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Multiplicative Interaction in Generalized Linear Models

Fred A. van Eeuwijk

DLO-Centre for Plant Breeding and Reproduction Research (CPRO-DLO),
P.O. Box 16, 6700 AA Wageningen, The Netherlands

SUMMARY

Bilinear or biadditive multiplicative models for interaction in two-way tables provide the major means for studying genotype by environment interaction problems. In applications the typical accompanying assumptions are those of a normally distributed error and an identity link. These assumptions are unnecessarily restrictive. Introduction of multiplicative terms for interaction in generalized linear models removes these restrictions. Parameter estimates can be obtained by an iterative process of alternating generalized row and column regressions within a quasi-likelihood set-up. The best known examples of this class of generalized additive main effects and multiplicative interaction effects (GAMMI) models are the AMMI models (Gauch, 1988, *Biometrics* **44**, 705–715) and Goodman's RC-association models (Goodman, 1981, *Journal of the American Statistical Association* **76**, 320–334). The multiplicative interaction part of GAMMI models can be visualized through biplots. Two applications of GAMMI models are presented for data coming from plant breeding experiments. The first illustration deals with a log-bilinear model for count data with (extra) Poisson variation. The second illustration concerns a logit-bilinear model for disease incidence data with a special type of variance function, an extension of a model presented by Wedderburn (1974, *Biometrika* **61**, 439–447).

1. Introduction

In recent years there has been a revival of interest in the use of bilinear multiplicative models for interaction in the analysis of two-way genotype by environment tables in plant breeding. For a long time regression on the mean (Yates and Cochran, 1938; Mandel, 1961; Finlay and Wilkinson, 1963) was the most applied technique within this class of models. Work by Gauch and Zobel (Gauch, 1988; Gauch and Zobel, 1988, 1989; Zobel, Wright, and Gauch, 1988), elaborating on earlier work by Gollob (1968), Mandel (1969), and Freeman and Dowker (1973), shifted attention from the rather narrowly applicable regression on the mean model to a class of more versatile models, for which the interaction structure was derived from a singular value decomposition of the matrix of residuals from additivity. Various names are in use for these models, of which the acronym "AMMI" (models) from "additive main effects and multiplicative interaction" (models) is the most popular in the applied literature. Though we will adhere to AMMI model below, names like bilinear model (Gabriel, 1978; Denis, 1991), or, recently, biadditive model (Denis and Gower, 1992, 1994) probably reflect more accurately the structure of the model.

AMMI models represent an observation as consisting of a systematic component that includes the main effects, as well as one or more multiplicative interaction terms, besides a random component for residual variation or "error". In the context of plant breeding, the error term is generally assumed to be normally distributed. AMMI models perform well for a broad class of problems, especially when continuous variables like plant length are involved. However, for variables like disease or pest incidence on a plant, the appropriateness of AMMI models with normal error terms becomes doubtful. Such variables are typically non-normal, and when modeled by an AMMI model, heterogeneity of variance may be dealt with inadequately, while the scale of prediction may be equally unsatisfactory. Both phenomena may necessitate the inclusion of extra interaction terms.

Sometimes overriding reasons are postulated for modeling the response on the scale of observation, although this scale is apt to create problems of the above types. In these cases the scale

Key words: AMMI model; Biadditive model; Bilinear Model; Biplot; Disease resistance; GAMMI model; Genotype by environment interaction; GLM; Interaction; Plant breeding; Two-way table.

problem is solved by accepting the scale, whereas heterogeneity of variance is modeled by one or more extra multiplicative terms for interaction (Johnson and Graybill, 1972; Snijders and van Eeuwijk, 1991). When no such reasons to insist on the scale of observation can be formulated, transformation of the response may decrease scale problems. A linear or bilinear model is fitted to the transformed data, and distributional properties of the residuals are assumed to comply with those of the normal distribution.

An important aim of modeling is to provide an interpretation of the phenomenon under study, expressed in words appropriate to the area of application. Transformation may be omitted in some cases when heterogeneity of variance can be modeled by means of extra multiplicative terms in the systematic part of the model. However, for non-normal data modeled on the scale of observation, multiplicative interaction terms will very likely reflect both heterogeneity of variance and "real" multiplicative interaction (Snee, 1982; Hinkley, 1985). Transformation of the data on the scale of observation does not guarantee full disentanglement of these quantities. In the case of linear regression or analysis of variance a transformation is expected to produce homogeneity of variance, approximate normality of errors, and additivity of systematic effects. One transformation will seldom meet all three requirements. For example, for count data which follow a Poisson distribution and whose systematic effects are multiplicative, the square root transformation will achieve approximate constancy of variance, the power transformation with power two-third will provide approximate symmetry or normality, and the log transformation will produce additivity of the systematic effects. Thus, even after transformation of the data, estimated multiplicative terms are likely to reflect mixtures of heterogeneity of variance and multiplicative interaction.

Independent modeling of the systematic and random parts is needed, as in generalized linear models (GLMs). For GLMs, additivity of systematic effects can be specified on a transformed scale. Normality and constancy of variance are no longer required, because within a quasi-likelihood context (Wedderburn, 1974; McCullagh and Nelder, 1989) only the relation between mean and variance needs to be specified. A serious omission in the theory of GLMs is that little attention has been given to the incorporation of multiplicative terms for interaction.

Multiplicative models for interaction bridge the gap between the main effects model, in ANOVA as well as GLM sense, and the full interaction model with an interaction parameter for every cell in the two-way table (van Eeuwijk, 1992a). They also offer a means of visualizing the main features of interaction in low dimensional space (Gabriel, 1971; Kempton, 1984). Therefore, extension of the GLM theory by incorporating multiplicative terms for interaction is important. A first move in that direction, which related directly to GLM theory, was given by Pettitt (1989), who showed how Tukey's one-degree-of-freedom test for non-additivity (Tukey, 1949) can be generalized to the GLM context. Of more relevance is the work by Goodman (1981, 1986, 1991) on two-way tables of counts, termed RC-tables, though this emphasizes log-linear models. Here, Goodman's work will be expanded to the wider class of GLMs. The same iterative procedure can be used for all GLMs to estimate both additive main effects and multiplicative interaction effects. The method also works for incomplete tables.

In Section 2 the main features of GLMs and AMMI models will briefly be described. Section 3 contains the model description for a GAMMI model plus a description of an estimation procedure for its parameters, and some comments on the assessment of the number of multiplicative terms to retain. Section 4 describes Goodman's RC-association model as a special case of a GAMMI model. Section 5 deals with biplots as a means to visualize the interaction in GAMMI models. A first application is given in Section 6; a log-linear model with multiplicative interaction effects, or log-bilinear model, for count data. A second example, Section 7, deals with a logit-bilinear model for incidence data, consisting of proportions between 0 and 1. A discussion, Section 8, will end the paper.

