1. Introduction

The performance of a particular variety is the result of its genetic constitution and the environment in which it has been grown. In practice it is quite possible that a particular variety may not exhibit the same phenotypic performance under different environments or different varieties may respond differently to a specific environment. This variation, arising from the lack of correspondence between the genetic and non-genetic effects is known as the genotype-environment (GE) interaction. The presence of GE interaction reduces the correlation between phenotype and genotype, makes difficult to judge the genetic potential of variety and alters the relative ranking of different varieties. Because of these very reasons, before the successful release of particular variety on commercial basis plant breeders grow different varieties at different locations over the years just to determine the magnitude of GE interactions for ensuring the stability of varieties, under varying environments.

For a long time, most breeders used the term stability to characterize a genotype which showed a near constant yield whatever the environment conditions might be. This clearly implies that they look into a variety with a minimum variance over different environments. This idea of stability is in agreement with the concept of homeostatic widely used in genetics (Lerner, 1954) and may be called a ‘biological concept’ of stability.

A genotype showing a constant performance in all environments does not respond to improved growing conditions with increased yield, therefore most agronomists no longer regard this type of stability as desirable. Keeping this in mind, an appropriate measure of phenotypic stability, Wricke (1962) proposed the concept of ‘ecovalence’ the contribution of a genotype to the total GE interaction sum of squares. With small values of ecovalence this concept is referred as ‘agronomic concept of stability’ and has desirable properties in crop production.

In addition to this, there are several versions of what is meant by the term stability. This leads many plant breeders to wonder which stability statistics should be used for their particular problem. To answer some of these questions Freeman (1973), Verma and Gill (1975), Narain and Bhatia (1984) and Lin et al (1986) reviewed different methods of stability analysis by highlighting the advantages and limitations. Besides all this and following Federer & Scully (1988) there is still a need to look into an idea of stability which is more consistent with objectives of the breeder of a given variety. For that it will be necessary to study and consider various types of possible responses for varieties grown in environments which range from extremely poor or adverse to optimal conditions. The range of environments encountered in practice should be included in the range of environments being considered in experiments studying such concepts of stability. It is also necessary to precisely define what is meant by poor optimal environments. The goals and objectives of breeders are also to be precisely stated.
With this in mind the present article aims at firstly to discuss what an environment is and secondly some types of responses over a range of genotypes and environments. Then methodologies to detect a stable variety are highlighted. Lastly an empirical comparison of the three conventional regression techniques has been demonstrated.

2. Defining Environments
Most people consider an ‘environment’ to be a single trial at a single locality and in a single year. They then attempt to obtain a range of environments by selection ‘a random sample’ of locations and years. It is not clear how or if this can be accomplished. Others decide to select locations which cover the range of ‘conditions’ to be met in practice. The ‘conditions’ are not defined except to say that these are supposed to be the conditions encountered by farmers who grow these varieties. If the factors creating the environments or conditions are not define precisely, how can one cover a range of such ‘conditions or environments’? Thus the idea is that the researcher should know precisely what conditions he wishes to use and to create these conditions in an experiment. It therefore implies that genotype by environment interaction is not of much use unless one knows the elements making environments different e.g. according to forage crop specialist one can make any forage genotype come out on top simply by changing the dates of cutting. This statement shows the need of precisely defining the objectives of the farmers of these varieties. Note that a particular breeder’s objectives are rather immaterial unless he meets the needs of the farmers.

