

A NOTE ON THE ESTIMATION OF STABILITY PARAMETERS IN THE MODEL OF PERKINS AND JINKS

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1. Eberhart and Russell (1966) and Perkins and Jinks (1968a) introduced separate models for the study of linear component of the genotype-environment interaction. Eberhart and Russell expressed yield of a variety for a specific environment in terms of its mean yield over all the environments, the environmental index, the regression of yield upon the index and a deviation from linearity. Perkins and Jinks, too, gave a linear model but introduced the term additive genetic contribution while the regression used was that of the genotypic value for a specific environment upon the environmental index. The calculation of the genotypic values is a laborious task. The author has shown that these two regression coefficients are simply related and also given suitable formulae for use in the analysis of variance for the Perkins and Jinks' model. Perkins and Jinks (1968b) also developed a procedure for classifying varieties into groups by working out correlations between the deviations from regression of each environment for pairs of varieties. This aspect, too, has been treated by the author on the basis of original values instead of the genotypic values.

2. *The models of Eberhart & Russell and Perkins and Jinks:*
Eberhart & Russell's model is:

$$Y_{ij} = \mu_i + \beta_i^{-1} I_j + e_{ij} \quad \dots(1)$$

where Y_{ij} is the variety mean of the i th variety at the i th environment, μ_i is the mean of the i th variety over all the s environments, I_j the environmental index defined by:

$$I_j = \left(\sum_{i=1}^v Y_{ij} / v \right) - \sum_{i=1}^v \sum_{j=1}^s Y_{ij} / vs \quad \dots(2)$$

where v is the number of varieties and β'_i the regression coefficient of Y_j or I_j .

Perkins and Jinks presented the model :

$$Y_{ij} = \mu + d_i + I_j + g_{ij} + e_{ij} \quad \dots(3)$$

where μ is the general mean over all lines and environments, d_i the additive genetic contribution, I_j the additive environmental contribution, g_{ij} the genotype-environment interaction of the i th line in the j th environment and e_{ij} the corresponding experimental error. The restrictions imposed are :

$$\sum_i d_i = 0 ; \quad \sum_j I_j = 0 ; \quad \sum_{i,j} g_{ij} = 0 \quad \dots(4)$$

They further express g_{ij} as

$$g_{ij} = \beta_i I_j + f_{ij} \quad \dots(5)$$

where β_i is the linear regression of g_{ij} upon I_j while f_{ij} is the residual deviation from g_{ij} .

Least square estimate of μ , β_i and d_i are :

$$\left. \begin{aligned} \hat{\mu} &= \left(\sum_{i=1}^v \sum_{j=1}^s Y_{ij} \right) / sv \\ \hat{d}_i &= \left(\sum_{j=1}^s Y_{ij} \right) / s - \hat{\mu} \\ 1 + \hat{\beta}_i &= \left(\sum_{j=1}^s Y_{ij} I_j \right) / \sum_{j=1}^s I_j^2 \end{aligned} \right\} \dots(6)$$

$= \hat{\beta}_i^1$ of Eberhart and Russell.

3. Sum of squares of the genotype-environment interaction :

The sum of squares of each line is split up as sum of squares due to linear regression and sum of square due to deviations from linearity. The relation for the i th line is :

$$\sum_{j=1}^s \left(Y_{ij} - \frac{Y_{i.}}{s} \right)^2 = \frac{\left(\sum_{j=1}^s Y_{ij} I_j \right)^2}{\sum_{j=1}^s I_j^2} + \sum_{j=1}^s f_{ij}^2$$

$$= \left(1 + \hat{\beta}_1\right)^2 \sum_{j=1}^s I_j^2 + \sum_{j=1}^s f_{ij}^2 \quad \dots(7)$$

where Y_i is the total over all the j values for Y_{ij} .

Equation (7) would be used to test $1 + \hat{\beta}_i$ and not $\hat{\beta}_i$ for significance. However, for testing $\hat{\beta}_i$ against 0, the approach of Bucio Alanis (1966) is used. This approach is then further used to test the overall heterogeneity of $\hat{\beta}_i$ s. This is done by first calculating $\hat{d}_i + \hat{g}_{ij}$ as $Y_{ij} - \mu - I_j$ and then working out its regression upon I_j to obtain $\hat{\beta}_i$. For a large table such a procedure would be very laborious. In the present paper, simplified formulae are given to obtain the same results including the analysis of variance by using Y_{ij} directly instead of calculating $\hat{d}_i + \hat{g}_{ij}$.

In the first place it is easy to show that corresponding to (7) the residual sum of squares in respect of the genotypic value g_{ij} for the i th line is the same as in (7) i.e.

$$\sum_{j=1}^s \left(g_{ij} - \frac{\hat{g}_i}{s} \right)^2 = \hat{\beta}_i^2 \sum_{j=1}^s I_j^2 + \sum_{j=1}^s f_{ij}^2 \quad \dots(8)$$

where \hat{g}_i is the sum of all the j values of g_{ij} .

4. Analysis of variance:

For convenience of comparison the various sum squares using Y_{ij} are given along with those obtained from g_{ij} hereafter referred as (P & J).

