Bias in the Estimates of Sensitivity from
Incomplete G × E Tables

B.M.K. Raju and V.K. Bhatia
Indian Agricultural Statistics Research Institute, New Delhi –110 012
(Received : October, 2002)

SUMMARY

In sensitivity analysis, Perkins and Jinks [11] model may at times fail to perceive important interaction effects. In such cases Factorial Regression model, which can exploit the additional information (if available) on external environmental characteristics may be considered. Variety testing data are often unbalanced. Eeuwijk [7] while fitting Factorial Regression model to such data suggested an approximate method which involves fitting the mixed model to incomplete data and subsequently calculating the BLUPs of interactions for the cells having data in the incomplete two way table. The interactions of missing cells are estimated by zero so that the two way table of interactions be complete. The estimates of sensitivity obtained from this method have been shown to be biased towards zero in comparison to the usual method for the single covariate case.

Key words : Sensitivity, Factorial regression, Unbalanced data, Substituted BLUP, Ignored BLUP.

1. Introduction

The existence of interaction reflecting differences among varieties in their ability to maintain performance over a wide range of environmental conditions has long been recognized (Finlay and Wilkinson [8]) and exploited by several researchers. This ability, which is an important property of a variety, is usually referred to as the sensitivity or adaptability of a crop variety to the environment. As an alternative to linear formulations of interaction (Finlay and Wilkinson [8]), which identify the interaction as a source but does not analyze its multiplicative formulations, which permit the interpretation of interaction as differential genotypic sensitivity to environmental variable(s) may be chosen in an attempt to quantify the variety's contribution to genotype × environment interaction, including the most popular Joint Regression. Perkins and Jinks [11] model consists in regressing the estimated interactions of each variety on the environmental index, obtained as observed environmental mean minus the grand

mean. The resulting regression coefficient may be interpreted as linear sensitivity of the variety to environmental change.

Jukka Ofversten [9] proposed that conditional expectation of yield given the environment be used as a measure for natural environment when variety-testing data are used to evaluate varietal sensitivity. In this context, he introduced a procedure that combines EM algorithm for the incomplete data with standard maximum likelihood estimation of mixed model parameters, which resulted in consistent maximum likelihood estimators. However, with a groundnut data this methodology was shown to be very inferior to Substituted BLUP and Ignored BLUP methodologies proposed by Raju [12] for joint regression with incomplete data. The underlying concepts of these two methodologies will be discussed in detail in the coming sections of this paper. Nabugoomu *et al.* [10] described REML analysis for estimation of variety means and sensitivity coefficients when locations are treated as random variables and is compared with least squares analysis. Alison Smith *et al.* [2] extended the spatial mixed model of Cullis *et al.* [4] to include multiplicative models for the variety effects in each environment.

For some data sets the linear regression accounts for only a small portion of interaction sum of squares. When the component of deviation from linear regression is significant, Perkins and Jinks [11] model fails to perceive important interaction effects. If some information on external environmental characteristics such as weather parameters, soil characteristics is available, it may come in handy to explain the important interaction effects using a technique called Factorial Regression, (Baril *et al.* [3]) which can accommodate this additional information in an efficient manner.

The Factorial Regression (FR) model serves as a means of finding the underlying physiological causes of observed sensitivities. The regression on the environmental mean or row regression model (Yates and Cochran [14]; Finlay and Wilkinson [8]) can be seen as a special type of Factorial Regression model with only one non measurable, concomitant variable on the environmental factor. The environmental main effect can be called internal covariate as it is derived from the data table itself.

Most often the data obtained from multi-environment testing are unbalanced. It may be incidental or accidental. The variety sortment changes over the years and not all varieties are tested in all the environments since the genotypes change from year to year. As new varieties become available, older ones become obsolete which makes the data set unbalanced. Some causes for the accidental unbalancedness are poor germination, damage of crop on account of pests and diseases and floods etc. The aim of this paper is to determine the statistically sound methodology with respect to bias for evaluating the sensitivities of Factorial Regression when data set under study is unbalanced.

