

## Use of AMMI in Simultaneous Selection of Genotypes for Yield and Stability

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### SUMMARY

Multi-environmental trials (MET), generally, have significant main effects and significant multiplicative genotype  $\times$  environment interaction effect. AMMI offers a more appropriate statistical analysis to deal with such situations, compared to traditional methods like ANOVA, PCA and linear regression. In this paper, a family of simultaneous selection indices is proposed, which selects genotypes for both high yield and stability in MET using AMMI model. A comparison between proposed indices and existing simultaneous selection indices is also made. To assist agronomists and plant breeders, a user-friendly computer programme is developed and demonstrated with real data.

*Key words* : Simultaneous selection indices, Stability, AMMI, Multi-environmental trials.

### 1. INTRODUCTION

Genotype  $\times$  environment interaction (GEI) continues to be a challenging issue among plant breeders, geneticists, and production agronomists who conduct crop performance trials across diverse environments. GEI can reduce progress from selection. The methods of partitioning GEI into components attributable to each genotype measure the contribution of each genotype to GEI. A universally acceptable selection criterion that takes GEI into consideration does not exist. Whenever an interaction is significant, the use of main effects, e.g. overall genotypes means across environments, is questionable. Hence, stability of performance should be considered as an important aspect of yield trials. Researchers need a statistic that provides a reliable measure of stability or consistency of performance across a range of environments, particularly one that reflects the contribution of each genotype to the total GEI. In literature a large number of stability measures are available (Prabhakaran and Jain (1994)). However, the stability measure alone is of limited use. For a successful breeding or cultivar testing programme, both stability and yield (or any other trait) must be considered simultaneously. Also integration of stability of performance with yield through suitable measures will help in selecting cultivars in a more refined manner. One

approach would be to integrate measures of performance and stability as a most informative index.

Kang and Pham (1991) discussed several methods of simultaneous selection for yield and stability and relationships among them. The development and use of Yield-Stability statistic (YSi) has enabled incorporation of stability in the selection process (Kang (1993)). Kang's Yield-Stability statistic (Kang (1993)) has been evaluated and found to be useful for recommending varieties (Pazdernik *et al.* (1997)). However, Bajpai and Prabhakaran (2000) observed that Kang's rank-sum method has an inherent weakness that it is weighing heavily towards yield performance, apart from the arbitrariness in the scoring procedure. Accordingly they proposed three new indices which were found to be superior to Kang (1993) indices. Dashiell *et al.* (1994) evaluated the usefulness of several stability statistics for simultaneously selecting for high yield and stability of performance in soybean. Fernandez (1991) also evaluated stability statistics for similar purposes.

This study proposes a family of simultaneous selection indices using Additive Main Effects and Multiplicative Interaction (AMMI). The AMMI model is chosen when main effects (genotypic, environmental) and genotype  $\times$  environment interaction (GEI) effects are both important in yield trials (Gauch ((1988), (1992)),

Zobel *et al.* (1988)). It also captures non-linear GEI, left unaccounted by the joint regression technique. AMMI discards noise rich residuals, after fitting main effects, and decomposes the residual matrix by singular value decomposition. Nachit *et al.* (1992) showed that AMMI model was more effective in partitioning the GEI sum of squares than the linear regression model. Yan *et al.* (2000) advocated a graphical presentation of main effect of genotype (G) and genotype  $\times$  environment interaction (GE) as a 'GGE' biplot. However, the inferences drawn from biplots will be valid only when the first PCA or the first two PCAs explain a large proportion of interaction variation. Whenever more than two axes are retained in the AMMI model, the biplot formulation of interaction becomes complex. Consequently the conclusions drawn on stability of varieties will be imprecise. However, the plant breeders would like to identify varieties which are stable and high yielding when the PCA axes retained in the AMMI model will be more than two, if the axes together accumulate considerable portion of interaction variation. Thus, there is a need to develop selection indices under such circumstances. A comparison between the proposed indices and the improved simultaneous selection indices by Bajpai and Prabhakaran (2000) will help in judging the superiority of the former over the latter. Kang and Magari (1995) proposed a computer program (STABLE) for calculating Kang's Yield-Stability statistic. We also give a listing of a user-friendly programme to judge superior genotypes for both yield and stability. Before introducing the new family of selection indices based on AMMI model, a brief outline of AMMI procedure and biplots is given.

