Modeling Unstructured Heterogeneity Along with Spatially Correlated Errors in Field Trials

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SUMMARY

In this paper we consider analysis of two experimental data sets for evaluating lentil genotypes. One of these data sets comes from an incomplete block design and the other one from a complete block design. The incomplete blocks contribute to the experimental error reduction and spatially correlated plot-errors can be modeled using autoregressive scheme that may lead to further improvement in the assessment of the genotypes. Such an approach was applied in several other studies to model the linear trends and spatially correlated errors. However, the assumption of a constant error variance restricts the scope of the analysis in many agricultural field trials, and in other situations in general, where heterogeneity of error variances is a reality. In this study, we have approached the problem first by fitting a model with constant error variance and generating the residuals. Using the squared residuals, we use K-cluster means technique to group the experimental units for similar squared-residuals. Next, we allow the error variances to vary with the group of the experimental units which need not require any spatial restrictions to model the error variances. The number of heterogeneous errors and the experimental units belonging to the heterogeneous clusters are obtained using the AIC criterion values followed by a groups merger scheme based on insignificant change in the residual maximum log likelihood values. The final models with heterogeneous variances were used to evaluate the precision of the genotype means comparisons. We found a substantial improvement on the efficiency of the pair-wise comparisons over the other ways of analysis. We recommend the application of this procedure in any general situation permitting unstructured heterogeneity.

Key words: Heterogeneous error variances; Spatially correlated errors; Variogram; Clustering; Field trials.

1. INTRODUCTION

Control of field variability is normally done by applying blocking methods where experience with the obvious landscape configuration guides the formation of the blocks for assigning the treatments such as genotypes of a crop to the field-plots, i.e. the experimental units. Furthermore, the design may consist of complete blocks or incomplete blocks allowing a certain degree of balance under a constant error variance model. Such approaches are discussed in standard texts on design and analysis of experiments (see for example, Fisher 1990, Cochran and Cox 1992, Cox and Reid 2002 and Hinkelmann and Kempthorne 2007). In the context of field experiments, the experimental units on a rectangular layout would generally be correlated due to their fixed physical proximity, and, in addition, there might be presence of local fertil-

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ity trends. Analysis approaches in these situations have been developed in order to account for blocking effects and correlated errors in space and time (see Gilmore et al. 1997, Cullis and Gleeson 1991 and Grondona et al. 1996). Various criteria such as Akaike information criteria (AIC) have been used for selection of appropriate covariance models in these areas (see Wolfinger 1996 and Singh et al. 2003).

The approaches used in the analysis to capture spatial variability in field trials have been found useful in enhancing the breeding efficiency of crop variety improvement programs (Sarker et al. 2001, Malhotra 2004). The underlying models in most of these analyses have assumed homogeneous error variances across all the plots of the layout. We believe that in reality, experimental errors need not be homoscedastic even after accounting for various local fertility trends and or autocorrelations across various directions in the layout. This may be due to variety of reasons. In field trials, lack of homogeneity may be attributed to ineffective cover cropping in the preceding season, or the farmers' fields used for experimentation having been subjected to the application of crop management input factors to the where-needed plots or sections of the field. In a well designed blocking experiment, the uniform application of the management practices over the whole of a block might have been overlooked or ignored. It is also possible that the prevalence or distribution of underground parasites such as *orobanche* in legume fields or *striga* in the sorghum fields, may follow irregular pattern and make the nearest neighbor adjustment unreliable (Wilkinson et al. 1983). Therefore, it is essential to allow for heterogeneous error variances in the field trials in addition to accounting for the other factors. The heterogeneous error variance need not follow any spatial structure on the field layout. The general objective of this study, therefore, is to address the unstructured heterogeneity of error variances in evaluation of variety trials and apply on lentil data.

The identification of the sources and the structure of heterogeneity is based on residuals from the fitted model found most suitable when the heterogeneity was ignored. The squared residuals were used to form clusters or groups of homoscedastic experimental units and to identify the structure of homogeneity, if any, by using an empirical or non-parametric approach. The use of squared residuals for studying the homogeneity of variances have also been found robust to the departure from normality (Levene 1960). Since, no clear structure is expected in the residuals, non-hierarchical approach or K-means clustering could be applied to obtain the prevailing clusters of units with homoscedastic units. Other alternative methods of clustering could also be used (Everitt et al. 2001). The most appropriate cluster could be determined from the trend of a criterion values and the change in the log-likelihood value for the heterogeneous models. This study uses data from two lentil trials with relatively high coefficient of variation that are described in Section 2. The statistical methods for identifying the structure of heterogeneous errors are given in Section 3, computational details appear in Section 4 and results are summarized in Section 5.

