

ADDIS ABABA UNIVERSITY  
SCHOOL OF GRADUATE STUDIES  
FACULTY OF SCIENCE  
DEPARTMENT OF STATISTICS

CONSTRUCTION AND ANALYSES OF COMPLETE DIALLEL CROSS  
THROUGH PARTIALLY BALANCED INCOMPLETE BLOCK DESIGNS

By

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A Thesis Submitted to the School of Graduate Studies Addis Ababa University  
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## Declaration

I, the undersigned, declare that the thesis is my original work, has not been presented for a degree in any university and that all sources of material used for the thesis have been duly acknowledged.

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## ABSTRACT

Experimental designs for complete diallel cross system IV with equal number of replications of each cross has been studied extensively in the literature. In this paper, we have proposed incomplete block designs for complete diallel cross (CDC) system IV with unequal number of replications for crosses through two-associate classes of partially balanced incomplete block (PBIB (2)) designs where none of two treatments which are  $i^{\text{th}}$  associates occur together in exactly  $\lambda_i$  blocks ( $i = 1, 2$ ) is zero. In addition to the block effects and general combining abilities (gca) effects, the model also includes the parameter of specific combining abilities (sca) effects. The procedure of analyses of these designs has also been developed. The analysis includes the analysis of variance and the estimation (intra-block, inter-block and combined) of general and specific combining abilities. Tests of certain hypotheses concerning some general parameters are also given. The efficiency (optimality) of the proposed designs is also considered in comparison to randomized complete block designs (RCBD). The method of analysis (intra-block, inter-block and combined) has been illustrated with the help of numerical data.

# CHAPTER ONE

## INTRODUCTION

### *1.1. Background of the Study*

Research in genetics is based almost exclusively on experimental investigation, different facets of in genetics using different techniques. The interpretation of and conclusions drawn from these experiment is often based on statistical analyses of some sort. This implies in turn that the design of such experiments must be based, implicitly or explicitly, on statistical considerations in order to obtain data that are relevant to experimenter's questions in the sense that if analyze appropriately they will provide answers to these questions.

One of the main aims of genetical investigation involving crops is to develop improved crop varieties using genetic architecture. When there are a numbers of strains of a crop of one type of investigation consisting of crossing between such strains to evolve new varieties. Through these types of investigation the combining capabilities of the strains can be studied. Normally highly inbred parental lines are considered for such investigation. If there be  $p$  such lines or strains, and each line is crossed with each other line, then there will be  $p^2$  crosses in all. All these crosses constitute what is called complete diallel crosses. For assessing the yielding ability all these crosses are tried in an experiment where these crosses are taken as treatments. The usual designs are adopted for such experiments. The purpose of analyzing of the data collected from such trials is to estimate using appropriate model of the effects or yielding abilities of the original  $p$  lines. When there are large numbers of crosses incomplete block designs can be adopted. Again, when  $p$  line is large, the number of crosses becomes large and sometimes unmanageable.

It is obviously impossible to cover and summarize all aspects of design for genetical experiments in one single paper. A selection therefore has to be made based on personal preference and on the theme of study. A natural choice then is to discuss experiments in quantitatively genetics or, more precisely, certain types of such experiments.

### **1.1.1. Purpose of Genetical Experiments**

Within the framework of this paper, following Hinkelmann (1975), we shall classify experiments in quantitative genetics into two groups: comparative experiments and exploratory experiments.

#### **1.1.1.1. Comparative Experiments**

Comparative experiments in quantitative genetics have the same purpose that comparative experiments have in general: to compare treatments and draw conclusions from the comparisons for practical applications or further theoretical investigations. The “treatments” in a genetical experiment are genetic entities, such as individuals (plant, animal), lines, clones, strains, populations. The main objective is to compare these entities in some form on their genetic merits and predict their performance in or ability to transmit this performance to future generations.

For example, suppose we consider the cross between individuals  $i$  (male), and  $j$  (female) and observe the performance (with regard to some quantitative trait) of their offspring.  $y_{ijk}$  is a phenotypic value of the  $k^{\text{th}}$  offspring; it is composed additively of two parts: a genetic component and an environment component. The genetic component, in turn, is broken down into four parts: a contribution due to (i) male  $i$ ,  $g_i$ , (ii) female,  $j$ ,  $g_j$ , (iii) interaction between  $i$  and  $j$ ,  $s_{ij}$ , and (iv) particular genotype of the  $k^{\text{th}}$  offspring  $\varepsilon_{ijk}$ .

#### **1.1.1.2. Exploratory Experiments**

The main difference between a comparative experiment and an exploratory experiment can be best explained in terms of underlying linear model: the genetic components of a comparative model are considered to be fixed effects, whereas those for an explanatory experiment are considered to be random effects. In other words: the inferences to be drawn from these two types of experiments are quite different and aimed at answering different questions. An explanatory experiment is designed to answer questions such as: what is the genetic structure of a population; i.e., what types of gene action are present in the population;

or: Is there any interaction between genotypes and environment present and if so, of what type is this interaction.

The objectives of comparative and exploratory experiments are that: how can these objectives be achieved? This brings us to the actual design aspects for genetical experiments, which means finding ways to generate data that are appropriate for answering relevant questions of a comparative or exploratory nature. There are two design aspects involved in this problem of generating data: (i) the mating design, (ii) the environmental design. Although the separation into these aspects is not unique to genetical experiments it is perhaps more pronounced here and the techniques are different from those used for the more familiar types of experiments.

### **1.1.2. Diallel Crosses**

The term *diallel* is a Greek word and implies all possible crosses among a collection of male and female animals. Hayman (1954a, 1954b) defined diallel cross as the set of all possible crosses between several genotypes, which may be individuals, clones, homozygous lines etc. Diallel cross is most balanced and systematic experiment to examine continuous variation. The genetic information related to parental population is available in early generation ( $F_1$  itself). Thus, it is useful to breeding strategy without losing much time. Many improvements with respect to generalization of diallel crosses enlarge its scope and utility.

Diallel crosses are used mainly (1) to estimate the genetic components of variation of a quantitative character and (2) to estimate the combining abilities of different inbred lines involved in the crosses.

The concept of combining ability is becoming increasingly important in plant and animal breeding. It is the measure of gene action and helps in evaluation of inbreds in terms of their genetic value and in the selection of parents for hybridization. Superior cross combinations can be identified by this technique. It is a special useful in connection with 'testing' procedures, in which it is desired to study and compare the performance of lines or hybrid combination. There are two types combining abilities: general combining ability and specific combining ability. In this paper, we consider the definitions of general and specific combining ability when the testing procedure utilizes a diallel cross system. It was with such a system that the terms general and specific combining ability were originally defined by

Sprague and Tatum (1942). They defined the terms as follows: “the term ‘general combining ability’ is used to designate the average performance of a line in hybrid combination....the term ‘specific combining ability’ is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis average performance of a line involved”. General combining ability is analogous to the main effect of a factorial experiment. It is estimated from half-sib families. Specific combining ability refers to a pair of inbred lines involved in a cross. It indicates cases in which certain combinations do relatively better or worse than would be expected on the basis of *gca* effects of the two lines involved in it. It is the derivation of a particular cross from the experimentation on the basis of average *gca* effects of the two lines involved. It is analogous to an interaction effect of factorial experiment discussed by Parsad (2000).

By diallel crossing system is meant one in which a set of inbred lines is chosen and crosses among these lines made. This procedure gives rise to a maximum of  $p^2$  combinations. Data from such combinations can be most conveniently set out in a  $p \times p$  table in which  $y_{ii}$  represents the mean value for the  $i^{\text{th}}$  inbred and  $y_{ij}$  the mean value for the first generation progeny ( $F_1$ ) resulting from crossing the  $i^{\text{th}}$  and  $j^{\text{th}}$  inbreds and  $y_{ji}$  represents its reciprocal. Thus, the  $p^2$  combinations can be divided into three groups, (1) the  $p$  parental lines themselves, (2) one set of  $\frac{1}{2} p(p-1)$   $F_1$ 's hybrid, and (3) the set of  $\binom{p}{2} = \frac{1}{2} p(p-1)$   $F_1$ 's reciprocal hybrid.

Diallel crossing techniques may vary depending upon whether or not the parental inbreds or the reciprocal  $F_1$ 's are included or both. With this as a basis for classification (sometimes known as Griffing classification of diallel cross), there are four possible experimental methods: (1) Parents, one set of  $F_1$ 's and reciprocal  $F_1$ 's are included (all  $p^2$  combinations); (2) Parents and one set of  $F_1$ 's are included but not the reciprocal  $F_1$ 's ( $\frac{1}{2} p(p+1)$  combinations), i.e., include  $p$  parents and  $\binom{p}{2}$   $F_1$ 's hybrids; (3) One set of  $F_1$ 's and reciprocal  $F_1$ 's are included but not the parents ( $p(p-1)$  combinations), i.e., including  $\binom{p}{2}$   $F_1$ 's hybrids

and  $\binom{p}{2}$   $F_1$ 's reciprocals; and (4) One set of  $F_1$ 's but neither parents nor reciprocal  $F_1$ 's is included ( $\frac{1}{2}p(p-1)$  combinations), i.e.,  $\binom{p}{2}$   $F_1$ 's only.

With regard to sampling assumptions, it is necessary to distinguish between (1) the situation in which the parental lines simply or the experimental material as a whole are assumed to be a random sample from some population about which inferences are to be made, and (2) the situation in which the lines are deliberately chosen and cannot be regarded as a random sample from any population. This second assumption can be expressed somewhat differently by stating that the experimental material constitutes the entire population about which valid inferences can be made.

These two different assumptions give rise to different estimation problems and different tests of hypotheses regarding combining ability effects.

Among the four types of diallel crosses discussed by Griffing (1956), here we shall consider only the designs used for the 4<sup>th</sup> types of analysis. That are the designs for diallel cross experiment involving  $\frac{1}{2}p(p-1)$  crosses of types  $(ixj = jxi)$  for  $i < j$  and  $i, j = 1, 2, \dots, p$ . This is called System IV mating design of Griffing. It is also known as modified diallel system or half diallel we shall refer to it as a complete diallel cross (CDC), the most commonly used diallel cross in plant breeding.

Diallel crossing is a very useful method for conducting plant and animal breeding experiments, especially for estimating combining ability effects of lines. Diallel crosses in which all possible distinct crosses in pairs among the available lines are taken are called complete diallel crosses. Diallel crosses in which only a fraction of all possible crosses among the available lines are taken are called partial diallel crosses. When the number of lines is large, it is desirable to adopt partial diallel crosses.

A common experimental design in genetics is the diallel cross, in which pairs of distinct lines (strains) are crossbred in order to estimate genetic effects. Let  $p$  denote the number of lines and it is desired to perform a diallel cross experiment involving  $v = \frac{1}{2}p(p-1)$  crosses of the type  $ixj$ , between lines  $i$  and  $j$ , where  $i < j = 1, \dots, p$ . This is the complete diallel

cross experimental method IV mating design Griffing (1956) with  $p$  inbred lines. Griffing (1956) discussed in detail the analysis of complete diallel cross experimental method IV mating design experiment in randomized complete block design (RCBD).

To obtain unbiased estimates of the population parameters of general combining ability variance ( $\sigma_{gca}^2$ ) and specific combining ability variance ( $\sigma_{sca}^2$ ), it is necessary to modify diallel cross system. The inclusion of inbreeds vitiates this properties of the estimates obtained from experimental data. This method could be chosen for genetic investigation when maternal inheritance is not suspected, i.e., reciprocal crosses give the same result. Also this method requires lesser number of experimental units. This has received much attention now a days because  $gca$  are important while selecting inbred lines for hybrid discussed by Parsad (2000).

In this paper, a simple method of construction of mating-environmental designs CDC system IV is proposed by using two associate classes of partially balanced incomplete block (abbreviated PBIB (2)) designs with  $\lambda_i \neq 0$  ( $i = 1,2$ ). A method of analysing these designs is also described. The statistical analysis includes the analysis of variance and the estimation (intra-block, inter-block and combined) of general and specific combining abilities. Tests of certain hypotheses concerning some general parameters are also given.

### ***1.2. Motivation/ Statement of the Problem***

Diallel crosses as mating designs are used to study the genetic properties of inbred lines in plant and animal breeding experiments. Most of the theory of diallel cross designs is based on standard linear model assumption. The model does not include the parameter representing the specific combining abilities and also the general combining ability effects and block effects are taken to be fixed. In this paper, we address this problem by including the parameter of specific combining ability and block effects as a random variable.

### ***1.3. Objectives of the Study***

- To give method of construction of mating designs for complete diallel cross (CDC) system IV through two-associate classes partially balanced incomplete block (PBIB(2)) designs.

- To develop environmental designs for the crosses obtained through mating designs.
- To give method of analysis to estimates the effect of general combining ability (gca) and specific combining ability (sca).
- To compare the efficiency (optimality) of proposed environmental designs in comparison to randomized complete block design (RCBD).

#### **1.4. Application of Results**

- The study will contribute a new method for obtaining complete diallel cross and as well as method of analysis in the presence of specific combining ability.
- The study will also boost further research in plant and animal breeding.
- The result of this study provides information to researchers and further investigation on diallel crosses.
- The results help for practitioners to understand and adjust their investigation programs.
- The results help as a basis for further study in this area.

#### **1.5. Limitations of the Study**

The study has the following limitations.

- Two-associate classes of partially balanced incomplete block (PBIB (2)) designs are used in method of construction as auxiliary designs. The catalogue of the plans of PBIB (2) designs has been prepared by Clatworthy (1973). It may be possible that many researchers do not access to this catalogue.
- The mating designs for diallel crosses are not available for every value of inbred line  $p$ .
- In mating designs each cross is not replicated equal number of times. Due to this reason, these designs are not found to be optimal but in the literature optimal designs

in the presence of specific combining consume large number of experimental units in comparison of our proposed designs.

# CHAPTER TWO

## Literature Review

### *2.1. The General Literature Review about the Environmental Design used in the Study*

Incomplete block designs have become highly developed as statistical tool for the planning, conduct, analysis, and interpretation of scientific experimentation conducted in laboratories and test installations where high degree of experimental control is desirable or even necessary to cope with the experimental variability that in variably arises throughout the conduct of the experiment. Historically use of the designs began with balanced incomplete block (BIB) designs introduced by Yates (1936a) and developed by Fisher and Yates (1938), and Bose (1939) and extensively tabled in Fisher and Yates (1963) and Cochran and Cox (1957) along with the lattice designs of Yates (1936b, 1937) and Cochran and Cox (1957) all of which were developed for use in agricultural and biological experiments. Further refinements in statistically based experimental arrangements of the first type were developed by Youden (1937, 1951) and the second by Harshbarger (1946, 1947) and Nair (1951). Bose and Nair (1939) developed a very general class of incomplete block designs, which they called partially balanced incomplete block designs with  $m$  associate classes (abbreviated PBIB ( $m$ ) designs). These designs include the balanced incomplete block (BIB) designs and the square and rectangular lattice designs as special cases. Generally, they have the advantage of an extremely large selection of experimental arrangements from which investigators may choose the ones best suited to their needs. Beside the advantage of control of experimental variation through blocking technique, they offer (1) the opportunity to select plans of smaller size (few repetitions of the treatments, varieties, test conditions etc), (2) Statistical analysis of the experimental data by relatively simple computational procedures, and (3) Simplicity of presentation and interpretation of the results from comparative experiments in terms of clear-cut statements about their precision based on modern statistical developments.

In the United States and England during the period of World War II, a strong interest was developed in industry and in government to adapt the developments in probability and small sample theory to the control of quality of production processes of industry. The interest was

extended after the war to the introduction of statistical procedures to the experimental problems of the physical and engineering sciences. This effort has been particularly significant in the vast expensive investigative activity associated with atomic power and aerospace developments. Today there is intense interest in current developments in probability and statistics for possible application to research and development in all branches of sciences, engineering, health and medical research, business, and in fact, in any area where decisions need be made on the basis of incomplete information. Thus the incomplete block designs have potential for application to many fields of investigation.

By 1952 R.C. Bose and a group of his advanced degree students at the University North Carolina (including S.S. Shrikhande, W.S. Connor, T. Shimamoto, and W. H. Clatworthy) has sufficiently extended and developed the partially balanced incomplete block designs with two associate classes (PBIB(2) designs) that several hundreds were now available. With the encouragement Gertrude Cox, Director of the Institute of Statistics, consolidated University of North Carolina, and with support of the Agricultural Experiment Station, North Carolina State College, some 375 of these PBIB(2) designs were classified, catalogued and generally put into convenient form for use by experimenters. A monograph was published by Bose, Clatworthy and Shrikhande (1954) very soon after Bose and Shimamoto (1952) had developed the concept of association schemes, on which the classification of PBIB (2) designs, is based. Since in 1952 the concept of association schemes has been the subject of intensive research by statisticians interested in combinatorial problems of the design of experiments. The intimate relations between association schemes and certain types of graphs have attracted many mathematicians interested in the graph theory to join in their investigation. The resulting improved insight into the construction problems of PBIB(2) designs accompanying the improved knowledge of association schemes, leads to the construction of literally hundreds of new designs of PBIB(2) type since the publication by Bose, Clatworthy, and Shrikhande (1954).

