VARIANCE-DISTANCE RELATIONSHIPS IN AGRICULTURAL FIELD PLOT EXPERIMENTS

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by

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CONTENTS

ABSTRACT

Methods for examining how the errors of agricultural field plot experiments are related to the distances between plots are developed for a two-dimensional layout. Knowledge of the errors is useful for investigating the suitability of experimental designs and methods of analysis for various field situations.

The methods of postblocking and pairblocking are extended to two dimensions to allow the calculation of error laws for the semi-variance of the difference in yields of plots **p** rows and **q** columns apart. The techniques are applied to results of past variety trials. The two-dimensional version is applied to two UK trials series, while the one-dimensional version is applied to a tropical series of trials. The error laws derived, the exponential variance error laws, are used to improve recommendation for design and analysis of future trials.

The classical method of analysis of the variety trials used is also described in this work and the efficiency of such analysis assessed. In particular, for row and column designs that have the property of adjusted orthogonality, the estimate of the ratio of the row stratum variance to the row × column stratum variance can be expressed as a function of the error mean squares from the analysis of the incomplete block column component design and row and column design. Similarly, the estimate of the ratio of the column stratum variance to the row × column stratum

variance can also be expressed as a function of the error mean squares from the analysis of the incomplete block row component design and row and column design.

Knowledge of the error variance law can be used to derive spatial methods of analysis for individual trials. The simplest first difference neighbour analysis, derived from the linear variance rule has row and column analysis without recovery of information as its simplest case when no trend effect is present.

ANOVA	Analysis of variance
APV	Average pairwise variance of all varietal differences
AR	Autoregressive
ARIMA	Autoregressive integrated moving average
CV	Coefficient of variation
dfs	Degrees of freedom
DW	Durbin-Watson statistics
EMS	Error mean square
EV	Exponential variance
FD	First-difference
GLM	General linear models
GLS	Generalised least squares
IB	Incomplete block
i.i.d.	Independently and identically distributed
LV	Linear variance
ML	Maximum likelihood
MS(K)	Error mean square in blocks of size **k**
MS(r,c)	Within-block EMS in blocks of dimension (**r**,**c**)
MS1(r,c)	Within-row and column, within block EMS in blocks of dimension (**r**,**c**)
NN	Nearest neighbour
1-D	One-dimensional
RC	Row and column
RCB	Randomized complete block
REML	Residual maximum likelihood

$\phi(x)$	Semi-variance, i.e. half the variance, of the difference between plots at distance **x** apart
$\phi(p,q)$	Semi-variance of the difference between plots **p** rows and **q** columns apart
2-D	Two-dimensional

int(v/k)	: integer part of **v/k**
I	: identity matrix of appropriate dimension
I_t	: **t**×**t** identity matrix
J_r	: **r**×**r** matrix of ones
min(A,B)	: minimum between **A** and **B**
X^T	: transpose of **X**
tr(X)	: trace of **X**
V^+	: Moore-Penrose generalised inverse of **V**
⊗	: Kronecker product of matrices

Chapter 1

INTRODUCTION

1.1. Aim of project

The aim of this thesis is to provide a method of examining the variability of agricultural field plot experiments in terms of error laws relating the variance of the difference between two plots to their distance apart, when the plots are arranged in two dimensions.

The general purpose of field experiments is to provide precise and meaningful comparisons between measurements made on different treatments applied to a collection of experimental units. In order to achieve this, it is important to reduce or control the field variation not due to treatments effects.

In agricultural field plot experiments, the experimental unit consists of rectangular plots of land disposed spatially in a field. If the field is uniform, plot data is spatially independent. However, it has long been recognised that fields are rarely uniform (Mercer & Hall, 1911). Since plots are arranged spatially, their responses will necessarily show patterns of associations; plots close together are more likely to have similar response than those separated (Student, 1923). The main cause of interplot association arises from underlying patterns of plot to plot variability, for example, due to soil variation. Other forms of dependence are introduced

by experimental treatments, such as competition between different plant varieties in neighbouring plots, but these will not be considered in this work.

Classical methods for analysis of field trials attempt to take account of the interplot correlation by allocating plots to homogeneous blocks and using randomization. More recently, alternative analyses using spatial processes have been suggested. They endeavour to take account of spatial correlation in plot responses by using a more realistic covariance structure which gives a better approximation to the plot to plot variation.

Although the analysis of data allowing particular types of correlation between neighbouring plots has received much attention in recent years, very little work is available on examining the correlation structure of field plot trials containing different treatments. The study of field variability in the presence of differential treatments is important because this is the type of data that experimentalists have to work with. Uniformity trials (field plot experiments in which no treatments are applied) commonly used to study field variation in the past, usually provide information only for the field and season for which they are carried out. Furthermore, any variation due to treatment by plot interactions will not be manifested in the results. Even though useful, a small number of uniformity trials can never experience the same range of environmental conditions as series of variety trials.

At present, there are three techniques that allow us to

examine the error structure of field plot trials in the presence of treatments:

i) Postblocking (Patterson & Hunter, 1983);

ii) Pairblocking (Ainsley, 1985);

iii) Variograms (Grondona & Cressie, 1991).

The variogram was first used for studying time series (Jowett, 1952). It is also used in spatial processes and has recently been applied in the context of field plot experiments.

The postblocking method was previously used to predict the optimum block size for incomplete block designs. Pairblocking is a refinement of postblocking. Both give the same type of information.

So far, these methods have been applied to field trials considering only the arrangement of plots in one dimension, even if the trial has a two-dimensional layout. For a trial with plots arranged in two dimensions the correlation between neighbouring plots in one direction is considered negligible, as would occur, for example, with long and narrow plots. However, in practice many trials with plots arranged spatially in two dimensions have small plots and there may be significant correlations between neighbouring plots in both directions. The question how the error structure of a trial data should best be described in this case remains open.

This thesis sets out to tackle this important problem with two main objectives. Firstly, to extend the principles of postblocking and pairblocking to examine how the covariance between two plots depends on their distance

apart in two dimensions. Secondly to show how the method can be employed when designing and analysing future trials.

1.2. Layout of the thesis

In Chapter 1 (Section 1.3) the literature is reviewed looking at how the relationship between plots has been considered as the years went by and how the designs and methods for analysis of field trials evolved with it.

Chapter 2 describes the classical analysis of block designs and row and column designs with the purpose of introducing techniques that will be used in later chapters.

There are many different types of field experiments, for example, fungicides, herbicides, fertilizers, variety trials, etc. Data and experience of variety trials are, however, readily available and these form the basis for this investigation. Chapter 3 describes the variety trials data used in this study and also examines the effectiveness of applying the classical analyses.

The techniques used to obtain the covariance structure of field trials in terms of error laws are introduced in Chapter 4 for one dimension and extended to two dimensions in Chapter 5. The error laws relate the variance of the difference between two plots to their distance apart in one and two dimensions. Here the individual plot response depends on the variety applied. After the effect of the variety has been removed, serial correlation between plots

at various "lags" are calculated. The term "lag" comes from times series but now denotes distance between two plots rather than the time interval between observations. The postblocking and pairblocking methods used to examine these correlations are described in Chapter 4. Example of their application to tropical series of variety trials from Brazil is also given. Extensions of both postblocking and pairblocking to two dimensions are derived in Chapter 5.

In Chapter 6 the error structures of two UK series of variety trials are examined in the light of the techniques derived in Chapter 5. The error laws derived as well as the techniques used are compared.

When an error law based on data from large number of trials is known, the information it provides may be used to improve recommendations for the design and analysis of future trials. Chapter 7 shows how the knowledge of the error law can be employed to predict efficiency of analysis and block dimensions for incomplete block and row and column designs to be used when designing new trials. In Chapter 8 an attempt is made to describe how the error law may be used in the spatial analysis of individual trials. The relationship of the spatial analysis to classical methods is also examined from a theoretical and empirical standpoint.

Finally, in Chapter 9 the conclusions of this investigation are presented and possible areas for further work are identified.

1.3. Literature review

1.3.1. Field variation and plot correlations

Background knowledge and characterization of field variation allow development of methods for its control or reduction. Suitable experimental designs and methods of analysis for various field situations can then be recommended so that field plot trials can be conducted as efficiently as possible. Early works made no attempt to control field variation until studies indicated that data from adjacent plots were correlated (Harris, 1915, 1920).

The relationship between agricultural field plots has been examined in terms of its correlation structure in the absence and presence of differential treatments applied to the plots. When there are no differential treatments, the plot data are known as uniformity data. Examples of data sets presented in the literature include Mercer & Hall (1911) on wheat and mangold yields, Batchelor & Reed (1918) on fruit trees, Wiebe (1935) on wheat yields, Laycock (1955) on tea yields, Kempton & Howes (1981) on barley yields and Williams & Luckett (1988) on cotton and barley yields. The study of uniformity trials was the basis for development of early techniques to reduce experimental variability.

Early investigations with uniformity data were concerned with the determination of optimum plot sizes and shapes (Fairfield Smith, 1938). In contrast Kempton & Howes (1981) used their uniformity trial to study the

validity of various methods for reducing error variation (see also Besag & Kempton, 1986; and Lill, Gleeson & Cullis, 1988). Williams & Luckett (1988) examined their uniformity data in terms of the correlation between neighbouring plots.

The approach of examining data in terms of correlation between neighbouring plots or units was, however, considered much earlier by Student (1923). He produced a shade diagram of plot fertility for Dr Beaven's 1913 barley experiment and noted that

"...the correlation between the shading of neighbouring plots is obvious to the eye".

He tabulated the average variance of the difference between two plots in terms of their physical separation in the field and found that there was a marked tendency for differences between the more distant plots to be less accurate. Wiebe (1935) also studied the correlation between plots when the distance between them was varied and showed that as the distance increases the correlation decreases. Physical distances were used in these two works.

Li & Keller (1951) calculated the serial correlation between adjacent plots in a uniformity trial, to obtain information on trend of soil variation and compare relative efficiencies of different plot sizes and shapes.

Spatial correlations at various lags had been calculated for several uniformity studies (Whittle, 1954). However, the idea of describing the correlation between plots at distance x apart as a monotonic decreasing

function of $\mathbf{x}$, within 1 and 0, was not put forward until Martén (1970). Four such laws of attenuation were studied by simulation in Pearce (1976a).

Correlation structure of uniformity data have also been considered in two dimensions. Whittle (1954) examined the two-dimensional autocovariance function of Mercer & Hall and Batchelor & Reed's uniformity trials. However, a detailed interpretation of the results of the two-dimensional autocovariance of Mercer & Hall's data was given in McBratney & Webster (1981). Brewer & Mead (1986) developed and fitted a two-dimensional continuous second order field variation model to Kempton & Howes (1981) barley uniformity trial.

Uniformity trials have also been examined in different contexts. Discussions in the framework of spatial lattice data is given in Ripley (1981, 1984) with further references therein. Similar work has also been done in soil science (Burrough, 1983a, b) and in geostatistics (Cressie, 1991).

The value of uniformity trials is widely appreciated. However, as Williams & Luckett (1988) pointed out, few have the resources to perform them, and few of the trials now available are relevant to current field trial practice. Notable among uniformity data is the frequent use of Mercer & Hall's data even in the present day (Modjeska & Rawlings, 1983; Cressie, 1991, Chapter 4). Results from uniformity trials, for both correlation and variance, are very specific to the particular field studied (Modjeska & Rawlings, 1983).

In contrast, a vast amount of data from variety trials become available every year, but relatively, little work has been done toward examining the correlation structure of field plot experiments in the presence of treatment effects. Patterson & Hunter (1983) drew attention to the subject and introduced the exponential variance (EV) model to describe a one-dimensional variance-distance relationship in field trials. They derived an identity relationship between the semi-variance of the difference in yields of plots at distance $\mathbf{x}$ apart, $\phi(\mathbf{x})$, and the expected error mean square in blocks of different sizes, $\mathbf{k}$. Average error mean squares were then evaluated for different block sizes for a set of cereal variety trials and were found to be in agreement with the assumption that semi-variances followed an exponential variance law.

An alternative version of Patterson & Hunter's method was developed by Ainsley (1985). Here each postblock consists of two plots, which are not necessarily physically adjacent in the field. The error mean square in blocks of two plots at distance $\mathbf{x}$ apart, provides an estimate of the semi-variance between the two plots. As in Patterson & Hunter's method, a single trial is analysed several times. The idea of analysing a trial in different ways had previously been used in other contexts, see for instance Yates (1940a) and Pearce (1976b, 1983). The validity of the methods was established in Ainsley, Paterson & Patterson (1987).

Since Patterson & Hunter (1983) the applicability of the EV model to field plot trials has been appreciated by

other researchers. Kempton (1984) used a linear approximation to the EV model, for short distances, to predict optimal frequency of check plots in unreplicated trials. Williams & Luckett (1988) fitted the EV rule to an Australian barley uniformity trial and made suggestions about design and analysis for barley variety trials. Pilarczyk (1990) has fitted the EV model to a large series of Polish variety trials.

More recently a variogram estimation method somewhat similar to Patterson and Hunter (1983) and Ainsley (1985) methods has been proposed in the context of field experiments (Grondona & Cressie, 1991). In principle, the method consists of removing treatment effects and local control effects, for example block effects, by median polish (Cressie, 1991, Chapter 3) and estimating the variogram from the residuals. Grondona & Cressie (1991) applied the method to a series of six experiments, with dummy treatments, imposed on Mercer & Hall's data. They calculated individual and combined variograms and found that, among the classes of models fitted, the exponential semivariogram model gave the best fit.

So far the examination of correlation structure of field plot experiments with differential treatments has not yet been addressed in two dimensions. However, the classical methods to control field variation in one and two dimensions are at least as old as the work of Fisher (1925).

1.3.2. Classical methods for controlling field variation

Classical experimental design and analysis is based on three principles - replication, randomization and local control (Fisher, 1925). Local control and replication help to reduce the effect of field variation and allow more precise treatment estimation. Randomization neutralizes the effect of spatial correlation and produces a valid analysis of variance (Yates, 1938). Fisher (1925) developed the randomized complete block design where each block contains as many plots as there are treatments, and each treatment occurs once in each block. Blocks are used for controlling local variation and are chosen to cover a uniform area, so that plots are less variable within a block than within the experimental area as a whole.

In many field experiments, such as variety trials, the number of treatments to be tested is too large to be accommodated in a single homogeneous block. This requires the use of smaller incomplete blocks to control field variation. However, methods of field operation require that the design be resolvable, that is, blocks must still be capable of arrangement in complete replications. To satisfy these requirements Yates (1936, 1939) introduced lattice designs. Here each replicate is arranged in **k** blocks of **k** plots, so that the designs are only available when the number of treatments is a perfect square. This limitation of lattice designs was later overcome by Patterson & Williams (1976) with the introduction of a general class of incomplete block designs called alpha

designs for any number of varieties. Patterson, Williams & Hunter (1978) presented a compact catalogue of such designs. Patterson & Silvey (1980) introduced an extension to α-designs, called generalized lattice designs which includes Yates' square lattices and Harsbarger's (1949) rectangular lattices as special cases.

Another classical means for controlling field variation uses a double blocking systems (Yates, 1933) which remove variation in two dimensions. Two orthogonal block systems are now used, one representing rows and the other columns. Yates (1937, 1940a) introduced the lattice square designs to allow adjustment for rows and columns when plots are arranged in two-dimensional array.

As with lattice designs, lattice squares are only available when the number of varieties is a perfect square. However, less restrictive designs, such as the row and column alpha designs (John & Eccleston, 1986) and the nested row and column designs for two replicates (Patterson & Robinson, 1989) are available. However, no general method is yet available to construct efficient designs for any number of treatments. Nevertheless, as a result of close interaction with practical experimentation, row and column designs have recently been proposed to address specific field requirements (see Williams & John, 1989; Seeger, 1991). Discussion of designs using single or double blocking systems and their associated methods of analysis is available in several textbooks on experimental designs (see, for example, Cochran & Cox, 1957; Kempthorne, 1952; John, 1987).

Blocking in one and two dimensions has proved effective in practice to control field variation (Patterson & Hunter, 1983; Kempton & Howes, 1981; Robinson, Kershaw & Ellis, 1988). However, an argument against blocking is that the underlying model is artificial and only partially allows for the association between neighbouring plots in the plot covariance matrix. In the analysis of an incomplete block design the pairwise variance between any two plots within a block is the same, and the pairwise variance between any two plots in two different blocks is the same. For a row and column design, the pairwise variance between any two plots in a row is the same, and similarly for columns. Although hardly realistic, these classical methods may be justified by randomization theory on the grounds that on average, over all randomizations, the estimation of standard errors of treatment estimates from the analysis is unbiased.

1.3.3. Spatial methods for control of field variation

An alternative approach to the control of field variation is to use spatial or neighbour methods. Although the first method based on spatial considerations (Papadakis, 1937; Bartlett, 1938) were proposed as early as incomplete block designs, only recently they have started be well studied. Neighbour methods attempt to control the variation in a more realistic way than the classical methods, using covariance structure that gives better approximation to the true plot to plot variation.

The field variation is modelled as a continuous trend with an assumed error structure, and in some cases there are differencing of the plot data to reduce the trend component to a simpler form. Most of the spatial methods for field trials have concentrated on one-dimensional layouts.

Bartlett (1978) considered theoretical aspects of the method of Papadakis (1937) which adjusts plot values by covariance on neighbouring plots residuals. Following this several one-dimensional neighbour models have been proposed (Kempton & Howes, 1981; Wilkinson, Eckert, Hancock & Mayo, 1983; Patterson & Hunter 1983; Green, Jennison & Seheult, 1985; Williams, 1986a; Besag & Kempton, 1986; Gleeson & Cullis, 1987). Dagnelie (1990) presented an overview of the Papadakis' method and other neighbour methods developed up to 1988. Azais, Denis, Dhorne & Kobilinsky (1990) gave an unified presentation of the main neighbour analysis methods.

Patterson (1983) pointed out that the NN analysis of Wilkinson *et al.* (1983) is a special case of the exponential variance model of Patterson & Hunter (1983). Also, the linear variance (LV) model of Williams (1986a) and first difference model (with errors-in-variables) of Besag & kempton (1986) can be developed as a limiting case of the EV model.

Kempton (1985a) showed that most neighbour methods lead to approximately equivalent estimators for treatment contrasts which are frequently more efficient than the estimators from traditional block models. Conditions under

which these estimators are unbiased under the assumed true model are given in Zimmerman & Harville (1989). However, as there is no valid randomization theory, the estimates of standard errors may not be valid if the plot yields do not follow the assumed model. Glasbey (1988) proposed variance estimates for treatments that are less dependent on the assumption about error variance.

The validity of the standard errors estimates in neighbour methods has been investigated empirically using uniformity data (see Kempton & Howes, 1981; Wilkinson *et al.*, 1983; Besag & Kempton, 1986; Williams, 1986b; Lill *et al.*, 1988; and Baird & Mead, 1991). With the exception of the iterated Papadakis model (Bartlett, 1978), error estimates from the neighbour models were found to be approximately valid.

The potential of neighbour methods to increase efficiency over the standard analyses has been shown in a number of empirical studies. Cullis & Gleeson (1989), in a study of over one thousand field trials, found that for most trials the independent first differenced trend model (Besag & Kempton, 1986) was adequate and on average there was a significant reduction (42%) in variance of varietal yield differences compared with randomized complete block (RCB). Kelly (1988) studying a series of barley trials found that in 45 out of 49 trials the independent first differenced trend model was adequate and in general there was an increase of efficiency over the incomplete block (IB) analysis.

In these studies, neighbour methods have been applied

to trials with RCB, IB or row and column (RC) designs which are not necessarily optimal for neighbour types analysis. Williams (1985) considered a criterion for the construction of optimal neighbour designs. He proposed a two-stage procedure where an efficient resolvable incomplete block design can be used as a starting point. An algorithm based on this procedure has already been developed (Wild & Williams, 1987). However, computer searches give little insight into the features that lead to efficiency and may miss some efficient designs. Martin & Eccleston (1991) developed some theoretical approximations to allow studies of the design features that lead to high efficiency under known dependence structure.

Although every effort has been put into developing one-dimensional neighbour methods, situations occur where they may be not fully efficient. For example a trial with a rectangular array of small plots may show gains from two-dimensional analysis if substantial correlation between plots may exist in both directions; see Kempton & Howes (1981) and Robinson *et al.* (1988).

Few two-dimensional methods have been proposed, so that there is limited experience of reasonable models. Martin (1990) suggested the use of time series models and put forward that many of the problems of two-dimensional analysis can be overcome by using separable lattice processes. Zimmerman & Harville (1991) proposed an approach to two-dimensional analysis in which the observations are regarded as realizations of random field.

Using uniformity data they demonstrated that their approach can be as successful or more successful than one-dimensional (1-D) spatial analysis or classical (RCB and RC) analysis. Cullis & Gleeson (1991), following the suggestion of Martin (1990), have extended the one-dimensional ARIMA model of Gleeson & Cullis (1987) to two dimensions. Also using uniformity data they showed the potential gain from using a two-dimensional (2-D) spatial analysis rather than a classical row and column analysis.

Two-dimensional neighbour methods are claimed to be at least as successful as the classical methods based on the efficiency of analysis using few uniformity trials. However no method can be recommended based solely on increases in efficiency. Other considerations, for example validity under randomization, should be taken into account (Bartlett, 1983, 1984, 1985). For one-dimensional analysis evidence of empirical validity has been demonstrated in a number of works, but there is no guarantee that the same will hold for two dimensions. Study of validity in a comprehensive study over large set of trials has yet to be done.

Until these studies are completed the cautious recommendation of Bartlett (1978) that the neighbour methods should be considered as possible ancillary device for improving the accuracy of treatment comparisons still holds.

Chapter 2

BLOCKING SYSTEMS

2.1. Introduction

Field plots experiments usually occupy an area of land that becomes large as the number of treatments increase. The greater the area the less homogeneous it is. One of the most effective ways of increasing the precision of a field experiment is to control this variation by blocking. Certain restrictions may be imposed upon the arrangement of the plots, so that part of the influence of the heterogeneity may be eliminated.

Two different blocking systems may be used in practice. A single block system is introduced when plots lying in close neighbourhood are grouped together into blocks aiming to maximize the variation between blocks and leaving as little variation as possible among plots within blocks. When plots in a field are disposed to form a rectangular grid two orthogonal block systems may be introduced which aim to eliminate possible differences which may exist between whole rows of plots and between whole columns of plots. Designs for trials using a single block system are called block designs and those using two orthogonal block systems are known as row and column (RC) designs.

This chapter describes the analysis of resolvable block designs and row and column designs with reference to

variety trials. These techniques will be applied in later chapters. The resolvability property is considered because it provides useful advantages for the experimenter in the field and in the analysis of the results. For example, the analysis of any resolvable design can be reverted to randomized complete block analysis if the blocks turn out to be ineffective at controlling variation. Although this procedure introduces some loss of accuracy in individual pairwise variances the estimated average pairwise variance is still unbiased (Yates, 1948).

2.2. Block structure and randomization

The way that plots are or can be grouped in blocks, regardless of the treatments applied, defines the block structure of the design. Similarly, the set of treatments applied to the plots defines the treatment structure. For instance, for an IB variety trial the block structure is plots within blocks within superblocks. For a nested RC variety trial the block structure is rows crossed with columns which are then nested within blocks. The treatment structure in both trials includes just one factor, varieties.

The blocking structure of a trial defines what blocking comparisons can be made, for example within blocks, between blocks, within row and column, etc., and every simple block structure has a complete randomization theory (Nelder, 1965a). The randomization procedure for any simple block structure consists of any permutation of the

labelling of the plots which preserves the block structure. For example, the blocks and the plots within blocks may be labelled arbitrarily. There is no link between the $\mathbf{i}^{th}$ plot in the $\mathbf{j}^{th}$ block and the $\mathbf{i}^{th}$ plot in the $\mathbf{j}'^{th}$ block. When the blocks do not contain the same number of plots this arbitrary labelling can not be achieved since the randomization set in this circumstance is not transitive (Bailey, 1981, 1991).

In terms of variety trials, the vector of observed yields in field order, can be considered as one member of the population of all possible vectors of yields that could occur under different randomizations of the trial. The randomization distribution is derived from this population of all possible yield vectors, assuming that there is no treatment differences, that is, taken the null experiment in which all plots receive the same treatment. The form of the plot covariance matrix of this distribution can be calculated from the form of the block structure and then be used in the process of estimation.

The design, randomization and the analysis of design of experiments are very closely interrelated (Nelder, 1965a, b; Bailey, 1981, 1991). Nevertheless, the interest in this work is mainly in the analysis of field plot trials. Nelder (1965a, b) gave details of the randomization theory and showed how the randomization procedure for various designs with orthogonal block structure defines the form of the plot covariance matrix.

2.3. Block designs

The block designs encompass two main categories of designs, the randomized complete block (RCB) designs and the incomplete block (IB) designs. The RCB designs are appropriate for variety trials if the number of varieties is small. However, the number of varieties is often large and the adoption of RCB designs may result in an increase of error variance due to larger block size: incomplete block designs may then be used instead. In IB designs the number of plots in a block is smaller than the number of varieties to increase the homogeneity of the blocks. The IB designs considered here are based on the general class of designs for $\mathbf{v}$ varieties with plots arranged in $\mathbf{t}$ superblocks each carrying a complete replication in $\mathbf{s}$ blocks of $\mathbf{k}$ plots (Patterson & Williams, 1976).

The efficiency of analysis of an IB variety trial depends very much on how the blocks are formed in the field. The blocks can be defined in various ways according to the grouping of plots and optimum choice will depend on the background knowledge of the field variation. Practical aspects of the formation of blocks are discussed for instance by Pearce (1983, Chapter 2) and Mead (1988, Chapter 2). In practice, for trials with $\mathbf{v} \leq \mathbf{64}$ variety, small blocks roughly equal to $\sqrt{\mathbf{v}}$ are recommended (Patterson & Hunter, 1983). However, this may be different for very large number of varieties. In addition, the shape of the block may be quite as important as its size. These points are investigated in Chapter 7.

Before a trial be set out in the field the design should be proper randomized. The randomization scheme of the IB design consists of the following steps:

i) randomize the plot labels within each block,

ii) randomize the block labels within each superblock,

iii) randomize the superblock labels,

iv) randomize the variety labels.

Step (**iv**) is only concerned with the treatment structure rather than the block structure of the design. It has no influence on the form of the plot covariance matrix. However, it is useful to avoid repeatedly confounding the same degrees of freedom in a trial series.

This randomization procedure for an IB design guarantees that the data can be divided into four orthogonal strata. The four strata being respectively the mean stratum; the superblock stratum, containing contrasts between superblocks; the block stratum, containing contrasts between blocks within superblocks; and the plot stratum, containing contrasts between plots within blocks.

Once varieties are applied to the plots, the expected value of the yield from a particular plot will depend on which variety is applied to that plot. An appropriate model for the standard analysis of the results of an resolvable IB variety trial may be given by

$$E(y) = X\tau$$

$$Var(y) = V$$

where,

y is the **n**×**1** vector of field plot yields (**n=tv**),

X is the **n**×**v** design matrix for varieties,

τ is the **v**×**1** vector of variety effects,

V is the **n**×**n** plot covariance matrix, determined by the randomization procedure.

Over the randomization distribution defined by the randomization scheme the errors within each stratum are homogeneous and the plot covariance matrix **V** of the randomization model may be written as

$$V = \xi_o G + \xi_t (P_S - G) + \xi_b (P_B - P_S) + \xi_w (I - P_B) \qquad (2.3.1)$$

where,

ξ_o, ξ_t, ξ_b, and ξ_w, are the stratum variances, and

G, $\mathbf{P}_S - \mathbf{G}$, $\mathbf{P}_B - \mathbf{P}_S$, and $\mathbf{I} - \mathbf{P}_B$ are the projection matrices that define respectively the four orthogonal strata of the data. The matrices

$$G = 1(1^T 1)^{-1} 1^T$$

for $\mathbf{1}^T = (1,\ldots,1)$ is the grand mean projector,

$$P_S = Z_0 (Z_0^T Z_0)^{-1} Z_0^T$$

for $\mathbf{Z}_0$ the **n**×**t** design matrix for superblocks, is the projection matrix for superblocks, and

$$P_B = Z (Z^T Z)^{-1} Z^T$$

for **Z** the **n**×**ts** design matrix for blocks, is the projection matrix for blocks.

If instead of the randomization model a random effects error model is assumed, the plot covariance matrix can be specified as

$$V = \sigma^2(I + \varphi P_B) \qquad (2.3.2)$$

where,

σ^2 and φ are variance parameters to be estimated.

These two plot covariance matrices given in (2.3.1) and (2.3.2) can be shown to be the same, noting that the stratum variances in (2.3.1) are

$$\xi_o = \xi_t = \xi_b = \sigma^2 + k\sigma_b^2$$

$$\xi_w = \sigma^2.$$

The plot covariance matrix in the form of (2.3.2) is important because it can also be applied when block sizes differ. However, the randomization plot covariance matrix for this situation is no longer available.

The aim of the analysis of an IB variety trial is to provide estimates of variety differences and their standard errors. Of the four strata of the data only the block stratum and the plot stratum contain variety information: these are respectively the inter-block information and intra-block information. Using $\mathbf{V}$ given in (2.3.2) the combined variety effect estimates can be obtained by generalized least squares (GLS) analysis as the solution to the normal equation

$$(X^TV^+X)\tau = X^TV^+y$$

where $\mathbf{V}^+$ is the Moore-Penrose generalized inverse of $\mathbf{V}$ (Rao, 1973, page 26).

This normal equation can be convenient rewritten as

$$A_c\tau = q_c$$

where,

$$A_C = fA_I + (1 - f)X^TX$$

$$q_C = fq_I + (1 - f)X^Ty$$

for,

$$A_I = X^T(I - P_B)X$$

$$q_I = X^T(I - P_B)y$$

$$f = \frac{1}{1 + \varphi^{-1}} \quad \text{and} \quad \varphi = \frac{k\sigma_b^2}{\sigma^2} .$$

If $\mathbf{f = 1}$, i.e. $\varphi^{-1} = 0$, the analysis only takes account of the intra-block variety information. An intra-block analysis is based on the plot stratum. When carrying out analysis in Chapters 4 and 6 the interest is in this stratum.

For given values of σ^2 and $\mathbf{f}$ the combined variety estimates are given by

$$\hat{\tau} = A_C^{-1}q_C$$

and the variances by

$$\text{var}(\hat{\tau}) = \sigma^2 A_C^{-1}.$$

The average variance of all pairwise varietal differences (APV) is then given by

$$\text{APV} = \frac{2\sigma^2}{v - 1}\left\{\text{trace}(A_C^{-1}) - \left[t(1 - f)\right]^{-1}\right\}. \qquad (2.3.3)$$

In practice estimates of σ^2 and σ_b^2 are required to obtain the estimate of τ. Nelder (1968) gave details of how variance parameters may be obtained for a class of

generally balanced designs. Patterson & Thompson (1971) gave the residual maximum likelihood (REML) method to estimate variances in block designs. Both methods give identical results when blocks have the same size. However, these variance parameters are usually estimated by equating mean squares to their expectation in the intra-block analysis (Yates, 1939, 1940b; Cochran & Cox, 1957, Chapter 10, 11). The error mean square in the plot stratum gives an unbiased estimate of σ^2. The estimate of σ_b^2 is obtained by equating the blocks eliminating variety sum of squares to its expectation.

Speed, Williams & Patterson (1985) showed how the combined analysis may be simplified by expressing the estimator of σ_b^2 as a function of the RCB and IB error mean squares. From their results the estimate of **f** can directly be obtained as

$$\hat{f} = \frac{(v - 1)(\hat{\sigma}^2_{RCB} - \hat{\sigma}^2_{IB})}{(v - 1)\hat{\sigma}^2_{RCB} - (v - s)\hat{\sigma}^2_{IB}}$$

where

$$\hat{\sigma}^2_{RCB} = \frac{y^T\left\{(I-P_S) - (I-P_S)X\left[X^T(I-P_S)X\right]^+ X^T(I-P_S)\right\}y}{(t - 1)(v - 1)}$$

is the error mean square of an ordinary randomized complete block analysis and

$$\hat{\sigma}^2_{IB} = \frac{y^T\left\{(I-P_B) - (I-P_B)X\left[X^T(I-P_B)X\right]^+ X^T(I-P_B)\right\}y}{n - ts - v + 1} \qquad (2.3.4)$$

is the error mean square of an intra-block analysis which

estimate σ^2.

