CHAPTER VIII
USE OF AMMI IN SIMULTANEOUS SELECTION OF GENOTYPES FOR YIELD AND STABILITY

8.1. Introduction

Multi-location trials (MLT), generally, have significant main effects and significant multiplicative genotype x environment interaction (GEI) effects. Additive Main Effects and Multiplicative Interaction (AMMI) model offers a more appropriate statistical analysis to deal with such situation, compared to traditional methods of ANOVA, Principal Component Analysis and linear regression, which are discussed in length in previous chapters. In this chapter, a family of simultaneous indices was estimated as proposed by Rao and Prabhakaran [66], which selects genotypes for both high yield and stability in MLT using AMMI model. A comparison between proposed indices and existing simultaneous selection indices with reference to french bean MLT is also made.

8.2. Genotype x environment interaction (GEI)

Genotype x environment interaction (GEI) is the challenging issue to the plant breeders, geneticists and production agronomist who conduct crop performance trials across diverse environments. GEI can reduce the progress from selection. The method of partitioning GEI into components attributable to each genotype measures the contribution of each genotype to GEI. A universally acceptable selection criterion that takes GEI into consideration does not exit. 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, large numbers of stability measures are available (Prabhakaran and Jain [61]). However, the
stability measure alone is of limited use. For successful breeding or cultivar testing programme, both stability and yield (or any other trait) must be considered simultaneously. The estimates of the integration of stability of performance with yield through suitable measures will also 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 [35] discussed several methods of simultaneous selection for yield and stability and relationship among them. The development and use of Yield-Stability statistic (YSₘ) has enabled incorporation of stability in the selection process (Kang [34]). Kang’s Yield-Stability statistic has been evaluated and found useful for recommending varieties (Pazdernik et al. [57]). However, Bajpai and Prabhakaran [4] observed that Kang’s rank-sum method has an inherent weakness that it is weighing heavily towards yield performance, apart from the arbitrariness in scoring procedure. Accordingly, they proposed new indices which were found to be superior to Kang’s [34] indices. Dashiell et al. [13] evaluated the usefulness of several stability statistics for simultaneously selecting for high yield and stability of performance in soybean. Fernandez [17] also evaluated stability statistics for similar purpose.

### 8.3. AMMI model and biplots

This study proposes a family of simultaneous selection indices using Additive Main Effects and Multiplicative Interaction (AMMI). The AMMI model is chosen when main (genotypic and environmental) and GEI effects are both important in yield trials (Gauch [23 and 24], Zobel et al. [89]). 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. [51] showed that, AMMI model was more effective in partitioning the GEI sum of squares than the linear regression model. Yan et al. [88] advocated a graphical presentation of main effects of genotype (G) and GEI as a ‘GGE’ biplot. However, the inferences drawn from biplots will be valid only when
first PCA or first two PCA s 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 genotypes which are stable and high yielding when the PCA axes retained in AMMI model will be more than two, if the axes together accumulate considerable portion of interaction variation. Thus, to cater the need to develop selection indices under such circumstances Rao and Prabhakaran [66] proposed new yield stability indices.

A user-friendly SAS programme for judging superior genotype for both yield and stability is also demonstrated in annexure.

8.4 AMMI Procedure

The AMMI model is discussed in depth in Chapter VII, but for the sake of continuity the AMMI procedure is briefed here. The AMMI model for T genotypes and S environments is given as

\[
Y_{ij} = \mu + g_i + e_j + \sum \lambda_n \alpha_{in} \tau_{jn} + \theta_{ij} \quad (8.1)
\]

\[
\theta_{ij} \sim N(0, \sigma^2); \quad i = 1, 2, \ldots, T; \quad j = 1, 2, \ldots, S.
\]

Where, \(Y_{ij}\), the mean seed yield of \(i\)th genotype in \(j\)th environment; \(\mu\), the general mean; \(g_i\), \(i\)th genotypic effect; \(e_j\), \(j\)th environmental effect; \(\lambda_n\), eigen value of \(n\)th PCA axis; \(\alpha_{in}\) and \(\tau_{jn}\), principal component scores for principal component axis (PCA) \(n\) of \(i\)th genotype in \(j\)th environment, respectively; \(\theta_{ij}\), residual effect; \(n'\) 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 [23 and 24]). The residual combines the PCA scores from \(N=n'\) discarded axes,