The vast development of new designs of PBIB (2) type are the extremely widespread frequent referencing of Clatworthy (1973) by scholars all over the world, and the very high potential for use of these combinatorial arrangements in scientific experimentation.

## ***2.2. The Use of Mating Designs in the Environmental Designs***

A Diallel is a mating scheme used by plant breeders and geneticists to test for general and specific combining ability as well as genetic effects behind quantitative traits (Hallauer and Filho, 1988).

In a full diallel, all parents are crossed to make hybrids in all possible combinations. Variations include partial diallel with and without parents. Full diallel require twice as many crosses and entries in experiments, but allows for testing for maternal effects. If maternal effects are assumed to be negligible, then a partial diallel without reciprocals is effective.

Common analysis methods utilize general linear models to identify heterotic groups (Griffing, 1956), estimate general combining ability (gca), specific combining ability (sca)(Gardner and Eberhart, 1966), interactions with testing environments, years, and estimates of additive, dominant, and epistatic genetic effects discussed by Hayman (1958), and Sprague and Tatum, 1942).

Other common mating designs used to study quantitative genetics effects include regression, generation (Hayman, 1958), triple test cross (Kearsey and Jinks, 1968), and the mating schemes proposed by Comstock and Robinson (1948) called by plant breeders North Carolina (NC) I nested design, NC II factorial design, and NC III testcross mating designs.

Plant breeders frequently study the genetic properties of inbred lines using complete diallel crosses (CDC) or partial diallel crosses (PDC) as mating designs. Most common diallel cross experiment (CDCs or PDCs) have been evaluated using a completely randomized design (CRD) or a randomized complete block design (RCBD) with suitable number of replications as environmental design (e. g., Kempthorne and Curnow, 1961; Curnow, 1963; Hinkelmann and Kempthorne, 1963; Arya, 1983). Due to the limitation of homogeneous experimental units in a block to accommodate all the chosen crosses, the estimates of genetic parameters would not be precise enough if a complete block design was adopted for the large number of crosses. The number of inbred lines increases, the number of crosses increases rapidly. For example, with  $p=5$  lines there are only 10 crosses. While for  $p =10$  the number of crosses is 45 and when  $p=15$  it becomes 105. Laying out the design, as a randomized complete block design, even with a moderately large number of lines, will, however, result in to large blocks

and consequently large intra-block variances due to loss of homogeneity. It results in to high coefficient of variation (CV) and hence reduced precision on the comparisons of interest.

In order to overcome this problem, one may use incomplete block designs like balanced incomplete block (BIB) designs and partially balanced incomplete block (PBIB) designs with two-associate classes, cyclic designs, nested designs etc by treating the crosses as treatments for one-way elimination of heterogeneity settings. Under such circumstances, the use of suitable incomplete block designs is inevitable and is suggested, by Braaten (1965), Aggrawal (1974), Das and Giri (1986), Ceranka and Mejza (1988), Agarwal and Das (1990), and Divecha and Ghosh (1994). Hinkelmann (1975) stresses the importance of embedding mating designs in environment designs. Gupta and Kageyama (1994), Dey and Midha (1996), Mukerjee (1997), Das, Dey and Dean (1998), Ghosh and Divecha (1997), Parsad, Gupta, and Srivastava (1999) and Sharma (2000), Sharma (2005) addressed the problem of finding optimal designs by using nested incomplete block designs (NBIB), triangular PBIB designs, nested balanced block (NBB) designs, GD PBIB designs, PBIB designs and circular designs respectively. Singh and Hinkelmann (1995) consider the use of partial diallel crosses in incomplete block designs, give methods for constructing mating-environment designs and evaluate their efficiencies.

These designs have interesting optimality properties while making inferences on a complete set of orthonormalised treatment contrasts. However, in diallel cross experiments the main interest of the experimenter in making comparisons among general combining ability of lines and, therefore, using these designs as mating designs may result in poor precision for the comparisons among lines. Further, the analysis of a diallel cross experiments in incomplete blocks depends on the incidence of lines in blocks, rather than the incidence of experiments or crosses in blocks. Another approach advocated in the literature is to start with an incomplete block design, write all the pairs of treatments within a block, and identify these pairs of treatments as crosses by treating treatments of the original incomplete block designs as lines and use the resulting design as a design for diallel crosses. Das and Giri (1986) used this approach for complete diallel crosses (CDC) experiments by using BIB designs. Later, using the same technique with PBIB designs, designs have been obtained for partial diallel crosses (PDC) experiments. Sharma (1998) obtained designs for partial diallel crosses through circular designs. Sharma and Sileshi have considered MS- Optimal partial diallel cross designs (2007), optimal block designs (2009), incomplete block designs for CDC

experiments I and III (2009). Chai and Mukerjee (1999) obtained optimal designs for diallel crosses with specific combining abilities. In this paper, we considered incomplete block designs for CDC experiment method IV. Experiment Method IV is chosen for the following reasons:

1. It represents the most commonly used diallel crossing systems.
2. When the necessary assumptions concerning the sampling nature the set of inbreds can be validity made, it is possible to give an exact genetic interpretation to the general and specific combining ability variances.
3. Reciprocal genotypic effects are generally non-existent in plant data. Therefore, it is not necessary to introduce the additional complication of reciprocal  $F_1$ 'S.

### ***2.3. Definitions and Concepts of Partially Balanced Incomplete Block Designs***

The definition of PBIB designs is based on the concept of association schemes and it is therefore necessary to first introduce this concept. This section definitions and concepts of partially balanced incomplete block designs are available in any statistical design and analysis of experiments such as John (1971), Clatworthy (1973), Dey (1986) and Sharma (2000).

#### **2.3.1. m- Class Association schemes**

Given  $v$  treatment symbols  $1, 2, \dots, v$  a relation satisfying the following conditions is an m-class association scheme ( $m \geq 2$ ).

- i. Any two treatment symbols  $\alpha$  and  $\beta$  are either  $1^{st}, 2^{nd}, \dots, m^{th}$  associate, the relation of association being symmetric, i.e., if the symbol  $\alpha$  is the  $i^{th}$  associate of  $\beta$ , then  $\beta$  is the  $i^{th}$  associate of  $\alpha$ .
- ii. Each symbol  $\alpha$  has  $n_i$   $i^{th}$  associates, the number  $n_i$  being independent of  $\alpha$ .
- iii. If any two symbols  $\alpha$  and  $\beta$  are  $i^{th}$  associates, then the number of the symbols that are  $j^{th}$  associates of  $\alpha$  and  $k^{th}$  associate of  $\beta$  is  $p_{jk}^i$  and is independent of the pair of  $i^{th}$  associates  $\alpha$  and  $\beta$ .

The numbers  $v$ ,  $n_i$  and  $p_{jk}^i$  ( $i, j, k = 1, 2, \dots, m$ ) are called the parameters of the  $m^{\text{th}}$  association scheme. These parameters are not all independent but connected the following parametric relations:

$$\sum_{i=1}^m n_i = v - 1; \quad (2.1)$$

$$\sum_{k=1}^m p_{jk}^i = n_j - \delta_{ij} \quad (2.2)$$

Where  $\delta_{ij}$  is the Kronecker's delta i.e.,  $\delta_{ij} = 1$  if  $i = j$  and is zero otherwise;

$$n_i p_{jk}^i = n_j p_{ik}^j \quad (2.3)$$

The relation  $p_{jk}^i = p_{kj}^i$  always holds because of symmetry, that is, from the fact that  $\alpha$  is an  $i^{\text{th}}$  associate of  $\beta$ , then  $\beta$  is an  $i^{\text{th}}$  associate of  $\alpha$ .

### 2.3.2. Definition of a Partially Balanced Incomplete Block Designs with m-associate classes and the relations between its parameters

We now formally define a PBIB design with m association classes based on the notion of association schemes.

**Definition 2.1.** Given an association scheme with m classes ( $m \geq 2$ ) we have a PBIB design based on the association scheme, if it is possible to arrange the  $v$  treatments in  $b$  blocks, such that

- i. Each block contains  $k$  ( $< v$ ) distinct treatments;
- ii. Each treatment occurs in  $r$  blocks;
- iii. If the treatments  $\alpha$  and  $\beta$  are mutually  $i^{\text{th}}$  associates in the association scheme, then  $\alpha$  and  $\beta$  occurs together  $\lambda_i$  blocks, where the integer  $\lambda_i$  does not depend on the pair  $(\alpha, \beta)$  so long as they are mutually  $i^{\text{th}}$  associates  $i = 1, 2, \dots, m$ . Further, not all  $\lambda_i$ 's are equal.

The integers  $b, r, k, \lambda_i$  are called the parameters of the PBIB design. Note that the definition of PBIB design is based on the existence of an association scheme. Consequently, if some specified values of  $v, n_i, p_{jk}^i$ , there are no association scheme with some  $m$ , there is no PBIB design with m-association classes based on the scheme. The following relations connect the parameters of PBIB design as also the parent association scheme:

$$vr = bk; \quad (2.4)$$

$$\sum_{i=0}^m n_i \lambda_i = rk, \quad (2.5)$$

where  $\lambda_0 = r$ .

Let  $\mathbf{N}$  be the incidence matrix of PBIB with  $m$ -associate classes. Then from the above definition, it follows that the diagonal elements of  $\mathbf{NN}'$  are all equal to  $r$ . Further, in each row of  $\mathbf{NN}'$  there are precisely  $n_1$  positions filled with  $\lambda_1$ ,  $n_2$  positions filled with  $\lambda_2$ , ...,  $n_m$  positions filled with  $\lambda_m$ , apart from the single entry  $r$ . Thus

$$\mathbf{NN}'\mathbf{1} = (r + \sum_{i=1}^m n_i \lambda_i) \mathbf{1} \quad (2.6)$$

Where,  $\mathbf{1}$  is  $v \times 1$  vector with all elements unity.

Again,

$$\mathbf{NN}'\mathbf{1} = \mathbf{N}(\mathbf{N}'\mathbf{1}) = k(\mathbf{N}\mathbf{1}) = rk\mathbf{1} \quad (2.7)$$

From (2.6) and (2.7), we have

$$rk = r + \sum_{i=1}^m n_i \lambda_i \quad (2.8)$$

or

$$\sum_{i=1}^m n_i \lambda_i = r(k - 1) \quad (2.9)$$

### 2.3.3. Two- Associate Classes of Partially Balanced Incomplete Block Designs

Among the association schemes and PBIB designs, the two class associate schemes and the two-associate classes of PBIB designs have received most attention. In this section, we study some two class association schemes and the two-associate classes of PBIB designs.

#### 2.3.3.1. Definition of a Partially Balanced Incomplete Block Designs with Two Associate Classes and the Relations between its Parameters

**Definition 2. 2.** Following Bose, Clatworthy, and Shrikhande (1954), an incomplete block design is said to be partially balanced incomplete block design with two associate classes if it satisfies the following requirement:

- i. The experimental material is divided into  $b$  blocks of  $k$  units each, different treatments being applied to the units in the block.
- ii. There are  $v$  ( $>k$ ) treatments each of which occurs in  $r$  blocks.

- iii. There can be established a relation of association between any two treatments satisfying the following requirements:
- Two treatments are either first associates or second associates.
  - Each treatment has exactly  $n_i$   $i^{\text{th}}$  associates ( $i = 1, 2$ ).
  - Given any two treatments which are  $i^{\text{th}}$  associates, the number of treatments common to the  $j^{\text{th}}$  associate of the first and the  $k^{\text{th}}$  associate of the second is  $p_{jk}^i$  and is independent of the pair of treatments we start with. Also  $p_{jk}^i = p_{kj}^i$  ( $i, j, k = 1, 2$ ).
- iv. Two treatments which are  $i^{\text{th}}$  associates occur together in exactly  $\lambda_i$  blocks ( $i = 1, 2$ )

For a proper partially balanced incomplete block design  $\lambda_1 \neq \lambda_2$ . If  $\lambda_1 = \lambda_2$  the design becomes a balanced incomplete block design.

The numbers  $v, r, k, b, n_1, n_2, \lambda_1$  and  $\lambda_2$ , are called the parameters of the first kind, where as the numbers  $p_{jk}^i$  ( $i, j, k = 1, 2$ ) are called the parameters of the second kind.

It is to be noted that the association relations between the treatments of partially balanced incomplete design are governed solely by the requirements of (iii) of the definition 2.2 and do not depend up on how the treatments are distributed in blocks. The association scheme depends only on the parameters  $n_1, n_2$  and  $p_{kj}^i$

$$\left. \begin{aligned} vr &= bk \\ n_1 + n_2 &= v - 1 \\ n_1\lambda_1 + n_2\lambda_2 &= r(k - 1) \end{aligned} \right\} \quad (2.10)$$

$$\left. \begin{aligned} p_{11}^1 + p_{12}^1 &= n_1 - 1 \\ p_{21}^1 + p_{22}^1 &= n_2 \\ p_{11}^2 + p_{12}^2 &= n_1 \\ p_{21}^2 + p_{22}^2 &= n_2 - 1 \end{aligned} \right\} \quad (2.11)$$

$$\left. \begin{aligned} n_1 p_{12}^1 &= n_2 p_{11}^2 \\ n_1 p_{22}^1 &= n_2 p_{12}^2 \end{aligned} \right\} \quad (2.12)$$

We can exhibit the parameters  $p_{jk}^i$  of the second kind as the element of the two symmetric matrices

$$\mathbf{P}_1 = \begin{bmatrix} p_{11}^1 & p_{12}^1 \\ p_{21}^1 & p_{22}^1 \end{bmatrix} \quad \mathbf{P}_2 = \begin{bmatrix} p_{11}^2 & p_{12}^2 \\ p_{21}^2 & p_{22}^2 \end{bmatrix} \quad (2.13)$$

Since the above matrices are symmetric, it is unnecessary to write down the elements  $p_{21}^1$  and  $p_{21}^2$  explicitly. These values will accordingly be omitted in the rest of the monograph. The computed quantities  $\mathbf{P}_1$  and  $\mathbf{P}_2$  arise in the analysis of these designs.

### 2.3.4. The Classification of PBIB Designs

From practical viewpoint, two associate classes of PBIB designs are important and exhaustive list of these designs is available in Clatworthy (1973) and Clatworthy (1956). Here we briefly define some of the well known two-associate class association schemes and give their parameters. Bose and Shimamoto(1952) have classified the two associate classes of PBIB designs into many categories, namely, Group Divisible(GD), consisting of three subtypes: singular(S), semi-regular (SR) and regular (R), Triangular (T), Latin square type (LS<sub>i</sub>), cyclic (C), partial geometry (PG) and miscellaneous (M).

#### 2.3.4.1. Group Divisible (GD) PBIB (2) Designs

The largest, simplest and perhaps most important class of PBIB (2) design. A GD designs is a PBIB (2) designs for which the treatments may be divided into m groups of n distinct treatments each such that belong to the same group are the first associates and two treatments that belongs to different groups are second associates. The GD designs association scheme is an  $mxn$  array of the treatment symbols (1,2,...,  $mn = v$ , say).

For GD designs is clear that

$$v = mn, \quad n_1 = n - 1, \quad n_2 = n(m - 1) \quad (2.14)$$

From the general condition  $n_1\lambda_1 + n_2\lambda_2 = r(k-1)$ , we have for GD designs

$$(n-1)\lambda_1 + n(m-1)\lambda_2 = r(k-1). \quad (2.15)$$

From the definition of the parameters  $p_{jk}^i (i, j, k = 1, 2)$  and consideration of the association scheme it is clear that

$$\mathbf{P}_1 = (p_{jk}^i) = \begin{bmatrix} n-2 & 0 \\ 0 & n(m-1) \end{bmatrix}, \mathbf{P}_2 = (p_{jk}^i) = \begin{bmatrix} 0 & n-1 \\ n-1 & n(m-2) \end{bmatrix} \quad (2.16)$$

For any GD design  $\lambda_2 > 0$  is necessary condition, since if  $\lambda_2 = 0$  then the treatments that belong to groups that never occur together in a block and the design breaks up into  $m$  disconnected set of blocks of a degenerate form of the design (called a disconnected design) that does not permit estimation of comparison of treatments belong to different groups. When zero-valued  $\lambda$  in GD design is  $\lambda_2$ , it is always be put into the proper form with  $\lambda_1 = 0$  by renaming the associate classes.