2. GLMs and AMMI Models

In a GLM for the random variable y the known link function $g(\cdot)$ transforms the expectation of y , $\mathcal{E}(y) = \mu$, to the linear predictor $\eta = \mathbf{x}^T \boldsymbol{\beta}$, where the vector \mathbf{x} contains the values of the independent variables and the vector $\boldsymbol{\beta}$ the unknown parameters (McCullagh and Nelder, 1989). A quasi-likelihood setting will be adopted, so that the variance of y , $\text{var}(y)$, equals $\phi V(\mu)$, with ϕ the dispersion parameter and $V(\cdot)$ the variance function (Wedderburn, 1974). As shown by Wedderburn the estimates for the parameters $\boldsymbol{\beta}$, collected in $\boldsymbol{\beta}$, can be obtained by an iteratively reweighted linear regression of a linearized form of the link function applied to the observations, y , on the independent variables, \mathbf{x} . This linearized form of the link, the link-adjusted dependent variate z , has the form $z = \eta + (y - \mu) \delta\eta/\delta\mu$. The weighting variate, w , is defined by $w = 1/\text{var}(z) = (\delta\mu/\delta\eta)^2/V(\mu)$. For each cycle of the iterative process the values for z and w are updated. The system

of quasi-likelihood equations that is solved by the iteratively reweighted regression can be written as $\Sigma [(y - \mu)/V(\mu)] \delta\mu/\delta\beta_i = 0$.

The AMMI model for a random variable y_{ij} occurring in row i and column j of a two-way table reads

$$\mathcal{E}(y_{ij}) = \nu + \alpha_i + \beta_j + \sum_{k=1}^K \sigma_k \gamma_{ki} \delta_{kj}, \quad (1)$$

with ν the general mean, α_i the additive row effect ($i = 1, \dots, I$), and β_j the additive column effect ($j = 1, \dots, J$). Both main effects have sum to zero identifiability constraints. The interaction consists of a sum of multiplicative terms, often loosely referred to as axes, whose number, K , is less or equal to the rank of the matrix of residuals from additivity, the latter being the minimum of $I - 1$ and $J - 1$. The multiplicative interaction parameters for the rows, also row scores, are denoted by γ_{ki} , with k indicating the axis and i the row. The column scores are denoted by δ_{kj} , with k the axis and j the column. The singular value corresponding to axis k is represented by σ_k . It can be interpreted as a measure of association between row and column scores, and indicates the importance of the axis. Squares of singular values, eigenvalues, are equal to the sum of squares explained by an axis. Identifiability constraints for the multiplicative terms include sum to zero and orthonormality. Testing is usually based on the assumption of normality.

3. GAMMI Models

The generalized form for the structural part of the AMMI model follows straightforwardly from its model formulation in (1);

$$\eta_{ij} = \nu + \alpha_i + \beta_j + \sum_{k=1}^K \sigma_k \gamma_{ki} \delta_{kj}. \quad (2)$$

Adopting quasi-likelihood, a wide range of variance functions comes available for modeling the random component. An AMMI model is a GAMMI model with identity link and constant variance.

Fixing the values of β_j and δ_{kj} reduces model (2) to a GLM over the rows, whereas fixing the values of α_i and γ_{ki} reduces model (2) to a GLM over the columns. This property of the GAMMI model can serve as the basis for an estimation procedure for the parameters.

The following alternating GLM procedure, using iteratively reweighted least squares, provides estimates for the parameters of the GAMMI model with specified link and variance function. (A Genstat procedure doing the required calculations is available upon request from the author.)

3.1 Forming Initial Values for the Column Main and Interaction Effects

When a GAMMI model with K axes is to be fitted and no results are available from fits with $M < K$ axes, fit a main effects model to the two-way table, $\eta_{ij} = \nu + \alpha_i + \beta_j$, and save the estimates $\hat{\beta}_j$ of the column main effects. Also choose arbitrary column scores, $\hat{\delta}_{kj}$, for the axes 1 to K . These scores must not be all equal, and should be standardized and orthonormalized;

$$\sum_{j=1}^J \hat{\delta}_{kj} = 0, \quad \sum_{j=1}^J \hat{\delta}_{kj}^2 = 1, \quad \text{for } k = 1, \dots, K,$$

$$\sum_{j=1}^J \hat{\delta}_{kj} \hat{\delta}_{k'j} = 0, \quad \text{for } k \neq k'.$$

When parameter estimates are available for GAMMI models with $M < K$ axes, the values of $\hat{\beta}_j$ and $\hat{\delta}_{kj}$, with k now from 1, \dots , M , can be used as initial values for the GLM of the next step. For the $\hat{\delta}_{kj}$ values belonging to the axes $M + 1$, $M + 2$, \dots , K , arbitrary values can again be chosen.

3.2 Estimating the Row Main and Interaction Effects

Put $b_j = \hat{\beta}_j$, and $d_{kj} = \hat{\delta}_{kj}$, and fit the row regression

$$\eta_{ij} = \nu + \alpha_i + b_j + \sum_{k=1}^K \gamma_{ki} d_{kj}.$$

The values of b_j are supposed to be known and do not need to be estimated. They are called offsets in Genstat and GLIM. The d_{kj} values represent concomitant variables on the column factor. The parameters α_i and $\gamma_{1i}, \gamma_{2i}, \dots, \gamma_{Ki}$ are the intercept and slopes for the regression of the entries of row i on the variables d_1, d_2, \dots, d_K . The row main effects, $\hat{\alpha}_i$, need not necessarily be centered within the iteration process, this may just as well be done after convergence. In a package like Genstat this amounts to omitting the constant from the fitting process.

3.3 Centering and Orthogonalizing the Row Interaction Effects

$$\sum_{i=1}^I \hat{\gamma}_{ki} = 0, \quad \text{for } k = 1, \dots, K,$$

$$\sum_{i=1}^I \hat{\gamma}_{ki} \hat{\gamma}_{k'i} = 0, \quad \text{for } k \neq k'.$$

3.4 Estimating the Column Main and Interaction Effects

Put $a_i = \hat{\alpha}_i$ and $c_{ki} = \hat{\gamma}_{ki}$, and fit the column regression

$$\eta_{ij} = \nu + a_i + \beta_j + \sum_{k=1}^K c_{ki} \delta_{kj}.$$

Now the a_i values form offsets, while the c_{ki} values represent concomitant variables on the row factor. The parameters β_j and $\delta_{1j}, \delta_{2j}, \dots, \delta_{Kj}$ are the intercept and slopes for the regression of the entries of column j on the variables c_1, c_2, \dots, c_K . Again, there is no need to center the column main effects, β_j , within the procedure.

3.5 Standardizing and Orthonormalizing the Column Interaction Effects

For the calculations involved in the standardization and orthonormalization of the column interaction effects, see Section 3.1. If convergence has occurred, stop, otherwise go back to Section 3.2 using the values for $\hat{\beta}_j$ and $\hat{\delta}_{kj}$ from Sections 3.4 and 3.5.

Change in deviance of either or both the row and column regression can be used as the convergence criterion, or changes in estimates of either or both row and column parameters. Upon convergence the residual deviance of the row regression will be equal to that of the column regression. Estimates are maximum quasi-likelihood estimates.

