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A shifted multiplicative model cluster analysis for grouping environments without genotypic rank change *

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Summary. The shifted multiplicative model (SHMM) is used with a cluster method to identify subsets of sites in an international maize (*Zea mays* L.) trial without genotypic rank-change. For cluster analysis, distance between two sites is defined as the residual sum of squares after fitting SHMM with one multiplicative term ($SHMM_1$) if $SHMM_1$ does not show genotypic rank-change. However, if $SHMM_1$ does show genotypic rank-change, the distance between two sites is defined as the smaller of the sums of squares owing to genotypes within each of the two sites. Calculation of distance between two sites is facilitated by using the site regression model with one multiplicative term ($SREG_1$), which can be reparameterized as $SHMM_1$ when only two sites are considered. The dichotomous splitting procedure, used on the dendrogram obtained from cluster analysis, will first perform SHMM analyses on each of the last two cluster groups to join (end of the dendrogram). If $SHMM_1$ does not give an adequate fit, the next step is to move down the branches of the tree until groups of sites (clusters) are found to which $SHMM_1$ provides an adequate fit and primary effects of sites are all of the same sign. Five final groups of sites to which $SHMM_1$ provides an adequate fit and primary effects of sites are all of the same sign were obtained. The procedure appears to be useful in identifying subsets of sites in which genotypic rank-change interactions are negligible.

Key words: Genotype-environment interaction – Crossover interaction – Separability – Shifted multiplicative model – Distance measure – Cluster analysis – *Zea mays* L.

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Introduction

Variation in genotypic yield response in different environments is known as genotype-environment interaction (GEI). The GEI complicates the identification of superior genotypes for a range of environments. However, in plant breeding, GEI is critical only if it involves significant crossover interaction (COI), that is, significant reversal in genotypic rank across environments (Baker 1990). Although a great number of statistical methods have been investigated and proposed to study GEI (Crossa 1990; Freeman 1990), most of them fail to distinguish between significant COI (change in genotypic rank) and noncrossover interaction (NCOI) (no change in genotypic rank) (Baker 1990).

A test for the absence of significant COI in connection with analysis of variance was described by Azzalini and Cox (1984). It involves calculating the difference between all pairs of genotypes in all possible pairs of environments. Baker (1988) suggested using this test with a significance level of 0.1 to compensate for its conservativeness. Gail and Simon (1985) developed a likelihood ratio test for the hypothesis that there is NCOI between two treatments evaluated in different trials. In the context of a variety trial, where more than two genotypes are evaluated in different environments, the use of this test to assess the significance of COI between all possible pairs of genotypes is subject to criticism concerning the comparison-wise and experiment-wise error rates (Baker 1988).

Gregorius and Namkoong (1986) pointed out that phenotypes result from specific genotype responses [$\gamma(g)$] to specific environmental effects [$\varepsilon(e)$]; therefore, these effects are not independent (non-separable), and a joint multiplicative operation [$\gamma(g)\varepsilon(e)$] should be defined. In the context of the analysis of variance, all the variation

would be attributed to the joint effect of genotype and environments (interaction) without main effects. The authors defined (1) "separability of genotypic effects from environmental effects", (2) "separability of environmental effects from genotypic effects", and (3) complete (or mutual) separability when both (1) and (2) hold. In situation (1) there are no genotypic rank-changes across environments, and in situation (2) there are no environmental rank-changes across genotypes. Although no statistical method was given, Gregorius and Namkoong (1986) suggested that an effective statistical analysis should assess the failure of separability between genotypes and environments.

The shifted multiplicative model (SHMM) was developed by Seyedsadr and Cornelius (1992) for analyzing nonadditivity in a two-way table. In the context of a variety trial, the SHMM model provides a powerful analytical tool for determining separability of genotypic effects from environmental effects, separability of environmental effects from genotypic effects, and complete separability.

The general relationships between the primary effects of environments and genotypes of the SHMM model with one multiplicative term ($SHMM_1$) and Gregorius and Namkoong's definition of separability are described by Cornelius et al. (1992). These authors defined sufficient conditions for the absence of statistically significant genotypic rank-change interactions: (1) $SHMM_1$ is an adequate model for fitting the data and (2) primary effects of environments have the same sign. Absence of statistically significant environmental rank-change interactions is achieved when (1) holds and (3) primary effects of genotypes have the same sign. The absence of statistical significance of both environmental rank-change interactions and genotypic rank-change interactions occurs when (1), (2), and (3) all hold.

In most crop cultivar trials, GEI is complex, and separability of genotypic effects does not occur. Cornelius et al. (1992) described an exploratory method using SHMM to find subsets of environments that do have within-subset separability of genotypic effects. Environments are grouped by inspection of computed estimates of model parameters ("primary", "secondary", "tertiary", etc., effects of environments) from a SHMM analysis of the entire data set in a search for subsets in which $SHMM_1$ is an adequate descriptive model, i.e., no statistically significant evidence for lack of fit is found. Separate SHMM analyses performed on the initial subsets may suggest further subdivisions or rearrangements of the original groupings. While in principle, the exploratory method of Cornelius et al. (1991) is always workable, it seems likely that, in practice, it will be increasingly difficult and time consuming as the number of environments increases. The purpose of this paper is to present a strategy that employs cluster analysis in conjunction with SHMM analysis to find subsets of environments in which separability of genotypic effects holds.

Materials and methods

Data from a CIMMYT international maize variety trial (EVT 13) conducted in 1987 were analyzed. The trial had eight open pollinated varieties grown in 59 locations (Table 1) and used a randomized complete block design with four replications at each location. The trait analyzed was grain yield (kg ha^{-1}) adjusted to 15% moisture. Details of the CIMMYT maize breeding program and field testing procedures are described in Pandey et al. (1986) and Vasal et al. (1982).

SHMM statistical analysis

SHMM with t multiplicative terms ($SHMM_t$) is represented by $y_{ij}=\beta+\sum_{k=1}^{t}\lambda_k\,\alpha_{ik}\,\gamma_{jk}+e_{ij}$ (Seyedsadr and Cornelius 1992; Cornelius et al. 1992) where y_{ij} is the yield of the i^{th} genotype in the j^{th} environment; β is the shift parameter; λ_k is the singular value for the axis k; α_{i1} and γ_{j1} are the "primary effects" of the i^{th} genotype and the j^{th} environment, respectively, α_{i2} and γ_{j2} are their "secondary effects", etc; e_{ij} is a random error.