#### 2.3.4.1.1. Combinatorial Properties of GD Designs

Bose and Connor (1952) have made a careful study of the combinatorial properties of GD designs, and classified into three subtypes depending on values assumed by the quantities

$$Q = r - \lambda_1 \quad \text{and} \quad rk - v\lambda_2 = p \quad (2.17)$$

They considered the  $vxb$  incidence matrix  $\mathbf{N} = (n_{ij})$  of a GD design. The determinant of the treatment structure matrix,  $\mathbf{NN}'$  is

$$\det(\mathbf{NN}') = rk(rk - v\lambda_2)^{m-1} (r - \lambda_1)^{m(n-1)} \quad (2.18)$$

They classified GD designs into three types from a consideration of the expression for  $\det(\mathbf{NN}')$  as follows

1. Singular (S) if  $r - \lambda_1 = 0$
2. Non-singular if

a. Semi-regular (SR) if  $r - \lambda_1 > 0$  and  $rk - v\lambda_2 = 0$

b. Regular (R) if  $r - \lambda_1 > 0$  and  $rk - v\lambda_2 > 0$

For GD designs, the parameters are  $v, r, k, m, n, \lambda_1, \lambda_2$  and  $p_{jk}^i$  ( $i, j, k = 1, 2$ ). The number of experimental units in the design is  $n = vr = bk$  and the size of the design.

We list below several of the more important results from the Bose and Connor (1952) combinatorial properties of GD designs:

1. The necessary and sufficient condition for PBIB (2) designs to be GD is that  $p_{12}^1 = 0$  or  $p_{12}^2 = 0$ . Note that to be consistent with the definition of the association scheme, we need to interchange the associate classes when  $p_{12}^2 = 0$ . This involves an interchange (1) the values of  $\lambda_1$  and  $\lambda_2$  (2) the values of  $n_1$  and  $n_2$ , and (3) reordering of the quantities  $p_{jk}^i$  in the matrices  $\mathbf{P}_1$  and  $\mathbf{P}_2$ . Once this has been done so that it is  $p_{12}^1$  that assumes the value 0, then the expression  $rk - v\lambda_2$  may be correctly evaluated.
2. For any group divisible designs, it is necessary that  $r - \lambda_1 \geq 0$  and  $rk - v\lambda_2 \geq 0$ .
3. For a singular group divisible design (SGD)  $b \geq m$ .
4. For a SGD design (since  $r = \lambda_1$ ),  $\det(\mathbf{N}\mathbf{N}') = 0$ .
5. For a semi-regular group divisible (SRGD) design  $k$  is divisible by  $m$ . If  $k = cm$ , then every block must contain  $c$  treatments from each group.
6. For a semi-regular group divisible (SRGD) design is  $b \geq v - m + 1$ .
7. A necessary condition for the existence of a symmetrical ( $v = b$ ) regular GD design is that  $(r^2 - v\lambda_2)^{m-1} (r - \lambda_1)^{m(n-1)} = p^{(m-1)} Q^{m(n-1)}$  is perfect square.
8. If a symmetrical ( $v = b$ ) regular GD design exists, then:

- a. If  $m$  is even, then  $p = r^2 - v\lambda_2$  must be a perfect square and further if  $m = 4t + 2$  and  $n$  is even, the Hilbert norm residue symbols  $(Q, (1))_p = -1$  for all primes  $p$ .
- b. If  $m$  is odd and  $n$  is even,  $Q = r - \lambda_1$  is perfect square and  $((-1)^\alpha n\lambda_2, p)_p = +1$  for all primes  $p$ , where  $\alpha = \frac{1}{2}m(m-1)$ .
- c. If  $m$  and  $n$  are both odd,  $((-1)^\alpha n\lambda_2, p)_p, ((-1)^\beta n, Q) = +1$  for all primes  $p$ , where  $\alpha = \frac{1}{2}m(m-1)$  and  $\beta = \frac{1}{2}n(n-1)$ .

### 2.3.4.2. Triangular PBIB (2) Designs

A partially balanced incomplete block designs with two associate classes is said to be triangular if the number of treatments is  $v = \frac{1}{2}p(p-1)$  and the associate scheme is an array of  $p$  rows and  $p$  columns with the following properties.

1. The positions in the principal diagonals (running from upper left-hand to lower right-hand corner) are left blank.
2. The  $\frac{1}{2}p(p-1)$  positions above the principal diagonal are filled by the numbers  $1, 2, \dots, \frac{1}{2}p(p-1)$  corresponding to the treatments.
3. The  $\frac{1}{2}p(p-1)$  positions below the principal diagonal are filled by so that the array is symmetrical about the principal diagonal.
4. For any treatment  $i$  the first associates are exactly those treatments which lie in the same rows (in the same columns) as  $i$ .

The following relations hold:

$$v = \frac{1}{2}p(p-1), \quad n_1 = 2(p-2), \quad n_2 = \frac{1}{2}(p-2)(p-3) \quad (2.19)$$

$$\mathbf{P}_1 = \begin{bmatrix} p-2 & p-3 \\ p-3 & \frac{1}{2}(p-3)(p-4) \end{bmatrix}, \quad \mathbf{P}_2 = \begin{bmatrix} 4 & 2p-8 \\ 2p-8 & \frac{1}{2}(p-4)(p-5) \end{bmatrix} \quad (2.20)$$

where  $p \leq 5$ . (The case  $p = 4$  has  $p_{12}^2 = 0$  so that it is also the group divisible type and is classified in this way. We note further that for  $p = 2$  or  $3$   $n_2 = 0$ , so that there is only one associate class and the design, if it exists, degenerates to the PBIB (1) design.)

### 2.3.4.3. Latin Square Types (LS) PBIB (2) Designs

Consider a set of  $v = p^2$  treatments and association scheme which consist of an  $p \times p$  array of the distinct symbols  $1, 2, \dots, p^2$  on which a set of  $i-2$  mutually orthogonal Latin square (MOLS) are superposed. Let  $LS_1$  first associate of a treatment  $\alpha$  consist of the  $p-1$  other treatments lying in the same row of an array with  $\alpha$ , the set of  $p-1$  other treatments in the same column of an array with  $\alpha$ , and then  $p-1$  other treatments corresponding to the same letters as  $\alpha$  in each of the Latin squares. All other treatments are second associates of  $\alpha$ . Such an association scheme is called a Latin square types ( $LS_i$ ) PBIB (2) design association scheme.

A PBIB (2) designs based on a Latin square type ( $LS_i$ ) association scheme is called a Latin square type ( $LS_i$ ) PBIB (2) design.

For these association schemes, it is clearly that

$$v = n^2, \quad n_1 = i(n-1), \quad n_2 = (n-1)(n-i+1) \quad (2.21)$$

$$\mathbf{P}_1 = \begin{bmatrix} i^2 - 3i + n & (i-1)(n-i+1) \\ (i-1)(n-i+1) & (n-i)(n-i+1) \end{bmatrix}, \quad \mathbf{P}_2 = \begin{bmatrix} i(i-1) & i(n-i) \\ i(n-i) & (n-i)^2 + i - 2 \end{bmatrix} \quad (2.22)$$

From these relations and the definition, it is clearly that certain restrictions on the parameters  $i$  and  $n$  are necessary. First of all, for a given  $n$  the definition depends upon the existence of a set of MOLS so that a positive integral values of  $n$  for which a maximum number of squares exist  $0 \leq i-2 \leq n-1$  or  $2 \leq i \leq n+1$ . We note that when  $i = n+1$ ,  $n_2$  becomes 0, and any design based on such association scheme would necessary degenerate to a PBIB (2) design. If  $i = n$ , then  $p_{12}^2 = 0$  the design, if it exists, must be of GD type. To avoid these probabilities we shall require  $i \leq n-1$ .

#### 2.3.4.4. Cyclic (C) PBIB (2) Designs

Let the treatment be designated by the integers  $1, 2, \dots, v$ . Let first associates of treatment  $i$  be given by  $i + d_1, i + d_2, \dots, i + d_{n_1} \pmod{v}$

Provided the  $d$ 's satisfying the following conditions:

1. The  $d$ 's are different and  $1 < d_j < v, j = 1, 2, \dots, n_1$ ;
2. Among the  $n_1(n_1 - 1)$  differences  $d_j - d_{j'} (j, j' = 1, 2, \dots, n_1 : j \neq j')$

Reduced mod  $v$  each of the numbers  $d_1, d_2, \dots, d_{n_1}$  occurs at  $\alpha$  times whereas each of the numbers  $e_1, e_2, \dots, e_{n_2}$  occurs at  $\beta$  times where  $\alpha \neq \beta$  and where  $d_1, d_2, \dots, d_{n_1}, e_1, e_2, \dots, e_{n_2}$  are the numbers  $1, 2, \dots, v$  such an association scheme is said to be a cyclic design, or a PBIB (2) design based on the association scheme.

To reduce an integer  $x \leq v$  and positive, which is an unconventional procedure for retention of treatment symbols  $1, 2, \dots, v$ .

A PBIB (2) design for which the relationships among the  $v$  treatments are given by the cyclic association scheme defined above is itself is known as a cyclic types of partially balanced design.

For a cyclic PBIB (2) design it is clearly necessary that

$$n_1\alpha + n_2\beta = n_1(n_1 - 1) \tag{2.23}$$

The parameters of the second kind are determined by  $\alpha, \beta$  ( $\alpha \neq \beta$ ),  $n_1$  and  $n_2$  so that

$$\mathbf{P}_1 = \begin{bmatrix} \alpha & n_1 - \alpha - 1 \\ n_2 - n_1 + \alpha + 1 \end{bmatrix} \quad \mathbf{P}_2 = \begin{bmatrix} \beta & n_1 - \beta \\ n_2 - n_1 + \beta + 1 \end{bmatrix} \quad (2.24)$$

### 2.3.4.5. Partial Geometries (PG) PBIB (2) Designs

A partial geometry  $(r, k, t)$  has been defined by Bose (1963) a system of undefined points and lines and an undefined relation called incidence satisfying the following four axioms:

- i. Any two points are incident with not more than one line.
- ii. Each point is incident with  $r$  lines.
- iii. Each line is incident with  $k$  points.
- iv. If the point  $P$  is not incident with the line  $l$ , then there pass through  $P$  exactly  $t$  lines ( $t \geq 1$ ) intersecting  $l$ .

From this beginning Bose showed that the number  $v$  of points and the number  $b$  of lines in the partial geometry.

$$v = \frac{1}{t} k [(r-1)(k-1) + t] \quad (2.25)$$

$$b = \frac{1}{t} r [(r-1)(k-1) + t] \quad (2.26)$$

We also proved that a necessary condition for the existence of partial geometry  $(r, k, t)$  is that the number

$$\alpha = \frac{1}{t} r k [(r-1)(k-1)(k+r-t-1)] \quad (2.27)$$

is integral.

Another of Bose's basic results is the following: Given a partial geometry  $(r, k, t)$  there exists a dual partial geometry  $(r, k, t)$  obtained by interchanging the role of points and lines in the given geometry.

The partial geometry  $(r, k, t)$  has an association scheme wherein two points are first associates if they are incident with a line of the geometry and they are second associates if they are not incident with a line.

It then follows from Bose (1963) that the association scheme of a partial geometry  $(r, k, t)$  has parameters

$$n_1 = r(k-1), n_2 = \frac{1}{t}(r-1)(k-1)(k-t) \quad (2.28)$$

$$p_{11}^1 = (t-1)(r-1) + k - 2, p_{11}^2 = rt \quad (2.29)$$

$$1 \leq t \leq r, 1 \leq t \leq k \quad (2.30)$$

Then it becomes evident that if a partial geometry  $(r, k, t)$  exists, it is a PBIB (2) designs with parameters  $r, k, \lambda_1 = 1, \lambda_2 = 0$  and having other parameters. Thus, the corresponding PBIB (2) design would have the parameters

$$\left. \begin{aligned} v &= \frac{1}{t}k[(r-1)(k-1) + t], r = r, \lambda_1 = 1 \\ b &= \frac{1}{t}r[(r-1)(k-1) + t], k = k, \lambda_2 = 0 \\ n_1 &= r(k-1), n_2 = \frac{1}{t}(r-1)(k-1)(k-t) \end{aligned} \right\} \quad (2.31)$$

$$\left. \begin{aligned} P_2 &= \left[ \begin{array}{cc} (t-1)(r-1) + k - 2 & (r-1)(k-t) \\ & \frac{1}{t}(r-1)(k-1) + (k-t-1) \end{array} \right] \\ P_2 &= \left[ \begin{array}{cc} rt & r(k-t-1) \\ \frac{1}{t}[(r-1)(k-1)(k-2t) + t(rt-k)] & \end{array} \right] \end{aligned} \right\} \quad (2.32)$$

Wherein

$$1 \leq t \leq r, 1 \leq t \leq k$$

#### **2.3.4.6. Miscellaneous (M) PBIB (2) Designs**

Those simple design of Bose, Clatworthy and Shrikhande (1954) for which  $\lambda_1 \geq 2$  and  $\lambda_2 = 0$  were constructed in all cases by replicating entire plans of our partial geometries. Since they cannot be classified as partial geometries (for which  $\lambda_1 = 1$ ), a new category called miscellaneous was formed to include these and other new designs for which the other classifications are not appropriate. Most of the miscellaneous (M) PBIB (2) designs are characterized by one zero  $\lambda$  but there are 8 instances of designs that have both  $\lambda$ 's different from zero.

Note that when a PBIB design with two associate classes is said to be simple if either (i)  $\lambda_1 \neq 0, \lambda_2 = 0$  or (ii)  $\lambda_1 = 0, \lambda_2 \neq 0$ . It may happen that a design of the simple category may belong to some other category as well.

# CHAPTER THREE

## METHOD OF CONSTRUCTION

### *3.1. Method of Construction of the Mating-Environmental Design*

In this section, we give a method of construction of mating-environment design for complete diallel cross system IV.

The method is simply stated as follows: Take, for  $p$  lines under evaluation and numbered randomly, two-associate classes of PBIB design with parameters  $p, r, k, b, n_i, \lambda_i, p_{jk}^i (i, j, k = 1, 2)$  such that none of the  $\lambda_i$ 's is zero. Take all possible distinct pair of combinations of treatment in each block of partially balanced incomplete block designs. Thus, we get  $\frac{1}{2}bk(k-1)$  crosses arranged in  $b$  blocks, each containing  $\frac{1}{2}k(k-1)$  crosses. Since one of the  $\lambda_i$ 's is greater than one, it leads to repetition of some crosses without making the design complex. We shall refer to the PBIB designs that led to CDC plans as the auxiliary designs or A-design. If  $\mathbf{N}$  is the incidence matrix of the A-design with  $v$  treatments, then the incidence matrix of the resulting design, which is of order  $v \times b$ . Thus, the resulting design is an incomplete block design for the CDC plan with parameters  $v' = \frac{1}{2}p(p-1)$ ,  $b' = b$ ,  $k' = \frac{1}{2}k(k-1)$ ,  $\mathbf{r} = (\lambda_1, \lambda_2)$ , that is each cross is repeated either  $\lambda_1$  times or  $\lambda_2$  times depending whether the pair of lines forming a cross are first associates or second associates. We shall call the resulting design the mating-environmental design, or simply the M-E design. The actual number of crosses that are being used in the plan is  $\frac{1}{2}bk(k-1)$  and, out of these,  $\frac{1}{2}vn_i$  crosses appear in the design  $\lambda_i$  times ( $i = 1, 2$ ).

Since the total number of parameters  $\frac{1}{2}p(p-1) + b + 1$  are to be estimated by the model considered in chapter four. Therefore, we searched those PBIB (2) designs from the catalogue of Clatworthy (1973) in which  $\frac{1}{2}bk(k-1) \geq \frac{1}{2}p(p-1) + b + 1$  i.e., total number of observations must be greater than or equal to the number of parameters to be estimated. The list of those selected PBIB (2) designs is given in Appendix A.

### Example 3.1

Let us consider the construction of a CDC plan involving  $p = 9$  lines. From the catalogue of Clatworthy (1973), a LS26 PBIB (2) design with parameters  $p = 9$ ,  $b = 9$ ,  $r = 4$ ,  $k = 4$ ,  $\lambda_1 = 1$ ,  $\lambda_2 = 2$ ,  $n_1 = 4$  and  $n_2 = 4$  is taken. It is our auxiliary design with association matrices  $\mathbf{P}_1$  and  $\mathbf{P}_2$

$$\mathbf{P}_1 = \begin{bmatrix} 1 & 2 \\ & 2 \end{bmatrix}, \quad \mathbf{P}_2 = \begin{bmatrix} 2 & 2 \\ & 1 \end{bmatrix} \text{ is taken.}$$

Now making distinct crosses in each block according to our scheme, we get  $\frac{1}{2}k(k-1) = 6$  crosses in each block. Thus, we get  $\frac{1}{2}bk(k-1) = 54$  crosses arranged in  $b = 9$  blocks. Now, we get M-E design with parameters  $v' = 36$ ,  $b' = 9$ ,  $k' = 6$ ,  $\mathbf{r}' = (1, 2)$ . The plans of auxiliary and M-E designs are given below.