An alternative way to obtain the APV given in (2.3.3) is to calculate

$$APV = \frac{2\hat{\sigma}^2}{tE^*} \qquad (2.3.5)$$

where $\mathbf{E}^*$ is approximately given by

$$E^* = E + (1 - E)(1 - \hat{f})$$

for

$$E = \frac{v - 1}{t \ \text{trace}(A_I^+)}$$

the efficiency factor of the design.

The use of $\mathbf{E}^*$ is very convenient mainly when predicting efficiency of analysis for IB designs to be used in future trials. The efficiency for a single analysis measures the APV relative to that for a RCB analysis. Chapters 4 and 7 explore the convenience of use of $\mathbf{E}^*$.

Detailed exposition of the combined analysis for block designs is also given in John (1987, Chapter 8).

2.4. Row and column design

The use of a double block system, e.g. rows and columns, is more restrictive than one block system in terms of choice of designs. Two block systems are unlikely to be equally effective in field conditions and it is important that both component blocks have reasonable efficiency. Another useful property is that of adjusted orthogonality (Eccleston & Russel, 1975, 1977) when the

two sets of blocks are orthogonal after eliminating varieties.

Several row and column designs are presented and discussed in Pearce (1983, Section 6.6) and John (1987, Chapter 5). However, most of them fail to satisfy the usual requirements of variety trials, viz resolvability, large number of varieties and few replicates (≤ 4), and therefore are of limited practical use. Useful row and column designs for variety trials have been provided by Yates (1937, 1940a) and Patterson & Robinson (1989). The family of row and column α - designs given by John & Eccleston (1986), although not resolvable, might also be useful. Although the emphasis is on row and column designs that are resolvable and have the property of adjusted orthogonality, the analysis presented can be extended to any row and column design.

In a typical resolvable RC variety trial, **v** varieties are set out in **t** blocks each forming one replicate. The plots in each block are arranged in **r** rows and **c** columns. The RC design is randomized subject to the rules:

i) randomize the rows within each replicate,

ii) randomize the columns within each replicate,

iii) randomize the replicates,

iv) assign the varieties at random to the numbers **1** to **v**.

As with IB designs, the stage (**iv**) only concerns with the treatment structure. The random allocation of varieties does not affect the form of the plot covariance matrix. Nevertheless, stage (**iv**) is useful in the design

of series of trials (Patterson & Robinson, 1989).

The data in the analysis of the RC design can be divided into five orthogonal strata. This is ensured by the randomization procedure. The five strata are respectively the mean stratum, the block stratum, the row stratum, the column stratum and the row × column stratum, containing interaction contrasts between rows and columns within blocks. The appropriate model for the analysis is

$$E(y) = X\tau$$

$$Var(y) = V$$

where,

$\mathbf{y}$, $\mathbf{X}$, τ, $\mathbf{V}$ are defined as for IB designs except that $\mathbf{V}$ is now determined by the randomization procedure of a RC design.

As the errors are homogeneous within each stratum, over the randomization distribution, the plot covariance matrix is given by

$$V=\xi_o G+\xi_t (P_S-G)+\xi_r (P_R-P_S)+\xi_c (P_C-P_S)+\xi_w (I+P_S-P_R-P_C) \quad (2.4.1)$$

where,

ξ_o, ξ_t, ξ_r, ξ_c and ξ_w, are the stratum variances, and

$\mathbf{G}$, $\mathbf{P}_S - \mathbf{G}$, $\mathbf{P}_R - \mathbf{P}_S$, $\mathbf{P}_C - \mathbf{P}_S$, and $\mathbf{I} + \mathbf{P}_S - \mathbf{P}_R - \mathbf{P}_C$ are the projection matrices that define the five orthogonal strata of the data. The matrices $\mathbf{G}$ and $\mathbf{P}_S$ are the same as for IB designs. The others are defined as follow:

$$P_R = Z_1 (Z_1^T Z_1)^{-1} Z_1^T$$

is the row projection matrix, where $\mathbf{Z}_1$ is the $\mathbf{n \times tr}$ design

matrix for rows,

$$P_c = Z_2(Z_2^T Z_2)^{-1} Z_2^T$$

is the column projection matrix, where $\mathbf{Z}_2$ is the **n×tc** design matrix for columns.

For the stratum variances given by

$$\left.\begin{aligned} \xi_o = \xi_t &= \sigma^2 + c\sigma_r^2 + r\sigma_c^2 \\ \xi_r &= \sigma^2 + c\sigma_r^2 \\ \xi_c &= \sigma^2 + r\sigma_c^2 \\ \xi_w &= \sigma^2 \end{aligned}\right\} \qquad (2.4.2)$$

the plot covariance matrix for the randomization model given in (2.4.1) is the same as that for the model with random row and column effects which is given by

$$V = \sigma^2(I + \varphi_r P_R + \varphi_c P_C) \qquad (2.4.3)$$

where,

σ^2, φ_r, and φ_c are variance parameters to be estimated.

In the analysis, of the five strata only the row stratum, the column stratum and the row × column stratum provide information on varietal contrasts. The estimates of variety effects are obtained by combining the information available from the three strata. As for IB designs, the GLS analysis can be used to provide an estimator of variety effects. The combined estimates of variety effects are again obtained as a solution to the normal equation

$$(X^T V^+ X)\tau = X^T V^+ y$$

where $\mathbf{V}$ for example can be given by (2.4.3).

Analogous to the combined analysis of IB designs, the normal equation can be rearranged as

$$A_{Co}\tau = q_{Co}$$

with $\mathbf{A}_{Co}$ and $\mathbf{q}_{Co}$ defined as

$$A_{Co} = f_1 A_{I1} + f_2 A_{I2} - f_0 A_B + (1 - f_3) X^T X$$

$$q_{Co} = f_1 q_{I1} + f_2 q_{I2} - f_0 q_B + (1 - f_3) X^T y$$

where

$$A_{I1} = X^T(I - P_R)X \quad , \quad q_{I1} = X^T(I - P_R)y$$

$$A_{I2} = X^T(I - P_C)X \quad , \quad q_{I2} = X^T(I - P_C)y$$

$$A_B = X^T(I - P_S)X \quad , \quad q_B = X^T(I - P_S)y$$

$$f_1 = \frac{1}{1 + \varphi_1^{-1}} \quad , \quad f_2 = \frac{1}{1 + \varphi_2^{-1}} \quad , \quad f_3 = \frac{1}{1 + \varphi_3^{-1}} \quad , \quad f_0 = f_1 + f_2 - f_3$$

for

$$\varphi_1 = \frac{c\sigma_r^2}{\sigma^2} \quad , \quad \varphi_2 = \frac{r\sigma_c^2}{\sigma^2} \quad \text{and} \quad \varphi_3 = \varphi_1 + \varphi_2 \ .$$

Clearly if both $\mathbf{f}_1 = \mathbf{1}$ and $\mathbf{f}_2 = \mathbf{1}$ no variety information is recovered from the row stratum and the column stratum. Consequently, only the information from the row × column stratum is used. This mean that an intra-row and column analysis is performed. This type of analysis is one of those used in Chapter 6.

If $\mathbf{f}_1 \neq \mathbf{1}$ and $\mathbf{f}_2 \neq \mathbf{1}$, the matrix $\mathbf{A}_{Co}$ is non-singular and so the combined variety estimates are obtained as for

IB designs,

$$\hat{\tau} = A_{Co}^{-1} q_{Co}$$

with

$$\text{var}(\hat{\tau}) = \sigma^2 A_{Co}^{-1}.$$

The APV is then obtained by

$$\text{APV} = \frac{2\sigma^2}{v - 1} \left\{ \text{trace}(A_{Co}^{-1}) - \left[t(1 - f_3) \right]^{-1} \right\}. \qquad (2.4.4)$$

Usually, the parameters σ^2, σ_r^2 and σ_c^2 are unknown and have to be estimated to obtain the estimate of τ and its variance. The methods provided by Nelder (1968) and Patterson & Thompson (1971) can also be applied for row and column designs to obtain the estimates of these variance components.

When row and column designs satisfy the adjusted orthogonality condition (John, 1987, page 97, 98) the estimation of σ^2, σ_r^2 and σ_c^2 can be simplified. For these designs, the estimates of σ_r^2 and σ_c^2 can be obtained by equating adjusted row and column sums of squares to their expectations, that is, using identical method of estimation for the row and column component designs as used for IB designs (Eccleston & John, 1986). This succeeds as a direct result of the orthogonality between rows and columns after adjusting for varieties. An unbiased estimate of σ^2 is given by the error mean square in the row × column stratum.

Another advantage of RC designs satisfying the adjusted orthogonality condition is that the results of Speed *et al.* (1985) can be extended to them. This mean that σ_r^2 and

σ_c^2 can be obtained as a function of the error mean squares from the analysis of the IB row component design, IB column component design and RC design.

Consider, for example, the analysis of the IB row component design. From (2.3.4) the error sum of square can be written as

$$SQ_e^{IBR} = y^T D_R y$$

where

$$D_R = (I - P_R) - (I - P_R)X\left[X^T(I - P_R)X\right]^+ X^T(I - P_R).$$

Using the results in Searle (1982, page 355) its expectation under the row and column model is given by

$$E(SQ_e^{IBR}) = \text{trace}\left(D_R \text{Var}(y)\right)$$

for Var(y) given in (2.4.1).

Since

$$(I - P_S)D_R(I - P_S) = D_R ,$$

then

$$E(SQ_e^{IBR}) = \text{trace}\left\{D_R\left(\xi_r(P_R - P_S) + \xi_c(P_C - P_S) + \xi_w(I + P_S - P_R - P_C)\right)\right\}$$

$$= \text{trace}\left(D_R(\xi_c P_C + \xi_w I - \xi_w P_C)\right)$$

once

$$(I - P_R)P_R = 0 \quad \text{and} \quad (I - P_R)P_S = 0.$$

Now

$$\text{trace}(D_R) = tv - tr - v + 1$$

$$\text{trace}(D_R P_C) = tc - t - c + 1$$

and so

$$E(SQ_e^{IBR}) = (t-1)(c-1)(\xi_c - \xi_w) + \left[t(v-r) - (v-1)\right]\xi_w.$$

Hence the expectation of the error mean square in the IB row component analysis is

$$E(MS_e^{IBR}) = \frac{(t-1)(c-1)}{t(v-r) - (v-1)} (\xi_c - \xi_w) + \xi_w.$$

As $E(MS_e) = \xi_w$ is the expectation of the error mean square in the RC analysis then follows that

$$E(MS_e^{IBR}) - E(MS_e) = \frac{(t-1)(c-1)}{t(v-r) - (v-1)} (\xi_c - \xi_w). \quad (2.4.5)$$

If the randomized complete block analysis is considered under the RC model, the relationship

$$E(MS_e^{RCB}) - E(MS_e) = \frac{r-1}{v-1} (\xi_r - \xi_w) + \frac{c-1}{v-1} (\xi_c - \xi_w)$$

can be shown. MS_e^{RCB} is the error mean square in the RCB analysis.

Replacing the stratum variances in (2.4.5) by the expression given in (2.4.2) an estimate of σ_c^2 is given by

$$\hat{\sigma}_c^2 = \frac{t(v-r) - (v-1)}{(v-r)(t-1)} (MS_e^{IBR} - MS_e). \quad (2.4.6)$$

Analogous, an estimate of σ_r^2 is

$$\hat{\sigma}_r^2 = \frac{t(v-c) - (v-1)}{(v-c)(t-1)} (MS_e^{IBC} - MS_e) \quad (2.4.7)$$

where MS_e^{IBC} is the error mean square in the analysis of the IB column component design.

The error mean squares MS_e^{IBR}, MS_e^{IBC} and MS_e are obtained from (2.3.4). For MS_e^{IBR}, $\mathbf{P}_B$ is replaces by $\mathbf{P}_R$ and **ts** by **tr**. Similarly, for MS_e^{IBC} the projection matrix $\mathbf{P}_C$

and **tc** are used. MS_e is obtained replacing $\mathbf{I-P}_B$ by $\mathbf{I+P}_S-\mathbf{P}_R-\mathbf{P}_C$ and **ts** by **t(r + c - 1)**.

Finally, from (2.4.6) and (2.4.7) the estimates of $\mathbf{f}_1$ and $\mathbf{f}_2$ and consequently $\mathbf{f}_3$ and $\mathbf{f}_0$ are readily obtained.

As with IB designs, the APV given in (2.4.4) for RC designs can alternatively be calculated as in (2.3.5) but with $\mathbf{E}^*$ replaced by

$$E^* = \left\{\left[E_r+(1-E_r)(1-\hat{f}_1)\right]^{-1}+\left[E_c+(1-E_c)(1-\hat{f}_2)\right]^{-1}-1\right\}^{-1} \quad (2.4.8)$$

where $\mathbf{E}_r$ and $\mathbf{E}_c$ are respectively the efficiency factor of the row and column component designs. This relationship was obtained noting that the information matrices compound $\mathbf{A}_{Co}$ are spanned by a common set of eigenvectors (John 1987, page 98) and following the procedure used by John (1987, page 194, 196).

The $\mathbf{E}^*$ that can be obtained using expression (2.4.8) is only an approximation. However an exact value for $\mathbf{E}^*$ when the design has the same number of rows and columns (**r=c=s**) is given by

$$E^* = \left[1 + \frac{t}{s+1}\left(\frac{\hat{f}_1}{t-\hat{f}_1}+\frac{\hat{f}_2}{t-\hat{f}_2}\right)\right]^{-1}$$

derived from the results of Williams, Ratcliff & Ewijk (1986). This expression is considered in Chapter 3 when generating contours of predicted efficiency for RC analysis and the proportion of variety information lost in ignoring between RC information. Expression (2.4.8) is considered in Chapter 7.

Eccleston & John (1986) and John (1987, Chapter 8) also considered the recovery of row and column information in row and column designs with adjusted orthogonality. The details were given for designs like RC α - designs and no mention was made on the possibility of estimating σ_r^2 and σ_c^2 as given in (2.4.6) and (2.4.7). However, for a RC α - design is possible to show that the estimates of σ_r^2 and σ_c^2 can be given as

$$\hat{\sigma}_r^2 = \frac{v(t-1) - (c-1)}{v(t-1)} (MS_e^{IBC} - MS_e)$$

and

$$\hat{\sigma}_c^2 = \frac{v(t-1) - (r-1)}{v(t-1)} (MS_e^{IBR} - MS_e).$$

It is important to notice that for these designs **v=r(c/t)** and the replicates are housed together in a single block. RC α - designs are also considered in Chapter 7.

Chapter 3

DATA

3.1. Introduction

Three series of field plot variety trials data have been assembled for this project. The data available consisted of plot yields and field randomizations of varieties for each trial.

All data sets have been used in previous research. The Brazilian data was supplied by the "Empresa Goiana de Pesquisa Agropecuária - EMGOPA" a Brazilian research institute and was partially used for recommendation of maize varieties (Ruschel, Eleutério, Araujo, Seraphin & Santos, 1987). The data entitled SCRI data, from the Scottish Crop Research Institute, Dundee, was included by Robinson *et al.* (1988) in an investigation of two-dimensional yield variability. Reference to this data is also made in Patterson & Robinson (1989). The third data set, PBI data, from the Plant Breeding Institute, Cambridge, was reported in Kempton & Howes (1981).

Descriptions of these data sets are given in this chapter. In addition the efficiency or effectiveness of the designs used are also reported.

3.2. Description of trials data

The Brazilian data set consists of plot yields of 183

maize trials from the central area of Brazil. Grain yield is usually the most important economic trait considered in maize (Hallauer & Miranda Fo, 1981, Chapter 5). However only the ear (grain plus cob less husk) yield is examined here as this measurement was recorded in all trials. Studies based on grain yield may give very different results.

Of the 183 trials, 160 were designed as lattice designs (Cochran & Cox, 1957, Chapters 10). The remaining trials used randomized complete block (RCB) designs. The distribution of the trials designed as lattice designs over the years is given in Table 3.2.1. These trials were grown between 1976/77 and 1987/88 covering a range of geographical locations. Most trials had no missing values and the maximum number missing in any trial was 12. Trials had 2-6 replicates and the plots consisted of 1, 2 or 4 rows of plants, 3-10 m in length and 1 m apart.

The plots in each block in most of the trials were arranged in one-dimensional array but the arrangement of the blocks within replicates (i.e. superblocks) is unknown. Unfortunately, it was not possible to reconstruct the field layout of the varieties as complete field plot plans were not available. The importance of retaining complete plans and other relevant trials information for future trial monitoring or special investigation is mentioned elsewhere, for example by Pearce (1983, Chapter 10).

The SCRI data set consists of 60 spring barley trials, each comparing 100 varieties in two replicates. Of these

Table 3.2.1. Classification of the three trial series by crop, design and year.

Data set	Crop	Lattice designs	Year 76	77	78	80	81	82	83	84	85	86	87
		4×5									11		
		5×5				2	1						
		6×6	1							3			
		6×7				7	4	2	5	5	5	9	4
Brazilian	Maize	7×7				5	10	14	20	15	11		
		8×8										2	1
		9×9						1			2	1	
		10×10						1			2	12	2
		16×16									1	1	
Brazilian	Maize	-	1			14	15	18	25	23	32	25	7
SCRI	Barley	10×10†				7	14	11	7	21			
PBI	Barley	7×7		27	17								

- All Brazilian maize trials

† $\alpha(0,1)$ design or generalized lattice design

trials, 10 have missing plots but not more than 6 values in any case. The varieties were arranged as alpha (0,1) designs (Patterson *et al.*, 1978). The plots vary from 0.6 to 1.2 m wide and from 2 to 5 m long. Replicates were laid out in a 10×10 array with the columns running parallel to the longer plot side. All trials were carried out between 1980 and 1984 (Table 3.2.1).

The PBI data involves 44 spring barley trials in 4 replicates of 49 varieties arranged as a 7×7 lattice square designs (Cochran & Cox, 1957, Chapter 12). The replicates were laid down immediately adjacent to each other in a two by two array. The plot size was 1.50 m wide by 4.25 m long. Row neighbours were defined to be those plots with a longer edge in common. All trials were carried out between 1977 and 1978 (Table 3.2.1). Sowing, harvesting and all intermediate farming practices were carried out column by column.

The range of the mean yield and RCB coefficients of variation (CV) for all three series of trials are listed in Table 3.2.2. The greater variability in yield for maize trials is emphasised in this table.

3.3. Validity of analyses

Often trials designed in one way are analysed in another way (Patterson & Hunter, 1983; Robinson *et al.*, 1988; Cullis & Gleeson, 1989; Baird & Mead, 1991). A common analysis is the calculation of an estimate of the efficiency of a trial analysis. Here a resolvable

Table 3.2.2. Summary of design, coefficient of variation (CV) and yield from three trials series.

Data set	Lattice designs	Num. of trials	CV% Range	CV% Mean	Yield‡ Range	Yield‡ Mean
Brazilian	4×5	11	8.3-19.1	14.83	3.4-9.6	6.21
	5×5	3	20.9-35.9	27.46	3.6-6.4	4.83
	6×6	4	11.2-21.2	15.90	3.3-8.2	5.91
	6×7	41	6.9-34.4	16.98	2.0-10.0	6.05
	7×7	75	8.0-56.4	17.58	1.3-10.0	5.89
	8×8	3	10.5-11.5	11.01	6.6-9.2	7.80
	9×9	4	15.2-22.6	18.48	4.9-7.9	5.78
	10×10	17	10.2-20.3	14.20	4.8-9.0	6.90
	16×16	2	11.2-16.1	13.69	7.8-8.2	8.00
Brazilian	-	160	6.9-56.4	16.87	1.3-10.0	6.10
SCRI	10×10†	60	5.1-16.4	9.19	1.1-5.5	2.38
PBI	7×7	44	4.0-18.2	7.78	1.8-3.8	3.00

- All Brazilian maize trials

† $\alpha(0,1)$ design or generalized lattice design

‡ Brazilian and SCRI:t/ha; PBI: kg/plot

incomplete block (IB) trial is analysed by the proper incomplete block method and as a randomized complete block. Similarly, a resolvable row and column (RC) trial is analysed by the proper row and column method and as a RCB, and even as an IB.

An analysis remains weakly valid under the usual randomization criterion of validity (Grundy & Healy, 1950; Fisher, 1970) if the variety mean square and the error mean square have the same expectation in the absence of variety effects, or equivalently, the estimated average variance of all variety differences is unbiased. Yates (1939, 1940b), when developing his lattices designs and lattice squares, showed that the RCB analysis of a trial designed as a lattice or a resolvable balanced incomplete block is weakly valid under the criterion of Grundy & Healy. Speed *et al.*(1985) extended Yates' results to any resolvable block designs. Additionally, they showed that recovery of inter-block information is simplified by expressing the variance component of blocks as a function of the complete and incomplete block error mean squares. Following Speed *et al.*'s results, it is shown in Chapter 2 that the recovery of inter-row and inter-column information is also simplified for resolvable RC designs which have the property of adjusted orthogonality.

Conversely, an IB analysis of a trial designed as RCB is also valid if the incomplete blocks are contained within replicates (Ainsley *et al.*, 1987).

Although, in some cases a different analysis from that appropriate for the original design may be weakly valid,

as mentioned above, this will not always be true. In these other circumstances, however, the effect of a possible bias in the analysis of any single trial may be reduced if results are averaged over a number of trials.

3.4. Results of block analyses

The efficiency of a trial analysis was measured by comparing results from the incomplete block analysis or row and column analysis with those from a randomized complete block analysis. The efficiencies were calculated as described in Yates (1939, 1940a) and Patterson & Robinson (1989). The approach involves analysing the results of each trial at least twice -

a) the appropriate incomplete block or row and column analysis with recovery of information;

b) the conventional randomized complete block analysis.

The efficiency is given by the ratio between the average variance of varietal differences in analysis (**b**) and the average variance of varietal differences in analysis (**a**).

The average variance of varietal differences for each trial were obtained using the REML program. REML uses the method of residual maximum likelihood (Patterson & Thompson, 1975; Robinson, 1987) to estimate the variability of each blocking factor and uses this information to obtain efficient estimates of variety effects, recovering all inter-block information.

The efficiencies of trial analyses using rows as incomplete blocks (row analysis), columns as incomplete

blocks (column analysis) or row and column analysis are summarized in Table 3.4.1. Results varied greatly from one trial to another and from one series to another. The distribution of efficiencies is positively skewed for most of the data sets considered.

The lattice designs were very effective using rows as incomplete blocks, but not as effective as using row and column analysis where this was available. Mean efficiencies of the row analysis were 1.12, 1.41 and 1.20 for the Brazilian, SCRI and PBI trials respectively (Table 3.4.1), corresponding to average reductions of 11%, 29% and 17% in average pairwise variance of varietal yield differences. Efficiencies for maize trials are lower than for spring barley trials. The reason for this is not clear; two possible contributory factors are the greater variability of maize yields and the trial design and layout.

For the Brazilian trials it was not possible to use columns as incomplete blocks (see Section 3.2). However, the efficiency using columns as incomplete blocks for SCRI and PBI trials was not so high as for the row analysis. This suggests no clear pattern in fertility within columns and consequently weaker correlations between adjacent plots.

Efficiencies results for SCRI trials row analysis of 1.26 for median and 1.41 for mean are similar to the values of 1.23 and 1.43 for median and mean efficiency reported by Patterson & Hunter (1983), who examined 244 generalized lattice trials for cereals. Results for SCRI

Table 3.4.1. Efficiency of row (R), column (C) and row and column (RC) analysis relative to randomized complete block (RCB) for three series of trials.

Data set	Lattice designs	Number of trials	Efficiency (RCB=1.00) Mean R	Mean C	Mean RC	Median R	Median C	Median RC
	4×5	11	1.04			1.01		
	5×5	3	1.42			1.11		
	6×6	4	1.13			1.02		
	6×7	41	1.20			1.10		
Brazilian	7×7	75	1.09			1.03		
	8×8	3	1.00			1.00		
	9×9	4	1.03			1.01		
	10×10	17	1.12			1.07		
	16×16	2	1.12			1.12		
Brazilian	-	160	1.12			1.05		
SCRI	10×10†	60	1.41	1.15	1.76	1.26	1.04	1.61
PBI	7×7	44	1.20	1.04	1.38	1.09	1.02	1.24

- All Brazilian maize trials

† $\alpha(0,1)$ design or generalized lattice design

trials also compare closely with those reported by Cullis & Gleeson (1989) for 219 IB variety trials from Australia (mean efficiency = 1.50) and by Kelly (1988) for 49 Australian barley trials, designed as 8×8 row lattices (median efficiency = 1.25). However, these efficiencies are considerably higher than for the PBI barley trials (Table 3.4.1) and for a parallel set of 118 winter wheat trials (Kempton, 1985b). These latter trials were designed as a complete 5×5 lattice squares with similar plot size to the barley trials and had a median efficiency of 1.12 and mean of 1.24.

The larger number of varieties in the SCRI trials seems to contribute to the difference in efficiency between SCRI trials and PBI barley and wheat trials. The plot sizes, CV% and range in yields are not very different for both series of trials (Table 3.2.2) but they might also contribute to the difference in the efficiency. The pattern in fertility is another factor that might contribute to the difference in the efficiency. A strong fertility pattern is expected to increase efficiency. The high efficiency for SCRI trials suggests that they have a much stronger fertility pattern within rows than PBI barley and wheat trials. Consequently a much stronger relationship between plots apart within rows is expected for SCRI trials than for PBI barley and wheat trials. The efficiencies for PBI barley and wheat trials are also comparable. This suggests that they may present the same type of pattern in fertility within rows.

The PBI trials were designed for a row and column

analysis. However the SCRI trials were not, so the optimal efficiency is unlikely to have been achieved. The SCRI and PBI trials were most efficient when row and column analysis was considered. The introduction of column effects in the SCRI trials increased the median efficiency from 1.26 for row analysis alone, to 1.61, while the mean efficiency increased from 1.41 to 1.76 (Table 3.4.1). For PBI trials the gains were more modest. The median efficiency increased from 1.09 to 1.24, while the mean efficiency increased from 1.20 to 1.38. These gains in efficiency correspond to average reductions of 43% and 28% in average pairwise variance of varietal yield differences for SCRI and PBI trials when using RC analysis, compared with 29% and 17% reductions for row analysis. Kempton (1985b) also noted increases in efficiency by taking account of column effects in addition to rows. Using RC analysis in his trials resulted in average reduction of 32% in average pairwise variance of varietal yield differences, compared with 19% reductions for row analysis.

In general, the results of efficiency for SCRI trials are consistent with those obtained by Robinson *et al.* (1988) and Patterson & Robinson (1989). Similarly, the results for PBI trials are also consistent with those of Kempton & Howes (1981) and Kempton (1985b).

For more detailed examination, contours of predicted efficiency for RC analysis (compared with RCB) were derived for different ratios σ_r^2/σ^2 and σ_c^2/σ^2 where σ_r^2, σ_c^2 are variance components for rows, columns and σ^2 the error

mean square. Contours of the proportion of variety information lost in ignoring between RC information were also produced. A 10x10 RC design with 2 replicates and a 7x7 lattice square with 4 replicates were considered.

The contours were produced using results given in Chapter 2 Section 2.4. The distribution of observed efficiencies and proportions of information lost in ignoring between RC information obtained for SCRI and PBI trials are plotted together with the respective contour in Figures 3.4.1, 3.4.2, 3.4.3 and 3.4.4.

The observed ratios of variance components for SCRI vary approximately from 0.0 to 5.2 for σ_r^2/σ^2 and from 0.0 to 2.2 for σ_c^2/σ^2 (Figure 3.4.1). Whereas for PBI, σ_r^2/σ^2 vary from 0.0 to 1.9 and σ_c^2/σ^2 from 0.0 to 1.2 (Figure 3.4.3).

It is important to notice that the observed points in Figures 3.4.1 and 3.4.2 for SCRI are for $\alpha(0,1)$ design analysed as a RC design while the contours are for a real RC design. These figures show that if the SCRI trials had been designed as a proper RC design they would be somewhat more efficient and consequently the proportion of information lost in ignoring between RC analysis would be less. For example, for the observed efficiency of 4.49 (Figure 3.4.1) the expected value is 4.79, whereas for the observed proportion of information lost of 0.08 (Figure 3.4.2) the expected value is 0.04. For PBI trials the observed efficiencies and proportions of information lost agree with the predicted contours (Figures 3.4.3 and 3.4.4).

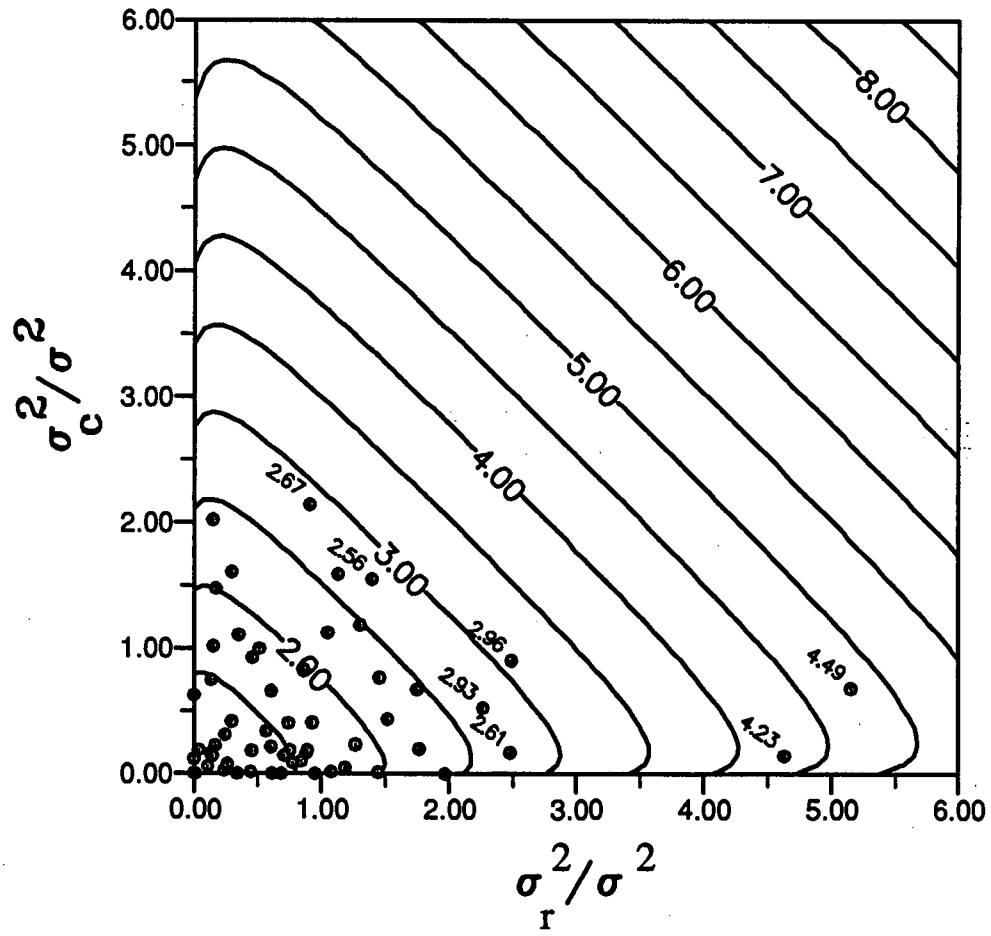


Figure 3.4.1. Efficiency contour and observed efficiency (SCRI) of row and column analysis for a 10x10 row and column design in 2 replicates (σ_r^2, σ_c^2 variance component for row, column and σ^2 the error mean square).

