

Stability Variance of Genotype \times Environment Interaction in $m \times m$ Latin Square Layout

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Abstract

In the presence of diverse and unpredictable environmental conditions, it is important to study the tangle of the genotypic responses of the various genotypes in specified environments. The use of justified model and its analysis is required to analyze the complex rootlets with or within the triple frame of genotype, environment and their interaction. Therefore, in the present study, an attempt is made to investigate the situation in which the experimenters want to study phenotypic value of the genotype in a particular environment receiving different treatments in $m \times m$ Latin Square layout and its respective stability measure.

Key Words: L.S.D., ANOVA, GEI, Stability Measure, etc.

1. Introduction

In agricultural experiments, a large number of genotypes are comprehensively tested over a wide range of environmental conditions such as locations, years, growing seasons, etc. and the underlying statistical and genetical theories are simultaneously used to constitute this system which in-together all may be rather complicated. The occurrence of the genotype \times environment interaction (GEI) effect further embroils the selection of superior genotypes for a population of environments under consideration. The presences of the GEI particular genotypes are being most stable in particular environments, whereas in the absence of GEI, the superior genotype in one environment may be regarded as the most stable genotype in all. In general, GEI plays a vital role in multi-environmental plant breeding trials, when the genotypes under consideration exhibit inconsistent relative performance over environments. Significant GEI outgrowth arises from the changes in the magnitude of differences among genotypes and/or changes in the relative ranking of the genotypes in different environments. The presence of GEI reduces the progress from selection in any single environment.

A variety of statistical procedures are available to analyze the results of multi-environment trials. One of the most common methods in a GEI study is to reckon the simple averages across replications for a genotype in an environment and then analyzing the means. The most popular methods have used analysis of variance combined with joint regression analysis to determine the environmental stability of the genotypes (Plaisted and Peterson, 1959; Plaisted, 1960; Wricke, 1962; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966;

Perkins and Jinks, 1968; Parul et al., 2015; Laxmi et al. 2015; Chetan et al. 2016). Freeman and Perkins (1971) developed a different approach having rectification to the various shortcomings. The first short-coming which relates to the analysis part was removed by a modification in the method of analysis. The second relates to their model and it was met by introduction of an independent measure of the environments. Shukla (1972) proposed a stability measure by partitioning the GE sum of squares into component for each genotype separately. A genotype is considered stable if its stability variance (σ_i^2) is equal to the within environmental variance (σ_0^2).

There are other alternative methods of analyzing the data in a two-way layout such as Additive Main Effects and Multiplicative Interaction (AMMI) model which combines the conventional analysis of variance for additive main effects with the principal components analysis (PCA) for the non-additive residuals (Raju, 2002). AMMI is frequently applied in yield trials in agricultural research when both main effects and interaction are important. In practice, most of the experimental situation may arise in which the experimenters want to study phenotypic value of the genotype in the particular environment receiving different treatments. Therefore, in the present study, an attempt is made to investigate such type of situation in $m \times m$ Latin Square layout and its respective stability measure.

2. Methodology

Let y_{ijk} ($i, j, k = 1, 2, \dots, m$) denote the phenotypic value of the i^{th} genotype in the j^{th} environment receiving k^{th} treatment. The tripe (i, j, k) assumes only m^2 of the possible m^3 values of an Latin Square (L.S.) selected by the experimenter. If \mathcal{S} represent the set of m^2 values, then $(i, j, k) \in \mathcal{S}$. If a single observation is made per experimental unit, then the heuristically liner model:

$$y_{ijk} = \mu + d_i + E_j + t_k + g_{ijk} + \epsilon_{ijk} \quad \forall i, j, k = 1, 2, \dots, m$$

Where, μ is general mean effect; d_i is additive effect of the i^{th} genotype; E_j is the effect of j^{th} environment; t_k is the effect due to k^{th} treatment on i^{th} genotype in j^{th} environment; g_{ijk} is GEI receiving k^{th} treatment; ϵ_{ijk} is the error due to the random component assumed to be normally distributed with mean zero and variance σ_e^2 i.e. $\epsilon_{ijk} \sim N(0, \sigma_e^2)$, with μ, d_i and E_j are constants.

