestivum cultivars of wheat for the characters grain yield, thousand grain weight, harvest index, water use efficiency, etc.

Punjab Agricultural University, Ludhiana

- Sh. M. Ashraf Bhat, Ph.D. student from Department of Plant Breeding and Genetics was advised on the analysis of data pertaining to 37 inbred lines (maize), all at advanced stage of development, selected for estimating the genetic diversity using molecular markers (SSR).

Banaras Hindu University, Varanasi

- Dr. Arun Kumar Joshi, Professor, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences and Visiting Scientist at CIMMYT Mexico was advised on (i) analysis of data pertaining to experiments conducted with resource conservation technology viz. zero tillage and conventional tillage in combination with different varieties of wheat to identify varieties that are good for zero tillage /conventional tillage and (ii) analysis of data pertaining to the experiment conducted for detecting the variation in 963 diverse lines of wheat for stay green trait. The experiment was conducted using randomized complete block design with three replications for three years. He was also advised on the analysis of data pertaining to an experiment on 100 diverse lines for stay green, canopy temperature difference and yield traits. The 100 lines comprised of 25 lines from each of the four groups, stay green, moderately stay green, moderately non-stay green and non-stay green. The experiment was conducted using a randomized complete block design with three replications for three years. There were three dates of sowing in each of the year.

➢ Publications

Research Papers: 23 (12 published, 4 Accepted for Publication and 7 Communicated/Under Revision); Popular Articles: 3; Book Chapters: 2; Electronic Book: 1; Monograph: 1.

(A) Research Papers
Published

1. **Rajender Parsad**, V.K.Gupta and Sudhir Gupta (2005). Optimal designs for experiments on two-line and four-lines crosses. *Utilitas Mathematica*, **68**, 11-32.
2. **Rajender Parsad** and Subrata Kumar Satpati (2005). Nested block designs for comparing test treatments with a control. *Utilitas Mathematica*, **68**, 271-281.
3. Ajit Kaur Bhatia, **Rajender Parsad**, S.K. Sharma and Rajinder Kaur (2005). Statistical assessment of different crop rotations. *J. Farming Systems Research & Development*, **11(2)**, 190-196.
4. Rama Krishna Singh, R. Srivastava and **Rajender Parsad** (2005). Robustness of standard re-inforced balanced incomplete block designs against exchange of a test treatment. *Journal of Indian Society of Agricultural Statistics*, **59(3)**, 228-232.
5. Abhishek Rathore, **Rajender Parsad** and V.K.Gupta (2006). Computer aided search of efficient block designs for making all possible pairwise treatment comparisons. *Journal of Statistics and Applications: A Publication of 'Forum of Interdisciplinary Mathematics',* **1(1),** 15-33.
6. Gunanand Choudhary, Jitendra Kumar, Suresh Walia, **Rajender Parsad** and Balraj S. Parmar (2006). Development of controlled release formulations of Carbofuran and evaluation of their efficacy against *Meloidogyne incognita*. *Journal of Agricultural and Food Chemistry*, **54**, 4727-4733.
7. D.M. Kadam, D.V.K. Samuel and **Rajender Parsad** (2006). Optimisation of pre-treatments of solar dehydrated cauliflower. *Journal of Food Engineering*, **77**, 659-664.
8. Gunanand Choudhary, Jitendra Kumar, Suresh Walia, **Rajender Parsad** and Balraj S. Parmar. (2006). Controlled release of carbofuran into water from polymeric matrices. *Pesticide Research Journal*, **18**, 65-69.
9. S.K.Swain, J.P.Gupta, P.K. Sahoo, Abhijit Kar and **Rajender Parsad** (2006). Studies on rupture characteristics of drum roasted cashew nut. *Journal of Agricultural Engineering*, **43(3)**, 122-125.
10. Ananta Sarkar and **Rajender Parsad** (2006). Block designs for 2-colour microarray experiments: An overview. *Pusa AgriScience*, 38-54.
11. R. Srivastava, **Rajender Parsad**, Amitava Dey and V.K. Gupta (2006). A-efficient block designs for asymmetrical slope ratio assays. *Journal of Statistics and Applications: A Publication of 'Forum for Interdisciplinary Mathematics'*, **1(2-4)**, 185-192.
12. **Rajender Parsad**, V.K. Gupta and R. Srivastava (2007). Designs for cropping systems research. *Journal of Statistical Planning and Inference*, **137**, 1687-1703.