After convergence, $\sum_{i=1}^I \hat{\gamma}_{ki}^2$ will be equal to the "eigenvalue" corresponding to axis k , that is the square of the "singular value", σ_k . The parameter σ_k represents a general association parameter, a generalized singular value. Except for the AMMI model case there seems to be no simple relation between the amount of deviance corresponding to axis k and the square of the singular value.

The number of multiplicative terms to be retained in GAMMI models can be assessed by generalizing well-known tests for AMMI models. First, there are the likelihood ratio tests for the first eigenvalue (Johnson and Graybill, 1972), for the second given the first (Hegemann and Johnson, 1976) and for subsequent eigenvalues (Yochmowitz and Cornell, 1978). These tests compare the percentage explained by a particular term with the total amount still to be explained, and do not need an estimate for error (over-/under-dispersion). They were shown to perform well in simulations by Williams and Wood (1993), and Cornelius (1993), but require special tables of critical values, which have been developed only for certain combinations of row and column numbers.

Well performing F -tests that do not require special tables and are easy to calculate were described by Cornelius (1993). An independent estimate of error (over-/under-dispersion), however, is necessary, and this may cause problems (Milliken and Johnson, 1989, p. 3).

A simple test, proposed by Gollob (1968), attributes $(I - 1) + (J - 1) - (2k - 1)$ degrees of freedom to the eigenvalue corresponding to axis k , this being the difference between the number of parameters to be estimated and the number of identification constraints imposed. (Goodman (1981) arrived at an equivalent number of degrees of freedom for the interaction terms in log-bilinear models.) The corresponding mean square is then tested against an estimate of error (under-/over-dispersion). For AMMI this procedure is too liberal under the null hypothesis of no interaction (Williams and Wood, 1993). However, in the presence of multiplicative interaction which clearly dominates noise, Gollob's rule has been shown to be satisfactory (Goodman and Haberman, 1990; Gauch, 1992). Thus, when the first eigenvalue(s) are particularly large relative to the remainder, it

is safe to attribute degrees of freedom following Gollob and pool the remaining terms for an estimate of error (under-/over-dispersion). Sequential application of this procedure, testing successive eigenvalues against pooled error estimates, usually works quite satisfactorily. Furthermore, testing seldom needs to be extended to more than the first three eigenvalues, as, in practice, there are rarely grounds for including more than two axes (Milliken and Johnson, 1989, p. 48). As a check, the sizes of multiplicative effects may be inspected when deciding on whether a particular term should be retained. Note that addition of another multiplicative term for GAMMI models requires recalculation of the terms already included. Because of differential cell weighting, successive dimensionalities are not nested in the way they are for AMMI models with equal cell weighting.

Residuals for diagnostic purposes can, after convergence, be obtained from the row regression as well as the column regression. Row and column regression residuals will deviate slightly from each other, because the calculation of the row regression residuals assumes that the column parameters are known rather than estimated, while for the column regression residuals the estimation of the row parameters is similarly ignored. In practice, however, differences between both types of residuals are small. Another possibility is to create regressors from the products of row and column interaction parameters in the same way as Tukey's one-degree-of-freedom test for non-additivity can be given a regression interpretation (Snedecor and Cochran, 1980, Ch. 15.8), and fit a model with main effects and these regressors. The residuals from this model are a compromise between those of the row regression and the column regression. In Sections 6 and 7, describing applications, reference will be made to this last type of residuals.

4. The RC Association Model as an Example of a GAMMI Model

A second example of a class of GAMMI models, besides the AMMI models, consists of Goodman's RC association models for $I \times J$ tables of counts (Goodman, 1979, 1981, 1986, 1991). These models assume either a multinomial distribution that applies to the whole of the $I \times J$ table, or a multinomial distribution that applies to each of the I rows independently, or to each of the J columns independently, or a Poisson distribution that applies to each of the $I \times J$ cells independently. Let P_{ij} be the probability for an observation to fall in the i th row and j th column of the table, then

$$P_{ij} = \alpha_i \beta_j \exp \left(\sum_{k=1}^K \sigma_k \gamma_{ki} \delta_{kj} \right), \quad (3)$$

represents the RC association model, with α_i and β_j being positive parameters. As identification constraints for the multiplicative interaction terms, Goodman (1991, p. 1094) advises to use the same constraints as for the AMMI model when the marginals are not fixed (unweighted association), and to make identification dependent on the marginals in case of fixed marginals (weighted association).

By taking logarithms, model (3) is transformed to the equivalent log-bilinear model,

$$\eta_{ij} = \log(P_{ij}) = \nu + \alpha_i + \beta_j + \sum_{k=1}^K \sigma_k \gamma_{ki} \delta_{kj}, \quad (4)$$

which can be identified as a GAMMI model with a logarithmic link function. The main effects of (4) are, of course, the logarithmic transforms of those in (3).

5. Visual Displays of Interaction by Means of Biplots

Biplots constitute a powerful tool for displaying interaction which is described by the multiplicative terms in an AMMI model (Gabriel, 1971; Kempton, 1984). In a biplot, rows and columns are represented by points in two- or three-dimensional space. The coordinates of the points are determined by the row and column scores. The singular values are allocated to the row and column scores in different ways depending on whether the interest is in the relations between the rows, between the columns, or between the rows and columns. When, for AMMI models, the row scores $\gamma'_{ki} = \gamma_{ki} \sigma_k$ are plotted, distances between row points are proportional to the amount of interaction between the rows (Kempton, 1984). Plotting δ'_{kj} , with $\delta'_{kj} = \delta_{kj} \sigma_k$, transfers this relation to the column points. After considering the row and column points as the end points of vectors starting at the origin, simple geometry can show that the amount of interaction, or non-additivity, between a row and column can be approximated by the inner product between their vectors in the biplot. This inner product can be determined from a biplot by projecting either row or column vector on the other, and then multiplying the length of the projection with the length of the vector on which projection takes place.

For the broader class of GAMMI models, it is still possible to visualize the interactions by means of biplots, but their interpretation depends on the particular link function.

For RC association models it is the form of non-independence rather than non-additivity, that is relevant. Goodman (1991) defines two forms of non-independence.

First, where

$$\lambda_{ij} = \log\left(\frac{P_{ij}}{\alpha_i \beta_j}\right) = \sum_{k=1}^K \sigma_k \gamma_{ki} \delta_{kj},$$

and second, the log-odds ratio,

$$\pi_{ij} = \log\left(\frac{P_{ij}P_{st}}{P_{it}P_{sj}}\right) = \sum_{k=1}^K \sigma_k (\gamma_{ki} - \gamma_{ks})(\delta_{kj} - \delta_{kt}),$$

defined for the cells in the rows i and s , and the columns j and t . The scaled row parameter $\gamma'_{ki} = \gamma_{ki}\sigma_k$, can be interpreted as the slope of a weighted linear regression of the non-independence measure λ_{ij} on the column scores, δ_{kj} : $\sum_{j=1}^J \lambda_{ij}\delta_{kj} = \gamma'_{ki}$. When the γ'_{ki} are used as coordinates for the row points in a biplot, the squared distance between two row points approximates the non-independence between the two rows, because

$$\sum_{k=1}^K (\gamma'_{ki} - \gamma'_{ks})^2 = \sum_{j=1}^J (\lambda_{ij} - \lambda_{sj})^2.$$

Similar relations can be deduced for δ'_{kj} and γ_{ki} . Therefore, Goodman (1986, p. 269; 1991, p. 1107) recommends for displays of row points alone to use $\gamma'_{ki} = \gamma_{ki}\sigma_k$, and for column points alone $\delta'_{kj} = \delta_{kj}\sigma_k$.

