Generalized AMMI Models for Assessing The Endurance of Soybean to Leaf Pest

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ABSTRACT

AMMI (Additive Main Effect Multiplicative Interaction) model for interactions in two-way table provide the major mean for studying stability and adaptability through genotype × environment interaction (GEI), which modeled by full interaction model. Eligibility of AMMI (Additive Main Effect Multiplicative Interaction) model depends on that assumption of normally independent distributed error with a constant variance. In the study of genotypes' resistance, disease and pest (insect) incidence on a plant for example, the appropriateness of AMMI model is being doubtful. We can handle it by introducing multiplicative terms for interaction in wider class of modeling, Generalized Linear Models. Its called Generalized AMMI model. An algorithm of iterative alternating generalized regression of row and column estimates its parameters. GAMMI log-link model will be applied to the Poisson data distribution. GAMMI log-link models give us good information of the interaction by its log-odd ratio.

Keywords: AMMI, GEI, GAMMI, log-link

INTRODUCTION

The AMMI model represents observations into a systematic component that consists of main effect and interaction effect through multiplication of interactions components, apart from random errors component. Basically, the AMMI analysis combines both additive analysis of variance for the main effect of treatment and analysis of multiple main components uses bilinear modeling for the interaction effect, by using singular value decomposition (SVD) of its interaction matrix (Mattjik & Sumertajaya 2002, Hadi & Sa'diyah 2004, Mattjik 2005). Sometimes, goodness of fit AMMI models which have normally distributed errors with constant variances cannot be satisfied. Statistical modeling plays the most important role in the providing interpretation of interest phenomenon, and representing it into appropriate language of application field.

Transformation can be omitted if homogeneity of variances can be modeled by multiplication of interactions components in the systematic model. However, for non-normally distributed data which is modeled in the observation scale, multiplication of interactions components maybe represent both homogeneity of variances and true multiplication of interactions. It means that there is no warranty that transformation of data in the observation scale be able to separates them.

Transformation, in the regression analysis and analysis of variance cases, has three goals, i.e., to obtain homogeneity of variances, normally of errors, and additional of systemic effects. It is not easy to obtain a satisfaction transformation for all need. So, after transforming, multiplicative component maybe still represents mixture of heterogeneity of variances and multiplicative effects (Hadi *et al.* 2007).

While, in the additive models, we have widely known generalized linear models (GLM) as a modeling class of non-normally distributed data. In GLM additiveness of systemic effects is given into normally scale. Normally (and homogeneity) of variances is not necessary again. It is because the (quasi) likelihood just need to fix the relationship between mean and variance only.

Multiplicative models (bilinear) bridge the gap between the main effect models (in ANOVA and GLM) and completely interaction models with interaction parameters for each cell in two way table. This models are also give a visually pattern of the main interaction through biplot. Therefore, developing of GLM theory by accommodate the multiplicative component of interaction is very necessary.

The power of multiplicative AMMI model is placed on visualized interactions by using biplot. Van Eeuwijk (1995) proposed the multiplicative model in term of GLM as an extension of AMMI model called as generalized AMMI (GAMMI) model. In the GAMMI model, it is possibly to visualize interactions. However, as proposed by Van Eeuwijk 1995 that interpretation of the AMMI model must be investigated again, because it depends on link function used in spite of distance its points still represents non-additiveness or dependence. This paper discusses fitting bilinear model in term of GLM, especially for discrete observations, Poisson and Binomial distributions.

Generalized linear models

Classical Linear models have some characteristics, i.e., errors or response variables are normally distributed with constant variances, independent variances of means, and errors or response variables are independent of each other. In the larger model class, it is not depend on these assumptions. Nelder & Wedderburn (1972) discussed GLM which is not depend on these assumptions but it just depends on link function that links between means μ_i and linear predictors η_i of probability distribution model used (Mc Chullagh & Nelder 1989).