2. Factorial Regression Model

Let us consider the basic ANOVA model for two-way crossed classification with interaction i.e.

$$Y_{ijr} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{ijr} \qquad (2.1)$$

$$i = 1, 2, ..., K; j = 1, 2, ..., N; r = 1, 2, ..., R$$

where

Y_{ijr} is the yield of r-th replicate of i-th variety in j-th environment

μ is the grand mean

α_i is the main effect of i-th variety such that $\displaystyle\sum_i \alpha_i = 0$

β_j is the main effect of j-th environment such that $\displaystyle\sum_j \beta_j = 0$

$(\alpha\beta)_{ij}$ is the interaction effect of i-th genotype in j-th environment such that

$$\sum_i (\alpha\beta)_{ij} = 0 \text{ and } \sum_j (\alpha\beta)_{ij} = 0$$

ε_{ijr} is the error associated with Y_{ijr}

Whenever the information on external environmental characteristics is available, this additional information can be accommodated in equation (2.1) in an optimum manner to interpret the interaction. The Factorial Regression model with environmental covariates (Denis ([5], [6]) Snedecor and Cochran [13]) has the form

$$Y_{ijr} = \mu + \alpha_i + \beta_j + \sum_{h=1}^{H} \Phi_{hi} X_{hj} + \delta_{ij} + \varepsilon_{ijr} \qquad (2.2)$$

where Φ_{1i} to Φ_{Hi} are sensitivities of i-th variety to environmental variables X_1 to X_H such that $\displaystyle\sum_i \Phi_{hi} = 0$ and $\displaystyle\sum_j X_{hj} = 0$; where H is the number of covariates included in the model. δ_{ij} is the component of deviation from regression.

After fitting the main effects μ, α_i, and β_j, one can introduce these concomitant variables on the levels of environmental factor in an attempt to describe the interaction

$$(\alpha\beta)_{ij} = \sum_{h=1}^{H} \Phi_{hi} X_{hj} + \delta_{ij} \qquad (2.3)$$

Now the $(\hat{\alpha\beta})_{ij}$'s for each genotype i, can be regressed on to environmental covariates X_1 to X_H to obtain the sensitivity coefficients for that genotype.

Application of this methodology to balanced data is straightforward. However, to an incomplete genotype × environment table no model with interaction, like $E(Y_{ijr}) = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij}$ can be fitted. For the missing cells, interaction parameters will be unspecified. To circumvent this problem, Eeuwijk [7] suggested an approximate method, which consists in treating appropriate terms in the model (2.1) as random so that the interaction for the missing cell may be estimated by its expectation (zero). One can reasonably treat environment effect as random since the environments in variety testing are chosen at random; consequently the interaction effect also becomes random. Now the Best Linear Unbiased Predictor (BLUP) estimates of interactions for the cells having data in the incomplete two-way table may be obtained from mixed model equations and the interactions for the missing cells may be estimated by zero (the expected value of interaction term) so that the two-way table of interactions be complete. Now the evaluation of sensitivities of model (2.2) is straightforward. Besides, treating the environment effect as random, it will have some desirable consequences in the sense that the corresponding BLUP estimator corrects for possible random environmental contributions to the genetic effects and thus for selection bias. Thus the bias creeping in due to the selection of environments is nullified.

3. Biased Estimates of Sensitivity

One cannot use the methodology suggested by Eeuwijk [7] if the interaction is treated as fixed. Further, one may be interested to see what happens if one does not estimate the interactions of missing cells with zero and just ignore them and proceed with the interactions obtainable from BLUP procedure. Let us consider the case of regression of interactions of particular genotype on a single environmental covariate and designate the method where zero is substituted for the interactions of missing cells, as 'Substituted method' and the method where missing cells are ignored as 'Ignored method'. Let N be the number of environments in the two-way table of genotype × environments and the genotype be grown in n environments and is absent in n' environments such that $n + n' = N$. Corresponding to Substituted method there will be two types of interactions viz., BLUP interactions and zero imputed interactions. Let the BLUP interaction for the non-missing cells be Y_i such that $\sum_{i}^{n} Y_i = 0$ and the zero imputed interaction for the missing cells be $Y_i \cdot$ such that $Y_i \cdot = 0$ for

every i^* (for n' cells). Let the values of environmental covariates be X_i and X_{i^*} corresponding to Y_i and Y_{i^*} respectively.

$C(i) = n$, $C(i^*) = n'$ and $C(i) + C(i^*) = N$ where C = cardinality

Obviously for the Ignored method there will be no Y_{i^*}; Further, X_{i^*} corresponding to the missing cells will be ignored. So, Y_i and X_i will only be utilized in the computation of sensitivity coefficients.