Where, \(N= \min (T-1, S-1)\). The other constraints in model (8.1) are

\[
\sum \alpha_{in}^2 = \sum \tau_{jn}^2 = 1 \forall n
\]

\[
\sum_i \alpha_{in} \alpha_{in'} = \sum_j \tau_{jn} \tau_{jn'} = 0 \quad \text{and}
\]

\[
\lambda_1 > \lambda_2 > \lambda_3 > \ldots \ldots > \lambda_{n'} > 0 \quad \text{and} \quad n \neq n'
\]
The model in (8.1) can be reparameterized as

$$Y_{ij} = \mu + g_i + e_j + Z_{ij}$$  \hspace{1cm} (8.2)

where, $Z_{ij} = \sum \lambda_n \alpha_{in} \tau_{jn} + \theta_{ij}$

Let, the estimate of interaction in the $({i,j})$th cell $Z_{ij}$ be

$$\hat{Z}_{ij} = \hat{Y}_{ij} - \hat{\mu} - \hat{g}_i - \hat{e}_j.$$  

Using matrix notation, denote

$Z = (\hat{Z}_{ij})$ a matrix of order $T \times S$. Now, the estimates of the parameters of the model are

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

$\hat{\alpha}_n =$ the principal components of the rows of the sum of squares and cross product matrix $ZZ'$ and

$\hat{\tau}_{in} =$ the principal components of the columns of the sum of squares and cross product matrix $Z'Z$.

Using these one can write

$$\hat{Z}_{ij} = \sum_{n=1}^{N} \hat{\lambda}_n \hat{\alpha}_{in} \hat{\tau}_{jn}$$  \hspace{1cm} (8.3)

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

Also, using factor analytic decomposition, $Z$ may be written as

$$Z = A D B'$$  \hspace{1cm} (8.4)

where, $A$ is $T \times N$ orthogonal matrix, $D$ is $N \times N$ diagonal matrix with elements $\lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_{n'} \geq \ldots \geq \lambda_N$, $B$ is $N \times S$ orthogonal matrix, $N$ is the rank of $Z$. The matrices $A$, $D$ and $B$ of the equation (8.4) can be obtained from the eigen vectors and eigen values of $ZZ'$ of the order $T \times T$. The matrix $A$ consists of the eigen vectors (principal components $\alpha_{in}$) of $ZZ'$ and the diagonal matrix $D$ with square root of eigen values as diagonal elements of $ZZ'$. The matrix $B$ consists of eigen vectors (principal components $\tau_{jn}$) and can be obtained by solving $B = Z'AD^{-1}$. For many practical situations, the number of PCA
axes to be retained is determined by testing the mean squares of each axis with the estimate of residual through F-statistic (Gollob [27]; Gauch [23]). The mean sum of squares of each PCA axis is equal to the ratio of square of corresponding eigen value and the degrees of freedom of each axis is obtained as \( T+S-1-2n \).

The model formulation for AMMI shows its interaction part consisting of summed orthogonal products. Because of this form the interaction lends itself to graphical display in the form of so called biplots (Gabriel [22]). Here, it is assumed that the first two PCA axes suffice for an adequate description of GEI.

### 8.5. Simultaneous selection indices based on AMMI model

It is evident from the earlier section that the scope of the biplots is very much limited. The inferences drawn from biplots will be valid only when 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. Rao and Prabhakaran [66] proposed a new family of simultaneous selection indices which can select varieties for both yield and stability.

Let \( \alpha^*_n = \alpha_n \tau_n \) be a \( T \times 1 \) vector of modified genotypic scores corresponding to the \( n^{th} \) PCA axis of \( ZZ' \), where \( \lambda_n \) is the eigen value and \( \alpha_n \) is corresponding eigen vector of \( ZZ' \). Suppose that \( n' \) of the \( N \) axes retained in the AMMI model to explain GEI, then the stability measure of \( i^{th} \) variety can be determined as the end point of its vector \((\alpha^*_{1i}, \alpha^*_{2i}, \ldots, \alpha^*_{n'i})\) from the origin \( O'_{1 \times n'} \). This can be taken as squared euclidean distance between the vectors \( \delta' = (\alpha^*_{1i}, \alpha^*_{2i}, \ldots, \alpha^*_{n'i}) \) from the origin, in the \( n' \)-dimensional euclidean space. We consider a stability measure, \( \text{ASTAB}_i \) as