Lines (varieties).

$$SS(V) = \left(\sum_{i=1}^v Y_i^2 \right) / s - \left(\sum_{i=1}^v \sum_{j=1}^s Y_{ij} \right)^2 / sv$$

with $(v-1)$ df

$$\dots(9)$$

$$= s \sum_{i=1}^v d_i^2 \quad (P \& J)$$

Environments (Joint Regression):

$$SS(S) = v \sum_{j=1}^s I_j^2 \text{ with } (s-1) \text{ df} \quad \dots(10)$$

$$= v \sum_{j=1}^s I_j^2 \quad (\text{P \& J})$$

Lines × Environments:

$$SS(V \times S) = \sum_{i=1}^v \sum_{j=1}^s Y_{ij}^2 - \left(\sum_{i=1}^v \sum_{j=1}^s Y_{ij} \right)^2 / sv - SS(V) - SS(S)$$

with $(v-1)(s-1)$ df ... (11)

Heterogeneity between regressions (linear components of interaction)

$$SSLI(V) = \sum_{i=1}^v \left\{ \left(\sum_{j=1}^s Y_{ij} I_j \right)^2 / \sum_{j=1}^s I_j^2 \right\} - SS(S)$$

$$= \sum_{i=1}^v \beta_i^2 \sum_{j=1}^s I_j^2 \quad (\text{P \& J}) \quad \dots(12)$$

Remainder (Deviations from regression)

$$SSRI(V) = \sum_{i=1}^v \left\{ \left(\sum_{j=1}^s Y_{ij}^2 - \frac{Y_i^2}{s} \right) - \left(\sum_{j=1}^s Y_{ij} I_j \right)^2 / \sum_{j=1}^s I_j^2 \right\}$$

$$= \sum_{i=1}^v \sum_{j=1}^s f_{ij}^2 \dots (\text{P \& J}) \text{ with } (v-1)(s-2) \text{ df} \quad \dots(13)$$

Pooled error

Pooled experimental error is obtained from individual analysis of environments.

5. *Correlations between deviations from regression of genotypic values upon the environmental index for pairs of varieties.*

Perkins and Jinks (1968b) proposed the grouping of varieties on the basis of correlating the deviations f_{ij} for pairs of varieties (v_1, v_2) .

This aspect requires the computation of the following quantities:

$$\sum_{j=1}^s f_{ij}^2 = \left\{ \sum_{j=1}^s \left(\hat{g}_{ij} - \frac{\hat{g}_{i\cdot}}{s} \right)^2 \right\} - \hat{\beta}_i^2 \sum_{j=1}^s I_j^2 \quad \dots(14)$$

$i = 1, 2$

$$\sum_{j=1}^s f_{1j} f_{2j} = \left\{ \sum_{j=1}^s \left(\hat{g}_{1j} - \frac{\hat{g}_{1\cdot}}{s} \right) \left(\hat{g}_{2j} - \frac{\hat{g}_{2\cdot}}{s} \right) \right\} - \hat{\beta}_1 \hat{\beta}_2 \sum_{j=1}^s I_j^2 \quad \dots(15)$$

It may be easily shown that (14) and (15) can be easily obtained by using Y_{ij} in place of \hat{g}_{ij} . Using $\hat{\beta}'_i$ from (6) we get :

$$\sum_{j=1}^s f_{ij}^2 = \left\{ \sum_{j=1}^s \left(Y_{ij} - \frac{Y_{i\cdot}}{s} \right)^2 \right\} - \hat{\beta}'_i{}^2 \sum_{j=1}^s I_j^2 \quad \dots(16)$$

$i = 1, 2$

$$\sum_{j=1}^s f_{1j} f_{2j} = \left\{ \sum_{j=1}^s \left(Y_{1j} - \frac{Y_{1\cdot}}{s} \right) \left(Y_{2j} - \frac{Y_{2\cdot}}{s} \right) \right\} - \hat{\beta}'_1 \hat{\beta}'_2 \sum_{j=1}^s I_j^2 \quad \dots(17)$$

The correlation coefficient r_{12} is then given by:

$$r_{12} = \frac{\sum_{j=1}^s f_{1j} f_{2j}}{\left\{ \left(\sum_{j=1}^s f_{1j}^2 \right) \left(\sum_{j=1}^s f_{2j}^2 \right) \right\}^{\frac{1}{2}}} \quad \dots(18)$$

It is thus seen that the entire work involving the use of \hat{g}_{ij} may be simply done by using Y_{ij} with suitable formulae.

6. SUMMARY

In the study of genotype-environment interaction by using the model proposed by Perkins and Jinks, some computational difficulties, because of the calculations with genotypic values, can be considerably reduced by using the original values with appropriate formulae. It has been shown that the regression coefficient $\hat{\beta}'_i$ of Eberhart and Russell is simply related to $\hat{\beta}_i$ of Perkins and Jinks.

The aspect of grouping of varieties by correlating the residual deviations from linear regression between pairs of varieties can also be dealt easily by using the original values in place of the genotypic values.

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