Having discussed conditions, the next question is that what are factors causing poor, fair or optimal growing conditions or environments? Certainly, the amount of water available for a crop at critical times in the growing season is a prime factor. A second one is soil type and fertility. A third could be the number and kind of insects present as well as the type of amount of disease. Another important factor would be biological, not necessarily calendar, date of planting and harvest. Other factors could be amount of sunshine, fog, wind elevation etc. Besides, the factors making environment different, it is necessary to precisely defined what is meant by poor, fair and good environments with respect to the characteristic being measured. Once the factors affecting variation in environments can be conducted which include this range of variation for most factors. Breeders do this to some extent when they make their selections under low fertility and high fertility conditions, when they make their selections under low fertility and high fertility conditions, when they make selections under inter-cropping, when selections are made under low and high disease or insect infestations, when selections are made under low and high disease or insect infestations, when selections are made under drought and non-drought conditions etc. Here it is emphasized that in particular for dry-land agriculture, rather than considering changing environments for only one or two factors, selections should be made considering all factors, or at least the major ones, affecting varieties response grown under various known environmental conditions.

3. Types of Responses
Responses of varieties to varying environments can be of various types. There is no set pattern or form of response. Following Federer & Scully (1988), some possible responses of varieties to changing environments are shown in Figure 1.
Response of type R₁ would be for a low yielding which did not make use of the better environmental conditions. Note that the extreme case of a type R₁ response is where a variety has zero yield under any environment.

The response R₂ is for a variety that performs well (compared to R₁) at poor environments in a linear manner. This variety will have a small slope when its yield Y is plotted against the environmental index X. Likewise, its variance in yield over all environments is small. R₁, however, has zero slope and zero variance which under several proposed, stability measures (Lin et al 1986) will be optimal, R₂ will also rate high in stability under these measures. However, R₂ will be much preferred to R₁ from a farmer’s view point and needs. R₃ is a variety that responds poorly to poor environments but responds in a linear fashion to increasing environment indices up to some point X₀. After X₀, the R₃ response tends change with X in a curvilinear manner and reaches some asymptotic level. The high slope and high variance of R₃ will make it an ‘unstable’ variety under some current definitions in the literature. In good environments, R₃ will be superior to R₂ from a farmer’s point if view and if only good environments are to be considered, R₃ will be the selected variety. Likewise, if poor environments are encountered infrequently, R₃ may still be selected over the stable variety R₂. This will depend upon whether or not the farmer can afford to have the low yields of R₃ in poor environments on an infrequent basis.

The R₄ type of response will be the desirable one for many farmers. R₄ gives relatively high yields in poor environment and is able to take advantage of increasingly optimal environments. Although, this variety response will have a relatively high slope and variance and will be classified as unstable, but it will be the desired response that many farmers will want. This is in agreement with Verma et al (1978) and Pooni and Jinks (1980) where they suggest a segmented regression approach rather than the sigmoid response curve given in Figure 1.
There are various types of response of the form given by $R_4$. Some of these are given in Figure 2. It is assumed that to have a desirable form of response that there is some minimum level of response at poor conditions which can be tolerated i.e. $Y_0$. This level is that level for farmer which is at least required for the family’s survival. All acceptable varieties must be above this level in all environments to be encountered. Response type $T_1$ will be for a variety that only responds well to quite good environments. Response $T_2$ is similar to $R_3$ in Figure 1. Varieties with response $T_3$ respond in a linear manner to increasing environmental indices upto some point $X_0$. Varieties which respond to increasingly optimal conditions very quickly and then level off are of type $T_4$. This type of response will be certainly be desired over all the other types of responses if the goal is to maximize yields over all environments.

![Diagram of types of desirable responses](image)

Varieties having $T_2$ response will be those having a type of threshold value of the environment before they can take advantage of a more favourable environment. For each cross, a breeder can evaluate the various kinds of responses to determine which of the responses $T_1$ to $T_4$ are encountered, how frequently, and from what type of parents.