Auxiliary design plan1					M-E Design of Complete Diallel Cross Plan 2							
Blocks	Treatments				Blocks	Treatments (Crosses)						
↓					↓							
1	1	6	9	2	1	1x6	1x9	1x2	6x9	6x2	9x2	
2	6	8	2	4	2	6x8	6x2	6x4	8x2	8x4	2x4	
3	8	1	4	9	3	8x1	8x4	8x9	1x4	1x9	4x9	
4	9	2	5	7	4	9x2	9x5	9x7	2x5	2x7	5x7	
5	2	4	7	3	5	2x4	2x7	2x3	4x7	4x3	7x3	
6	4	9	3	5	6	4x9	4x3	4x5	9x3	9x5	3x5	
7	5	7	1	6	7	5x7	5x1	5x6	7x1	7x6	1x6	
8	7	3	6	8	8	7x3	7x6	7x8	3x6	3x8	6x8	
9	3	5	8	1	9	3x5	3x8	3x1	5x8	5x1	8x1	

# CHAPTER FOUR

## ANALYSIS

### *4.1. Introduction*

A statistical model is actually a linear relation of effect different levels of a number of factors involved in an experiment along with one or more terms of representing error effects. There are three types of models in statistical design and analysis of experiment: fixed effects model, mixed effects model and random effects model.

Fixed effects model are models in which both variety (treatment) effects and block effects of the factors are constants (fixed) and only error effect(s) is (are) random. Intra-block estimates are obtained from treatment contrasts obtained within the blocks. These arise from through the model commonly known as the fixed effects model (and also Griffing (1956) called model I) in which additive components which include treatment effects  $\tau_{ij}$  and block effects  $\beta_k$  are fixed but unknown constants.

Mixed effects model are models in which some factors have fixed effects and some random effects. Mixed effects model are either the variety effects are random variables and the block effects are constants (Griffing designate as mixed A model) or the variety effects are constants and the block effects are random variables (Griffing designate as mixed B model).

Random effects model are models where all the factors have random effects.

In this paper, we are considered both fixed and mixed (mixed B type) of the model without interactions of treatment and block effects of PBIB (2) designs as environmental (experimental) designs.

## 4.2. Intra-Block Analysis

### 4.2.1. The Model

The statistical linear model for genetic yield from a complete diallel cross plan of type IV for data obtained in PBIB (2) designs may be expressed in the form

$$y_{ijk} = \mu + g_i + g_j + s_{ij}^{(1)} + s_{ij}^{(2)} + \beta_k + \varepsilon_{ijk}, \quad i < j, i, j = 1, 2, \dots, p; k = 1, 2, \dots, b. \quad (4.1)$$

where  $y_{ijk}$  is the response of (ixj) cross in the  $k^{\text{th}}$  block,  $\mu$  is the general mean,  $g_i(g_j)$  is the general combining ability (gca) effect of the  $i^{\text{th}}(j^{\text{th}})$  line (variety),  $s_{ij}^{(1)}$  and  $s_{ij}^{(2)}$  are the specific combining ability (sca) of those crosses in which (ixj) lines are first associates and second associates respectively,  $\beta_k$  is the  $k^{\text{th}}$  block effect and  $\varepsilon_{ijk}$  is the error component i.e. environmental effect. It is assumed to be normally distributed with mean zero and constant variance  $\sigma^2$ , i.e.,  $\varepsilon_{ijk} \sim N(0, \sigma^2)$ .

Equation (4.1) can also be written as

$$y_{ijk} = \mu + \tau_{ij} + \beta_k + \varepsilon_{ijk} \quad (4.2)$$

Where

$$\tau_{ij} = g_i + g_j + s_{ij}^{(1)} + s_{ij}^{(2)}$$

Where  $\tau_{ij}$  denotes the effect of (ixj)<sup>th</sup> cross and the rest of terms have already defined in equation (4.1).

For the analysis of data obtained from complete diallel cross (CDC) system IV through two associate classes of partially balanced incomplete block (PBIB (2)) designs, we will follow Singh and Hinkelmann (1998) two stage procedures for estimating gca and sca effects with some modification. The first stage is to consider the proposed designs to estimate cross effects, say,  $\boldsymbol{\tau} = (\tau_{12}, \tau_{13}, \dots, \tau_{(p-1)(p)})'$ . Equation (4.2) may be expressed in matrix notation as

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{X}\boldsymbol{\tau} + \mathbf{D}\boldsymbol{\beta} + \boldsymbol{\varepsilon} \quad (4.3)$$

where  $\mathbf{y}$  be an  $n \times 1$  (column) vector of observations,  $\mathbf{1}$  is the  $n \times 1$  (column) vector of ones,  $\mu$  is a general mean,  $\mathbf{X}$  is an  $n \times v$  design matrix of ones and zeros for treatments, that is, the  $(h, l)^{\text{th}}$  element of  $\mathbf{X}$  is 1 if the  $h^{\text{th}}$  observation pertains to the  $l^{\text{th}}$  cross, and is zero otherwise,  $\boldsymbol{\tau} = (\tau_{12}, \tau_{13}, \dots, \tau_{(p-1)(p)})'$  is a  $v \times 1$  vector of treatment effects,  $\mathbf{D}$  is an  $n \times b$  design matrix for blocks, that is, the  $(h, k)^{\text{th}}$  element of  $\mathbf{D}$  is 1 if the  $h^{\text{th}}$  observation pertains to the  $k^{\text{th}}$  block, and is zero otherwise,  $\boldsymbol{\beta} = (\beta_1, \beta_2, \dots, \beta_b)'$  is a  $b \times 1$  vector of block effects and  $\boldsymbol{\varepsilon}$  is an  $n \times 1$  vector of residuals. In intra-block analysis, it is assumed that vector  $\boldsymbol{\beta}$  is fixed and  $\boldsymbol{\varepsilon}$  is normally distributed with  $E(\boldsymbol{\varepsilon}) = \mathbf{0}$ , the variance-covariance matrix of the error vector is  $\sigma^2\mathbf{I}$  and  $\text{Cov}(\boldsymbol{\beta}, \boldsymbol{\varepsilon}) = \mathbf{0}$ , where  $\mathbf{I}$  is the identity matrix of conformable order.

Thus, the expected value and variance of the observation on the  $(i, j)^{\text{th}}$  treatment in the  $k^{\text{th}}$  block are  $E(\mathbf{y}) = \mathbf{1}\mu + \mathbf{X}\boldsymbol{\tau} + \mathbf{D}\boldsymbol{\beta}$  and  $V(\mathbf{y}) = \sigma^2\mathbf{I}$ .

#### 4.2.2. Estimation of Model Parameters

From Clatworthy (1973) with some modification, the least square estimators of  $\mu$ ,  $\boldsymbol{\beta} = (\beta_1, \beta_2, \dots, \beta_b)'$ ,  $\boldsymbol{\tau} = (\tau_{12}, \tau_{13}, \dots, \tau_{(p-1)(p)})'$  can be expressed in the normal equations

$$\begin{pmatrix} \frac{1}{2}bk(k-1) & \frac{1}{2}k(k-1)\mathbf{1}' & r\mathbf{1}' & 0 & 0 \\ \frac{1}{2}k(k-1)\mathbf{1} & \frac{1}{2}k(k-1)\mathbf{I} & \mathbf{N}' & 1 & 0 \\ r\mathbf{1} & \mathbf{N} & r\mathbf{I} & 0 & \mathbf{1} \\ 0 & \mathbf{1}' & 0 & 0 & 0 \\ 0 & 0 & \mathbf{1}' & 0 & 0 \end{pmatrix} \begin{pmatrix} \hat{\mu} \\ \hat{\boldsymbol{\beta}} \\ \hat{\boldsymbol{\tau}} \\ \theta_1 \\ \theta_2 \end{pmatrix} = \begin{pmatrix} G \\ \mathbf{B} \\ \mathbf{T} \\ 0 \\ 0 \end{pmatrix} \quad (4.4)$$

Where  $\mathbf{1}' = (1, 1, \dots, 1)$ ,  $\theta_1$  and  $\theta_2$  are Lagrangian multipliers entering in the minimization. Dimensions of the sub-matrices may be inferred from the dimensions of  $\mathbf{N}$  and  $\mathbf{N}'$ . On the right hand side of equation (4.4)  $G$  is the grand total of all observations,  $\mathbf{B}$  is the vector of block totals and  $\mathbf{T}$  is vector of treatment (cross) totals.

The inverse of the matrix of normal equations can be written

$$\begin{pmatrix}
 \frac{2}{bk(k-1)} & & \mathbf{0.1}' & & \mathbf{0.1} & & -\frac{1}{b} & -\frac{2}{p(p-1)} \\
 \mathbf{0.1} & \frac{2}{k(k-1)}\mathbf{I} + \frac{4}{k^2(k-1)^2}\mathbf{N}'\mathbf{C}^-\mathbf{N} - \frac{2}{bk(k-1)}\mathbf{J} & & -\frac{2}{k(k-1)}\mathbf{N}'\mathbf{C}^- & & \frac{1}{b}\mathbf{1} & & \mathbf{0.1} \\
 \mathbf{0.1} & & -\frac{2}{k(k-1)}\mathbf{C}^-\mathbf{N} & & \mathbf{C}^- & & \mathbf{0.1} & \frac{2}{p(p-1)}\mathbf{1} \\
 -\frac{1}{b} & & \frac{1}{b}\mathbf{1}' & & \mathbf{0.1}' & & 0 & 0 \\
 -\frac{2}{p(p-1)} & & \mathbf{0.1}' & & \frac{2}{p(p-1)}\mathbf{1}' & & 0 & 0
 \end{pmatrix}$$

$$= \begin{pmatrix}
 \frac{2}{bk(k-1)} & \mathbf{0.1}' & \mathbf{0.1} & -\frac{1}{b} & -\frac{2}{p(p-1)} \\
 \mathbf{0.1} & \mathbf{E} & \mathbf{F}' & \frac{1}{b}\mathbf{1} & \mathbf{0.1} \\
 \mathbf{0.1} & \mathbf{F} & \mathbf{C}^- & \mathbf{0.1} & \frac{2}{p(p-1)}\mathbf{1} \\
 -\frac{1}{b} & \frac{1}{b}\mathbf{1}' & \mathbf{0.1}' & 0 & 0 \\
 -\frac{2}{p(p-1)} & \mathbf{0.1}' & \frac{2}{p(p-1)}\mathbf{1}' & 0 & 0
 \end{pmatrix} \quad (4.5)$$

Where

$$\mathbf{C}^- = \frac{1}{2}k(k-1)\left[\frac{1}{2}k(k-1)r - \mathbf{N}\mathbf{N}' + \frac{1}{2}k(k-1)\mathbf{J}\right]^{-1} - \frac{2}{p(p-1)}\mathbf{J}, \quad \mathbf{J} = \mathbf{1}\mathbf{1}' \text{ is a matrix of all}$$

ones,

$$\mathbf{F} = -\frac{2}{k(k-1)}\mathbf{C}^-\mathbf{N}, \quad \mathbf{E} = \frac{2}{k(k-1)}\mathbf{I} + \frac{4}{k^2(k-1)^2}\mathbf{N}'\mathbf{C}^-\mathbf{N} - \frac{2}{bk(k-1)}\mathbf{J}$$

The  $v \times v$  matrix  $\mathbf{C}^-$  is the basic matrix of the analysis and its computation should present no problems because  $(\frac{1}{2}k(k-1)r - \mathbf{N}\mathbf{N}' + \frac{1}{2}k(k-1)\mathbf{J})$  is well conditioned for PBIB designs.

The estimators of the parameters of the design and their variance are as follows:

i. Grand mean

$$\hat{\mu} = \frac{2G}{bk(k-1)} \quad (4.6)$$

with  $V(\hat{\mu}) = \frac{2}{bk(k-1)} \sigma^2$

ii. Treatment (cross) values

$$\hat{\tau} = \mathbf{DB} + \mathbf{C}^{-1}\mathbf{T} = \mathbf{C}^{-1}\left(\mathbf{T} - \frac{2}{k(k-1)}\mathbf{NB}\right) = \mathbf{C}^{-1}\mathbf{Q} \quad (4.7)$$

Where  $\mathbf{Q} = \mathbf{T} - \frac{2}{k(k-1)}\mathbf{NB}$

with

$$V(\tau_{ij}) = \text{Diag}(\mathbf{C})\sigma^2 = c_{ii}\sigma^2 = c_{11}\sigma^2$$

Treatment difference =  $\hat{\tau}_{ij} - \hat{\tau}_{lm}$ ,  $i < j, m < l, i \neq m, j \neq l$ ,  $i, j, m, l = 1, 2, \dots, p$

$$V(\hat{\tau}_{ij} - \hat{\tau}_{lm}) = 2\sigma^2(c_{ijij} - c_{lmlm})$$

Note that there will be two values for this variance depending on whether  $\hat{\tau}_{ij}$  and  $\hat{\tau}_{lm}$  are first associates and second associates, respectively.

iii. Block Effects

$$\hat{\beta} = \mathbf{EB} + \mathbf{F}'\mathbf{T} = \frac{2}{k(k-1)}(\mathbf{B} - \mathbf{N}'\hat{\tau}) \quad (4.8)$$

with  $V(\hat{\beta}_i) = \varepsilon_{ijk}\sigma^2 = \varepsilon_{121}\sigma^2$

Difference between blocks =  $\hat{\beta}_i - \hat{\beta}_j$  with  $V(\hat{\beta}_{ij} - \hat{\beta}_{lm}) = 2\sigma^2(\varepsilon_{ijij} - \varepsilon_{kk})$

iv. Predicted Values

$$\hat{\mathbf{y}} = \mathbf{1}\hat{\mu} + \mathbf{X}\hat{\boldsymbol{\tau}} + \mathbf{D}\hat{\boldsymbol{\beta}} \quad \text{or} \quad \hat{y}_{ijk} = \hat{\mu} + \hat{\tau}_{ij} + \hat{\beta}_k \quad \text{with} \quad (4.9)$$

$$V(\hat{y}_{ijk}) = \left( \frac{2}{bk(k-1)} + c_{ij} + \varepsilon_{kk} + 2d_{ijk} \right) \sigma^2$$

v. Variance

$$\hat{\sigma}^2 = \frac{SS_{error}}{df_{error}} = \frac{\mathbf{y}'\mathbf{y} - \hat{\mathbf{y}}'\hat{\mathbf{y}}}{b\left[\frac{1}{2}k(k-1) - 1\right] - \frac{1}{2}p(p-1)} = MS_E \quad (4.10)$$

The least squares (LS) method for data analysis of a proposed designs leads to the following reduced normal equations.

$$\mathbf{C}\boldsymbol{\tau} = \mathbf{Q} \quad (4.11)$$

$$\hat{\boldsymbol{\tau}} = \mathbf{C}^{-}\mathbf{Q}$$

Where

$$\mathbf{C} = \mathbf{R}^{\delta} - \mathbf{N}\mathbf{k}^{-\delta}\mathbf{N}' \quad (4.12)$$

$$\mathbf{Q} = (Q_1, \dots, Q_v)' = \mathbf{T} - \mathbf{N}\mathbf{k}^{-\delta}\mathbf{B} \quad (4.13)$$

In the above expressions, (4.12) and (4.13),  $\mathbf{R}^{\delta}$  and  $\mathbf{k}^{-\delta}$  are the diagonal matrices of the replication of the crosses and block size of the proposed design of order  $v \times v$  and  $b \times b$  respectively.  $\mathbf{N} = \mathbf{X}'\mathbf{D}$  is the  $v \times b$  incidence matrix of the designs. Note that the assignment of treatments to blocks can be represented by incidence matrix,  $\mathbf{N}$ , of the design when  $\mathbf{N}$  is the  $v \times b$  matrix which take the value 1 in the  $(ixj, k)^{th}$  cell if treatment  $ixj$  occurs in block  $k$  and zero otherwise.  $\mathbf{T} = \mathbf{X}'\mathbf{Y}$  is the  $v \times 1$  vector of treatment totals and  $\mathbf{B} = \mathbf{D}'\mathbf{Y}$  is the  $b \times 1$  vector of block totals. The sum of squares due to crosses is  $\mathbf{Q}'\mathbf{C}^{-}\mathbf{Q}$  with degree of freedom (d.f.) = rank ( $\mathbf{C}$ ) =  $v-1$ , where  $\mathbf{C}^{-}$  is the generalized inverses of  $\mathbf{C}$  with property  $\mathbf{C}\mathbf{C}^{-}\mathbf{C} = \mathbf{C}$ , and expectation and variance of  $\mathbf{Q}$  is

$$E(\mathbf{Q}) = \mathbf{C}\boldsymbol{\tau} \quad \text{and} \quad V(\mathbf{Q}) = \mathbf{C}\sigma^2 \quad (4.14)$$

The vector  $\mathbf{Q}$  is called the vector of adjusted treatment totals. The adjusted treatments totals will always sum to zero i.e.,  $\mathbf{Q}'\mathbf{1}_v = 0$ . Where  $\mathbf{1}_v$  is  $v \times 1$  vector with all elements unity. Equations  $\mathbf{C}\boldsymbol{\tau} = \mathbf{Q}$  are sometimes called reduced normal equations for treatment effects. Since  $\mathbf{C}\mathbf{J}_v = \mathbf{0}$ , follows that  $\mathbf{C}$  is a singular matrix and thus,  $\text{Rank}(\mathbf{C}) \leq v - 1$ . Further, if  $\mathbf{p}'\boldsymbol{\tau}$  is a linear combination of treatment effects, then the necessary condition for  $\mathbf{p}'\boldsymbol{\tau}$  to estimable is that  $\mathbf{p}'\mathbf{1} = 0$ . A treatment contrasts  $\mathbf{p}'\boldsymbol{\tau}$  is called an elementary contrast if the vector  $\mathbf{p}$  has only two non-zero entries, 1 and -1, the other entries being zero. We now give the following definition from Dey (1986).