Accepted for Publication

13. Subrata Kumar Satpati, **Rajender Parsad**, V.K. Gupta and A.K. Nigam. Computer Aided Search of Efficient Nested Incomplete Block Designs for Correlated Observations. *Journal of Combinatorics, Information and System Sciences.*

14. Subrata Kumar Satpati, **Rajender Parsad** and V.K. Gupta. Efficient block designs for dependent observations: A computer aided search. *Communications-in-Statistics: Theory & Methods*, **36(6)**.
15. Jitendra Kumar, G. Singh, R.K. Palta, Suresh Walia, **Rajender Parsad** and B.S. Parmar. Field appraisal of controlled release formulations of carbofuran against the rice leaffolder, cnaphalocrocis medinalis (guenee). *Indian Journal Agricultural Sciences*.
16. **Rajender Parsad**. A note on semi-Latin squares. *Journal of Indian Society of Agricultural Statistics.*

Communicated/Under Revision

17. Ananta Sarkar, **Rajender Parsad** and M.R. Vats. Multivariate analysis of variance of data from long term fertilizer experiments. *Journal of Indian Society of Agricultural Statistics.*
18. Ananta Sarkar, **Rajender Parsad**, Abhishek Rathore and V.K. Gupta. Efficient block designs for microarray experiments. *Statistical Applications in Genetics and Molecular Biology*.
19. Ananta Sarkar, **Rajender Parsad**, V.K. Gupta and Abhishek Rathore. Efficient row-column designs for microarray experiments. *Biostatistics*.
20. V.K. Gupta, **Rajender Parsad** and Lal Mohan Bhar. Supersaturated designs for asymmetrical factorial experiments. *Journal of Statistical Theory and Practice*.
21. A.K. Joshi, O. Ferrara, M.R. Bhatta, G. Singh, E. Duveiller, R. Sharma, R. Chand, B. Arun, D.B. Pandit, N.C.D. Barma, M.M. A.B. Siddique, S.Y. Das, R.N. Sharma and **Rajender Parsad.** Sources of resistance to spot blotch pathogen *Bipolaris sorokiniana* of wheat for warm humid regions of south Asia. *Field Crops Research.*
22. B.N. Mandal, **Rajender Parsad** and V.K. Gupta. Computer-aided construction of polygonal designs. *Journal of Statistical Planning and Inference*.
23. B.N. Mandal, Rajender Parsad, V.K. Gupta and U.C. Sud. A family of distance balanced sampling plans. *Biometrika.*

(B) Popular Article/Bulletin

1. ***राजेन्द्र प्रसाद***, *अरुण कुमार निगम, विनोद कुमार गुप्ता एवं अजीत कुमार* (2006). *अनुसंधान केन्द्रों और किसानों के खेतों पर किये गये कृषि परीक्षणों की अभिकल्पना एवं विश्लेषणः एक पुनरावलोकन । सांख्यिकी विमर्श, भारतीय कृषि सांख्यिकी अनुसंधान संस्थान, नई दिल्ली ।*
2. **Rajender Parsad** and V.K. Gupta (2007). Statistical issues for experimentation in national agricultural research system. *Proceedings of XIV National Conference of Agricultural Research Statisticians*, 144-151.
3. V.K. Gupta and **Rajender Parsad** (2007). Status of agricultural experimentation in national agricultural research system. *Proceedings of XIV National Conference of Agricultural Research Statisticians*, 58-68.

(C) Book Chapters Published

1. V.K. Gupta and **Rajender Parsad** (2006). Statistical Designing of Experiments with Emphasis on Hill Agriculture. Sustainable Production from Agricultural Watersheds in North West Himalaya. Eds. HS Gupta, AK Srivastava and J.C. Bhatt, Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora, 457-474.
2. **Rajender Parsad,** Anshu Dixit, P.K. Malhotra and V.K. Gupta (2007). Geoinformatics in precision farming: An overview. In the Book entitled "*Geoinformatics Applications for*

sustainable development" Eds. A.K.Singh and U.K. Chopra, 39-78, New India Publishing Agency, New Delhi.