2. EXPERIMENTAL DATA

Two trials consisting of genetic materials for a preliminary yield trial (PYT) and an advanced yield trial (AYT) were evaluated in block designs at an experimental station of the International Center for Agricultural Research in the Dry Areas ($ICARDA$) at Breda in northern Syria. Data on seed yield were examined. Trial 1, a PYT, had 25 genotypes and was evaluated in a square lattice with 4 replications on a 4×25 rectangular layout in 2005. In field trials, the coefficient of variation (CV) is normally used as an indicator or a measure of experimental error variability. The analysis using randomized complete block design resulted in a CV of 51% for seed yield. Trial 2, an AYT, was conducted in randomized complete blocks with 30 genotypes and 3 replications on a

3×30 layout in 2003 and gave a CV of 41% for seed yield. In the PYT, the plot size was $4m \times 1.5m$, and in the AYT it was $4m \times 3m$ with a standard row-to-row distance of $30cm$ for lentil crop. However, at maturity, actual harvest area per plot was $4.5m^2$ and $9m^2$ for the PYT and the AYT, respectively. Analysis was performed based on net harvested area per plot.

3. MODELING HETEROGENEITY OF SPATIALLY CORRELATED ERRORS

The two data sets were first analyzed by fitting the best spatial models described in Singh et al. (2003) to screen the AIC best model out of the group of models generated by various combinations of complete or incomplete blocks, fixed linear, random cubic spline or no trend, and first-order autocorrelated along rows and columns or independent errors. In the two trials, the best model for seed yield was found to be randomized complete blocks with first-order autoregressive errors along rows. At this stage, each model was based on the assumption of homogeneous error variances. In order to examine any possible indication of heterogeneity, the residuals obtained from the fitted models in above can be plotted and their variograms can be examined as well (see Sarker et al. 2001 for details on obtaining the variograms). Figures $(1-4)$ exhibit 3D plots of residuals and their variograms for the two trials. We noticed no clear spatial patterns in the residuals (Figures 1 and 2). This can be expected since we have screened various models accounting for the presence of linear trends in the field layout and the residuals are computed from the best models as obtained using Singh et al. (2003). Another way to explore the variability is in terms of the variograms, which indicate the presence of different levels of variability between the residuals over the layouts. For instance, in Fig. 3, the variogram of the residuals in the PYT (2005) indicates that there is a variation in the variances of the plot residuals: $0.40 - 0.65$ for plots within 2 plot-units, fluctuating values within $0.4 - 0.6$ for distances from $3 - 22$ units and variation from 0.2 to 0.6 for plots separated by more than 22 plot-units. There is no clear spatial pattern to allow modelling of the variogram with different values for nearly the same distances. In Fig. 4 ($AYT, 2003$), the variogram indicates different levels of variances: less than 0.3 for distances within 5 plot-units, between $0.3 - 0.4$ is fairly constant between 5 to 23 plot-units, while a higher value of nearly 0.48 and low values close to 0.2 are observed for distances exceeding 23 plot units. Here also, there is no clear spatial pattern for distances more than 23 units. Thus, these cases support the need of examining non-spatial or unstructured heterogeneity in the plot error variances.

In addition to the visual approach of exploring heterogeneity in the above data, we also applied the method presented in Chaubey (1981) for detecting the presence of heterogeneity of variances in the data. The residuals were ordered based on their absolute values. The variances were computed using these ordered residuals from (a) two groups formed from the highest/lowest 50% of the residuals, and (b) three groups from lowest/highest 33% of the residuals. The F-test was used with residual degrees of freedom equally allotted. As can be seen in Table 1, there is an indication of presence of the heterogeneous error variance in the data.

In the presence of heterogeneity, the next question is to identify the experimental units groups with heterogeneous errors variances. For this purpose, we follow the following two-step procedure.