Let us designate the sensitivity coefficient obtained from Substituted method as b_s and sensitivity coefficient obtained from Ignored method as b_I. In the aforesaid notations b_s and b_I may be written as under

$$b_s = \frac{\sum_i^n \left[X_i - \left(\frac{\sum_i^n X_i + \sum_{i^*}^{n'} X_{i^*}}{N} \right) \right] Y_i + \sum_{i^*}^{n'} \left[X_{i^*} - \left(\frac{\sum_i^n X_i + \sum_{i^*}^{n'} X_{i^*}}{N} \right) \right] Y_{i^*}}{\sum_i^n \left[X_i - \left(\frac{\sum_i^n X_i + \sum_{i^*}^{n'} X_{i^*}}{N} \right) \right]^2 + \sum_{i^*}^{n'} \left[X_{i^*} - \left(\frac{\sum_i^n X_i + \sum_{i^*}^{n'} X_{i^*}}{N} \right) \right]^2}$$

$$b_I = \frac{\sum_i^n \left[X_i - \left(\frac{\sum_i^n X_i}{n} \right) \right] Y_i}{\sum_i^n \left[X_i - \left(\frac{\sum_i^n X_i}{n} \right) \right]^2}$$

Let us compare the numerators of b_s and b_I. Since $Y_{i^*} = 0$ for every i^* (for n' cells), the numerator of b_s may be written as

$$\text{Numerator of } b_s = \sum_i^n \left[X_i - \left(\frac{\sum_i^n X_i + \sum_{i^*}^{n'} X_{i^*}}{N} \right) \right] Y_i$$

$$= \sum_i^n X_i Y_i - \frac{\left(\sum_i^n X_i + \sum_{i^*}^{n'} X_{i^*} \right)}{N} \sum_i^n Y_i$$

$$= \sum_i^n X_i Y_i - 0 \qquad\qquad \left[\because \sum_i^n Y_i = 0 \right]$$

$$= \sum_i^n X_i Y_i$$

Similarly

Numerator of $b_I = \sum_{i=1}^n X_i Y_i$ $\qquad\qquad \left[\because \sum_i^n Y_i = 0 \right]$

Hence the numerators of both b_s and b_I are same.

Let us now compare the denominators of b_s and b_I.

Denominator of b_s – Denominator of b_I

$$= \sum_i^n \left[X_i - \frac{\left(\sum_i^n X_i + \sum_{i^*}^{n'} X_{i^*} \right)}{N} \right]^2 + \sum_{i^*}^{n'} \left[X_{i^*} - \frac{\left(\sum_i^n X_i + \sum_{i^*}^{n'} X_{i^*} \right)}{N} \right]^2$$

$$- \sum_i^n \left[X_i - \frac{\left(\sum_i^n X_i \right)}{n} \right]^2$$

$$= \sum_i^n \left[X_i - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right]^2 - \sum_i^n [X_i - \overline{X}]^2 + \sum_{i^*}^{n'} \left[X_{i^*} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right]^2$$

$$= \sum_i^n \left[X_i - \overline{X} + \overline{X} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right]^2 - \sum_i^n [X_i - \overline{X}]^2 + \sum_{i^*}^{n'} \left[X_{i^*} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right]^2$$

$$= \sum_i^n \left[(X_i - \overline{X})^2 + \left\{ \overline{X} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right\}^2 + 2(X_i - \overline{X}) \left\{ \overline{X} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right\} \right]$$

$$- \sum_i^n [X_i - \overline{X}]^2 + \sum_{i^*}^{n'} \left[X_{i^*} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right]^2$$

$$= \sum_{i}^{n} [X_i - \overline{X}]^2 + \sum_{i}^{n} \left[\overline{X} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right]^2 + 2 \left[\overline{X} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right] \sum_{i}^{n} [X_i - \overline{X}]$$

$$- \sum_{i}^{n} [X_i - \overline{X}]^2 + \sum_{i^*}^{n'} \left[X_{i^*} - \frac{[n\overline{X} + n'\overline{X}_*]}{N} \right]^2$$

$$= \sum_{i}^{n} \left[\overline{X} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right]^2 + \sum_{i^*}^{n'} \left[X_{i^*} - \frac{(n\overline{X} + n'\overline{X}_*)}{N} \right]^2 \geq 0$$