(D) Electronic Book

An electronic book on **Advances in Data Analytical Techniques** has been compiled, edited and developed by Rajender Parsad, V.K. Gupta, Lal Mohan Bhar and V.K. Bhatia. The E-book consists of chapters on 66 topics described in more than 920 pages. The topics covered in this electronic book have been categorized into six modules namely Computer Usage and Statistical Software Packages, Basic Statistical Techniques consisting of Statistical methods and Inference, Design of Experiments and Sample Surveys, Diagnostics and Remedial Measures, Applications of Multivariate Techniques, Modelling and Forecasting Techniques in Agriculture and Other Useful Techniques such as Bio-informatics, Geoinformatics, Microarrays, DNA Fingerprinting, nanotechnology in agriculture etc. This book is available at IASRI website (www.iasri.res.in).

(E) Monographs

Rajender Parsad, V.K. Gupta, P.K. Batra, S.K. Satpati and Pabitra Biswas (2007). α-Designs. IASRI, New Delhi.

➢ Awards and Recognitions

Awards

- **Associate Fellow** of National Academy of Agricultural Sciences, New Delhi from January 01, 2007.

Recognitions

- **Member, Organizing Committee** and **Chairman, Publication and Souvenir Committee** of the **International Conference on Statistics and Informatics in Agricultural Research** organized at IASRI, New Delhi during December 27-30, 2006.
- **Convener** *for the* Theme on **Emerging Issues in Areas of Basic Statistical Research** during **International Conference on Statistics and Informatics in Agricultural Research** organized at IASRI, New Delhi during December 27-30, 2006.
- **Convener** of a s**ymposium on Information Extraction from Data Investigation** and **Chaired** a session on Contributed Papers during 9th Annual Conference of Society of Statistics, Computer and Applications held at Department of Statistics, Saurashtra University Rajkot during November 11-13, 2006.
- Nominated as M**anaging Editor of Journal of Econometric Applications and Theory**, A publication of Forum for Interdisciplinary Mathematics.
- Nominated as **Joint Secretary**, **Forum for Interdisciplinary Mathematics**.
- Acted as referee for Journal of Statistical Planning and Inference, Journal of Statistical Theory and Practice, ARS Combinatoria
- Member, Editorial Board for सांख्यिकी विमर्श 2006-2007.
- संस्थान में आयोजित 01 से 30 सितम्बर, 2007 क दौरान आयोजित किये गये हिन्दी चेतना मास में निम्न कार्यकमों के आयोजन में सहभागिताः
  1. सदस्य उप–समिति शोध पत्र पोस्टर प्रदर्शन प्रतियोगिता
  2. अध्यक्ष उप–समिति, वाद–विवाद प्रतियोगिता
  3. मूल्यांकन, निबन्ध लेखन प्रतियोगिता