\[
\text{ASTAB}_i = d_i (\delta', 0) = \alpha^2_{1i}, \alpha^2_{2i}, \ldots, \alpha^2_{n'i},
\]

\[
= \sum_{n=1}^{n'} \lambda_n \alpha^2_{ni} = \sum_{n=1}^{n'} \lambda_n \alpha^2_{ni} \tag{8.5}
\]
The algebraic expression of the above said stability measure can also be derived from the spectral decomposition of ZZ’ matrix. As we know that

$$ZZ' = \lambda_1 \alpha_1 \alpha_1' + \lambda_2 \alpha_2 \alpha_2' + \ldots + \lambda_n \alpha_n \alpha_n' + \ldots + \lambda_N \alpha_N \alpha_N'$$

The diagonal element of ZZ’ i.e. $$\sum_{j=1}^{S} Z_{ij}^2$$, is nothing but the interaction effect of ith genotype over S environments.

Therefore,

$$\sum_{j=1}^{S} Z_{ij}^2 = \lambda_1 \alpha^2_{i1} + \lambda_2 \alpha^2_{i2} + \ldots + \lambda_N \alpha^2_{iN} = \sum_{j=1}^{S} \lambda_{ij} \alpha^2_{ni} \quad (8.6)$$

The stability measure mentioned in (8.5) is also equal to the expression given in (8.6) when N=n’, where n’ being the number of PCA axes retained in AMMI model. A variety is considered more stable when the value of ASTABI is lower. The proposed selection indices (Ij) consists of (i) a yield component, measured as the ratio of the average performance of jth genotype to the overall mean performance of the genotypes under test, and (ii) a stability component, measured as the ratio of stability information (1/ASTABI) of jth genotype to the mean stability information of all the genotypes under test. The simultaneous selection index can be given as

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

where, $$\alpha$$ is the ratio of the weights given to the yield ($$w_1$$) and stability components ($$w_2$$) with restriction that, $$w_1 + w_2 = 1$$. The weights considered in the index are, in general, as per the plant breeders’ requirement. By considering 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 I1, I2, I3 and I4.

To estimate the index values and ranks, a user-friendly SAS programme is also demonstrated (Annexure ).

8.6. Empirical study
The data used for comparing various simultaneous selection indices are collected from University Multi-Location Trials (MLT) of sixteen French bean (*Phaseolus vulgaris* L.) genotypes including three checks viz., ACPR-5, ACPR-9, ACPR-11, ACPR-94034, ACPR-94035, ACPR-94036, ACPR-94037, ACPR-94038, ACPR-94039, ACPR-94040, Red Cloud, PDR-5, EC-49844, HPR-35, Vaghyा and HUR-137. These genotypes were grown in 1.8 x 4.0 m² plot with 30 and 10 cm spacing between and within rows, respectively in a randomized block with three replications during *kharif* 1996-2001 at five different locations, viz., Ganeshkhind, Pune, Karad, Borgaon and Kolhapur, in the rajmash growing region of plain zone. All the treatments received uniform recommended dose of fertilizers, timely inter-culturing and plant protection measures. The data generated on seed yield of rajmash were analysed as per Zobel *et al.* [89] and Gauch and Zobel [26], using IRRISTAT software developed by International Rice Research Institute, Philippines.

8.7. Results and discussion

The ANOVA based on AMMI model is presented in Table 8.1. It is evident from the data in Table 8.1 that the utility of biplots to explain efficiently the interaction is very much limited, since the first two PCA axes explain 64 per cent 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 four axes must be retained for explaining stability or using the Rao and Prabhakaran [66] simultaneous selection indices. Accordingly, the index and stability values are calculated by retaining four PCA axes in the model. The rank orders based on yield, stability (ASTABi) indices for each genotype and for different α values presented in Table 8.2 revealed that the high yielding genotype ACPR-94035 was found to be stable followed by the genotypes ACPR-94036 and ACPR-94039. These results are in accordance with the findings of Nimbalkar *et al.* [53 and 56].
8.8. Summary and conclusions

Multi-location trials (MLT), generally, have significant main effects and significant multiplicative genotype x environment interaction effects. Additive Main Effect and Multiplicative Interaction model (AMMI) offer a more appropriate statistical analysis to deal with such situation, compared to traditional methods of ANOVA, Principal Component Analysis and linear regression. In this chapter, a family of simultaneous indices was estimated as proposed by Rao and Prabhakaran [66], which selects genotypes for both high yield and stability in MLT using AMMI model. A comparison between proposed indices and existing simultaneous selection indices with reference to french bean MLT is also made. The results revealed that the high yielding genotype ACPR-94035 was found to be stable followed by the genotypes ACPR-94036 and ACPR-94039. The user-friendly SAS programme and results of the same are demonstrated in annexure.
Table 8.1. AMMI ANOVA for seed yield (13 french bean genotypes and 3 checks tested at 16 environments).