Step-1 : *Formation of clusters*: Based on the best model selected using Singh et al. (2003), we first applied K-means clustering on its squared residuals using the criterion which maximizes between group sum of squares. The number of groups, set *a priory,* varied from $K = 2, ...10$. The change in the criterion values were noted with successive values of K, the number of groups or clusters of the experimental units. The value of K, for which the change was not substantial

was considered as the potential number of clusters. For each set of clusters of the experimental units, we modeled the data using the spatial errors as per the best model and a random factor where error variances were allowed to vary with the cluster of units obtained for a chosen value of K. For example, if $K = 3$, there were three error variances, σ_1^2, σ_2^2 and σ_3^2. For such a fitted model, we computed the likelihood value in terms of $-2ln$ ($REML$: residual maximum likelihood) value and the successive increase in its values with a unit increase in k. At this stage, it is not likely to have a nested structure defining the heterogeneous with increase in the number of groups, we can not apply a test of significance (such as chi-square) on the decrease in the $-2ln(REML)$, however, we can use Akaike information criterion (AIC) to decide on the number of groups, smaller AIC is better. We used Genstat (Payne et al. 2009) for the computation which produces a quantity called 'deviance' which is equal to $-2ln(REML)$ ignoring a constant which depend on the fixed effect terms. We used the quantity $AICD$ which expresses AIC in terms of the deviance where $AICD$ = deviance - $2q$ where q is the number of covariance parameters (Singh et al. 2003).

Step-2: *Fusion of the clusters*: Step-1 provides a number of clusters, say K, with heterogeneous error variances ($\sigma_j^2, j = 1...K$). Let the deviance at this step be D_0. The error variances were arranged in order, we merged those two clusters which were the closest for the values of their error variance estimates. Then the model was fitted with, now, the reduced number of clusters ($K - 1$) and the deviance was computed, say D_1. Since the fusion of the clusters presents a nested structure of the units, it is possible to test the hypothesis of the equality of the variance components of the two merged clusters. In the case of equality of the variances, the difference $D_1 - D_0$ will follow a chi-square distribution with 1 degree of freedom. If the observed difference is greater than the chi-square value at the chosen level of significance, then the number of clusters K available at Step-1 will be taken as final, and the estimation of the genotypes effects will proceed with the K error variances. If the observed difference is smaller than the chi-square value, then the $K - 1$ merged clusters will be considered for further analysis repeating the process of fusing the clusters with closest error variance estimates, and evaluating the change in the deviance against the value of chi-square with 1 degree of freedom.

4. ESTIMATION OF THE VARIANCE-COVARIANCE PARAMETERS

We present here a general model and a computational procedure for estimation of the variance-covariance parameters. Let $\mathbf{y} = (y_{ijk})$ be the vector of responses or yield from the plot receiving the i-th genotype (treatment) in the k-th incomplete block of the j-th replication of the design used. The vector $\mathbf{y}$ can, equivalently, be denoted also by $\mathbf{y} = (y_{RC})$ as well where R, C denote the row and column coordinates of the plot associated with indices i, j, k. The model for y_{ijk} is given by:

$$y_{ijk} = \mu + \pi_j + \beta_{jk} + \tau_i + \epsilon_{RC}$$

where μ is the general mean, π_j is the effect of replication j, β_{jk} is the effect of block k in the replication j, τ_i is the effect of treatment i, and ϵ_{RC}s are random errors with an auto-covariance structure along/across rows/column. Let N be the number of the experimental units. The N errors presented as the vector $\epsilon = (\epsilon_{RC})$ may have the heterogeneous variances, σ_l^2 $(l = 1, ..., K)$, where K is the number of clusters of the N experimental units. The diagonal matrix of variances for the N errors can be written as $\sigma^{2\delta}$ using the associated σ_l^2 for a given plot. Further, suppose that the model selection using Singh et al. (2003) resulted in an auto-correlated errors across columns with correlations expressed as $corr(\epsilon_{RC}, \epsilon_{R'C'}) = \phi^{|C-C'|}$, then

the above model can more compactly be written as:

$$y = X\alpha + Z\beta + \epsilon$$

where X is the design matrix associated with factors with effects assumed as fixed, α say, consisting of genotypes effects τ_i's and μ, and Z is the design matrix with factors with effects assumed random, β say, consisting of replication effects, π_j's etc. The variance-covariance of the plot-error vector ϵ can be written as