Least Square Estimation of Parameters

The normal equations for estimating μ, d_i, E_j, t_k and g_{ijk} are obtained by using the principle of least square. If \mathcal{S}_i is the possible pair (j, k) associated with a fixed value of i and similarly \mathcal{S}_j and \mathcal{S}_k ; and $\hat{\mu}, \hat{d}_i, \hat{E}_j, \hat{t}_k$ and \hat{g}_{ijk} are the estimates of μ, d_i, E_j, t_k and g_{ijk} respectively. Then

$$\frac{\partial E}{\partial \mu} = \sum_{\mathcal{S}} (y_{ijk} - \hat{d}_i - \hat{\mu} - \hat{E}_j - \hat{t}_k - \hat{g}_{ijk}) = 0$$

$$\frac{\partial E}{\partial d_i} = \sum_{\mathcal{S}_i} (y_{ijk} - \hat{d}_i - \hat{\mu} - \hat{E}_j - \hat{t}_k - \hat{g}_{ijk}) = 0$$

$$\frac{\partial E}{\partial E_j} = \sum_{\mathcal{S}_j} (y_{ijk} - \hat{d}_i - \hat{\mu} - \hat{E}_j - \hat{t}_k - \hat{g}_{ijk}) = 0$$

$$\frac{\partial E}{\partial t_k} = \sum_{\mathcal{S}_k} (y_{ijk} - \hat{d}_i - \hat{\mu} - \hat{E}_j - \hat{t}_k - \hat{g}_{ijk}) = 0$$

$$\frac{\partial E}{\partial g_{ijk}} = \sum_{\mathcal{S}} (y_{ijk} - \hat{d}_i - \hat{\mu} - \hat{E}_j - \hat{t}_k - \hat{g}_{ijk}) = 0$$

Further, since in an L.S. layout each i and each j exactly once with each k in triplet $(i, j, k) \in \mathcal{S}$ and consequently \mathcal{S}_k consists of m pairs (i, j) . The solution of these equation will provide the estimates of different parameters i.e.

$$\hat{\mu} = \bar{y}_{...}$$

$$\hat{d}_i = \bar{y}_{i..} - \bar{y}_{...}$$

$$\hat{E}_j = \bar{y}_{.j.} - \bar{y}_{...}$$

$$\hat{t}_k = \bar{y}_{..k} - \bar{y}_{...}$$

$$\hat{g}_{ijk} = \frac{1}{m^2} \{ (m^2 + 2)\bar{y}_{...} - (\bar{y}_{i..} + \bar{y}_{.j.} + \bar{y}_{..k}) \}$$

Analysis of Variance

$$\sum_{(i,j,k) \in \mathcal{S}} (y_{ijk} - \bar{y}_{...})^2 = \sum_{(i,j,k) \in \mathcal{S}} \left[\begin{aligned} &(\bar{y}_{i..} - \bar{y}_{...}) + (\bar{y}_{.j.} - \bar{y}_{...}) + (\bar{y}_{..k} - \bar{y}_{...}) \\ &+ \frac{1}{2}(y_{ijk} - \bar{y}_{i..} - \bar{y}_{.j.} - \bar{y}_{..k}) \\ &+ \left\{ \frac{1}{2}(y_{ijk} - \bar{y}_{i..} - \bar{y}_{.j.} - \bar{y}_{..k}) + 2\bar{y}_{...} \right\} \end{aligned} \right]^2$$

Since the algebraic sum of deviation from mean is zero, therefore

$$\sum_{(i,j,k) \in \mathcal{S}} (y_{ijk} - \bar{y}_{...})^2 = \sum_{\mathcal{S}_i} (\bar{y}_{i..} - \bar{y}_{...})^2 + \sum_{\mathcal{S}_j} (\bar{y}_{.j.} - \bar{y}_{...})^2 + \sum_{\mathcal{S}_k} (\bar{y}_{..k} - \bar{y}_{...})^2$$