This implies that denominator of b_s is always greater than or equal to the denominator of b_1 which makes the b_s biased towards zero. If we interpret this result in a more formal way, zero imputation for the interaction of missing cells is contributing nothing to the numerator of b_s but the corresponding covariate values are causing rise in the denominator of b_s. The sign of sensitivity coefficient remains same for both Substituted and Ignored methods since the sign is determined by the numerator only. Similarly one may study the impact of zero substitution for the interaction of missing cells on the regression sum of squares. We know that, Regression SS = Sensitivity coefficient × Numerator. As the estimate of sensitivity coefficient is biased towards zero in the Substituted method, the Regression SS for the Substituted method will always be less than or equal to that of Ignored method causing biased fitting in Substituted method, which ultimately leads to biased co-efficient of determination (R^2). So it is better not to include the levels of covariate corresponding to the missing cells as there is no corresponding contribution to numerator from non zero realizations of random interaction effects. It is thus evident that Ignored method may be statistically superior atleast for the single covariate case.

When the case of regression of interactions on more than one environmental covariate at a time is considered, one may not arrive at any conclusion for the numerical comparison of Substituted method with Ignored method. In this case sum of cross products between the covariates come into picture and the signs and magnitude of sensitivity coefficients for the Ignored method over the Substituted method would remain unpredictable. However when the interaction is treated as fixed, Ignored method is the only option one may be left with.

4. Illustration

For the sake of illustration, the data reported by Aastveit [1] is considered and presented in Table 1. The data set represents plant height of genotypes of barley. The experiment has been carried out at AS Norway, over a period of 9 years in an RBD with 4 blocks. The sowing date was same for all 15 genotypes

but differed from year to year. The data in Table 1 are the average values of plant height over 4 replications for different years. The data on different climatic variables corresponding to the years taken in Table 1 are presented in Table 2, which was also taken from the same source i.e. Aastveit [1]. The data in Table 2 shows sowing time in days after 1st April (ST) and average rainfall (mm) per day at six growth periods, $(R_1, ..., R_6)$. It may be noted that six growth periods reflect stages of grain maturity, not the calendar dates.

Table 1. Yearly plant heights of barley measured in cm., averaged over 4 replicates for 15 genotypes

	1974	1975	1976	1977	1978	1979	1980	1981	1982	Average
G-1	81.0	67.3	71.5	64.3	55.8	84.9	86.2	88.0	72.0	74.56
G-2	72.3	60.3	60.8	55.3	48.8	78.1	80.4	85.3	69.8	67.90
G-3	79.3	67.8	64.8	57.5	46.8	80.2	81.8	87.8	71.8	70.87
G-4	88.5	70.8	76.3	69.5	64.0	90.8	97.3	97.8	86.0	82.33
G-5	78.5	67.5	72.5	61.0	50.3	78.7	82.7	87.3	66.0	71.61
G-6	89.3	74.5	80.5	67.8	60.8	86.3	90.2	100.0	81.3	81.19
G-7	94.3	73.0	80.3	68.5	63.8	96.0	100.7	106.5	85.3	85.38
G-8	88.8	63.8	66.8	78.5	70.3	86.1	104.3	102.0	82.5	82.57
G-9	91.3	67.0	73.8	75.8	71.5	90.5	100.6	102.8	86.3	84.40
G-10	91.8	65.5	77.0	80.0	73.5	88.0	104.7	102.0	87.3	85.53
G-11	86.0	69.8	73.8	77.3	75.5	88.8	106.4	103.8	86.8	85.36
G-12	91.0	71.8	81.0	65.5	54.5	87.9	84.8	91.8	77.8	78.46
G-13	75.5	56.5	67.0	64.3	58.8	86.7	85.2	91.8	76.0	73.53
G-14	96.8	81.5	86.3	73.3	59.3	97.0	96.1	95.8	90.3	86.27
G-15	97.0	83.3	86.8	72.0	49.3	91.3	94.6	95.5	80.8	83.40
Average	86.76	69.36	74.61	68.71	60.20	87.42	93.07	95.88	80.00	79.56