For simultaneous displays, the recommendation is to use $\gamma^*_{ki} = \gamma_{ki}\sigma_k^{1-c}$ and $\delta^*_{kj} = \delta_{kj}\sigma_k^c$ ($0 \leq c \leq 1$), where choice of c depends on whether the emphasis is on rows or columns. The inner product of row and column points in a simultaneous biplot approximates the non-independence measure λ_{ij} when γ and δ are scaled as γ^* and δ^* , as can be seen from

$$\begin{aligned} \lambda_{ij} &= \log\left(\frac{P_{ij}}{\alpha_i \beta_j}\right) = \\ &= \sum_{k=1}^K \sigma_k \gamma_{ki} \delta_{kj} = \sum_{k=1}^K \gamma^*_{ki} \delta^*_{kj} = |\boldsymbol{\gamma}^*_i| |\boldsymbol{\delta}^*_j| \cos(\boldsymbol{\gamma}^*_i, \boldsymbol{\delta}^*_j), \end{aligned} \quad (5)$$

where $\boldsymbol{\gamma}^*_i$ and $\boldsymbol{\delta}^*_j$ denote vectors of length K . In the same biplot, the inner product of a difference of row points with a difference of column points approximates the log-odds ratio

$$\begin{aligned} \pi_{ij} &= \log\left(\frac{P_{ij}P_{st}}{P_{it}P_{sj}}\right) = \sum_{k=1}^K \sigma_k (\gamma_{ki} - \gamma_{ks})(\delta_{kj} - \delta_{kt}) \\ &= \sum_{k=1}^K (\gamma^*_{ki} - \gamma^*_{ks})(\delta^*_{kj} - \delta^*_{kt}) = |\boldsymbol{\gamma}^*_i - \boldsymbol{\gamma}^*_s| |\boldsymbol{\delta}^*_j - \boldsymbol{\delta}^*_t| \cos(\boldsymbol{\gamma}^*_i - \boldsymbol{\gamma}^*_s, \boldsymbol{\delta}^*_j - \boldsymbol{\delta}^*_t), \end{aligned} \quad (6)$$

with $\boldsymbol{\gamma}^*_i$, $\boldsymbol{\gamma}^*_s$, $\boldsymbol{\delta}^*_j$, and $\boldsymbol{\delta}^*_t$ vectors of length K . Simultaneous biplots thus provide a powerful tool for visualizing non-independence in two-way tables of counts analyzed by means of RC association models.

For other GAMMI models the interpretation of the biplot relations has still to be investigated. Nevertheless, distances between points of either rows or columns will always indicate some form of non-additivity or non-independence. Simultaneous displays should be interpreted with more care, but here the inner products of row and column points will still approximate non-additivity on the linear predictor scale.

6. An Application of a Log-Bilinear Model to Counts of Potato Cyst Nematodes on Potatoes

Table 1 gives the number of newly formed cysts on 11 potato genotypes for five potato cyst nematode populations belonging to the species *Globodera pallida* (part of a larger table in Arntzen and van Eeuwijk (1992)). The numbers are means over four or five replicates. An assessment of the genetic similarity of the potato cyst nematode populations was required. We will concentrate mainly on illustration of the possibilities for modeling and visualizing the interaction with an appropriate GAMMI model.

Table 1
Mean number of cysts of five nematode populations on eleven potato genotypes

Potato genotype	Nematode population				
	P2-22	Rookmaker	75-884-4	74-768-20	1077
12380	2.8	18.6	5.6	136.8	8.2
Vantage	2.6	31.8	5.4	107.2	17.0
AM78-3778	4.5	5.25	2.0	9.8	6.2
(VT ⁿ) ² 62-33-3	19.6	96.2	85.4	307.0	29.4
Desiree	333.0	402.6	339.0	549.6	374.0
Maritta	421.0	426.8	221.8	630.4	260.8
Astarte	118.4	122.4	145.4	102.4	106.2
Elles	3.6	58.0	43.8	123.4	9.6
Pansta	23.4	199.0	208.4	83.8	104.6
Mara	134.2	216.0	257.2	277.4	204.4
Saturna	269.0	384.6	361.6	477.8	356.8

Using the alternating GLM algorithm described above, a sequence of nested models was fitted. The link function was chosen to be the natural log and the distribution to be the Poisson distribution. The differences in deviance corresponding to the inclusion of individual terms are given in Table 2.

Table 2
Deviance table for nematode data

Source	Degrees of freedom	Deviance	Mean deviance
PCN population	4	690.57	127.64
Potato genotype	10	7111.38	711.14
Axis 1	13	715.96	55.07
Axis 2	11	351.10	31.92
Axis 3	9	43.72	4.86
Residual	7	34.62	4.94
Total	54	8947.35	

The criterion for inclusion of a multiplicative interaction term (axis) was an *F*-test for the ratio of the mean deviance for the particular interaction term to a current estimate for the over-dispersion, the latter being either the mean deviance of the rest or Pearson’s chi-square divided by the residual degrees of freedom:

$$\left\{ \sum_i \sum_j \frac{(y_{ij} - \hat{\mu}_{ij})^2}{\hat{\mu}_{ij}} \right\} / df_{\text{residual}}$$

In the following examples, the difference between these estimators for over-/under-dispersion was negligible. The estimate for the over-dispersion for the model with three multiplicative axes on the basis of the residual deviance was 4.94; on the basis of Pearson’s chi-square it was 5.05. Table 2 shows that a model with two axes (GAMMI-2 model) was satisfactory, because the ratio of the mean deviance for the third axis to the residual mean deviance for a model with three axes was 4.86/4.94 = .98, which is not significant when compared with the $P \leq .05$ point of an $F_{[9;7]}$ distribution. The residual deviance estimate for over-dispersion for the GAMMI-2 model was $(43.72 + 34.62)/(9 + 7) = 4.90$; the Pearson chi-square estimate was 4.91. Plots of Pearson and deviance residuals against fitted values and linear predictor values revealed no severe anomalies. A plot of the link-adjusted dependent variate,

$$z = \left[\eta + (y - \mu) \frac{d\eta}{d\mu} \right]_{\hat{\eta}, \hat{\mu}},$$

against the linear predictor, $\hat{\eta}$, can indicate the inappropriateness of the link function when clear deviations from linearity occur (McCullagh and Nelder, 1989, Chap. 12). However, no deviations from linearity were observed. Hence the GAMMI-2 model with log link and Poisson distribution appeared to fit the data well.