$$R = \sigma^{\delta}(corr(\epsilon_{RC}, \epsilon_{R'C'}))\sigma^{\delta}$$

The computation of the estimates of the parameters associated with the fixed effects α, variance components of the factors in β, correlation parameter ϕ are given in the various computing software such as GENSTAT and SAS. Generally, the matrix R has a structure of correlations and variances. In the two datasets, while the correlations between the plot errors ϵ_{RC} have a spatial structure, the (plot) error variances do not. For example, neither there is an assumed structure in terms of σ_l^2 over the positions of the units nor the variances are totally unstructured as there are $K \ll N$ distinct variances. Let REP, GENO, ROWS and COLS stand for the replication, genotype (treatment), rows and columns factors and YIELD for the response variate. Let HGROUP stand for the factor with the K levels representing heterogeneous variances units. The key Genstat directives to compute the variances, autocorrelation and standard errors are:

```
Vcomponents[Fixed=GENO]REP+HGROUP.ROWS.COLS ; constraints=positive
VStructure[Term=HGROUP.ROWS.COLS]diag, AR; Factor=HGROUP, COLS
Reml[prin=m,c,w,mean,d; workspace=50; maxcycle=150;pse=d] YIELD
```

The above codes produce a common σ_e^2 (error variance) and other variances as ratios d_l or σ_l^2 where $\sigma_l^2 = (d_l + 1)\sigma_e^2$ signifies the error variance corresponding to the l^{th} cluster, which varies with the level of the grouping factor HGROUP, $l = 1...K$.

5. RESULTS & DISCUSSION

Following the test by Chaubey (1981), Table 1 gives estimates of error variances based on ordered absolute residuals for assumed two and three groups. As can be noted from the computed F-values for all the three data sets, there is an indication of the heterogeneity in the error variances. This supports our venture to explore the heterogeneous clusters of units.

Table 2 gives the information on distribution of experimental units with homogeneous error variances obtained using a K-cluster means and the AICD (AIC values expressed as deviance, see Singh et al. 2003). It may be seen that the number of heterogenous groups inferred at this step are 3 for each of the two trials. Table 3 provides the estimates of the variance components at Step -1 (i.e. when selected using AIC criterion) and Step -2 (i.e. closest groups were fused and tested for the change in deviance values against chi-square). For Trial 1, fusion of two closest clusters resulted in significant increase in deviance ($P < 0.001$), therefore, the three heterogeneous groups with $60, 13$ and 27 units were considered for using the models for the evaluation of the genotypes. For Trial 2, the three clusters obtained from Step - 1 were fused into two clusters with an insignificant increase in the deviance. When merged again (now into a single group), there was a significant increase in the deviance, implying the presence of only two heterogenous groups of units.

Table 1: Preliminary indication of heterogeneity of error variances using approximate F-tests in the data on seed yields of the two trials at Breda, Syria

(a) Trial 1: Preliminary yield trial, 2005				
Two groups:	$s_1^2 = 10.01$	$s_2^2 = 20.26$	$F_{36,36} = s_2^2/s_1^2 = 2.02$	$P-$value$= 0.0204$
Three groups:	$s_1^2 = 10.0$	$s_3^2 = 30.23$	$F_{24,24} = s_3^2/s_1^2 = 3.02$	$P-$value$= 0.0046$
(b) Trial 2: Advanced yield trial, 2003				
Two groups:	$s_1^2 = 10.00$	$s_2^2 = 20.21$	$F_{29,29} = s_2^2/s_1^2 = 2.02$	$P-$value$= 0.033$
Three groups:	$s_1^2 = 10.00$	$s_3^2 = 36.85$	$F_{13,14} = s_3^2/s_1^2 = 3.02$	$P-$value$= 0.0093$

Note: F-test is based on Chaubey (1981) adapted to the fitted models.

Table 2: Clusters of experimental units with heterogeneous error variances on seed yield data in the two trials

k	Cluster sizes	Criterion value	Change in criterion value	q	Deviance	AICD
(a) Trial 1: Preliminary yield trial, 2005						
1	100	-	-	3	71	77
2	78, 22	10.23	-	5	48.06	58.06
3	60, 13, 27	5.75	-4.48	6	33.76	**45.71**
4	5, 49, 30, 16	2.85	-2.90	7	32.02	46.02
(b) Trial 2: Advanced yield trial, 2003						
1	90	-	-	3	43.54	49.54
2	12, 78	7.64	-	5	17.33	27.33
3	10, 19, 61	4.19	-3.45	6	5.82	**17.28**
4	2, 8, 19, 61	1.28	-2.91	7	NC	

Note: Bold letters indicate that the corresponding clusters were identified with heterogeneous error variances. q = number of covariance parameters.
AICD = AIC (Akaike information criterion) expressed in terms of deviance (Singh et al. 2003).

