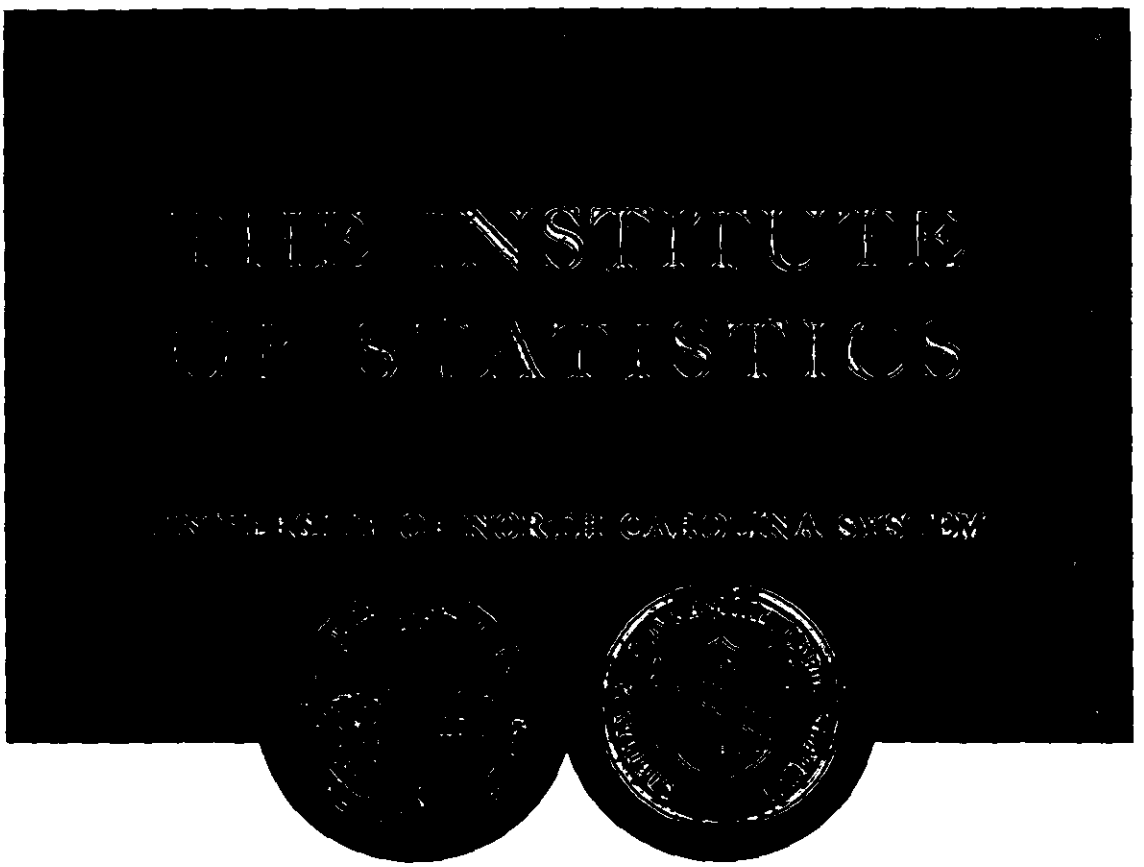


A COMPARISON OF METHODS THAT INCLUDE ESTIMATION OF SPATIAL VARIATION IN THE ANALYSIS OF DATA FROM YIELD TRIALS

by

Cavell Brownie, Daryl T. Bowman, and Joe W. Burton

Institute of Statistics Mimeo Series No. 2236

September, 1992

NORTH CAROLINA STATE UNIVERSITY
Raleigh, North Carolina

MIMEO SERIES #2236

Cavell Brownie, D
Daryl T. Bowman and
Joe W. Burton

A COMPARISON OF METHODS THAT INCLUDE ESTIMATION OF SPATIAL VARIATION IN THE ANALYSIS OF DATA

A Comparison of Methods that Include Estimation of Spatial Variation in the Analysis of Data from Yield Trials.

Cavell Brownie,

Daryl T. Bowman*,

and

Joe W. Burton

Cavell Brownie, Dep. of Statistics, Box 8203, Daryl T. Bowman and Joe W. Burton, Crop Science Dep., Box 7620, North Carolina State University, Raleigh, NC 27695. *Corresponding author.

Abbreviations: CE, correlated errors; NN, nearest neighbor; RCBD, randomized complete block design.

A Comparison of Methods that Include Estimation of Spatial Variation in the Analysis of Data from Yield Trials.

ABSTRACT

In large yield trials, variation in soil fertility (or, more generally, yield potential) can result in substantial heterogeneity within blocks, and hence in treatment estimates with poor precision. Methods for improving precision include statistical analyses in which this spatial variation is accounted for in the estimation of treatment or entry means. Three such types of "spatial" analysis are reviewed; trend analysis, the Papadakis method, and analyses based on "correlated errors" models which account for spatial variation through correlations between yields of neighboring plots. It is noted that, unlike the classical analyses which can be justified solely on the basis of the randomization employed in the experimental design, validity of these "spatial analyses" in typical field situations is not guaranteed. Properties of these techniques are discussed and the subjectivity involved in specifying a model for the spatial variation is emphasized. Performance of the methods is illustrated using data from two corn *(Zea mays* L.) yield trials and a soybean (*Glycine max* L.) trial, each of which showed evidence of heterogeneity within blocks. In comparison to the classical randomized blocks analysis, precision tended to be best for the trend and the trend plus correlated errors analyses, with the Papadakis method intermediate. Results for ranking of entries differ across analyses because each analysis adjusts for spatial variation in a different way. Although using a spatial analysis technique can improve precision, it can be difficult to determine which specific analysis is the most appropriate for a given data set.

Many field trials in agriculture, including trials to determine genotypic yield potential, are carried out using a complete block design. As is well known, the purpose of blocking is to increase precision by ensuring that within a block treatments are evaluated with respect to similar environmental (and operational) conditions. Heterogeneity among plots within a block causes the estimate of a difference between two treatments to vary across blocks, and the greater the heterogeneity within blocks, the greater the variation in estimates of treatment effect and the poorer the precision of the study. Even with uniform cultivation practices, there may be considerable variation in soil properties among plots in a block, and in general, the larger the required block size, the greater is the within-block heterogeneity. Accordingly, efficiency of the randomized complete block design (RCBD) tends to be poor in trials involving a large number of treatments. To increase precision in such a trial, one approach is to reduce block size by employing an incomplete block design such as a lattice, lattice square, or one of the more flexible but potentially less efficient α-designs (Patterson et al., 1978). Another approach is to use a method of analysis which utilizes information in plot position to estimate and "correct for" spatial variation in yield potential due, for example, to differences among plots in soil fertility, moisture, or even pest populations. These analyses require contiguous or regularly spaced plots, arranged in a strip or rectangular grid, but given an appropriate layout can be applied to data from a complete or incomplete block design.

Increasing efficiency via an analysis which includes estimation of spatial variation in yield potential has been the focus of a number of recent articles in the agronomy and soil science literature. Several methods have been described, including trend analysis (Kirk et al., 1980; Tamura et al., 1988; Bowman, 1990), and the Papadakis method (e.g., Warren and Mendez, 1982), also called nearest neighbor (NN) analysis (Bhatti et al., 1991), or Productivity Covariate analysis (Longer and Risley, 1983). There is considerable confusion in terminology, however, and the properties and relative merits of different methods (and the many variations on each) are not well understood. Another potential source of confusion is that in promoting trend or NN analyses, there has been a tendency to compare different methods of analysis

solely on the basis of error mean squares calculated for a limited number of data sets. Recommendations have been based on the assumption that the best method is that which produces the smallest calculated 'error', and there has been little attention given to validity of estimates of precision or corresponding tests of hypothesis. In making comparisons with the traditional randomized block analysis, there has also been a tendency to misrepresent the properties of this analysis, especially properties that are a consequence of randomization which is an integral part of the experimental design.

The goals of this article are therefore (i) to review the role of randomization in the classical analysis, (ii) to describe the main types of analysis which include estimation of spatial variation, and (iii) to provide a more balanced assessment of the properties of these methods, including comparisons with the classical analyses. Illustrative examples are taken from corn (*Zea mays* L.) and soybean *(Glycine max* L.) yield trials, and treatments are referred to as entries throughout.

VALIDITY OF THE RCB ANALYSES

The assumptions usually listed for validity of the RCB analysis include independent and identically distributed (iid) errors. It is less frequently noted that the classical analysis can be justified solely on the basis of the chance distribution induced by the design principle of random assignment of entries to plots within blocks (Kempthorne, 1952). This property of the RCBD is reviewed here because of a concern that promoting the use of procedures which account for spatial variation could actually lead to suggestions that randomization is either inappropriate or unnecessary when systematic heterogeneity is present.