*Definition 4.1.* A block design is said to be connected if all elementary treatment contrasts are estimable.

The property of connectedness is related to the rank of  $\mathbf{C}$  matrix of the design. The result is contained in the following theorem.

*Theorem 4.1.* A block design is connected if and only if  $\text{Rank}(\mathbf{C}) = v - 1$ .

Another definition of connectedness, given by Bose (1947), is as follows:

*Definition 4.2.* A treatment  $ixj, i < j$  and a block  $k$  in block design are said to be associated if the treatment  $i$  appears in the block  $k$ . Two treatments are said to be connected if it is possible to pass from one to the other through a chain consisting alternatively of treatments and blocks such that any two members of a chain are associated. A design is said to be connected if every pair of treatments is connected.

Now we will utilize the above equations to estimate the genetic parameters in proposed designs. We will give below the estimation procedure of genetic parameters in complete diallel cross (CDC) system IV through partially balanced incomplete block (PBIB) designs.

### 4.2.2.1. Estimation of gca and sca of the Proposed Designs

Let  $\hat{\tau}$ ,  $\hat{\mathbf{g}}$  and  $\hat{\mathbf{s}}$  are estimates of  $\boldsymbol{\tau}$ ,  $\mathbf{g}$  and  $\mathbf{s}$  respectively in intra-block analysis. The second stage is to utilize the fact that the cross effects can be expressed in terms of gca and sca. To achieve this, we define the cross *gca* relation matrix  $\mathbf{Z}$  of the mating design. So we can write

$$\tau_{ij} = g_i + g_j + s_{ij} \quad (4.15)$$

where  $g_i$  ( $g_j$ ) is the gca for the  $i^{\text{th}}$  ( $j^{\text{th}}$ ) parent and  $s_{ij}$  ( $s_{ij} = s_{ji}$ ) is the sca for the cross between the  $i^{\text{th}}$  and the  $j^{\text{th}}$  parents where ( $i < j = 1, 2, \dots, p$ ) and we also assume that

$\sum_{i=1}^p g_i = 0$ ,  $\sum_{i < j=1}^p s_{ij} = 0$  for all  $i$ . In matrix notation, model (4.15) can be written as

$$\boldsymbol{\tau} = \mathbf{Z}\mathbf{g} + \mathbf{s} \quad (4.16)$$

where  $\mathbf{g} = (g_1, g_2, \dots, g_p)'$ ,  $\mathbf{s} = (s_{12}, s_{13}, \dots, s_{p(p-1)})'$  and  $\mathbf{Z} = (z_{ui})$  ( $u = 1, 2, \dots, v$ ;  $i = 1, 2, \dots, p$ ) is the cross and gca relation matrix.

$$z_{ui} = 1 \text{ if the } u^{\text{th}} \text{ cross has only one parent } i \text{ or parent } j .$$

$$= 0, \text{ otherwise.}$$

That is,  $\mathbf{Z}$  is crosses and line relation matrix.

Now

$$\mathbf{C}\boldsymbol{\tau} = \mathbf{CZ}\mathbf{g} + \mathbf{C}\mathbf{s} \quad (4.17)$$

with

$$\mathbf{E}(\mathbf{Q}) = \mathbf{CZ}\mathbf{g} + \mathbf{C}\mathbf{s}, \quad V(\mathbf{Q}) = \mathbf{C}\sigma^2 \quad (4.18)$$

Since the matrix  $\mathbf{C}$  is singular, we use the unified theory of least square due to Rao (1973). We get the estimator of general combining ability  $\mathbf{g}$  from equation (4.17) and imposing to  $\mathbf{Z}'\mathbf{C}\mathbf{s} = \mathbf{0}$ .

$$\hat{\mathbf{g}} = (\mathbf{Z}'\mathbf{C}\mathbf{C}^{-1}\mathbf{CZ})^{-1}\mathbf{Z}'\mathbf{Q} = (\mathbf{Z}'\mathbf{CZ})^{-1}\mathbf{Z}'\mathbf{C}\hat{\boldsymbol{\tau}} = \mathbf{P}_1\hat{\boldsymbol{\tau}} \quad (4.19)$$

Where

$$\mathbf{P}_1 = (\mathbf{Z}'\mathbf{CZ})^{-1}\mathbf{Z}'\mathbf{C} \quad (4.20)$$

with variance

$$\begin{aligned} V(\hat{\mathbf{g}}) &= \mathbf{P}_1\mathbf{C}^{-1}\mathbf{P}_1'\sigma^2 \\ V(\hat{\mathbf{g}}) &= (\mathbf{Z}'\mathbf{CZ})^{-1}\sigma^2 \end{aligned} \quad (4.21)$$

and

$$SS_{gca} = \mathbf{Q}'\mathbf{Z}(\mathbf{Z}'\mathbf{CZ})^{-1}\mathbf{Z}\mathbf{Q} \quad (4.22)$$

The estimator of  $\mathbf{s}$  is: From (4.16), we get

$$\hat{\mathbf{s}} = \hat{\boldsymbol{\tau}} - \mathbf{Z}\hat{\mathbf{g}} \quad (4.23)$$

$$\hat{\mathbf{s}} = \mathbf{C}^{-1}\mathbf{Q} - \mathbf{Z}(\mathbf{Z}'\mathbf{CZ})^{-1}\mathbf{Z}'\mathbf{Q} \quad (4.24)$$

$$\hat{\mathbf{s}} = [\mathbf{C}^{-1} - \mathbf{Z}(\mathbf{Z}'\mathbf{CZ})^{-1}\mathbf{Z}']\mathbf{Q} \quad (4.25)$$

$$\hat{\mathbf{s}} = [\mathbf{C}^{-1}\mathbf{C} - \mathbf{Z}(\mathbf{Z}'\mathbf{CZ})^{-1}\mathbf{Z}'\mathbf{C}]\hat{\boldsymbol{\tau}} = \mathbf{P}_2\hat{\boldsymbol{\tau}}$$

$$\text{Where } \mathbf{P}_2 = \mathbf{C}^{-1}\mathbf{C} - \mathbf{Z}(\mathbf{Z}'\mathbf{CZ})^{-1}\mathbf{Z}'\mathbf{C} \quad (4.26)$$

With variance

$$V(\hat{\mathbf{s}}) = \mathbf{P}_2\mathbf{C}^{-1}\mathbf{P}_2'\sigma^2 \quad (4.27)$$

Since  $\mathbf{P}_1\mathbf{1}_v = \mathbf{P}_2\mathbf{1}_v = \mathbf{0}$ ,  $\mathbf{P}_1\mathbf{P}_2' = \mathbf{0}$ ,  $\text{rank}(\mathbf{P}_1) = p-1$  and  $\text{rank}(\mathbf{P}_2) = \frac{1}{2}p(p-3)$ , it follows that the  $\hat{\mathbf{g}}$  and  $\hat{\mathbf{s}}$  are represented by treatment contrasts that carries  $p-1$  and  $\frac{1}{2}p(p-3)$  degrees of freedom respectively. It means that the proposed design allows for general combining abilities and specific combining abilities to be estimated independently. The total sum of squares and the block sum of squares are calculated in the usual way.

The sum of squares due to  $\hat{\mathbf{s}}$  is

$$\begin{aligned}
 SS_{sca} &= SS_{cross} - SS_{gca} = \hat{\mathbf{t}}' \mathbf{Q} - \hat{\mathbf{t}}' \mathbf{C}' \mathbf{Z} (\mathbf{Z}' \mathbf{C} \mathbf{Z})^{-1} \mathbf{Z}' \mathbf{Q} \\
 &= \hat{\mathbf{t}}' [\mathbf{I} - \mathbf{C}' \mathbf{Z} (\mathbf{Z}' \mathbf{C} \mathbf{Z})^{-1} \mathbf{Z}'] \mathbf{Q} \\
 &= \mathbf{Q}' \mathbf{C}^{-1} \mathbf{Q} - \mathbf{Q}' \mathbf{Z} (\mathbf{Z}' \mathbf{C} \mathbf{Z})^{-1} \mathbf{Z}' \mathbf{Q} \\
 &= \mathbf{Q}' [\mathbf{C}^{-1} - \mathbf{Z} (\mathbf{Z}' \mathbf{C} \mathbf{Z})^{-1} \mathbf{Z}'] \mathbf{Q}
 \end{aligned} \tag{4.28}$$

The Analysis of variance (ANOVA) is then given in Table 4.1.

Table 4.1. Intra-block Analysis of Variance

Source of variation	Degrees of freedom	Sum of squares
Blocks	b-1	$\frac{2}{k(k-1)} \mathbf{NB} - \frac{\mathbf{G}^2}{bk}$
Crosses (adjusted )	$\text{rank}(\mathbf{C}) = \frac{1}{2} p(p-1) - 1$	$\mathbf{Q}' \mathbf{C}^{-1} \mathbf{Q}$
gca	$\text{Rank}[(\mathbf{Z}' \mathbf{C} \mathbf{Z})^{-1}] = p-1$	$\mathbf{Q}' \mathbf{Z} (\mathbf{Z}' \mathbf{C} \mathbf{Z})^{-1} \mathbf{Z}' \mathbf{Q}$
sca	$\text{rank}(\mathbf{C}) - \text{rank}[(\mathbf{Z}' \mathbf{C} \mathbf{Z})^{-1}] = \frac{1}{2} p(p-3)$	$\mathbf{Q}' (\mathbf{C}^{-1} - \mathbf{Z} (\mathbf{Z}' \mathbf{C} \mathbf{Z})^{-1} \mathbf{Z}') \mathbf{Q}$
Residual	by subtraction	by subtraction
Total	$n - 1$	$\mathbf{y}' \mathbf{y} - \frac{2G^2}{bk(k-1)}$

Where  $G$  = grand total of all the  $n = \frac{1}{2} bk(k-1)$  observations.

### 4.2.3. Properties of M-E Designs

In section 3.1, we have described one method of employing complete diallel crosses in incomplete block designs. Obviously, there are other methods. Whenever one has such choice it is useful to compare competing designs. This can be accomplished by means of the efficiency factors of those designs. Since we present an embedding of two types of designs, a mating design (M) and an environmental design (E) (see e.g. Singh and Hinkelmann, 1995), the efficiency comparison of such a mating-environmental design will be relative to a CDC-orthogonal block design (say, RCBD) combination.

For a complete diallel cross (CDC) in a randomized complete block design (RCBD) with  $b$  block and one offspring per experimental units, we have (Griffing, 1956)

$$V(\mathbf{C}'\hat{\mathbf{g}}) = \frac{\mathbf{C}'\mathbf{C}}{b(p-2)}\sigma^2 \quad (4.29)$$

More specifically, we are interested in elementary gca comparisons i.e.,  $g_i - g_j$ , in the context of our proposed design where we have either  $\lambda_1$  or  $\lambda_2$  replications for each mating. We may take  $b = 2$  for RCBD, then

$$V(\hat{g}_i - \hat{g}_j) = \frac{\sigma^2}{p-2}, \text{ for all } i, j (i \neq j) \quad (4.30)$$

For corresponding M-E design, we can write

$$V(\hat{g}_i - \hat{g}_j) = (c^{ii} + c^{jj} - 2c^{ij})\sigma^2 = V_{ij}\sigma^2, \text{ say where } (\mathbf{Z}'\mathbf{C}\mathbf{Z})^{-1} = (P_1^{ii}).$$

The average variance all elementary gca contrast is then

$$av_{i \neq j} V(\hat{g}_i - \hat{g}_j) = \frac{2}{p(p-1)} \sum_{i \neq j} V_{ij}\sigma^2 \quad (4.31)$$

If we denote for short expressions in (4.30) and (4.31) by  $V_C$  and  $V_P$ , respectively, then the efficiency factor of the M-E design is given by

$$E_F = \frac{V_C}{V_p} = \frac{p(p-1)/2(p-2)}{\sum_{i \neq j} V_{ij}} \quad (4.32)$$

### 4.3. Inter-Block Analysis

While discussing the intra-block analysis of block designs it was stated that the block as well as treatment effects are fixed. If the block effect is regarded as a random variable, the analysis slightly changed. Under the assumption of random block effects, the analysis is termed inter-block analysis or recovery of inter block information.

The need for recovery of inter-block information was first felt by Yates (1940) in the context of incomplete block designs, because he noticed that since the allocation of treatments to incomplete block designs is made at random, it is reasonable to assume that the block effects themselves are random variables, instead of fixed. Yates (1940) noticed that if the experimental material is fairly heterogeneous, treating the block effects as fixed results in the loss of information contained in the block totals.

In this section the analysis of block designs with recovery of inter-block information is dealt for binary, proper designs. We consider the model (4.2) in intra-block analysis

$$y_{ijk} = \mu + \tau_{ij} + \beta_k + \varepsilon_{ijk} \quad (4.33)$$

All the terms are already defined in the intra-block analysis.

With the additional assumption that the block effects,  $\beta_k$  are random variables such that

- i.  $E(\beta_k) = 0$ ,  $\text{var}(\beta_k) = \sigma_\beta^2$ ;  $\text{cov}(\beta_k, \beta_{k'}) = 0, k \neq k', k, k' = 1, 2, \dots, b$ ;
- ii.  $\beta_k$  are uncorrelated with error terms  $\varepsilon_{ijk}$ 's.

Mixed effects model in matrix notation

$$\mathbf{y} = \mathbf{1}\mu + \mathbf{X}\boldsymbol{\tau} + \mathbf{D}\boldsymbol{\beta} + \boldsymbol{\varepsilon} \quad (4.34)$$

All the terms are already defined in (4.3). In mixed effects model, it is assumed that vector  $\boldsymbol{\beta}$  is random variable with  $E(\boldsymbol{\beta}) = \mathbf{0}$ ,  $V(\boldsymbol{\beta}) = E(\boldsymbol{\beta}\boldsymbol{\beta}') = \sigma_b^2 \mathbf{I}$ ,  $\text{Cov}(\boldsymbol{\beta}, \boldsymbol{\varepsilon}) = \mathbf{0}$ ,  $E(\boldsymbol{\beta}, \boldsymbol{\varepsilon}') = \mathbf{0}$  where  $\mathbf{I}$  is the identity matrix of conformable order. Hence,  $\text{Cov}(\mathbf{y}) = \sigma^2 \mathbf{I} + \sigma_b^2 \mathbf{D}\mathbf{D}'$ .

#### 4.3.1. Estimation of Mixed Model Parameters

Let  $\tilde{\boldsymbol{\tau}}$ ,  $\tilde{\mathbf{g}}$  and  $\tilde{\mathbf{s}}$  are estimates of  $\boldsymbol{\tau}$ ,  $\mathbf{g}$  and  $\mathbf{s}$  respectively in inter-block analysis. In the analysis of fixed and mixed model, the variance components  $\sigma^2$  and  $\sigma_b^2$  play an important role. In particular, the method of estimation depends on whether  $\sigma^2$  and  $\sigma_b^2$  are known or not. Practically the variance components  $\sigma^2$  and  $\sigma_b^2$  are not known and such a situation will be considered here. Under the assumption that  $\sigma^2$  and  $\sigma_b^2$  are unknown, the so called intra-and inter-block analyses are very helpful in the analysis of results based on the fixed and mixed effects model.

In this paper, we will consider PBIB (2) designs only. Our consideration will be restricted to estimation and testing hypotheses concerning contrasts of treatment parameters, i.e., to linear functions  $\mathbf{c}'\boldsymbol{\tau}$ ,  $\mathbf{c}'\mathbf{g}$  and  $\mathbf{c}'\mathbf{s}$  where  $\mathbf{c}'\mathbf{1} = 0$ .  $\boldsymbol{\tau}$ ,  $\mathbf{g}$  and  $\mathbf{s}$  are already defined in the models (4.3) and (4.16).

Under these conditions, one may regard the block totals,  $B_{k'}$ 's as observations, where

$$B_{k'} = k' \mu + \sum_{i < j} n_{ijk'} \tau_{ij} + (k' \beta_{k'} + \sum_{i < j} \varepsilon_{ijk'}) \quad (4.35)$$

The new 'error' term may be denoted by

$$d_{k'} = k' \beta_{k'} + \sum_{i < j} \varepsilon_{ijk'} \quad (4.36)$$

Then,

$$E(d_{k'}) = 0 \quad \text{var}(d_{k'}) = k'^2 \sigma_\beta^2 + k' \sigma^2. \quad (4.37)$$

Where  $k' = \frac{1}{2} k(k-1)$

The inter-block estimators are then obtained by minimizing the sum of squares due to new 'errors', i.e.,  $\sum_{k'}^b d_{k'}$ , where

$$\sum_{k'}^b d_{k'} = \sum_{k'}^b (\beta_{k'} - k' \mu - \sum n_{ijk} \tau_{ij})^2 \quad (4.38)$$

The right hand side of (4.38) can be written in matrix notation as

$$(\mathbf{B} - k' \mu \mathbf{1} - \mathbf{N}' \boldsymbol{\tau})' (\mathbf{B} - k' \mu \mathbf{1} - \mathbf{N}' \boldsymbol{\tau}) \quad (4.39)$$

The normal equations are

$$\begin{bmatrix} bk' & \mathbf{1}' \mathbf{R}^\delta \\ k' \mathbf{R}^\delta \mathbf{1} & \mathbf{N} \mathbf{N}' \end{bmatrix} \begin{bmatrix} \mu \\ \boldsymbol{\tau} \end{bmatrix} = \begin{bmatrix} \mathbf{G} \\ \mathbf{N} \mathbf{B} \end{bmatrix} \quad (4.40)$$

All the terms have already defined in intra- block analysis section.