4. Regression Method for Assessing Stability

**EBERHART AND RUSSELL MODEL**

The more widely used method for detecting stable varieties is the regression approach (Eberhart and Russell 1966). Let us consider that there are $t$ varieties whose performance has tested in $s$ environments. Considering $Y_{ij}$ as the mean observation of the $i$th variety in $j$th environment, the following model of the stability of varieties under different environments is

$$Y_{ij} = m + B_i I_j + \delta_{ij} \quad (i=1,2,\ldots,t \text{ and } j=1,2,\ldots,s)$$

where

- $Y_{ij} =$ Mean of $i$th variety in $j$th environment,
- $m =$ Mean of all the varieties over all the environments,
- $B_i =$ The regression coefficient of the $i$th variety on the environmental index which measures the response of this variety to varying environments,
I_j = The environmental index which is defined as the deviation of the mean of all the varieties at a given location from the overall mean.

\[ I_j = \sum_{i} y_{ij}/t - \sum_{i} \sum_{j} y_{ij}/ts \]

With

\[ \sum_{j} I_j = 0 \]

and \( \delta_{ij} \) The deviation from regression of the ith variety at jth environment.

STABILITY PARAMETERS: Two parameters of stability are calculated: (a) The regression coefficient which is the regression of the performance of each variety under different environments on the environmental means over all the genotypes. This is estimated as follows:

\[ B_i = \sum_{j} y_{ij} I_j / \sum_{j} I_j^2 \]

where,

\[ \sum_{j} y_{ij} I_j \] is the sum of products and

\[ \sum_{j} I_j^2 \] is the sum of squares,

(b) Mean square deviations \( (S_i^2) \) from linear regression.

\[ = \frac{\sum \delta_{ij}^2}{(s-2)} - \frac{S_r^2}{r} \]

where,

\[ \sum \delta_{ij}^2 = \left[ \sum y_{ij}^2 - \frac{\left( \sum y_{ij} I_j \right)^2}{\sum I_j^2} \right] \]

And \( S^2_e = \) the estimate of pooled error.

The various computational steps involved in the estimation are as follows:

I. Computation of environmental index \( (I_j) \) We know that Ij is defined as:

\[ I_j = \frac{\sum_{j} Y_{ij} - \sum_{i} \sum_{j} Y_{ij}}{t s} \]

\[ = \frac{Total of all the varieties at jth location}{Number of varieties} - \frac{Grand total}{Total number of observations} \]
II. Computation of regression coefficient \((b_i)\) for each variety:

\[
\sum Y_{ij} I_j
\]

\[
b_i = \frac{\sum Y_{ij} I_j}{\sum I_j^2}
\]

PERKINS AND JINKS’ MODEL

From stability point of view, the variance due to genotype x environmental interaction being the most important, Perkins and Jinks (1968) proposed that a regression of genotype x environment interaction on environmental index should be obtained rather than regression of mean performance \((Y_{ij})\) on the latter as done in the Eberhart and Russell’s model. For describing \(Y_{ij}\), the mean performance of \(i\)th variety in \(j\)th location, they proposed following model:

\[
Y_{ij} = m + d_i + e_i + g_{ij} + e_{ij}
\]

where, \(m\) is the general mean,
\(d_i\) is the additive genetic effect,
\(e_i\) is the additive environmental effect,
\(g_{ij}\) is the genotype x environmental interaction effect, and
\(e_{ij}\) is the error associated with each observation.

These effects are defined as follows:

\[
m = Y../st
\]

\[
d_i = (Y_i./s) - m
\]

\[
e_i = (Y.i/t) - m
\]

\[
g_{ij} = Y_{ij} - m - d_i - e_i
\]

and further, they defined

\[
g_{ij} = \beta_i e_j + \delta_{ij}
\]

Putting the values of \(g_{ij}\) in above model,

\[
Y_{ij} = m + d_i + e_j + \beta_i e_j + \delta_{ij} + e_{ij}
\]

\[
= m + d_i + e_j + \beta_i e_j + \delta_{ij} + e_{ij}
\]