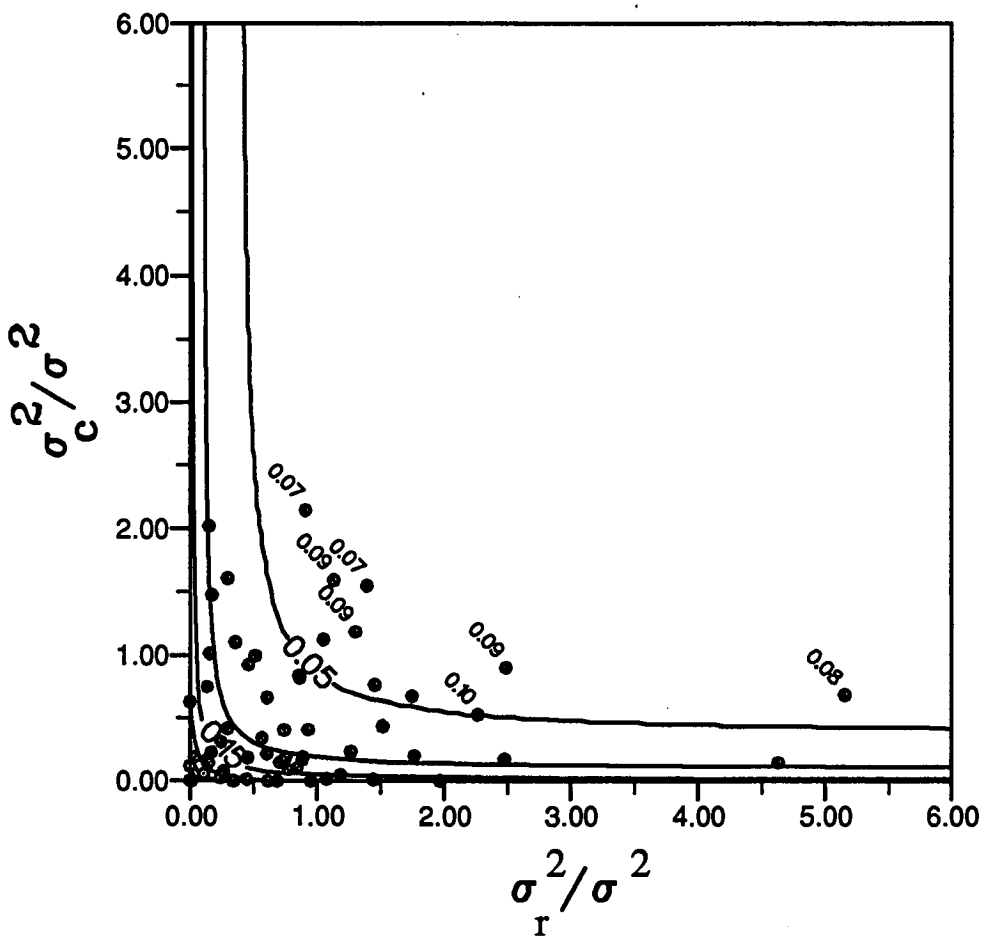


Figure 3.4.2. Proportion contour and observed proportion (SCRI) of information lost in ignoring between row and column information for a 10×10 row and column design in 2 replicates (σ_r^2, σ_c^2 variance component for row, column and σ^2 the error mean square).

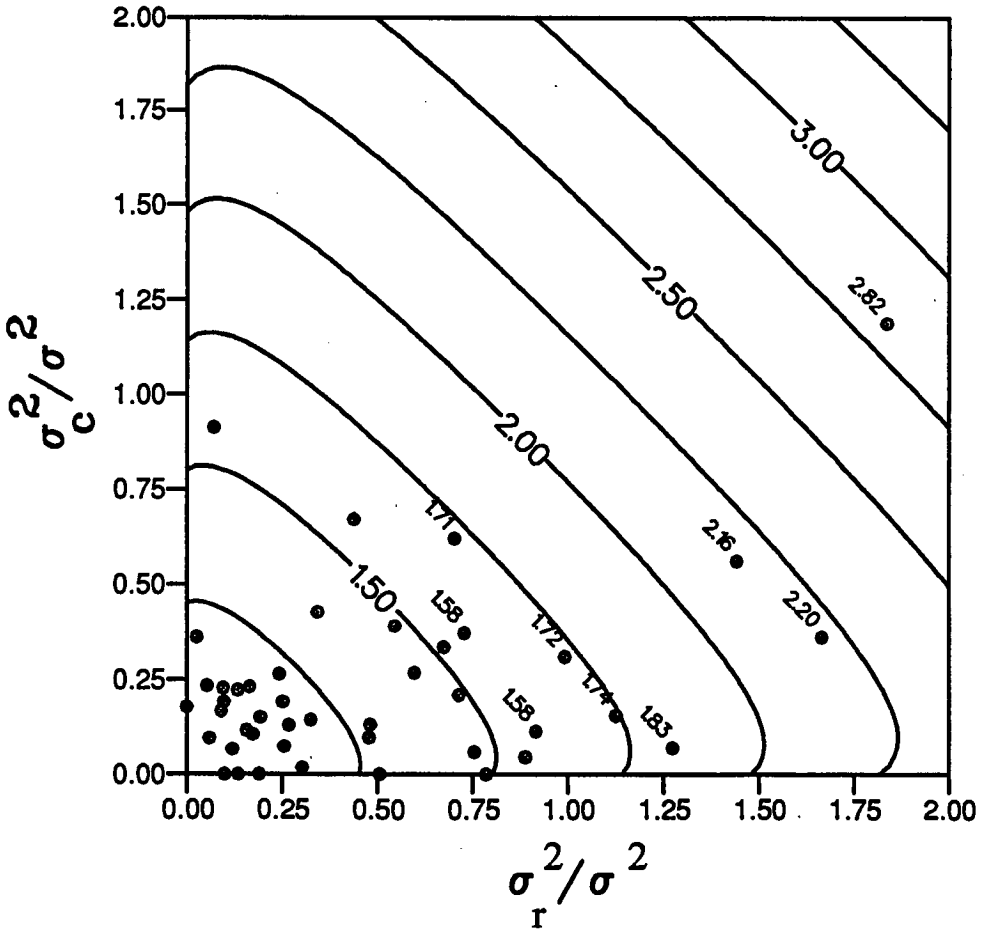


Figure 3.4.3. Efficiency contour and observed efficiency (PBI) of row and column analysis for a 7×7 lattice square design in 4 replicates (σ_r^2, σ_c^2 variance component for row, column and σ^2 the error mean square).

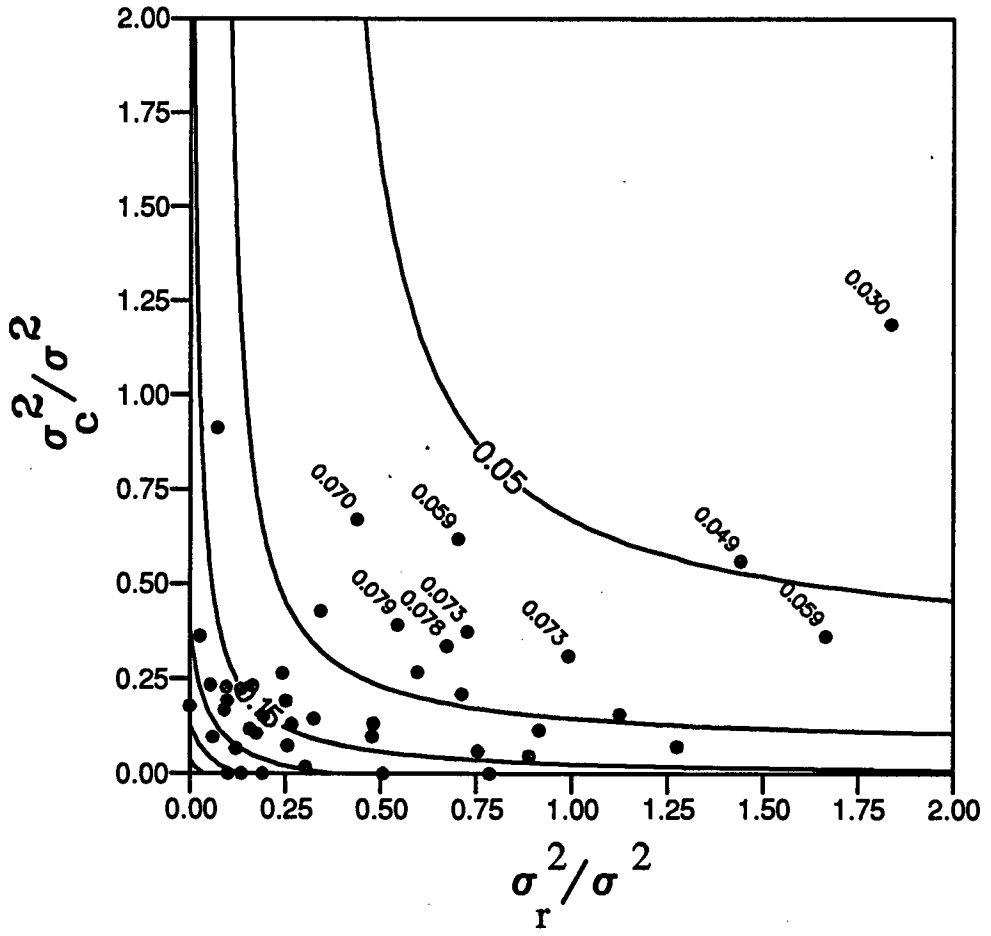


Figure 3.4.4. Proportion contour and observed proportion (PBI) of information lost in ignoring between row and column information for a 7×7 lattice square design in 4 replicates (σ_r^2, σ_c^2 variance component for row, column and σ^2 the error mean square).

A striking characteristic of Figures 3.4.1 and 3.4.3 is the suggestion that row and column are to some extent, complementary. In other words, trials with large ratio σ_r^2/σ^2 did not tend to show particularly large ratio σ_c^2/σ^2 and vice versa. However trials with both ratios small are very common.

In general, if one or both ratios of variance components are large the RC design is highly efficient (Figures 3.4.1 and 3.4.3). However, if both ratios are very small the design has low efficiency and recovery of between RC information is essential (Figures 3.4.2 and 3.4.4). It is suggested that recovery of between RC information should be done routinely for every trial since in the majority of cases, ignoring this information results in a significant reduction in efficiency.

3.5. Selection of data for future analyses

All three series of trials will be used for further analyses, although for the Brazilian trials only those designed as a 7×7 lattices will be used. This comprises 75 trials each with 4 replicates and with plots consisting of 2 rows of 4 m length. This subset was chosen because it is the largest number of trials of one design and has a good distribution over years.

Because of the lack of information on layout, the 75 Brazilian trials will not be used to develop any methodology. They will however be used as an example to introduce postblocking and pairblocking for one-

dimensional case in tropical cereal data.

The SCRI and PBI series will be used in developing postblocking and pairblocking to two dimensions and for neighbour analysis.

Chapter 4

SEMI-VARIANCES IN ONE DIMENSION

4.1. Introduction

In the previous chapter the direct calculation of efficiency of trial analysis was used to assess the effectiveness and to demonstrate the necessity of recovering inter-block and inter-row and column information for incomplete block (IB) and row and column (RC) designs.

Although very informative on past trials, efficiency calculations do not directly answer questions about the planning of future trials. For example, assuming that the plot size and the trial layout remain unchanged, what is the predicted trials efficiency of a new series of trials for a specific number of varieties ? What block size should be chosen ? Information on the variance of the difference between pairs of plots within a block, can however give guidance on these and similar questions.

The intra-block error mean square (EMS) of a blocked trial provides an estimate of half the average variance of the difference between all pairs of plots within a block: when plots are uncorrelated this is the average variance of an observation (John, 1987). However, when examining variability of agricultural field trials data where neighbouring plots are correlated this identity does not hold. The semi-variance of the difference between pairs of

plots is therefore

$$\text{semi-variance } (ij) = \sigma^2(1 - \rho_{ij}).$$

For one-dimensional layout of plots, assuming that the correlation between two plots depends only on the distance between them,

$$\rho_{ij} = \rho(|i - j|)$$

$$= \rho(x)$$

for plots $\mathbf{x}$ apart,

the semi-variance $\phi(\mathbf{x})$ can be related to $\mathbf{x}$, where $2\phi(\mathbf{x})$ is the variance of a difference between two plots $\mathbf{x}$ apart. Once the information on semi-variances is available this relationship may be expressed in terms of error rules.

Information on semi-variances $\phi(\mathbf{x})$ can be made available directly through their values or indirectly through EMS using the relationship between $\mathbf{MS}(\mathbf{k})$ and $\mathbf{k}$, where $\mathbf{MS}(\mathbf{k})$ is the average EMS in blocks of $\mathbf{k}$. If the semi-variances are known, the mean squares are also known.

This chapter gives the relationship between $\mathbf{MS}(\mathbf{k})$ and $\mathbf{k}$ in terms of $\phi(\mathbf{x})$ and describes the methods developed by Patterson & Hunter (1983) and Ainsley (1985) to obtain information on semi-variances. It also describes an exponential variance rule relating semi-variances to plot distances. Additionally the range of application and the effectiveness of the methods are extended to tropical cereal data.

4.2. Expectation of mean square within blocks of size k

Consider a one-dimensional block of size **k**, where **k** is the number of plots. If the correlation between two plots depends only on their distance **x** apart, the relationship between the expected within-block mean square **MS(k)** and **k** is given as a weighted sum of semi-variances $\phi(x)$ for all possible **x**, that is

$$MS(k) = \sum_{x=1}^{k-1} W(x;k)\ \phi(x). \qquad (4.2.1)$$

The weight function **W(x;k)** gives the proportion of pairs of plots **x** apart and is defined as

$$W(x;k) = \frac{2\ N(x;k)}{k(k-1)},$$

where

$$N(x;k) = k - x \qquad 0 < x < k,$$

gives the number of pairs of plots **x** apart.

The expansion of expression (4.2.1) gives

$$MS(k) = \frac{2}{k(k-1)} \sum_{x=1}^{k-1} (k - x)\ \phi(x) \qquad (4.2.2)$$

as shown in Patterson & Hunter (1983).

4.3. Postblocking analysis

Patterson & Hunter (1983) developed a technique which they called postblocking to study the relationship between **MS(k)** and **k** on cereal variety trials. Postblocking groups

the plots into artificial blocks after the trial has been completed. The purpose of the analysis is to estimate **MS(k)** and hence to investigate the error structure of the data.

To use the method of postblocking consider a one-dimensional arrangement of field plots with **v** plots, where **v** is the number of varieties. For any block size **k**, **2≤k≤v**, blocks are imposed on the array by subdividing it into **s** blocks of **k** adjacent field plots each where **s = int(v/k)**. The first block starts in the first field plot of the array. The successive blocks start at field plots **k+1**, **2k+1**, ..., **(s-1)k+1**. If **k** is not a factor of **v** the remaining plots are omitted from the analysis. The analysis is carried out as if the trial had been randomized as an IB(k) design and an estimate of the within-block error mean square **MS(k)** is obtained. The design assumed is determined by the way in which the imposed blocks partition the original randomization.

The process is repeated with the first block starting on each field plot **2**, **3**, ..., **k** or **v-k+1**. Separate error estimates are obtained for each analysis, which is labelled as one pass of the data.

The number of passes of the data for postblocking in blocks of **k** is

$$k \quad \text{if} \quad k \le (v+1)/2$$

or

$$v-k+1 \qquad \text{otherwise.}$$

Figure 4.3.1 gives an example of the passes required for

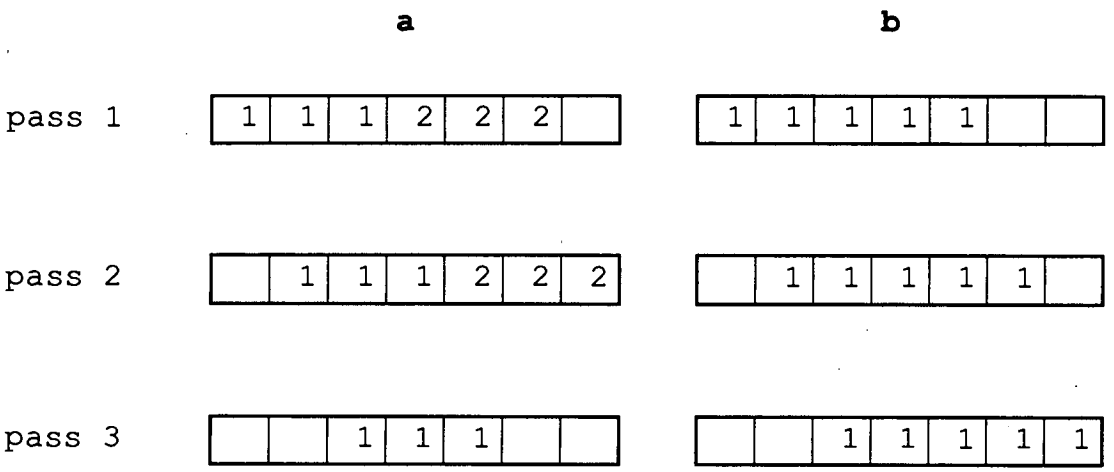


Figure 4.3.1. Passes required for postblocking a trial on 7 varieties in **a**) blocks of 3 and **b**) blocks of 5. Each superblock of the trial is postblocked in the same way. Plots identified with the same number make up a block.

postblocking an arrangement of seven field plots in blocks of 3 and 5.

Postblocking in blocks of **k** involves at least two passes of the data. Therefore different estimates of the error mean square are obtained. A combined estimate of **MS(k)** is then formed as the average of the calculated error mean squares weighted by their degrees of freedom.

4.4. Pairblocking analysis

Pairblocking is a version of postblocking devised by Ainsley (1985) to provide direct estimates of $\phi(\mathbf{x})$. Each postblock consists of two plots at a distance **x** apart. The error mean square within blocks of two plots provides an estimate of the semi-variance of the difference between such plots.

The variance of the difference in yield between plots at a distance **x** apart in the absence of treatments (as in a uniformity trial), is estimated as:

$$\frac{\sum_{i=1}^{v-x}\sum_{j=1}^{s}(y_{ij}-y_{i+x,j})^2}{S(v-x-1)}$$

where $\mathbf{y}_{ij}$ is the yield of the $\mathbf{i}^{th}$ plot in $\mathbf{j}^{th}$ array. However, in field trials each plot within a superblock receives a different variety. In these circumstances the difference between the yields of plots distance **x** apart is due to the differences in varieties and also due to an error component which may depend on the distance apart of

the plots; that is, for the usual additive model,

$$y_i - y_{i+x} = \tau_i - \tau_{i+x} + \varepsilon_i - \varepsilon_{i+x}$$

$$\neq \varepsilon_i - \varepsilon_{i+x}$$

unless $\tau_i = \tau_{i+x}$, where τ_i is the true yield of the variety applied to the $\mathbf{i}^{th}$ field plot. Pairblocking provides a method of estimating the semi-variances $\phi(\mathbf{x})$ even in the presence of differential treatments.

In pairblocking, the trial results are also analysed several times. Instead of increasing the block size from analysis to analysis as in postblocking, blocks of size two are retained throughout and the component plots of the blocks are moved further apart.

In order to get all information given by the difference in the yields of two plots, pairblocking analysis includes two passes of the data. Pass one starts in the first field plot of the array and pass two starts in the field plot **x+1** (see Figure 4.4.1).

For a large distance **x** apart the passes may omit many plots particularly on the second pass when at least **x** plots are omitted. As a result less of the data are used in calculating $\phi(\mathbf{x})$ when **x** is large than when it is small. Thus the estimates of $\phi(\mathbf{x})$ for large **x** are likely to be more variable than for small **x**.

Each pass of the data gives an estimate of $\phi(\mathbf{x})$ and the two estimates obtained are then weighted by their degrees of freedom (dfs) to form a combined estimate. The consequence of this procedure was examined by Ainsley

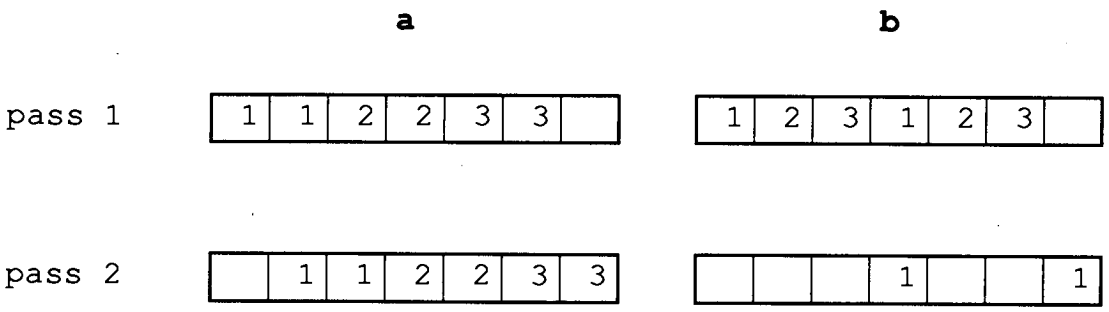


Figure 4.4.1. One superblock of a trial on 7 varieties showing the blocks formed in each pass. The two plots in each block are at **a**) distance 1 apart to estimate $\phi(1)$ and at **b**) distance 3 apart to estimate $\phi(3)$. Plots identified with the same number make up a block.

(1985). For small distances apart when the ratio of the error dfs on the two passes is close to one, the combination of the estimates of $\phi(\mathbf{x})$ from the two passes by their dfs was found to be more efficient then using the result of a single pass. On the other hand, for large distances apart when the second pass tends to have only a few dfs for error, the estimate of $\phi(\mathbf{x})$ from a single pass was found to be slightly more efficient than using a weighted combination of the results of the two passes. Finally the rule of combining the estimates of $\phi(\mathbf{x})$ weighting by their dfs for error df≥4 was derived.

With an appropriate definition of the blocks, a standard intra-block ANOVA can be used to estimate $\phi(\mathbf{x})$ directly. Since this involves analysis of results of a trial in blocks other than those of the design, the validity of such analysis depends on a relationship between the set of randomizations of the actual design and the set of randomizations of the design used in the analysis. Ainsley (1985) and Ainsley *et al.* (1987) showed that estimated variances of new strata created by postblocking or pairblocking are valid (unbiased under randomization) when each such stratum is wholly nested within an original stratum.

When performing postblocking or pairblocking analysis successive values of $\mathbf{MS}(\mathbf{k})$ or $\phi(\mathbf{x})$ are estimated. Clearly, from the method of calculation, these estimates will not be independent. Indication of the size of the correlations can be obtained by calculating the expected correlation between semi-variances when there are no variety effects

and the plot yields have a known distribution. Ainsley (1985) investigated the variances and correlations between successive estimates of $\phi(\mathbf{x})$ in this way. The main conclusion was that correlations between successive values of $\phi(\mathbf{x})$ are substantially smaller than those between successive $\mathbf{MS}(\mathbf{k})$ values which are, in general, very highly correlated. The implications of this were also pointed out. Plots of empirical semi-variances would be expected to be more variable and less smooth than the corresponding empirical error mean squares plots and also more directly interpretable.

4.5. Exponential variance rule relating semi-variances to plot distances

Once the information on semi-variances $\phi(\mathbf{x})$ are available either through postblocking or pairblocking, the relationship between the $\phi(\mathbf{x})$ and the distance $\mathbf{x}$ apart can be established.

Patterson & Hunter (1983) wishing to summarize the relationship between $\mathbf{MS}(\mathbf{k})$ and $\mathbf{k}$ for cereal trials suggested an exponential variance (EV) rule. For an exponential process in one dimension the covariance between two plots $\mathbf{x}$ apart is $\lambda\rho^{x}$, where λ and ρ are defining parameters. The relationship between $\phi(\mathbf{x})$ and $\mathbf{x}$ is then given as:

$$\phi(x)=\sigma^2(1 - \lambda\rho^{x}) . \qquad (4.5.1)$$

The EV rule is widely used in other applications of distance laws such as geostatistics (see, for example,

Clark, 1979) and has a simple theoretical interpretation (Patterson & Hunter, 1983). Considering the error on any given plot as the sum of a component generated by a simple first-order autoregressive process and a white noise error component, the EV parameters can be interpreted as:

σ^2 the total variance per plot,

λ the proportion of the total variance attributable to the autoregressive component,

$\lambda\rho$ the overall correlation between neighbouring plots.

Besag (1977) used error models of this type in analysis of Mercer & Hall's (1911) wheat data.

Despite this theoretical interpretation the prime importance of the EV rule is to describe the relationship between $\phi(\mathbf{x})$ and $\mathbf{x}$. However, other error models such as proposed by Fairfield Smith (1938) and Patterson & Ross (1963) are known to be inadequate for field trial data.

Assuming the exponential relationship between $\phi(\mathbf{x})$ and $\mathbf{x}$ given in (4.5.1) the corresponding error mean squares are derived using (4.5.1) in (4.2.2) as:

$$MS(k) = \sigma^2 \left[1 - \frac{2\lambda}{k(k-1)} A_k(\rho)\right], \qquad (4.5.2)$$

where

$$A_k(\rho) = \sum_{x=1}^{k-1} (k - x)\,\rho^x = \frac{k\rho}{(1-\rho)} - \frac{\rho(1-\rho^k)}{(1-\rho)^2}.$$

For known parameters λ and ρ the expression (4.5.2) can be used to predict the within-block error mean square for blocks of size $\mathbf{k}$.

4.6. Application to tropical cereal data

So far, the only yield trials investigated in terms of error rule, using postblocking or pairblocking, on a large scale have been of cereal varieties in temperate climates (see Patterson & Hunter, 1983; Ainsley, 1985; and Pilarczyk, 1990). Plots were long and thin and laid out in a single line within each replicate.

To extend the range of application of postblocking and pairblocking and to consider whether similar error rule hold for results from other variety trials, the correlation structure and the use of error rules for the Brazilian maize data described in Section 3.2 is examined.

The maize data are very different from those UK cereal trials. For example, they come from the tropics and the crop, plot sizes and trial designs are all different. The extent to which neighbouring plots are correlated may be expected to depend on some of these factors, and the correlation structure could consequently be very different from that found for cereals in the UK.

Postblocking and pairblocking analysis of 75 maize trials were carried out using SAS GLM routines (SAS Institute, 1985; Freund & Littell, 1981). Analysis of this data was restricted because there was no information on the arrangement of the blocks within replicates (i.e. superblocks). Artificial blocks were not allowed to cross the original block boundaries. This limited the range of values assumed for $\mathbf{k}$ and $\mathbf{x}$.

The mean squares $\mathbf{MS}(\mathbf{k})$ for artificial block of size $\mathbf{k}$,

k=2,...,7 were calculated by the method of postblocking of Section 4.3. Average results over all 75 trials are given in Table 4.6.1 and are plotted in Figure 4.6.1. Alternatively the semi-variances $\phi(\mathbf{x})$ for distances apart **x, x=1,...,5** were obtained by the method of pairblocking of Section 4.4. Average results over all 75 trials are also given in Table 4.6.1. These results are plotted in Figure 4.6.2.

The size of the error mean squares (Table 4.6.1) are higher than those found for cereal in the UK. This suggests a much large variation in the maize data. A striking feature of the error mean squares plots (Figure 4.6.1) is the smoothness when compared with the semi-variances plots (Figure 4.6.2). This was expected and it means that the correlation between successive **MS(k)** values may be higher than correlation between successive $\phi(\mathbf{x})$ values (see, also Section 4.4). Further examination of Figures 4.6.1 and 4.6.2 reveal that the curves could be described by exponential error rules.

Postblocking and pairblocking are alternative methods which provide information on semi-variances $\phi(\mathbf{x})$. Postblocking gives information indirectly through error mean squares whereas pairblocking gives direct information from the empirical values of $\phi(\mathbf{x})$. In the absence of error the methods are theoretically equivalent. However they are likely to give different results when applied to trial data. For example, an exponential error rule derived via each method would probably present small differences between the two sets of parameters. These differences

Table 4.6.1. Average values of within-block error mean squares MS(k) and semi-variances $\phi(x)$ in 75 Brazilian maize trials $(t/ha)^2$.

Postblocking		Pairblocking	
Block size (k)	MS(k)	Distance apart (x)	$\phi(x)$
2	0.674	1	0.674
3	0.728	2	0.836
4	0.760	3	0.836
5	0.783	4	0.928
6	0.804	5	0.966
7	0.831		

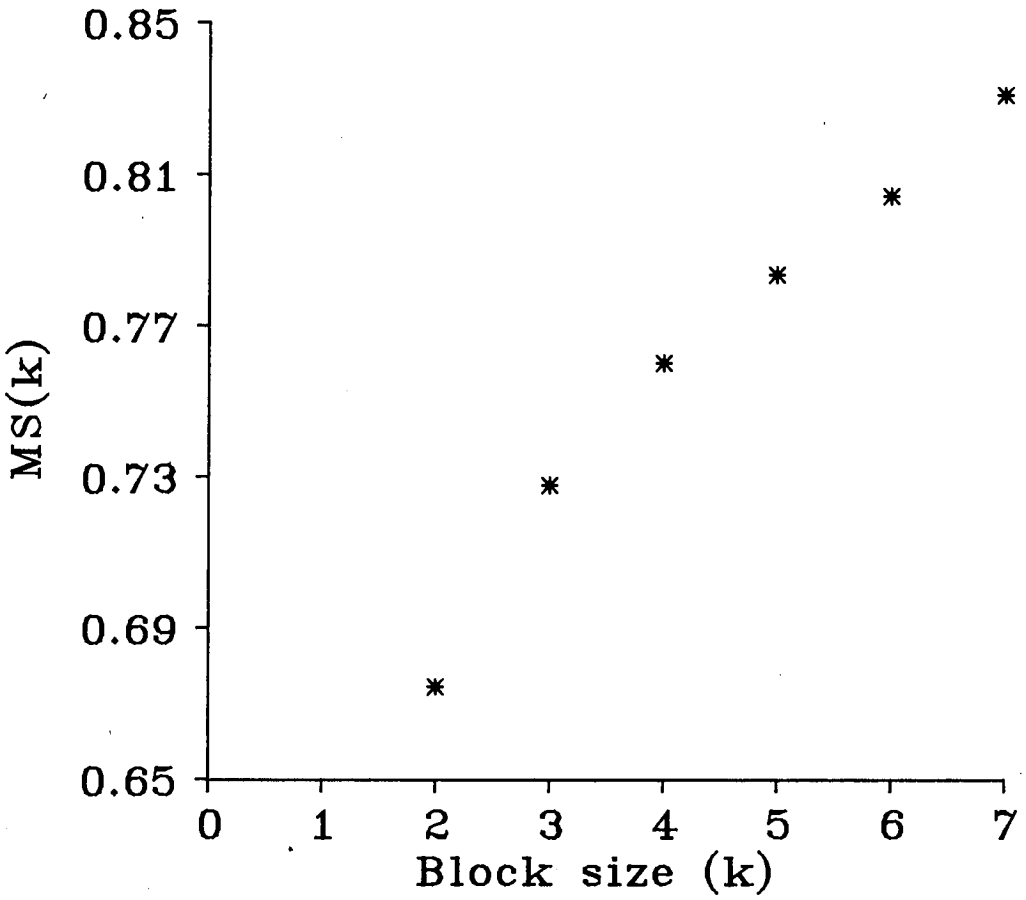


Figure 4.6.1. Values of MS(k) averaged over 75 maize trials

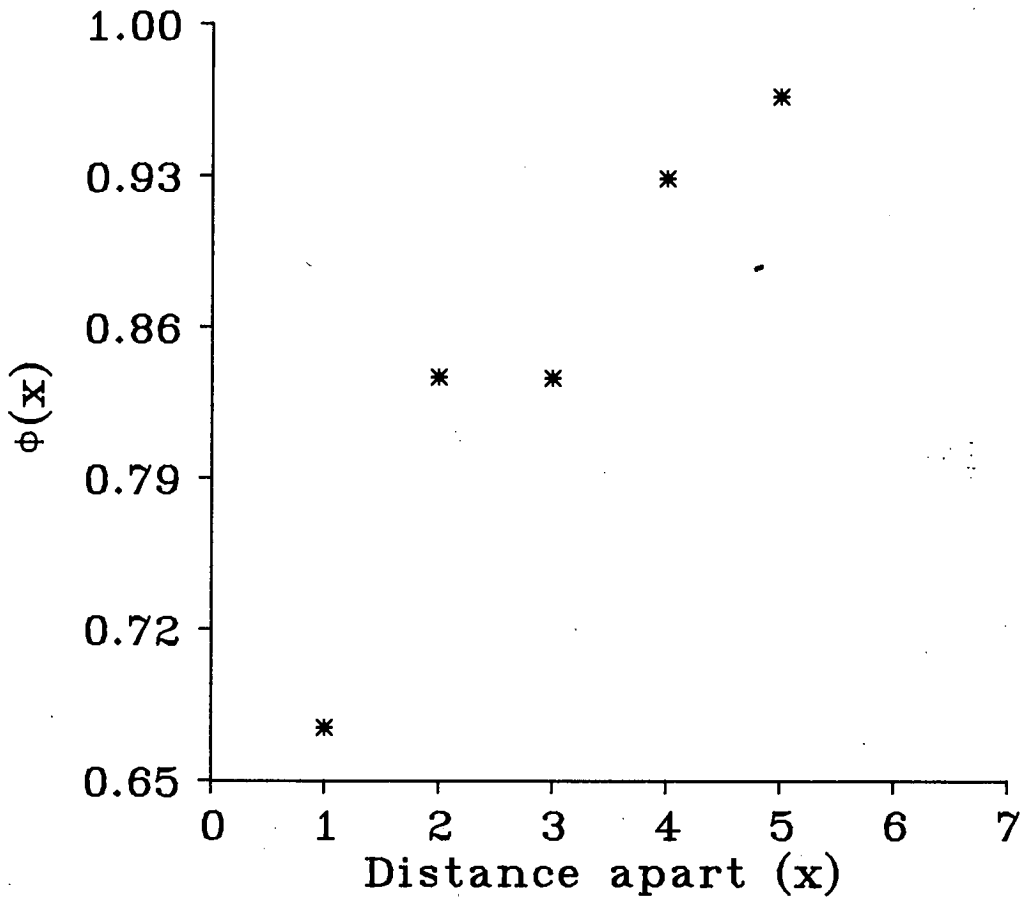


Figure 4.6.2. Values of $\phi(x)$ averaged over 75 maize trials

would be mainly due to different weightings of observations implicitly used in the fitting of the model via each method, although differences in the range of distances apart **x** covered by the two methods would also contribute. In addition, particularly for this data set, the limited range of distances imposed by block size would also contribute to enhance the difference between the two sets of parameters. Despite these practical differences between the two methods, they produce similar conclusions as will be seen below.