➢ Conferences/ Workshops organized

- A training programme on ***Design and Analysis of Experiments for Rapeseed-Mustard Varietal Trials*** for the plant breeders and statisticians of All India Co-ordinated Research Project on Rapeseed-Mustard, National Research Centre on Rapseed-Mustard, Bharatpur was organized during May 10-11, 2006. 13 participants attended the training programme. 8 participants were from State Agricultural Universities and 5 from ICAR Institutes. The topics covered in this training programme included Fundamentals of Design of Experiments, MS-Excel: Analysis of Experimental Data, SPSS: An Overview, Combined Analysis of Data and Stability Analysis. Participants have analyzed some of the data sets on their own. The preparation of data and important characters such as seed yield, oil content and plant stand were finalized on which replicated data shall be collected. It was also decided that the randomized layout should also be provided along with data to the co-ordinating unit.
- A Workshop-cum-training programme on ***Design and Analysis of Farmers Participatory Research Trials*** for the research personnel involved in the conduct of farmers participatory research trials under the aegis of Rice Wheat Constortium for Indo-Gangetic Plains was organized during August 10-12, 2006. This workshop-cum-training programme aimed at the theme of statistical principles involved in the conduct of farmers participatory research trials. It was attended by 20 participants. Out of 20 participants, 7 were from RWC-CIMMYT, 2 from IRRI, 2 from Banaras Hindu University, 4 from different ICAR Institutes, 4 from SAUs and 1 from State Department of Agriculture. The topics discussed were fundamentals of design of experiments, contrast analysis, analysis of covariance, biplot graphic display, SAS and ASreml. The main emphasis was laid on case studies. Several real data sets were analyzed by the participants using SAS. The workshop-cum-training programme was conducted in participatory mode. A lot of discussions took place. It was decided that some treatments such as conventional tillage may be kept common for all the farmers. The data may be analyzed on grain yield, straw yield, thousand grain weight and returns over variable cost. To investigate the effect of resource conversation technologies on the soil physical and biological properties, long term experiments with reference to resource conservation technologies may be conducted at some of the ICAR institutes. The clear cut definition and identification of treatments was done and all the centres were asked to present their data as per the terminology finalized. The variables on which the data is to be supplied were also finalized along with EXCEL sheets.
- Organized a symposium on ***Information Extraction from Data Investigation*** as Convener during the 9th Annual Conference of Society of Statistics, Computer and Applications held at Department of Statistics, Saurashtra University Rajkot during November 11-13, 2006.
- Organized four Sessions on the ***Theme 2: Emerging Issues in Areas of Basic Statistical Research*** as Convener along with Professor Sudhir Gupta, Northern Illinois University, USA during International Conference on Statistics and Informatics in Agricultural Research organized by at I.A.S.R.I., New Delhi during December 27-30, 2006 to celebrate the Diamond Jubilee of Indian Society of Agricultural Statistics at NASC Complex, New Delhi.

➢ Teaching and Research Guidance

A) Teaching

Year	Trimester	Course	Taught Jointly with	Number of Lectures Taken
2005-06	Trimester II	AS 171: Bioinformatics-I (3L+1P)	Dr. V.K. Bhatia, Dr. A.R. Rao & Dr. K.V. Bhatt	9 (8L + 1P)
2005-06	Trimester III	AS 163: Statistical Inference (4L + 1P)	Dr. L.M. Bhar	31(25L+6P)
2005-06	Trimester III	AS 208: Bio-informatics-II (2L+1P)	Dr. V.K. Bhatia and Dr. K.V. Bhat	6 (6L+0P)
2006-07	Trimester - I	AS 200: Design of Experiments-II (1L+1P)	Dr. Cini Varghese	18 (15L +3P)
2006-07	Trimester-II	AS 171: Bioinformatics-I (3L+1P)	Dr. V.K. Bhatia and Dr. K.V. Bhat	19 (15L+4P)

B) Research Guidance (P.G. Students Guided)

- **Chairman Advisory Committee**:
  - 2 Ph.D. (Agricultural Statistics) : Continuing
  - Sh. Ananta Sarkar, Roll No. 8976 completed his Ph.D. (Agricultural Statistics). Title of his thesis was **A Study on Design and Analysis of Microarray Experiments**.

The salient achievements of the above research investigation are:
In microarray experiments, the four experimental factors are array (*A*), dye (*D*), variety (*V*) and gene (*G*). These four experimental factors give rise to 2^4 -1= 15 possible experimental effects excluding the general mean. Out of these 15 possible experimental effects, seven effects viz. array (*A*), dye (*D*), variety (*V*), gene (*G*), array-gene interaction (*AG*), dye-gene interaction (*DG*), variety-gene interaction (*VG*) effects are of main interest to the experimenter. In the present investigation, we have considered experimental situations where the same set of genes is spotted on each array. Therefore, gene/gene specific effects (*G*, *AG*, *DG*, *VG*) are orthogonal to global effects (*A*, *D*, *V*). Optimality aspects of designs for microarray experiments, can therefore, be studied leaving gene specific effects from the model, *i.e*., by taking only array, dye and variety effects in the model. Designs that are good under the model containing global effects are also good under the model containing both global and gene specific effects.