The reason for randomization in experimental design is to provide unbiased estimates of treatment effects or contrasts, and to provide valid estimates of residual variation or precision (Steel and Torrie, 1980). When heterogeneity or even systematic trends are present within blocks, assuming only additivity of entry effects, randomization ensures that, averaging over all possible assignments or layouts, the difference between two entries is estimated without bias. (Alternatively, we may think of the difference between entry means being unbiased when

averaged over a large number of blocks.) Randomization also provides a framework in which the traditional estimates of precision, and tests of hypothesis, are valid (Williams, 1986; Baird and Mead, 1991). Thus 'biases' in treatment means reported by Tamura et al. (1988) represent results for a single field layout and ignore the role of randomization in the RCBD entirely. Also, contrary to statements in Bhatti et al. (1991), validity of the traditional analysis does not require that 'soil . . . properties exhibit random variability with little or no spatial correlation.' Also incorrect are statements in Kirk et al. (1980) to the effect that estimates of error and tests of significance for the "standard" analysis are biased. The presence of undetected systematic variation within blocks does not invalidate the classical RCB analysis, rather it strengthens the case for random allocation of treatments. On the other hand, substantial heterogeneity within blocks results in estimates that are highly variable, so that a nontraditional method of analysis might be considered in order to improve precision.

To motivate the nontraditional analyses, suppose that for a particular trial there is considerable spatial heterogeneity in the site, and that the yield potential (e.g., fertility) happens to be known for every plot. An efficient analysis would make use of these values and accordingly adjust observed yields to obtain estimates of differences between entries. In practice, plot yield potentials will, of course, be unknown but it seems reasonable to consider the joint estimation of fertility trends and entry effects. To do this requires making assumptions about the nature of spatial variation, and validity of the resulting "spatial" analysis will depend on whether model assumptions are met or not. The problem is therefore to compare two different types of analysis where each has a different basis for validity. The physical process of randomization provides a basis for validity of the classical RCB analysis, while the validity of analyses which estimate spatial variation depends on assumptions that are impossible to verify for a single data set. To permit meaningful comparisons among analyses, it is important, therefore, to investigate conditions under which the non-traditional analyses yield valid tests of hypotheses and estimates of precision. Results of such investigations are reported for the non-traditional spatial analyses described below.

ANALYSES WITH ESTIMATION OF SPATIAL VARIATION

The analyses described below assume a rectangular axb layout of plots, with row position indexed by R_i, i = 1,...,a, and column position by C_j, j = 1,...,b. Each of the t entries is replicated r times, so that the total number of plots in the grid is ab = rt. For the plot in row i and column j, plot (i,j), let Y_{ij} represent the observed yield, T_{ij} the unknown yield potential, and $\tau_{k(ij)}$ the effect for the entry assigned to this plot. Then a model which incorporates spatial variation is

$$Y_{ij} = \mu + \tau_{k(ij)} + T_{ij} + \epsilon_{ij} \qquad [1]$$

where μ is an overall mean, $\tau_{k(ij)}$ and T_{ij} are assumed to be fixed effects, and the ϵ_{ij} are random errors with $E(\epsilon_{ij}) = 0$.

As noted in Zimmerman and Harville, 1991, spatial variation can be incorporated in this model at two levels. Major trends can be modelled as part of the mean through the T_{ij} term, and small scale dependence can be included by allowing correlations between the plot errors ϵ_{ij}. The methods of analysis discussed below differ in the assumptions made about the T_{ij} and ϵ_{ij}. The linear model for the RCB analysis is a special case of Eq. [1] with the ϵ_{ij} assumed iid and the value of T_{ij} depending only on the complete block or replicate in which plot (i,j) is located.

Trend Analysis.

The term trend analysis has been used to describe an analysis based on the model in Eq. [1] with the ϵ_{ij} assumed to be iid, and T_{ij} assumed to be a polynomial function of R_i and C_j (for more detail, see Kirk et al., 1980; Tamura et al., 1988; Bowman, 1990; or Warren and Mendez, 1982, who use the term polynomial regression rather than trend analysis). As an example, assume that yield potential can be represented by a 2nd degree polynomial response surface (c.f. Zimmerman and Harville, 1991). Then trend analysis corresponds to fitting the model in Eq. [1] with

the ϵ_{ij} assumed iid, $Var(\epsilon_{ij}) = \sigma^2$, and

$$T_{ij} = b_1R_i + b_2C_j + b_3R_i^2 + b_4C_j^2 + b_5R_iC_j \, . \qquad [2]$$

Note that block effects are not included in Eqs. [1] and [2] on which trend analysis is based. This is because one of the arguments given for trend analysis is that boundaries between contiguous blocks are artificial in the sense that yield potential is not likely to change abruptly along straight lines corresponding to these boundaries. Including a term for blocks in Eq. [1] or [2] would result in a model for yield potential with discontinuities along block boundaries, whereas trend analysis assumes that yield potential varies in a smooth manner.

Under the model given by Eqs. [1] and [2], estimates of the entry means (corrected for differences in yield potential between plots) and of the parameters $b_1, \ldots, b_5$, as well as tests of significance, are easily obtained using PROC GLM in SAS (version 6.07; SAS Institute, Cary, NC). Kirk et al. (1980) explain that fitting the polynomial response surface corresponds to partitioning out of "error" the systematic component of heterogeneity, and estimates of precision are based on the remaining random component only. Examples are given of the increase in (calculated) precision achieved by reducing error in this way.

Although trend analysis can result in increased efficiency, potential shortcomings of this approach should not be overlooked. These include problems associated with overfitting or with using an incorrect model. Overfitting occurs if the true function for T_{ij} is a polynomial but we fit a polynomial with too many terms. Fitting an incorrect model occurs if too few terms are fitted, or if the true function cannot be modeled as a polynomial. Overfitting tends to add noise (rather than bias) to estimates of entry means, and can lead to poor performance because of near confounding between polynomial terms and entry effects. Fitting an incorrect model will result in biased estimates of entry effects and can lead to inflated (i.e., larger than nominal) type I error rates. For data sets where strong trends are evident, however, numerical studies suggest that the increase in precision will often more than compensate for bias which results when the polynomial is at best an approximation (e.g., Zimmerman and Harville, 1991).

An important component of trend analysis, therefore, is deciding how to select the polynomial function for T_{ij}. One approach is to always use a polynomial of high degree.

Warren and Mendez, 1982, suggested an 8th degree polynomial, but did not assess validity of estimates of precision or tests of significance. Another approach is to select the terms of the polynomial by means of an algorithm analogous to procedures used for variable selection in stepwise regression (Kirk et al., 1980; Tamura et al., 1988). This selection algorithm involves performing a number of preliminary tests of significance to determine the terms to be included in T_{ij}. As a consequence, p-values based on the final model are likely to be liberal (too small), and estimates of precision are likely to be optimistic. In a limited numerical study, Tamura et al. (1988, Table 3) indeed found inflated Type I error rates for the test for differences between entries. To improve Type I error rate properties, Tamura et al. suggested that a significance level of .01 be used in determining the polynomial terms to be included in T_{ij}.

Variations on trend analysis therefore include different procedures for choosing the polynomial for T_{ij}. Other variations involve specifying functions other than polynomials based e.g., on Fourier series expansions (Warren and Mendez, 1982). Problems associated with specifying the degree of the polynomial function for T_{ij} are also encountered with other types of series approximation.

Papadakis analysis.

Although it is difficult to describe a rigorous basis for this analysis (e.g., Kempton and Howes, 1981), the Papadakis method has considerable intuitive appeal. A residual is calculated for each plot by subtracting the appropriate entry mean from the plot yield. A measure of yield potential, X_{ij}, is then computed for each plot as the average of the residuals for the neighboring plots. Adjusted means are obtained for entries by treating the measures X_{ij} as values of a covariate. That is, adjusted means for entries are based on fitting the model

$$Y_{ij} = \mu + \tau_{k(ij)} + bX_{ij} + e_{ij} \qquad [3]$$

where, for interior plots,

$$X_{ij} = 1/4\ (r_{i,j-1} + r_{i,j+1} + r_{i-1,j} + r_{i+1,j}), \qquad [4]$$

$$r_{ij} = Y_{ij} - \bar{Y}_{k(ij)}, \qquad [5]$$

and $\bar{Y}_{k(ij)}$ is the mean yield for the entry assigned to plot (i,j).

For border plots, X_{ij} is the mean of the r_{ij} for the 2 or 3 neighboring plots.

As with trend analysis, blocks are ignored when carrying out the Papadakis analysis. Again, this is because including block effects would introduce seemingly artificial discontinuities in yield potential for plots that are adjacent but in different blocks. The Papadakis analysis is sometimes described as an analysis of covariance, but note that X_{ij} is not a true covariate because the r_{ij} are calculated from the observed yields Y_{ij}. Versions of the Papadakis analysis are also referred to as nearest neighbor analyses (Bhatti et al., 1991; Pearce and Moore, 1976), however the term (nearest) neighbor analysis is also used in a generic way to denote any analysis which utilizes information from neighboring plots in accounting for spatial variation. The Papadakis analysis, including calculation of adjusted entry means, can readily be implemented using SAS (see Appendix).

Variations on the Papadakis method include using different subsets of residuals to compute X_{ij}. For example, X_{ij} may be computed from residuals of neighbors in the same row only [$X_{ij} = 1/2\ (r_{i,j-1} + r_{i,j+1})$]. Also, more than one "covariate" may be fitted, so that Eq. [3] may contain one "covariate" for residuals in the same row and a second for residuals in the same column (e. g., Zimmerman and Harville, 1991). Yet another variation is the iterated Papadakis method (e. g., Bartlett, 1978) in which Eq. [3] represents step 1, and the adjusted means from Eq. [3] are used to calculate step 2 residuals $r_{ij}^{(2)}$ and yield potentials $X_{ij}^{(2)}$. Step 2 adjusted means are then obtained by fitting the model in Eq. [3] with X_{ij} replaced by $X_{ij}^{(2)}$. The process is repeated until adjusted means from consecutive steps are approximately the same.