Pre-multiplying both sides of (4.40) by the non-singular matrix

$$\begin{bmatrix} \mathbf{1} & \mathbf{0} \\ \frac{1}{2b} \mathbf{R}^\delta \mathbf{1} & \mathbf{I} \end{bmatrix}$$

We obtain the following equations:

$$\begin{bmatrix} bk' & \mathbf{1}' \mathbf{R}^\delta \\ 0 & \mathbf{N} \mathbf{N}' - \frac{1}{b} \mathbf{R}^\delta \mathbf{1}' \mathbf{1} \mathbf{R}^\delta \end{bmatrix} \begin{bmatrix} \mu \\ \boldsymbol{\tau} \end{bmatrix} = \begin{bmatrix} \mathbf{G} \\ \mathbf{N} \mathbf{B} - \frac{1}{b} \mathbf{G} \mathbf{R}^\delta \mathbf{1} \end{bmatrix} \quad (4.41)$$

The solution of the equations (4.40) (or equivalently (4.41)) is obtained by taking the side condition  $\mathbf{1}' \mathbf{R}^\delta \boldsymbol{\tau} = \mathbf{0}$ . The solution is

$$\begin{aligned} \tilde{\mu} &= \frac{\mathbf{G}}{bk'} \\ \tilde{\boldsymbol{\tau}} &= (\mathbf{N} \mathbf{N}')^{-1} (\mathbf{N} \mathbf{B} - \frac{1}{b} \mathbf{G} \mathbf{R}^\delta \mathbf{1}) = (\mathbf{N} \mathbf{N}')^{-1} \mathbf{P} \end{aligned} \quad (4.42)$$

where  $\mathbf{P} = \mathbf{N} \mathbf{B} - \frac{\mathbf{G} \mathbf{R}^\delta \mathbf{1}}{b}$  and  $\mathbf{N}$  is the incidence matrix of the design under consideration.

The expectation and variance of  $\mathbf{P}$  is

$$E(\mathbf{P}) = \mathbf{NN}'\boldsymbol{\tau} \quad \text{and} \quad V(\mathbf{P}) = \mathbf{NN}'(k'^2 \sigma_b^2 + k' \sigma^2) \quad (4.43)$$

Following equation (4.9), we can write  $\boldsymbol{\tau} = \mathbf{Z}\mathbf{g} + \mathbf{s}$ , where  $\boldsymbol{\tau}$ ,  $\mathbf{Z}$ ,  $\mathbf{g}$  and  $\mathbf{s}$  have their usual meaning as defined in intra-block analysis. Now

$$\mathbf{NN}'\boldsymbol{\tau} = \mathbf{NN}'\mathbf{Z}\mathbf{g} + \mathbf{NN}'\mathbf{s} \quad (4.44)$$

Hence

$$\tilde{\mathbf{g}} = (\mathbf{Z}'\mathbf{NN}'\mathbf{Z})^{-1}\mathbf{Z}'\mathbf{P} \quad (4.45)$$

with variance

$$V(\tilde{\mathbf{g}}) = (\mathbf{Z}'\mathbf{NN}'\mathbf{Z})^{-1}(k'^2 \sigma_b^2 + k' \sigma^2) \quad (4.46)$$

The sum of squares due to general combining ability in inter-block analysis is

$$SS_{gca} = \tilde{\mathbf{g}}'\mathbf{Z}'\mathbf{P} = \mathbf{P}'\mathbf{Z}[\mathbf{Z}'(\mathbf{NN}')\mathbf{Z}]^{-1}\mathbf{Z}'\mathbf{P} \quad (4.47)$$

with d.f. = rank $[\mathbf{Z}'(\mathbf{NN}')\mathbf{Z}]^{-1}$ .

Inter-block estimator of sca from equation  $\boldsymbol{\tau} = \mathbf{Z}\mathbf{g} + \mathbf{s}$

$$\tilde{\mathbf{s}} = \tilde{\boldsymbol{\tau}} - \mathbf{Z}\tilde{\mathbf{g}} = [(\mathbf{NN}')^{-} - \mathbf{Z}[\mathbf{Z}'(\mathbf{NN}')\mathbf{Z}]^{-1}\mathbf{Z}']\mathbf{P} \quad (4.48)$$

With

$$V(\tilde{\mathbf{s}}) = [I - \mathbf{Z}(\mathbf{Z}'\mathbf{NN}'\mathbf{Z})^{-1}\mathbf{Z}'](k'^2 \sigma^2 + k' \sigma^2)$$

and its sum of squares is

$$\begin{aligned} SS_{sca} &= SS_{cross} - SS_{gca} = \mathbf{P}'(\mathbf{NN}')^{-}\mathbf{P} - \mathbf{P}'\mathbf{Z}(\mathbf{Z}'(\mathbf{NN}')\mathbf{Z})^{-}\mathbf{Z}'\mathbf{P} \\ &= \mathbf{P}'[(\mathbf{NN}')^{-} - \mathbf{Z}(\mathbf{Z}'(\mathbf{NN}')\mathbf{Z})^{-}\mathbf{Z}']\mathbf{P} \end{aligned} \quad (4.49)$$

The inter-block analysis of variance is given in Table 4.2.

Table 4.2. Inter-block Analysis of Variance

Source of variation	Degrees of freedom	Sum of squares
Blocks (adjusted)	b-1	$\hat{\boldsymbol{\tau}}' \mathbf{Q} + \frac{2}{k(k-1)} \sum_k^b \mathbf{B}_k^2 - \sum_{i < j} \frac{\mathbf{T}_{ij}^2}{r_{ij}}$
Crosses (unadjusted)	$\frac{1}{2} p(p-1) - 1$	$\sum_{i < j} \frac{T_{ij}^2}{r_{ij}} - CF$
gca (unadjusted)	(p-1)	$\mathbf{P}' \mathbf{Z} [\mathbf{Z}' (\mathbf{N}\mathbf{N}') \mathbf{Z}]^{-1} \mathbf{Z}' \mathbf{P}$
sca (unadjusted)	$\frac{1}{2} p(p-3)$	$\mathbf{P}' [(\mathbf{N}\mathbf{N}')^{-1} - \mathbf{Z} (\mathbf{Z}' (\mathbf{N}\mathbf{N}') \mathbf{Z})^{-1} \mathbf{Z}'] \mathbf{P}$
Residual	by subtraction	by subtraction
Total	$\frac{1}{2} bk(k-1) - 1$	$\mathbf{y}' \mathbf{y} - \frac{2G^2}{bk(k-1)}$

Where  $G =$  grand total of all the  $n = \frac{1}{2} bk(k-1)$  observations and  $CF = \frac{2G^2}{bk(k-1)}$ .

#### 4.4. Combined of Intra- and Inter-Block Analysis

Now, we have two estimators of  $\boldsymbol{\tau}$ , the intra- block estimator is given by  $\hat{\boldsymbol{\tau}} = \mathbf{C}^{-1} \mathbf{Q}$  and the inter-block estimator given by  $\tilde{\boldsymbol{\tau}} = (\mathbf{N}\mathbf{N}')^{-1} (\mathbf{N}\mathbf{B} - \frac{r_{ij} G \mathbf{1}}{b})$ . Finally, Kempthorne (1952, 1957) suggested the construction of best linear unbiased estimator (BLUE) of the treatment differences by combining  $\hat{\boldsymbol{\tau}}$  and  $\tilde{\boldsymbol{\tau}}$ , weighting inversely as their variances. That is, the BLUE of  $\hat{\tau}_{ij} - \tilde{\tau}_{ij}$  is given by

$$\tau_{ij}^* = \frac{\hat{\tau}_{ij} / V(\hat{\tau}_{ij}) + \tilde{\tau}_{ij} / V(\tilde{\tau}_{ij})}{1 / V(\hat{\tau}_{ij}) + 1 / V(\tilde{\tau}_{ij})} \quad (4.50)$$

Since  $\tilde{\tau}_{ij}$  is a function of  $\sigma_b^2$  and  $\sigma_b^2$  can be estimated as

$$\hat{\sigma}_b^2 = \frac{[MS_{block (adjusted)} - MS_{error}]/b - 1}{v(r - 1)} \quad (4.51)$$

Where  $v = \frac{1}{2}p(p-1)$ ,  $r = \frac{n_1\lambda_1^2 + n_2\lambda_2^2}{n_1\lambda_1 + n_2\lambda_2}$  is the weighted average of the replication of the crosses.

Note: The above suggestion will also be used in pooling the estimates of gca and sca obtained by intra and inter block analysis, i. e.,

$$g_i^* = \frac{\hat{g}_i / V(\hat{g}_i) + \tilde{g}_i / V(\tilde{g}_i)}{1 / V(\hat{g}_i) + 1 / V(\tilde{g}_i)}$$

$$s_{ij}^* = \frac{\hat{s}_{ij} / V(\hat{s}_{ij}) + \tilde{s}_{ij} / V(\tilde{s}_{ij})}{1 / V(\hat{s}_{ij}) + 1 / V(\tilde{s}_{ij})}$$

## 4.5. Hypotheses Testing

### 4.5.1. Fixed and Mixed Effects Model

Since the analyzed combining abilities are expressible in terms of the contrasts of treatment parameters, it is sufficient to consider the test of hypotheses concerning contrasts. Suppose we consider  $h(\leq \frac{1}{2}p(p-1) - 1 = v - 1)$  contrasts of treatment parameters  $c'_1 \tau, c'_2 \tau, \dots, c'_h \tau$  where  $c'_i \mathbf{1} = 0$  for  $i = 1, 2, \dots, h$ . If we are interested in testing the hypotheses:

i. Testing crosses

$$H_0: \mathbf{C}'\boldsymbol{\tau} = \mathbf{0} \quad \text{against} \quad H_1: \mathbf{C}'\boldsymbol{\tau} \neq \mathbf{0}$$

Where  $\mathbf{C} = (c_1, c_2, \dots, c_h)$ ,  $\text{rank}(\mathbf{C}) = h$ , then the appropriate F-statistic

$$F_{cal} = \frac{MS_{cross}}{MS_{error}} = \frac{SS_E / \frac{Q' C^{-1} Q}{v-1}}{SS_E / b[\frac{1}{2}k(k-1)-1] - \frac{1}{2}p(p-1) - 1} \quad (4.53)$$

ii. Testing general combining ability (gca)

$$H_0: \mathbf{C}'\mathbf{g} = \mathbf{0} \text{ against } H_1: \mathbf{C}'\mathbf{g} \neq \mathbf{0}$$

Where  $\mathbf{C} = (c_1, c_2, \dots, c_h)$ ,  $\text{rank}(\mathbf{C}) = h$ , then the appropriate F-statistic

$$F_{cal} = \frac{MS_{gca}}{MS_{error}} = \frac{SS_E / \frac{Q' \mathbf{Z}(\mathbf{Z}'\mathbf{C}^{-1}\mathbf{Z})^{-1}\mathbf{Z}'\mathbf{Q}}{p-1}}{SS_E / b[\frac{1}{2}k(k-1)-1] - \frac{1}{2}p(p-1) - 1} \quad (4.54)$$

iii. Testing specific combining ability (sca)

$$H_0: \mathbf{C}'\mathbf{s} = \mathbf{0} \text{ against } H_1: \mathbf{C}'\mathbf{s} \neq \mathbf{0} \text{ with}$$

$$F_{cal} = \frac{MS_{sca}}{MS_{error}} = \frac{SS_E / \frac{Q' \mathbf{Z}(\mathbf{C}^{-1} - \mathbf{Z}'\mathbf{C}^{-1}\mathbf{Z})^{-1}\mathbf{Z}'\mathbf{Q}}{\frac{1}{2}p(p-3)}}{SS_E / b[\frac{1}{2}k(k-1)-1] - \frac{1}{2}p(p-1) - 1} \quad (4.55)$$

In the analysis of combining abilities the interesting hypotheses concerning the gca and sca effects can be formulated as follows:

1.  $H_0 : g_i = 0$ ; for all  $i$ ,
2.  $H_0 : s_{ij} = 0$ ; for all  $i < j$ ,
3.  $H_0 : g_i = 0$ ; for fixed  $i$ ,
4.  $H_0 : g_i - g_j = 0; i \neq j$ ,
5.  $H_0 : s_{ij} = 0$ ; for fixed  $i < j$ ,
6.  $H_0 : s_{ij} = s_{il}; i < j, l, j \neq l$ ,
7.  $H_0 : s_{ij} - s_{ml} = 0; i < j, m < l, i \neq m, j \neq l$ ,

where  $i, j, m, l = 1, 2, \dots, p$ .

The diallel crossing system is often of interest to the breeders dealing with estimation and testing of general and specific combining abilities. In this paper we consider one type of diallel crossing system, type IV according to the classification by Griffing (1956). With respect to the above, we need the significance levels of the appropriate F-tests used to test the same hypothesis. Now we will describe the intra- and inter- block analyses of F-test for each of the hypotheses 1-7.

Table 4.3. F-statistics for testing hypotheses 1-7

Hypotheses	F <sub>fixed</sub> (intra-block)	F <sub>mixed</sub> (inter-block)
1	$\frac{SS_{gca} / p - 1}{MS_E}$	$\frac{SS_{gca} / p - 1}{MS_E}$
2	$\frac{SS_{sca} / \frac{1}{2} p(p - 3)}{MS_E}$	$\frac{SS_{sca} / \frac{1}{2} p(p - 3)}{MS_E}$
3	$\frac{p \hat{g}_i^2}{MS_E}$	$\frac{p \tilde{g}_i^2}{MS_E}$
4	$\frac{(\hat{g}_i - \hat{g}_j)^2}{2MS_E}$	$\frac{(\tilde{g}_i - \tilde{g}_j)^2}{2MS_E}$
5	$\frac{p(p - 1)(\hat{s}_{ij})^2}{2MS_E}$	$\frac{p(p - 1)(\tilde{s}_{ij})^2}{2MS_E}$
6	$\frac{(\hat{s}_{ij} - \hat{s}_{il})^2}{2MS_E}$	$\frac{(\tilde{s}_{ij} - \tilde{s}_{il})^2}{2MS_E}$
7	$\frac{(\hat{s}_{ij} - \hat{s}_{lm})^2}{2MS_E}$	$\frac{(\tilde{s}_{ij} - \tilde{s}_{lm})^2}{2MS_E}$

If hypothesis 1 is true under  $H_0$ , then the  $F_{\text{fixed}}$ -statistic in intra-block and  $F_{\text{mixed}}$ -statistic in inter-block have the F- distribution with  $p - 1$  and  $n - b - v + 1$  degrees of freedom, respectively.

If hypothesis 2 is true under  $H_0$ , then the  $F_{\text{fixed}}$ -statistic in intra-block and  $F_{\text{mixed}}$ -statistic in inter-block have the F- distribution with  $\frac{1}{2} p(p - 3)$  and  $n - b - v + 1$  degrees of freedom, respectively.

If hypotheses 3-7 (they are individual hypotheses) are true, then the  $F_{\text{fixed}}$ -statistics and  $F_{\text{mixed}}$ -statistics have the F- distributions with 1 and  $n - b - v + 1$  degrees of freedom, respectively.

# CHAPTER FIVE

## ILLUSTRATIVE EXAMPLE

### 5.1. Introduction

For illustrating the theory given in this paper, let us consider the data on maize yield reported by Griffing (1956) on page 482. The author used a randomized complete block design for complete diallel cross system IV with  $v = 36$  genotypes. From this study we have taken the data on  $y =$  cob weight of maize for numerical illustration.

The most commonly used statistical software for statistical design and analysis of experiments such as SAS, STATA, SPSS, S-PLUS, MS-Excel, which we are not going to employ in our analysis directly. We employed MS-Excel and S-PLUS statistical softwares for calculating analysis of variance and estimation of model parameters.

There are 36 crosses and the design has nine blocks, each of size six. Eighteen crosses were replicated twice and the remaining eighteen crosses were replicated once. The number of observations is 54. The layout and observations in parentheses are given below.