The shift parameter has an important role in determining the type of separability existing in the data set. When the $SHMM_1$ values are plotted against primary effects of environments or genotypes, the diagram shows a set of concurrent regression lines, i.e., which intersect at one point. The expected value of y at the point of concurrence (i.e., intersection) is β. If $SHMM_1$ is an adequate model and its graph with environmental primary effects (γ_{j1}) as the abscissa is such that all of the phenotypic values are located to the left or to the right of the point or concurrence (0, β), then genotypic effects are separable from environmental effects (Cornelius et al. 1992). If this is not so, COI (change in genotypic rank; in fact, complete rank reversal) involving environments on opposite sides of the point of concurrence occurs, and primary effects of genotypes are said to be "non-separable". For genotypes and environments with only one or neither type of separability, the value of β will necessarily be contained within the range of the phenotypic values. For genotypes and environments with nearly additive effects, β will have a numerically large value (Seyedsadr and Cornelius 1992). The only COI pattern that $SHMM_1$ can display is complete rank reversal left and right of the point of concurrence. Since COI seldom has such an extreme pattern, its existence is most commonly revealed by failure of $SHMM_1$ to adequately fit the data.

The SHMM model has the following somewhat annoying properties: (1) the least squares estimate of the shift parameter β depends on estimates of the multiplicative terms and, except in the special case where t is 1 less than the smaller dimension of the two-way table of data, an iterative algorithm is needed to compute the estimates; (2) changing the number of multiplicative terms in the model changes the estimates of all model parameters.

Finding subsets of sites for which $SHMM_1$ fits adequately. Clustering method, distance measures, and dichotomus split procedure

Experimental sites in this international trial were clustered on the basis of a distance measure between two sites defined as the residual sum of squares, RSS ($SHMM_1$), when $SHMM_1$ is fitted to the data from these two sites only, provided that the fitted $SHMM_1$ does not show genotypic rank change. Otherwise, the

Table 1. Sites included in EVT 13 (1987)

Code Number	Country	Location	Altitude (masl)	Latitude
1	Philippines	Los Baños	–	14° N
2	Philippines	Karaan	700	7° N
3	Philippines	Smarc	20	7° N
4	Philippines	Smarc (2)	20	7° N
5	Argentina	Córdoba	–	31° S
6	Bolivia	Mairana	–	17° S
7	Bolivia	Sapirangui	–	–
8	Brazil	Jardinopolis	600	21° S
9	Brazil	Capinopolis	621	18° S
10	Brazil	S. Cruz Palm.	–	–
11	Colombia	Turipana	13	8° N
12	Colombia	Ciat	965	3° N
13	Colombia	Tulenapa	–	–
14	Colombia	Cri Motilonia	120	10° N
15	Colombia	Cri Motilonia (2)	120	10° N
16	Ecuador	Porto Viejo	44	1° S
17	Paraguay	Caacupe	228	25° S
18	Paraquay	Cpt. Miranda	200	27° S
19	Peru	La Molina	251	12° S
20	Peru	Cajamarca	2,628	7° S
21	Peru	Yurimaguas	184	5° S
22	Surinam	Tijgerkreek	1	3° N
23	Belize	Central Farm	61	17° N
24	Costa Rica	Los Diamantes	900	10° N
25	México	Poza Rica	60	20° N
26	México	Cd. Obregón	40	26° N
27	México	La Huerta	500	21° N
28	Panamá	Tocumen	14	9° N
29	Panamá	Rio Hato	5	8° N
30	Panamá	Guarape	15	8° N
31	Panamá	La Honda	17	8° N
32	México	Ocotlan	1,200	20° N
33	México	Jalisco	–	–
34	Dom. Rep.	Unphu	–	–
35	Mauritania	Kaedi	10	16° N
36	Congo	Loudima	165	4° S
37	Congo	Loudima (1)	165	4° S
38	Ivory Coast	Ferkessedougou	330	9° N
39	Ivory Coast	Bouake	360	7° N
40	Ghana	Nyankpala	185	9° N
41	Ghana	Kwadaso	270	6° N
42	Ghana	Damongo	–	9° N
43	Senegal	Keur Samba G.(1)	15	13° N
44	Senegal	Keur Samba G.(2)	15	13° N
45	Senegal	K. Samba (3)	15	13° N
46	Zaire	Mvuazi	505	5° S
47	Zeire	Kiyaka	739	5° S
48	Bangladesh	Yoydebpu	8	24° N
49	Bangladesh	Ishurdi	14	24° N
50	Bangladesh	Jessore	6	23° N
51	Bangladesh	Rangpur	34	25° N
52	Indonesia	Mojosari	28	8° S
53	Indonesia	Muneng	10	8° S
54	Indonesia	Yogyakarta	–	8° S
55	Taiwan	Po-Tzu-Chia-I	5	23° N
56	Thailand	Tak Fa	87	15° N
57	Thailand	Phraputh	–	17° N
58	Vietnam	Song Boi	16	22° N
59	Vietnam	Hung Loc	180	10° N

distance is defined as RSS ($SHMM_1$) under a constraint that the fitted $SHMM_1$ does not show genotypic rank change. If a pair of sites, say sites 1 and 2, shows genotypic COI in the fitted $SHMM_1$, then $\hat{\gamma}_{11}$ and $\hat{\gamma}_{21}$ differ in sign. Suppose that $\hat{\gamma}_{11}<0$ and $\hat{\gamma}_{21}>0$. We will then choose the better of two possible constrained solutions:

1) $\hat{\beta}=\bar{y}_{.1}, \hat{\gamma}_{11}=0, \hat{\gamma}_{21}=1, \hat{\lambda}_1\,\hat{\alpha}_{i1}=y_{i2}-\bar{y}_{.1}$, $RSS=\Sigma_i(y_{i1}-\bar{y}_{.1})^2$;
2) $\hat{\beta}=\bar{y}_{.2}, \hat{\gamma}_{11}=-1, \hat{\gamma}_{21}=0, \hat{\lambda}_1\,\hat{\alpha}_{i1}=y_{.2}-\bar{y}_{i1}$, $RSS=\Sigma_i(y_{i2}-\bar{y}_{.2})^2$.