Table 2. Climatic variables of the different years

Climatic variables	1974	1975	1976	1977	1978	1979	1980	1981	1982	Average
ST	17.00	21.00	26.00	48.00	35.00	39.00	35.00	38.00	27.00	31.78
R_1	0.00	1.66	0.80	0.21	0.37	1.35	0.67	0.23	2.58	0.87
R_2	0.16	1.84	2.05	3.62	0.66	3.92	3.45	3.20	3.29	2.47
R_3	1.59	1.68	0.81	0.36	0.75	1.05	2.75	4.36	0.01	1.48
R_4	2.65	0.08	0.40	3.46	6.72	2.22	6.20	3.01	2.76	3.06
R_5	1.70	0.02	1.02	0.15	3.32	0.86	1.05	4.14	3.31	1.73
R_6	2.21	0.01	1.06	4.65	0.88	2.49	3.60	0.54	2.54	2.00

ST: Sowing time, measured in days after April 1
$R_1,...,R_6$: average rainfall(mm.) per day in the 6 growth periods

First, the sensitivities of the 15 varieties under investigation corresponding to each of the covariates are evaluated by taking one covariate at a time. The model used for this is

$$Y_{ijr} = \mu + \alpha_i + \beta_j + \Phi_{hi}X_{hj} + \delta_{ij} + \varepsilon_{ijr}$$

The corresponding results are presented in Table 3. The environmental index (internal covariate, β_j) has also been considered as 8th covariate and the sensitivities corresponding to this are presented in Table 3 as 8th column, which eventually are equivalent to Perkins and Jinks [11] regression coefficients. The results presented in Table 3 can be interpreted as following: If we consider the first covariate sowing time, in days after 1st April, the genotypes G-1, G-3, G-4, G-5, G-6, G-7, G-12, G-14 and G-15 can take the advantage of early sowing as the sign of sensitivity coefficients for these genotypes is negative. Similarly the genotypes G-2, G-8, G-9, G-10, G-11 and G-13 will be in better position if sowing is delayed, as these genotypes possess positive sign for the sensitivity coefficient. A similar kind of interpretation can be made for the other covariates too. If we take the environmental index (the internal covariate), thought of the joint (net) effect of so many complex covariates such as soil fertility, climate, management practices and so on, obtained from the two-way table itself, the genotypes G-2, G-3, G-4, G-7, G-8, G-9, G-15 can exploit the favorable environmental conditions, whereas genotypes G-1, G-5, G-6, G-10, G-11, G-12, G-13 and G-14 can be recommended for poor environmental conditions. The SS due to regression is also given in Table 3 for each covariate. The genotype × environment interaction SS is found to be 2541.39. Perkins and Jinks [11] model is explaining only 4% of the interaction SS; and is likely to miss important interaction effects. On the other hand, R_4 is explaining 66% of the interaction SS. This additional information on rainfall is exploited to explain the interaction.

To show that Substituted method is biased in comparison to Ignored method, artificial unbalancedness is created by purposefully discarding some data in Table 1. The details of discarded data are given in Table 4. In order to obtain BLUP estimates of interaction, one need to have replicated data, so three replicates are generated for the data in Table 1 such that average over these 3 replications is equal to the mean value in Table 1. Let us call this unbalanced replicated barley data as Ubarley. The BLUP estimates of interactions are obtained from Ubarley with the following constraints

$$\sum_i (\alpha\beta)_{ij} = 0$$

and
$$\sum_j (\alpha\beta)_{ij} = 0$$

Table 3. Co-efficients of sensitivity of the 15 genotypes when one covariate is taken in the Factorial Regression model at a time