## 2. AMMI PROCEDURE

### AMMI Model

The AMMI model for T genotypes and S environments is given as

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{n'} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij} \quad (1)$$

$$\theta_{ij} \sim N(0, \sigma^2); i = 1, 2, \dots, T; j = 1, 2, \dots, S$$

where,  $Y_{ij}$  is the mean yield of  $i$ th genotype in the  $j$ th environment;  $\mu$  is the general mean;  $g_i$  is the  $i$ th genotypic effect;  $e_j$  is the  $j$ th location effect;  $\lambda_n$  is the eigen value of the PCA axis  $n$ ;  $\alpha_{in}$  and  $\gamma_{jn}$  are the  $i$ th

genotype and  $j$ th environment PCA scores for the PCA axis  $n$ ;  $\theta_{ij}$  is the residual;  $n'$  is the number of PCA axes retained in the model. Ordinarily the number  $n'$  is judged on the basis of empirical consideration of F-test of significance (Gauch (1988), (1992)). The residual combines the PCA scores from the  $N - n'$  discarded axes, where  $N = \min(T - 1, S - 1)$ . The other constraints in the model (1) are

$$\sum_i \alpha_{in}^2 = \sum_j \gamma_{jn}^2 = 1 \quad \forall n$$

$$\sum_i \alpha_{in} \alpha_{in'} = \sum_j \gamma_{jn} \gamma_{jn'} = 0$$

$$\text{and } \lambda_1 > \lambda_2 > \dots > \lambda_{n'} > 0 \quad n \neq n'$$

The model in (1) can be reparameterized as

$$Y_{ij} = \mu + g_i + e_j + Z_{ij} \quad (2)$$

$$\text{where } Z_{ij} = \sum_{n=1}^{n'} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij}$$

Let the estimate of interaction in the  $(i, j)$ th cell  $Z_{ij}$  be  $\hat{Z}_{ij} = Y_{ij} - \hat{\mu} - \hat{g}_i - \hat{e}_j$ . Using matrix notation, denote  $\mathbf{Z} = (\hat{Z}_{ij})$  a matrix of order  $T \times S$ . Now, the estimates of the parameters of the model are

$$\hat{\lambda}_n = \text{the non-zero eigen values of } \mathbf{Z}'\mathbf{Z} \text{ or } \mathbf{Z}\mathbf{Z}' \text{ (in descending order)}$$

$$\hat{\alpha}_{in} = \text{the principal components of the rows of the sum of squares and cross product matrix } \mathbf{Z}\mathbf{Z}' \text{ and}$$

$$\hat{\gamma}_{jn} = \text{the principal components of the columns of the sum of squares and cross product matrix } \mathbf{Z}'\mathbf{Z}$$

Using these we can write

$$\hat{z}_{ij} = \sum_{n=1}^N \hat{\lambda}_n \hat{\alpha}_{in} \hat{\gamma}_{jn} \quad (3)$$

It follows that,  $\alpha_{in}^* = \lambda_n^c \hat{\alpha}_{in}$  is the  $i$ th genotype PCA score for the  $n$ th axis, and  $\gamma_{jn}^* = \lambda_n^{1-c} \hat{\gamma}_{jn}$  is the  $n$ th PCA score of the  $j$ th environment; where  $c$  is a scaling constant varying between 0 to 1.