RSS for these constrained solutions is the sum of squares owing to genotypes within the site. The mean of the site was chosen for $\hat{\beta}$. Thus, the distance will be defined as RSS ($SHMM_1$) if the fitted $SHMM_1$ does not show genotypic COI and $\min[\Sigma_i(y_{i1}-\bar{y}_{.1})^2, \Sigma_i(y_{i2}-\bar{y}_{.2})^2]$ otherwise. This distance measure has properties similar to Euclidean distance measures commonly used in cluster analysis. If we write the matrix of $SHMM_1$ residuals as $\hat{\lambda}_2\,\hat{\boldsymbol{\alpha}}_2\,\hat{\gamma}'_2$, where $\hat{\boldsymbol{\alpha}}_2$ and $\hat{\gamma}_2$ are normalized vectors, then whether the solution is a constrained solution or not, RSS ($SHMM_1$) can be expressed as $\|\hat{\lambda}_2\,\hat{\boldsymbol{\alpha}}_2\|^2=\|\hat{\lambda}_2\,\hat{\gamma}_2\|^2$ where $\|\cdot\|$ denotes the Euclidean norm.

By exploiting certain properties of SHMM in the special case where the smaller dimension of the two-way table of data is two, we can compute the distance matrix without need for an iterative algorithm. Seyedsadr and Cornelius (1991b) proved that if $s\leq g$, where s is the number of sites and g the number of genotypes, then the least squares residuals of $SHMM_{(s-1)}$ are identical to those of $SREG_{(s-1)}$ where SREG denotes the site regressions model, $y_{ij}=\mu_j+\Sigma_k\,\theta_k\,\zeta_{ik}\,\delta_{jk}+e_{ij}$. Thus, if $s\leq g$, RSS ($SHMM_{(s-1)}$)=RSS ($SREG_{(s-1)}$). The RSS is zero if $s=g$, but greater than zero if $s<g$. Whereas in general the least squares fitting of SHMM requires an iterative algorithm, the least squares fitting of SREG is obtained without iteration by putting $\mu_j=\bar{y}_{.j}$ and obtaining estimates of the multiplicative terms from the singular value decomposition of the matrix **W** where $w_{ij}=y_{ij}-\bar{y}_{.j}$. Consequently, RSS ($SHMM_{(s-1)}$) can be easily obtained as RSS ($SREG_{(s-1)}$).

In particular, in a SHMM analysis of a subset of data from two sites, RSS ($SHMM_1$) can be obtained as RSS ($SREG_1$). In fact, if there are only two sites, $SREG_1$ can be reparameterized as $SHMM_1$ by putting $\gamma_{j1}=\delta_{j1}$, $\beta=(\delta_{21}\,\mu_1-\delta_{11}\,\mu_2)/(\delta_{21}-\delta_{11})$, $\alpha_{i1}=(\zeta_{i1}-\zeta_0)/\phi$, and $\lambda_1=\phi\,\theta_1$, where $\zeta_0=(\mu_1-\mu_2)/\theta_1(\delta_{21}-\delta_{11})$ and $\phi=[\Sigma_i(\zeta_{i1}-\zeta_0)^2]^{1/2}$. This transformation is derived by considering the two nonparallel regression lines for the two sites in the $SREG_1$ parameterization (plotted with value of ζ_{i1} as the abscissa) and translating the origin to the abscissa (ζ_0) at the point of intersection. Since $SHMM_2$ will fit the data from two sites exactly, RSS ($SHMM_1$)=RSS ($SREG_1$) is also the sequential sum of squares owing to secondary effects in a separate analysis of a pair of sites.

Thus, the distance matrix can be computed by the following simple strategy. Once and for all compute the matrix $\mathbf{Q}=\mathbf{W}\mathbf{W}'$ for the entire data set. Then, for each pair of sites, extract the 2×2 submatrix of **Q** for that pair of sites and obtain its eigenvalues and eigenvectors. To confirm that a graphical display of the fitted $SHMM_1$ for the pair of sites will not predict genotypic rank reversal from one site to the other, it is sufficient to confirm that the product of the two elements of the eigenvector associated with the larger eigenvalue is positive. If this hold, put the distance equal to the smaller eigenvalue [this is RSS ($SHMM_1$)]. Otherwise, put the distance equal to the smaller of the two diagonal elements of the 2×2 submatrix of **Q**.

Once distance matrix has been obtained, the complete linkage method (or furthest neighbor technique) for combining clusters is utilized. In this method the distance between two clusters is calculated as the distance between their two furthest points. A

"dendrogram" showing the steps where clusters were combined provides a useful visual representation of the cluster analysis.

To identify as large as possible clusters to which $SHMM_1$ gives an adequate fit, we use a dichotomous splitting procedure in which we first perform SHMM analyses on each of the two last cluster groups (end of dendrogram) to determine whether or not $SHMM_1$ gives a satisfactory fit to those groups. If $SHMM_1$ does not give an adequate fit, the next step is to move down the branches of the tree (within each group) until clusters (groups of sites) are found to which $SHMM_1$ does provide an adequate fit and primary effects of sites ($\hat{\gamma}_{j1}$) are all of the same sign.

A SAS program that calculates the distance matrix and does cluster analysis is provided in the appendix.

Criteria for assessing the adequacy of $SHMM_1$ for fitting a subset of environments

To determine how well the $SHMM_1$ model fits a particular subset of environments obtained by the cluster method, several approximate tests were used to assess the significance of secondary and tertiary effects in explaining the data. These are the approximate F tests, F_1 and F_{GH1}, described by Cornelius et al. (1992) for testing terms in a SHMM model against a pooled error mean square, the Seyedsadr and Cornelius (1991 b) (SC) test, the Seyedsadr and Cornelius/Schott and Merasinghe test (SC/SM) test (Cornelius et al. 1992) and a test constructed by analogy to the test of Yochmowitz and Cornell (1978) (YC) for sequential tests of components in additive main effects and multiplicative interaction (AMMI) models. The YC procedure tests the k^{th} multiplicative term as though it were the first in a problem with the smaller dimension of the two-way table reduced to $\min(s, g)-k+1$. This is based on a theoretical argument that appears not to be strictly valid for SHMM models, but in practice we find the test to be a useful criterion that is generally less conservative than the SC/SM test. Yochmowitz and Cornell (1978) give a method for computing approximate probabilities (P-values) for AMMI models for only a few small values of the smaller dimension of the two-way table of data, but these probabilities can be computed approximately for a wide range of table dimensions by the method of Johnson and Graybill (1972). For AMMI models this requires the computer simulation results of Mandel (1971) for expectations and standard deviations of the sum of squares owing to the first interaction component. For SHMM, the simulation results given by Seyedsadr and Cornelius (1991 b) for the first SHMM component are substituted for Mandel's AMMI results. Formulas which closely approximate these simulation results as functions of $r=\max(s, g)$ and $c=\min(s, g)-k+1$ and which may be used in computer programs to eliminate the need for table lookups are given by Seyedsadr and Cornelius (1991 a). The simulation results are available and the approximation formulas are valid only for $r \leq 99$ and $c \leq 19$.