STABILITY PARAMETERS: In this approach also, the same two parameters, regression co-efficient and the deviation from regression are used as the parameters of stability. In comparison to Eberhart and Russell’s model, the regression co-efficient in this model is different in the sense that Perkins and Jinks proposed to calculate the regression of genotype x environment interaction value on the environmental index. In terms of this model, the earlier model of Eberhart and Russell is thus regression of \((e_j+g_{ij})\) on \(e_i\). The regression of \(e_j\) on \(e_j\) being one, and regression of \(g_{ij}\) on \(e_j\) being \(\beta_i\) the \(b_i\) value of Ebehart and Russel model is thus:

\[
b_i = 1 + \beta_i
\]

\[
\beta_i = b_i - 1
\]
FREEMAN AND PERKINS’ MODEL
In the previous two models, the mean performance of a variety in a given environment \((Y_{ij})\) is regressed over the environmental index defined as \((\sum Y_{ij}/t) - \sum Y_{ij}/st\). Obviously, the estimation of these two variables is not independent. This being an object ional point, Freeman and Perkins (1971) proposed independent estimate of environmental index in the following two ways: (i) Divide the replications into two groups, so that the one group may be used for measuring the average performance of varieties in various environments and the other groups, averaging over the varieties is used for estimating the environmental index. (ii) Use one or more varieties as check and assess the environmental index on the basis of their performance.

Another objection of Freeman and Perkins to other two models was about the partitioning of the degrees of freedom. Though S.S. due to environment (linear) of Eberhart and Russell’s model being the same as S.S. due to environment (joint regression) of Perkins and Jinks’ model, yet the degree of freedom is 1 in the former and \((s-1)\) in the latter.

For describing \(Y_{ijk}\), i.e., performance of kth replicate of ith genotype in the jth environment, Perkins and Jinks proposed the following model:

\[ Y_{ijk} = m + d_i + e_j + g_{ij} + e_{ijk} \]

where,
- \(m\) = general mean,
- \(d_i\) = additive genetic effect of ith genotype,
- \(e_j\) = additive jth environmental effect,
- \(g_{ij}\) = genotype environment interaction effect and
- \(e_{ijk}\) = the error associated with kth observation.

Consider some measure \(x_j\) of the environment, \(x_j\) being the same for all genotypes. In the previous models \(x_j\) has been taken as \(\bar{Y}_j\), or the deviation of this form the general mean. But this may not be valid to assume \(x_j\) to be a linear function of \(\bar{Y}_{ij}\). In fact the relationship can be expressed as:

\[ \bar{Y}_{ij} - \bar{Y}_i = B_i(x_{j\bar{x}}) + \text{error term} \]

where, \(\bar{x}\) is the mean of \(x_j\).

It is convenient to write \(Z_j\) for \((x_{j\bar{x}})\) and \(B_i\) is estimate of \(b_i\), where,

\[ b_i = \sum_j \sum_k Y_{ij}Z_j / \sum_j \sum_k Z_j^2 \]

Estimation of environmental index: Considering 3 replications, there can be 3 different ways to estimate \(I_j\) or \(Z_j\) and to perform the analysis: (i) The values of replication 3 are used for measuring \(Z_j\) and those of replication 1 and 2 for variety mean. (ii) Replication 2 for \(Z_j\) and replication 1 and 3 for mean of varieties, and (iii) Replication 1 for \(Z_j\) and replications 2 and 3 for mean. We shall take up one of these situations, say replication 3 for measuring \(Z_j\) and replication 1 and 2 for variety mean, and demonstrate the estimation of the stability.
parameters. To distinguish the $I_j$ values estimated in other two models from its value in this model, another symbol $Z_j$ has been used.

5. Crossover Interactions

Let us consider that treatments A and B are tested in environments 1 and 2. Let $\bar{Y}_{A1}$ and $\bar{Y}_{A2}$ be the means of treatment A in environments 1 and 2, respectively, and $\bar{Y}_{B1}$ and $\bar{Y}_{B2}$ be the means of treatment B in environments 1 and 2, respectively. The treatment effects in each environment are defined as

$$d_1 = \bar{Y}_{A1} - \bar{Y}_{B1}; \quad d_2 = \bar{Y}_{A2} - \bar{Y}_{B2}$$

No interaction and all types of interactions can be illustrated in the space of treatment effects by plotting $d_1$ and $d_2$.