Table 3: Number of experimental units and estimates of variance components for various groups when the heterogeneous groups were selected using AIC criterion or fused using the change in the deviance, and corresponding deviance from the fitted model for seed yield data from the two trials conducted at Breda, Syria.

(a) Trial 1: Preliminary yield trial, 2005

(i) Overall grouping: Deviance $= 33.76, \text{DF} = 68$

Group (l)	No. of Units (N_l)	$\hat{\sigma}_l^2$
1	60	0.15
2	13	2.12
3	27	0.85

(ii) Groups 1 and 3 merged: Deviance $= 54.3, \text{DF} = 69$

Group (l)	No. of Units (N_l)	$\hat{\sigma}_l^2$
1	87	0.371
2	13	2.587

Change in deviance = 20.54, DF=1 , P-value < 0.001

(b) Trial 2: Advanced yield trial, 2003

(i) Overall grouping: Deviance $= 5.28, \text{DF} = 54$

Group (l)	No. of Units (N_l)	$\hat{\sigma}_l^2$
1	10	1.515
2	19	0.973
3	61	0.0998

(ii) Groups 1 and 2 merged: Deviance $= 3.88, \text{DF} = 55$

Group (l)	No. of Units (N_l)	$\hat{\sigma}_l^2$
1	29	1.0642
2	61	0.0961

Change in deviance $= -1.4, \text{DF} = 1, \text{P} - \text{value} = 1.00$

(iii) All the groups merged: Deviance = 43.54, DF= 57

Group (l)	No. of Units (N_l)	$\hat{\sigma}_l^2$
1	90	0.501

Change in deviance $= 39.66, \text{DF} = 2, \text{P} - \text{value} < 0.001$

Note: DF = degrees of freedom associated with the deviance (residuals).

Table 4: Position of experimental units grouped (1-3) according to heterogeneous error variances on the rectangular layouts for the three trials conducted at Breda, Syria

Trial 1: Seed yield (Preliminary yield trial, 2005)
Using three heterogeneous groups selected on AIC criterion.

	Columns														
Rows	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	1	3	1	1	1	3	3	1	1	1	1	1	1	2	1
2	1	1	3	1	3	1	1	2	1	1	3	2	1	1	1
3	1	3	1	3	2	1	3	1	1	3	3	2	3	1	1
4	1	1	1	1	3	3	1	1	1	1	2	2	3	3	1

	Columns									
Rows	16	17	18	19	20	21	22	23	24	25
1	3	1	1	3	2	1	3	1	3	3
2	1	1	1	2	1	1	2	1	1	1
3	1	3	3	1	3	1	1	1	3	1
4	3	1	2	3	2	1	1	1	1	2

Trial 2: Seed yield (Advanced yield trial, 2003)
(a) Using three heterogeneous groups selected on AIC criterion

	Columns														
Rows	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	2	1	2	3	3	3	2	3	3	2	2	2	1	3	3
2	3	3	3	3	3	2	1	1	3	3	2	3	3	2	3
3	3	3	3	1	3	3	3	2	3	3	3	3	3	3	2

	Columns														
Rows	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	2	3	3	3	3	1	1	2	1	1	2	3	3	3	3
2	2	3	3	3	3	2	3	3	3	3	3	2	3	2	3
3	3	3	3	3	3	3	3	3	3	3	1	2	3	3	3

(b) Merged to two heterogeneous groups

	Columns														
Rows	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	1	1	1	2	2	2	1	2	2	1	1	1	1	2	2
2	2	2	2	2	2	1	1	1	2	2	1	2	2	1	2
3	2	2	2	1	2	2	2	1	2	2	2	2	2	2	1

	Columns														
Rows	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1	1	2	2	2	2	1	1	1	1	1	1	2	2	2	2
2	1	2	2	2	2	1	2	2	2	2	2	1	2	1	2
3	2	2	2	2	2	2	2	2	2	2	1	1	2	2	2

Table 5: Estimates of variance components, Wald test statistics value and significance level, and average estimated variance error of pair-wise genotypes comparison and efficiency of the design-analysis models for seed yield data from the two trials conducted at Breda, Syria