In addition to the above-mentioned tests, it is useful to note that the $SHMM_1$ model is adequate for fitting a subset of environments if the mean squares due to secondary and tertiary effects and the $SHMM_1$ residual are smaller than the residual mean square obtained when the appropriate model was fitted to the entire data set. However, the appropriate statistical significance tests for such comparisons are not available.

When the above criteria do not provide a clear answer as to whether or not $SHMM_1$ adequately fits a specific group of environments we recommend following the dichotomous split indicated by the dendrogram one step further. Then, if a sizeable reduction in the mean squares owing to secondary and tertiary effects have not occurred, this further subdivision is ignored, and $SHMM_1$ is considered to have been adequate at the previous step; otherwise the subdivision is considered appropriate.

Statistical test for assessing significance of crossover interaction

The three tests considered here for assessing significant COI are based upon the null hypothesis that the parametric cell means for a particular group of sites do not contain any COIs, the alternative hypothesis being that some COIs exist. From a breeder's perspective, a Type II (accepting a false null hypothesis) error is more serious than a Type I error (rejecting a true null hypothesis) since this will imply using certain genotypes for a set of environments in which one assumes there are no COIs when in fact there are. This suggests that a test that gives experiment-wise α-level protection at a cost of having low power to detect the true interactions should not be used.

Test 1

The test proposed by Azzalini and Cox (1984) requires calculating differences between all possible pairs of genotypes in all possible pair of environments. The test considers that for any pair of genotypes and environments a significant COI occurs only if the absolute value of the genotypic difference exceeds some critical value in both environments and the difference has a COI pattern, i.e., the difference between the two genotypes differs in sign from one environment to the other. The critical value used by this test is $t_\alpha \sigma\sqrt{2}$ where t_α (not Student's t) is a table value from Azzalini and Cox and σ is the standard error of a cell mean. The test has an experiment-wise error rate of α, and its power for detecting COIs will decrease as the number of genotypes and environments increases.

Test 2

This test was used by Cornelius et al. (1992) and is similar to the Azzalin-Cox (1984) test except that it uses a comparison-wise error rate (α) of 0.05 for the *t*-tests of the simple genotypic differences within environments.

Test 3

Cornelius et al. (1992) also defined an interaction-wise Type I error rate, i.e., error rate per 2×2 subtable tested for COIs, using critical value of $t_\theta \sigma\sqrt{2}$ where t_θ is the value of Student's t such that $P(t > t_\theta) = \theta$. Then the probability of making a Type I error (declaring a 2×2 subtable to have COI when, in fact, it does not) is $2\theta^2$. Putting $2\theta^2 = \alpha$ gives $\theta = (\alpha/2)^{1/2}$.

Results and discussion

Grouping sites with separable genotypic effects

The SHMM analysis of the entire EVT 13 data shows significant ($P < 0.05$) primary effects by all test criteria (Table 2). Secondary effects were significant by the F_1 and F_{GH1} tests and tertiary effects only by the F_1 tests. Given that the mean square of the tertiary effect (160) is smaller than the remainder mean square (170), we can conclude that $SHMM_2$ adequately fits these data. This nonseparability of the genotypic effects from site effects predicts a different norm of response of the genotype under different environments. While some genotypes have a positive response (yield increase) to specific environmental conditions, other show negative performance (yield decrease), and this trend is not consistent for all genotypes and sites.

From a plant breeder's perspective these results indicate that it is not possible to select one or two superior

Table 2. Analysis of variance (ANOVA) and SHMM analysis for grain yield (kg ha^{-1}) of EVT 13 (1987)

Source of variation	*df*	MS × 10^{-3}
ANOVA		
Model's corrected total	471	2,194
Genotype (G)	7	2,947[a]
Site (S)	58	16,324[a]
G × S	406	162[b]
Pooled error	1,239	111
SHMM analysis		
Model's corrected total	471	2,194
Primary effects	98.20	9,862[c-g]
Secondary effects	82.23	196[f,g]
Tertiary effects	70.45	160[g]
Remainder	220.10	170

[a] Significant ($P<0.05$) when tested against the interaction
[b] Significant ($P<0.05$) when tested against the pooled error
[c] Significant ($P<0.05$) by the test of Yochmowitz and Cornell (1978)
[d] Significant ($P<0.05$) by the tests of Seyedsadr and Cornelius (1991a, b, 1992), Schott (1986) and Marasinghe (1985)
[e] Significant ($P<0.05$) by the test of Seyedsadr and Cornelius (1991a, b, 1992)
[f] Significant ($P<0.05$) by the F_{GH1} test
[g] Significant ($P<0.05$) by the F_1 test

genotypes across a wide range of environments. Therefore, it is necessary to split the total set of sites into more homogeneous site groups with each group having no significant genotypic rank reversal trends, i.e., an appropriate subset of sites should be such that genotypic effects are "separable" from environmental effects. The breeder will then be interested in which genotypes are superior in each specific subset and in how the predicted rank order of genotypes changes from one subset to another. The cluster method in conjunction with a dichotomous splitting was used to identify subsets of sites were separability of genotypes holds.

The dendrogram of 59 sites is depicted in Fig. 1. All 59 sites are first partitioned into two major groups, A and B. The dichotomous split procedure is initiated by analyzing the two major groups of sites and examining whether $SHMM_1$ gives an adequate fit. $SHMM_1$ is unsatisfactory for fitting groups A and B because they have large and significant secondary and tertiary components (Table 3). Thus, the dichotomous split continues moving down within the two main branches of the tree to the next split where groups A1, A2, B1, and B2 (Fig. 1) are analyzed. $SHMM_1$ model adequately fits group A1 where secondary effects are not significant. However, $SHMM_1$ does not provide a good fit to sites in group A2 (significant mean square for secondary and tertiary effects by F_{GH1} and F_1 tests, Table 3). Group A2 is subdivided into groups A3 and A4 (Fig. 1). $SHMM_1$ is adequate for group A3, but not for group A4 where mean squares