$B_1$	$B_2$	$B_3$	$B_4$	$B_5$	$B_6$	$B_7$	$B_8$	$B_9$
1x2 (31.8)	2x4 (30.8)	1x4 (23.3)	2x5 (39.6)	2x3 (27.9)	3x4 (23.7)	1x5 (45)	3x6 (35.5)	1x3 (34.7)
1x6 (39)	2x6 (34.2)	1x8 (35.7)	2x7 (30.9)	2x4 (29.1)	3x5 (41.4)	1x6 (37)	3x7 (36.3)	1x5 (47)
1x9 (40.1)	2x8 (36.9)	1x9 (38.3)	2x9 (31.4)	2x7 (32.8)	3x9 (32.4)	1x7 (35.1)	3x8 (32.1)	1x8 (39)
2x6 (33.1)	4x6 (35.7)	4x8 (35.2)	5x7 (43.6)	3x4 (25.2)	4x5 (42.6)	5x6 (40.1)	6x7 (43.2)	3x5 (39.1)
2x9 (28.5)	4x8 (32.7)	4x9 (41.3)	5x9 (44.2)	3x7 (34.9)	4x9 (43.7)	5x7 (40.2)	6x8 (41.8)	3x8 (30.4)
6x9 (41.5)	6x8 (43.5)	8x9 (35.2)	7x9 (41.1)	4x7 (35.6)	5x9 (42)	6x7 (39.1)	7x8 (38.3)	5x8 (41.8)

## 5.2. Presentation, Interpretation and Implications of Results

The following exhibit the vectors  $\mathbf{R}^\delta, \mathbf{k}^\delta, \mathbf{T}, \mathbf{B}$  and  $\mathbf{Q}$  are given in this section and the matrices  $\mathbf{N}, \mathbf{Z}$  and  $\mathbf{C}$  are given in Appendix B. The analysis of variance (intra- and inter-block) for cob weight are given in Table 5.1 and 5.2 respectively, and the estimates of genotype and sca from intra- and inter- block analyses are given in Tables 5.3, 5.4, 5.5 and 5.6. The combined estimates of sca are given in table 5.7. The statistical inferences obtained from hypotheses are also given in Table 5.8.

The first step in the analysis is to calculate analysis of variance i.e., the degrees of freedom, the sum of squares, the mean squares and the F-ratio in the intra-and the inter-block analyses, which are summarized in Table 5.1 and Table 5.2, respectively.

Table 5.1. The Estimate of Intra-block Analysis of Variance

Source of variation	Degrees of freedom	Sum of squares	Mean Squares	$F_{cal}$	$F_{critical}$ at $\alpha = 0.05$
Blocks	8	314.27	39.28375	16.1628	
Crosses (adjusted)	35	1141.865	32.62471	13.4231	4.2035
gca (adjusted)	8	876.3333	109.5417	45.0696	3.0717
sca(adjusted)	27	265.5317	9.834506	4.0463	3.3003
Residual	10	24.305	2.4305		
Total	53	1480.44			

Table 5.2. The Estimate of Inter-block Analysis of Variance

Source of variation	Degrees of freedom	Sum of squares	Mean Squares	F <sub>cal</sub>	F <sub>critical</sub> $\alpha = 0.05$
Blocks(adjusted)	8	25.07			
Crosses (unadjusted)	35	1431.065	40.88757	16.8227	4.2035
gca	8	336.5233	37.39148	15.38427	3.0717
sca	27	1094.542	42.09777	17.32062	3.3003
Residual	10	24.305	2.4305		
Total	53	1480.44			

From the intra- and inter- block analysis of variance, Table 5.1 and Table 5.2, we conclude that genotype, gca and sca are significant at 5% level of significance. The analysis of variances tends to render the information about the basic nature of the parental materials involved in diallel crossing. Thus, the significant variation among gca and sca, indicate potential genetic differences among the parents chosen.

Since gca and sca are significant in the above analysis of variance, the gca effects ( $g_i$ ) for each parent and sca effects ( $s_{ij}$ ) for each cross combination can be calculated using the formulae in chapter four.

$\mathbf{R}^{\delta} = \text{diag.}(1, 1, 1, 2, 2, 1, 2, 2, 1, 2, 1, 2, 2, 1, 2, 2, 2, 1, 2, 2, 1, 1, 1, 1, 2, 2, 1, 2, 1, 2, 2, 2, 1, 1, 1, 1)$ .

$\mathbf{k}^{\delta} = \text{diag.}(6, 6, \dots, 6)$ , there are 36 diagonal elements with each has 6 value.

The followings are the vector of treatment total ( $\mathbf{T}$ ), block total ( $\mathbf{B}_k$ ) and adjusted treatment total ( $\mathbf{Q}$ ) respectively.

$\mathbf{T}$	$\mathbf{B}_k$	$\mathbf{Q}$
31.8	214	-3.8667
34.7	213.8	-3.9667
32.3	218	-4.0333
92	230.8	13.9167
76	185.5	0.9167
35.1	225.8	-4.3167
74.7	236.5	-0.3
78.4	227.2	6.4
27.9	232	-3.0167
59.9		-6.65
39.6		1.1333
67.3		-4
63.7		-5.6833
36.9		1.2667
59.9		-14.2333
48.9		-19.65
80.5		4.2
35.5		-2.3667
71.2		2.4167
62.5		-14.0333
32.4		-5.2333
42.6		4.9667
35.7		0.0667
35.6		4.6833
67.9		-4.0667
85		11.0333
40.1		0.6833
83.8		5.9167
41.8		3.1333
86.2		10.1
82.3		5.0167
85.3		11.8
41.5		5.8333
38.3		0.4333
41.1		2.6333
35.2		-1.1333

The next step is estimation of effects of the crosses (genotypes) in the intra- and inter-block analyses, i.e., the calculation of the vectors  $\hat{\tau}$  and  $\tilde{\tau}$  respectively, the elements which are arranged in the following triangular tables:

-in the intra-block analysis the estimated genotype (cross) effects are

Table 5.3. The Estimates of Genotype (Cross) Effects of in Intra-block Analysis

ixj	2	3	4	5	6	7	8	9
1	-4.3958	-1.7958	-3.2292	10.6375	2.7875	0.8708	1.3375	3.3375
2		-9.7125	-7.4958	1.6542	-3.0875	-5.9292	-0.3792	-7.1208
3			-12.9292	3.4292	-2.2792	-2.0958	-5.8875	-4.7458
4				5.4542	-1.5792	-2.0125	-2.4542	6.1625
5					5.8708	5.8125	5.3042	5.5542
6						5.1458	5.1208	5.3042
7							0.5208	3.1542
8								-0.3292

-in inter-block analysis the estimated genotype (cross) effects are

Table 5.4. The Estimates of Genotype (cross) Effects of in Inter-block Analysis

ixj	2	3	4	5	6	7	8	9
1	-1.8727	0.7373	-0.6667	4.4593	1.7053	3.3013	0.3393	-2.2257
2		-6.6907	-6.7307	1.8893	-1.7647	-4.8807	0.2853	-0.1237
3			-4.81970	2.90030	0.98730	-5.61570	1.70630	2.02930
4				2.0293	0.2853	-6.6907	-0.6787	1.1103
5					3.3013	5.2913	0.7373	3.9583
6						4.2453	1.1233	-1.8727
7							0.9873	1.8893
8								-0.6667

Now, use formulae given in the previous chapter, we can estimate the gca and sca effects.

General Combining Ability (gca) effects: The estimates of gca effects are as follows:

-in the intra-block analysis,  $\hat{g}_i$ , where  $i = 1, 2, \dots, 9$ , are

1.5667    -5.11    -6.05    -2.8367    6.7367    2.5467    1.5633    -0.8133    2.3967

With variance  $v(\hat{g}_i) = 0.3241$  and  $\text{cov}(\hat{g}_i, \hat{g}_j)$  has two values depending on whether  $(\hat{g}_i, \hat{g}_j)$  are first associates or second associates. Thus,

$$\text{Cov}(\hat{g}_i, \hat{g}_j) = \begin{cases} -0.054 & , \text{ for first associates} \\ -0.027 & , \text{ for second associates} \end{cases}$$

- in the inter-block analysis, they are

-1.8278   -4.9278   -3.2778   -2.6444   6.6889   3.1556   -0.7278   1.9722   1.5889

- in the combined analysis, they are

1.6025   -4.0563   -4.8529   -2.1295   5.9842   2.4331   1.5996   -0.4147   2.3059

The gca effects ( $g_i$ ) represent the additive nature of gene action. A high general combiner (parent) is characterized by its better breeding value when crossed with a number of other parents. Depending upon the character concerned, the nature (direction/ sign) and magnitude (size) of  $g_i$  are both concerned. Besides, mean performance of the parent is also considered in unison with  $g_i$  since the former offers reliability/authenticity to  $g_i$  as a guide to selection of parent. Further, the other associated parameters,  $\sigma_{g_i}^2$  (gca variance) and  $\sigma_{s_{ij}}^2$  (sca variance) with each parent play significant role in choice of parents, for instance, a parent showing high  $\sigma_{g_i}^2$  and low  $\sigma_{s_{ij}}^2$  with high  $g_i$  and high mean would certainly be a right choice as a component of synthetic variety. Similarly, a parent with high  $\sigma_{g_i}^2$  and  $\sigma_{s_{ij}}^2$  is a better parent for creating high-yielding specific combinations, as high  $\sigma_{s_{ij}}^2$  arises mainly from its highly differential (specific) ability to transmit its characters (genes) into its hybrid progenies.

Thus, in the present example, by using the hypothesis 3 all are significant except for  $g_8$ . But only  $g_1, g_5, g_6, g_7$  and  $g_9$  (they bring significantly different with each other) for intra-block analysis. In case of inter-block analysis are also all significant except  $g_7$ . But only  $g_5, g_6$  and  $g_9$  are brought positive significant. The estimates of combined are also interpreted in similar fashion.

The estimates of sca effects are arranged in triangular tables:

-in the intra-block analysis estimates are

Table 5.5. The Estimates of sca Effects of in Intra-block Analysis

ixj	2	3	4	5	6	7	8	9
1	-0.8525	2.6875	-1.9592	2.3342	-1.3258	-2.2592	0.5842	-0.6258
2		1.4475	0.4508	0.0275	-0.5242	-2.3825	5.5442	-4.4075
3			-4.0425	2.7425	1.2242	2.3908	0.9758	-1.0925
4				1.5542	-1.2892	-0.7392	1.1958	6.6025
5					-3.4125	-2.4875	-0.6192	-3.5792
6						1.0358	3.3875	0.3608
7							-0.2292	-0.8058
8								-1.9125

$$V(s_{ij}) = \begin{cases} 2.8862 & , \text{ for } s_{ij}^{(1)} \\ 1.4436 & , \text{ for } s_{ij}^{(2)} \end{cases}$$

Table 5.6. The Estimates of sca Effects of in Inter-block Analysis

ixj	2	3	4	5	6	7	8	9
1	4.8829	5.8429	3.8056	-0.4018	0.3776	5.8569	0.1949	-1.9868
2		1.5149	0.8416	0.1282	0.0076	0.7749	3.2409	3.2152
3			1.1026	-0.5108	1.1096	-1.6101	3.0119	3.7182
4				-2.0151	-0.2258	-3.3184	-0.0064	2.1659
5					-6.5431	-0.6698	-7.9238	-4.3194
6						1.8176	-4.0044	-6.6171
7							-0.2571	1.0282
8								-4.2278

Table 5.7. The Estimates of sca Effects of in Combined Analysis

ixj	2	3	4	5	6	7	8	9
1	-4.1627	15.7028	-7.4557	-0.9378	-0.5006	-13.2317	0.1138	1.2434
2		2.1928	0.3794	0.0035	-0.0040	-1.8462	17.9680	-14.1711
3			-4.4571	-1.4008	1.3583	-3.8495	2.9391	-4.0622
4				-3.1318	0.2911	2.4529	-0.0077	14.3003
5					22.3284	1.6661	4.9061	15.4600
6						1.8827	-13.5651	-2.3877
7							0.0589	-0.8286
8								8.0856

Specific combining ability (sca) effects:

The sca effects ( $s_{ij}$ ) Signify the role of non- additive gene action. It is denotes highly specific combining ability leading to highest performance of some specific cross combinations. That is why, it relates to a particular cross. The  $s_{ij}$  are also seen in relation to their size and sign. In our example, the crosses 4x9, 2x8 and 6x8 manifest the highest  $s_{ij}$  in positive direction in intra-block analysis. In inter-block and combined estimates of sca interpreted in similar way.

As we can see from the results of this example, the combined estimates (especially gca) are nearly the estimates obtained from intra-block analysis. This follows from the fact that main part of information about contrasts of treatment parameters is included in intra-block analysis. The differences between intra-block estimates and combined estimates are more perceptible if more information is contained in the inter-block analysis. In planning experiment it is desirable to have more information in the inter-block analysis, but such a situation is not always possible.

The efficiency factor of the intra-block M-E design in relation to RCBD is

$$E_F = \frac{V_c}{V_p} = \frac{p(p-1)}{\sum_{i \neq j} 2(p-2)} = 0.8817$$

This implies that complete diallel cross obtained through PBIB (2) designs is 88.2% efficient in comparison to RCBD, which is considered to be 100% efficient. In other words, complete diallel cross obtained through RCBD is more efficient by 11.8% than PBIB (2) design for this

particular example. But we cannot use the RCBD for the above type of experiment because RCBD is advisable to use less or equal to only 12 or 13 treatments. If we use large number (more than 12 or 13) of treatments, it will create heterogeneity in the block as mention in the literature review section 2.2.

Now, we consider some statistical inferences from hypotheses testing in table 5.8 are given below.

Table 5.8. Statistical Inferences

Serial Number	Hypotheses	$F_{\text{fixed}}$ (intra-block)	$F_{\text{mixed}}$ (inter-block)	$F_{\text{critical}}$ at $\alpha = 0.05$
1	$\mathbf{g} = \mathbf{0}$	45.0696**	15.3842**	3.0717
2	$\mathbf{s} = \mathbf{0}$	4.0463**	17.3206**	3.3003
3	$g_1 = 0$	22.0909**	30.0669**	4.9646
4	$g_1 - g_2 = 0$	9.1705**	1.977	4.9646
5	$s_{12} = 0$	10.7645**	353.151**	4.9646
6	$s_{12} - s_{13} = 0$	2.578	0.1896	4.9646
7	$s_{12} - s_{34} = 0$	2.0934	2.9399	4.9646

Note: \*\* significant at  $\alpha = 0.05$  level of significance.

A comparison of individual line performances is of considerable interest to a plant breeder. Inferences on their basis can be made by testing hypotheses 1-7 (Table 5.8). The first and the second hypotheses of gca and sca effects are significant, respectively, for both intra- and inter- block analyses, at 5% level of significance. This means that at least one of gca and sca effects are different from zero. In the above table, we have taken only one sample hypothesis for illustrative purpose for each hypothesis 3-7. In similar way, we can exhaustively list and test all the hypotheses 3-7 as mentioned in page 45. Since the overall gca and sca are significant, we can further test the individual gca and sca effects in the hypotheses 3 and 5.

gca and sca are statistically significant of the first parental line, and the combination of the first and the second parental lines, respectively, for both intra- and inter- block analyses at 5% level of significance. From hypothesis 4, there is statistical difference between the first and the second parental lines of gca for intra-block analysis but not inter-block analysis. The objective of testing hypotheses 6 and 7 are to know the difference between two sca from fix one parental line and vary the others (hypothesis 6), and vary both parental lines for each sca (hypothesis 7). From table 5.8, both hypotheses 6 and 7 are statistically insignificant for both intra- and inter-block analyses at 5% level of significance.

### ***5.3. Discussion***

The appropriateness of the various kinds of diallel crossing methods depends on the experimental material and the objectives of the experiment. When information on general and specific combining ability for a specific set of lines is described in connection with a plant or animal breeding problem, experimental method 4 is most applicable. In plant material if it can be assumed that there will be no genotypic reciprocal effects; method 4 is the most suitable.

In most combining ability analyses in which a chosen set of lines is used interest center on the performance of  $F_1$ 's. Therefore, the parental lines need not be included. However, in certain instances it might be advisable to include the parents.

When a set of inbred lines is used in a diallel crossing system a genetic interpretation in terms of quantitative inheritance is made possible by the fact that the analysis is really a "gamete" combining ability analysis. Thus the genetic properties of a diploid individual may be regarded as the combination of the genetic properties of the two gametes which united to form the individual. Therefore in statistical analysis we may regard the genotypic effect of an individual as the summation effects contributed by each gamete (i. e., set of genes in the gamete) and the interaction of gametes (i. e., the interaction of the genes in one gamete with those in the other).