(a) Trial 1: Preliminary yield trial, 2005

Variance components	Estimates	WStat	DF	P-value	Av. var.	Eff(%)
RCB, homogeneous	$\sigma_e^2 = 0.630 \pm 0.1036$	36.07	24	0.094	0.3194	100
Homogeneous	$\sigma_e^2 = 0.64 \pm 0.111$	40.36	24	0.055	0.2953	108
	$\phi = -0.27 \pm 0.128$					
Heterogeneous	$\sigma_e^2 = 0.15 \pm 0.035$	74.88	24	0.001	0.1495	214
	$d_1 = 0.00 \pm 0.00$					
	$d_2 = 12.93 \pm 6.78$					
	$d_3 = 4.62 \pm 2.29$					
	$\phi = -0.56 \pm 0.246$					

(b) Trial 2: Advanced yield trial, 2003

Variance components	Estimates	WStat	DF	P-value	Av. var.	Eff(%)
RCB, homogeneous	$\sigma_e^2 = 0.470 \pm 0.0871$	43.41	29	0.096	0.3132	100
Homogeneous	$\sigma_e^2 = 0.501 \pm 0.109$	60.84	29	0.014	0.2346	134
	$\phi = 0.46 \pm 0.116$					
Heterogeneous	$\sigma_e^2 = 0.0822 \pm 0.0304$	194.32	29	$< .001$	0.0933	336
	$d_1 = 12.27 \pm 6.87$					
	$d_2 = 0.198 \pm 0.4151$					
	$\phi = 0.80 \pm 0.121$					

Note: WStat = Wald statistic for testing equality of genotype effects (assumed fixed). DF =Degrees of freedom of the genotype. Av. var. = Average variance of difference of estimated effects between a pair of genotypes. AIC= Akaike information criterion. P- value= P- value based on the Wald test. Eff(%)= Percent efficiency over RCB (randomized complete block design) model.

Further, the spatial distribution of the experimental plots are exhibited on the layout schema (Table 4) for the various heterogeneous groups resulted at Step -1 and/or at the final stage of the formation of heterogeneous clusters. In these two trials, nearly 60% of the units have lowest level of error variability. The positions of the units from the other clusters are reasonably spread throughout the field layout.

Using the chosen combination of autocorrelation (spatial errors) and heterogeneous variances for the errors in the model, the estimates of various variances and autocorrelation parameters are given in Table 5. Table 5 also exhibits the P-value for equality of the genotypes effects based on the Wald statistic and the average variance of estimated difference of pair-wise genotypes effects. The efficiency (%) values are given in comparison with the standard randomized complete block design model. It may be noted that the best models, without heterogeneity components in, fail to detect significant statistical differences in genotypes effects in Trials 1 (P-values 0.055) while the P-