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>SS</th>
<th>MSS</th>
<th>% SS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Treat combinations</td>
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<td>4.47E+07</td>
<td>175204.70588**</td>
<td>100.0</td>
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<td>Genotypes</td>
<td>15</td>
<td>5.90E+06</td>
<td>393058.6667**</td>
<td>13.2</td>
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<td>Environments</td>
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<td>2.31E+07</td>
<td>1537980**</td>
<td>51.6</td>
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<td>G x E Interaction</td>
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<td>1.57E+07</td>
<td>69829.3333**</td>
<td>35.2</td>
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<td>PCA 1</td>
<td>29</td>
<td>5.94E+06</td>
<td>204766.5517**</td>
<td># 37.795</td>
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<td>PCA 2</td>
<td>27</td>
<td>4.16E+06</td>
<td>154161.8519**</td>
<td># 26.492</td>
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<tr>
<td>PCA 3</td>
<td>25</td>
<td>1.50E+06</td>
<td>60088.4**</td>
<td># 9.561</td>
</tr>
<tr>
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<td>23</td>
<td>1.32E+06</td>
<td>57443.4783**</td>
<td># 8.409</td>
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<td>Residual</td>
<td>121</td>
<td>2.79E+06</td>
<td>23038.4298</td>
<td># 17.743</td>
</tr>
<tr>
<td>Error</td>
<td>512</td>
<td>3.60E+06</td>
<td></td>
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</table>

*, **: Significant at 5 and 1 % levels, respectively.

#: as a per cent of GEI SS
Table 8.2. Effect of variation of weights on the rank orders of french bean varieties in the simultaneous selection indices.

<table>
<thead>
<tr>
<th>Sr.No.</th>
<th>Genotypes</th>
<th>Yield (kg/ha)</th>
<th><strong>Yield based rank</strong></th>
<th>Stability (x 10^6)</th>
<th><strong>Stability based rank</strong></th>
<th>( \alpha = 1.00 )</th>
<th>( \alpha = 0.67 )</th>
<th>( \alpha = 0.43 )</th>
<th>( \alpha = 0.25 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>ACPR-5</td>
<td>1183</td>
<td>12</td>
<td>1.68</td>
<td>10</td>
<td>1.84</td>
<td>1.53</td>
<td>1.31</td>
<td>1.14</td>
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<tr>
<td>2</td>
<td>ACPR-9</td>
<td>1315</td>
<td>9</td>
<td>2.49</td>
<td>14</td>
<td>1.64</td>
<td>1.43</td>
<td>1.28</td>
<td>1.16</td>
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<tr>
<td>3</td>
<td>ACPR-11</td>
<td>1159</td>
<td>13</td>
<td>2.83</td>
<td>15</td>
<td>1.44</td>
<td>1.26</td>
<td>1.12</td>
<td>1.03</td>
</tr>
<tr>
<td>4</td>
<td>ACPR-94034</td>
<td>1335</td>
<td>8</td>
<td>2.31</td>
<td>13</td>
<td>1.70</td>
<td>1.48</td>
<td>1.31</td>
<td>1.19</td>
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<td>5</td>
<td>ACPR-94035</td>
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<td>1</td>
<td>0.96</td>
<td>2</td>
<td>2.79</td>
<td>2.25</td>
<td>1.85</td>
<td>1.56</td>
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<td>4</td>
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<td>1.63</td>
<td>1.42</td>
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<td>11</td>
<td>Red cloud</td>
<td>1338</td>
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<td>1.51</td>
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<tr>
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<td>HUR-137 (NC)</td>
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<td>16</td>
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<td>1.43</td>
<td>1.19</td>
<td>1.00</td>
</tr>
</tbody>
</table>

\( \alpha \) is the ratio of the weights given to the stability components \((w_2)\) and yield \((w_1)\) with restriction that \(w_1 + w_2 = 1\).

\( \alpha \) 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 \((w_1 = 0.8, \ w_2 = 0.2)\)