Properties of the Papadakis analysis are difficult to determine theoretically. Several numerical studies (e.g., Binns and Jui, 1985) of the performance of the method have concluded that the uniterated version lacks efficiency, while the iterated method produces tests with inflated Type I error rates. The inefficiency of the uniterated version is attributed, in part, to the fact that plot yield potentials and entry effects are not estimated jointly. Studies comparing versions with X_{ij} calculated from different subsets of residuals (e.g., Pearce and

Moore, 1976; Longer and Risley, 1983) have confirmed that no single version will be best for all fields or patterns of soil heterogeneity. Selecting the best "covariate(s)" for a particular data set leads to problems analogous to those associated with choosing the polynomial function in trend analysis.

Models with correlated errors.

The most recently developed methods of analysis are based on models that account for small scale variation in soil properties through correlations between the plot errors ϵ_{ij}. Typically, these models assume that the strength of the correlation between two errors, Corr (ϵ_{ij}, ϵ_{lm}), is greatest for adjacent plots, and diminishes as the distance between the plots increases. These models and corresponding analyses are more complex to describe and implement than are either trend analysis or the Papadakis method. Most of the proposed models are included in the general formulation given by Zimmerman and Harville (1991), but only methods that are easily implemented with SAS are considered here. For example, Zimmerman and Harville (1991) studied a modification of the model in Eq. [1] where T_{ij} is a second degree polynomial and the correlation between plots decays exponentially as the distance between the plots (or plot centers) increases. Specifically, this model is given by Eqs. [1] and [2], with

$$\text{Cov}(\epsilon_{ij}, \epsilon_{lm}) = \sigma^2 \text{ Corr } (\epsilon_{ij}, \epsilon_{lm}) = \sigma^2 e^{-\theta d(ij,lm)}, \qquad [6]$$

where d(ij,lm) = the distance between (the centers of) plots (i,j) and (l,m).

Variations on this model include specifying other polynomial functions for T_{ij} and/or alternative covariance structures for the errors ϵ_{ij}. The latter include 1-dimensional correlation structures, for example serial correlations between plots within the same row only. This approach models large scale spatial trends through "fixed-effect" polynomial terms for the mean, as does trend analysis, but it also allows for small scale dependence through correlations between neighboring plots. This "correlated errors" modification of trend analysis is thus subject to the same problems as trend analysis with respect to specifying the polynomial function for T_{ij}. In addition, the need to select a specific covariance function provides another

opportunity for subjectivity to enter the analysis. If the polynomial function for the trend and the covariance function have both been specified, the new PROC MIXED in SAS can be used to carry out an appropriate analysis (see Appendix).

In theory, inferences provided by this "trend plus correlated errors" (trend+CE) analysis are valid if the assumptions of Eqs. [1], [2] and [6] are correct for an appropriate target population. In practice, it will be difficult to determine if these assumptions are even approximately correct for a given data set, and properties of the analysis when the trend+CE model is incorrect are not easily derived analytically. Accordingly, Zimmerman and Harville carried out a numerical study using uniformity trial data to assess performance of the analysis based on Eqs. [1], [2] and [6]. They found that this trend+CE analysis was more efficient than an uniterated Papadakis analysis, and considerably more efficient than the RCB analysis. The trend+CE analysis was also more efficient than the corresponding trend analysis with iid errors.

To assess validity of each method, Zimmerman and Harville compared the averages (over different randomizations or layouts) of two measures of precision: one based on the predicted variance for that model, and the other an empirical estimate possible because of the absence of treatment effects in uniformity trials. Results suggested that estimates of precision based on the trend+CE model generally agreed well with the empirical estimates. In comparison, estimates of error produced by both the Papadakis and trend analyses were found to differ considerably from the empirical estimates, the Papadakis estimates being consistently pessimistic. As expected, validity of the RCB analysis was demonstrated, even though systematic heterogeneity was evident in the uniformity trial yields.

Zimmerman and Harville (1991) caution that the favorable results for the model with covariance as in Eq. [6] (and for related models with asymmetric correlation structures) are preliminary, being based on 3 data sets each with a limited number of plots. They also note that there is no simple solution to the problem of how to select an appropriate covariance function for a given data set when trend and entry effects may be present. Results in

Zimmerman and Harville are sufficiently promising, however, to warrant further investigation of analyses based on models with correlated errors to account for spatial variation in data from large yield trials.

EXAMPLES

Properties of the analyses described above are illustrated using data from two corn yield trials (Bowman, 1985) and a soybean trial. Each corn trial included 30 commercial entries, the experimental design being a 6x5 rectangular lattice in 3 replicates (c.f., Cochran and Cox, 1957), laid out with the 18 incomplete 5-plot blocks arranged in an 18x5 grid (see Fig. 1). The soybean trial contained 180 inbred lines or entries in 3 replicates, with entries in 10 sets of 18 in a split plot type of arrangement (c.f., Cochran and Cox, 1957, p. 388). Each complete block or replicate was 70m x 35m in area, with plots arranged in a 15×12 grid. However replicates were not contiguous, being separated by alleys. More detail is given for the corn trials than for the soybean trial partly because the corn trials allow comparisons with incomplete block designs and partly because presentation of results is easier with 30 than with 180 entries.

Corn trials 1 and 2.

To examine the data from each trial for systematic trends in yield potential, residuals r_{ij} were calculated as in Eq. [5] and plotted against row position R_i and, separately, against column position C_j. The following series of analyses was then applied to the data from each trial:

(a) the RCB analysis,

(b) the lattice analysis with incomplete block effects assumed random,

(c) a Papadakis analysis with a single "covariate" as in Eqs. [3] and [4],

(d) trend analysis with the polynomial function for T_{ij} selected using the Tamura et al. (1988) modification of a program developed by Kirk et al. (1980),

(e) trend+CE, a correlated errors modification of (d) with the polynomial for T_{ij} as in (d), and $\mathrm{Corr}(\epsilon_{ij}, \epsilon_{lm})$ as in Eq. [6], and

(f) CE, a correlated errors modification of the RCB analysis with fixed effects for

replicates and Corr(ϵ_{ij}, ϵ_{lm}) as in Eq. [6].

SAS code for carrying out each of these analyses is given in the Appendix.

Comparing results for these different analyses is not a straightforward matter. This is because for a given trial, the true ranking of entries and the actual pattern of spatial heterogeneity are both unknown. Conceptually, there are also difficulties relating to the implied target populations if block effects are assumed random in the traditional analyses. In fact, there is no completely objective way to determine which analysis is the most appropriate for a single data set. Nevertheless, it is informative to compare certain results from these analyses, keeping in mind what is known about the properties of each.

Ideally, comparisons of precision among analyses should be based on the variances or standard errors of estimated entry effects or contrasts. For each data set and analysis, a model based estimate of the standard error can be calculated for each adjusted entry mean. The average of these standard errors then provides a measure of precision for comparing analyses (Table 1). Other articles (e.g., Warren and Mendez, 1980; Kirk et al., 1982; Tamura et al., 1988) have based comparisons of precision on the error mean square. This is reasonable for the RCB, trend and Papadakis analyses since the standard error of an adjusted entry mean is largely determined by the (square root) of the error mean square. For the CE models, however, because of the more complex variance structure, precision cannot be summarized using a single mean square analogous to the error mean square. Accordingly, the root error mean square is reported in Table 1 for the RCB, trend and Papadakis analyses, but there is no corresponding entry for CE and trend+CE analyses. For the lattice analysis, precision depends on whether incomplete blocks are assumed random or fixed, the latter being more closely analogous to the fixed effects model of trend analysis. It was decided to perform the lattice analyses with incomplete blocks random, but the square root of intrablock error is given in Table 1 as an indication of precision of the lattice analysis with fixed block effects.

To further examine differences between analyses, comparisons were also made of the estimates of yield potential used in obtaining adjusted entry means. Lastly, these adjusted

means were compared across analyses to illustrate that the different methods of accounting for spatial variation can lead to quite different results with respect to ranking of entries. This seems important to emphasize because it will usually be impossible to determine which analysis produces the most accurate ranking of entries for a given trial.

Plots of residuals, corrected for entry effects only (see Eq. [5]), against row position showed evidence of systematic trends in yield potential for both trials (Fig. 2). Plotting residuals against column position was less informative. The model selection procedure in Tamura et al. (1988) on the whole supported this visual assessment resulting in a 4th degree polynomial on row position for trial 1, and a polynomial involving both row and column terms for trial 2. Consequently, substantial reductions in "unexplained variation" can be achieved by a nontraditional analysis, and average standard errors are largest for the RCB analysis which accounts for spatial heterogeneity only through differences between the 3 complete replicates (Table 1). For trial 1 where the rows correspond to incomplete blocks, and trend appears to depend mainly on row position, the lattice analysis is effective. For trial 2, where yield potential seems to depend to some extent on both row and column position, the lattice analysis is comparatively less effective. Accordingly, trend analysis produces an increase in precision comparable to that for the lattice in trial 1, but appears more efficient than the lattice in trial 2. The Papadakis analysis is intermediate between the RCB and trend analyses in both cases.