$$\begin{aligned}
 & + \frac{1}{4} \sum_{(i,j,k) \in \mathcal{S}} (y_{ijk} - \bar{y}_{i..} - \bar{y}_{.j.} - \bar{y}_{..k}) \\
 & + \sum_{(i,j,k) \in \mathcal{S}} \left\{ \frac{1}{2} (y_{ijk} - \bar{y}_{i..} - \bar{y}_{.j.} - \bar{y}_{..k}) + 2\bar{y}_{...} \right\}^2
 \end{aligned}$$

or

$$T.SS = SS.G + SS.E_n + SS.T + SS.I + SS.E_r$$

where $T.SS$ is the total sum of square and $SS.G (S_G^2)$, $SS.E_n (S_{E_n}^2)$, $SS.T (S_T^2)$, $SS.I (S_I^2)$ and $SS.E_r (S_{E_r}^2)$ represent sum of square due to genotypes, environments, treatment and error respectively.

ANOVA Table

Source of Variation	Degree of Freedom (d.f.)	Mean Sum of Square	Variance Ratio
Genotype	$(m - 1)$	$s_G^2 = S_G^2 / (m - 1)$	$F_G = S_G^2 / S_{E_r}^2$
Environment	$(m - 1)$	$s_{E_n}^2 = S_{E_n}^2 / (m - 1)$	$F_{E_n} = S_{E_n}^2 / S_{E_r}^2$
Treatment	$(m - 1)$	$s_T^2 = S_T^2 / (m - 1)$	$F_T = S_T^2 / S_{E_r}^2$
Interaction	$\frac{1}{2}(m - 1)(m - 2)$	$s_I^2 = S_I^2 / \frac{1}{2}(m - 1)(m - 2)$	$F_I = S_I^2 / S_{E_r}^2$
Error	$\frac{1}{2}(m - 1)(m - 2)$	$s_{E_r}^2 = S_{E_r}^2 / \frac{1}{2}(m - 1)(m - 2)$	
Total	$(m^2 - 1)$		

Stability Measure

The stability variance of i^{th} genotype as its variance across environments after considering the main effect of environment. Since the genotype main effect is constant, the stability variance is thus based on the residua matrix in two-way classification. The stability statistics is termed stability variance (σ_i^2) and is estimated as

$$\begin{aligned}
 \sigma_i^2 = \frac{1}{(m^2 - 1)} & \left[\sum_{(i,j,k) \in \mathcal{S}} (m\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} - \bar{y}_{..k} + 2\bar{y}_{...})^2 \right. \\
 & \left. - \frac{1}{m^2} \sum_{(i,j,k) \in \mathcal{S}} \{ (m^2 + 2)\bar{y}_{...} - (\bar{y}_{i..} + \bar{y}_{.j.} + \bar{y}_{..k}) \}^2 \right]
 \end{aligned}$$

A genotype is called stable if its stability variance σ_i^2 is equal to the environmental variance σ^2 which means that $\sigma_i^2 = 0$. A relatively large value of σ_i^2 will thus indicate greater instability of i^{th} genotype. As the stability variance is the difference between two sums of squares, it can be negative, but negative estimate of variance is not uncommon in variance component problems. Negative estimate of σ_i^2 may take be zero as usual (Shukla, 1972).

3. Discussion and Conclusion

Genotype x Environment Interactions (GEIs) are an important source of variation in any crop production experiment. On the basis of this idea, genotypes with a minimal variance for yield across different environments are considered stable. The term stability is sometimes used to characterize a genotype, which shows a relatively constant yield, independent of changing environmental conditions. Numerous stability measures with these different approaches have been worked out. Diversity of these statistics and their relationships for equivalence of response to environment and their inter-relationships have given rise to interest for further studies. Therefore, with exuberance in this direction, in present study a different approach is used to frame design to analyze the GEI. In present investigation, an attempt is made to diagrammatize the experimental situation in which the experimenters want to analyze phenotypic value of the genotype in the particular environment which receives the desired treatment with $m \times m$ Latin Square layout. The stability variance is a tool which measures the potential of a genotype in different varying environments and characterizes the relative performance of a genotype. Therefore, simultaneous efforts are made to diagrammatize the respective stability variance (σ_i^2).

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