The line where $d_1 = d_2$ represents the situation in which there are differences in treatment means but not in treatment-environment interaction; when $d_1 = d_2 = 0$ (at the origin), there are no differences in treatment means and no interaction. Qualitative or crossover interaction will occur in the second and fourth quadrants when $d_1 < 0$ and $d_2 > 0$ or $d_1 > 0$ and $d_2 < 0$. The rest of the cases are non-cross-over interactions and consist of all the points in the first and third quadrants, excluding those lying on the line where $d_1 = d_2$.

In case of cross over interactions, one-way to identify the sub-sets of treatments for certain environments are to use the technique of biplots. Before the details of biplots is mentioned the details of Additive Main Effects and Multiplicative Interaction (AMMI) is given as under

6. Additive Main Effects and Multiplicative Interaction (AMMI)

In stability analysis, Additive Main Effects and Multiplicative Interaction (AMMI) model is given by

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

$$\theta_{ij} \sim N(0, \sigma^2) \quad i = 1,2,...,t; \quad j = 1,2,...,s.$$

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 $n$; $\alpha_{in} \gamma_{jn}$ are the $i$-th genotype $j$-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 combined the PCA scores from the $N$ - $n'$ discarded axes, where $N=\min (t-1, s-1)$. The other constraints in the model (1) are

$$\sum_{i} \alpha_{in}^2 = \sum_{j} \gamma_{jn}^2 = 1 \forall n; \sum_{i} \alpha_{in} \alpha_{in}^* = \sum_{j} \gamma_{jn} \gamma_{jn}^* = 0, n \neq n^*; \text{ and } \lambda_1 > \lambda_2 > ... > \lambda_{n'} > 0.$$

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The model in (1) can be reparameterized as
\[ Y_{ij} = \mu + g_i + e_j + Z_{ij} \] (2)

where \[ Z_{ij} = \sum_{n=1}^{n'} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij}. \]

The AMMI is required at first instance for the estimation of genotype and location main effects by ANOVA. Subsequently residuals from additively of these effects are then partitioned into:
- The multiplicative term of the model, of which the estimated parameters relate to the statistically significant axes of a double-centred principal components analysis performed on the genotype location (GL) interaction matrix and
- a deviation from the model term:

The proportion of GL interaction variation accounted for by each PC axis is equal to the relative size of its eigenvalue. The further scaling of eigenvectors through multiplication by \[ \sum \lambda_n \] allows for a straightforward estimation of the GLij effects expected on the PC axis n by multiplication of the scaled genotype and location scores on that axis.

There are several possible AMMI models characterized by a number of significant PC axes ranging from zero (AMMI-0, i.e. additive model) to a minimum between (t-1) and (s-1), where t = number of genotypes and sl=number of locations. The full model (AMMI-F), with the highest number of PC axes, provides a perfect fit between expected and observed data. Models including one (AMMI-1) or two (AMMI-2) PC axes are usually the most appropriate where there is significant GL interaction. Due to their simplicity, they provide a notable reduction of dimensionality for the adaptation patterns relative to observed data.

While principal components analysis is usually executed on the correlation matrix, for AMMI modelling it is executed on the covariance matrix. Furthermore, two (not one) analyses are performed simultaneously: in the analysis the genotypes are individuals (rows) and the locations original variables (columns); in the other, vice versa.
- The first axis (PC 1) maximizes the variation of GL effects in one dimension (i.e. it minimizes the sum of squared projections of the points off that axis).
- The second axis (PC 2) maximizes the residual variation in a second dimension that must be perpendicular to PC 1 (correlation is therefore zero between PC 1 and PC 2 scores, for both genotypes and locations).