To enhance interpretation, a simultaneous biplot was made with the constant $c = .5$ (Figure 1). The association parameters for the two axes were 3.54 and 2.23, respectively. (For GAMMI-3 the parameters were 3.54, 2.30, and 0.52, illustrating the lack of orthogonality of the axes and the unimportance of the third axis.) For AMMI models the correlations between main effects and interaction scores can be used to diagnose models with a simpler structure. When, for example, only one axis is significant and its environmental scores are highly correlated with the environmental main effects, a regression on the environmental mean model (Yates and Cochran, 1938; Mandel, 1961; Finlay and Wilkinson, 1963) gives an adequate description of the data. For our potato cyst data the main effect for the nematode populations was correlated almost completely with the scores on the first axis, $r = .999$. In contrast, the genotype scores for axis 1 were only modestly correlated with the genotypical main effect. In combination this means that the first axis of the interaction could be of the "Finlay-Wilkinson type," i.e., the nematode population main effect reflects some aspect of the environment toward which the potato genotypes differ in sensitivity. Axis 2 would then represent some other aspect of the environment not addressed by the first axis. Although this is an appealing interpretation, one must be cautious about interpreting axes separately. We are dealing with a lower rank representation of a phenomenon of which it would be rather unlikely, although not impossible, that environmentally important directions coincide with axes whose estimation is

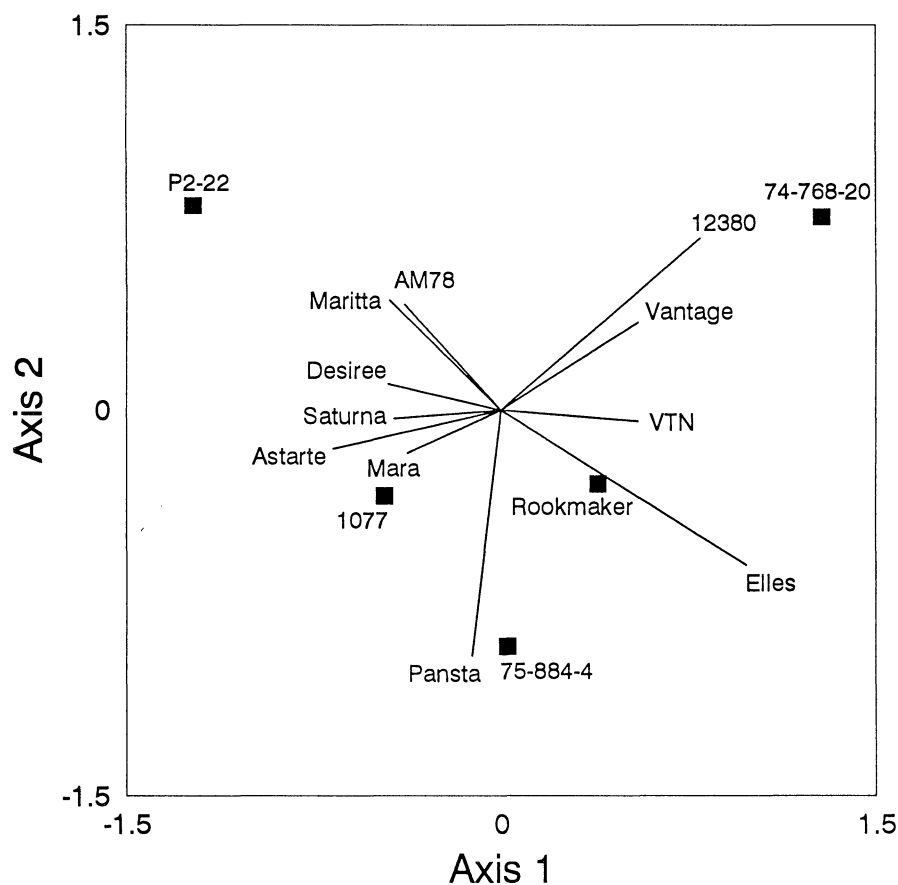


Figure 1. Biplot of the interaction in nematode data from GAMMI-2 model with log link and over-dispersed Poisson distribution. Nematodes populations are represented by squares; potato genotypes by lines.

determined solely by a mathematical criterion. Therefore, it is better to consider the biplot of Figure 1 as a whole.

Considering Figure 1 as a whole, the nematode cyst populations are located roughly on a parabola from top left via bottom middle to top right in order of aggressiveness, the potential to form cysts on potatoes, irrespective of the genotype of the potato. Along the same parabola, the potato genotypes, with the exception of AM78, are ordered from susceptible to resistant.

The biplot for the interaction of the log-bilinear model can conveniently be used for finding pairs of potato genotypes and pairs of nematode cyst populations with an odds-ratio of unity, or a log-odds ratio of zero. As an example, consider the genotypes 12380 and Mara in combination with the cyst populations P2-22 and 75-884-4. The line through the genotypes in Figure 1 is orthogonal to the line through the cyst populations, indicating a zero log-odds ratio. From Table 1 it can be verified that the odds-ratio is indeed close to one.

7. A Logit-Bilinear Model for *Fusarium* Head Blight Incidence in Winter Wheat

In the classical introductory paper on quasi-likelihood, Wedderburn (1974) illustrated the method with barley disease incidence data consisting of percentages of leaf area affected by leaf blotch. Wedderburn used a quasi-likelihood model with logit link and variance function $V(\mu) = \mu^2(1 - \mu)^2$, in which μ was expressed as a proportion. We will illustrate for wheat disease incidence data how that model can be extended usefully by including multiplicative terms for interaction.

Data are taken from Snijders and van Eeuwijk (1991, Table 1) and are reproduced in Table 3. They consist of assessments of the percentage of leaf area affected by *Fusarium* head blight for 17 winter wheat genotypes. The genotypes were inoculated by four *Fusarium* head blight strains over a period of 3 years. Year-Strain combinations, 12 in number, together defined the environmental dimension of the genotype by environment table. The entries of Table 3 are averages over replications within years. The main research question with respect to these data was whether the winter wheat genotypes exhibited so-called horizontal resistance (Vanderplank, 1984). This broadly means that susceptibility of genotypes does not depend on the strain of the pathogen, with the statistical implication of non-existence of interaction between genotype and pathogen.

Table 3

Incidence data (%) on 17 winter wheat genotypes for four strains of Fusarium culmorum over 3 years. SVP-line code: first two digits indicate year of crossing; next three, crossing number; after hyphen, selection number. (From Snijders and van Eeuwijk, 1991, Table 1).