Also, using factor analytic decomposition,  $\mathbf{Z}$  may be written as

$$\mathbf{Z} = \mathbf{ADB}' \quad (4)$$

where  $\mathbf{A}$  is  $T \times N$  orthonormal matrix,  $\mathbf{D}$  is  $N \times N$  diagonal matrix with elements  $\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_{n'} \geq \dots \geq \lambda_N$ ,  $\mathbf{B}$  is  $N \times S$  orthonormal matrix,  $N$  is the rank of  $\mathbf{Z}$ . The matrices  $\mathbf{A}$ ,  $\mathbf{D}$  and  $\mathbf{B}$  of equation (4) can be obtained from the eigen vectors and eigen values of  $\mathbf{ZZ}'$  of the order  $T \times T$ . The matrix  $\mathbf{A}$  consists of the eigen vectors (principal components  $\alpha_{in}$ ) of  $\mathbf{ZZ}'$  and the diagonal matrix  $\mathbf{D}$  with square root of eigen values as diagonal elements of  $\mathbf{ZZ}'$ . The matrix  $\mathbf{B}$  consists of the eigen vectors (principal components  $\gamma_{jn}$ ) can be obtained by solving  $\mathbf{B} = \mathbf{Z}'\mathbf{A}\mathbf{D}^{-1}$ . For many practical situations, the number of PCA axes to be retained is determined by testing the mean square of each axis with the estimate of residual through F-statistic (Gollob (1968), Gauch (1988)). The mean sum of squares of each PCA axis is equal to the ratio of square of the corresponding eigen value and the degree of freedom of each axis obtained as  $T + S - 1 - 2n$ .

The model formulation for AMMI shows its interaction part consists of summed orthogonal products. Because of this form the interaction lends itself to graphical display in the form of so-called biplots (Gabriel (1971)). Here, it is assumed that the first two PCA axes suffice for an adequate description of the GEI.

### 3. SOME SIMULTANEOUS SELECTION INDICES BASED ON AMMI MODEL

It is evident from earlier sections that the scope of biplots is very much limited. The inferences drawn from biplots will be valid only when the first two PCAs explain a large portion of interaction variation. In situations, where more than two PCA axes are needed to accumulate considerable portion of GEI variation, what should be the approach for identifying varieties which are high yielding as well as stable. Keeping this in mind, we propose here a new family of simultaneous selection indices which can select varieties for both yield and stability.

Let  $\alpha_n^* = \alpha_n \lambda_n$  be a  $T \times 1$  vector of modified genotypic scores corresponding to the  $n$ th PCA axis of  $\mathbf{ZZ}'$ ; where  $\lambda_n$  is the eigen value and  $\alpha_n$  is the corresponding eigen vector of  $\mathbf{ZZ}'$ . Suppose that  $n'$  of the  $N$  axes are retained in the AMMI model to explain genotype  $\times$  environment interaction, then the stability measure of  $i$ -th variety can be determined as the end point of its vector  $(\alpha_{1i}^*, \alpha_{2i}^*, \dots, \alpha_{n'i}^*)$  from the origin

$O'_{1 \times n'}$ . This can also be taken as the squared euclidean distance between the vector  $\delta' = (\alpha_{1i}^*, \alpha_{2i}^*, \dots, \alpha_{n'i}^*)$  from the origin, in the  $n'$ -dimensional Euclidean space. We consider a stability measure,  $ASTAB_i$  as

$$\begin{aligned} ASTAB_i &= d_i(\delta, \mathbf{0}) = \alpha_{1i}^{2*} + \alpha_{2i}^{2*} + \dots + \alpha_{n'i}^{2*} \\ &= \sum_{n=1}^{n'} \alpha_{ni}^{2*} = \sum_{n=1}^{n'} \lambda_n \alpha_{ni}^2 \end{aligned} \quad (5)$$

The algebraic expression of the above said stability measure can also be derived from the spectral decomposition of the  $\mathbf{ZZ}'$  matrix. As we know that

$$\mathbf{ZZ}' = \lambda_1 \alpha_1 \alpha_1' + \lambda_2 \alpha_2 \alpha_2' + \dots + \lambda_n \alpha_n \alpha_n' + \dots + \lambda_N \alpha_N \alpha_N'$$

The  $i$ th diagonal element of  $\mathbf{ZZ}'$  i.e.,  $\sum_{j=1}^S Z_{ij}^2$ , is nothing but the interaction effects of  $i$ -th genotype over  $S$  environments.