The exponential variance model, equation (4.5.1), was fitted via postblocking and pairblocking to derive an error rule for the maize data. An autoregressive (AR) error term (maximum second order) was included to allow for correlation between successive values but was found to be non-significant. The curves were fitted using a BASIC program based on a iterative method of curve fitting (Williams, 1959, Chapter 4) and a correlated error structure was fitted by regression (Box & Newbold, 1971). The AR error term produced no substantial change in each set of results so that the simplest model of an i.i.d. error term was assumed.

The EV model fitted to the values of mean squares led to the equation

$$\phi(x) = 0.970\ [1 - 0.582\ (0.520)^{x}]$$

estimated from **MS(k)** values (Table 4.6.1) satisfying **MS(k)** in expression (4.5.2). When fitted directly to $\phi(\mathbf{x})$ values (Table 4.6.1), the estimated equation was

$$\phi(x) = 1.021\ [1 - 0.501\ (0.659)^{x}].$$

The parameters together with the standard errors appear in Table 4.6.2.

The two sets of results exhibit slight differences as was expected. However, either set of parameter estimates are very different from those for cereal in the UK (Table 4.6.2). The values of λ and ρ are much smaller in the maize data. The product $\lambda\rho$ indicates the correlation between neighbouring plots and large values of both suggest a high correlation which falls away slowly with distance. Thus if both parameters are large the use of IB or neighbour analysis would be expected to increase the efficiency of analysis. However for the maize data these parameters are small and blocking methods are expected to be much less useful. Neighbour methods may also be less useful.

To determine how useful the blocking methods are for these maize trials, the efficiency of using various sizes of IB designs has been predicted from the knowledge of the error rule.

For a particular error rule the efficiency of a trial on **v** varieties designed in **s** blocks of **k** plots in each superblock can be approximately calculated using the formula in Patterson & Hunter (1983)

$$\mathcal{E} = \gamma \left[E + \frac{(1 - E)(s - 1)}{\gamma(v - 1) - (v - s)} \right]$$

where **E** is the efficiency factor of the design (Patterson

Table 4.6.2. Parameter estimates and standard errors of EV model via postblocking and pairblocking - Brazilian maize data.

Parameters	Estimates (± se) via Postblocking	Pairblocking
σ^2	0.970 (± 0.042)	1.021 (± 0.135)
λ	0.582 (± 0.071)	0.501 (± 0.101)
ρ	0.520 (± 0.108)	0.659 (± 0.226)

For comparison, Patterson & Hunter (1983) give estimates $\sigma^2 = 0.209$, $\lambda = 0.725$, and $\rho = 0.942$ for a series of UK cereal trials.

et al., 1978) and γ is the ratio of mean squares **MS(v)/MS(k)**. For unequal block size an average value of γ can be used. The expected values of the mean squares are obtained from expression (4.5.2).

The results of efficiency for trials in 2, 3 or 4 replicates of 49 varieties are given in Table 4.6.3. They were considered separately for postblocking and pairblocking in order to test whether the differences between the two methods could drastically affect the inference made.

Examination of Table 4.6.3 shows that postblocking and pairblocking lead to the same conclusions and minor differences between the set of EV estimates are not important.

Clearly, reduction in block size leads to a reduction in the error mean squares (large γ). The optimum block size is the result of a balance between having a small error mean square (large γ) and a reasonable proportion of the within-blocks information (high **E**).

The optimum block size for maximum efficiency relative to randomized complete block can be chosen between 5 and 6 for trials with more then two replicates. When there are only two replicates very small blocks should be avoided. In this case a block of 7 is predicted to give the greatest efficiency. These results are consistent with those obtained for cereals in the UK (Patterson & Hunter, 1983).

The results achieved and discussed in this section illustrate the usefulness and the effectiveness of

Table 4.6.3. Predicted efficiencies ($\mathcal{E}$) of incomplete block designs for 49 varieties in blocks of 4-13 based on EV rule via postblocking and pairblocking for Brazilian maize trials.

Number of blocks	Block size†	Effic. factor	Postblocking γ	Postblocking $\mathcal{E}$	Pairblocking γ	Pairblocking $\mathcal{E}$
		Two replicates				
13 (3)‡	4	0.565	1.261	0.981	1.316	0.996
10 (1)	5	0.676	1.206	1.002	1.262	1.024
9 (5)	6	0.714	1.188	1.008	1.242	1.032
7 (0)	7	0.800	1.145	**1.022**	1.195	**1.049**
6 (5)	9	0.821	1.122	1.014	1.168	1.039
5 (1)	10	0.857	1.100	1.014	1.138	1.037
4 (3)	13	0.889	1.076	1.010	1.107	1.030
		Three replicates				
13 (3)	4	0.662	1.261	1.043	1.316	1.068
10 (1)	5	0.752	1.206	**1.050**	1.262	1.079
9 (5)	6	0.781	1.188	**1.050**	1.242	**1.081**
7 (0)	7	0.842	1.145	1.048	1.195	1.080
6 (5)	9	0.859	1.122	1.037	1.168	1.067
5 (1)	10	0.889	1.100	1.033	1.138	1.060
4 (3)	13	0.914	1.076	1.025	1.107	1.047
		Four replicates				
13 (3)	4	0.691	1.261	1.062	1.316	1.089
10 (1)	5	0.775	1.206	**1.064**	1.262	**1.096**
9 (5)	6	0.802	1.188	1.063	1.242	**1.096**
7 (0)	7	0.857	1.145	1.057	1.195	1.091
6 (5)	9	0.874	1.122	1.046	1.168	1.077
5 (1)	10	0.900	1.100	1.040	1.138	1.067
4 (3)	13	0.923	1.076	1.030	1.107	1.053

† Designs with almost block size are classified by the larger of the two block size.

‡ Number of blocks for the small block size

postblocking and pairblocking to derive error rules for crops where the management of crop and trials are entirely different from those for cereals in the UK.

Chapter 5

SEMI-VARIANCES IN TWO DIMENSIONS

5.1. Introduction

The previous chapter presented an account of the use of postblocking and pairblocking to provide information on semi-variances in one dimension.

Postblocking and pairblocking as originally devised have mainly been used when either the plots are long and narrow or the trials have a one-dimensional layout. In these situations the correlation between plots are assumed to exist solely in one direction, dependent only on the distance between them.

When the plot shape is square or near-square and the trial layout is in a rectangular array, correlations between plots may exist in both directions. For a separable process (Martin, 1990), the correlation between two plots **p** rows and **q** columns apart depends on the product of the correlations between plots in the same row and in the same column:

$$\rho_{ij,hk} = \rho(|i - h|)\ \rho(|j - k|)\ ,$$

$$= \rho(p)\ \rho(q)\ .$$

The semi-variance between plots **p** rows and **q** columns apart is therefore

$$\phi(p,q) = \sigma^2 \left[1 - \rho(p)\ \rho(q)\right].$$

At this point one might ask how the information about a two-dimensional semi-variance $\phi(\mathbf{p},\mathbf{q})$ would be obtained and used in studying error structure of field trials. A further question is how this information would be employed for testing the efficiency of a range of row and column (RC) and incomplete block (IB) designs to decide whether they might be appropriate for future trials. This latter question will be discussed in later chapters.

Concerning the former question, Ainsley *et al.* (1987) suggested that pairblocking may be useful to give information on semi-variances in two dimensions. However postblocking can also be used once the relationship for the error mean square (EMS) for blocks of $(\mathbf{r},\mathbf{c})$ is established. A block of $(\mathbf{r},\mathbf{c})$ has dimension $\mathbf{r}$ and $\mathbf{c}$ and is laid down in $\mathbf{r}\times\mathbf{c}$ array, $\mathbf{r}$ being the number of rows and $\mathbf{c}$ the number of columns of the array. The size of the block is automatically given by its dimensions.

The approaches of postblocking and pairblocking are compatible: mean squares can be derived from semi-variances $\phi(\mathbf{p},\mathbf{q})$ and vice-versa. Thus, in this chapter the relationship between the EMS and block dimensions is established and extensions of postblocking and pairblocking methods to two dimensions are devised to obtain information on semi-variances. Finally, a two-dimensional exponential variance rule is discussed and a method of fitting described.

5.2. Expectation of mean square within r×c blocks

If the correlation between two plots depends only on the distance between them, the relationship between the expected mean square and semi-variances can be derived as follows.

Consider a **r**×**c** block where **r** is the number of rows and **c** is the number of columns. One may consider two possible mean squares, the within-block mean square **MS(r,c)** and the within-row and column within block mean square **MS1(r,c)**. Each of these mean squares is given as a weighted sum of semi-variances $\phi(p,q)$ for all possible **p** and **q**, but with different weightings, that is

$$\left.\begin{aligned} MS(r,c) &= \sum_{p=1}^{r-1} W(p,0;r,c)\phi(p,0) + \sum_{q=1}^{c-1} W(0,q;r,c)\phi(0,q) \\ &\quad + \sum_{p=1}^{r-1}\sum_{q=1}^{c-1} W(p,q;r,c)\phi(p,q) \\ &\text{and} \\ MS1(r,c) &= \sum_{p=1}^{r-1} W_1(p,0;r,c)\phi(p,0) + \sum_{q=1}^{c-1} W_1(0,q;r,c)\phi(0,q) \\ &\quad - \sum_{p=1}^{r-1}\sum_{q=1}^{c-1} W_1(p,q;r,c)\phi(p,q)\,. \end{aligned}\right\} \quad 5.2.1$$

The weight functions give the proportion of pairs of plots **p** rows **q** columns apart. For **MS(r,c)** the proportion of pairs of plots is given in relation to the total number of pairs of plots within the block with the weight

function defined as

$$W(p,q;r,c) = \frac{2\,N(p,q;r,c)}{rc(rc-1)},$$

where $\mathbf{N(p,q;r,c)}$, for $\mathbf{p<r}$ and $\mathbf{q<c}$, is a function defined by

$$N(p,q;r,c) = r(c-q) \qquad \text{when } p = 0,$$

$$N(p,q;r,c) = c(r-p) \qquad \text{when } q = 0,$$

$$N(p,q;r,c) = 2(r-p)(c-q) \qquad \text{when } p \neq 0 \text{ and } q \neq 0,$$

which gives the number of pairs of plots **p** rows and **q** columns apart.

In contrast, for $\mathbf{MS1(r,c)}$ the weight function is defined as

$$W_1(p,q;r,c) = \frac{2\,N(p,q;r,c)}{rc(c-1)} \qquad \text{when } p = 0,$$

$$W_1(p,q;r,c) = \frac{2\,N(p,q;r,c)}{rc(r-1)} \qquad \text{when } q = 0,$$

$$W_1(p,q;r,c) = \frac{2\,N(p,q;r,c)}{rc(r-1)(c-1)} \qquad \text{when } p \neq 0 \text{ and } q \neq 0,$$

where $\mathbf{N(p,q;r,c)}$ is defined as before.

Expanding $\mathbf{MS(r,c)}$ and $\mathbf{MS1(r,c)}$ in (5.2.1) leads to the expressions

$$MS(r,c) = \frac{2}{rc(rc-1)}\Big[\sum_{p=1}^{r-1} c(r-p)\phi(p,0) + \sum_{q=1}^{c-1} r(c-q)\phi(0,q) + \sum_{p=1}^{r-1}\sum_{q=1}^{c-1} 2(r-p)(c-q)\phi(p,q)\Big] \qquad (5.2.2)$$

and

$$MS1(r,c) = \frac{2}{rc(r-1)(c-1)} \left[(c-1) \sum_{p=1}^{r-1} c(r-p)\phi(p,0) + \right.$$

$$\left. (r-1) \sum_{q=1}^{c-1} r(c-q)\phi(0,q) - \sum_{p=1}^{r-1} \sum_{q=1}^{c-1} 2(r-p)(c-q)\phi(p,q) \right] \quad (5.2.3)$$

in terms of $\phi(\mathbf{p},\mathbf{q})$.

The mean square in formula (5.2.2) is the same as the within-block error mean square in blocks of dimension $(\mathbf{r},\mathbf{c})$. Similarly, the mean square in formula (5.2.3) is the same as the within-row and column, within block error mean square in blocks of dimension $(\mathbf{r},\mathbf{c})$, that is, the intra-row and column error mean square.

5.3. Postblocking in two dimensions

As in one dimension, postblocking is the analysis of a superimposed arrangement of groups of plots into artificial blocks after the trial has been completed. The error mean square of a trial designed in artificial blocks of dimension $(\mathbf{r},\mathbf{c})$, $\mathbf{MS}(\mathbf{r},\mathbf{c})$ or $\mathbf{MS1}(\mathbf{r},\mathbf{c})$, is an estimator of half of the average variance of the difference between all pairs of plots within each block.

Consider a two-dimensional arrangement of field plots in a $\mathbf{R}\times\mathbf{C}$ array, where $\mathbf{R}$ is the number of rows and $\mathbf{C}$ the number of columns. $\mathbf{R}$ and $\mathbf{C}$ may be assumed to be the dimension of superblocks if they are separated or the dimension of the trial if they are adjacent.

A general way of postblocking this array for any block

of dimension **(r,c)** with **1≤r≤R**, **1≤c≤C** and **rc>1**, is to impose blocks on the array by subdividing it into **s** blocks of **(r,c)** adjacent field plots each. The first block starts in the first field plot of the array, which has coordinates **(1,1)** and successive blocks start at **(1,c+1)**, **(1,2c+1)**, ..., **(r+1,1)**, **(r+1,c+1)**, ... If **r** is not a factor of **R** and/or **c** is not a factor of **C** the remaining plots are omitted from the analysis. The analysis proceeds as if the trial had been randomized as an IB**(r,c)** or RC**(r,c)** design and an estimate of the error mean square in block of **(r,c)**, **MS(r,c)** or **MS1(r,c)** is obtained.

The procedure is repeated with the first block starting at field position of the array **(1,2)**, **(1,3)**, ..., **(r,c)** or **(r,C-c+1)** or **(R-r+1,c)** or **(R-r+1,C-c+1)** and separate error estimates are obtained for each pass of the data.

The number of passes of the data for postblocking in blocks of **(r,c)** is

$$\min(r,\ R-r+1)\min(c,\ C-c+1).$$

An example of the passes required for postblocking an arrangement of field plots in a 10×10 array in blocks of (2,5) is given in Figure 5.3.1.

Postblocking in blocks of **(r,c)** involves at least two passes of the data. For each pass, different estimates of the error mean square are obtained. An overall estimate of **MS(r,c)** or **MS1(r,c)** may then be calculated as the average of the error mean squares weighted by their individual degrees of freedom. This weighting is suggested by the Normal-Law theory under which the error sum of squares has

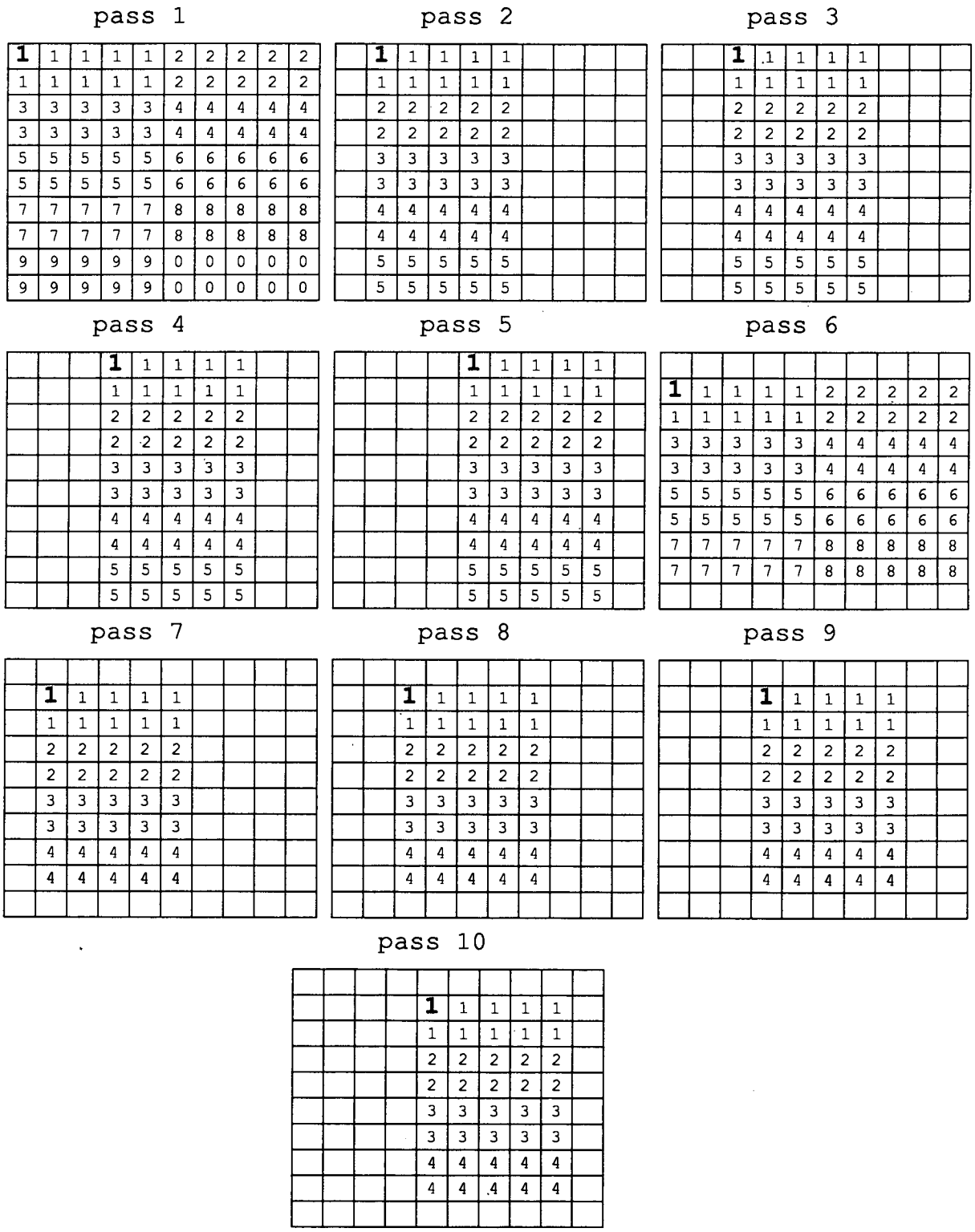


Figure 5.3.1. Passes required for postblocking a trial on 100 varieties in blocks of (2,5). Each superblock of the trial is postblocked in the same way. Plots with the same number make up a block. Each pass is defined by the starting position (bold type) in the first block.

a χ^2 distribution with variance proportional to the degrees of freedom. As the EMSs are likely to be correlated, optimal weighting among linear combinations of the individual EMSs is not possible since these correlations are unknown. However ignoring dependence should not drastically increase the variance of the combined estimate.

The purpose of the analysis is to estimate **MS(r,c)** or **MS1(r,c)**, and it is important to notice that the design assumed for each pass is determined by the way in which the imposed blocks partition the original randomization. The design will not have any structure or advantageous properties that could be used to simplify the analysis.

In two dimensions there are many possible blocking arrangements and some of them have a very high number of passes. In addition, many of the passes may omit a large proportion of the data and the remaining data will often be very unbalanced. In large trials this could substantially increase the time taken to calculate all possible **MS(r,c)** or **MS1(r,c)** values for little additional information. Therefore, in practice **MS(r,c)** or **MS1(r,c)** were calculated only where no data in the trial were omitted from the analysis. Hence, the points were those which both **r** and **c** were factors of **R** and **C** respectively. Only the first pass of the data was considered.

5.4. Pairblocking in two dimensions

In one dimension, pairblocking is a refinement of

postblocking analysis which has the objective of providing direct estimates of semi-variances. Its extension to two dimensions also provides direct estimates of semi-variances, $\phi(p,q)$, for plots **p** rows and **q** columns apart: one dimension could be considered as a particular case when the distance in one of the directions is zero. Just as in one dimension, pairblocking in two dimensions is expected to give similar results to those given by Postblocking. This will be shown in the next chapter.

Consider **S** two-dimensional arrays of plots with **r** rows and **c** columns each. If every plot was given the same variety, as in a uniformity trial, the variance of the difference in yield between plots distance **p** and **q** apart could be estimated as:

$$\frac{\sum_{i=1}^{r-p}\sum_{j=1}^{c-q}\sum_{k=1}^{S}[(y_{ijk} - y_{i+p,j+q,k})^2 + B(y_{i+p,j,k} - y_{i,j+q,k})^2]}{S\,[(r-p)(c-q)\,2^B - 1]}$$

where y_{ijk} is the yield of the plot at the i^{th} - row and j^{th} - column in the k^{th} - array and **B** is 1 if both **p** and **q** are different from zero and 0 otherwise. Nevertheless, in variety trials each plot within a superblock receives a different variety. Pairblocking provides a way of estimating the semi-variances, $\phi(p,q)$, even in the presence of differential treatments.

The intra-block EMS from a blocked trial in which each block contains only two plots provides an estimate of half the variance of the difference between the yields of the

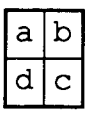
two plots. If blocks of size two were used but the component plots of each block were **p** rows and **q** columns apart the EMS would estimate $\phi(\mathbf{p},\mathbf{q})$. This idea is exploited in the extension to two dimension.

As in pairblocking in one dimension, the trial data are analysed several times using separate passes of the data.

The passes fall into two groups, which we shall call case 1 and case 2. In order to get all information given by the difference in the yields of two plots, each case includes a maximum of four passes of the data.

In both cases, for pass one the first block starts in the first field plot of the array. For pass two it starts in the field plot at **q** columns apart from the first field plot of the array. In pass three the beginning is in the field plot at **p** rows apart from the first field plot of the array and in pass four it is in the field plot at **p** rows and **q** columns apart from the first field plot of the array.

The direction of the blocks in each pass are defined following the diagram



where **ac** are diagonal plots and **bd** are cross diagonal plots.

Pass one and three involve blocks with plots **a** and **c** and pass two and four involve blocks with plots **b** and **d**, for case 1. For case 2, each pass involve blocks with plots **a** and **c** and blocks with plots **b** and **d**.

As an example, for a trial on 100 varieties with replicates forming a 10×10 array, the EMS from an analysis in blocks of two with the component plots 1 row and 1 column apart (Figure 5.4.1) estimate $\phi(1,1)$ in each pass of the data, that from an analysis in block of two with component plots 2 rows and 1 column apart (Figure 5.4.2) estimate $\phi(2,1)$ in each pass of the data, etc.

Empirical comparisons of estimates for the different passes and cases (Table 5.4.1 and Table 5.4.2) showed that they lead to the same results. For example, in the PBI data it was found that there are no differences in $\phi(1,1)$ among passes (Pr=0.55) or among cases (Pr=0.97). In practice, only the passes for case 1 were used to estimate $\phi(\mathbf{p},\mathbf{q})$ because programming was easier. The estimates of $\phi(\mathbf{p},\mathbf{q})$ are then weighted by their dfs to form a combined estimate.

If **p** or **q** is zero the method reduces to using pairblocking in one dimension, and there are only two passes of the data. Then, the method permits us to verify if it is possible to use the results of pairblocking in one dimension for **p=0** (varying **q**) and for **q=0** (varying **p**) to predict the semi-variances in two dimensions. This may be done through comparison between the observed values of semi-variances obtained in two dimensions and those predicted from one dimension.

Case 1

pass 1

1	2	3	4	5	6	7	8	9	
	1	2	3	4	5	6	7	8	9
10	11	12	13	14	15	16	17	18	
	10	11	12	13	14	15	16	17	18
19	20	21	22	23	24	25	26	27	
	19	20	21	22	23	24	25	26	27
28	29	30	31	32	33	34	35	36	
	28	29	30	31	32	33	34	35	36
37	38	39	40	41	42	43	44	45	
	37	38	39	40	41	42	43	44	45

pass 2

	1	2	3	4	5	6	7	8	9
1	2	3	4	5	6	7	8	9	
	10	11	12	13	14	15	16	17	18
10	11	12	13	14	15	16	17	18	
	19	20	21	22	23	24	25	26	27
19	20	21	22	23	24	25	26	27	
	28	29	30	31	32	33	34	35	36
28	29	30	31	32	33	34	35	36	
	37	38	39	40	41	42	43	44	45
37	38	39	40	41	42	43	44	45	

pass 3

1	2	3	4	5	6	7	8	9	
	1	2	3	4	5	6	7	8	9
10	11	12	13	14	15	16	17	18	
	10	11	12	13	14	15	16	17	18
19	20	21	22	23	24	25	26	27	
	19	20	21	22	23	24	25	26	27
28	29	30	31	32	33	34	35	36	
	28	29	30	31	32	33	34	35	36

pass 4

	1	2	3	4	5	6	7	8	9
1	2	3	4	5	6	7	8	9	
	10	11	12	13	14	15	16	17	18
10	11	12	13	14	15	16	17	18	
	19	20	21	22	23	24	25	26	27
19	20	21	22	23	24	25	26	27	
	28	29	30	31	32	33	34	35	36
28	29	30	31	32	33	34	35	36	

Case 2

pass 1

1	2	3	4	5	6	7	8	9	10
2	1	4	3	6	5	8	7	10	9
11	12	13	14	15	16	17	18	19	20
12	11	14	13	16	15	18	17	20	19
21	22	23	24	25	26	27	28	29	30
22	21	24	23	26	25	28	27	30	29
31	32	33	34	35	36	37	38	39	40
32	31	34	33	36	35	38	37	40	39
41	42	43	44	45	46	47	48	49	50
42	41	44	43	46	45	48	47	50	49

pass 2

	1	2	3	4	5	6	7	8	
	2	1	4	3	6	5	8	7	
	9	10	11	12	13	14	15	16	
	10	9	12	11	14	13	16	15	
	17	18	19	20	21	22	23	24	
	18	17	20	19	22	21	24	23	
	25	26	27	28	29	30	31	32	
	26	25	28	27	30	29	32	31	
	33	34	35	36	37	38	39	40	
	34	33	36	35	38	37	40	39	

pass 3

1	2	3	4	5	6	7	8	9	10
2	1	4	3	6	5	8	7	10	9
11	12	13	14	15	16	17	18	19	20
12	11	14	13	16	15	18	17	20	19
21	22	23	24	25	26	27	28	29	30
22	21	24	23	26	25	28	27	30	29
31	32	33	34	35	36	37	38	39	40
32	31	34	33	36	35	38	37	40	39

pass 4

	1	2	3	4	5	6	7	8	
	2	1	4	3	6	5	8	7	
	9	10	11	12	13	14	15	16	
	10	9	12	11	14	13	16	15	
	17	18	19	20	21	22	23	24	
	18	17	20	19	22	21	24	23	
	25	26	27	28	29	30	31	32	
	26	25	28	27	30	29	32	31	

Figure 5.4.1. Possible passes of the data array. One 10×10 superblock of a trial on 100 varieties for each pass and each case. The two plots in each block are 1 row and 1 column apart, to estimate $\phi(1,1)$. Plots identified with the same number make up a block.

Case 1

pass 1

1	2	3	4	5	6	7	8	9	
10	11	12	13	14	15	16	17	18	
	1	2	3	4	5	6	7	8	9
	10	11	12	13	14	15	16	17	18
19	20	21	22	23	24	25	26	27	
28	29	30	31	32	33	34	35	36	
	19	20	21	22	23	24	25	26	27
	28	29	30	31	32	33	34	35	36

pass 2

	1	2	3	4	5	6	7	8	9
	10	11	12	13	14	15	16	17	18
1	2	3	4	5	6	7	8	9	
10	11	12	13	14	15	16	17	18	
	19	20	21	22	23	24	25	26	27
	28	29	30	31	32	33	34	35	36
19	20	21	22	23	24	25	26	27	
28	29	30	31	32	33	34	35	36	

pass 3

1	2	3	4	5	6	7	8	9	
10	11	12	13	14	15	16	17	18	
	1	2	3	4	5	6	7	8	9
	10	11	12	13	14	15	16	17	18
19	20	21	22	23	24	25	26	27	
28	29	30	31	32	33	34	35	36	
	19	20	21	22	23	24	25	26	27
	28	29	30	31	32	33	34	35	36

pass 4

	1	2	3	4	5	6	7	8	9
	10	11	12	13	14	15	16	17	18
1	2	3	4	5	6	7	8	9	
10	11	12	13	14	15	16	17	18	
	19	20	21	22	23	24	25	26	27
	28	29	30	31	32	33	34	35	36
19	20	21	22	23	24	25	26	27	
28	29	30	31	32	33	34	35	36	

Case 2

pass 1

1	2	3	4	5	6	7	8	9	10
11	12	13	14	15	16	17	18	19	20
2	1	4	3	6	5	8	7	10	9
12	11	14	13	16	15	18	17	20	19
21	22	23	24	25	26	27	28	29	30
31	32	33	34	35	36	37	38	39	40
22	21	24	23	26	25	28	27	30	29
32	31	34	33	36	35	38	37	40	39

pass 2

	1	2	3	4	5	6	7	8	
	9	10	11	12	13	14	15	16	
	2	1	4	3	6	5	8	7	
	10	9	12	11	14	13	16	15	
	17	18	19	20	21	22	23	24	
	25	26	27	28	29	30	31	32	
	18	17	20	19	22	21	24	23	
	26	25	28	27	30	29	32	31	

pass 3

1	2	3	4	5	6	7	8	9	10
11	12	13	14	15	16	17	18	19	20
2	1	4	3	6	5	8	7	10	9
12	11	14	13	16	15	18	17	20	19
21	22	23	24	25	26	27	28	29	30
31	32	33	34	35	36	37	38	39	40
22	21	24	23	26	25	28	27	30	29
32	31	34	33	36	35	38	37	40	39

pass 4

	1	2	3	4	5	6	7	8	
	9	10	11	12	13	14	15	16	
	2	1	4	3	6	5	8	7	
	10	9	12	11	14	13	16	15	
	17	18	19	20	21	22	23	24	
	25	26	27	28	29	30	31	32	
	18	17	20	19	22	21	24	23	
	26	25	28	27	30	29	32	31	

Figure 5.4.2. Possible passes of the data array. One 10×10 superblock of a trial on 100 varieties for each pass and each case. The two plots in each block are 2 rows and 1 column apart, to estimate $\phi(2,1)$. Plots identified with the same number make up a block.

Table 5.4.1. Mean $(kg/plot)^2$ and standard error of $\phi(1,1)$ for each pass for the two cases (PBI data).

Passes	Case 1	Case 2
1	0.052 (± 0.0066)	0.051 (± 0.0051)
2	0.053 (± 0.0061)	0.051 (± 0.0060)
3	0.047 (± 0.0043)	0.048 (± 0.0043)
4	0.045 (± 0.0041)	0.046 (± 0.0053)
Mean	0.050 (± 0.0053)	0.049 (± 0.0050)

The standard errors should not be used for comparing individual estimates of semi-variances in the table, since the semi-variances are not independent.

Table 5.4.2. Means $(kg/plot)^2$ and standard errors of semi-variances, $\phi(p,q)$, for plots p rows and q columns apart averaged over all four passes for each case (PBI data).