Wheat genotype	1986				1987				1988			
	IPO 39-01	329-01	348-01	436-01	39-01	329-01	348-01	436-01	39-01	329-01	348-01	436-01
SVP 72017-17-5-10	2.0	1.5	3.0	1.5	7.3	.8	.5	2.1	5.3	2.7	2.0	2.7
SVP 77076-4	9.0	1.0	3.0	1.5	13.5	.3	.1	.2	7.0	1.7	3.3	3.7
Arina	8.0	2.5	5.0	4.0	12.0	.3	.1	2.8	6.3	1.0	2.0	3.3
SVP 77076-38	18.0	1.0	4.5	7.0	8.9	.2	.1	.7	2.0	2.3	1.3	1.7
SVP 77076-1	6.0	3.0	1.0	1.5	11.1	.1	.4	2.7	7.0	4.7	5.0	8.3
Saiga	4.5	7.5	4.5	9.0	15.5	1.1	.3	1.7	9.3	9.7	6.0	11.7
SVP 77078-30	9.0	13.0	1.0	2.5	17.8	.6	.4	8.4	15.7	5.3	3.3	4.7
SVP 72003-4-2-4	23.5	4.0	9.5	3.5	16.3	.7	.4	1.4	5.0	6.3	7.3	13.7
SVP 77079-15	27.5	4.5	2.5	8.5	35.2	1.9	.5	5.8	3.3	6.3	4.0	8.3
SVP 75059-28	11.0	3.5	3.0	1.5	54.0	1.2	1.2	19.3	4.0	2.7	1.3	6.3
SVP 73030-8-1-1	60.0	7.0	7.5	9.0	36.3	3.0	5.0	7.5	13.0	4.7	5.0	5.7
SVP 73016-2-4	47.0	18.0	14.5	22.5	44.1	5.4	3.5	11.6	6.7	12.5	3.3	4.0
SVP 73012-1-2-3	67.5	16.0	17.5	17.0	34.2	7.0	2.5	9.3	11.0	9.0	6.0	25.7
SVP 75059-46	25.5	5.0	5.0	10.5	69.3	5.0	1.7	13.2	30.0	22.3	20.0	20.3
Nautica	62.5	20.5	20.0	30.5	32.2	1.3	.8	4.8	40.0	25.0	18.0	20.3
SVP 75059-32	32.5	5.0	9.0	42.5	57.3	5.2	4.3	30.5	37.7	14.7	28.3	31.0
SVP 72005-20-3-1	62.5	16.5	27.5	23.0	58.5	3.7	2.7	21.7	36.7	26.3	13.3	20.3

Data were first transformed to logits and analyzed by an AMMI model. An analysis of variance (Table 4) shows the AMMI-2 model to be satisfactory. From a biplot of the interaction (Figure 2), it can be seen that the interaction was mainly caused by the differential influence of years on the incidence rates for the genotypes, the interaction between genotypes and strains seems relatively unimportant from the biplot; i.e., environments occur in year clusters, not in strain clusters.

The impression that genotype by strain interactions were less important than genotype by year

Table 4
Analysis of variance for AMMI-3 model fitted to two-way table of logit transformed Fusarium head blight incidences in winter wheat

Source	Degrees of freedom	Sum of squares	Mean square
Year-Strain combination	11	224.09	20.37
Wheat genotype	16	171.60	10.73
Axis 1	26	28.17	1.08
Axis 2	24	23.20	0.97
Axis 3	22	9.11	0.41
Residual	104	30.60	0.29
Total	203	486.77	

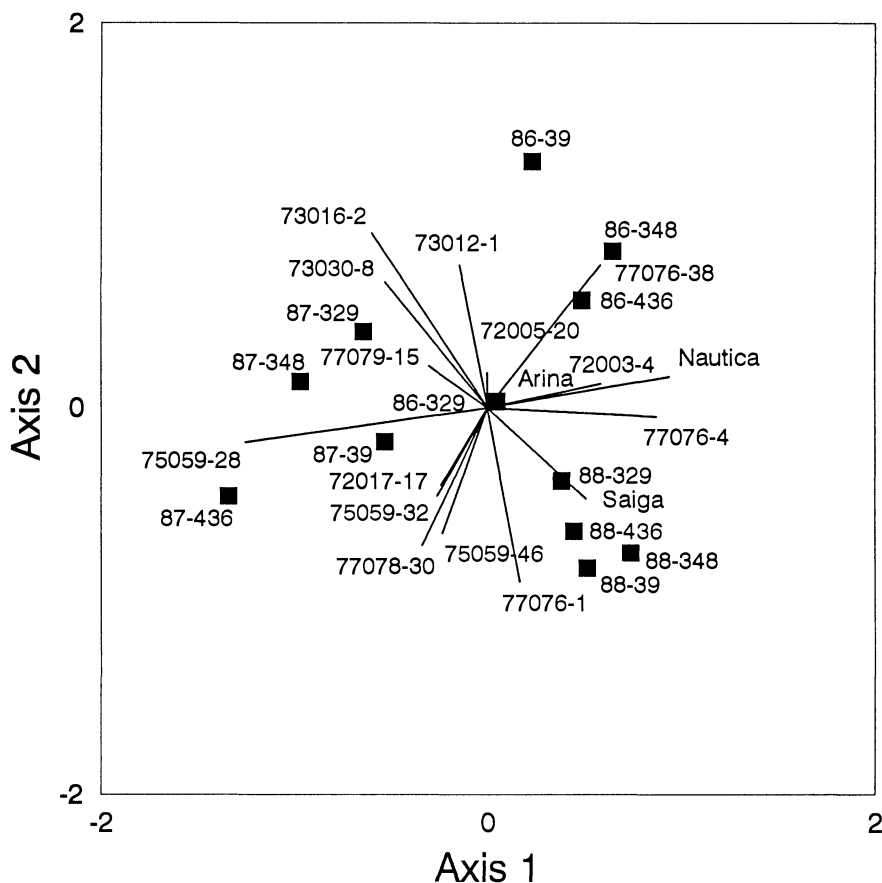


Figure 2. Biplot of the interaction in the *Fusarium* head blight data following from AMMI-2 model on logit transformed data. Year by strain combinations are represented by squares; wheat genotypes by lines.

interactions can be tested somewhat more rigorously by performing a three-way analysis of variance with the factors genotype, strain, and year on the table of mean incidence proportions (logit transformed). As an estimate for the error we used the three-factor interaction. From Table 5 we see that the mean square for the three factor interaction, .33, was almost equal to our estimate for the error derived from the AMMI-2 analysis, $(9.11 + 30.60)/(22 + 104) = .32$. Hence there are good reasons to assume that there was indeed no “real” three-factor interaction. Genotype by strain interaction was not found significant, and the resistance may therefore be classified as horizontal. Furthermore, the conjecture of significant genotype by year interaction is also confirmed by Table 5. The AMMI analysis combined with the three-way ANOVA gives a reasonably clear picture of what is happening. A plot of standardized residuals versus fitted values shows no notable anomalies (Figure 3a).