In 2-colour microarray experiments, only two varieties labelled with two different dyes can be accommodated on one array; therefore, arrays may be considered as blocks of size 2. Further, array effects may be taken as random. To deal with the problem of obtaining efficient designs when array effects are random, the lower bounds to the A- and D-efficiencies of the designs in a given class of designs have been obtained for block designs under mixed effects model. The existing algorithm based on exchange and interchange of treatments has been modified by incorporating the procedure of computing lower bounds to A- and D-efficiencies under mixed effects model. The algorithm developed is general in nature and can be used for generation of efficient block designs for any $2 \le k < v$, where v is the number of treatments (varieties) and k is block size. Using this algorithm, efficient block designs for microarray experiments have been obtained in the parametric range $3 \le v \le 16$, $v \le b \le v(v-1)/2$ and $17 \le v \le 25$ **;** $b = v$ and $k = 2$, where b is the number of arrays/ blocks. A total of 569 designs including all the 14 unreduced

balanced incomplete block designs in this parametric range have been obtained. Efficient block designs obtained under fixed effects model have been compared with the best available designs (designs with highest lower bound to A-efficiency) in literature and 2-associate partially balanced incomplete block designs. 30 designs are found to be more efficient than the best available block designs. The robustness aspects of designs obtained and best available block designs have been investigated under mixed effects model. Out of 30 more efficient designs, 7 designs are found to be strongly robust, 18 designs are found to be robust and the remaining 5 designs are non-robust.

Efficient block designs for 2-colour microarray experiments have been obtained under a restricted model involving array and variety effects. The dye effects have been ignored from the model, since in microarray experiments, the two varieties appearing on the array are to be labeled with two different dyes. If the variety at position 1 in a block is labeled with dye 1 and the variety at position 2 is labeled with dye 2, then the block contents should be so arranged that the varieties are most balanced with respect to dyes. Further, if dye effects are included in the model, then the structure of the design becomes that of a row-column design where arrays represent columns, dyes represent rows and varieties represent treatments. Efficient row-column designs have been obtained in the parametric range $3 \le v \le 10, v \le b \le v(v-1)/2$; $11 \le v \le 25, b = v$ and $(v, b) =$ (11, 13), (12, 14), (13, 14) and (13, 15), where b is the number of arrays/columns by modifying the existing exchange and interchange algorithm of row-column designs. A total of 139 designs have been obtained. Efficient row-column designs obtained under fixed effects model are then compared with the best available designs (block designs with highest A-efficiency under row-column set up after rearranging the block contents in such a fashion that the varieties are most balanced with respect to dyes) and even designs (designs in which replication of each variety is even). 45 designs are found to be more efficient than the best available designs and 90 designs obtained are more efficient than the best even designs. Robustness aspects of designs obtained and best available designs are then investigated under mixed effects model. Out of 45 more efficient designs, 9 designs are found to be strongly robust, 22 designs are found to be robust and the remaining 14 designs are not-robust.

The catalogues of all efficient block designs and row-column designs obtained and the best available designs have been prepared along with their lower bounds to A-and D-efficiencies under fixed/mixed effects models and their robustness status. Strength of the algorithm for obtaining block designs/ row-column designs for 3-colour microarray experiments has also been demonstrated with the help of examples.

After the conduct of experiment using an appropriate design, the next step is analysis of data to identify differentially expressed genes from microarray experiments. We have developed analytical procedure based on single-step mixed effects model as well as two-stage linear mixed effects models considering array effects as random to identify differentially expressed genes from microarray experiments. The analytical techniques developed have been illustrated using real life data sets.

- **Co-Chairman Advisory Committee:** 2 M.Sc. (Agricultural Statistics) students completed.
- **Member Advisory Committee:** 6 students (1 Ph.D. and 5 M.Sc.) completed their respective degrees.