Distance apart (p,q)	Case 1	Case 2
1,1	0.050 (± 0.0053)	0.049 (± 0.0050)
2,1	0.053 (± 0.0053)	0.055 (± 0.0054)
1,2	0.051 (± 0.0051)	0.051 (± 0.0052)
2,2	0.054 (± 0.0049)	0.054 (± 0.0048)

5.5. Exponential variance rule in two dimensions

Information about semi-variance $\phi(\mathbf{p},\mathbf{q})$ can be obtained directly by pairblocking or indirectly by postblocking in two dimensions. Once this information is available, the prime importance is to describe the relationship between the semi-variance $\phi(\mathbf{p},\mathbf{q})$ and the distances $\mathbf{p}$ and $\mathbf{q}$. Any error law which predicts similar semi-variances between two plots related to their distances apart will be appropriate. In one dimension, Patterson & Hunter (1983) used the exponential variance law.

In the one-dimensional exponential variance model, covariances between plots $\mathbf{x}$ apart are $\lambda\rho^{x}$, where λ and ρ are unknown parameters. For a separable (1,1) dimensional exponential process in two dimensions, the covariance between two plots $\mathbf{p}$ rows and $\mathbf{q}$ columns apart is $\lambda\rho_v^p\rho_h^q$ (Martin, 1990). The semi-variance of the difference between two plots $\mathbf{p}$ rows and $\mathbf{q}$ columns apart, $\phi(\mathbf{p},\mathbf{q})$, is then given as:

$$\phi(p,q)=\sigma^2(1-\lambda\rho_v^p\rho_h^q)\,. \qquad (5.5.1)$$

Although emerging from an empirical investigation, this two-dimensional exponential variance law has a simple theoretical interpretation. For example, if the error on any given plot is regarded as the sum of a component generated by a doubly-geometric process and a white noise error component, the parameters of this law could be interpreted as:

σ^2 the total variance per plot,

λ the proportion of the total variance attributable to the doubly-geometric component,

$\lambda\rho_v\rho_h$ the overall correlation between neighbouring plots in different rows and columns.

Martin (1979) describes the doubly-geometric process as a natural extension of the one-dimensional Markov process. Applications are found in image processing (Habibi, 1972), remotely-sensed data (Campbell, 1985) and in variety trial (Martin, 1990). Mardia (1980) suggested its use in geostatistics.

Substituting (5.5.1) in (5.2.2) and (5.2.3) the error means squares are derived as:

$$MS(r,c) = \sigma^2 \left[1 - \frac{2\lambda}{rc(rc-1)} A_{rc}(\rho_v,\rho_h)\right] \qquad (5.5.2)$$

where

$$A_{rc}(\rho_v,\rho_h) = cA_r(\rho_v) + rA_c(\rho_h) + 2A_r(\rho_v)A_c(\rho_h) ,$$

and

$$MS1(r,c) = \sigma^2 \left[1 - \frac{2\lambda}{rc(r-1)(c-1)} A1_{rc}(\rho_v,\rho_h)\right] \qquad (5.5.3)$$

where

$$A1_{rc}(\rho_v,\rho_h) = c(c-1)A_r(\rho_v) + r(r-1)A_c(\rho_h) - 2A_r(\rho_v)A_c(\rho_h).$$

$A_r(\rho_v)$ and $A_c(\rho_h)$ are defined as in (4.5.2).

The parameters ρ_v and ρ_h in the error model (5.5.1) determine the correlation between pairs of plots in the same column (vertical direction) and in the same row (horizontal direction) respectively. If the parameters ρ_v

and ρ_h and λ are known, the expression (5.5.2) can be used to predict the intra-block error mean square for blocks of dimension $(\mathbf{r},\mathbf{c})$. Similarly, the expression (5.5.3) can also be used to predict the intra-row and column error mean square. The next section describes a way to estimate these model parameters.

5.6. Fitting an exponential model to ϕ and to MS in two dimension

With the empirical mean squares obtained from the method in Section 5.3 or with the semi-variances obtained from the method in Section 5.4, the parameters of the error model σ^2, λ, ρ_v and ρ_h can be estimated using one of the relationships given in (5.5.1), (5.5.2) or (5.5.3).

The method of fitting regression equations that are linear in the parameters to be estimated or reducible to linear form is straightforward (see Draper & Smith, 1981). However, when, as here, the regression equations are nonlinear in the parameters to be estimated analysis is more difficult and iterative methods of estimation are usually required. Williams (1959, Chapter 4) presents suitable iterative methods together with approximate tests of significance for the parameter estimates.

Following Williams (1959) the general form of regression equation that is nonlinear in one parameter is

$$Y = b_0 + b_1 f(x,\upsilon),$$

where $\mathbf{f}(\mathbf{x},\upsilon)$ is some nonlinear function of υ.

If $\delta\upsilon$ is a preliminary adjustment of the initial

estimate υ_0 of υ, then to $\mathbf{o}(\delta\upsilon)$

$$f(x,\upsilon_0+\delta\upsilon) = f(x,\upsilon_0) + \delta\upsilon \left[\frac{\partial f(x,\upsilon)}{\partial\upsilon}\right]_{\upsilon=\upsilon_0}.$$

Thus in order to estimate the linear parameters $\mathbf{b}_0$, $\mathbf{b}_1$ of the regression equation, the first approximation

$$Y = b_0 + b_1 f(x,\upsilon_0) + b_2 \left[\frac{\partial f(x,\upsilon)}{\partial\upsilon}\right]_{\upsilon=\upsilon_0},$$

where $\mathbf{b}_2 = \mathbf{b}_1\delta\upsilon$, can be used.

Moreover, in a regression equation of the type

$$Y = b_0 + b_1 f(x,\upsilon)\ g(z,\vartheta),$$

where $\mathbf{f}(\mathbf{x},\upsilon)$ is some nonlinear function of υ and $\mathbf{g}(\mathbf{z},\vartheta)$ is some nonlinear function of ϑ, the first approximation is

$$Y = b_0 + b_1 f(x,\upsilon_0)\ g(z,\vartheta_0) + b_2 \left[\frac{\partial f(x,\upsilon)}{\partial\upsilon}\right]_{\upsilon=\upsilon_0} g(z,\vartheta_0) +$$

$$b_3 f(x,\upsilon_0) \left[\frac{\partial g(z,\vartheta)}{\partial\vartheta}\right]_{\vartheta=\vartheta_0}$$

where $\mathbf{b}_2 = \mathbf{b}_1\delta\upsilon$ and $\mathbf{b}_3 = \mathbf{b}_1\delta\vartheta$.

This principle is used in fitting an exponential model to ϕ and MS.

5.6.1. Fitting the exponential model to $\phi(p,q)$

Let us consider the nonlinear system

$$y_i(p,q) = \sigma^2(1-\lambda\rho_v^p\rho_h^q) + \varepsilon_i\ , \qquad (5.6.1)$$

$$\text{for } i = 1,2,\ldots,n,$$

where $\mathbf{y}_i(\mathbf{p},\mathbf{q})$ is the $\mathbf{i}^{th}$ semi-variance $\boldsymbol{\phi}(\mathbf{p},\mathbf{q})$ and the ε_i are assumed to be independent identically distributed (i.i.d.) variables.

The exponential equation can be rearranged and written as

$$y_i(p,q) = \sigma^2(1 - \lambda) + \sigma^2\lambda(1 - \rho_v^p\rho_h^q).$$

If it is defined that

$$a = \sigma^2(1 - \lambda),$$

$$b = \sigma^2\lambda,$$

$$f(p,\rho_v) = \rho_v^p ,$$

$$g(q,\rho_h) = \rho_h^q ,$$

and considering $\mathbf{v}$ as an estimate of ρ_v and $\mathbf{h}$ as an estimate of ρ_h, so that the values of $\mathbf{f}(\mathbf{p},\rho_v)=\mathbf{v}^p$ and $\mathbf{g}(\mathbf{q},\rho_h)=\mathbf{h}^q$ can be calculated, the exponential equation becomes, to a first approximation,

$$y_i(p,q) = a + b\left[1 - (v^ph^q + \delta v\ pv^{p-1}h^q + \delta h\ qv^ph^{q-1})\right]$$

$$= a + b(1 - v^ph^q) - b_1(pv^{p-1}h^q) - b_2(qv^ph^{q-1})$$

$$= a + b\,x_i + b_1x_{1i} + b_2x_{2i} ,$$

where

$$b_1 = b\,\delta v = b(\rho_v - v) ,$$

$$b_2 = b\,\delta h = b(\rho_h - h) ,$$

$$x_i = 1 - v^ph^q ,$$

$$x_{1i} = - p\ v^{p-1}h^{q} ,$$

$$x_{2i} = - q\ v^{p}h^{q-1}.$$

The equation is linear in the four parameters **a**, **b**, $\mathbf{b}_1$ and $\mathbf{b}_2$ and can therefore be fitted by ordinary least squares to obtain estimates $\hat{\mathbf{a}}$, $\hat{\mathbf{b}}$, $\hat{\mathbf{b}}_1$ and $\hat{\mathbf{b}}_2$.

In practice (5.6.1) can be fitted as

$$E\ [Y_i(p,q)] = A + b\ X_i + b_1 X_{1i} + b_2 X_{2i} ,$$

to give estimates of **A**, **b**, $\mathbf{b}_1$ and $\mathbf{b}_2$ and their covariance matrix **V**, where,

$$Y_i(p,q) = y_i(p,q) - \bar{y}$$

$$X_i = x_i - \bar{x}$$

$$X_{1i} = x_{1i} - \bar{x}_1$$

$$X_{2i} = x_{2i} - \bar{x}_2$$

$$A = a + b\ \bar{x} + b_1\bar{x}_1 + b_2\bar{x}_2 - \bar{y} .$$

Better estimates of ρ_v and ρ_h are

$$v_1 = \frac{\hat{b}_1}{\hat{b}} + v \text{ and } h_1 = \frac{\hat{b}_2}{\hat{b}} + h$$

respectively, and $\mathbf{v}_1$ replaces **v** and $\mathbf{h}_1$ replaces **h** and the procedure is repeated until convergence. This is taken to be when the ratio $\frac{\hat{\mathbf{b}}_1}{\hat{\mathbf{b}}} < 10^{-5}$ and $\frac{\hat{\mathbf{b}}_2}{\hat{\mathbf{b}}} < 10^{-5}$.

At each stage, revised estimates of the original

parameters are

$$\hat{\sigma}^2 = \hat{A} + \bar{y} + \hat{b}(1 - \bar{x}) - \hat{b}_1\bar{x}_1 - \hat{b}_2\bar{x}_2 ,$$

$$\hat{\lambda} = \frac{\hat{b}}{\hat{A} + \bar{y} + \hat{b}(1 - \bar{x}) - \hat{b}_1\bar{x}_1 - \hat{b}_2\bar{x}_2} ,$$

$$\hat{\rho}_v = \frac{\hat{b}_1}{\hat{b}} + v \text{ and } \hat{\rho}_h = \frac{\hat{b}_2}{\hat{b}} + h.$$

The approximate estimates of their variances and covariances are $\mathbf{V1} = \mathbf{J}\ \mathbf{V}\ \mathbf{J}^T$ where $\mathbf{J}$ is the Jacobian matrix of the transformation, that is

$$J = \begin{bmatrix} \frac{\partial\sigma^2}{\partial A} & \frac{\partial\sigma^2}{\partial b} & \frac{\partial\sigma^2}{\partial b_1} & \frac{\partial\sigma^2}{\partial b_2} \\ \frac{\partial\lambda}{\partial A} & \frac{\partial\lambda}{\partial b} & \frac{\partial\lambda}{\partial b_1} & \frac{\partial\lambda}{\partial b_2} \\ \frac{\partial\rho_v}{\partial A} & \frac{\partial\rho_v}{\partial b} & \frac{\partial\rho_v}{\partial b_1} & \frac{\partial\rho_v}{\partial b_2} \\ \frac{\partial\rho_h}{\partial A} & \frac{\partial\rho_h}{\partial b} & \frac{\partial\rho_h}{\partial b_1} & \frac{\partial\rho_h}{\partial b_2} \end{bmatrix}.$$

5.6.2. Fitting the exponential model to MS(r,c)

Consider the nonlinear system

$$y_i(r,c) = \sigma^2 \left[1 - \frac{2\ \lambda}{rc(rc - 1)} A_{rc}(\rho_v, \rho_h)\right] + \varepsilon_i , \quad (5.6.2)$$

$$\text{for } i = 1,2,\ldots,n,$$

where $\mathbf{y}_i(\mathbf{r},\mathbf{c})$ is the $\mathbf{i}^{th}$ error mean square for block of $(\mathbf{r},\mathbf{c})$ and the ε_i are assumed to be i.i.d. $\mathbf{A}_{rc}(\rho_v,\rho_h)$ is

given as in (5.5.2). Employing the principle of first approximation as in Section 5.6.1, the exponential equation becomes

$$y_i(r,c) = \sigma^2(1-\lambda) + \sigma^2\lambda\Big\{1 - \frac{2}{rc(rc-1)}\Big[\sum_{p=1}^{r-1} c(r-p)\,(v^p + \delta v\; p\; v^{p-1}) + \sum_{q=1}^{c-1} r(c-q)\,(h^q + \delta h\; q\; h^{q-1}) + \sum_{p=1}^{r-1}\sum_{q=1}^{c-1} 2(r-p)(c-q)\,(v^p h^q + \delta v\; p v^{p-1} h^q + \delta h\; q v^p h^{q-1})\Big]\Big\}$$

$$= a + b\left[1 - \frac{2}{rc(rc-1)}\,A_{rc}(v,h)\right] - b_1\,\frac{2}{rc(rc-1)}\left[cA_{r-1}(v) + 2A_{r-1}(v)A_c(h)\right] - b_2\,\frac{2}{rc(rc-1)}\left[rA_{c-1}(h) + 2A_r(v)A_{c-1}(h)\right]$$

$$= a + b\,x_i + b_1 x_{1i} + b_2 x_{2i}\,,$$

where

$$a = \sigma^2(1-\lambda)\,, \qquad b = \sigma^2\lambda\,,$$

$$b_1 = b\,\delta v = b(\rho_v - v)\,, \qquad b_2 = b\,\delta h = b(\rho_h - h)\,,$$

$$x_i = 1 - \frac{2}{rc(rc-1)}\,A_{rc}(v,h)\,,$$

$$x_{1i} = -\frac{2}{rc(rc-1)}\left[cA_{r-1}(v) + 2A_{r-1}(v)A_c(h)\right]$$

and

$$x_{2i} = -\frac{2}{rc(rc-1)}\left[rA_{c-1}(h) + 2A_r(v)A_{c-1}(h)\right],$$

with

$$A_{r-1}(v) = \sum_{p=1}^{r-1} (r-p)\,p\; v^{p-1} \quad \text{and} \quad A_{c-1}(h) = \sum_{q=1}^{c-1} (c-q)\,q\; h^{q-1}.$$

$A_{rc}(v,h)$, $A_r(v)$ and $A_c(h)$ follow from (5.5.2).

The equation is linear in the four parameters **a**, **b**, $\mathbf{b}_1$ and $\mathbf{b}_2$ and so can be fitted by ordinary least squares to obtain estimates $\hat{\mathbf{a}}$, $\hat{\mathbf{b}}$, $\hat{\mathbf{b}}_1$ and $\hat{\mathbf{b}}_2$.

Henceforth the procedure is the same as in Section 5.6.1.

To accommodate **MS1(r,c)** together with **MS(r,c)**, changes are made in the variables $\mathbf{x}_i$, $\mathbf{x}_{1i}$, and $\mathbf{x}_{2i}$.

5.6.3. Fitting models with correlated errors

Autocorrelation in error terms ε frequently occurs with data which are taken serially in time or space.

If the errors in (5.6.1) or (5.6.2) are not independent an additional problem of fitting correlated error emerges. A discussion about models with autocorrelated errors can be found, for example in Wetherill (1986, Chapter 13).

A regression technique to fit an integrated moving average error term to some economic time series data was used by Box & Newbold (1971). The model was adapted by Patterson & Hunter (1983) to fit an autoregressive error term (see Ainsley, 1985).

Consider the system

$$y_t = f(t,\boldsymbol{\theta}) + \varepsilon_t \qquad (5.6.3)$$

with

$$\varepsilon_t = \sum_{i=1}^{m} \alpha_i \varepsilon_{t-i} + \eta_t \qquad (5.6.4)$$

$$\text{for } t = 1,2,\ldots,n,$$

where $\mathbf{f(t,\theta)}$ is the function of the $\mathbf{s}$ dimensional parameter vector $\boldsymbol{\theta}$, the errors ε_t follow a $\mathbf{m}^{th}$ order autoregressive process and the η_t are independent and identically distributed. The function may be fitted iteratively as follows.

Let $\underline{\alpha}^0$ to be an initial estimate of $\underline{\alpha}=(\alpha_1,\alpha_2,\ldots,\alpha_m)^T$. Then, after substituting the augmented error structure and differencing (5.6.3)

$$y_t - \sum_{i=1}^{m} \alpha_i^0 \, y_{t-i} = f(t,\theta) - \sum_{i=1}^{m} \alpha_i^0 \, f(t-i,\theta) + \eta_t$$

or

$$Y_t = F(t,t-1,\ldots,t-m;\theta) + \eta_t \qquad (5.6.5)$$

where,

$$Y_t = y_t - \sum_{i=1}^{m} \alpha_i^0 \, y_{t-i}$$

and

$$F(t,t-1,\ldots,t-m;\theta) = f(t,\theta) - \sum_{i=1}^{m} \alpha_i^0 \, f(t-i,\theta).$$

Now the equation may be fitted by ordinary least square to give an estimate $\hat{\boldsymbol{\theta}}^1$ of $\boldsymbol{\theta}$, since the errors η_t in (5.6.5) are i.i.d. If $\mathbf{f(t,\theta)}$ is a nonlinear function, the fitting is itself an iterative procedure.

Estimates of residuals

$$\hat{\varepsilon}_t = y_t - f(t, \hat{\theta}^1),$$

are now obtained from (5.6.3) and a new estimate of α is calculated by fitting the regression (5.6.4).

Suppose that the new estimate is $\underline{\alpha}^1 = \underline{\alpha}^0 + \underline{\omega}$, where $\underline{\omega} = (\omega_1, \omega_2, \ldots, \omega_m)^T$. Then fitting

$$\hat{\varepsilon}_t = \sum_{i=1}^{m} \alpha_i^1 \hat{\varepsilon}_{t-i} + \eta_t,$$

as

$$\hat{\varepsilon}_t - \sum_{i=1}^{m} \alpha_i^0 \hat{\varepsilon}_{t-i} = \sum_{i=1}^{m} \omega_i \hat{\varepsilon}_{t-i} + \eta_t$$

estimates of ω_i are found by regression of

$$\hat{\varepsilon}_t - \sum_{i=1}^{m} \alpha_i^0 \hat{\varepsilon}_{t-i} \text{ on } \hat{\varepsilon}_{t-1}, \hat{\varepsilon}_{t-2}, \ldots, \hat{\varepsilon}_{t-m}.$$

The revised estimate of α is then $\hat{\underline{\alpha}}^1 = \hat{\underline{\alpha}}^0 + \hat{\underline{\omega}}$ which replaces $\underline{\alpha}^0$ in (5.6.5), and the process continues until convergence.

According to Barnard, Jenkins & Winsten (1962) the estimates given by this procedure approximate to the maximum likelihood estimates for θ.

Chapter 6

PARAMETER ESTIMATES OF THE TWO-DIMENSIONAL EXPONENTIAL VARIANCE MODEL

6.1. Introduction

This chapter presents the results of applying postblocking and pairblocking to the SCRI and PBI data sets described in Section 3.2.

Postblocking and pairblocking analysis were carried out as described in the previous chapter using SAS GLM routines (SAS Institute, 1985; Freund & Littell, 1981).

The exponential equation,

$$\phi(p,q)=\sigma^2(1-\lambda\rho_v^p\rho_h^q),$$

was fitted with and without an autoregressive (AR) error term included by the method given in Section 5.6. The following criteria - the significance of the Durbin-Watson (DW) statistic for autocorrelation in residuals (Durbin & Watson, 1951; Savin & White, 1977), the significance of the AR terms (maximum second-order), the best fitting and the simplicity of the analysis - were considered in choosing the order of the autoregressive process. The program used was based on a BASIC procedure written by Professor H. D. Patterson of the Department of Mathematics and Statistics, Edinburgh University, who has kindly permitted me to use and modify it.

Average results over all trials are examined for 60

spring barley trials from SCRI (Section 6.2) and for 44 spring barley trials from PBI (Section 6.3).

The results for these two trial series are compared in Section 6.4.

6.2. SCRI error structure

All 60 trials comprised two replicates of 100 varieties arranged in a 10×10 array.

Because of the restricted replication, pairblocking could not be employed as there were insufficient degrees of freedom for the error mean square to estimate $\phi(\mathbf{p},\mathbf{q})$. However, postblocking was possible except for block of size 2. The artificial blocks were not allowed to cross superblock boundaries since the two replicates were not adjacent in the field.

6.2.1. Exponential variance model via postblocking

Average mean squares, $\mathbf{MS}(\mathbf{r},\mathbf{c})$, for artificial block dimensions (1,5), (1,10), (2,2), (2,5), (2,10), (5,1), (5,2), (5,5), (5,10), (10,1), (10,2), (10,5) and (10,10), and $\mathbf{MS1}(\mathbf{r},\mathbf{c})$ for block dimensions (5,5), (5,10), (10,5) and (10,10), calculated by the method of Section 5.3 are given in the second column of Table 6.2.1.

The exponential variance (EV) model was first fitted to $\mathbf{MS}(\mathbf{r},\mathbf{c})$ values using expression (5.5.2) and gave the estimated function

$$\phi(p,q) = 0.064\ [1 - 0.654\ (0.776)^{p}\ (0.935)^{q}]. \qquad (6.2.1)$$

Table 6.2.1. Actual and expected error mean squares in 60 trials $(t/ha)^2$ - SCRI data.

	Block size (r,c)	Actual mean square	Expected mean square (5.5.2) and (5.5.3) with $\phi(p,q)$ equations (6.2.1)	(6.2.2)
	1, 5	0.027	0.027	0.026
	1,10	0.030	0.031	0.030
	2, 2	0.031	0.030	0.028
	2, 5	0.033	0.031	0.030
	2,10	0.035	0.034	0.034
	5, 1	0.036	0.038	0.037
MS+,	5, 2	0.039	0.037	0.036
	5, 5	0.039	0.038	0.038
	5,10	0.041	0.041	0.041
	10, 1	0.043	0.045	0.045
	10, 2	0.046	0.045	0.045
	10, 5	0.046	0.045	0.046
	10,10	0.047	0.047	0.048
	5, 5	0.020	(0.024)"	0.022
MS1′	5,10	0.021	(0.025)	0.023
	10, 5	0.021	(0.025)	0.023
	10,10	0.023	(0.027)	0.025

+ used to estimate parameters in equation (6.2.1)

′ used to estimate parameters in equation (6.2.2)

" predicted values

An alternative semi-variance function

$$\phi(p,q) = 0.070\ [1 - 0.724\ (0.796)^{p}\ (0.934)^{q}] \qquad (6.2.2)$$

was also estimated from simultaneous fitting to **MS(r,c)** and **MS1(r,c)** values using expressions (5.5.2) and (5.5.3).

The parameter estimates and standard errors (Table 6.2.2) were calculated by the method given in Sections 5.6.2 and 5.6.3 using a first-order AR error term. The DW test indicated that higher order autoregressive terms were not required.

Fitted values of the mean squares according expressions (5.5.2) and (5.5.3) with $\phi(\mathbf{p},\mathbf{q})$ given by equation (6.2.1) are in column 3 of Table 6.2.1. Fitted mean squares with $\phi(\mathbf{p},\mathbf{q})$ given by equation (6.2.2) are in column 4.

Examination of Table 6.2.1 shows that the exponential variance law gives a reasonably good fit to the data. A further examination for those blocks actually laid out on the field, highlighted in Table 6.2.3, also confirms this.

The equations (6.2.1) and (6.2.2) are comparable. The parameters and standard errors in Table 6.2.2 and the fitted values in Table 6.2.1 using these parameter estimates are similar.

The largest difference between the two sets of parameters is in the estimated values of λ. However the difference between these estimates is still small and has little effect on the fitted values which are the real quantities of interest (Tables 6.2.1 and 6.2.3).

A detailed examination of Tables 6.2.1 and 6.2.3 shows that it is worthwhile using **MS1(r,c)** values together with

Table 6.2.2. Parameter estimates and standard errors of the EV model via postblocking - SCRI data.

Parameters	Estimates (± se) from MS(r,c) with AR(1) error term	Estimates (± se) from MS(r,c) and MS1(r,c) with AR(1) error term
σ^2	0.064 (± 0.009)	0.070 (± 0.015)
λ	0.654 (± 0.034)	0.724 (± 0.036)
ρ_v	0.776 (± 0.084)	0.796 (± 0.103)
ρ_h	0.935 (± 0.032)	0.934 (± 0.034)
DW^+	2.088 ns	1.945 ns

+ Durbin-Watson statistic

ns - not significant at 5%

Table 6.2.3. Actual error mean squares with the standard error of mean, and predicted ones for block dimensions actually used in designing the trial $(t/ha)^2$ - SCRI data.

Design	Array	Actual mean square	Predicted mean square from expressions (5.5.2) and (5.5.3)† with $\phi(p,q)$ equations (6.2.1)	(6.2.2)
RCB	10×10	0.048 (± 0.005)	0.047	0.048
IB	1×10	0.030 (± 0.003)	0.031	0.030
IB	10×01	0.043 (± 0.005)	0.045	0.045
RC	10×10	0.023 (± 0.003)	0.027†	0.025†

MS(r,c) values in the fitting procedure whenever possible. As a result the exponential variance rule with the semi-variances given by equation (6.2.2) is considered for this data set.

6.3. PBI error structure

Although there are fewer trials and varieties in the PBI series than the SCRI series, each PBI trial has 4 replicates. Each replicate forms a superblock of 49 varieties in a 7×7 array, and the superblocks are arranged in a 2×2 array. This means that both postblocking and pairblocking can be used to derive the exponential variance model. As there were no differences in the management of superblocks, postblocking and pairblocking were applied allowing the imposed blocks to cross superblocks boundaries.

6.3.1. Exponential variance model via postblocking

Values of **MS(r,c)** for block dimensions (1,2), (1,7), (1,14), (2,1), (2,2), (2,7), (2,14), (7,1), (7,2), (7,7), (7,14), (14,1), (14,2), (14,7) and (14,14), and values of **MS1(r,c)** for block dimensions (2,7), (2,14), (7,2), (7,7), (7,14), (14,2), (14,7) and (14,14), calculated as described in Section 5.3 are given in the second column of Table 6.3.1.

The EV model was first fitted to **MS(r,c)** values using expression (5.5.2) and gave the estimated function

Table 6.3.1. Actual and expected error mean squares in 44 trials $(kg/plot)^2$ - PBI data.

	Block size (r,c)	Actual mean square	Expected mean square (5.5.2) and (5.5.3) with $\phi(p,q)$ equations (6.3.1)	(6.3.2)
	1, 2	0.041	0.041	0.039
	1, 7	0.045	0.047	0.045
	1,14	0.052	0.052	0.051
	2, 1	0.046	0.046	0.043
	2, 2	0.046	0.045	0.043
	2, 7	0.049	0.050	0.048
	2,14	0.054	0.054	0.053
MS^{+},	7, 1	0.053	0.054	0.053
	7, 2	0.054	0.054	0.053
	7, 7	0.056	0.056	0.056
	7,14	0.060	0.059	0.059
	14, 1	0.057	0.059	0.059
	14, 2	0.058	0.059	0.059
	14, 7	0.060	0.061	0.061
	14,14	0.063	0.062	0.063
	2, 7	0.035	(0.040)"	0.037
	2,14	0.041	(0.041)	0.038
	7, 2	0.035	(0.039)	0.036
MS1'	7, 7	0.038	(0.042)	0.039
	7,14	0.042	(0.045)	0.042
	14, 2	0.037	(0.040)	0.037
	14, 7	0.039	(0.044)	0.041
	14,14	0.045	(0.048)	0.045

+ used to estimate parameters in equation (6.3.1)

' used to estimate parameters in equation (6.3.2)

" predicted values

$$\phi(p,q) = 0.068\ [1 - 0.456\ (0.716)^{p}\ (0.856)^{q}]. \quad (6.3.1)$$

Alternatively, the EV model was also fitted to simultaneous **MS(r,c)** and **MS1(r,c)** values using expressions (5.5.2) and (5.5.3) and gave the estimated semi-variance function

$$\phi(p,q) = 0.070\ [1 - 0.519\ (0.731)^{p}\ (0.866)^{q}]. \quad (6.3.2)$$

Table 6.3.2 shows the parameter estimates with the standard errors. They were calculated as described in Sections 5.6.2 and 5.6.3. No autocorrelation in error terms was detected in fitting equation (6.3.1), but a first-order AR error term was included for equation (6.3.2).

Values of fitted mean squares according to expressions (5.5.2) and (5.5.3) with $\phi(\mathbf{p},\mathbf{q})$ given by equations (6.3.1) and (6.3.2) are presented in column 3 and 4 of Table 6.3.1 respectively. In addition mean squares for those block dimensions used in the trial design are in Table 6.3.3.

These results (Tables 6.3.1 and 6.3.3) show that the EV model fits reasonably well to the data.

The fitted values (Table 6.3.1) and the parameter estimates with standard error (Table 6.3.2) according to equations (6.3.1) and (6.3.2) are very close to each other.

As with the SCRI trials, the greatest difference between the two sets of parameters is in the $\hat{\lambda}$ values. Again the difference between these estimates is small and has little effect on the fitted values which are the real

Table 6.3.2. Parameter estimates and standard errors of the EV model via postblocking - PBI data.

Parameters	Estimates (± se) from MS(r,c) with i.i.d. error term	Estimates (± se) from MS(r,c) and MS1(r,c) with AR(1) error term
σ^2	0.068 (± 0.002)	0.070 (± 0.003)
λ	0.456 (± 0.017)	0.519 (± 0.019)
ρ_v	0.716 (± 0.054)	0.731 (± 0.052)
ρ_h	0.856 (± 0.030)	0.866 (± 0.026)
DW$^+$	2.131 ns	2.184 ns

+ Durbin-Watson statistic

ns - not significant at 5%

Table 6.3.3. Actual error mean squares with the standard error of mean, and predicted ones for block dimensions actually used in designing the trial $(kg/plot)^2$- PBI data.

Design	Array	Actual mean square	Predicted mean square from expressions (5.5.2) and (5.5.3)† with $\phi(p,q)$ equations (6.3.1)	(6.3.2)
RCB	7×7	0.056 (± 0.005)	0.056	0.056
IB	1×7	0.045 (± 0.005)	0.047	0.045
IB	7×1	0.053 (± 0.006)	0.054	0.053
RC	7×7	0.038 (± 0.005)	0.042†	0.039†

quantities of interest. However, the additional use of **MS1(r,c)** values together with **MS(r,c)** values seems to be worthwhile in the fitting procedure, whenever possible. In fact the EV rule with $\phi(\mathbf{p},\mathbf{q})$ given by equation (6.3.2) should be considered.

6.3.2. Exponential variance model via pairblocking

Values of $\phi(\mathbf{p},\mathbf{q})$ were directly calculated as described in Section 5.4. These $\phi(\mathbf{p},\mathbf{q})$ for plots within the same row (0,1), (0,2), ..., (0,10), for plots within the same column (1,0), (2,0), ..., (10,0) and for all **(p,q)** for **p**=1...4, **q**=1...4. are given in Table 6.3.4.

The EV model was first fitted to those $\phi(\mathbf{p},\mathbf{q})$ for which either **p** or **q** are zero. The estimated equation was

$$\phi(p,q) = 0.067\ [1 - 0.486\ (0.719)^{p}\ (0.820)^{q}]. \qquad (6.3.3)$$

When fitted to *all* derived values of $\phi(\mathbf{p},\mathbf{q})$, the estimated equation was

$$\phi(p,q) = 0.068\ [1 - 0.490\ (0.727)^{p}\ (0.822)^{q}]. \qquad (6.3.4)$$

These equations were fitted using the method described in Sections 5.6.1 and 5.6.3. An i.i.d. error term was assumed as an AR error term did not produce any significant change in the results. The standard errors of parameter estimates are given in Table 6.3.5.