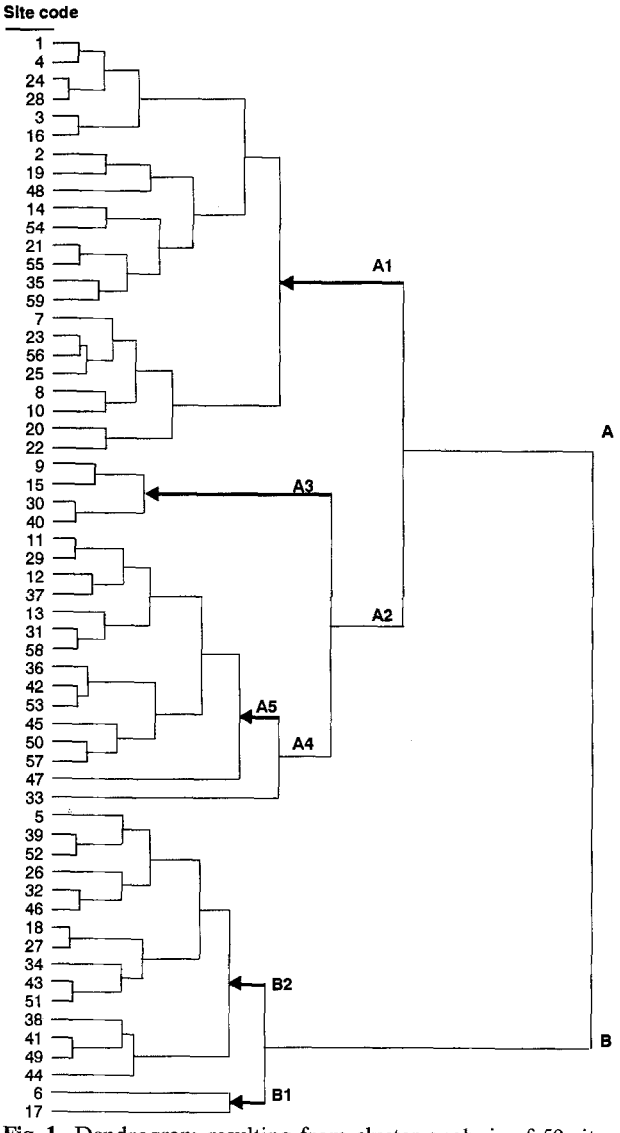

Fig. 1. Dendrogram resulting from cluster analysis of 59 sites included in EVT13

owing to secondary and tertiary effects (172 and 141, respectively) are significant by the F_1 test. Because site 33 joins the rest of the sites late in the dendrogram, its exclusion from A4, to form group A5, clearly improves the fit of $SHMM_1$ (mean square of secondary effects is 111 and not significant). Site 33 is left as an ungrouped site.

Although, the mean square owing to secondary effects is large in group B1 (312 not significant), we can regard $SHMM_1$ as satisfactory for fitting these data due to the large value of the pooled error variance (301) (mean square error of sites 6 and 17 were 263 and 339, respectively). The large error variance, of course, increases the risk of failing to detect true genotypic rank changes. It is clear from the SHMM analysis of group B2 that $SHMM_1$ is satisfactory for this group (only primary effects are significant).

Table 3. Mean squares of SHMM analyses for various site groups of EVT 13 (1987) formed using the cluster methodology based on the RSS ($SHMM_1$) fitted under the constraint that the model does not have genotypic rank change

	Group A	Group A1 [+]	Group A2
		$\times 10^{-3}$	
Component 1	8,476[a-e]	6,385[a-e]	7,775[a-e]
Component 2	156[d,e]	133	202[d,e]
Component 3	168[d-e]	135	227[d,e]
Remainder	147	118	122
Error	109	111	106
$SHMM_1$ residuals	153	126	170
	Group A3	Group A4	Group A5
Component 1	4,620[a-e]	5,496[a-e]	4,628[a-e]
Component 2	103	172[e]	111
Component 3	170	141[e]	116
Remainder	13	134	118
Error	121	102	98
$SHMM_1$ residuals	115	147	115
	Group B	Group B1	Group B2
Component 1	7,761[a-e]	878[c-e]	6,189[a-e]
Component 2	255[a-e]	312	112
Component 3	170[e]	–	121
Remainder	133	–	129
Error	115	301	91
$SHMM_1$ residuals	179	312	122

[a] Significant ($P<0.05$) by the test of Yochmowitz and Cornell (1978)
[b] Significant ($P<0.05$) by the tests of Seyedsadr and Cornelius (1991 a, b, 1992), and Schott (1986) and Marasinghe (1985)
[c] Significant ($P<0.05$) by the test of Seyedsadr and Cornelius (1991 a, b, 1992)
[d] Significant ($P<0.05$) by the F_{GH1} test
[e] Significant ($P<0.05$) by the F_1 test
[+] *Site composition of the final groups:* group A1 = 1, 2, 3, 4, 7, 8, 10, 14, 16, 19, 20, 21, 22, 23, 24, 25, 28, 35, 48, 54, 55, 56, 59; group A3 = 9, 15, 30, 40; group A5 = 11, 12, 13, 29, 31, 36, 37, 42, 45, 47, 50, 53, 57, 58; group B1 = 6, 17; group B2 = 5, 18, 26, 27, 32, 34, 38, 39, 41, 43, 44, 46, 49, 51, 52

Cluster analysis based on the proposed distance measure produces five final groups of sites with a $SHMM_1$ that does not display genotypic crossover being an adequate model in each group. These groups, marked with an arrow in Fig. 1, are A1, A3, A5, B1, and B2. Within each of these groups of sites, because of the absence of significant COI, consistent conclusions can be made regarding the performance of the eight genotypes. Four of these groups (A1, A3, A5, and B2) have complete separability. Group B1 has primary effects of genotypes which are not all of the same sign and, consequently, site effects are not separable from genotypic effects in that group.

The plots of the $SHMM_1$ model fitted to the five final groups of sites are presented in Figs. 2–6. Note that primary effects of sites (abcissa) are all of the same sign.

Table 4. All possible 2×2 interactions (I), crossover interactions (COI), and significant crossover interactions obtained by test 1, test 2, and test 3 for sites in different final groups and for sites in the same final group

Allocation of sites	I	COI	Test 1[a]	Test 2	Test 3
Among final groups	35,140	15,374	1	276	2,482
Within final groups	12,768	4,339	0	6	352
Group A1	7,084	2,550	0	6	213
Group A3	168	50	0	0	0
Group A5	2,548	677	0	0	71
Group B1	28	9	0	0	2
Group B2	2,940	1,053	0	0	66

[a] Test 1 is the Azzalini and Cox test; test 2 is the simple *t*-test; test 3 is the *t*-test with the joint 0.05 significant protection

Groups A1 and A5 have shift parameter values so far outside the range of the data ($-33{,}133$ kg ha^{-1} and 91,624 kg ha^{-1}, respectively) that the regression lines appear nearly parallel (Figs. 2 and 4). This indicates that genotypic and environmental effects are essentially additive in those two groups.