Therefore

$$\sum_{j=1}^S Z_{ij}^2 = \lambda_1 \alpha_{1i}^2 + \lambda_2 \alpha_{2i}^2 + \dots + \lambda_N \alpha_{Ni}^2 = \sum_{n=1}^N \lambda_n \alpha_{ni}^2 \quad (6)$$

The stability measure mentioned in (5) is also equal to the expression given in (6) when  $N = n'$ ,  $n'$  being the number of PCA axes retained in the AMMI model. A variety is considered more stable when the value of  $ASTAB_i$  is lower. The proposed selection indices ( $I_j$ ) consists of (i) a yield component, measured as the ratio of the average performance of the  $j$ th genotype to the overall mean performance of the genotypes under test, and (ii) a stability component, measured as the ratio of stability information ( $1/ASTAB_j$ ) of the  $j$ th genotype to the mean stability information of all the genotypes under test. The simultaneous selection index can be given as

$$I_j = \frac{\bar{Y}_j}{\bar{Y}_{..}} + \alpha \frac{(1/ASTAB_j)}{\left( \frac{1}{T} \sum_{j=1}^T ASTAB_j \right)} \quad (7)$$

where  $\alpha$  is the ratio of the weights given to the stability components ( $w_2$ ) and yield ( $w_1$ ) with a restriction that  $w_1 + w_2 = 1$ . The weights considered in the index are, in general, as per the plant breeders' requirement. By considering the values of  $\alpha$  as 1.0 ( $w_1 = w_2 = 0.5$ ), 0.66 ( $w_1 = 0.6, w_2 = 0.4$ ), 0.43 ( $w_1 = 0.7, w_2 = 0.3$ ) and 0.25

( $w_1 = 0.8$ ,  $w_2 = 0.2$ ), a new family of indices consists of four indices  $I_1$ ,  $I_2$ ,  $I_3$  and  $I_4$  are proposed in this paper.

#### 4. COMPARISON OF THE SIMULTANEOUS SELECTION INDICES

In this section we compare the performance of the proposed selection indices among themselves as well as with the existing indices (Bajpai and Prabhakaran (2000)). The comparisons are made on the basis of Spearman's rank correlations. The rank correlations are worked out between yield based ranks and index-based ranks, stability based ranks and index based ranks so as to assess the performance of the selection indices. Also the percentage of high yielders and highly stable varieties present in the top 50% varieties selected on the basis of index values are worked out.

The data used for comparing various simultaneous selection indices are collected from multi-location year trials of released and pre-released varieties of groundnut conducted in different agro-climatic zones of Andhra Pradesh. The data are supplied by Regional Agricultural Research Station (RARS), Palem and quoted by Raju (1998). The experiments were conducted in 20 environments and the same 15 genotypes. Each experiment was laid in randomized block design (RBD) with three replications. The pod yields were expressed as kilogram per hectare (kg/ha). The mean data over the replicates for the 15 genotypes and 20 environments are considered for the AMMI analysis. The ANOVA based on AMMI model is presented in Table 1. It is evident from Table 1 that the use of biplots to explain efficiently

the interaction is very much limited, since the first two PCA axes explain only 55% of the total interaction variation. Hence it may not be advisable to conclude either on stability or simultaneous selection based on these two axes. It is evident that at least six axes must be retained for explaining stability or using the proposed simultaneous selection indices. Accordingly the index values and stability values are calculated by retaining 6 PCA axes in the model. The rank orders based on yield, stability (ASTAB<sub>i</sub>), proposed index and Bajpai index for each genotype and for different  $\alpha$  values are presented in Table 2. Table 3 shows the rank correlations between yield, stability with the proposed indices and Bajpai indices. Significant correlations of order 0.59, 0.61, 0.64 and 0.78 are observed between yield and proposed index when value of  $\alpha$  is taken as 1.0, 0.67, 0.43 and 0.25 respectively, whereas with the Bajpai's index the correlations are to the extent 0.49, 0.51, 0.55 and 0.64. Further, the correlations indicate superiority of the proposed index over the Bajpai's index. Also Table 3 indicates the extent of high linear relationship between the rank orders of proposed index with the stability. Besides, these correlations are at par with the correlations observed between stability and Bajpai's index. The proportion of high yielders and stable performers present in the 50% top selected genotypes based on simultaneous selection index values are presented in Table 4. From this table, it is evident that among the top 50% varieties selected based on the proposed indices, around 70% are the high yielders and 85% are high stable performers. Since the proposed indices show significant correlations with both high yield and stability as well as selects large