	ST	R_1	R_2	R_3	R_4	R_5	R_6	β_j
G-1	-0.015	0.077	-0.277	-0.632	-0.445	-1.051	-0.330	-0.099
G-2	0.015	1.549	0.518	0.144	-0.155	0.217	-0.539	0.001
G-3	-0.184	1.819	-0.053	0.392	-1.153	-0.680	-0.995	0.040
G-4	-0.006	1.194	0.263	-0.261	0.332	0.521	0.146	0.021
G-5	-0.112	-0.765	-0.722	0.190	-1.132	-1.491	-1.166	-0.093
G-6	-0.180	0.228	-0.948	0.321	-0.961	0.236	-1.562	-0.038
G-7	-0.063	-0.197	0.230	1.645	-0.027	0.939	-0.636	0.226
G-8	0.417	-3.484	0.730	1.009	2.798	1.546	2.354	0.043
G-9	0.227	-1.756	0.088	0.213	1.749	1.672	1.061	0.006
G-10	0.293	-2.718	0.111	-0.206	2.233	1.442	1.933	-0.043
G-11	0.352	-1.398	0.722	0.597	2.457	1.678	1.066	-0.061
G-12	-0.306	0.623	-1.328	-1.014	-1.827	-1.165	-1.105	-0.048
G-13	0.308	0.179	1.321	-0.554	0.827	1.240	0.599	-0.015
G-14	-0.321	3.320	-0.225	-1.698	-1.839	-1.800	-0.244	-0.019
G-15	-0.427	1.329	-0.432	-0.146	-2.857	-3.304	-0.581	0.078
Reg SS	759.89	258.77	99.11	133.62	1667.61	578.48	351.80	105.70
Rem SS	1781.50	2282.62	2442.28	2407.77	873.78	1962.91	2189.59	2435.50
R^2	0.30	0.10	0.04	0.05	0.66	0.23	0.14	0.04

Table 4. Details of discarded data

Variety	Environment	Plant Height
2	8	85.3
4	1	88.5
7	3	80.3
8	8	102.0
13	4	64.3

Table 5. Co-efficients of sensitivity of 15 genotypes from Substituted BLUP methodwhen one covariate is taken at a time

	ST	R_1	R_2	R_3	R_4	R_5	R_6
G-1	-0.005	0.014	-0.128	-0.322	-0.286	-0.640	-0.214
G-2	0.005	1.097	0.328	-0.050	-0.097	0.024	-0.258
G-3	-0.114	1.140	0.017	0.339	-0.744	-0.400	-0.644
G-4	-0.014	0.614	0.097	-0.077	0.209	0.375	0.102
G-5	-0.068	-0.531	-0.416	0.209	-0.730	-0.924	-0.754
G-6	-0.112	0.111	-0.562	0.294	-0.620	0.192	-1.011
G-7	-0.037	-0.166	0.194	1.141	-0.028	0.639	-0.421
G-8	0.253	-1.989	0.392	0.217	1.813	0.685	1.730
G-9	0.152	-1.171	0.108	0.224	1.133	1.121	0.685
G-10	0.194	-1.793	0.122	-0.047	1.445	0.972	1.249
G-11	0.232	-0.940	0.517	0.472	1.590	1.124	0.688
G-12	-0.193	0.367	-0.807	-0.570	-1.179	-0.713	-0.716
G-13	0.180	0.214	0.816	-0.184	0.525	0.942	0.221
G-14	-0.203	2.110	-0.094	-1.012	-1.187	-1.124	-0.159
G-15	-0.271	0.823	-0.228	-0.009	-1.845	-2.097	-0.377
Reg. SS	302.14	101.82	36.73	48.90	696.73	233.68	156.82
Rem. SS	753.22	953.54	1018.62	1006.46	358.63	821.68	898.53
R^2	0.29	0.1	0.03	0.05	0.66	0.22	0.15

The coefficients of sensitivity obtained for 15 genotypes from the Substituted BLUP method when one covariate is taken at a time are presented in Table 5. Each column in Table 5 refers to a particular covariate and is independent of other columns since the sensitivities in each column are obtained by an independent regression. The splitting up of interaction SS (1055.36) into Regression SS and Remainder SS as well as the co-efficient of determination (R^2) corresponding to each covariate are also presented in Table 5. The sensitivity coefficients for 15 genotypes corresponding to Ignored BLUP method when one covariate is taken at a time are presented in Table 6. The splitting up of interaction SS as well as the co-efficient of determination (R^2) corresponding to each covariate are also presented in Table 6. As expected, the coefficients of sensitivity in Table 6 for the genotypes, which are present in all the environments remained same to that of Table 5. One may compare the

magnitudes of sensitivities for the genotypes G-2, G-4, G-7, G-8 and G-13, which are not present in all the environments in Table 5 and Table 6. With every covariate, the magnitude of sensitivity in Table 5 is less than or equal to the corresponding sensitivity in Table 6, revealing the biasedness of Substituted method in comparison to Ignored method. We may also observe that regression SS or equivalently R^2 value in Table 5 is always less than or equal to the corresponding value in Table 6, revealing the biased fitting resulted from Substituted method. This finding enables us to recommend Ignored method in place of Substituted method. Further, Ignored method is valid for random as well as fixed interaction effects.