The final groups obtained comprise sites from diverse geographical areas as well as different altitudes and latitudes (e.g., group A3 includes Cajamarca in Peru at 2628 masl and Tijgerkreek in Surinam at 1 masl). Furthermore, each of the final groups contains sites with a wide range in mean yields, i.e., the groupings seem not to be associated with site productivity levels. Because information on environmental variables (e.g., temperature and rainfall) is not available, conclusions regarding the biological interpretation of these groups can not be made.

Assessing significant crossover interaction within and among groups of sites with separable genotypic effects

For EVT 13 with 59 sites and eight genotypes, the number of all possible interactions between any two genotypes with any two environments is $s(s-1)\,g(g-1)/4 = 47{,}908$; 41% of them (19,713) had the COI pattern, i.e., with genotypic rank-change (Table 4). Of the within-group interactions, 34% (4339) had the COI pattern, while 44% (15,374) of the among group interactions had COI pattern (Table 4). The magnitude of the COI for sites in different groups range from $-3{,}722$ to 3,962 kg ha^{-1} with a mean absolute value of 949 kg ha^{-1}, whereas the magnitude of the COI for sites in the same final group ranges from $-3{,}034$ to 2,490 kg ha^{-1} with a mean absolute value of 746 kg ha^{-1}.

The percentage of COI which were significant by Test 3 (the most liberal one) was 8% (352) within groups and 16% (2,482) among groups. The number of statistically significant COI for sites in the same final group is very

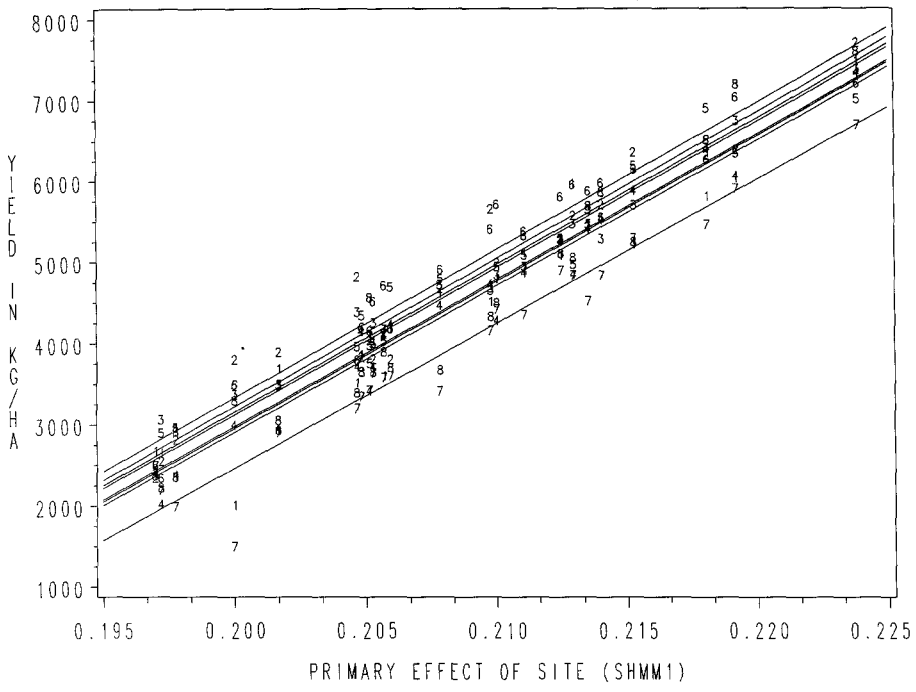

Fig. 2. $SHMM_1$ fitted to group A1. *Plotted points* are phenotypic mean; *straight lines* show the primary effects of eight genotypes; $\hat{\beta} = -33133$

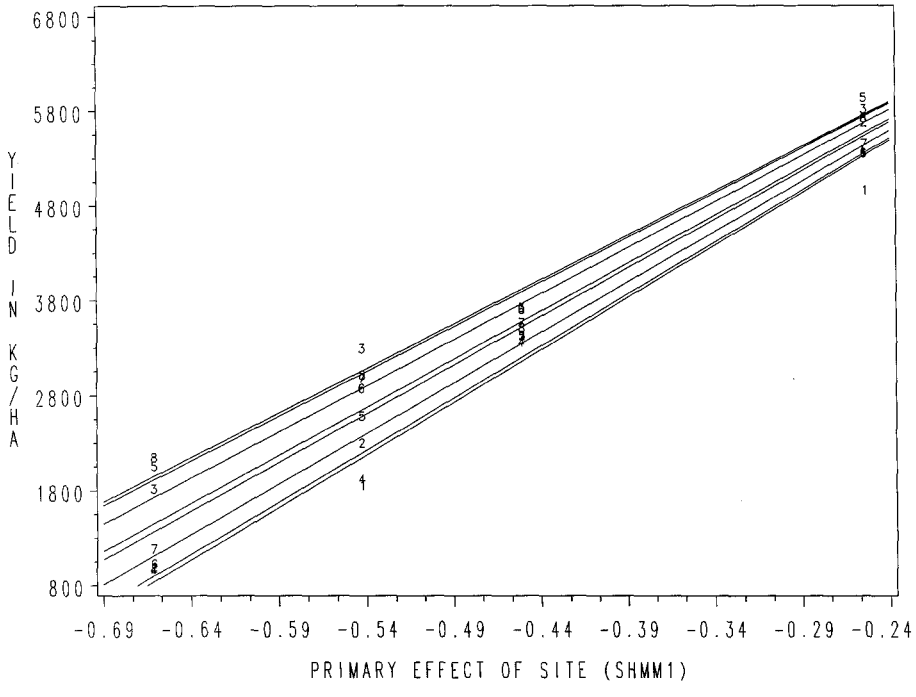

Fig. 3. $SHMM_1$ fitted to group A3. *Plotted points* are phenotypic means; *straight lines* show the primary effects of eight genotypes; $\hat{\beta} = 8136$

low for all three tests. Test 3 indicates that 8% (213) of the COI within group A1 were significant (Table 4); none of the COI were significant in group A3; 10% (71) of the COI were significant in group A5; 22% (2) and 6% (66) of the COI were significant for groups B1 and B2, respectively. It is interesting that half of the significant COI within group A5 (36 out of 71) involved site 47; this site joined the other sites of group A5 late on the dendrogram (Fig. 1). Test 2 detected 6 significant COI within group A1 (4 of them include site 3) and none within the other groups. Test 1 is the most conservative and did not detect any significant COI for sites in the same group. These results indicate the effectiveness of the distance measure used in the cluster analysis in reducing the number of significant COI with genotypic rank-change within the final groups of sites.