7. Biplots
A biplot is a scatter plot that graphically displays both the row factors and the column factors of a two-way data. The concept of biplots is very old and based on application to principal component analysis. Biplots have been used in data visualization and pattern analysis in various research fields, from psychology to economics to agronomy. This technique has extensively been used in the analysis of multi-environment trials.
Any \( n \times m \) matrix \( Y \) of rank \( r \) can be factorised as
\[
Y = GH'
\] (3)
into a \( n \times r \) matrix \( G \) and a \( m \times r \) matrix \( H \), both of rank \( r \). However, this factorization is not unique, because for any non-singular matrix \( R \), one can have
\[
Y = (GR') (HR^{-1})'.
\]
Thus, factorization in (1) can be written as
\[
y_{ij} = g_i'h_j,
\]
where \( y_{ij} \) is the \((i,j)\)-th element of \( Y \), \( g_i \) is the \( i \)th row of \( G \) and \( h_j \) is the \( j \)th column of \( H \). Thus the factorization assigns \( g_1, ..., g_n \) to each of \( n \) rows and \( h_1, ..., h_m \) to each of \( m \) columns of \( Y \) by means of \((n+m)\) vectors of \( Y \) in \( r \)-space. Thus for rank one matrix \( y_{ij} \) is simply the product \( g_i h_j \) having a multiplicative structure, in contrast to additive structure \( y_{ij} = \beta_i + \tau_j \), assumed for matrices in a two-way analysis of variance.

In a matrix of rank two, the effects \( g_1, ..., g_n \) and \( h_1, ..., h_m \) are vectors of order two. These \( n+m \) vectors may be plotted in the plane, giving a representation of the \( nm \) elements of \( Y \) by means of the inner products of the corresponding row effect and column effect vectors. Such a plot will be referred to as a biplot since it allows row effects and column effects to be plotted jointly. The graphical representation is likely to be useful in allowing rapid visual appraisal of the structure of the matrix. An inner product of two vectors may be appraised visually by considering it as the product of the length of one of the vectors times the length of the other vector's projection on to it. This allows one to see easily rows or columns are proportional to which rows or columns (lying in the same direction), which entries are zero (right angles between row and column effects) etc.

A manual that includes SAS codes, and data examples for performing the analysis of the Additive Main Effects and Multiplicative Interaction (AMMI) model of multi-environment trials and for constructing the biplot is available at https://www.cimmyt.org/english/wps/biometrics.

**Biplot can also be generated using the MS-EXCEL in the following manner:**

Go to Scatter Plot → Choose series → Add Series → Give name, say gen → Define X and Y ranges for this series → Add new series → Give name say env → Define its X, Y ranges. This can be continued for as many series as we have, then next and finish. Now right click on graph → Format Plot Area → Remove Grid lines. In the patterns do area as none. Now click on any one of the Axis and Format Axis. In Patterns, Choose the following: Major Tick Mark type-outside; Minor Tick Mark type-none; Tick Mark labels-low. From Scale: Define minimum and maximum value in data set and define Major and Minor Units. For origin select values (X) axis crosses at 0 or at the desired number. From number, decimal places can be chosen. If one wants to label for each pint, click on the point and put label. Or one can define as many series as we have points and then label the points by series name.

In brief, we can say that biplot is a scatter plot of scores of treatments and environments of the first dimension (bilinear term) against the scores of treatments and environments of the
second dimension (bilinear term). A full description of the interpretation of the biplots of multiplicative models is given in Gower, J.C. and Hand, D.J. (1996). *Biplots*. Chapman and Hall, UK. Briefly, the treatment and environment scores are represented as vectors in a two-dimensional space. The treatment and environments vectors are drawn from the origin (0, 0) to the end points determined by their scores. An angle less than 90° or greater than 270° between a treatment vector and an environment vector indicates that the treatment has a positive response in that environment. A negative treatment response is indicated if the angle is between 90° and 270°.

References
SPAR 2.0: *Statistical Package for Agricultural Research* 2.0, Indian Agricultural Statistics Research Institute, New Delhi.