Examination of fitted values of $\phi(\mathbf{p},\mathbf{q})$ (Table 6.3.4) and the predicted error mean squares for those block dimensions used in the original design (Table 6.3.6)

Table 6.3.4. Actual and expected semi-variances, $\phi(p,q)$, in 44 trials $(kg/plot)^2$ - PBI data.

	Component plot (p,q)	Actual semi-variance	Expected semi-variance from equations (6.3.3)	(6.3.4)
	0, 1	0.040	0.040	0.041
	0, 2	0.045	0.045	0.045
	0, 3	0.049	0.049	0.049
	0, 4	0.050	0.052	0.053
	0, 5	0.057	0.055	0.055
	0, 6	0.057	0.057	0.058
	0, 7	0.061	0.059	0.060
	0, 8	0.061	0.060	0.061
	0, 9	0.064	0.062	0.062
p=0 or +′	0,10	0.063	0.063	0.063
q=0	1, 0	0.044	0.044	0.044
	2, 0	0.053	0.050	0.050
	3, 0	0.056	0.055	0.055
	4, 0	0.058	0.058	0.059
	5, 0	0.062	0.061	0.061
	6, 0	0.060	0.063	0.063
	7, 0	0.064	0.064	0.064
	8, 0	0.064	0.065	0.065
	9, 0	0.062	0.065	0.066
	10, 0	0.071	0.066	0.067
	1, 1	0.050	(0.048)"	0.048
	2, 1	0.053	(0.053)	0.054
	3, 1	0.058	(0.057)	0.057
	4, 1	0.062	(0.060)	0.060
	1, 2	0.051	(0.051)	0.052
	2, 2	0.054	(0.056)	0.056
	3, 2	0.059	(0.059)	0.059
p≠0 and′	4, 2	0.060	(0.061)	0.062
q≠0	1, 3	0.056	(0.054)	0.055
	2, 3	0.057	(0.058)	0.058
	3, 3	0.062	(0.060)	0.061
	4, 3	0.064	(0.062)	0.063
	1, 4	0.059	(0.056)	0.057
	2, 4	0.062	(0.059)	0.060
	3, 4	0.063	(0.062)	0.062
	4, 4	0.067	(0.063)	0.064

+ used in fitting equation (6.3.3)

′ used in fitting equation (6.3.4)

" predicted values

Table 6.3.5. Parameter estimates and standard errors of the EV model from pairblocking - PBI data.

Parameters	Estimates (± se) from $\phi(0,q)$ and $\phi(p,0)$ with an i.i.d. error term	Estimates (± se) from all $\phi(p,q)$ with an i.i.d. error term
σ^2	0.067 (± 0.002)	0.068 (± 0.002)
λ	0.486 (± 0.031)	0.490 (± 0.025)
ρ_v	0.719 (± 0.051)	0.727 (± 0.037)
ρ_h	0.820 (± 0.031)	0.822 (± 0.024)
DW$^+$	2.043 ns	1.789 ns

+ Durbin-Watson statistic

ns - not significant at 5%

Table 6.3.6. Actual error mean squares with the standard error of mean, and predicted mean squares for block dimensions used in trial design $(kg/plot)^2$ - PBI data.

Design	Array	Actual mean square	Predicted mean square from expressions (5.5.2) and (5.5.3)† with $\phi(p,q)$ equations (6.3.3)	(6.3.4)
RCB	7×7	0.056 (± 0.005)	0.056	0.056
IB	1×7	0.045 (± 0.005)	0.047	0.047
IB	7×1	0.053 (± 0.006)	0.052	0.052
RC	7×7	0.038 (± 0.005)	0.041†	0.041†

reveal that a good fit can be obtained using the EV rule.

If **p** or **q** is zero, pairblocking in two dimensions becomes pairblocking in one dimension. Results of pairblocking in one dimension (equation 6.3.3) may be used to predict the semi-variances in two dimensions.

Comparisons between observed $\phi(\mathbf{p},\mathbf{q})$ for **p** and **q** different from zero and those predicted from equation (6.3.3) are presented in Table 6.3.7. These results suggest that:

i) covariances between plots **p** rows and **q** columns apart are well approximated by $\lambda\rho_v^p\rho_h^q$, i.e. errors can be described by separable exponential processes;

ii) for this model the semi-variances in two dimensions can be predicted from those observed in one dimension.

Further evidence is given by comparing the parameters of equation (6.3.4) fitted to all values of $\phi(\mathbf{p},\mathbf{q})$, with those of equation (6.3.3).

For practical purposes there is no difference between the two sets of parameter estimates (Table 6.3.5), and the difference in their standard errors may be due to the difference in the number of observations used in the fitting procedure. It is recommended therefore that for pairblocking in two dimensions only pairs of plots in the same row or column (**p** or **q** equal to zero) need be considered. The relevant EV model is given by equation (6.3.3).

Table 6.3.7. Actual mean $(kg/plot)^2$ and standard errors of semi-variances $\phi(p,q)$, together with predicted values from equation (6.3.3) and the probability of difference between observed and predicted - PBI data.

		observed ± standard error			
		predicted prob > |T|			
p \ q	1	2		3	4
1	0.050 ±0.005	0.051 ±0.005	0.056 ±0.006	0.059 ±0.006	
	0.048 0.733	0.051 0.990	0.054 0.786	0.056 0.682	
2	0.053 ±0.005	0.054 ±0.005	0.057 ±0.006	0.062 ±0.006	
	0.053 0.967	0.056 0.725	0.058 0.921	0.059 0.698	
3	0.058 ±0.005	0.059 ±0.006	0.062 ±0.005	0.063 ±0.005	
	0.057 0.895	0.059 0.967	0.060 0.706	0.062 0.743	
4	0.062 ±0.006	0.060 ±0.006	0.064 ±0.007	0.067 ±0.005	
	0.060 0.729	0.061 0.777	0.062 0.757	0.063 0.445	

6.3.3. Comparison of postblocking and pairblocking in investigation of PBI trials error structure

The PBI trials error structure was investigated by two different methods, both of which give information about semi-variances, $\phi(\mathbf{p},\mathbf{q})$. In the absence of error the two methods are theoretically equivalent, but give different results when applied to trials data.

In postblocking the information about $\phi(\mathbf{p},\mathbf{q})$ is derived indirectly from the error mean square obtained from the trial analysis using different block dimensions. For pairblocking this information is obtained directly from empirical values of $\phi(\mathbf{p},\mathbf{q})$.

The parameters of the EV model via the error mean squares (Table 6.3.2) and via direct values of $\phi(\mathbf{p},\mathbf{q})$ (Table 6.3.5) suggest that the two approaches can be considered equivalent. The methods provide the same type of information about $\phi(\mathbf{p},\mathbf{q})$ although there are small differences among the sets of parameter estimates. To assess significance of these differences, a test for independent regression given in Steel & Torrie (1980, Chapter 10.8) was applied. This gave no evidence that the sets of parameters were different. Additional confirmation comes from comparing the predicted error mean squares in Tables 6.3.3 and 6.3.6.

The numerical differences between the two sets of results may be explained by the fact that

i) different weightings of observations were implicitly used in fitting the EV model directly to values of $\phi(\mathbf{p},\mathbf{q})$ and indirectly to error mean

squares;

ii) the error mean squares incorporate information about $\phi(\mathbf{p},\mathbf{q})$ for values of **p** and **q** up to 13, while direct values of $\phi(\mathbf{p},\mathbf{q})$ were only obtained for values of **p** and **q** up to 10.

Direct values of $\phi(\mathbf{p},\mathbf{q})$ for values of **p** and/or **q** over 10 could not be obtained or were very inaccurate due to the very high degree of imbalance in the data. However these further points provide additional information about the parameters values over a wider range of **p** and **q** which is used in postblocking. This seems to be an advantage of estimating $\phi(\mathbf{p},\mathbf{q})$ via error mean squares. EMS are also more highly correlated than $\phi(\mathbf{p},\mathbf{q})$ so observed curve seems better behaved.

In general, if the main purpose is to investigate whether an alternative blocking system would have been better than the one actually used, postblocking is the more appropriate method. But, if the objective is to derive underlying error law, pairblocking is the simpler and more natural approach when more than two replicates are available. The empirical semi-variances plot is also more directly interpretable than the corresponding empirical error mean squares plots.

6.4. Comparison of error laws for different trial series

The discussion in this section relates to the postblocking method employed for all series of trials.

The error structure of the SCRI and PBI series of

trials is well described by the exponential variance error law. Error models that can be considered a particular case of the two-dimensional EV model are well known, see for example Herzberg (1978), Martin (1979, 1990) and Zimmerman & Harville (1991).

The parameters for the EV model fitted via error mean squares given in equation (6.2.2) for SCRI trials and equation (6.3.2) for PBI trials are considered. They are given in Table 6.4.1. For comparison the results of Patterson & Hunter (1983) for the EV model in one dimension are also included.

Regarding the component along rows (horizontal) the estimates of the parameters σ^2, λ and ρ_h for SCRI trials may be compared with those of Patterson & Hunter's results (Table 6.4.1).

The parameter estimates are very similar with the exception of the estimated values of σ^2. The difference in these values of $\hat{\sigma}^2$ may be explained by the difference in plot size between the two data sets, the amalgamation of crops (mainly spring barley and winter wheat) in Patterson & Hunter's work and the difference in environmental condition between both trial sets. Small plots are likely to be less variable, which is the case in the SCRI trial series. It is also known that spring barley and winter wheat crops respond differently to changing growth conditions; spring barley tends to be less variable than winter wheat (Talbot, 1984).

The PBI yields were measured on different scale and care should be taken in the comparison with the other

Table 6.4.1. Exponential variance error law for three series of cereal variety trials.

Source	Plot length × width	Parameter estimates σ^2	λ	ρ_v	ρ_h
SCRI	2-5 × 0.6-1.2	0.070	0.724	0.796	0.934
PBI	4 × 1.5	0.070	0.519	0.731	0.866
PH†	20-25 × 2.0	0.209	0.725	-	0.942

† 1-D EV model of Patterson & Hunter (1983)

trial series. σ^2 depends on scale of measurement. If a particular yield was measured in kg and follow an EV law the effect of measuring it in tonnes would be to decrease the value of σ^2 by the factor of 10^6 leaving λ and ρ's unchanged. The effect of decreasing σ^2 alone is to decrease the range of the $\phi(\mathbf{p},\mathbf{q})$ curve; the curve becomes flatter. Curves for fitted equations (6.2.2) and (6.3.2) are presented in Figures 6.4.1 and 6.4.2.

The PBI EV model shows apparent differences when compared with the SCRI and Patterson & Hunter EV models (Table 6.4.1). These differences among EV laws are generally attributed to crop and/or plot size and others components as differences in trial sizes and distribution of the trials over the years and sites.

Reduction in plot size seems likely to decrease λ and ρ's (Patterson & Hunter, 1983). The SCRI trials have a much smaller plot size than those trials used by Patterson & Hunter (1983). However the reduction in λ and ρ_h values are too small to be attributed to the difference in plot size. On the other hand PBI and SCRI trials involve the same crop and the plots are about the same size and yet the reduction in λ and ρ's for PBI EV law are much more noticeable. Thus either the distribution of trials over the years and sites or the effect of trial size or possibly the effect of both could have produced these differences in the results. Robinson *et al.* (1988), in an investigation of two-dimensional yield variability, identified years, sites and plot sizes plus some interactions of these terms as the only factors

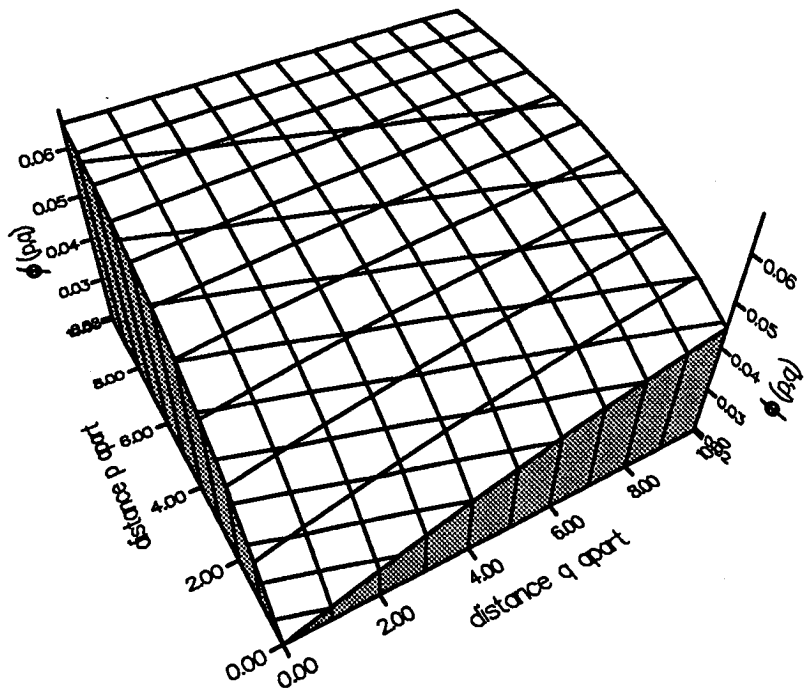


Figure 6.4.1. Fitted curve of semi-variances, $\phi(p,q)$, from equation (6.2.2) for SCRI trials $(t/ha)^2$.

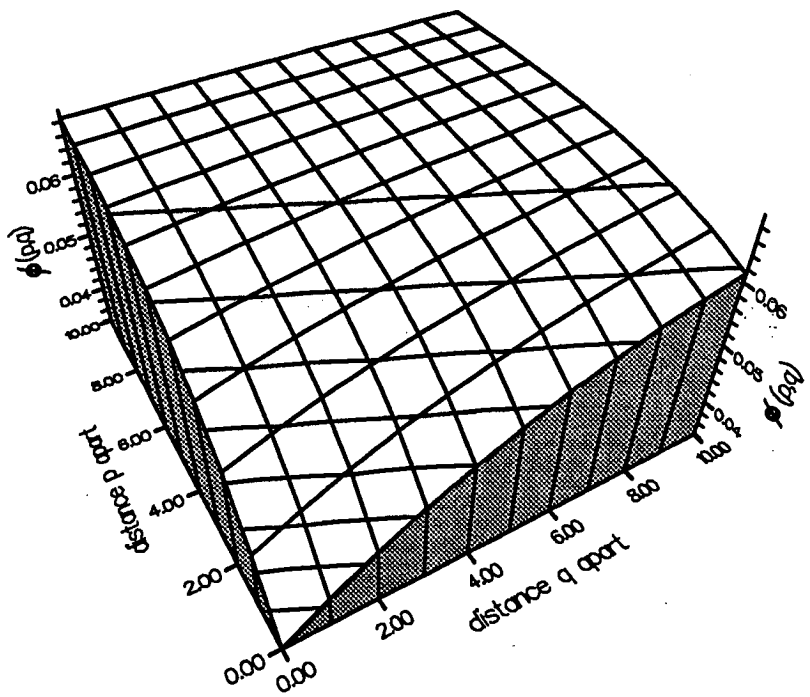


Figure 6.4.2. Fitted curve of semi-variances, $\phi(p,q)$, from equation (6.3.2) for PBI trials $(kg/plot)^2$.

affecting error variability. Therefore the Patterson & Hunter's (1983) conclusions appear to be equally appropriate for smaller, narrower plots.

For a two-dimensional array of plots where the plots are long and narrow, correlation between plots facing the narrow side may be assumed to be negligible. In contrast, if the plots are much smaller and squarer the patterns of variability may be different and a significant correlation is likely in both directions.

For SCRI and PBI trials which have small plots, correlation between plots sharing the narrow side (column) while not high, cannot be ignored. Kempton & Howes (1981) found this to be the case in their nearest neighbour analysis of 118 breeders' wheat trials at PBI. In 30% of their trials column effects were in fact larger than row effects. The same analysis applied to the PBI barley trials revealed that in 16 out of 44 trials column effects were again larger than row effects (Kempton, pers. comm.).

Large values of λ, ρ_v and ρ_h suggest a high correlation which falls slowly with interplot distance in both directions. In this case, the use of either IB designs with blocks in two dimensions (2-D) or RC designs would be expected to increase the efficiency of analysis. However, if either ρ_v or ρ_h is small the use of blocks in one dimension (1-D) is likely to be more efficient.

In the SCRI and PBI trials, correlations between plots within rows (horizontal direction) fall away slower with the distance than correlations within column (vertical direction) (Figures 6.4.1 and 6.4.2), reflecting the

rectangularity of plot dimensions.

The parameters λ and ρ's are reasonably large in the SCRI series and a 2-D analysis may be expected to provide increases in efficiency. The smaller parameter values in the PBI series suggests smaller increases in efficiency from IB and RC analysis. This is examined further in Chapter 7 and 8.

Chapter 7

APPLICATION OF THE FITTED TWO-DIMENSIONAL EXPONENTIAL VARIANCE MODEL: EFFICIENCY AND BLOCK DIMENSION

7.1. Introduction

It was shown in Chapter 6 that on the average, the plot to plot variability of the trials data is well described by the exponential variance error law. Each trial series is characterised by a set of parameters values which may depend on such factors as the location of trial sites, years of trialling, and plot and trial size.

This chapter shows how knowledge of the error law for series of field trials may be used to improve future recommendations about designs for individual trials. More specifically, knowledge of the relationship between the EMS and block dimension (i.e. block size and shape) is used to predict efficiency and optimal block dimension for incomplete block designs where blocks comprise a two-dimensional array of plots, and for row and column designs.

7.2. Prediction of efficiency and block dimension

Once the results of a trial are known, the effectiveness of the design may be assessed through direct calculation of relative precision of treatments contrasts. Yates (1940a) assessed effectiveness of his lattice square designs in this way (see also Chapter 3). Nevertheless in

the planning stage of a trial it may be that there are several possible designs to choose from and guidance is sought on their relative efficiencies. In this circumstance, recommendations for design is not simply a matter of choosing efficient combinations of varieties for each block. Decisions on the organization of the experimental area in plots, blocks, rows, and columns need to be considered. Results from past trials are useful to evaluate the different options.

In practice, for designs based on complete replicates, resolvable designs are preferable in field experiments. The resolvable property is useful in the field since operations like sowing or harvesting can be carried out in stages, replicate by replicate. Also, measurements may easily be made on only a proportion of the replicates if desired.

Once the general design is specified (i.e. incomplete block or row and column), the choice becomes one of selecting the block dimension with the aim of providing a balance between two requirements for efficiency: blocks with dimensions small enough to account for heterogeneity giving a small EMS and sufficiently large to provide a reasonable number of degrees of freedom for treatment comparisons.

If the particular error law is known, information on how the EMS depends on the block dimension can be used to predict efficiency of a particular design for future trials. Hence the optimal size and shape of the blocks for a particular number of varieties and replicates can be

calculated.

If previous results of a trial series are available, information derived on the error variance model can be used to investigate the potential for improvement in trial efficiency using alternative designs. This is special case of a "post-mortem" analysis discussed by Pearce (1976b, 1983).

Robinson *et al.* (1988) used direct calculation of efficiency, but the efficiencies were limited to those actually observed.

7.3. Incomplete Block designs

Patterson & Hunter (1983) gave an approximate formula for the efficiency of a trial analysis on **v** varieties designed with the plots of each replicate in **s** blocks of **k** plots, arranged in **v**×**1** array

$$\mathcal{E} = \gamma \left[E + \frac{(1 - E)(s - 1)}{\gamma(v - 1) - (v - s)} \right] \qquad (7.3.1)$$

where **E** is the efficiency factor of the design (Patterson *et al.*, 1978) and γ = **MS(v)/MS(k)** is the ratio of mean squares for the complete and incomplete block designs (see also Chapter 4). This formula can also be used for the efficiency of a trial analysis where the plots of each block form a two-dimensional **r**×**c** array, since

$$\gamma = \frac{MS(R,C)}{MS(r,c)}$$

where **MS(R,C)** is the error mean square of the trial as a

RCB design in **R**×**C** array and **MS**(**r**,**c**) is the intra-block error mean square of the trial as an IB design with blocks of (**r**,**c**). The values of these EMS are obtained from expression (5.5.2).

In many practical cases when none of the factors of **v** falls in the range of acceptable block sizes, designs with two block sizes differing by one plot are used (Patterson & Williams, 1976). In these circumstances, for unequal block size, average value of γ can be used.

Patterson & Hunter (1983) derived their formula using the approximation that all contrasts within a stratum have equal variance. This is considerably simpler than the more accurate method of calculating the average variance over all varietal contrasts for each design.

Taking the error laws developed in Chapter 6 for SCRI trials (equation 6.2.2) and PBI trials (equation 6.3.2) the predicted efficiency for trials in 2, 3 or 4 replicates of 48 and 100 varieties using IB designs with different block dimensions were calculated. The results are given in Table 7.3.1.

Trials for 48 varieties were used because the number of varieties can be factorized in a much wider range of block dimensions than trials for 49 varieties.

The error mean squares ratios (γ) and the efficiency factor (**E**) for each block dimension are given in Table 7.3.2.

The reduction in the error mean squares (large γ) depends not only on the block size but also on its shape. Situations occur where reducing block size does not reduce

Table 7.3.1. Predicted efficiency ($\mathcal{E}$) of incomplete block designs in blocks of different arrays of plots.

EV model... Num.of blocks	Block size†	Array r×c	48 varieties SCRI Replicates 2	SCRI 3	SCRI 4	PBI 2	PBI 3	PBI 4
12	4	1×4	1.17	1.29	1.32	1.02	1.09	1.11
8/4	4	4×1/1×4	1.03	1.10	1.12	0.98	1.03	1.05
8/4	4	4×1/2×2	1.00	1.07	1.09	0.97	1.02	1.04
12	4	2×2	1.09	1.18	1.21	1.00	1.06	1.08
8/2	5	5×1/1×4	1.01	1.07	1.08	0.98	1.02	1.03
6/2	6	1×6/6×1	1.17	1.23	1.25	1.03	1.07	1.08
6/2	6	1×6/3×2	1.22	1.28	1.30	1.05	1.09	1.10
8	6	6×1	0.99	1.01	1.01	0.99	1.01	1.01
6/2	6	2×3/6×1	1.12	1.17	1.19	1.03	1.07	1.08
6/2	6	2×3/3×2	1.16	1.22	1.24	1.05	1.09	1.10
8	6	3×2	1.12	1.17	1.19	1.03	1.07	1.08
6/1	7	1×7/6×1	1.21	1.26	1.28	1.05	1.08	1.09
6	8	1×8	**1.27**	**1.32**	**1.34**	1.05	1.09	1.10
6	8	2×4	1.23	1.28	1.30	**1.07**	**1.10**	**1.12**
4/2	8	4×2/2×4	1.13	1.17	1.18	1.04	1.07	1.08
4/2	8	4×2/1×8	1.14	1.18	1.20	1.03	1.06	1.07
3/2	10	2×5/3×3	1.20	1.24	1.25	**1.07**	**1.10**	1.11
3/1	12	2×6/6×2	1.17	1.19	1.20	1.06	1.08	1.08
4	12	6×2	1.01	1.03	1.03	1.01	1.03	1.03
4	12	3×4	1.19	1.22	1.23	**1.07**	**1.10**	1.10
3	16	2×8	1.22	-	-	1.06	-	-
2/1	16	4×4/2×8	1.15	-	-	1.06	-	-
			100 varieties					
20/5	4	1×4/2×2	1.22	1.38	1.43	1.03	1.13	1.16
20/5	4	4×1/2×2	1.02	1.12	1.15	0.97	1.04	1.07
25	4	2×2	1.14	1.28	1.32	1.01	1.10	1.13
20	5	1×5	1.32	**1.45**	**1.48**	1.09	1.17	1.19
20	5	5×1	1.02	1.09	1.11	0.99	1.04	1.05
15/2	6	2×3/5×1	1.24	1.33	1.36	1.08	1.14	1.16
15/2	6	3×2/1×5	1.22	1.31	1.34	1.06	1.13	1.14
10/5	7	1×7/2×3	1.34	1.42	1.45	1.10	1.16	1.18
10/5	7	7×1/3×2	1.07	1.12	1.14	1.02	1.06	1.07
10	10	1×10	**1.39**	1.43	1.45	1.11	1.14	1.15
10	10	10×1	1.00	1.01	1.02	1.00	1.01	1.02
10	10	2×5	**1.39**	1.43	1.45	**1.15**	**1.18**	**1.20**
10	10	5×2	1.17	1.21	1.22	1.07	1.10	1.11
2/5	15	3×5/7×2	1.16	1.19	1.19	1.07	1.09	1.10
2/5	15	5×3/2×7	1.31	1.34	1.35	1.13	1.15	1.16
5	20	2×10	1.32	1.34	1.35	1.13	1.14	1.15
5	20	10×2	1.02	1.03	1.03	1.02	1.03	1.04
4/1	20	4×5/2×10	1.26	1.28	1.29	1.13	1.14	1.15
4/1	20	5×4/10×2	1.17	1.19	1.20	1.09	1.10	1.11

† Designs with almost equal block size are classified by the larger of the two block sizes

- No design available

Table 7.3.2. Error mean square ratio (γ) and efficiency factor of IB design in blocks of different plot arrays.

			48 varieties				
			EMS ratio for EV model		Efficiency factor for replicates		
Num.of blocks	Block size†	Array r×c	SCRI	PBI	2	3	4
12	4	1×4	1.680	1.341	0.594	0.687	0.712
8/4	4	4×1/1×4	1.360	1.211	0.594	0.687	0.712
8/4	4	4×1/2×2	1.300	1.190	0.594	0.687	0.712
12	4	2×2	1.500	1.279	0.594	0.687	0.712
8/2	5	5×1/1×4	1.244	1.148	0.668	0.746	0.770
6/2	6	1×6/6×1	1.436	1.207	0.753	0.808	0.826
6/2	6	1×6/3×2	1.505	1.236	0.753	0.808	0.826
8	6	6×1	1.077	1.078	0.753	0.808	0.826
6/2	6	2×3/6×1	1.355	1.207	0.753	0.808	0.826
6/2	6	2×3/3×2	1.425	1.236	0.753	0.808	0.826
8	6	3×2	1.355	1.196	0.753	0.808	0.826
6/1	7	1×7/6×1	1.440	1.202	0.796	0.839	0.854
6	8	1×8	1.500	1.196	0.817	0.858	0.872
6	8	2×4	1.448	1.222	0.817	0.858	0.872
4/2	8	4×2/2×4	1.306	1.171	0.817	0.858	0.872
4/2	8	4×2/1×8	1.324	1.162	0.817	0.858	0.872
3/2	10	2×5/3×3	1.365	1.196	0.854	0.886	0.898
3/1	12	2×6/6×2	1.285	1.147	0.887	0.913	0.922
4	12	6×2	1.077	1.078	0.887	0.913	0.922
4	12	3×4	1.313	1.170	0.887	0.913	0.922
3	16	2×8	1.313	1.122	0.921	-	-
2/1	16	4×4/2×8	1.238	1.122	0.921	-	-
			100 varieties				
20/5	4	1×4/2×2	1.879	1.450	0.553	0.658	0.693
20/5	4	4×1/2×2	1.440	1.279	0.553	0.658	0.693
25	4	2×2	1.714	1.395	0.553	0.658	0.693
20	5	1×5	1.846	1.429	0.652	0.734	0.760
20	5	5×1	1.297	1.200	0.652	0.734	0.760
15/2	6	2×3/5×1	1.613	1.344	0.707	0.779	0.800
15/2	6	3×2/1×5	1.583	1.319	0.707	0.779	0.800
10/5	7	1×7/2×3	1.695	1.343	0.747	0.804	0.824
10/5	7	7×1/3×2	1.297	1.189	0.747	0.804	0.824
10	10	1×10	1.600	1.250	0.846	0.880	0.892
10	10	10×1	1.067	1.071	0.846	0.880	0.892
10	10	2×5	1.600	1.304	0.846	0.880	0.892
10	10	5×2	1.333	1.200	0.846	0.880	0.892
2/5	15	3×5/7×2	1.273	1.166	0.892	0.917	0.925
2/5	15	5×3/2×7	1.442	1.236	0.892	0.917	0.925
5	20	2×10	1.412	1.200	0.925	0.943	0.949
5	20	10×2	1.067	1.071	0.925	0.943	0.949
4/1	20	4×5/2×10	1.349	1.200	0.925	0.943	0.949
4/1	20	5×4/10×2	1.251	1.155	0.925	0.943	0.949

† Designs with almost equal block size are classified by the larger of the two block sizes

- No design available

the error mean square. For example, for a trial with 48 varieties, where the SCRI error law holds, changing from blocks of (1,8) to blocks of (2,2) does not reduce the error mean square (Table 7.3.2). However, changing to blocks of (1,4) gives appreciable reduction. Additional examples for both error laws and variety numbers are found in Table 7.3.2.

In general plot arrangements which have small numbers of rows give high reduction in EMS. This may be explained by the fact that correlations within rows (horizontal directions) are greater than within columns, according to the EV laws.

Inspection of Table 7.3.1 shows that overall, provided the EV rules hold, the maximum efficiency (in bold type) is achieved with block sizes between 5 and 12 for a variety of arrays of plots. The block size for the maximum efficiency is between 5 and 10 using SCRI EV law and between 8 and 12 using PBI EV law.

The results using SCRI EV law are similar to those given by Robinson *et al.* (1988), whose results suggest that the optimum block size is likely to lie between 5 and 10. This was expected since the SCRI EV law was derived over the same data used by Robinson *et al.* (1988).

Patterson & Hunter (1983) gave tables of predicted efficiency for trial series, assuming the one-dimensional exponential variance law. The optimal block size for $\mathbf{v \leq 64}$ varieties was generally near to $\sqrt{\mathbf{v}}$. The parameters of the SCRI EV law in one of the directions are very similar to the parameters of Patterson & Hunter EV law (see Chapter

6). For a trial on 48 varieties, using the SCRI EV law, the recommendations of Patterson & Hunter are equally valid (Table 7.3.1). However, for a trial on 100 varieties with more than 2 replicates the optimal block size is much smaller than $\sqrt{v}$.

The formula for efficiency of analysis given in (7.3.1) allows for between-block information. Up to 27% of the efficiency is due to between-block analysis but the optimum block dimension (i.e. block size and array of plots) for maximum efficiency is hardly affected by the between-block analysis.

The efficiency, on the SCRI error law, is found to be maximum for most of the blocks with plots arranged in one row. For trials on 48 varieties, block of (1,8) are predicted to give the greatest efficiency. For trials on 100 varieties with more than two replicates, maximum efficiency is achieved with block of (1,5). Blocks of (1,10) or (2,5) are the optimum block dimensions for trials on 100 varieties in two replicates.

On the PBI error law, different arrays with more than one row are found to give the maximum efficiency. This can be explained by the observation that the correlations in two directions are more nearly equal for PBI than for SCRI. In this case a near-square array of plots may give the greatest efficiency. For example for trials on 48 varieties, block of (2,4) are predicted to give the maximum efficiency, though larger blocks of dimensions 2×5 and 3×4 give similar efficiency for 2 or 3 replicated trials (Table 7.3.1). For trials on 100 varieties the

maximum efficiency is achieved with block of dimension (2,5).

Overall, the results in Table 7.3.1 show that blocking is likely to be more efficient for trials with larger numbers of varieties. Trials with larger replication are likely to required smaller block sizes to achieve the maximum efficiency. The potential gains from blocking are much smaller for PBI than for SCRI trials, as was expected from their respective parameters for the EV laws (refer back to Chapter 6).

7.4. Row and Column designs

Row and column and incomplete block designs are appropriate under different circumstances. Incomplete block designs are known to be effective when plots are long and narrow (Patterson & Hunter, 1983). However when the plots are small they are less appropriate (Fisher, 1935) and row and column designs such as lattice squares (Yates, 1937, 1940a) have been used. Although less flexible than incomplete block designs these row and column designs are no more difficult to use than a randomized complete block design now that software is available for efficient analysis (e.g. in Genstat).

When row and column effects are associated with agricultural operations, such as the direction of seed drilling, designs with complex block structure may be more appropriate. Seeger (1986) proposed designs for trials with sugar-beet seed considering this requirement. Special

requirements of cotton variety trials led Williams (1986c) to use designs with columns running across replicates. Williams & John (1989) and recently Seeger (1991) also considered the construction of such row and column designs. Here we consider traditional row and column designs such as those proposed by Yates (1937, 1940a).