Table 1. AMMI analysis of variance for groundnut data

Source	d.f.	Sum of squares	Mean square	Variance ratio
Genotypes	14	3565604.00	254686.00	12.63**
Environments	19	107622796.00	5664357.70	280.86**
G × E interaction	266	25408293.00	95519.90	4.74**
___ PCA1	32	10240492.00	320015.38	12.05**
___ PCA2	30	3899700.40	129990.01	4.90**
___ PCA3	28	2795398.80	99835.67	3.76**
___ PCA4	26	2377000.80	91423.11	3.44**
___ PCA5	24	1961588.90	81732.87	3.08**
___ PCA6	22	1372729.60	62396.80	2.35**
Residual	104	2761382.50	26551.75	
Average error	560	11294080.00	20168.00	

\*\* indicates  $P < 0.01$

Table 2. Effect of variation of weights on the rank orders of groundnut varieties in the simultaneous selection indices

Variety	Yield (tone/ hectare)	Yield based Rank	Stability based Rank	Proposed index				Bajpai's index			
				$\alpha = 1.0$	$\alpha = 0.67$	$\alpha = 0.43$	$\alpha = 0.25$	$\alpha = 1.0$	$\alpha = 0.67$	$\alpha = 0.43$	$\alpha = 0.25$
G1	1.51	2	8	6	6	6	5	5	5	5	4
G2	1.34	12	6	7	7	7	8	3	3	4	5
G3	1.38	7	13	13	13	12	12	13	13	13	13
G4	1.32	11	14	14	14	14	14	14	14	14	14
G5	1.30	13	15	15	15	15	15	15	15	15	15
G6	1.69	1	3	2	1	1	1	4	4	3	3
G7	1.46	4	2	3	3	3	3	2	2	2	2
G8	1.27	15	7	8	8	8	10	8	8	8	9
G9	1.37	8	9	9	9	9	9	10	10	10	10
G10	1.36	10	12	11	11	11	11	12	12	12	11
G11	1.37	9	4	4	4	4	6	6	7	7	7
G12	1.50	3	5	5	5	5	4	7	6	6	6
G13	1.46	5	10	10	10	10	7	9	9	9	8
G14	1.44	6	1	1	2	2	2	1	1	1	1
G15	1.27	14	11	12	12	13	13	11	11	11	12

proportion of high yielders and stable performers, they can be safely recommended to the breeders and production agronomists for selecting genotypes simultaneously for high yield and stability.

#### A Computer Programme

A SAS programme names Simultaneous selection of genotypes for yield and stability (SISGYS) is developed for selecting genotypes simultaneously for yield and stability. This programme requires genotype

Table 3. Rank correlations between simultaneous selection indices and yield, stability for groundnut data

Index Type	Weightage on components of index							
	$\alpha = 1.00$		$\alpha = 0.67$		$\alpha = 0.43$		$\alpha = 0.25$	
	Yield ( $w_1=0.5$ )	Stability ( $w_2=0.5$ )	Yield ( $w_1=0.6$ )	Stability ( $w_2=0.4$ )	Yield ( $w_1=0.7$ )	Stability ( $w_2=0.3$ )	Yield ( $w_1=0.8$ )	Stability ( $w_2=0.2$ )
Proposed index	0.596*	0.982**	0.614**	0.975**	0.639**	0.968**	0.782**	0.914**
Bajpai's index	0.493 <sup>NS</sup>	0.946**	0.514*	0.943**	0.553*	0.953**	0.639**	0.932**

\* indicates  $P < 0.05$  \*\* indicates  $P < 0.01$  NS indicates not significant