Several correlated errors models were fit to the data and only the most noteworthy results are reported. When the polynomial terms specified for T_{ij} were selected as in Tamura et al. (1988), there was little difference between results obtained with trend analysis (i.e., assuming the ϵ_{ij} iid) and the corresponding correlated errors (or trend+CE) analysis. This was true whether the correlation structure was assumed to be 2-dimensional as in Eq. [6] or 1-dimensional either within rows or within columns. On the other hand, accounting for spatial variation using a correlated errors structure but no trend other than replicate effects (CE analysis) did not appear to improve precision relative to the RCB analysis.

Estimates of plot yield potentials are presented for trial 1 in Fig. 3a. For the RCB,

lattice, and trend analyses, these estimates depend on row position only, while the Papadakis estimates are different for each plot. For comparison, the average of the Papadakis X_{ij} values for each row is plotted with the other 3 estimates. For the RCB analysis, yield potential is assumed to be the same for the 6 rows in each complete block, and the estimated trend is thus a step function. In contrast, the lattice and trend analyses suggest systematic variation within blocks 1 and 3, with yield potential tending to increase with row position. Comparing the lattice and trend estimates, the lattice estimates agree closely with the row averages of the residuals (not shown) resulting in a rough pattern in Fig. 3a, while the trend estimates are like a smoothed version of these points (corresponding approximately to fitting a 4th degree polynomial to the lattice estimates).

For trial 2, the surface estimated by trend analysis has gradients in both row and column directions, whereas the lattice estimates are necessarily constant within each row. As a consequence, estimates of yield potential from these analyses agree reasonably well in the center plot of each row (Fig. 3c) but agree less well for the extreme plots in each row (i.e., for plots in colums 1 and 5, Figs. 3b and 3d respectively). Like the trend analysis estimates, the Papadakis estimates of yield potential are different for each plot, but the Papadakis estimates are not obviously closer to the trend estimates than to the lattice estimates.

The test for entries was not significant for trial 1, but adjusted means are presented for both trials in Table 2, as both sets of means illustrate how results can differ according to the analysis used. Note that the greater differences among analyses in estimates of spatial variation for trial 2 are reflected in larger differences in adjusted means across analyses for trial 2 than for trial 1 (see Table 2). Also in both trials it is evident that estimated entry means for the analyses that adjust for spatial variation differ substantially from the estimates for the RCB analysis. Comparing the trend and lattice analyses for trial 1, the largest differences between adjusted means are for entries 27 and 28, with entry 27 ranked 3rd by the lattice analysis and only 11th by trend analysis. Both of these entries occur in rows for which the trend estimates of yield potential are on average higher than the lattice estimates, and so adjusted means are

lower for the trend than for the lattice analysis.

For trial 2, analyses differ considerably with respect to entry 10, which is the top ranking entry for the Papadakis and trend analyses, but is 4th for the lattice analysis. Entry 10 occured in two plots for which yield potential was estimated to be low under the trend analysis, and accordingly was adjusted upward relative to the other entries, giving a yield of 11807 kg ha^{-1} for trend analysis, compared to 10799 kg ha^{-1} for the lattice analysis. Although less important for interpretation of results, there was also a large difference in the estimated means for entry 25 in the different analyses (Table 2). Like entry 10, entry 25 was located in plots with low estimated yield potential under the trend analysis.

Soybean trial.

Residuals obtained after fitting entry effects only, when plotted against column position showed evidence of trends from left to right within each replicate (Fig. 4). Effects of row position were more difficult to elucidate from plots.

Yield was missing for two of the 540 plots in this large trial, and so the RCB analysis was modified by computing adjusted means for entries. Analyses which estimate spatial variation required no modification because of the missing plots, but did have to be modified slightly because replicates were not contiguous. The Papadakis analysis was implemented by calculating the "covariate" values X_{ij} as in Eq. [4] but using residuals from plots in the same replicate only. The Tamura et al. (1988) program could not be used to select the polynomial model for trend analysis because replicates were not contiguous, and also because the number of entries exceeded 50. Instead, based on the residual plots, PROC GLM was used to fit a polynomial within each replicate which included all first and second order terms plus cubic and quartic terms for rows. This model was then simplified by successively eliminating the highest order nonsignificant ($p>.01$, Tamura et al., 1988) terms. Two trend+CE analyses were carried out, trend(1)+CE using the polynomial row and column terms exactly as in trend analysis, and trend(2)+CE with only a linear column effect within each replicate. A 1-dimensional correlation structure with serial correlations within columns seemed more effective than the 2-

dimensional structure in Eq. [6], and was implemented with both trend(1)+CE and trend(2)+CE.

Evidence of spatial heterogeneity was reflected in the highly significant "covariate" in the Papadakis analysis, and also in highly significant row and column polynomial effects. Average standard errors were similar for the Papadakis, trend, and trend+CE analyses, and about 20% smaller than for the RCB analysis (Table 3). Correspondingly, the root error mean square for the Papadakis and trend analyses was about 80% that for the RCB analysis. The similarity between standard errors for the two trend+CE analyses suggests that, as noted by Zimmerman and Harville (1991), the correlation structure can to some extent 'absorb' large scale trend not accounted for in T_{ij}.

Comparing analyses in terms of estimated entry means, agreement tends to be greater among the trend and trend+CE analyses than between any of these and the RCB analysis (Figs. 5a, 5b). Comparing results for the top ranked entries, 11 entries were ranked in the top 20 by all five methods, and six of these were ranked in the top 10 by all methods.

DISCUSSION AND CONCLUSIONS

For each of the examples presented it is evident from plots of residuals that there were trends in yield potential which resulted in heterogeneity within complete blocks. For field sites like these, there is disagreement on whether to improve precision by using an incomplete block design or by using an analysis which accounts for (within block) spatial variation. Reasons for not using incomplete block designs such as the lattice or lattice square relate to the practical difficulties imposed by restrictions on the number of entries that can be included and the inconvenience incurred when a decision is made to include additional entries after field plans have been prepared. The main argument against using a nontraditional spatial analysis is that properties of these analyses for typical field situations are largely unknown, whereas a simple randomization argument provides validity for the traditional RCB and intrablock lattice analyses. The reason for using a nontraditional spatial analysis is that greater gains in precision can sometimes be achieved with such an analysis than with an incomplete block

design and the conventional analysis.

On the basis of examples discussed here (see also Kirk et al., 1980; Pearce and Moore, 1976; Bowman, 1990, etc.) and numerical studies in Zimmerman and Harville (1991), Baird and Mead (1991), Binns and Jui (1985), it seems clear that precision can be improved by using a nontraditional analysis without necessarily sacrificing validity. An example where the lattice design and analysis are ineffective and a spatial analysis is more efficient is provided by the second of the corn trials where gradients in yield potential are not 1-directional. Note, however, that this is not an argument against use of incomplete block designs, because a spatial analysis can be applied to data obtained with such designs.

Perhaps more difficult than deciding whether to use a nontraditional analysis, is the problem of selecting a particular spatial model and analysis. The examples given here illustrate clearly that Papadakis, trend, and correlated errors analyses will produce different rankings of entries for a given data set. Results will also depend on how the Papadakis "covariate" is calculated, on the polynomial used to model trend, and on the covariance structure assumed. No simple rules can be given for deciding which is the best analysis, instead some of the issues to be kept in mind are noted below.

In simple regression problems such as relating yield to rate of fertilizer applied, polynomials can be useful approximations to the true relationship. On the other hand, polynomials can be entirely inappropriate as when the response curve plateaus. Similarly, polynomials will not always be good approximations to the variation in yield potential in a field, and the presence of entry or variety effects in the data makes it harder to detect poor fit than in a simple regression problem. Approximating trend using a polynomial can increase precision without introducing substantial bias, but for a given trial results for one or more entries could be misleading if the yield potential surface is not well approximated by a polynomial model.

The Papadakis analysis will not be as efficient as trend or trend+CE analyses when an appropriate polynomial is assumed for T_{ij}. On the other hand, because the Papadakis analysis

relies less on a specific shape for the yield surface it will be less likely than trend analysis to produce adjustments to means that are extreme. This is apparent in both the soybean and second corn trial, where the Papadakis adjustments are on average substantially (about 40%) smaller than for trend and trend+CE analyses. Comparing the Papadakis and trend analyses, there is the usual trade-off between possible gains in efficiency versus increased bias incurred by making more stringent assumptions about the data (specifically, about the form of the yield surface).

Zimmerman and Harville (1991) and Baird and Mead (1991) claim that the best gains in precision overall are made with correlated errors models, and for the soybean trial the trend+CE analyses did seem to be effective. For the corn trials examined here, however, there seemed to be little to be gained by assuming errors correlated in comparison to trend analysis as implemented using the Tamura et al. (1988) program.

Considerable detail has been omitted in this review of spatial analysis techniques useful for yield trials. In particular, correlated errors models have received very brief treatment. A topic that has been ignored entirely is that of designs developed specifically for use with spatial analyses (see, e.g., Williams, 1985). Also the use of spatial analyses when the goal is to combine results from a series of trials over space and time has not been addressed here or elsewhere. Objective methods to assist in selecting the best analysis for a particular data set have not been developed but are clearly needed. It is hoped that by providing SAS code, researchers will be encouraged to implement several of these analyses and thus provide empirical information on their performance. Careful evaluation of the results by a number of researchers should then lead to better understanding of the methods and their advantages and limitations.