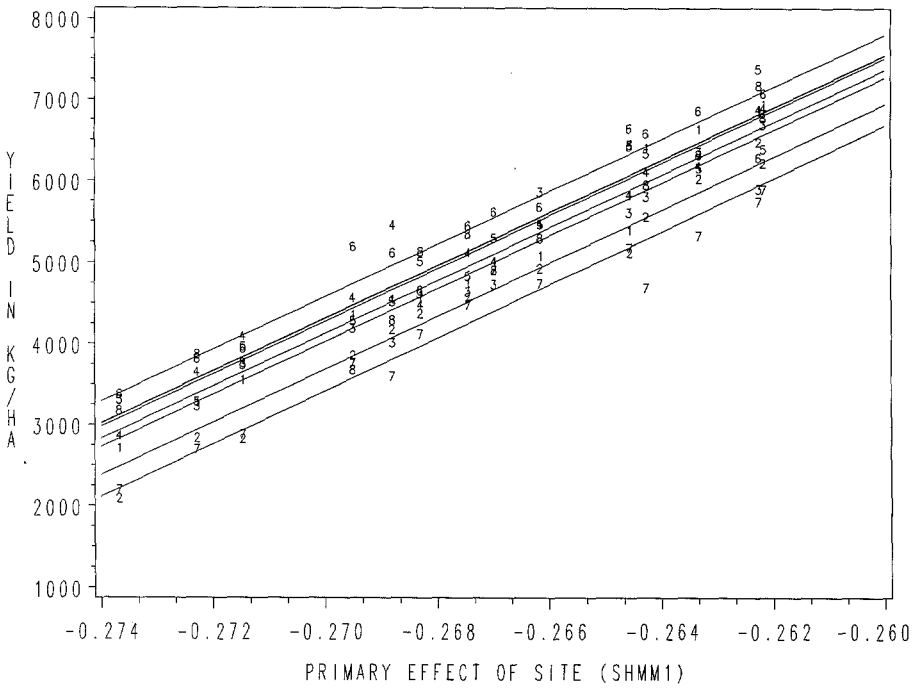

Fig. 4. $SHMM_1$ fitted to group A5. *Plotted points* are phenotypic means; *straight lines* show the primary effects of 8 genotypes; $\hat{\beta} = 91624$

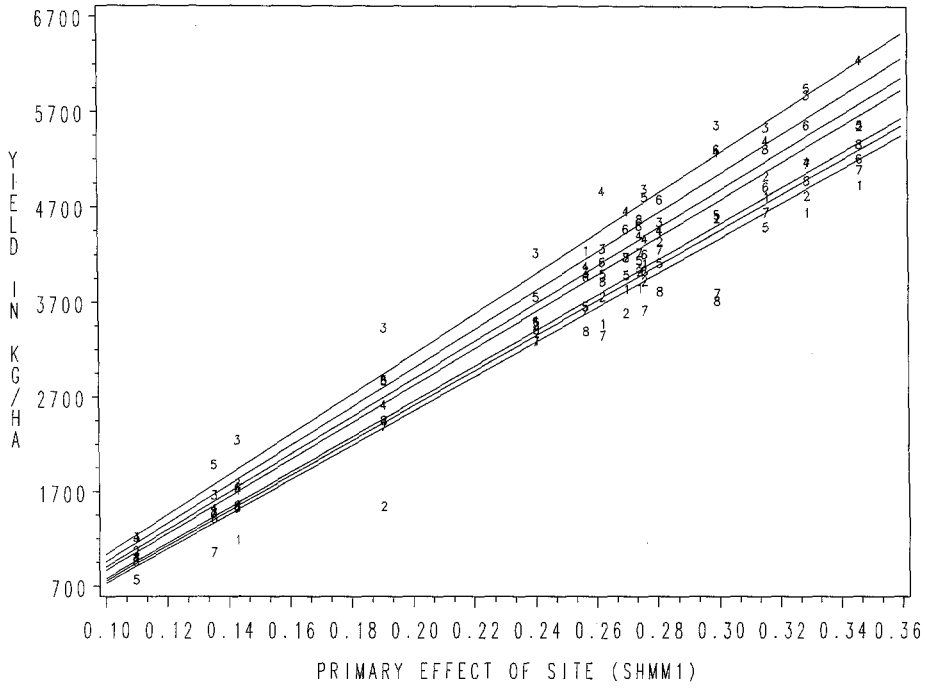

Fig. 5. $SHMM_1$ fitted to group B2. *Plotted points* are phenotypic means; *straight lines* show the primary effects of eight genotypes; $\hat{\beta} = -1083$

Under the null hypothesis that there are no significant COI with $\alpha = 0.05$, we expected Test 3 to find 354 significant COI in group A1, 8 in group A3, 127 in group A5, 1 in group B1, and 147 in group B2. In all the final groups (except B1) the observed number of significant COI given by the three tests is much lower than the number of COI expected under the null hypothesis.

Cornelius et al. (1992) used these three statistical tests to validate an exploratory method for identifying subsets of sites in which genotypic effects are separable from environmental effects. The method proved to be effective in forming groups of sites with very few significant COI. The clustering method used here also seems to be highly effective. Since the exploratory method is limited only by