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# Appendices

## Appendix A: Two –Associate Classes of Partially Balanced Incomplete Block Designs with Parameters

Ref. No	Parameters								$\frac{1}{2}p(p-1)+b+1$	$\frac{1}{2}bk(k-1)$
	$p$	$r$	$k$	$b$	$m(n_1)$	$n(n_2)$	$\lambda_1$	$\lambda_2$		
S2	6	4	4	6	3	2	4	2	22	36
S3	6	6	4	9	3	2	6	3	25	54
S4	6	8	4	12	3	2	8	4	28	72
S5	6	10	4	15	3	2	10	5	31	90
S6	8	3	4	6	4	2	3	1	35	36
S7	8	6	4	6	4	2	6	2	41	72
S8	8	9	4	18	4	2	9	3	47	108
S9	10	4	4	10	5	2	4	1	56	60
S10	10	8	4	20	5	2	8	2	66	120
S11	12	5	4	15	6	2	5	1	82	90
S12	12	10	4	30	6	2	10	2	97	180
S13	14	6	4	21	7	2	6	1	113	126
S18	8	3	6	4	4	2	3	2	35	60
S19	8	6	6	8	4	2	6	4	37	120
S20	8	9	6	12	4	2	9	6	41	180
S21	9	2	6	3	3	3	2	1	40	45
S22	9	4	6	6	3	3	4	2	43	90
S23	9	6	6	9	3	3	6	3	46	135
S24	9	8	6	12	3	3	8	4	49	180
S25	9	10	6	15	3	3	10	5	52	225
S26	10	6	6	10	5	2	6	3	56	150
S27	12	3	6	6	4	3	3	1	80	90
S28	12	5	6	10	6	2	5	2	77	150
S29	12	6	6	12	4	3	6	2	79	180
S30	12	9	6	18	4	3	9	3	85	270
S31	12	10	6	20	6	2	10	4	87	300
S32	14	3	6	7	7	2	3	1	99	105
S33	14	6	6	14	7	2	6	2	106	210
S34	14	9	6	21	7	2	9	3	113	315
S35	15	4	6	10	5	3	4	1	116	150
S36	15	8	6	20	5	3	8	2	126	300
S51	10	4	8	5	5	2	4	3	51	135

S52	10	8	8	10	5	2	8	6	56	280
S53	12	2	8	3	3	4	2	1	70	84
S54	12	4	8	6	3	4	4	2	73	168
S55	12	6	8	9	3	4	6	3	76	252
S56	12	8	8	12	3	4	8	4	79	336
S57	12	10	8	15	3	4	10	5	82	420
S58	12	10	8	15	6	2	10	6	82	420
S59	14	4	8	7	7	2	4	2	99	196
S60	14	8	8	14	7	2	8	4	106	392
S82	12	3	9	4	4	3	3	2	71	144
S83	12	3	9	8	4	3	6	4	75	288
S84	12	9	9	12	4	3	9	6	79	432
S85	15	6	9	10	5	3	6	3	116	360
S98	12	5	10	6	6	2	5	4	73	270
S99	12	10	10	12	6	2	10	8	79	540
S100	15	2	10	3	3	5	2	1	109	135
S101	15	4	10	6	3	5	4	2	112	270
S102	15	6	10	9	3	5	6	3	115	405
S103	15	8	10	12	3	5	8	4	118	540
S104	15	10	10	15	3	5	10	5	121	675
SR35	6	6	4	9	2	3	3	4	25	54
SR38	8	6	4	12	2	4	2	3	41	72
SR65	9	6	6	9	3	3	3	4	42	135
SR68	12	6	6	12	3	4	2	3	79	79
SR71	12	10	6	20	2	6	4	5	87	300
SR90	12	6	8	9	4	3	3	4	76	252
R43	6	6	3	12	2	3	3	2	28	36
R44	6	6	3	12	3	2	4	2	28	36
R45	6	7	3	14	3	2	2	3	30	42
R46	6	7	3	14	3	2	2	3	30	42
R47	6	8	3	16	2	3	5	2	22	48
R48	6	8	3	16	3	2	4	3	34	52
R49	6	9	3	18	2	3	6	2	34	52
R50	6	9	3	18	3	2	6	3	34	52
R51	6	9	3	18	3	2	2	4	34	52
R52	6	9	3	18	2	3	3	4	34	52
R53	6	10	3	20	2	3	7	2	36	60
R56	8	9	3	24	4	2	6	2	53	72
R58	8	9	3	24	2	4	2	3	53	72
R60	9	6	3	18	3	3	3	1	47	52
R61	9	7	3	21	3	3	4	1	58	63
R63	9	8	3	24	3	3	5	1	61	72
R64	9	9	3	27	3	3	6	1	64	81
R65	9	9	3	27	3	3	3	2	64	81

R66	9	10	3	30	3	3	7	1	67	90
R67	9	10	3	30	3	3	4	2	67	90
R68	9	10	3	30	3	3	1	3	67	90
R76	12	10	3	40	3	4	4	1	107	120
R94	6	4	4	6	2	3	3	2	22	36
R95	6	8	4	12	2	3	6	4	28	72
R96	6	8	4	12	3	2	4	5	28	72
R97	8	5	4	10	4	2	3	2	39	60
R98	8	8	4	16	2	4	4	3	45	96
R99	8	8	4	16	4	2	6	3	45	96
R100	8	9	4	18	2	4	5	3	47	108
R101	8	9	4	18	4	2	3	4	47	108
R102	8	10	4	20	2	4	6	3	49	120
R103	8	10	4	20	4	2	6	4	49	120
R104	9	4	4	9	3	3	3	1	46	54
R105	9	8	4	18	3	3	6	2	55	108
R107	10	10	4	25	2	5	5	2	71	150
R108	10	10	4	25	5	2	6	3	71	150
R110	12	8	4	24	6	2	4	2	91	144
R111	12	10	4	30	3	4	2	3	97	180
R115	15	8	4	30	5	3	6	1	136	180
R117	15	8	4	30	3	5	1	2	136	180
R133	8	5	5	8	2	4	4	2	37	80
R134	8	5	5	8	4	2	2	3	37	80
R135	8	10	5	16	2	4	8	4	45	160
R136	8	10	5	16	4	2	4	6	45	160
R137	9	5	5	9	3	3	4	2	46	90
R138	9	10	5	18	3	3	8	4	55	180
R139	10	5	5	10	5	2	4	2	56	100
R140	10	7	5	14	5	2	4	3	60	140
R141	10	10	5	20	2	5	5	4	66	120
R142	10	10	5	20	5	2	8	4	66	120
R143	12	5	5	12	3	4	4	1	79	120
R145	12	5	5	12	4	3	1	2	79	120
R146	12	10	5	24	3	4	8	2	91	240
R148	12	10	5	24	4	3	2	4	91	240
R149	15	10	5	30	5	3	8	2	136	300
R150	15	10	5	30	5	3	2	3	136	300
R164	8	9	6	12	2	4	7	6	41	480
R165	9	10	6	15	3	3	7	6	52	225
R166	10	6	6	10	2	5	5	2	56	150
R167	12	9	6	18	3	4	7	3	85	270
R168	15	9	9	15	3	5	5	1	131	540

R172	9	7	7	9	3	3	6	5	46	189
R173	12	7	7	12	3	4	6	2	79	252
R174	12	7	7	12	3	4	6	3	79	252
R175	12	7	7	12	6	2	2	4	79	252
R176	12	7	7	12	4	3	3	4	79	252
R177	14	7	7	14	7	2	6	3	91	294
R186	12	8	8	12	6	2	6	5	79	336
R187	14	8	8	14	2	7	7	2	91	392
R193	12	9	9	12	3	4	8	6	79	432
R194	15	9	9	15	3	5	8	4	121	540
R203	12	10	10	12	4	3	9	8	79	540
R204	14	10	10	14	2	7	8	6	106	630
R205	14	10	10	14	7	2	6	7	106	630
T13	10	9	3	30	6	3	1	4	76	90
T33	10	4	4	10	6	3	1	2	56	60
T34	10	8	4	20	6	3	3	2	76	120
T35	10	10	4	25	6	3	4	2	71	150
T36	10	8	4	20	6	3	2	4	66	120
T44	10	3	5	6	6	3	1	2	52	60
T45	10	6	5	12	6	3	3	2	58	120
T46	10	6	5	12	6	3	2	4	58	120
T47	10	9	5	18	6	3	3	6	64	180
T57	10	3	6	5	6	3	2	1	51	75
T58	10	6	6	10	6	3	4	2	56	150
T59	10	9	6	15	6	3	6	3	61	225
T60	10	6	6	10	6	3	3	4	56	150
T61	15	6	6	15	8	6	3	1	121	225
T62	15	4	6	10	8	6	1	2	116	150
T63	15	10	6	25	8	6	4	3	131	375
T64	15	8	6	20	8	6	2	4	126	300
T71	10	7	7	10	6	3	5	4	56	210
T84	15	9	9	15	8	6	6	4	121	540
T92	15	4	10	6	8	6	3	2	112	270
T93	15	8	10	12	8	6	6	4	118	540
LS13	9	8	3	24	4	4	1	3	61	72
LS14	9	10	3	30	4	4	2	3	67	90
LS15	9	10	3	30	4	4	1	4	67	90
LS26	9	4	4	9	4	4	1	2	46	54
LS27	9	8	4	18	4	4	2	4	55	108
LS49	9	5	5	9	4	4	2	3	46	90
LS50	9	10	5	18	4	4	4	6	55	180
LS72	9	4	6	6	4	4	3	2	43	54
LS73	9	8	6	12	4	4	6	4	49	108
C6	5	6	2	15	2	2	2	1	26	30

C13	5	6	3	10	2	2	4	2	21	30
C14	5	9	3	15	2	2	6	3	26	45
C15	5	9	3	15	2	2	5	4	26	45
C21	13	8	4	26	6	6	1	3	105	156
C23	13	6	6	13	6	6	3	2	92	195
C24	13	7	7	13	6	6	4	3	92	273
C29	13	10	10	13	6	6	8	7	92	585

## Appendix B : Matrices

### N : Incidence Matrix

$$\begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

### Z : Cross and gca Relation Matrix

1	1	0	0	0	0	0	0	0
1	0	1	0	0	0	0	0	0
1	0	0	1	0	0	0	0	0
1	0	0	0	1	0	0	0	0
1	0	0	0	0	1	0	0	0
1	0	0	0	0	0	1	0	0
1	0	0	0	0	0	0	1	0
1	0	0	0	0	0	0	0	1
0	1	1	0	0	0	0	0	0
0	1	0	1	0	0	0	0	0
0	1	0	0	1	0	0	0	0
0	1	0	0	0	1	0	0	0
0	1	0	0	0	0	1	0	0
0	1	0	0	0	0	0	1	0
0	1	0	0	0	0	0	0	1
0	0	1	1	0	0	0	0	0
0	0	1	0	1	0	0	0	0
0	0	1	0	0	1	0	0	0
0	0	1	0	0	0	1	0	0
0	0	1	0	0	0	0	1	0
0	0	1	0	0	0	0	0	1
0	0	0	1	1	0	0	0	0
0	0	0	1	0	1	0	0	0
0	0	0	1	0	0	1	0	0
0	0	0	1	0	0	0	1	0
0	0	0	1	0	0	0	0	1
0	0	0	0	1	1	0	0	0
0	0	0	0	1	0	1	0	0
0	0	0	0	1	0	0	1	0
0	0	0	0	1	0	0	0	1
0	0	0	0	0	1	1	0	0
0	0	0	0	0	1	0	1	0
0	0	0	0	0	1	0	0	1
0	0	0	0	0	0	1	1	0
0	0	0	0	0	0	1	0	1
0	0	0	0	0	0	0	1	1

$6C = 6R^{\delta} - NN'$ : **Matrix**

5	0	0	0	-1	0	0	-1	0	0	0	-1	0	0	-1	0	0	0
0	5	0	-1	0	0	-1	0	0	0	0	0	0	0	0	0	-1	0
0	0	5	0	0	0	-1	-1	0	0	0	0	0	0	0	0	0	0
0	-1	0	10	-1	-1	-1	0	0	0	0	0	0	0	0	0	-1	0
-1	0	0	-1	10	-1	0	-1	0	0	0	-1	0	0	-1	0	0	0
0	0	0	-1	-1	5	0	0	0	0	0	0	0	0	0	0	0	0
0	-1	-1	-1	0	0	10	-1	0	0	0	0	0	0	0	0	-1	0
-1	0	-1	0	-1	0	-1	10	0	0	0	-1	0	0	-1	0	0	0
0	0	0	0	0	0	0	0	5	-1	0	0	-1	0	0	-1	0	0
0	0	0	0	0	0	0	0	0	-1	10	0	-1	-1	-1	0	-1	0
0	0	0	0	0	0	0	0	0	0	5	0	-1	0	-1	0	0	0
-1	0	0	0	-1	0	0	-1	0	-1	0	10	0	-1	-1	0	0	0
0	0	0	0	0	0	0	0	0	-1	-1	-1	0	10	0	-1	-1	0
0	0	0	0	0	0	0	0	0	-1	0	-1	0	5	0	0	0	0
-1	0	0	0	-1	0	0	-1	0	0	-1	-1	-1	0	10	0	0	0
0	0	0	0	0	0	0	0	0	-1	-1	0	0	-1	0	0	10	-1
0	-1	0	-1	0	0	-1	0	0	0	0	0	0	0	0	-1	10	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
0	0	0	0	0	0	0	0	0	-1	-1	0	0	-1	0	0	-1	-1
0	-1	0	-1	0	0	-1	0	0	0	0	0	0	0	0	0	-1	-1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	-1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	-1
0	0	0	0	0	0	0	0	0	-1	0	-1	0	-1	0	0	0	0
0	0	0	0	0	0	0	0	0	-1	-1	0	0	-1	0	0	-1	0
0	0	-1	0	0	0	-1	-1	0	-1	0	-1	0	-1	0	0	0	0
0	0	-1	0	0	0	-1	-1	0	0	0	0	0	0	0	-1	-1	0
0	0	0	-1	-1	-1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	-1	-1	-1	0	0	0	0	-1	0	-1	0	-1	0	0	0
0	-1	0	-1	0	0	-1	0	0	0	0	0	0	0	0	0	-1	0
0	0	0	0	0	0	0	0	0	0	-1	0	-1	0	-1	-1	-1	0
0	0	0	-1	-1	-1	0	0	0	0	0	0	0	0	0	0	0	-1
0	0	0	0	0	0	0	0	0	-1	0	-1	0	-1	0	0	0	-1
-1	0	0	0	-1	0	0	-1	0	0	0	-1	0	0	-1	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-1
0	0	0	0	0	0	0	0	0	0	-1	0	-1	0	-1	0	0	0
0	0	-1	0	0	0	-1	-1	0	0	0	0	0	0	0	0	0	0

0	0	0	0	0	0	0	0	0	0	0	0	0	0	-1	0	0	0
0	-1	0	0	0	0	0	0	0	0	-1	0	0	0	0	0	0	0
0	0	0	0	0	0	-1	-1	0	0	0	0	0	0	0	0	0	-1
0	-1	0	0	0	0	0	0	-1	-1	-1	0	-1	0	0	0	0	0
0	0	0	0	0	0	0	0	-1	-1	0	0	-1	0	-1	0	0	0
0	0	0	0	0	0	0	0	-1	-1	0	0	-1	0	0	0	0	0
0	-1	0	0	0	0	-1	-1	0	0	-1	0	0	0	0	0	0	-1
0	0	0	0	0	0	-1	-1	0	0	0	0	0	0	-1	0	0	-1
-1	0	0	0	0	-1	0	0	0	0	0	0	0	0	0	0	0	0
-1	0	0	0	-1	-1	-1	0	0	0	0	0	0	-1	0	0	0	0
0	0	0	0	0	0	0	0	0	-1	0	-1	0	0	0	0	-1	0
0	0	0	0	-1	0	-1	0	0	0	0	0	0	-1	-1	0	0	0
-1	0	0	0	0	-1	0	0	0	-1	0	-1	0	0	0	0	-1	0
0	0	0	0	-1	0	-1	0	0	0	0	0	0	-1	0	0	0	0
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0	-1	-1	-1	0	0	0	-1	0	0	-1	-1	0	0	0	0	0	0
-1	-1	0	0	0	0	0	0	0	0	0	0	-1	-1	0	-1	0	0
10	-1	0	0	0	-1	0	0	0	0	0	0	-1	-1	0	-1	0	0
-1	10	0	0	0	0	0	0	0	0	-1	0	-1	-1	0	-1	0	0
0	0	5	-1	0	0	0	-1	0	0	0	-1	0	0	0	0	0	0
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-1	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	-1	0	10	-1	0	0	0	0	0	-1	0	0	0	-1
0	0	-1	-1	0	0	-1	10	0	0	0	-1	0	0	0	0	0	-1
0	0	0	0	0	0	0	0	5	-1	0	0	-1	0	0	0	0	0
0	0	0	0	0	0	0	0	-1	10	0	-1	-1	0	0	0	-1	0
0	-1	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0
0	0	-1	-1	0	0	0	-1	0	-1	0	10	0	0	0	0	-1	0
-1	-1	0	0	0	0	0	0	-1	-1	0	0	10	-1	0	-1	0	0
-1	-1	0	0	-1	0	-1	0	0	0	0	0	-1	10	0	-1	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0
-1	-1	0	0	0	0	0	0	0	0	0	0	-1	-1	0	5	0	0
0	0	0	0	0	0	0	0	0	-1	0	-1	0	0	0	0	5	0
0	0	0	0	0	0	-1	-1	0	0	0	0	0	0	0	0	0	5