REFERENCES

Baird, D. and R. Mead. 1991. The empirical efficiency and validity of two neighbour models. Biom. 47:1473-1487.

Bartlett, M. S. 1978. Nearest neighbour models in the analysis of field experiments. J. R. Stat. Soc., Ser. B 40:147-174.

Bhatti, A. U., D. J. Mulla, F. E. Koehler, and A. H. Gurmani. 1991. Identifying and removing spatial correlation from yield experiments. Soil Sci. Soc. Am. J. 55:1523-1528.

Binns, M. R., and P. Y. Jui. 1985. A simulation study of the nearest neighbour analysis method of Papadakis. Comm. Stat. - Simul. Comp. 14:159-172.

Bowman, D. T. 1985. Measured crop performance. I. Corn hybrids. North Carolina State Univ. Res. Rep. 102.

Bowman, D. T. 1990. Trend analysis to improve efficiency of agronomic trials in flue-cured tobacco. Agron. J. 82:499-501.

Cochran, W. G., and G. M. Cox. 1957. Experimental designs. John Wiley & Sons, New York.

Kempthorne, O. 1952. The design and analysis of experiments. John Wiley & Sons, New York.

Kempton, R. A., and C. W. Howes. 1981. The use of neighbouring plot values in the analysis of variety trials. Appl. Stat. 30:59-70.

Kirk, H. J., F. L. Haynes, and R. J. Monroe. 1980. Application of trend analysis to horticultural field trials. J. Am. Soc. Hort. Sci. 105:189-193.

Longer, D. E., and M. A. Risley. 1983. Improved precision in soybean variety trials. Proc. 13th Soybean Res. Conf. p. 22-28.

Patterson, H. D., E. R. Williams, and E. A. Hunter. 1978. Block designs for variety trials. J. Agric. Sci. 90:395-400.

Pearce, S. C., and C. S. Moore. 1976. Reduction of experimental error in perennial crops, using adjustment by neighbouring plots. Exp. Agric. 12:267-272.

Tamura, R. N., L. A. Nelson, and G. C. Naderman. 1988. An investigation of the validity and usefulness of trend analysis for field plot data. Agron. J. 80:712-718.

Warren, J. A., and I. Mendez. 1982. Methods of estimating background variation in field experiments. Agron. J. 74:1004-1009.

Williams, E. R. 1985. A criterion for the construction of optimal neighbour designs. J. R. Stat. Soc. B 47:489-497.

Williams, E. R. 1986. Neighbour analysis of uniformity data. Aust. J. Stat. 28:182-191.

Zimmerman, D. L., and D. A. Harville. 1991. A random field approach to the analysis of field-plot experiments and other spatial experiments. Biom. 47:223-239.

APPENDIX

The SAS (version 6.07) code included here was used to carry out the analysis of the corn trial data. The calculation of row and column positions (R, C) from plot numbers is specifically for plots in an 18x5 grid, and numbered in serpentine fashion, as indicated in Fig. 1. Note, however, that the PROC TREND code used to obtain the 4th degree polynomial for trend analysis is not included.

```
/*  SPATIAL.SAS */
******calculate row and column positions from plot number*****;
DATA SUB; SET 'inputfile';
        IF LOC=3;
        ROW=INT((PLOT-1)/5) +1;
        COL=MOD((PLOT-1),5) +1;
        IF MOD(ROW,2)=0 THEN COL=6-COL;
        KEEP LOC ROW COL YIELD ENT REP PLOT;
******calculate papadakis covariate******;
PROC SORT; BY ROW COL;
PROC GLM; CLASS ENT;
        MODEL YIELD=ENT;
        OUTPUT OUT=NEW R=RES;
DATA LEFT; SET NEW;
        COL=COL+1;
        IF COL <=5;
        LEFT=RES;
        KEEP LOC LEFT COL ROW ;
DATA RIGHT;SET NEW;
        COL=COL-1;
```

```
        IF COL >=1;
        RIGHT=RES;
        KEEP LOC RIGHT COL ROW ;
DATA TOP ; SET NEW;
        ROW=ROW-1;
        IF ROW >=1;
        TOP =RES;
        KEEP LOC TOP COL ROW ;
DATA BOTT; SET NEW;
        ROW=ROW+1;
        IF ROW <=18;
        BOTT=RES;
        KEEP LOC BOTT COL ROW ;
DATA TOG; MERGE SUB LEFT RIGHT TOP BOTT; BY LOC ROW COL;
        COV=MEAN(LEFT,RIGHT,TOP,BOTT);
PROC PRINT;
TITLE 'PAPADAKIS ANALYSIS';
PROC GLM; CLASS ENT;
        MODEL YIELD=ENT COV;
        LSMEANS ENT/OUT=PAPAD;
DATA A; SET SUB;
******calculate orthogonal polynomial contrasts for trend analysis;
R1=ROW-9.5; R2=R1*R1 - 323/12;
R3=R1*R2-64*R1/3;  R4=R1*R3- 81*R2/4;
PROC GLM DATA=A; CLASS REP ENT;
        MODEL YIELD=REP ENT;
```

```
        LSMEANS ENT/ OUT=RCBD;
TITLE 'RCB ANALYSIS';
PROC GLM DATA=A; CLASS ENT;
        MODEL YIELD=ENT R1 R2 R3 R4;
        LSMEANS ENT/OUT=TREND;
TITLE 'TREND ANALYSIS';
PROC MIXED DATA=A; CLASS REP ENT ROW COL PLOT;
        MODEL YIELD=REP ENT;
        REPEATED PLOT/TYPE=SP(POW)(ROW COL) SUB=REP;
        LSMEANS ENT;
        MAKE 'LSMeans' OUT=CE;
TITLE 'CE ANALYSIS';
PROC MIXED DATA=A; CLASS REP ENT ROW COL PLOT;
        MODEL YIELD=ENT R1 R2 R3 R4;
        REPEATED PLOT/TYPE=SP(POW)(ROW COL) SUB=REP;
        LSMEANS ENT;
        MAKE 'LSMeans' OUT=TRENDCE;
TITLE 'TREND+CE ANALYSIS';
PROC MIXED DATA=A; CLASS REP ENT ROW PLOT;
        MODEL YIELD=REP ENT;
        RANDOM ROW/ SUB=REP;
        LSMEANS ENT;
        MAKE 'LSMeans' OUT=LATTICE;
TITLE 'LATTICE ANALYSIS';
DATA B; SET RCBD; RCBDMN=LSMEAN;
        RCBDSE=STDERR; DROP LSMEAN STDERR;
```

```
DATA C; SET TREND; TRENDMN=LSMEAN; TRENDSE=STDERR;
      DROP LSMEAN STDERR;
DATA D; SET TRENDCE; TRCEMN=LSMEAN; TRCESE=SE;
      DROP LSMEAN SE DF T P_T LEVEL;
DATA E; SET CE; CEMN=LSMEAN; CESE=SE;
      DROP LSMEAN SE DF T P_T LEVEL;
DATA F; SET LATTICE; LATTMN=LSMEAN; LATTSE=SE;
      DROP LSMEAN SE DF T P_T LEVEL;
DATA G; SET PAPAD; PAPADMN=LSMEAN;
      PAPADSE=STDERR; DROP LSMEAN STDERR;
DATA MEANTOG; MERGE B G F C D E; DROP _NAME_;
PROC PRINT;
RUN;
```

Table 1. Square root of the calculated error mean square (REMS), average standard error of an entry mean (AVSE), error degrees of freedom (edf), and F ratio for the test of no entry effects, for six different analyses of data from two corn yield trials.

	Trial 1				Trial 2			
Analysis	REMS	AVSE	edf	F	REMS	AVSE	edf	F
	kg ha^{-1}				kg ha^{-1}			
RCBD	981	566	58	1.21	852	492	58	3.59
Lattice	772†	508	43‡	1.34	813†	490	43‡	3.54
Papadakis	863	501	59‡	1.04	786	454	59‡	3.90
Trend	808	475	56	1.39	599	362	53	7.05
Trend+CE	–§	470	56‡	1.34	–§	370	53‡	7.07
CE	–§	544	58‡	1.25	–§	505	58‡	5.81

† intrablock error.

‡ error or 'denominator' df, and F test, are approximate.

§ analysis does not yield an error mean square.

Table 2. Estimated yields for 30 commercial entries from five different analyses of the data from two corn trials. Entries are ranked according to the estimate from trend analysis.

Trial 1					
	Analysis method				
Entry	RCB	Lattice	Papadakis	Trend	CE
	kg ha^{-1}				
28	4553	4865	4618	4416	4495
3	4766	4842	5098	4676	5027
25	4425	4621	4519	4757	4297
26	4862	5149	5132	4842	4759
11	5310	4956	5183	5051	5028
4	5130	4959	5307	5252	5233
16	5497	5276	5274	5321	5281
12	5359	5070	5669	5364	5586
10	5590	5571	5738	5550	5670
5	5865	5583	5690	5644	5528
22	4864	5572	5227	5669	5135
20	5582	5484	6021	5674	5734
6	5825	5616	5701	5743	5765
24	5132	5526	5631	5766	5504
29	6253	6200	5724	5850	5604
30	6081	5892	5688	5864	5376
14	6206	5615	5753	5887	5583
13	6338	5976	5893	5888	5786
17	5746	5947	5680	5931	5562
27	6350	6332	6103	5964	5994
15	5824	5834	5779	5971	5683
2	5833	6267	6132	6021	5861
7	6387	6355	6009	6030	5885
23	5732	6041	5824	6058	5597
19	6256	6138	6020	6199	5856
18	5972	6217	6316	6265	6405
9	6094	6268	6612	6286	6341
1	6441	6233	6337	6287	6119
21	6204	6249	6127	6510	5948
8	6982	6805	6654	6727	6601

Table 2 continued.