➢ Presentations in Conferences/ Symposia/ Workshop/ Seminar and Other fora

- Presented 11 research papers (2 Invited by self, 4 invited and 5 contributed by co-authors)

No.	Name of the Conference/ Sumposia/ Workshop	Organizing Institution, Venue and Duration	Papers Presented
1.	Group Meeting of AICRP on STCR	I.A.S.R.I., New Delhi during November 02-03, 2006	- Design and Analysis of Experiments Under AICRP on STCR (V.K. Gupta*, **Rajender Parsad**)
2.	9th Annual Conference of Society of Statistics, Computer and Applications	Department of Statistics, Saurashtra University Rajkot during November 11-13, 2006.	- Statistical Analytical Techniques for Farmers' Participatory Research trials for Conservation Agriculture. (**Rajender Parsad*,** Jose Crossa and V.K. Gupta): **Invited Talk in** Symposium on **Information Extraction from Data Investigation**. - Super Saturated Designs: Some Thoughts (V.K. Gupta*, **Rajender Parsad** and Lal Mohan Bhar): **Special Invited Talk**
3.	International Conference on Statistics and Informatics in Agricultural Research as Diamond Jubilee of Indian Society of Agricultural Statistics at NASC Complex, New Delhi.	I.A.S.R.I., New Delhi during December 27-30, 2006	- Efficient Designs for 2-Colour Microarray Experiments (Ananta Sarkar, **Rajender Parsad***, V.K. Gupta and Abhishek Rathore): Invited Talk in Theme 4: Statistical and Computational Biology in Agriculture - Supersaturated Designs for Asymmetrical Factorial Experiments (V.K. Gupta*, **Rajender Parsad** and L.M. Bhar): Invited Talk in Theme 2: Emerging Issues in Areas of Basic Statistical Research. - Computer Aided Generation of Hadamard Matrices and Orthogonal Arrays (A. Dhandpani*, V.K. Gupta and **Rajender Parsad): Invited Talk in** Theme 3: Agricultural Informatics **Poster Presentations** - Robustness aspects of response surface designs against loss of data (R. Srivastava*, **Rajender Parsad**, Manisha Jain and P.K. Batra) - Robustness of BIB and GD designs for correlated observations (Seema Jaggi. **Rajender Parsad**, V.K.Gupta and Suman Kumar*) - Construction of Doubly Nested Balanced Incomplete Block Design (B.N. Mandal*, **Rajender Parsad** and V.K. Gupta) - Analysis of On-Farm Experiments over Farming Situations (D.N. Jha*, P.K. Batra and **Rajender Parsad)** - Analysis of Microarray Data (Ananta Sarkar*, **Rajender Parsad**, K.V. Bhat and V.K. Bhatia).

(* represents the author who presented the paper)

➢ Besides the above, I also attended the following:

- Brain Storming Session on Low and Declining Crop Responses organized by National Academy of Agricultural Sciences during February 20-21, 2006.
- XIII Annual Group Meeting of AICRP on Rapeseed and Mustard held at CCS HAU Hisar during August 02-04, 2006 as Resource Person.

➢ Special Lectures Delivered

A) Lectures Delivered in Training Programmes at IASRI, New Delhi

➢ 22 Lectures were delivered on the following topics during various training programmes held at I.A.S.R.I., New Delhi.

• Training programme on **Design and Analysis of Experiments for Rapeseed-Mustard Varietal Trials** for plant breeders and statisticians of AICRP on Rapeseed-Mustard (May 10-11, 2006).	**4 Lectures**
- File preparation in MS-Excel	1 Lecture
- Analysis of Variance, Analysis of Covariance, Multiple Comparison Procedures	1 Lecture
- Diagnostics in Designed Experiments	1 Lecture
- Combined Analysis of Experimental Data	1 Lecture
• Refresher course on **Small Area Estimation** for the senior and middle level officers from Central Statistical Organization (July 10-15, 2006)	**2 Lectures**
- SAS: An Overview	2 Lectures
• Summer School on **Sample Survey Techniques in Agricultural Research** (September 05-25, 2006).	**1 Lecture**
- SAS: An Overview	1 Lecture
• Training programme on **Biometrics in Agricultural Research** (October 03-November 30, 2006)	**3 Lectures**
- SPBD Release 1.0	1 Lecture
- SPFE 1.0	2 Lectures
• Training programme on **Statistical Methods for Agricultural Research with Use of Software** (November 01-21, 2006).	**4 Lectures**
- SAS: An overview and SAS: Statistical Procedures	2 Lecture
- Multiple Comparison Procedures	1 Lecture
- SPBD/SPFE/SPAD	1 Lecture
• Training programme on **Advances in Data Analytical Techniques** (February 08-28, 2007).	**8 Lectures**
- SAS: An Overview	1 Lecture
- Minitab: An Overview	1 Lecture
- SPBD/SPFE/SPAD	1 Lecture
- Hotelling T^2 and Multivariate Analysis of Variance	1 Lecture
- Principal Component Analysis, Factor Analysis and Discriminant Analysis	1 Lecture
- Response Surface Methodology	1 Lecture
- Multiple Comparison Procedure	1 Lecture
- Design and Analysis of Microarrays	1 Lecture