Table 6. Co-efficients of sensitivity of 15 genotypes from Ignored BLUP method when one covariate is taken at a time

	ST	R_1	R_2	R_3	R_4	R_5	R_6
G-1	-0.005	0.014	-0.128	-0.322	-0.286	-0.640	-0.214
G-2	0.005	1.196	0.342	-0.138	-0.097	0.038	-0.296
G-3	-0.114	1.140	0.017	0.339	-0.744	-0.400	-0.644
G-4	-0.021	0.724	0.164	-0.077	0.210	0.375	0.103
G-5	-0.068	-0.531	-0.416	0.209	-0.730	-0.924	-0.754
G-6	-0.112	0.111	-0.562	0.294	-0.620	0.192	-1.011
G-7	-0.039	-0.166	0.197	1.182	-0.035	0.660	-0.445
G-8	0.268	-2.168	0.408	0.601	1.813	1.076	1.988
G-9	0.152	-1.171	0.108	0.224	1.133	1.121	0.685
G-10	0.194	-1.793	0.122	-0.047	1.445	0.972	1.249
G-11	0.232	-0.940	0.517	0.472	1.590	1.124	0.688
G-12	-0.193	0.367	-0.807	-0.570	-1.179	-0.713	-0.716
G-13	0.293	0.234	0.908	-0.204	0.528	1.116	0.388
G-14	-0.203	2.110	-0.094	-1.012	-1.187	-1.124	-0.159
G-15	-0.271	0.823	-0.228	-0.009	-1.845	-2.097	-0.377
Reg. SS	320.84	104.85	38.11	50.92	696.80	241.69	166.09
Rem. SS	734.52	950.51	1017.25	1004.44	358.56	813.66	889.26
R^2	0.30	0.10	0.04	0.05	0.66	0.23	0.16

ACKNOWLEDGEMENT

REFERENCES

[1] Aastveit (1986). ANOVA interactions interpreted by partial least squares regression. *Biometrics*, **42**, 829-844.

[2] Alison Smith, Brian Cullis and Robin Thompson (2001). Analyzing variety by environment data using multiplicative mixed models and adjustments for spatial field trend. *Biometrics*, **57**, 1138-1147.

[3] Baril, C.P., Denis, J.B., Wustman, R. and Eeuwijk, F.A. Van (1995). Analysing genotype by environment interaction in Dutch potato variety trials using factorial regression. *Eeuphytica*, **82**, 149-155.

[4] Cullis, B. R., Gogel, B. J., Verbyla, A. P., and Thompson, R. (1998). Spatial analysis of multi-environment early generation trials. *Biometrics*, **54**, 1-18.

[5] Denis, J.B. (1980). Analyse de regression factorielle. *Biom. Praxim.*, **20**, 1-34.

[6] Denis, J.B. (1988). Two way analysis using covariates. *Statistics*, **19**, 123-132.

[7] Eeuwijk, F.A. Van (1995). Linear and bilinear models for the analysis of multi-environment trials, I, An inventory of models. *Euphytica*, **84**, 1-7.

[8] Finlay, K. and Wilkinson, G.N. (1963). The analysis of adaptation in a plant-breeding programme. *Australian Journal of Agricultural Research*, **14**, 742-754.

[9] Jukka, Ofversten (1998). Assessing sensitivity of agricultural crop varieties. *Journal of Agricultural, Biological and Environmental Statistics*, **3(1)**, 37-47.

[10] Nabugoomu, F., Kempton, R.A. and Talbot, M. (1999). Analysis of series of trials where varieties differ in sensitivity to locations. *Journal of Agricultural, Biological and Environmental Statistics*, **4**, 311-325.

[11] Pekins, J.M. and Jinks, J.L. (1968). Environmental and genotype-environmental components of variability, III, Multiple lines and crosses. *Heredity*, **23**, 339-346.

[12] Raju, B. M. K. (2002). On some statistical aspects of assessing sensitivity of crop varieties. Ph.D Thesis, P. G. School, IARI, New Delhi.

[13] Snedecor, G.W. and Cochran, W.G. (1980). *Statistical Methods.* 7th edition. Iowa State University Press, Ames, IO.

[14] Yates, F. and Cochran, W.G. (1938). The analysis of groups of experiments. *Journal of Agricultural Science*, Cambridge, **28**, 556-580.