Table 4. Proportion of high yielders (HY) and highly stable performers (HSP) present out of top 50% genotypes selected on the basis of simultaneous selection indices

Index Type	Weightage ( $\alpha$ )							
	$\alpha = 1.00$		$\alpha = 0.67$		$\alpha = 0.43$		$\alpha = 0.25$	
	HY	HSP	HY	HSP	HY	HSP	HY	HSP
Proposed index	0.71	0.86	0.71	0.86	0.71	0.86	0.86	0.86
Bajpai's index	0.71	0.86	0.71	0.86	0.71	0.86	0.71	0.86

Table 5. Output of the programme

Index Value	Rank	Yield (t/ha)	Rank1	Stability ( $\times 10^6$ )	Rank2
1.33	5	1.51	2	1.98	8
1.22	8	1.31	12	1.76	6
1.11	12	1.39	7	4.04	13
1.03	14	1.32	11	5.95	14
1.01	15	1.30	13	6.03	15
1.59	1	1.69	1	1.31	3
1.46	3	1.47	4	1.23	2
1.19	10	1.27	15	1.79	7
1.21	9	1.37	8	2.18	9
1.13	11	1.37	10	3.24	12
1.33	6	1.37	9	1.41	4
1.36	4	1.50	3	1.71	5
1.23	7	1.46	5	2.67	10
1.47	2	1.44	6	1.15	1
1.07	13	1.27	14	3.16	11

means over replications from individual locations. The input file should be in Excel and should contain a single field with yld as first row and the subsequent rows should be the mean yield over replications for each genotype nested within locations. The input file should be named 'data.xls'. The number of genotypes and the number of locations should be provided inside the programme codes. The programme calculates the following steps: (i) genotype's mean performance (ii) genotype's stability measure (ASTAB<sub>i</sub>) or d<sub>i</sub> (iii) genotype's index value I. Based on the index values genotypes are ranked. The genotype with highest index value will be ranked 1. The SAS codes developed for the purpose are given in ANNEXURE. To demonstrate the programme, the groundnut yields of 15 varieties in 20 locations, under cultivar  $\times$  location set up, are taken. The input data is arranged in a nested fashion as genotypes within locations and output (result) is as given in Table 5.

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### ANNEXURE

/\* SAS programme developed for finding the index values and ranks is as follows: \*/

```
data GE1;
proc import datafile='c:\data.xls' out=GE2;
proc iml;
use GE2;
var=10;loc=24;
read all var{yld} into yld;
y=shape(yld,loc,var);
y=y';
yi=y[,+]/loc;
yj=y[+,]/var;
ymean=yi[+,]/var;
x=repeat(1,var,loc);
do i=1 to var;do j=1 to loc;
x[i,j]=(y[i,j]-yi[i]-yj[j]+ymean);
end;
end;
f3=rank(1/yi);
```

```
xpx=x*x';
a=eigval(xpx);
b=eigvec(xpx);
a1=a[+,];
a2=a/a1;
a3=0;cnt=0;
do i=1 to var;
a3=a3+a2[i];
if a3<0.9 then cnt=cnt+1;
end;
cnt=cnt+1;
d=repeat(1,var,var);
do i=1 to cnt;
d[,i]=a[i]*b[,i];
end;
do i=1 to var;
e=1/sqrt((ssq(d[i,])));
f=f/e;
end;
e3=(1/f);
f4=rank(e3);
e1=f[+,]/var;
do i=1 to var;
e2=(yi[i]/ymean)+ w*(f[i]/e1); /* value of w can be given as
per requirement. For I1, w = 1.0; for I2, w = 0.66; for I3, w
= 0.43 and for I4, w = 0.25 */
f1=f1//e2;
end;
index=f1;
f2=rank(1/f1);
index_rank=f2;
stability=e3;
stab_rank=f4;
yield=yi;
yld_rank=f3;
do l=1 to var;
variety_number=variety_number//l;
end;
print variety_number index index_rank yield yld_rank
stability stab_rank;
run;
```