➢ Besides above, a Seminar on **Hands on Experience of Analysis of Farmers Participatory Research Trials Conducted By Rice-Wheat Consortium for Indo-Gangetic Plains** was delivered on July 28, 2006.

B) Invited Lectures Delivered

3 Invited Lectures are delivered Division of Agricultural Economics, IARI, New Delhi; Water Technology Centre, IARI, Faculty and Students, M.D. University, Rohtak.

- One lecture on **Multivariate Techniques: An Overview** to the participants of the training programme organized under center of Advanced Studies at Division of Agricultural Economics, IARI, New Delhi. (March 14, 2006).
- One lecture on **Fundamentals of Design of Experiments** at Water Technology Centre, IARI, New Delhi (December 04, 2006)
- One lecture on **Statistics: Career and Prospects** to the students and faculty of Department of Statistics, M.D. University, Rohtak during their study visit to IASRI, New Delhi on March 22, 2007.

➢ Visits Abroad

1. Deputed for a study visit on Hands-on Experience on Analysis of Farmer Participatory Research Trials conducted by Rice-Wheat Consortium for Indo-Gangetic Plains to CIMMYT, Mexico from May 24-June 28, 2006. During this study visit, I worked on ASREML (a statistical package that fits linear mixed effects models using Residual Maximum Likelihood (REML)) for spatial data analysis. Also worked on SAS to obtain biplots from Additive Main Effects and Multiplicative Interactions, and Sites Regression (SREG) models. Analyzed 5 data sets of RWC for IGP. In this analysis, farmers or villages are taken as blocks and resource conservation technology options as treatments. Farmers/villages effects were taken as random. Efforts were also made to find year × trt interactions and variety × treatment interactions. The efforts were also made to identify technology for a given variety or soil type. The results obtained were communicated to Dr R.K. Gupta and other scientists involved for their comments. The data file preparation for the analysis is very important. Some suggestions were also made on how to prepare the EXCEL files to maintain uniformity overall locations and years.

2. Deputed for participating in 14th Regional Technical Coordination Committee Meeting of the Rice-Wheat Consortium for Indo-Gangetic Plains held at Katmandu, Nepal during February 13-16, 2007. During this meeting, I presented a paper on **Statistical Tools for Farmers' Participatory Research Trials for Conservation Agriculture**.