Two types of designs are considered. First, designs on **v** varieties, that is the product of two integers **r** and **c**, where each block forms one replicate and the plots of each block are arranged in a **r**×**c** array. Second, designs as above but with all replicates housed together in a single block; **v** here is the product of **r** and **c/t**, **t** being the number of replicates.

The former designs are resolvable nested row and column designs and a series of them are presented in Haliburn (1980) and Patterson & Robinson (1989). Details of construction for some of the two replicated design in Patterson & Robinson (1989) are given in Bailey & Patterson (1991). The lattice squares included are those for which the index parameter **d** of Williams *et al.* (1986) is zero.

The second type of design, though not resolvable, are generated from resolvable α-designs (Patterson & Williams, 1976) and are known as row and column α-designs (John & Eccleston, 1986).

These two types of designs have the property of adjusted orthogonality, a concept introduced by Eccleston & Russel (1975, 1977). For such designs, the row effects adjusted for treatments are orthogonal to the column

effects adjusted for treatments. This property allows the properties of a row and column design to be determined from those of the separate row and column component designs.

According to Eccleston & McGilchrist (1985) an upper bound (**U**) for efficiency factor ($\mathbf{E}_{rc}$) of a row and column design is

$$E_{rc} \leq U = (E_r^{-1} + E_c^{-1} - 1)^{-1},$$

and this bound becomes the efficiency factor of the row and column design if the design has the property of adjusted orthogonality. Thus for a design with adjusted orthogonality, the efficiency factor is

$$E_{rc} = (E_r^{-1} + E_c^{-1} - 1)^{-1}$$

in terms of the separate row and column component designs, where $\mathbf{E}_r$ is the efficiency factor for the row component design and $\mathbf{E}_c$ is the efficiency factor for the column component design.

Given an error law, the efficiency of a trial with the first type of design approximates to

$$\gamma_{rc}\left\{\left[E_r + \frac{(1-E_r)(r-1)}{\gamma_r(v-1)-(v-r)}\right]^{-1} + \left[E_c + \frac{(1-E_c)(c-1)}{\gamma_c(v-1)-(v-c)}\right]^{-1} - 1\right\}^{-1} \quad (7.4.1)$$

where

$$\gamma_{rc} = \frac{MS(r,c)}{MS1(r,c)},$$

$$\gamma_r = \gamma'_c - \frac{t(c-1)}{(v-1)(t-1)}(\gamma'_c - 1)$$

and

$$\gamma_c = \gamma'_r - \frac{t(r-1)}{(v-1)(t-1)}(\gamma'_r - 1)$$

for,

$$\gamma'_r = \frac{MS(1,c)}{MS1(r,c)} \quad \text{and} \quad \gamma'_c = \frac{MS(r,1)}{MS1(r,c)}.$$

For the second type of design the efficiency is approximately

$$\gamma_{rc}\left\{\left[E_r + \frac{(1-E_r)}{\gamma_r c - (c-1)}\right]^{-1} + \left[E_c + \frac{(1-E_c)}{\gamma_c r - (r-1)}\right]^{-1} - 1\right\}^{-1} \quad (7.4.2)$$

where γ_{rc}, γ_r and γ_c is redefined as

$$\gamma_{rc} = \frac{MS(r,c/t)}{MS1(r,c)},$$

$$\gamma_r = \gamma'_c - \frac{(c-1)}{v(t-1)}(\gamma'_c - 1)$$

and

$$\gamma_c = \gamma'_r - \frac{(r-1)}{v(t-1)}(\gamma'_r - 1)$$

for γ'_r and γ'_c given as before. These expressions are obtained from the results given in Chapter 2.

The error mean squares MS and MS1 are given by the equations (5.5.2) and (5.5.3) and defined as follows:

i) **MS(r,c)** or **MS(r,c/t)** is the error mean square of the trial as a randomized complete block design in **r**×**c** or **r**×**c/t** array;

ii) **MS(1,c)** is the intra-block error mean square of the trial as a row-design;

iii) **MS(r,1)** is the intra-block error mean square of the trial as a column-design;

iv) **MS1(r,c)** is the intra-row and column error mean square of the trial as row and column design.

Consider, for example, the four-replicate resolvable row and column design for 49 varieties in a 7×7 array per replicate given in Table 7.4.1, the predicted efficiency given by (7.4.1) is 1.207, on the PBI EV law. A more accurate value, obtained by comparing average variances over all varietal contrasts, is 1.218. Similarly, for the two-replicate row and column α-design for 49 varieties in a 7×14 array given in Table 7.4.2, the predicted efficiency given by (7.4.2) is 1.048, on the same error law, and a more accurate value is 1.132, obtained comparing average variances over all varietal contrasts. The predicted efficiencies are slightly underestimated (Table 7.4.3). This is because equations (7.4.1) and (7.4.2) are derived on the assumption that all contrasts within each stratum have equal variance.

The row and column designs that have the property of adjusted orthogonality are in practice available for only a limited number of varieties. The wide range of block sizes available for block designs, for a given number of varieties and replicates, is not found for row and column designs. Therefore, it is not always possible to judge the optimum row and column dimension for maximum efficiency. For example, with a wider range of row and column designs we might compare the efficiencies of testing 100 varieties with the replicates represented as either a single 10×10

Table 7.4.1. Randomized plan of resolvable row and column design for four replicates of 49 varieties in 7×7 array per replicate.

Superblock 1							Superblock 2						
28	27	22	23	25	24	26	33	2	39	8	21	27	45
7	6	1	2	4	3	5	7	25	13	31	37	43	19
21	20	15	16	18	17	19	10	35	16	41	47	4	22
14	13	8	9	11	10	12	20	38	26	44	1	14	32
49	48	43	44	46	45	47	36	12	49	18	24	30	6
35	34	29	30	32	31	33	46	15	3	28	34	40	9
42	41	36	37	39	38	40	23	48	29	5	11	17	42

Superblock 3							Superblock 4						
27	38	9	7	29	18	47	21	44	40	29	6	10	25
37	6	26	17	46	35	8	30	11	7	45	15	26	41
49	11	31	22	2	40	20	46	27	16	12	31	42	1
32	43	21	12	41	23	3	5	35	24	20	39	43	9
15	33	4	44	24	13	42	22	3	48	37	14	18	33
10	28	48	39	19	1	30	13	36	32	28	47	2	17
5	16	36	34	14	45	25	38	19	8	4	23	34	49

Table 7.4.2. Unrandomized plan of row and column α-design for two replicates of 49 varieties in 7×14 array.

1	2	3	4	5	6	7	9	10	11	12	13	14	8
8	9	10	11	12	13	14	17	18	19	20	21	15	16
15	16	17	18	19	20	21	26	27	28	22	23	24	25
22	23	24	25	26	27	28	32	33	34	35	29	30	31
29	30	31	32	33	34	35	41	42	36	37	38	39	40
36	37	38	39	40	41	42	49	43	44	45	46	47	48
43	44	45	46	47	48	49	1	2	3	4	5	6	7

Table 7.4.3. Predicted efficiencies of trials for 49 varieties (**v**) as four-replicate resolvable row and column design in 7×7 array and as two-replicate row and column α-design in 7×14 array (on PBI EV error law).

v	array rxc	Eff. factor E_r	Eff. factor E_c	EMS ratios γ_r	EMS ratios γ_c	EMS ratios γ_{rc}	Efficiency P	Efficiency MA
49	7x7	0.857	0.857	1.299	1.128	1.436	1.207	1.218
49	7x14	0.828	0.800	1.192	1.188	1.333	1.048	1.132

P - Predicted using equation (7.4.1) or (7.4.2)

MA - Obtained by comparing average variances over all varietal contrasts

array or four 5×5 arrays.

Predicted efficiency calculated similarly to those shown in Table 7.4.3 are presented in Table 7.4.4 for different number of varieties **v** and array dimensions **r**×**c**. The EMS ratios and the efficiency factors used in the calculations are in Tables 7.4.5 and 7.4.6 respectively.

Provided that the EV laws hold, examination of Table 7.4.4 suggests that, as for block designs, row and column designs are likely to be more effective for large trials than for small ones.

The potential gains in efficiency from using row and column methods are much greater for SCRI trials than for PBI trials, as was expected. Up to 25% of the efficiency is due to between-row and column analysis.

Originally, the SCRI trials were designed as two replicated alpha (0,1) designs for 100 varieties. They were also analysed as 10×10 row and column designs. On the SCRI EV law, to attain results of the same precision by the use of RCB design 3 replicates would be required instead of 2. By the same error law, if the trials had been designed as RCB design for 49 varieties, the change to incomplete block design with optimal block dimension would have allowed the number of replicates to be reduced from 5 to 4 without losing precision. Similarly, the change to 7×7 row and column design would allow the number of replicates to be reduced from 6 to 4.

The PBI trials were designed as 4-replicate 7×7 lattice squares. According to the PBI EV rule, row and column analysis provides results of the same precision as would

Table 7.4.4. Predicted efficiencies of resolvable row and column design and row and column α-design for 25, 30, 49 and 100 varieties, in two, three or four replicates (According to EV model, eq. 6.2.2, for SCRI trials and, eq. 6.3.2, for PBI trials).

EV model...		SCRI			PBI		
	array	Replicates					
Variety	rxc	2	3	4	2	3	4
25	5x5	1.29	1.35	.	1.10	1.14	.
25+	5x10	1.28	.	.	1.06	.	.
30	5x6	1.30	.	.	1.07	.	.
30+	5x12	.	.	.	1.05	.	.
49	7x7	1.41	1.49	1.52	1.14	1.19	1.21
49+	7x14	.	.	.	1.05	.	.
100	10x10	1.52	.	.	1.17	.	.

+ Row and column α-design

Table 7.4.5. Error mean square ratios of resolvable row and column design and row and column α-design for 25, 30, 49 and 100 varieties, in two, three or four replicates (According to EV model, eq. 6.2.2, for SCRI trials and, eq. 6.3.2, for PBI trials).

EV model...		SCRI			PBI		
Variety	array rxc	EMS ratios γ'_r	γ'_c	γ_{rc}	γ'_r	γ'_c	γ_{rc}
25	5x5	1.182	1.682	1.727	1.105	1.316	1.368
25+	5x10	1.304	1.609	1.652	1.200	1.250	1.300
30	5x6	1.227	1.682	1.773	1.158	1.316	1.368
30+	5x12	.	.	.	1.225	1.250	1.300
49	7x7	1.217	1.783	1.870	1.154	1.359	1.436
49+	7x14	.	.	.	1.214	1.262	1.333
100	10x10	1.200	1.800	1.920	1.143	1.333	1.429

+ Row and column α-design

Table 7.4.6. Efficiency factors of resolvable row and column design and row and column α-design for 25, 30, 49 and 100 varieties, in two, three or four replicates.

replicates...		2		3		4	
	array	Efficiency factors					
Variety	rxc	E_r	E_c	E_r	E_c	E_r	E_c
25	5x5	0.750	0.750	0.800	0.800	.	.
25+	5x10	0.858	0.750	.	.	.	.
30	5x6	0.774	0.728	.	.	.	.
30+	5x12	0.879	0.728	.	.	.	.
49	7x7	0.800	0.800	0.842	0.842	0.857	0.857
49+	7x14	0.828	0.800	.	.	.	.
100	10x10	0.846	0.846	.	.	.	.

+ Row and column α-design

be obtained from 5 replicates with a RCB analysis.

The results in this section show that the techniques developed may be a useful guide in the search for the most efficient trial design. They also confirm that for small plot trials laid out in a two-dimensional array, correlation within columns, although smaller than correlation within rows, can not be ignored and, as pointed out by Kempton & Howes (1981) and Robinson *et al.* (1988), row and column designs are usually preferable to block designs.

Chapter 8

APPLICATION OF THE FITTED TWO-DIMENSIONAL EXPONENTIAL VARIANCE MODEL: INDIVIDUAL TRIAL ANALYSES

8.1. Introduction

So far, this study has shown that (**i**) the variability of trials data arranged in rectangular array of plots can be described by a two-dimensional exponential variance error law and (**ii**) this error law can be employed to predict efficiency of analysis of different blocking systems and optimum block dimensions to be used when designing future trials.

A new question that now arises is how the information about the error law may be used to improve the efficiency of the analysis of individual agricultural field trials.

The primary aim in agricultural field trials is usually the efficient estimation of treatment contrasts and the accurate estimation of their standard errors. This requires the control of underlying field variation arising from experimental management, trends in soil fertility and other environmental factors.

Plot to plot variation in field trials can be described in terms of its covariance structure. A poor approximation to the true covariance structure will result in an inefficient analysis and may produce bias in the estimates of standard errors.

Blocking, row and column and spatial or neighbour

methods have been used to control field variation. They can be considered as application of the generalized least squares.

Most of the spatial methods for field trials have concentrated on one-dimensional layouts. As a result few two-dimensional methods have been proposed, so that there is limited experience of reasonable models.

In yet another method (Two-dimensional EV analysis) generalized least squares can be proposed. It employs the plot covariance determined by the EV error model in two dimensions.

This chapter describes in Sections 8.2 and 8.3 how the two-dimensional EV error law and an approximation to it may be used in the analysis of individual field trial data to give efficient estimates of treatment and accurate estimates of their standard errors. Sections 8.4 and 8.5, develop and examine a two-dimensional first difference model based on Cullis & Gleeson's (1991) approach over the PBI and SCRI series of data.

Throughout this chapter matrix subscript in upper case is part of the label of the matrix. Whereas matrix subscript in lower case indicate the size of a square matrix.

8.2. Two-dimensional exponential variance analysis

The two-dimensional exponential variance (2-D EV) error law developed in Chapter 6 gives the relationship of the semi-variances of the difference in yields of plots **p** rows

and **q** columns apart. The semi-variance has form

$$\phi(p,q) = \sigma^2 (1 - \lambda\rho_v^p\rho_h^q). \qquad (8.2.1)$$

A model, for a trial arranged in resolvable superblocks of **r**×**c** plots each, which the plot covariance matrix take account of the information about semi-variances of the differences between plots apart is of the form

$$E(y)=X\tau$$

$$Var(y)= V = \sigma^2 [(1-\lambda) (I_n-R) + \lambda (I_n-R) H (I_n-R)] \qquad (8.2.2)$$

where,

y is the **n**×**1** vector of plot yields adjusted by their superblock means (**n=trc**),

X is the **n**×**v** design matrix for varieties,

τ is the **v**×**1** vector of variety effects,

R is the projection matrix for superblocks given by

$$R = I_t \otimes (J_{rc}/rc)$$

for **t** replicates, **r** rows and **c** columns,

and

$$H = I_t \otimes (P \otimes Q)$$

for

$$P = \begin{bmatrix} 1 & \rho_v & \rho_v^2 & \cdots & \rho_v^{r-1} \\ \rho_v & 1 & \rho_v & \cdots & \rho_v^{r-2} \\ \rho_v^2 & \rho_v & 1 & \cdots & \rho_v^{r-3} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho_v^{r-1} & \rho_v^{r-2} & \rho_v^{r-3} & \cdots & 1 \end{bmatrix}$$

and

$$Q = \begin{bmatrix} 1 & \rho_h & \rho_h^2 & \cdots & \rho_h^{c-1} \\ \rho_h & 1 & \rho_h & \cdots & \rho_h^{c-2} \\ \rho_h^2 & \rho_h & 1 & \cdots & \rho_h^{c-3} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ \rho_h^{c-1} & \rho_h^{c-2} & \rho_h^{c-3} & \cdots & 1 \end{bmatrix}.$$

The definition of **H** follows from the concept of separability for which

$$\rho(p,q) = \rho_v(p,0)\ \rho_h(0,q),$$

where $\rho_v(p,0)$ and $\rho_h(0,q)$ are the lag **p** and **q** correlations of the one-dimensional processes within columns and rows respectively (Martin 1990).

In the individual analysis of a trial to obtain estimates of variety differences and their standard errors, estimates of the parameters σ^2, λ, and ρ's have also been calculated. If the error model is appropriate and accurate estimates of λ and ρ's are available, the method is efficient and the variety effects are then estimated by

$$\hat{\tau} = (X^T\hat{V}^{-1}X)^{-1}X^T\hat{V}^{-1}y$$

and the standard errors of differences calculated from the estimates of the variance of $\hat{\tau}$,

$$\text{var}(\hat{\tau}) = (X^T\hat{V}^{-1}X)^{-1}.$$

If all variation present in a trial is due to white noise (λ=0 or ρ_v=0 or ρ_h=0 or yet ρ's=1) a 2-D EV analysis

with known parameters would be expected to be the same as a RCB analysis and the efficiency would therefore be the unity. In like manner, when neighbouring plots can be regarded as uncorrelated, a row and column analysis will give no more information than a RCB analysis. The efficiency is also the unity.

On the other hand when there is no white noise (λ=1) and the overall correlation between plots, $\lambda\rho_v\rho_h$, is very high a 2-D EV analysis would be expected to be most efficient.

Other analyses based on different models (with no white noise) can be considered as special cases of generalized least squares analysis under a 2-D EV model. For example, Herzberg (1978) in the discussion of Bartlett's (1978) paper considered the problem of the analysis of RCB designs using a 2-D EV model with λ=1. Similarly Zimmerman & Harville (1991) in their formulated random field linear model approach present a method of analysis called AEC (anisotropic exponential covariance) that also corresponds to a 2-D EV model with λ=1. They also show that the method is closely related to a two-dimensional Papadakis analysis under certain conditions.

For a full 2-D EV analysis, the values of the variance parameters must be estimated and this cannot be done by least squares techniques. Moreover, when the plot covariance matrix contains nonlinear parameters, estimation is more complicated. Methods of estimation which require the covariance matrix to be linear in the parameters have limited use when $\mathbf{V}$ is nonlinear in ρ's and

and cannot be rendered linear by reparameterization.

Originally it was intended to estimate the parameters of $\mathbf{V}$ by fitting a 2-D exponential curve to MS (mean squares) or to ϕ values calculated for individual trials using the methods of Chapter 5. However, the values for individual trials were found to be very variable and provided little useful information on the appropriate error law. Another possibility would be to use a 2-D EV error law with the parameters λ and ρ's estimated from $\phi(0,1)$, $\phi(1,0)$ and $\phi(1,1)$.

For a similar covariance matrix and making assumption of Gaussian yield, Besag (1978) suggested an iterative maximum likelihood approach for estimation of both variety and variance parameters. Similarly Zimmerman & Harville (1991) and Cullis & Gleeson (1991) made use of residual maximum likelihood (REML) approach, first proposed by Patterson & Thompson (1971), for estimation of both fixed variety effects and variance parameters. The performance of these methods have been well studied for one-dimensional data, see for example Lill *et al.* (1988) and Cullis, McGilchrist & Gleeson (1991). However little is known of their behaviour for two-dimensional data under a plot covariance matrix like $\mathbf{V}$.

A simple alternative method of estimating the variety effects in (8.2.2) would approximate $\mathbf{V}$ by a matrix that is linear in its parameters. We could then use the method equating sums of squares to their expectations (Yates, 1940a), maximum likelihood methods (Patterson & Thompson, 1971) or any other method for the simpler case of

estimating the parameters of a covariance matrix which has the form $\mathbf{V}=\sum_i \sigma_i^2 \mathbf{V}_i$, for known $\mathbf{V}_i$, to estimate the parameters of the covariance matrix.

An account of a first order approximation to **V** is considered in the following section.

8.3. Linear approximation to 2-D EV analysis

Williams (1986a), following a suggestion of Patterson (1983), developed a one-dimensional analysis based on first order approximation to the semi-variance of the difference between two plots **x** apart under a 1-D EV error law.

Similarly, using the development given in Section 5.6, when the correlation between neighbouring plots is close to unity (both values of ρ's close to 1) the semi-variance (8.2.1) of the difference between two plots **p** and **q** apart under the model (8.2.2) is approximated by

$$\phi(p,q) = \sigma_1^2 (1 + \Psi_v p + \Psi_h q) \qquad (8.3.1)$$

where,

$$\sigma_1^2 = \sigma^2 (1 - \lambda)$$

$$\Psi_v = \frac{\lambda}{1-\lambda} (1 - \rho_v)$$

$$\Psi_h = \frac{\lambda}{1-\lambda} (1 - \rho_h).$$

A model in which the plot covariance matrix takes account to these semi-variances has form

$$E(y) = X\tau$$

$$\text{Var}(y) = V_L = \sigma_1^2 (I_n - R)(I_n - \Psi_v L_V - \Psi_h L_H)(I_n - R) \qquad (8.3.2)$$

where,

$\mathbf{V}_L$ is the first order approximation to $\mathbf{V}$,

$\mathbf{y}$, $\mathbf{R}$, $\mathbf{X}$ and τ are defined as in Section 8.2,

$$L_V = I_t \otimes \left(\begin{bmatrix} 0 & 1 & 2 & 3 & \dots & r-1 \\ 1 & 0 & 1 & 2 & \dots & r-2 \\ 2 & 1 & 0 & 1 & \dots & r-3 \\ 3 & 2 & 1 & 0 & \dots & r-4 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ r-1 & r-2 & r-3 & r-4 & \dots & 0 \end{bmatrix} \otimes J_c \right)$$

and

$$L_H = I_t \otimes \left(J_r \otimes \begin{bmatrix} 0 & 1 & 2 & 3 & \dots & c-1 \\ 1 & 0 & 1 & 2 & \dots & c-2 \\ 2 & 1 & 0 & 1 & \dots & c-3 \\ 3 & 2 & 1 & 0 & \dots & c-4 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots \\ c-1 & c-2 & c-3 & c-4 & \dots & 0 \end{bmatrix} \right).$$

The estimation of σ_1^2 and Ψ's could be carried out for example by equating chosen sum of squares to their expectation under model (8.3.2), in analogy with Yates' method of analysis of lattice square design.

For the estimated values of σ_1^2 and Ψ's the variety effects would be estimated by

$$\hat{\tau} = (X^T \hat{V}_L^{-1} X)^{-1} X^T \hat{V}_L^{-1} y ,$$

and the estimates of variance of $\hat{\tau}$ by

$$\text{var}(\hat{\tau}) = (X^T \hat{V}_L^{-1} X)^{-1} .$$

The approximation of $\mathbf{V}_L$ to $\mathbf{V}$ is appropriate if both ρ's are large and the distance between plots is not too great. Moreover, the analysis will never be less efficient than a RCB analysis when Ψ's$\geq$0.

However a poor approximation would result in an inefficient analysis which may bias the estimates of standard errors of variety differences. Variances of differences between plots at very small or very large distance would be expected to be overestimated whilst those at intermediate distance underestimated.

The semi-variances under model (8.3.2) given in (8.3.1) are closely related to the semi-variances given by the 2-D ARIMA approach of Cullis & Gleeson (1991) if a two-dimensional first difference (2-D FD) model is considered. For values of **p**=0 or **q**=0 the semi-variances are equivalent.

In view of this partial relationship and considering that the Cullis & Gleeson (1991) approach although developed in general form has so far been applied only to uniformity data, it is worth considering the properties and the potential gain in efficiency of using the 2-D FD analysis over real field trials before attempting to develop a full 2-D EV analysis.

8.4. Two-dimensional first difference analysis

Gleeson & Cullis (1987) proposed for 1-D a general ARIMA model that includes the linear variance (LV) model of Williams (1986a) and the first difference model of

Besag & Kempton (1986). The method of estimation followed Besag (1974, 1978) but they used REML (Patterson & Thompson, 1971) to estimate variance parameters.

Cullis & Gleeson (1991) extended the 1-D ARIMA model to 2-D ARIMA model following Martin (1990) using the concept of separability and the property of rectangular separable lattice process variance; that is the variance matrix of a two-dimensional process is the Kronecker product of the variance matrices of one-dimensional processes. Here they used REML as method of estimation too.

Cullis & Gleeson (1991) illustrated the method for analysing a number uniformity trials and showed it was more efficient than classical RCB and row and column analyses. No extensive investigation of the 2-D model applied to variety trial data has been carried out to date.

Only the simplest 2-D first difference model from the ARIMA family will be considered here because of its close link with the 2-D first-order approximation of the 2-D EV model, and because it is the model that fits most data sets (see Cullis & Gleeson, 1991).

8.4.1. Model and parameter estimation

Based on Cullis & Gleeson (1991), the model for a 2-D first differenced data, within superblocks (or replicates), is

$$w = (I_t \otimes \Delta_C \otimes \Delta_R) y = \Delta y = \Delta X \tau + e$$

$$w = D\tau + e \qquad (8.4.1)$$

$$Var(e) = \sigma_f^2 \, I_t \otimes V_C \otimes V_R = \sigma_f^2 \, V_F$$

where,

$\mathbf{y} = vec(\mathbf{Y}^T)$, and $\mathbf{Y}$ is $\mathbf{tr}\times\mathbf{c}$ matrix of data indexed in field order comprised of $\mathbf{r}$ rows, $\mathbf{c}$ columns and $\mathbf{t}$ replicates.

$\mathbf{X}$ is the $\mathbf{n}\times\mathbf{v}$ design matrix for varieties ($\mathbf{n=trc}$).

τ is the $\mathbf{v}\times\mathbf{1}$ vector of variety effects.

Δ_C is the $(\mathbf{r-1})\times\mathbf{r}$ matrix that performs first difference inside columns (vertical direction).

Δ_R is the $(\mathbf{c-1})\times\mathbf{c}$ matrix that performs first difference inside rows (horizontal direction).

$\mathbf{e}$ is the $\mathbf{t(r-1)(c-1)}\times\mathbf{1}$ vector of residual trend together with the additional white noise of local errors after differencing.

$\mathbf{V}_C$ is the $(\mathbf{r-1})\times(\mathbf{r-1})$ matrix of the variance of the process inside column in 1-D and has form

$$V_C = \psi_c I_{r-1} + \Delta_C \Delta_C^T .$$

$\mathbf{V}_R$ is the $(\mathbf{c-1})\times(\mathbf{c-1})$ matrix of the variance of the process inside row in 1-D and has form

$$V_R = \psi_r I_{c-1} + \Delta_R \Delta_R^T .$$

Under model (8.4.1) the semi-variance of difference in yields plots $\mathbf{p}$ and $\mathbf{q}$ apart is

$$\phi(p,q) = \sigma_f^2 \, [1 + \psi_c p(1-x/2) + \psi_r q(1-x/2) - \psi_c \psi_r pq/4]$$

with

$$x = 0 \text{ for } p = 0 \text{ or } q = 0$$

or

$$x = 1 \text{ for } p,q \neq 0.$$

Making the assumption of Gaussian yields this model was applied to the PBI and SCRI data using the maximum likelihood (ML) method for estimation of variance parameters instead of REML.

For any particular value of ψ's, the ML estimate of τ is the generalized least squares on $\mathbf{w}$

$$\hat{\tau} = (D^T\hat{V}_F^{-1}D)^{-1}D^T\hat{V}_F^{-1}w. \qquad (8.4.2)$$

As regards ψ's, the ML estimates are obtained iteratively according to the cycle (Besag, 1978; Besag & Kempton, 1986):

(i) Estimate τ from (8.4.2) for the current ψ's.

(ii) Form $\hat{\mathbf{e}} = \mathbf{w} - \mathbf{D}\hat{\tau}$.

(iii) Obtain new ψ's to minimize

$$\ln\left|V_F\right| + t(r-1)(c-1)\ln(\hat{e}^TV_F^{-1}\hat{e}).$$

(iv) Return to (i) until convergence.

The stopping rule for the cycle is based on the residuals in (ii), when

$$\left|\frac{\hat{e}^T\hat{e} \text{ (actual cycle)}}{\hat{e}^T\hat{e} \text{ (prior cycle)}} - 1\right| < 10^{-5}.$$

The estimate of variance of $\hat{\tau}$ for given ψ's is

$$\text{var}(\hat{\tau}) = \hat{\sigma}_f^2 (D^T\hat{V}_F^{-1}D)^{-1} \qquad (8.4.3)$$

with

$$\hat{\sigma}_f^2 = \hat{e}^T \hat{V}_F^{-1} \hat{e} / [t(r-1)(c-1) - v - 1].$$

The standard errors of differences are calculated from (8.4.3).

For computational efficiency Besag & Kempton (1986) used a decomposition of the covariance matrix which is a special case of that in Besag (1978). They showed that $\mathbf{V}_R$ and $\mathbf{V}_C$ can be decomposed as:

$$V_R = C_R(\psi_r I_{c-1} + \Lambda_R) C_R$$

where $\mathbf{C}_R$ is the symmetric $(\mathbf{c-1})\times(\mathbf{c-1})$ matrix having $(\mathbf{i,j})$ element equal to

$$(2/c)^{1/2} \sin(\pi ij/c),$$

and Λ_R is the diagonal $(\mathbf{c-1})\times(\mathbf{c-1})$ matrix having $(\mathbf{i,i})$ element equal to

$$2[1 - \cos(\pi i/c)];$$

and

$$V_C = C_C(\psi_c I_{r-1} + \Lambda_C) C_C$$

where $\mathbf{C}_C$ is the symmetric $(\mathbf{r-1})\times(\mathbf{r-1})$ matrix having $(\mathbf{i,j})$ element equal to

$$(2/r)^{1/2} \sin(\pi ij/r),$$

and Λ_C is the diagonal $(\mathbf{r-1})\times(\mathbf{r-1})$ matrix having $(\mathbf{i,i})$ element equal to

$$2[1 - \cos(\pi i/r)].$$

Thus using the results of Searle (1982, pages 265-266 and 333) the terms involved in (8.4.2) and (iii) are readily calculated by noting that:

the $(\mathbf{i},\mathbf{j})$ element of $\mathbf{D}^T\hat{\mathbf{V}}_F^{-1}\mathbf{D}$ is

$$d_i^T\hat{V}_F^{-1}d_j=(\text{vec } D_i^T)^T[C_{CI}(\psi_c I_{r-1}+\Lambda_C)_I^{-1}C_{CI}\otimes C_R(\psi_r I_{c-1}+\Lambda_R)^{-1}C_R]\text{vec } D_j^T$$

$$=tr[C_R D_j^T\, C_{CI}(\psi_c I_{r-1}+\Lambda_C)_I^{-1}\, C_{CI} D_i C_R(\psi_r I_{c-1}+\Lambda_R)^{-1}],$$

the $(\mathbf{i})$ element of $\mathbf{D}^T\hat{\mathbf{V}}_F^{-1}\mathbf{w}$ is

$$d_i^T\hat{V}_F^{-1}w=(\text{vec } D_i^T)^T[C_{CI}(\psi_c I_{r-1}+\Lambda_C)_I^{-1}C_{CI}\otimes C_R(\psi_r I_{c-1}+\Lambda_R)^{-1}C_R]\text{vec } W^T$$

$$=tr[C_R D_i^T\, C_{CI}(\psi_c I_{r-1}+\Lambda_C)_I^{-1}\, C_{CI} W\, C_R(\psi_r I_{c-1}+\Lambda_R)^{-1}],$$

the value of $\mathbf{e}^T\hat{\mathbf{V}}_F^{-1}\mathbf{e}$ is

$$e^T\hat{V}_F^{-1}e=(\text{vec } E^T)^T[C_{CI}(\psi_c I_{r-1}+\Lambda_C)_I^{-1}C_{CI}\otimes C_R(\psi_r I_{c-1}+\Lambda_R)^{-1}C_R]\text{vec } E^T$$

$$=tr[C_R E^T\, C_{CI}(\psi_c I_{r-1}+\Lambda_C)_I^{-1}\, C_{CI} E\, C_R(\psi_r I_{c-1}+\Lambda_R)^{-1}]$$

and

$$\log\left|V_F\right| = t(c-1)\log\left|V_C\right| + t(r-1)\log\left|V_R\right|$$

$$= t(c-1)\log\left|\psi_c I_{r-1}+\Lambda_C\right| + t(r-1)\log\left|\psi_r I_{c-1}+\Lambda_R\right|$$

where

$$D=[d_1 d_2 \ldots d_v],\ d_i=\text{vec } D_i^T,\ w=\text{vec } W^T,\ e=\text{vec } E^T,\ C_{CI}=I_t\otimes C_C$$

and

$$(\psi_c I_{r-1}+\Lambda_C)_I^{-1}=I_t\otimes(\psi_c I_{r-1}+\Lambda_C)^{-1}.$$

The parameterization of Besag & Kempton (1986) can also be used, which means the use of α's instead of ψ's. The $\alpha' s=\frac{1}{\psi' s}$ come multiplying the second term of each variance matrix. The σ_f^2 is replaced by κ^*, and if a new value of σ_f^2 is needed it can be obtained by

$$\sigma_f^2 = \alpha_r \alpha_c \kappa^* .$$

8.4.2. Relationship to row and column analysis

Although derived from a different theoretical base, the 2-D first difference analysis is closely related to a classical row and column analysis as follows.