	Trial 2				
	Analysis method				
Entry	RCB	Lattice	Papadakis	Trend	CE
	kg ha^{-1}				
26	7839	7838	7794	7520	7866
24	7700	7778	7748	7846	7645
3	7971	8177	8551	8435	8405
28	8715	8743	8653	8437	8400
15	8907	8841	8596	8454	8320
20	8864	8773	8512	8512	8326
12	9326	9293	9073	8716	8760
13	8865	8907	8859	8822	8676
6	9427	9447	9483	9121	9091
2	9346	9358	9244	9261	9152
8	8841	8919	9314	9438	9323
21	9661	9639	9622	9501	9522
25	8737	8662	9106	9627	9307
14	9725	9699	9678	9631	9424
5	9417	9355	9257	9671	9278
27	10196	10153	10054	9730	10037
11	9991	10041	9826	9777	9689
30	9292	9365	9735	9782	9580
29	9789	9791	9704	10067	9813
7	10226	10169	10109	10172	9977
9	9850	9922	10269	10254	10068
22	10894	10842	10486	10385	10525
18	10602	10529	10368	10388	10132
23	9975	9834	10049	10392	10154
17	10976	10968	10636	10393	10549
19	10589	10599	10444	10448	10347
16	10679	10552	10802	10486	10440
1	10443	10469	10412	10530	10404
4	10980	11131	11057	10989	10876
10	10768	10799	11150	11804	11378

Table 3. Square root of the calculated error mean square (REMS), average standard error of an entry mean (AVSE), error degrees of freedom (edf), and F ratio for the test of no entry effects, for 5 different analyses of yields from a soybean trial involving 180 inbred lines or entries.

Analysis	REMS	AVSE	edf	F
	----------kg ha^{-1}----------			
RCBD	633	366	356	3.29
Papadakis	497	288	357†	5.12
Trend	504	298	345	4.54
Trend+CE (1)	- ††	278	345†	5.43
Trend+CE (2)	- ††	284	353†	5.27

† error or 'denominator' df and F test are approximate.

†† analysis does not yield an error mean square.

FIGURE CAPTIONS

Fig. 1. Field layout for corn trial 1, showing allocation of the 30 entries to plots which are numbered in serpentine fashion and arrayed in an 18x5 grid. The design is a 6x5 rectangular lattice, with six incomplete blocks (Rows) in each of three complete replicates (Reps).

Fig. 2. Residuals (plot yield – mean for entry) plotted against row position and identified by column position, (a) for corn trial 1, and (b) for corn trial 2.

Fig. 3. Estimated plot yield potentials (kg ha^{-1}) for RCB analysis (*), lattice analysis (Δ), Papadakis analysis (o), and trend analysis (+), plotted against row position. Estimates in (a) are for corn trial 1 and (o) represents the average of the Papadakis estimates for a row. Estimates in (b), (c), and (d), are for plots in columns 1, 3, and 5, respectively, for corn trial 2. The RCB (*) and lattice (Δ) estimates depend on row position only and are the same in (b), (c), and (d).

Fig. 4. Residuals (yield – mean for entry) for soybean trial plotted against column position. The basic-design was an RCBD with 180 entries in three replicates. Each replicate was a 15x12 grid of plots, but replicates were not contiguous in the field, being separated by alleys running between columns 12 and 13 and between columns 24 and 25.

Fig. 5. Agreement between adjusted entry means for three of the five analyses applied to the soybean yield data.

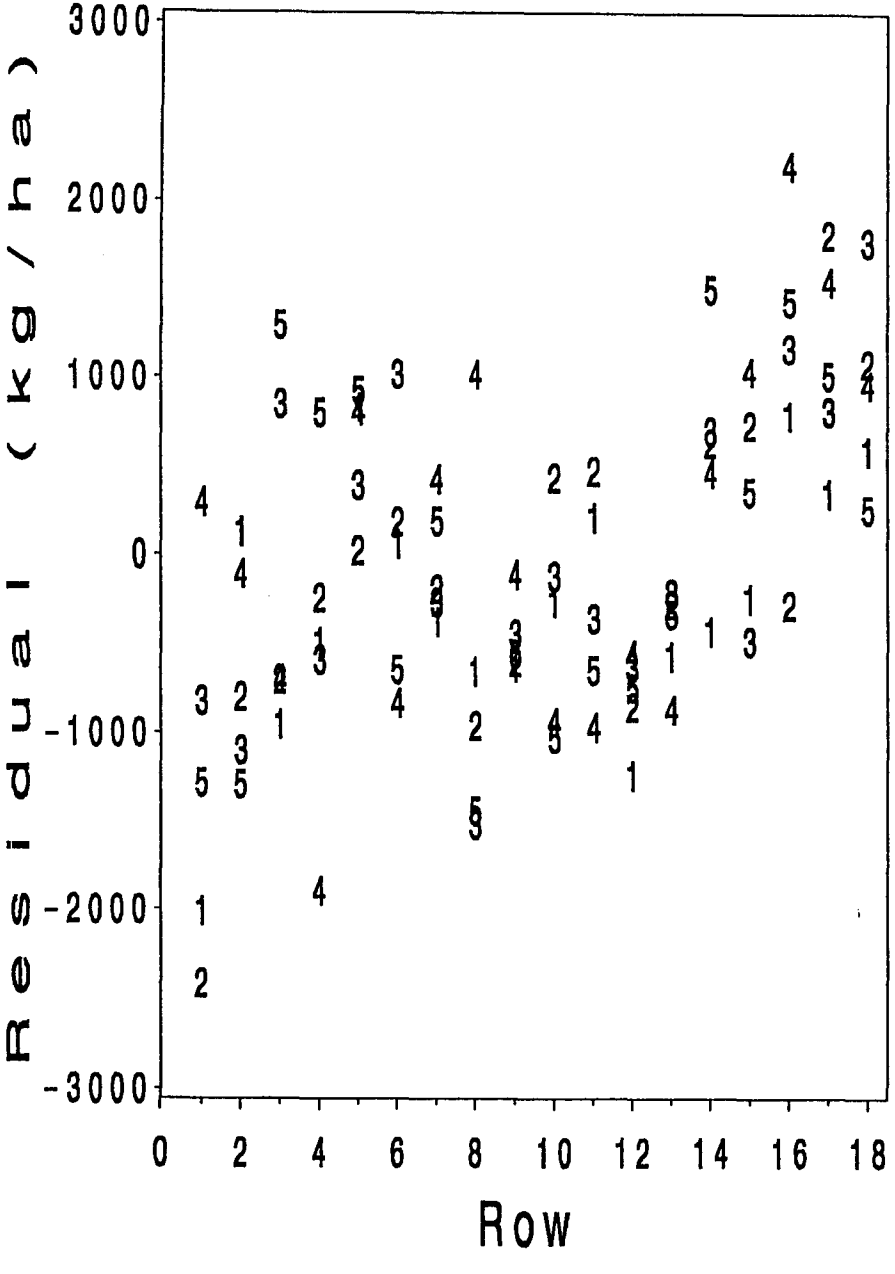
	90	89	88	87	86
	27	13	7	19	25
	81	82	83	84	85
	16	5	23	29	14
	80	79	78	77	76
Rep III	12	6	18	24	4
	71	72	73	74	75
	30	21	1	8	20
	70	69	68	67	66
	26	22	2	15	9
	61	62	63	64	65
	10	3	11	28	17
	60	59	58	57	56
	24	8	29	3	13
	51	52	53	54	55
	2	7	23	18	28
	50	49	48	47	46
	4	9	30	14	19
Rep II	41	42	43	44	45
	20	5	15	10	25
	40	39	38	37	36
	6	21	26	11	16
	31	32	33	34	35
	17	1	12	27	22
	30	29	28	27	26
	23	25	24	21	22
	21	22	23	24	25
	8	6	7	10	9
	20	19	18	17	16
	26	27	30	29	28
Rep I	11	12	13	14	15
	1	5	4	3	2
	10	9	8	7	6
	15	11	14	13	12
	1	2	3	4	5
	18	16	20	17	19