Next, we analyzed the same data with a GAMMI model with a logit link and a binomial

Table 5
Three-way analysis of variance for logit transformed Fusarium head blight incidences

Source	Degrees of freedom	Sum of squares	Mean square
Year	2	33.89	16.49
Fusarium strain	3	130.25	43.42
Strain-Year	6	59.96	9.99
Wheat genotype	16	171.60	10.73
Genotype-Year	32	43.86	1.37
Genotype-Strain	48	15.31	.32
Error	96	31.91	.33
Total	203	486.77	

distribution. Interaction was again describable by two multiplicative axes. However, a plot of (quasi-) deviance residuals against linear predictor was far from satisfactory (Figure 3b). The situation encountered here is clearly reminiscent of Wedderburn's leaf-blotch data on barley as treated in McCullagh and Nelder (1989, pp. 328–332) (see also Wedderburn, 1974). Therefore, a GAMMI model was fitted with logit link and with variance function $V(\mu) = \mu^2(1 - \mu)^2$, where μ is a proportion. The quasi-likelihood function corresponding to this combination of link and variance function is

$$Q(\mu; y) = \left[(2y - 1) \log \left(\frac{\mu}{1 - \mu} \right) - \frac{y}{\mu} - \frac{1 - y}{1 - \mu} \right] - \left[(2y - 1) \log \left(\frac{y}{1 - y} \right) - 2 \right] / \phi. \quad (7)$$

The function is not defined for $\mu = 0$ or 1 , or $y = 0$ or 1 . We had, however, no observations being equal to 0 or 1 , so will ignore this complication. Because the iterative weights are exactly unity, this type of GLM can be implemented particularly easily in our alternating GLM scheme. For an ordinary, i.e., non-alternating, GLM, an unweighted, but, still iterative, regression can be performed with as dependent variate $z = \hat{\eta} + (y - \hat{\mu})/\hat{\mu}(1 - \hat{\mu})$, in which $\hat{\eta}$ and $\hat{\mu}$ are the last updates for η and μ . The unity weights preserve the orthogonality properties in the iterative regression. These results carry over to our alternating GLM algorithm.

The results in Table 6 of the quasi-likelihood analysis were in close agreement with those of the AMMI analysis on the logit transformed data as given in Table 4. This similarity is also obvious from the comparison of the biplots (Figure 4, $c = .5$, and Figure 2) and the residual plots (Figures 3c and 3a). Table 6 indicates that two axes suffice. The association parameters for the GAMMI-2 model were $\sigma_1 = 5.20$ and $\sigma_2 = 4.57$.

The agreement between the quasi-likelihood analysis and the AMMI analysis on the logit transformed data is not surprising. The logit transform applied to the data themselves worked quite well when judged by its residual plot (Figure 3a), which exhibited good constancy of variance. Besides, a half-normal plot of the residuals (not shown) also was satisfactory, indicating approximate normality. On these grounds it might have been expected that the quasi-likelihood analysis used here would also do rather well. Because for both methods the weights are unity, the only difference between them is the use of a logit transform for the expected values (quasi-likelihood) instead of a logit transform for the observations (AMMI). In other situations the analyses may differ. For example, Wedderburn (1974) found differences, which were caused by observations either very close to one or zero.

8. Discussion

Estimation of main and interaction effects for the AMMI model is simple in case of a complete table, i.e., first fit a two-way ANOVA model to estimate the main effects and subsequently perform a singular value decomposition on the residuals (Gabriel, 1978). For incomplete tables Gabriel and Zamir (1979) proposed an iterative procedure of alternating row and column regressions with unit weights for presence and zero weights for absence. They also presented the idea of using weights inversely related to Poisson variance in the weighted singular value decomposition of a log transformed matrix of counts. This is very close to the GAMMI estimation procedure described in Section 3. In contrast to the fixed weights chosen by Gabriel and Zamir (1979), Gabriel and Odoroff (1984) proposed the use of iterative reweighing in a procedure for a more robust form of singular

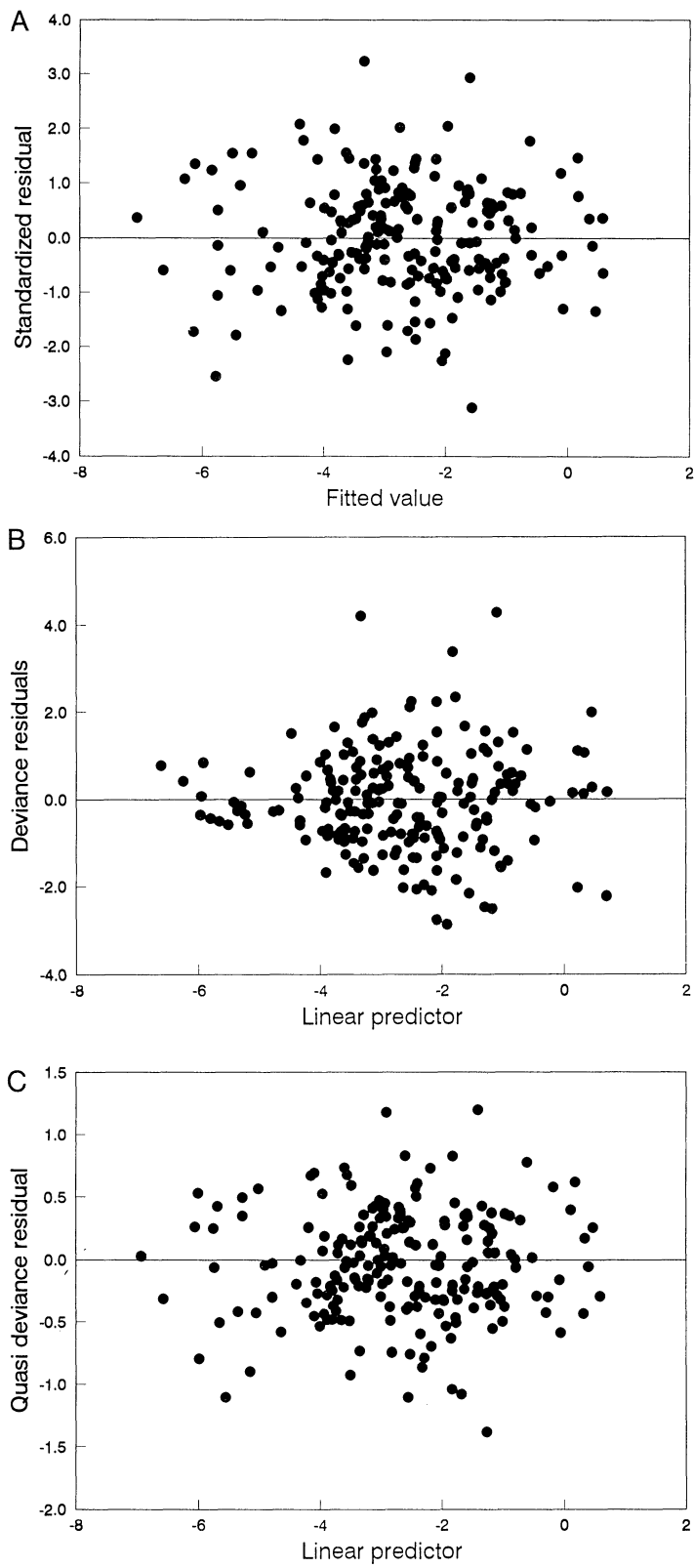


Figure 3. Residual plots for head blight data. (a) Standardized residuals versus fitted values from AMMI-2 model on logit transformed data. (b) Deviance residuals versus linear predictor from GAMMI-2 model with logit link and binomial distribution. (c) Quasi-deviance residuals versus linear predictor for GAMMI-2 model with logit link and variance function $V(\mu) = \mu^2(1 - \mu)^2$ (μ is expressed as a proportion).