Rewriting the estimate of τ in (8.4.2) in terms of $\mathbf{X}$ and $\mathbf{y}$

$$\hat{\tau} = (X^T\Delta^T V_F^{-1}\Delta X)^{-1} X^T\Delta^T V_F^{-1}\Delta y \ .$$

If the effects of trend are negligible, $\psi_r=\psi_c=0$, so that yields can be regard as uncorrelated, the matrix $\Delta^T\mathbf{V}_F^{-1}\Delta$ becomes

$$\Delta^T V_F^{-1}\Delta = (I_t\otimes\Delta_C^T\otimes\Delta_R^T)\,[I_t\otimes(\Delta_C\Delta_C^T)^{-1}\otimes(\Delta_R\Delta_R^T)^{-1}]\,(I_t\otimes\Delta_C\otimes\Delta_R)$$

$$= I_t\otimes[I_{rc} - (I_r\otimes J_c)/c - (J_r\otimes I_c)/r + J_{rc}/rc].$$

This identity ensures that, for $\psi_r=\psi_c=0$ (or $\alpha_r=\alpha_c=\infty$), $\hat{\tau}$ is the least squares estimate of τ based on the yields $\mathbf{y}$ and

$$I_t\otimes[I_{rc} - (I_r\otimes J_c)/c - (J_r\otimes I_c)/r + J_{rc}/rc]$$

is the sweep operator for removing the effects of row, column and replicate. This leads to an analysis that is identical to the row and column analysis when the row and column effects are considered fixed (intra-row and column analysis).

On the other hand, if $\psi_r=\psi_c=\infty$ (or $\alpha_r=\alpha_c=0$) so that the random sources of variation are negligible relative to the trend, the matrix $\Delta^T\mathbf{V}_F^{-1}\Delta$ becomes

$$\Delta^T V_F^{-1} \Delta = (I_t \otimes \Delta_C^T \otimes \Delta_R^T)\,(I_t \otimes I_{r-1} \otimes I_{c-1})\,(I_t \otimes \Delta_C \otimes \Delta_R)$$

$$= I_t \otimes (\Delta_C^T \Delta_C) \otimes (\Delta_R^T \Delta_R)\,.$$

The estimate of variety effects

$$\hat{\tau} = \{X^T [I_t \otimes (\Delta_C^T \Delta_C) \otimes (\Delta_R^T \Delta_R)]X\}^{-1} X^T [I_t \otimes (\Delta_C^T \Delta_C) \otimes (\Delta_R^T \Delta_R)]y,$$

then involves the observed yields **y** only through $[\mathbf{I}_t \otimes (\Delta_C^T \Delta_C) \otimes (\Delta_R^T \Delta_R)]\mathbf{y}$ which, except at end plots, represent second differences performed within rows and columns. As a result, $\hat{\tau}$ is approximately invariant to locally linear trend.

For the general case, where the trend components are between **0** and ∞, $\hat{\tau}$ is a compromise between the ordinary least squares estimate based on **w** (with maximum trend effect) and the ordinary least squares estimate based on **y** (with no trend effect) (Besag & Kempton, 1986). There is an analogy with the combination of intra- and inter-row and column information in the classical analysis of row and column designs.

In summary, for $\psi_r, \psi_c \neq 0$ (or $\alpha_r, \alpha_c \neq \infty$) the 2-D first difference analysis performs a kind of intra + inter-row and column analysis analogous to that carried out in the analysis of row and column designs when the row and column effects are considered random. Furthermore, it could be considered an alternative to row and column methods when the trend effects appear to be very strong.

The contrast between the two methods is that in the absence of trend the 2-D first difference analysis does not recover any information between rows and columns

whereas a full (intra+inter) row and column analysis does the maximum recovery of information and will certainly be more efficient. Conversely, in the presence of trend the 2-D first difference analysis recovers information from the trend (maximum at $\psi_r, \psi_c = \infty$ (or $\alpha_r, \alpha_c = 0$)) while the full row and column analysis does not fully recover this information and will usually be less efficient than the 2-D first difference analysis as the trend effects become strong.

8.4.3. Prediction of trend

The error term in model (8.4.1) can be rewritten as

$$e = \Delta\varepsilon + \Delta\eta = \Upsilon + \Delta\eta$$

where,

Δ is the **tn1**×**n** matrix that performs first difference (**n1=(r-1)(c-1)**),

ε is an **n**×**1** vector representing random trend and

η is an **n**×**1** vector comprising the local errors, assumed to be independent $N(0, \sigma_f^2)$ deviates.

Also, the Var(**e**) in (8.4.1) can be expanded to give

$$Var(e) = I_t \otimes (\psi_r \psi_c I_{n1} + \psi_c I_{r-1} \otimes \Delta_R \Delta_R^T + \psi_r \Delta_C \Delta_C^T \otimes I_{c-1} + \Delta_C \Delta_C^T \otimes \Delta_R \Delta_R^T) \sigma_f^2.$$

Assuming that after differencing the residual trends are stationary and independent of the local errors, that is

$$E(\Upsilon) = 0 \text{ and } cov(\Upsilon, \eta) = 0.$$

It can be shown that

$$\text{var}(\Upsilon) = I_t \otimes (\psi_r \psi_c I_{n1} + \psi_c I_{r-1} \otimes \Delta_R \Delta_R^T + \psi_r \Delta_C \Delta_C^T \otimes I_{c-1}) \sigma_f^2$$

$$= V_T \sigma_f^2 \qquad (8.4.4)$$

and

$$\text{var}(\Delta\eta) = I_t \otimes (\Delta_C \Delta_C^T \otimes \Delta_R \Delta_R^T) \sigma_f^2.$$

Although the trend effects are generally nuisance components to be removed through differencing before estimating treatment contrasts, there are occasions where their prediction are of interest; for example, to give an indication of the fertility pattern over an experimental site.

Using results from Henderson (1975), a best linear unbiased prediction of the residual trend Υ can be given as

$$\hat{\Upsilon} = \hat{V}_T \hat{V}_F^{-1} (w - D\hat{\tau}) \qquad (8.4.5)$$

for

$\hat{V}_T$ given in (8.4.4), $\hat{V}_F$ given in (8.4.1) and $\hat{\tau}$ in (8.4.2).

The estimates of the **n**-vector of trends, ε, from the **t(r-1)(c-1)**-vector of residual trends, $\hat{\Upsilon}$, is obtained minimizing the function of residual errors $\hat{\eta}^T\hat{\eta}$ subject to the side condition given in (8.4.5).

From the identity

$$\Delta\varepsilon = \hat{\Upsilon}$$

it is found that in each replicate or superblock

$$\varepsilon_{ij} = \varepsilon_{i1} - \varepsilon_{r1} + \varepsilon_{rj} - \sum_{k=i}^{r-1} \sum_{l=1}^{j-1} \hat{\Upsilon}_{kl} ,$$

$$i = 1,\ldots,r-1 \quad \text{and} \quad j = 2,\ldots,c$$

which leads to

$$\varepsilon = (I_t \otimes B)\xi - (I_t \otimes A)\hat{\Upsilon} \qquad (8.4.6)$$

for an **rc×(r-1)(c-1)** matrix **A** and an **rc×(r+c-1)** matrix **B** known.

Using (8.4.6) in the function of residual errors $\hat{\eta}^T\hat{\eta}$ and then minimizing with respect to ξ gives

$$\hat{\xi} = [I_t \otimes (B^TB)^{-1}B^T][y - X\hat{\tau} + (I_t \otimes A)\hat{\Upsilon}].$$

As a result in each replicate the trend effects are then predicted first obtaining

$$\hat{\varepsilon}_{i1} = [(r + c - 1)(y_{i1} - \hat{\tau}_{[i1]}) + (c - 1)\sum_{k\neq i=1}^{r}(y_{k1} - \hat{\tau}_{[k1]})$$

$$+ (r - 1)\sum_{l=2}^{c}(y_{i1} - \hat{\tau}_{[il]}) - \sum_{k\neq i=1}^{r}\sum_{l=2}^{c}(y_{kl} - \hat{\tau}_{[kl]})$$

$$+ \sum_{\substack{k=1\\ i\neq 1}}^{i-1}\sum_{l=1}^{c-1}(-k)(c - l)\hat{\Upsilon}_{kl} + \sum_{k=i}^{r-1}\sum_{l=1}^{c-1}(r - k)(c - l)\hat{\Upsilon}_{kl}]/rc$$

$$i = 1, \ldots, r$$

and

$$\hat{\varepsilon}_{rj} = [(r + c - 1)(y_{rj} - \hat{\tau}_{[rj]}) + (c - 1)\sum_{k=1}^{r-1}(y_{kj} - \hat{\tau}_{[kj]})$$

$$+ (r - 1)\sum_{l\neq j=1}^{c}(y_{rl} - \hat{\tau}_{[rl]}) - \sum_{k=1}^{r-1}\sum_{l\neq j=1}^{c}(y_{kl} - \hat{\tau}_{[kl]})$$

$$+ \sum_{k=1}^{r-1}\sum_{l=1}^{j-1}(k)(l)\hat{\Upsilon}_{kl} + \sum_{k=1}^{r-1}\sum_{l=j}^{c-1}(-k)(c - l)\hat{\Upsilon}_{kl}]/rc \quad ,$$

$$j = 2,\ldots,c$$

and using them in

$$\hat{\varepsilon}_{ij} = \hat{\varepsilon}_{i1} - \hat{\varepsilon}_{r1} + \hat{\varepsilon}_{rj} - \sum_{k=i}^{r-1}\sum_{l=1}^{j-1}\hat{\tau}_{kl} \ ,$$

$$i = 1,\ldots,r-1 \quad \text{and} \quad j = 2,\ldots,c$$

where $\hat{\tau}_{[..]}$ denotes the estimated treatment effect on the (..) plot.

8.5. First-difference model applied to PBI and SCRI trials

The SCRI and PBI trials described in Section 3.2 were analysed using the 2-D FD model described in Section 8.4. Ten of the SCRI trials had between 1 and 6 missing values which were replaced by their estimates from a randomized complete block analysis. This is adequate for comparative purposes and follows the procedure of Patterson & Hunter (1983).

In the 2-D FD model the plot neighbour relationship can operate within replicates or crossing replicates. This specification allows for situations where the superblocks (replicates) are physically separated in the field. The row and column size chosen correspond to those specified for the array of each replicate of the design. A further row and column size given by the whole trial was allowed for the PBI trials. In other words, for the SCRI trials the 2-D FD analysis was carried out only within superblocks, while for PBI trials in addition it was also allowed to cross superblocks boundaries where the

superblocks were arranged in 2×2 array.

The program used was based on a Genstat procedure written by Mr R Kempton of Scottish Agricultural Statistics Service (SASS) who has kindly permitted me to use and adapt it. The results of applying the 2-D FD analysis are summarized in Table 8.5.1 for SCRI trials and in Table 8.5.2 for PBI trials. For comparison the results for row and column and randomized complete block analyses are also given.

Although the parameterization in Section 8.4 follows Cullis & Gleeson (1991) all trials, except two of the SCRI, were analysed following the parameterization of Besag & Kempton (1986). This parameterization seems to be worthwhile to use when there is low effect of trend; it avoids the boundary restriction of α's=0 and the convergence is much quicker. The parameterization of Cullis & Gleeson (1991) is better when trend effects are large for the same reason.

The efficiency for a single row and column (or 2-D FD) analysis was measured as the ratio of (**a**) the average variance of all varietal differences from the randomized complete block analysis ignoring row and column to (**b**) the average variance of all varietal differences from the full (intra+inter) row and column (or 2-D FD) analysis (Yates, 1940a; Patterson & Robinson, 1989). In addition the efficiency of the 2-D FD analysis was also measured relative to the row and column analysis, following recommendations that comparison should also be made with the best available classical design (Patterson, 1983;

Bartlett, 1985).

The choice of which method of analysis is to be used depends upon the importance of validity or efficiency to those concerned. Baird & Mead (1991) show evidences that the generalized least squares estimator of treatment precision under ML estimation in one dimension is biased downward, although it is not known whether this is also true for two dimensions. So, in view of Tables 8.5.1 and 8.5.2 it is important to remember that the average variances for the 2-D FD model may be biased. For our analysis a less biased estimator for treatment precision was used (Martin, 1990) by correcting dfs for parameter estimates.

The distributions of statistics presented in Tables 8.5.1 and 8.5.2 are positively skewed as expected.

The 2-D FD analysis shows mean variances that are less, for SCRI trials, or equal, for PBI trials, to the mean variances of the row and column analysis. Nevertheless the variances have wider range than those given by the full row and column analysis.

Considering the analyses using the row and column size prescribed by the original row and column design (within replicates) and assuming estimates of error are unbiased a 2-D FD analysis of SCRI trials (Table 8.5.1) resulted in an increase in efficiency relative to a randomized complete block analysis of at least 70% in more than half of the trials, while a row and column analysis resulted in at least 60%. Smaller gains were achieved for PBI trials (Table 8.5.2). The increase in efficiency for 2-D FD

Table 8.5.1. Results of efficiency ($\mathcal{E}$), average variance of pairwise difference (APV) and others parameters for 2-D first differenced (2-D FD), intra row and column (RCtra), full row and column (RCter) and randomized complete block (RCB) analyses over 60 SCRI trials.

	Analysis	Min	25%	**50%**	75%	Max	**Mean**
$\mathcal{E}$	2-D FD cf. RCB	0.73	1.18	**1.75**	2.82	4.80	**2.00**
	RCtra cf. RCB	0.61	1.01	**1.31**	1.79	4.15	**1.49**
	RCter cf. RCB	0.96	1.29	**1.61**	2.06	4.49	**1.76**
	2-D FD cf. RCtra	0.96	1.09	**1.27**	1.49	2.06	**1.33**
	2-D FD cf. RCter	0.71	0.89	**1.06**	1.28	1.75	**1.10**
	RCter cf. RCtra	1.07	1.14	**1.19**	1.26	1.59	**1.22**
APV	2-D FD	0.008	0.011	**0.015**	0.040	0.142	**0.027**
	RCtra	0.008	0.015	**0.020**	0.051	0.149	**0.036**
	RCter	0.007	0.013	**0.017**	0.043	0.112	**0.029**
	RCB	0.008	0.019	**0.035**	0.079	0.155	**0.048**
α	row	0.000	0.000	**0.000**	0.002	1473	-
	column	0.000	0.000	**0.000**	0.006	2181	-
σ^2	2-D FD	0.000	0.000	**0.000**	0.000	0.013	**0.001**
	RCtra	0.005	0.010	**0.013**	0.033	0.098	**0.023**
	RCter	0.006	0.010	**0.013**	0.033	0.098	**0.023**
	RCB	0.008	0.019	**0.034**	0.079	0.155	**0.048**

Table 8.5.2. Results of efficiency ($\mathcal{E}$), average variance of pairwise difference (APV) and others parameters for 2-D first differenced (2-D FD), intra row and column (RCtra), full row and column (RCter) and randomized complete block (RCB) analyses over 44 PBI trials.

	Analysis	Min	25%	**50%**	75%	Max	**Mean**
$\mathcal{E}$	2-D FD cf. RCB	0.82	0.99	**1.17**	1.61	4.03	**1.38**
	2-D FD† cf. RCB	0.86	1.10	**1.21**	1.60	4.19	**1.46**
	RCtra cf. RCB	0.82	0.95	**1.08**	1.40	2.73	**1.22**
	RCter cf. RCB	1.03	1.11	**1.24**	1.56	2.82	**1.38**
	2-D FD cf. RCtra	0.98	1.00	**1.05**	1.13	1.54	**1.11**
	2-D FD cf. RCter	0.80	0.88	**0.92**	1.01	1.44	**0.98**
	2-D FD† cf. RCter	0.72	0.94	**1.00**	1.09	1.84	**1.03**
	RCter cf. RCtra	1.03	1.09	**1.14**	1.18	1.26	**1.14**
APV	2-D FD	0.007	0.013	**0.019**	0.027	0.157	**0.023**
	2-D FD†	0.006	0.012	**0.018**	0.024	0.148	**0.022**
	RCtra	0.007	0.015	**0.022**	0.028	0.154	**0.025**
	RCter	0.007	0.014	**0.019**	0.024	0.125	**0.022**
	RCB	0.012	0.019	**0.025**	0.032	0.128	**0.028**
α	row	0.000	1.697	**3.850**	119.6	1359	-
	row†	0.208	3.450	**6.797**	17.59	471.7	-
	column	0.116	2.463	**11.42**	341.8	3915	-
	column†	0.674	6.619	**9.332**	49.49	1221	-
σ^2	2-D FD	0.000	0.011	**0.020**	0.027	0.235	**0.024**
	2-D FD†	0.002	0.015	**0.024**	0.032	0.224	**0.029**
	RCtra	0.011	0.022	**0.034**	0.042	0.231	**0.038**
	RCter	0.011	0.022	**0.034**	0.042	0.231	**0.038**
	RCB	0.023	0.037	**0.051**	0.064	0.257	**0.056**

† row and column size 14x14

analysis was at least 15% in more than half of the trials whereas a row and column analysis was at least 20%. The improvement in efficiency relative to a row and column analysis is also important. The arithmetic mean and the median of the ratio of the pairwise variance of an full row and column analysis to that for a 2-D FD analysis are respectively 1.10 and 1.06 for SCRI trials and 0.98 and 0.92 for PBI trials.

The results in Table 8.5.2 also include the 2-D FD analysis with row and column size given by the whole trial (14×14); going across replicates. There is a small increase in efficiency, relative to an RCB analysis, in changing the row and column size from 7×7 to 14×14. The gains are 38% and 46% respectively. This is intuitively sensible since the increased area covered by a larger row and column array of plots is likely to be more variable and a larger array will enable more accurate estimation of that variability. Increasing efficiency of a neighbour analysis as the array of plots increase is also reported in Cullis & Gleeson (1989) and in Williams (1986a) for one dimension.

In Section 8.4.2 it is shown that when $\alpha_r, \alpha_c = \infty$ the intra-row and column analysis is the limiting case of the 2-D FD analysis. Figures 8.5.1 and 8.5.2 illustrate this. They show the square root of the efficiency of the 2-D FD, intra-row and column and full (intra+inter) row and column analyses relative to RCB analysis for each trial. Similar arguments to those in Section 8.4.2 were also used in one dimension by Besag & Kempton (1986) for $\alpha=\infty$.

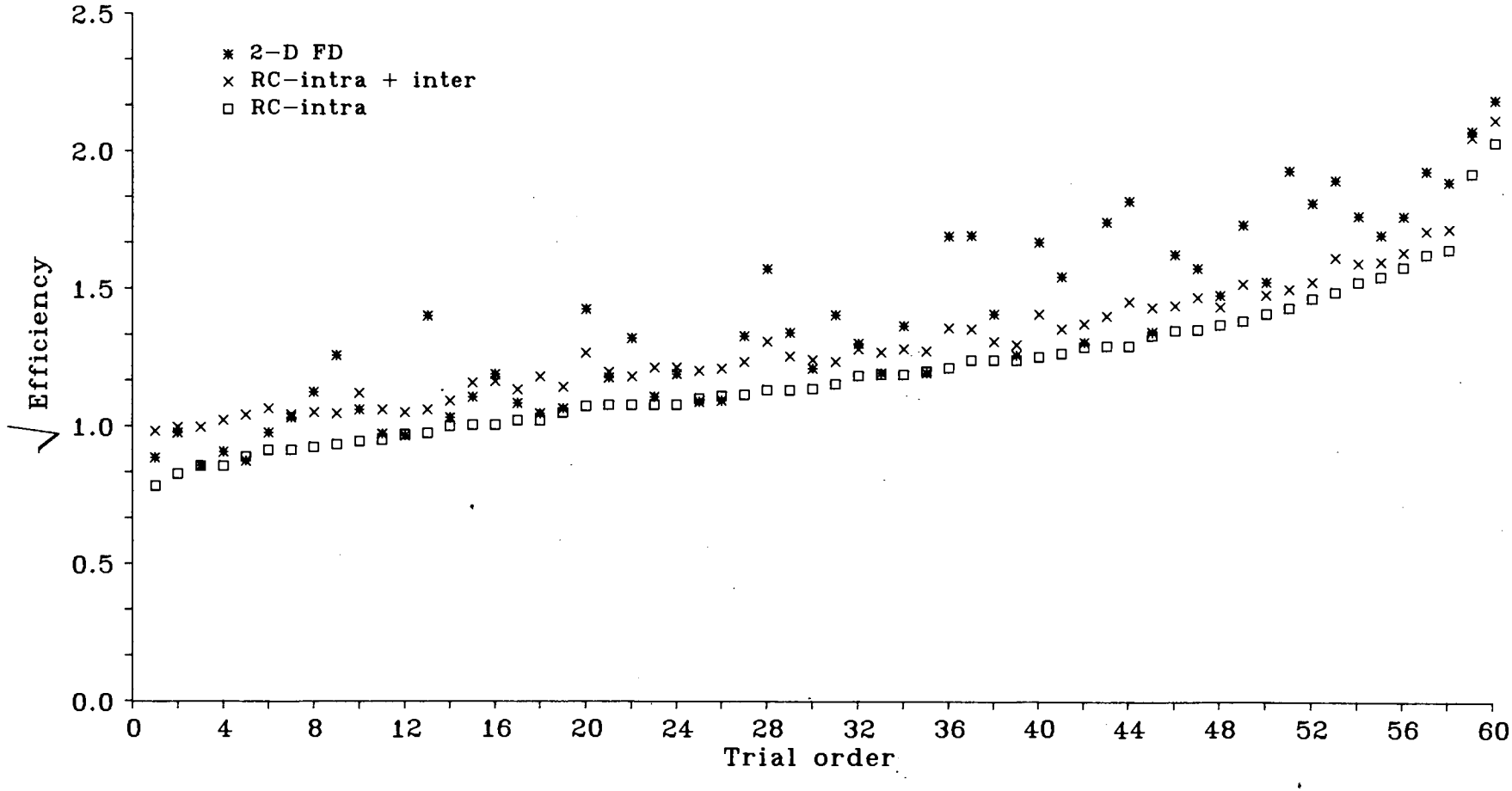


Figure 8.5.1. Efficiency of 2-D first differenced (*), full row and column (×) and intra row and column (□) analyses relative to randomized complete block analysis - SCRI trials

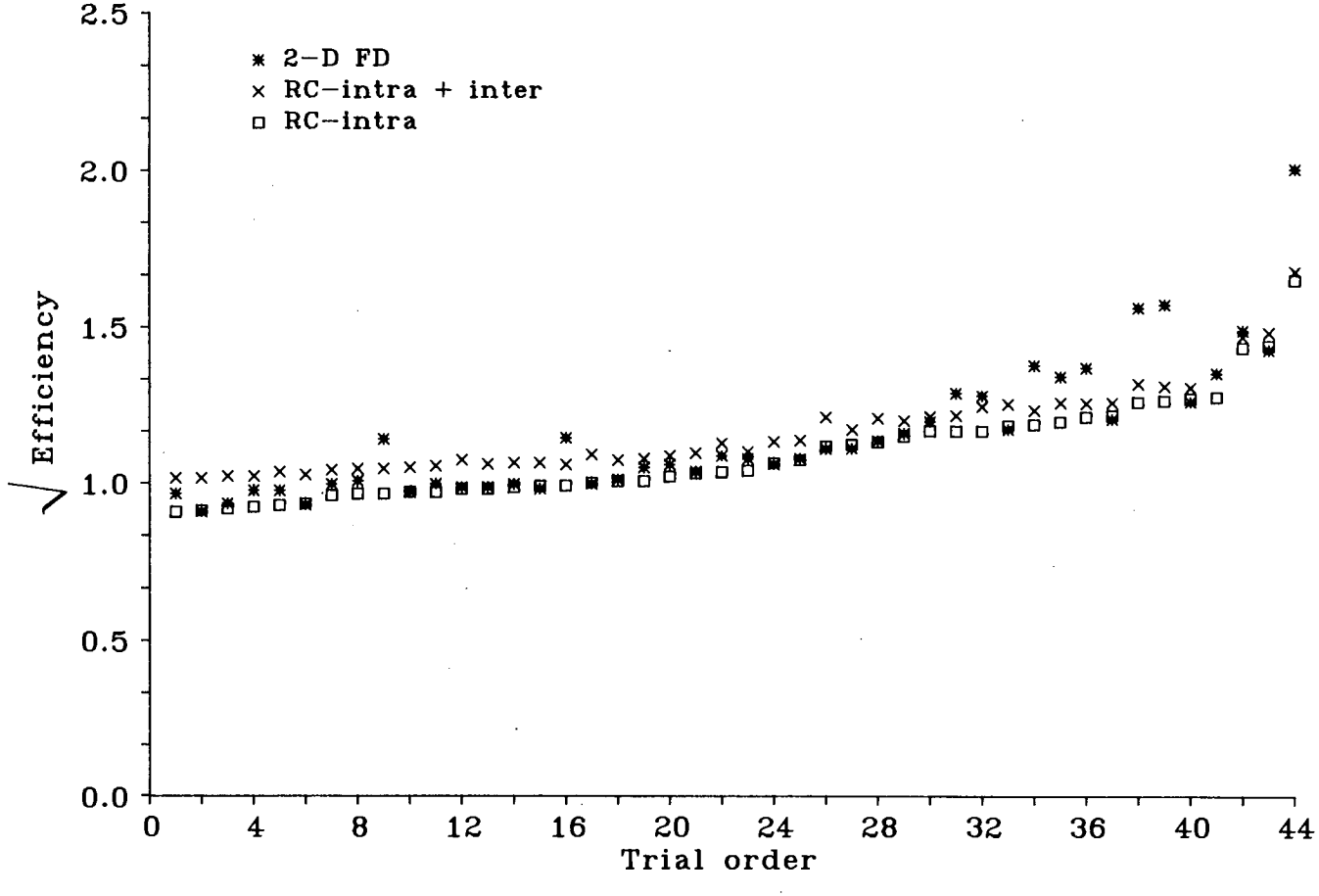


Figure 8.5.2. Efficiency of 2-D first differenced (*), full row and column (×) and intra row and column (□) analyses relative to randomized complete block analysis - PBI trials

Another feature illustrated in Figures 8.5.1 and 8.5.2 and already put forward in Section 8.4.2 is that where the full row and column analysis is making large gains over the RCB analysis, the gains of 2-D FD analysis is generally even larger. In other words when there is a sizeable trend the 2-D FD model is usually much more appropriate than the row and column model. This characteristic was also reported in one dimension for some neighbour analysis with relation to incomplete block analysis (Williams, 1986a, b; Baird & Mead, 1991). In 34 out of 60 SCRI trials and in 12 out of 44 PBI trials the 2-D FD analysis is more efficient than the full row and column analysis.

From the results of Chapter 6 it is possible to calculate the white noise level for SCRI and PBI trials under the 2-D EV model. Although the SCRI and PBI trials have different overall correlation between plots, the white noise level in the PBI trials is one and three quarter times larger than the white noise level in the SCRI trials. Patterson & Hunter (1983) show that change in the correlation and in the white noise level can have large effects on the efficiency of the analysis; the lower the white noise level the higher the efficiency. Examination of Tables 8.5.1 and 8.5.2 confirm this point.

Long narrow plots are important and widely used in variety trials (Patterson & Silvey, 1980). However the use of small plots is more typical in breeders' trials where limitations of seed and space result in compact trials restricting the use of long narrow plots. The results in

this section support previous findings that, when small plots are used, two-dimensional methods are preferable to one-dimensional methods (Kempton & Howes, 1981; Robinson *et al.*, 1988). They also confirm what was expected in Chapter 6 that 2-D analysis would increase efficiency in both data sets, the PBI gains being far behind those of SCRI gains.

The potential for increase efficiency from using a 2-D FD analysis, relative to a RCB analysis, is clearly evident in the results presented. The gains are modest when compared with those already achieved by the use of a full row and column analysis, being noticeable only when there is substantial trend. These gains are comparable with those related by Cullis & Gleeson (1989) in one dimension.

These results suggest that the 2-D FD model should be used when there is considerable trend. However at present there are no indications whether the estimates of error are unbiased or nearly so, as has been shown in one dimension (Kempton & Howes, 1981; Wilkinson *et al.*, 1983; Besag & Kempton, 1986; Williams, 1986b; Lill *et al.*, 1988; Baird & Mead, 1991). On the other hand the row and column model, although sometimes less appropriate in the presence of substantial trend, may always be justified by randomization theory. This ensures that on the average, over all randomizations, the estimates of standard error from the analysis are unbiased. Thus for the time being the neighbour model should be considered as useful non-routine method of analysis, while its theoretical

background is further developed.

Chapter 9

CONCLUSIONS

9.1. Introduction

This thesis has been mainly concerned with the methods of examining the errors of agricultural field plot experiments and its practical applications when plots are arranged in two dimensions.

This chapter presents the main achievements of these investigations and also suggests some possible areas for future work.

9.2. Main achievements

From the development and application of the methods derived in Chapter 5, the following conclusions can be made about variety trials with small plots:

i) On average, the plot to plot variability of trials data arranged in a rectangular array of plots can be described by a two-dimensional exponential variance error law.

ii) The derived error law can be employed to predict efficiency and optimal block dimensions to be used when designing future trials.

iii) The optimum block dimension for maximum efficiency is likely to be near-square if correlations in the two directions are nearly equal.

iv) The error laws for the SCRI and PBI trial series differ. It is suggested that this may be due to location of the trial sites, years of trialling, and plot or trial size.

v) Series of trials with error laws similar to those of SCRI and PBI trials are likely to benefit by the use of two-dimensional designs and analysis, for example row and column design and analysis.

vi) For SCRI and PBI trial series and other similar series of trials, the plot correlation structure can be utilised in a two-dimensional neighbour methods of analysis.

vii) The two-dimensional first difference neighbour analysis may be derived from the linear approximation to the exponential variance model. An intra-row and column analysis is its limiting case when no trend effect is present.

9.3. Additional achievements

Concerning the classical method of analysis the following main conclusions were derived:

i) The recovery of inter-row and column treatment information is simplified for row and column designs that have the property of adjusted orthogonality.

ii) For these designs, the estimate of the ratio of the row stratum variance to the row × column stratum variance can be expressed as a function of

the error mean squares from the analysis of the IB column component design and RC design. Similarly, the estimate of the ratio of the column stratum variance to the row × column stratum variance can also be expressed as a function of the error mean squares from the analysis of the IB row component design and RC design. The estimates of these two ratios are required for recovery.

iii) Inter-row and column treatment information should be recovered for every trial since ignoring this information can result in a substantial reduction in the efficiency of a trial analysis.

The application of postblocking and pairblocking in one dimension to tropical variety trials allow us to say:

i) Postblocking and pairblocking are very useful and effective to derive error laws for variety trials even when crop and the management of crop and trials are totally different from those for which the techniques were derived.

ii) On averaging over all trials, the exponential variance error law derived has very different parameters from those for cereal in the UK. The values of λ and ρ are much smaller in the cereal maize trials.

iii) The optimum block size for the most efficient IB design is likely to be approximately equal to the square-root of the number of varieties, as with UK cereal trials.

iv) Based on the values of the parameters in the error law, there is unlikely to be much benefit from using a neighbour analysis.

9.4. Possible topics for further research

In this work, the derivation and application of postblocking and pairblocking techniques to two dimensions to assess the possible benefits of applying various analyses to particular series of trials had been illustrated. An obvious extension is to trial series for other crops, variates and plot sizes and shapes.

The variance-distance model considered assume that errors are either random or due to soil variation. However, plants on neighbouring plots often compete with each other for air and light. Competition effects are far from random. They are likely to introduce biases which persist over replicates and even trials and seasons. Separation of soil and competition effects constitutes a very important practical issue.

The two-dimensional exponential variance error law was found to describe the error structure of trials data reasonably well. However, in practice, individual trials will not follow an exponential or any other functional error law exactly. The consequence of using a two-dimensional neighbour model when the error laws do not hold exactly is a matter that needs to be studied.

Dependent on the method of analysis, the analysis of a trial may be biased. The effect of a possible bias in the

analysis of any single trial may be reduced if results are averaged over a number of trials. Another theoretical research would be consider a broad study of the validity of postblocking and pairblocking to include applications where its validity does not apply.

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