18 12 6 1

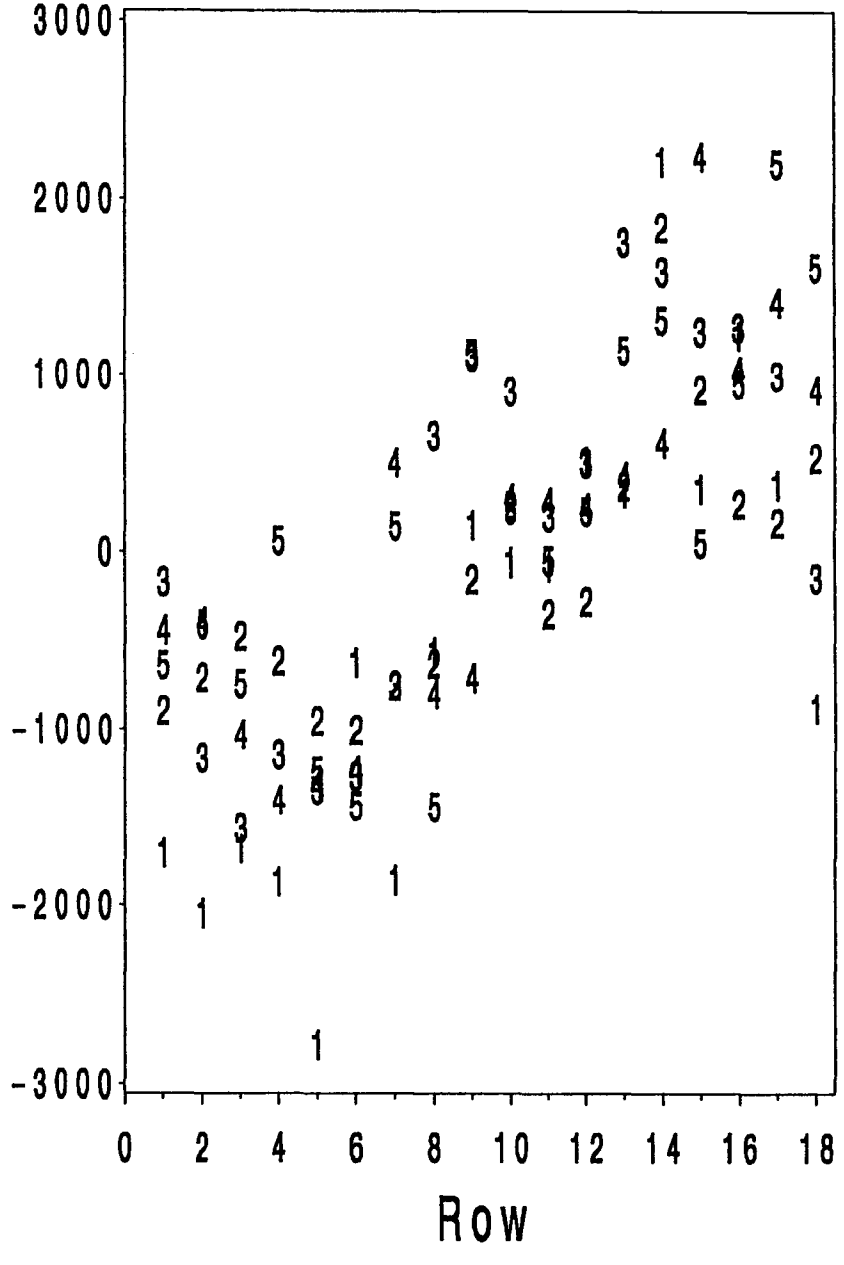
Row

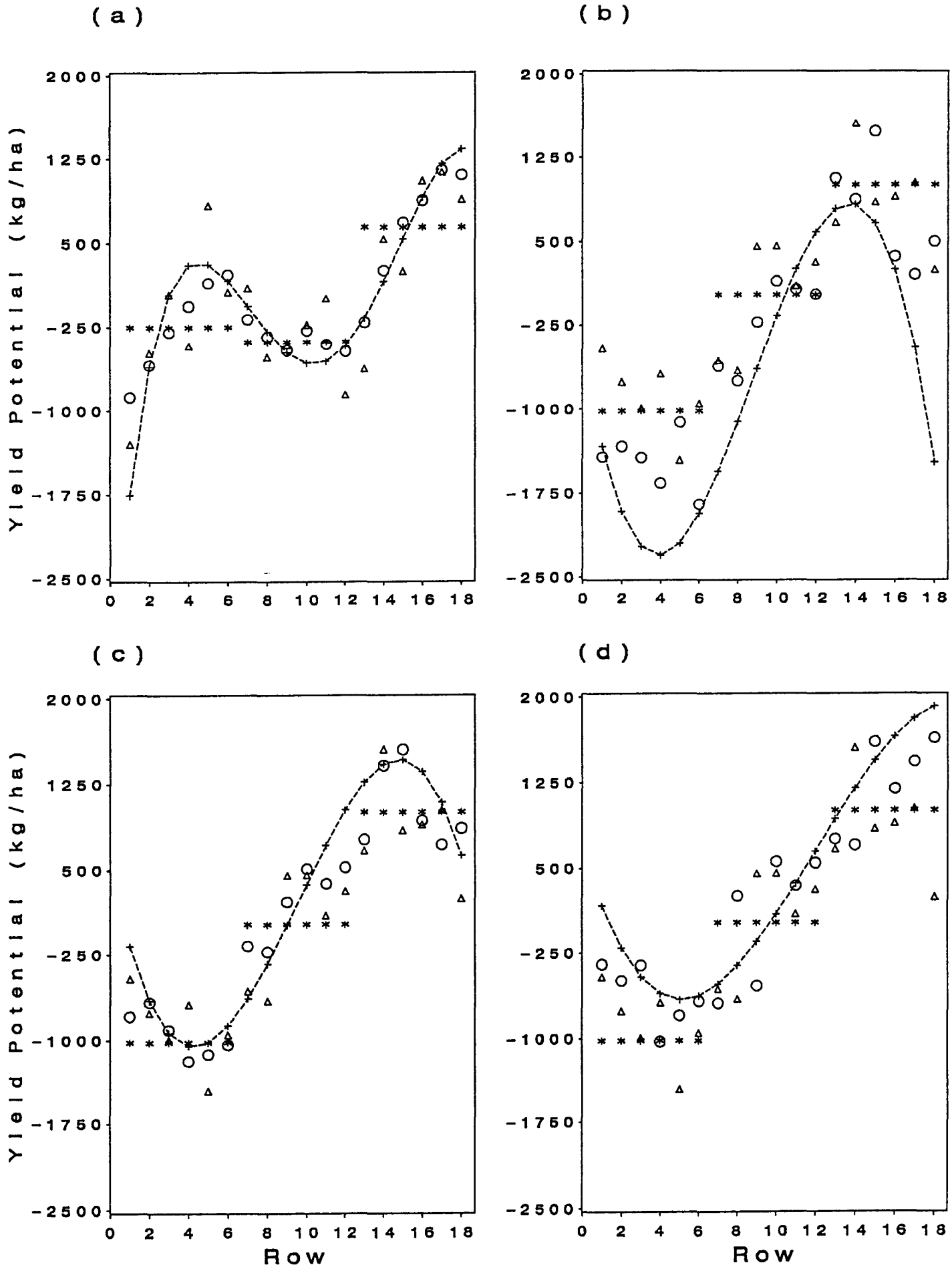
1 Column 5

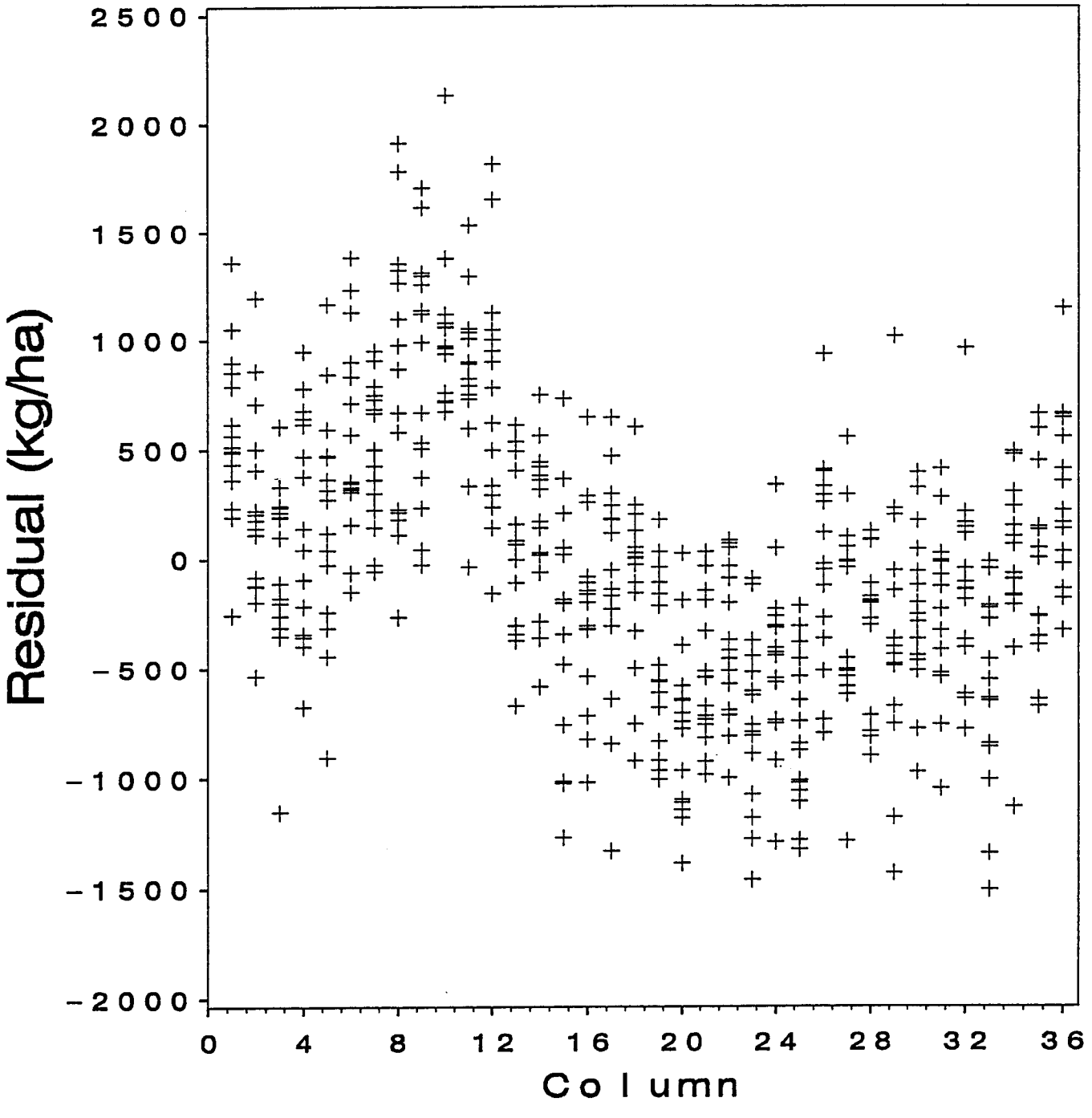
(a)