Table 6
Quasi-deviance table for Fusarium head blight incidences

Source	Degrees of freedom	Quasi-deviance	Mean quasi-deviance
Year-strain combination	11	150.85	13.71
Wheat genotype	16	145.26	9.08
Axis 1	26	26.13	1.01
Axis 2	24	19.49	.81
Axis 3	22	8.77	.40
Residual	104	29.36	.28
Total	203	379.86	

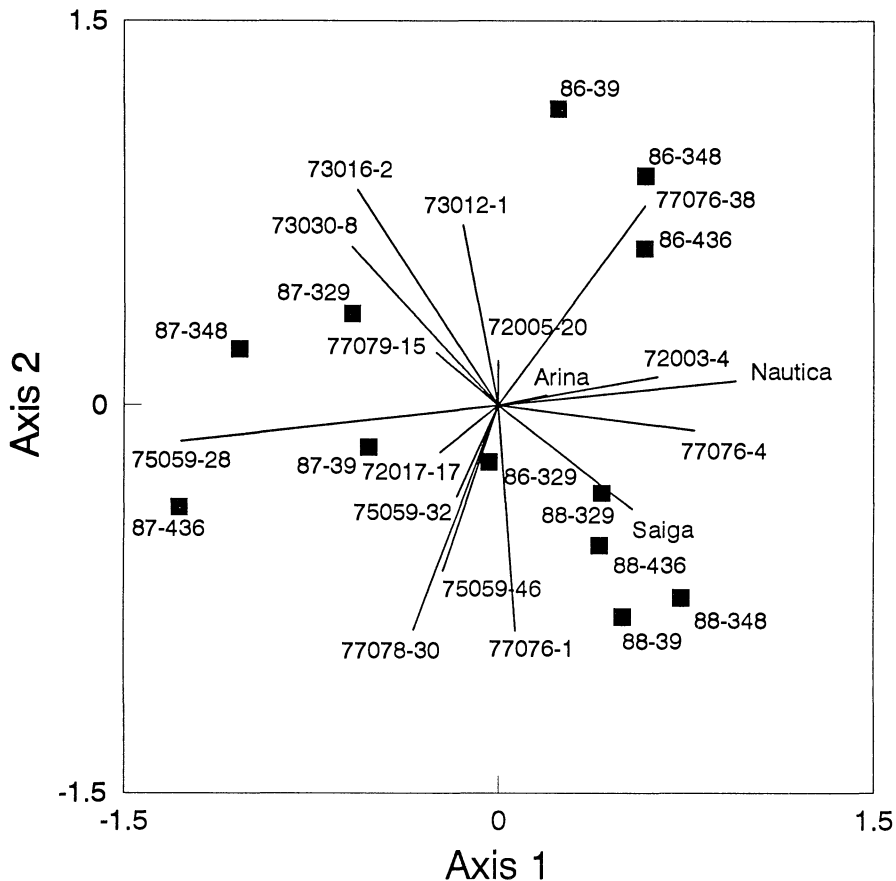


Figure 4. Biplot of the interaction in the *Fusarium* head blight data following from GAMMI-2 model with logit link and variance function $V(\mu) = \mu^2(1 - \mu)^2$ (μ is expressed as a proportion). Year by strain combinations are represented by squares; wheat genotypes by lines.

value decomposition. McNeil and Tukey (1975) elaborated a similar idea in the context of the diagnosis of models for two-way tables.

Though Gabriel and Zamir (1979) were already close to the use of alternating GLMs, Pettitt (1989) seems the first to explicitly propose iteration of alternating GLMs in a generalization of Tukey's one-degree-of-freedom test for non-additivity, which can be interpreted as a test for the presence of a restricted form of multiplicative interaction, namely the form for which there is only one multiplicative term and for which the row and column scores are proportional to the row and column main effects. In contrast to Pettitt, who left the possibilities for generalization to GAMMI unexplored, De Falguerolles and Francis (1992) acknowledged the possibility of using alternating GLMs for estimation of row and column parameters for a multiplicative interaction model. Their brief description, however, ignored the necessity of using offsets.

The use of offsets is essential for arriving at the maximum quasi-likelihood solution. Otherwise row and column regressions may reach different maxima, and the iterative scheme will continue

cycling between these two maxima. For weighted AMMI estimation (Gabriel and Zamir, 1979) the use of offsets reduces to subtraction of the column effects before the row regression and vice versa. Failure to use offsets will inevitably lead to convergence problems as observed by Gabriel and Zamir. Denis (1991) described an alternating least squares algorithm for weighted AMMI estimation including offsets.

The alternating GLM scheme can be extended to cover another generalization of the AMMI model; the reduced rank regression model (Davies and Tso, 1982; van Eeuwijk, 1992b). Reduced rank regression models can be derived from AMMI models by imposing the restriction on the scores that they have to be linear combinations of explicitly measured variables (Rao, 1964). AMMI model interaction scores can be forced to be linear combinations of explicitly measured variables simply by regressing them on the relevant variables. Thus row scores, γ_{ki} , are replaced by their fitted values from a regression on the appropriate explanatory variables between steps 2 and 3 (Sections 3.2 and 3.3) of the estimation scheme. Column scores, δ_{kj} , are likewise replaced by their fitted values between steps 4 and 5 (Sections 3.4 and 3.5). The generalization of reduced rank regression to generalized reduced rank regression will be obvious. With this generalization a wide range of techniques from AMMI analysis to the RC association model analog of canonical correspondence analysis (Ter Braak, 1986) can be covered by the same estimation procedure.

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RÉSUMÉ

Les modèles multiplicatifs bilinéaires ou biadditifs d'interaction dans des tableaux à deux facteurs fournissent les moyens essentiels d'étude des problèmes d'interaction genotype environnement. Dans les applications, les suppositions classiques sont celles d'une erreur Normalement distribuée et d'une fonction d'identité de lien. Elles sont inutilement restrictives. L'introduction de termes multiplicatifs pour l'interaction dans GLMs les supprime. On obtient les estimations des paramètres par un processus itératif alternant des régressions généralisées sur lignes et colonnes dans le cadre d'une quasi-vraisemblance. Les exemples les plus connus de cette classe de modèles généralisés d'effets principaux additifs et d'effets d'interaction multiplicatifs (GAMMI) sont les modèles AMMI (Gauch, 1988, *Biometrics* **44**, 705–715) et les modèles d'association RC de Goodman (Goodman, 1981, *Journal of the American Statistical Association* **76**, 320–334). On peut visualiser la partie multiplicative de l'interaction à l'aide de "biplots". On présente deux applications des modèles GAMMI sur des données provenant d'expériences de croisement de plantes. La première illustration traite d'un modèle log-bilinéaire pour des données de dénombrement avec variation poissonnienne. La seconde concerne un modèle logit-bilinéaire pour des données d'incidence d'une maladie avec un type particulier de fonction de variance, extension d'un modèle présenté par Wedderburn (1974, *Biometrika* **61**, 439–447).

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