Executive Summary

- In agricultural experiments, generally data on more than one character is observed. The experiments, where corresponding to the application of a treatment, more than one response variables are recorded, are known as multi-response experiments. Analytical procedures of analysis of data from multi-response experiments conducted using block designs have been developed. A method based on Euclidean distance and J-plot has also been developed for identification of the best treatment.
- To tackle the problem of outlier(s) in multi-response experiments, a test statistic has been developed for identification of a single outlier observation vector in complete multi-response experiments run in a block design.
- A catalogue of block designs with minimally connected designs with 4, 5, 6, 7 or 8 extra observations has been prepared alongwith lower bounds to A- and D- efficiencies and block contents.
- Extended Group Divisible (EGD) designs for three factors that permit the estimation of all main effects with no loss of information were obtained using self-complementary GD designs with replication number less than 6 and block size less than 11. A catalogue of such designs along with efficiencies for main effects and interactions was prepared. These designs are useful for crop sequence experiments.
- Results on non-existence of NPBIB designs based on group divisible designs has been obtained. Methods of construction of NPBIB designs based on Latin Square association scheme and Rectangular association scheme have been obtained and catalogued.
- Nested block designs for nearest neighbour correlation structure within sub-blocks of a block in a nested block design set up and for zero correlation structure in bigger blocks ignoring the sub-block classification were obtained.
- Analytical techniques based on mixed effects models and biplots have been developed for analysis of data generated from Farmers' participatory research trials for Resource Conservation Technologies conducted by the Rice-Wheat Consortium (RWC) for Indo-Gangetic Plains.
- Doubly nested partially balanced incomplete block designs have been introduced. Some general methods of construction of doubly nested partially balanced incomplete block designs are obtained using doubly nested balanced incomplete block (DNBIB) designs, nested balanced incomplete block designs and partially balanced incomplete block designs.
- Robustness of BIB and PBIB [Group Divisible (GD) and Cyclic] designs has been studied under correlated error structure [NN and AR(1)] for a given value of correlation coefficient in terms of A-efficiency.
- Binary variance balanced block designs have been shown robust in the presence of two outliers. Robust estimation procedure of treatment effects based on Least Median Squares has been developed.
- Developed a β-version of On-line Software for the generation of Hadamard matrices up to the order 1000.
- Supersaturated designs for asymmetrical factorial experiments have been obtained using resolvable orthogonal arrays and Hadamard matrices. Some criteria for comparing supersaturated designs for asymmetrical factorial experiments are also given.
- To disseminate the knowledge available on combinatorial aspects of designs and analytical procedures acquired to scientists engaged in research in the National Agricultural Research System. The advisory services are pursued rigorously. For the benefit of the experimenters

and practicing statisticians, Design Resources Server has been strengthened by adding 6574 efficient block designs for making all possible pairwise treatment comparisons.

- Taught **5** courses to M.Sc. and Ph.D. students and guided **1 Ph.D.** student as Chairman; 2 M.Sc. students as Co-Chairman and **5** M.Sc. and **1** Ph.D. students as member advisory committee. **2** Ph.D. students are working under my guidance.
- Published **12** research papers; **3** popular articles; **2** Book Chapters; **1** Electronic Book and **1** Monograph. **4** papers have been accepted for publication and **7** papers have been communicated. **11** papers are presented in International/National Conferences. Delivered **24** lectures in ad-hoc training programmes organized at IASRI and **3 invited lectures** in other academic organizations.
- Organized an International Conference on **Statistics and Informatics in Agricultural Research** as Member Organizing Committee and organized Four Sessions on the **Theme 2: Emerging Issues in Areas of Basic Statistical Research** as Convener along with Professor Sudhir Gupta, Northern Illinois University, USA during this conference.
- Organized a Symposium on **Information Extraction from Data Investigation** as Convener during the 9th Annual Conference of Society of Statistics, Computer and Applications
- Organized three training programmes (i) Design and Analysis of Experiments for Rapeseed-Mustard Varietal Trials; (ii) Design and Analysis of Farmers Participatory Research Trials and (iii) Advances in Data Analytical Techniques as Course Director. Deputed for a study visit on Hands-on-Experience on Analysis of Farmers' Participatory Research Trials Conducted by RWC for Indo-Gangetic Plains to CIMMYT, Mexico during May 24-June 28, 2006. Also deputed for participating in 14th Regional Technical Coordination Committee Meeting of RWC for Indo-Gangetic Plains held at Kathmandu, Nepal during February 14-15, 2007.
- Elected as **Associate Fellow** of **National Academy of Agricultural Sciences**. Nominated as **Managing Editor, Journal of Econometric Applications and Theory**, a publication of Forum for Interdisciplinary Mathematics and **Joint Secretary**, Forum for Interdisciplinary Mathematics.

03/9/07

Signature of Head of the Institute

सुखदेव शर्मा
S.D. SHARMA
निदेशक
Director
भा.कृ.सां.सं., (भा.कृ.अ.प.)
I.A.S.R.I., (I.C.A.R.)
लाइब्रेरी एवेन्यू, नई दिल्ली-110012
Library Avenue, New Delhi-110012

(Rajender Parsad) 03/09/07
Principal Investigator