Residual (kg/ha)
3000
2000
1000
0
-1000
-2000
-3000
0
2
4
6
8
10
12
14
16
18
Row

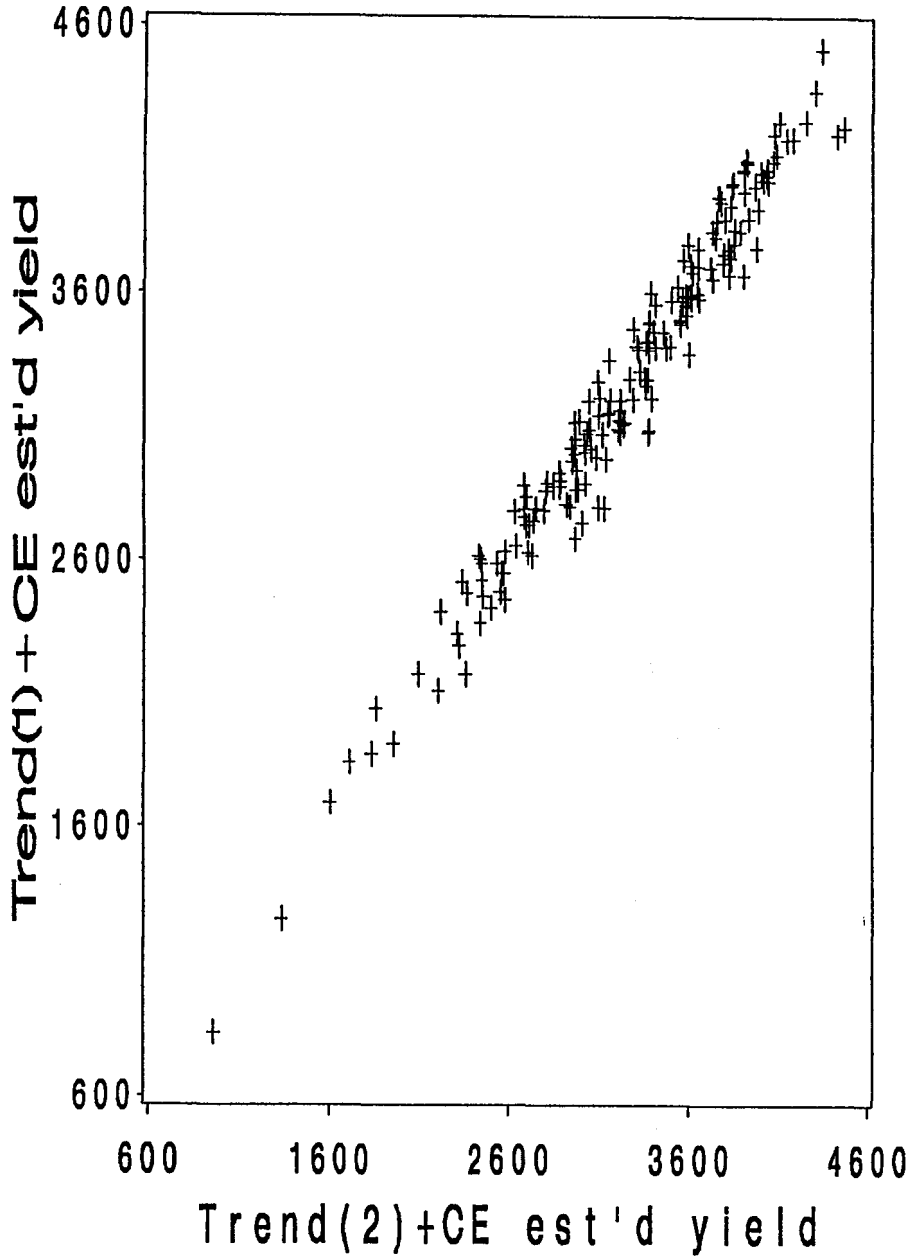
(b)


3000
2000
1000
0
-1000
-2000
-3000
0
2
4
6
8
10
12
14
16
18
Row

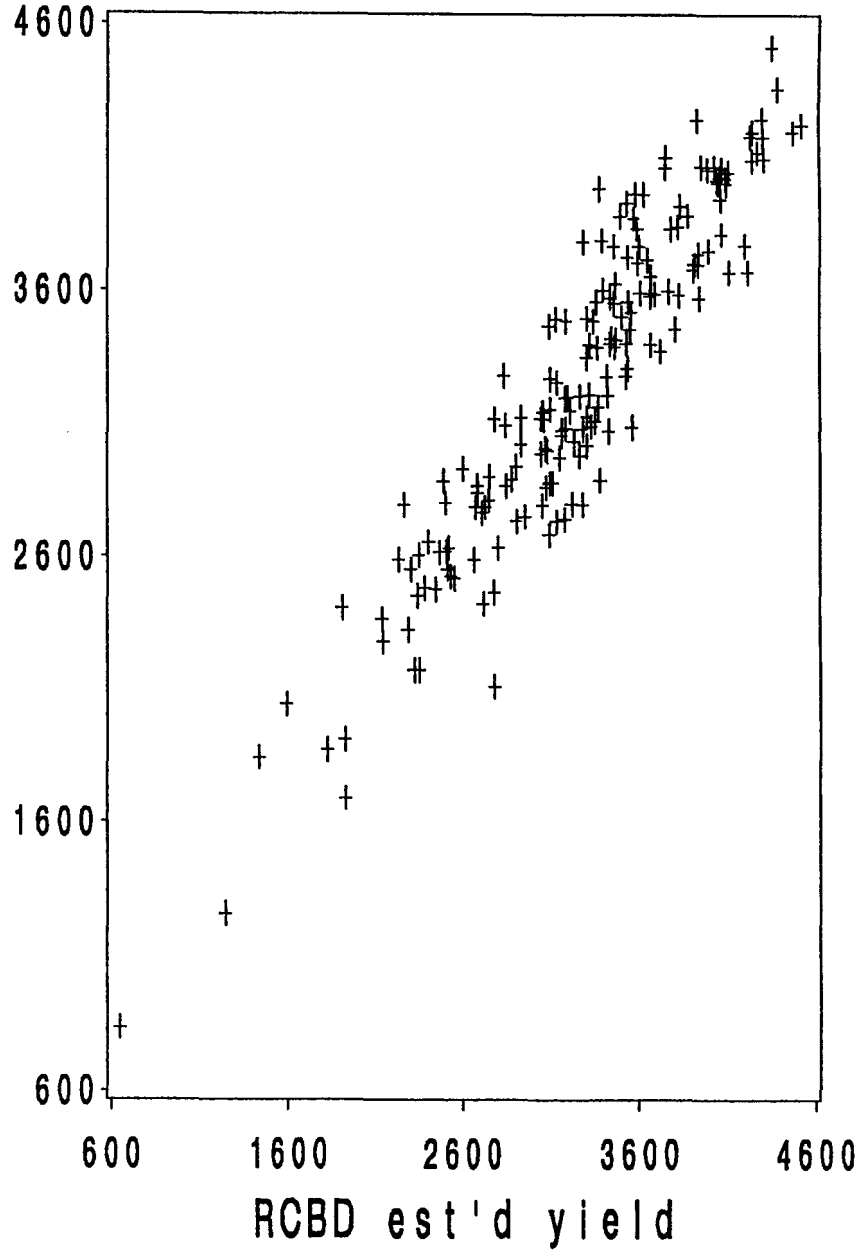

(a)
(b)
(c)
(d)
Yield Potential (kg/ha)
2000
1250
500
-250
-1000
-1750
-2500
0 2 4 6 8 10 12 14 16 18
Row


2500
2000
1500
1000
500
0
-500
-1000
-1500
-2000
Residual (kg/ha)
0
4
8
12
16
20
24
28
32
36
Column

(a)


4600
3600
2600
1600
600
Trend(1)+CE est'd yield
600
1600
2600
3600
4600
Trend(2)+CE est'd yield

(b)


4600
3600
2600
1600
600
600
1600
2600
3600
4600
RCBD est'd yield