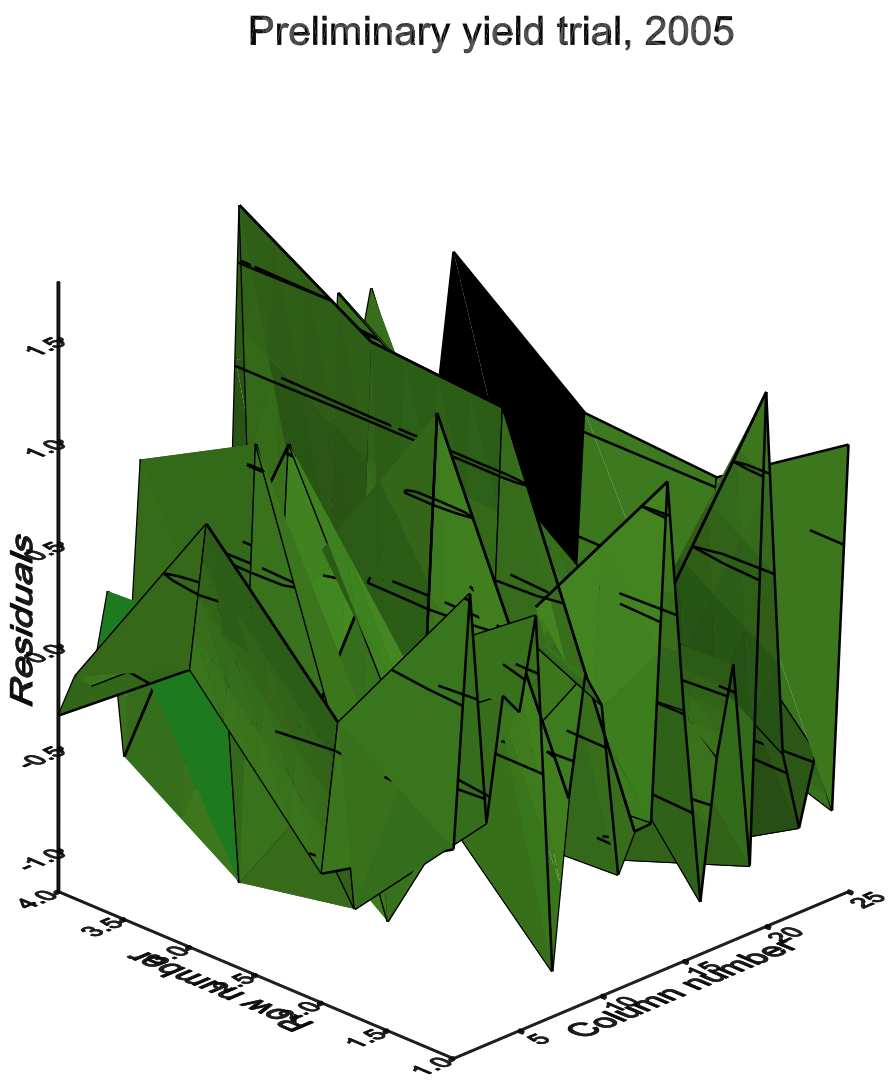

Figure 1: 3D plot of the residuals from RCB-AR model analysis of seed yields in the preliminary yield trials (2005) in 25 genotypes (RCB-AR model: The model incorporates random replication effects and first-order autoregressive plot-errors across columns)

value is 0.014 for Trial 2. An introduction of the heterogeneous error variances clearly shows an enhanced significance level (P-value ≤ 0.001) for genotype main-effects in both the cases. For the spatial models, reductions of 49% and 60% in the average variance of the difference of the genotypes effects for Trials 1 and 2 respectively can be considered substantial. While the spatial models for Trials 1 and 2 are more efficient than RCB model even without heterogeneity of error variances, incorporation of heterogeneity of error variances in the model has drastically improved the efficiency

of the pairwise comparisons of the genotypes. The efficiencies were found as 214% and 336% for the Trials 1 and 2, respectively.

The evaluation of these trials support the need for examining the presence of heterogeneous errors in the experimental units in field trials, and shows clearly that considerable improvement can be made by their identification and accounting at the analysis stage. Such an approach actually can easily be incorporated in most of the data analysis situations involving spatial, time or even unstructured experimental units, and, therefore, would enhance the efficiency of the associated plant breeding process.