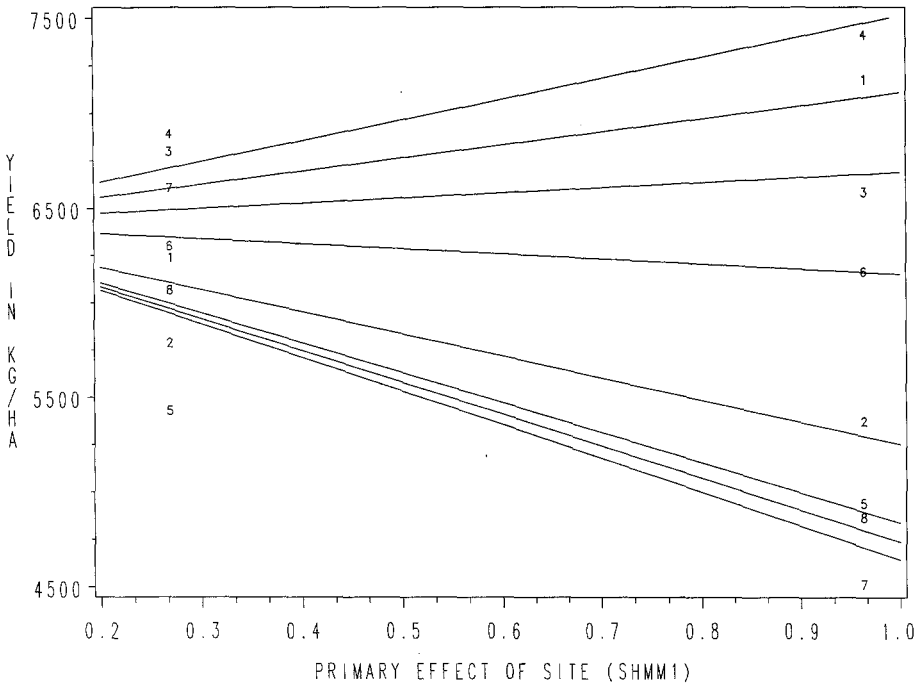

Fig. 6. $SHMM_1$ fitted to group A1. *Plotted points* are phenotypic means; *straight lines* show the primary effects of eight genotypes; $\hat{\beta}=6420$

the skill of the investigator and how exhaustively he is willing to pursue the analysis of alternative possible groupings, no claim can be made that the clustering method is superior. Its advantage lies in allowing the investigator to arrive at an interpretable result more quickly and easily in the analysis of some data sets, especially if the number of environments is large.

Conclusions

SHMM used in conjunction with the cluster method is a powerful tool by which to identify subsets of environments with genotypic separability. The complete linkage cluster procedure based on the proposed distance measure appears to do an excellent job of allowing the user of identify groups of environments in which genotypic rank-change interactions are negligible. This procedure can be effectively used for: (1) grouping environments with genotypic separability and (2) grouping genotypes and environments with complete separability.

In general, cluster analysis has some disadvantages: (a) many different distance measures can be used, yielding different results, (b) the truncation level of the classificatory hierarchies may be decided arbitrarily, and (c) numerous hierarchical clustering algorithms exist, all of which may produce different cluster groups. The advantage of the proposed distance measure between two sites is that it takes into account the existence of genotypic rank-change. Two sites with genotypic separability will join together in an early stage of the clustering process (see Fig. 1, sites 30 and 40), whereas a pair of sites (or groups of sites) without genotypic separability will meet in late stages of the process (see Fig. 1, group A5 and site 33). Furthermore, the dichotomous split, based on the adequacy of $SHMM_1$ to fit a particular cluster, provides a criterion for truncating the classificatory hierarchies. The procedure separates the groups (branches of the tree) into independent entities that are truncated at different levels according to whether $SHMM_1$ provides them a satisfactory fit. The extent to which the results depend on the choice of clustering algorithm requires further research, particularly in regard to the effectiveness of alternative algorithms in identifying subsets of environments with genotypic separability.

In further research we will investigate the utility of clustering genotypes or both genotypes and environments into groups that have genotypic separability.

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Appendix

*** This is the SAS program that calculates the distances between sites and does the cluster analysis;
*** Give the following information in macros: number of sites (NSITE), and Sxx where xx is the number of sites (SLAST);
MACRO NSITE 59% MACRO SLAST S59%
*** Give names 'S1' 'S2' ... in following macro which gives a statement needed later by PROC IML. There needs to be as many consecutively numbered names as there are sites (i.e., environments);
MACRO SNAMES SNAME={'S1' 'S2' 'S3' 'S4' 'S5' 'S6' 'S7' 'S8' 'S9' 'S10' 'S11' 'S12' 'S13' 'S14' 'S15' 'S16' 'S17' 'S18' 'S19' 'S20' 'S21' 'S22' 'S23' 'S24' 'S25' 'S26' 'S27'

```
'S28' 'S29' 'S30' 'S31' 'S32' 'S33' 'S34' 'S35' 'S36' 'S37'
'S38' 'S39' 'S40' 'S41' 'S42' 'S43' 'S44' 'S45' 'S46' 'S47'
'S48' 'S49' 'S50' 'S51' 'S52' 'S53' 'S54' 'S55' 'S56' 'S57'
'S58' 'S59'}'; %
```

```
*** Here insert appropriate syntax to read or construct a data
set named DS1 that contains variable SITE which identifies the
environment, variable GENOTYPE which identifies the culti-
var, and variable Y, the values of which will be the
SITE * GENOTYPE cell means of the response variable;
PROC SORT; BY SITE GENOTYPE;
PROC IML;
START;
USE DS1; READ ALL INTO Y VAR{Y};
YM=SHAPE (Y, NSITE); PRINT YM; R=NROW (YM); C=NCOL (YM);
DO I=1 TO R;
  SITEMEAN=SUM (YM(|I, *|))/C;
  YM(|I,*|)=YM(|I,*|)-J(1,C,SITEMEAN);
  END;
SSCP=YM * YM';
DIST=J(R, R, 0);
DO I=1 TO R-1;
  DO J=I+1 TO R;
  SUB=I || J;
  SSCP2=SSCP (|SUB, SUB|);
  CALL EIGEN (LAM, EVEC, SSCP2);
  DIST (|J, I|)=MIN (LAM);
  IF EVEC (|1, 1|) * EVEC (|2, 1|)<0 THEN
    DIST (|J, I|)=MIN (SSCP2 (|1, 1|), SSCP2 (|2, 2|));
END; END;
*** Get SNAME=statement from macro SNAMES; SNAMES
** PRINT DIST (|COLNAME=SNAME ROWNAME=SNAME|);
CREATE DS2 FROM DIST (|COLNAME=SNAME|); APPEND FROM DIST;
CREATE DS3 FROM SNAME (|COLNAME='SITE'|); APPEND FROM SNAME;
FINISH; RUN;
** PROC PRINT DATA=DS2;
DATA DS4 (TYPE=DISTANCE); MERGE DS2 DS3;
  KEEP S1-SLAST SITE;
** PROC PRINT;
PROC CLUSTER METHOD=COMPLETE; ID SITE; PROC TREE;
```

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