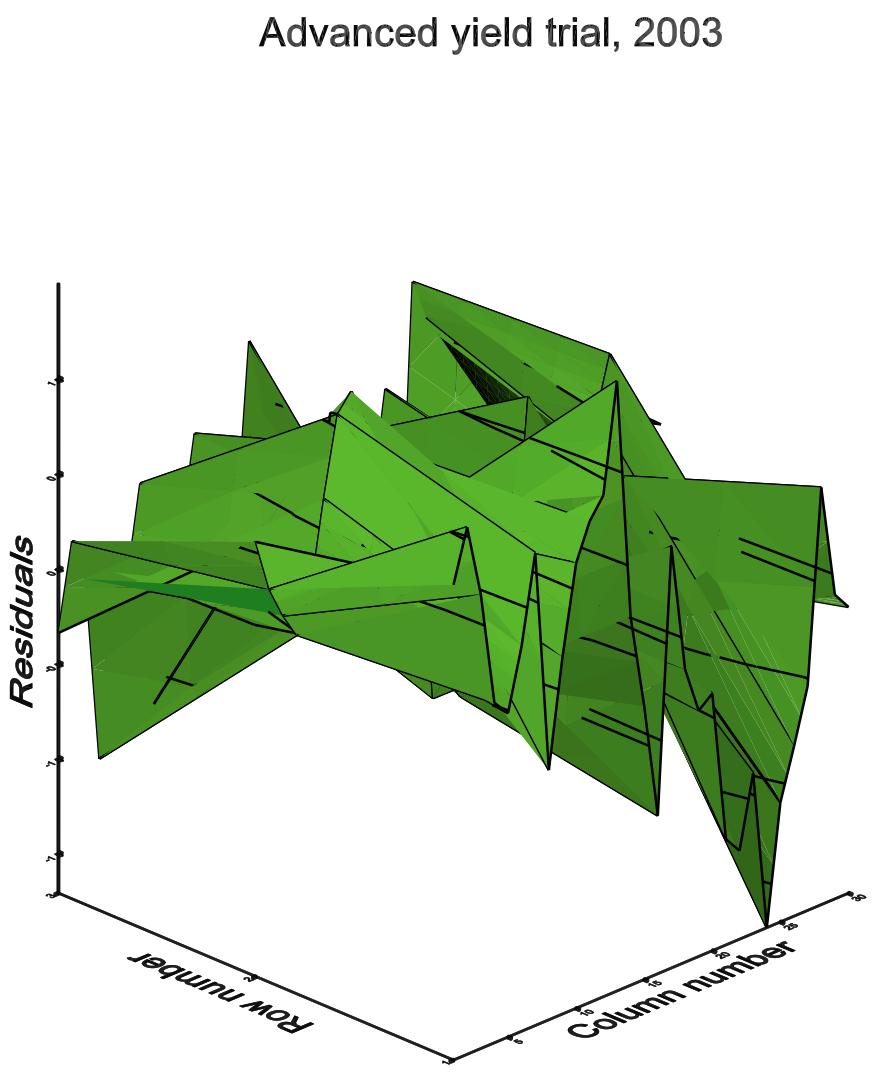

Figure 2: 3D plot of the residuals from RCB-AR model analysis of seed yields in the advanced yield trials (2003) in 30 genotypes (RCB-AR model: The model incorporates random replication effects and first-order autoregressive plot-errors across columns)

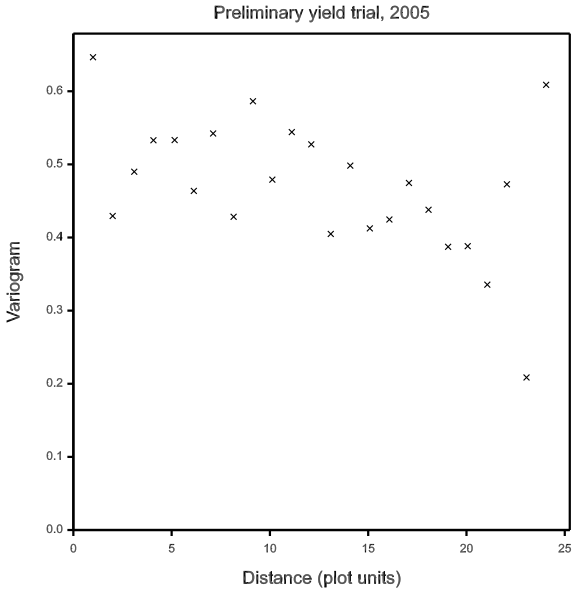

Figure 3: Variogram of the residuals from RCB-AR model analysis of seed yields in the preliminary yield trials (2005) in 25 genotypes (RCB-AR model: The model incorporates random replication effects and first-order autoregressive plot-errors across columns)

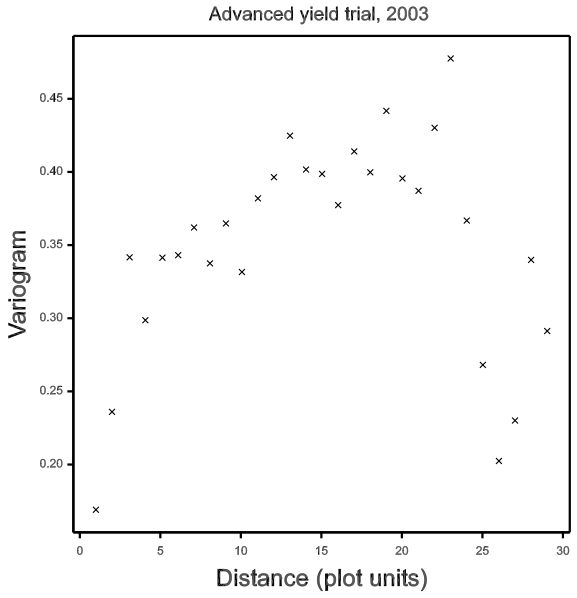

Figure 4: Variogram of the residuals from RCB-AR model analysis of seed yields in the advanced yield trials (2003) in 30 genotypes (RCB-AR model: The model incorporates random replication effects and first-order autoregressive plot-errors across columns)

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