Response variables y_i $(i = 1, 2, ..., n)$ are observation values of random variables Y_i assumed have certain distribution (exponential family) with means $E(y_i) = \mu_i$. In fact, a variance function of mean $V(\mu)$ which accompanies dispersion parameter, follows distribution assumptions $Var(y_i) = \phi\, V(\mu_i)$ where ϕ is a dispersion parameter (scale factor) and $V(.)$ is variance function. The means μ_i is linked to linear predictors $\eta_i = \sum_{j=1}^{p} \beta_j x_{ij}$ or $\eta = X\beta$ where $x_{\cdot j}$ are known predictor variables, and β_j are unknown parameters to be estimated by using link function $g_i(\mu_i) = \eta_i$. Although, each observation maybe has different link function, it rarely happens. So, the subscript i of function g_i can be ommited or $g_i(\mu_i)$ can be reduced to $g(\mu_i)$. Estimating of parameters β_j in vector β can be done by using weighted linear regression iteration procedure of

linearized link function which applies to observation (y) of predictor variable (x).

Table 1. Canonical Link functions in generalized linear models.

Respon distribution	Name	Link function
Normal	Identity	$\eta = g(\mu) = \mu$
Poisson	Log	$\eta = g(\mu) = log(\mu)$
Binomial	Logit	$\eta = g($
Negative Binomial	Log	$\eta = g(\mu) = log\left(\frac{\mu}{\mu + k}\right)$
Gamma	Invers	$\eta = g(\mu) = \frac{-1}{\mu}$

Linearized link functions or working variates (in GLIM), have form
$$z_i = \eta_i + g'(\eta_i),$$
or
$$z = \eta + (y - \mu)$$
(McChullagh & Nelder 1989, Van Eeuwijk 1995, Falguerolles 1996). Each observation also has prior weight $w_i = [Vc$, or $w = (\delta\mu/\delta\eta)$. In every iteration circle, values of x and z are updated. This method is known as iterative reweighted least square (IRLS).

In general, generalized linear model (GLM) has some characteristics as follows :

- Response variable **Y** has distribution in the exponential distribution family;

- Linear or systemic component links linear predictor η to multiplication between design **X** and parameter β, $\eta = X\beta$;

- Link function $g(\cdot)$ that links linear predictor to fitted values, follows monotonic and differentiable properties. The $g(\cdot)$ describes how the expected response mean is linked

to η, for example, $\eta = X\beta$ and

$$\mu = g^{-1}(\eta) = E(Y);$$

- Response variables may have no constant variances that their values are to be change as changing of their means, $\sigma_i^2 = f(\alpha_i)$

Generalized ammi model
In an experiment, responses observed sometimes is to be categorical data. It affects that AMMI model approach becomes unrelevant. So, it needs to make analysis by using other approach. For this case, AMMI model has also been developed to handle more general cases. This model approach is known as generalized AMMI (GAMMI) model (Van Eeuwijk 1995) or generalized bilinear models (GBMs) (Falguerlles 1996, Gabriel 1998). The GAMMI models are given as follows :

$$\eta_{ij} = \mu + \alpha_i + \beta_j + \sum_{k=1}^{K} \sqrt{\lambda_k}\, \gamma_{ki}\, \delta_{kj}$$

An AMMI model is a GAMMI model that its link function is to be identity with constant variance. By letting values of β_j and δ_{kj}, it reduces the model to GLM along the row; while letting values of α_i and γ_{ki} reduces the model to GLM along the column. This GAMMI model's characteristic can be used as base line to describe parameter estimate procedure. Other parameter estimate procedure usually uses iterative weighted least square.
Fitting GAMMI model is done iterativelly through some steps (Van Eeuwijk 1995, Falguerolles 1996). The number of multiplicative part in the GAMMI model can be determined by using generalized test of AMMI model as follows :
1. Likelihood ratio test for the first eigen value, and for the second eigen value if the first eigen value has been known, and for the next eigen values.This test compares percentage of those between that can be described by certain part and the total will be described; and it needs no error estimate.
2. F-test needs no special table, and be easy in computation. An independent error estimate (over/under dispersion) is needed and maybe gives problem.
3. Simple test with attribute degree of freedom $(I-1) + (J-1) + 1$ on the eigen value with respect to pivot *k*, becomes difference between the number of

parameters that will be estimated and the number of applied identification constraints. Appropriate mean square is then tested versus an error estimate (over/under dispersion). This test was proposed by Golob, 1968. When the first eigen value relatively more than the next eigen value, attribute degree of freedom will save to follow Golob, and collect next part to estimate error (over/under dsipersion). Sequential application of this procedure is to test eigen value of success versus collected estimate errors.

Adding other multiplicative components for GAMMI model needs recomputing of part that has been inputed. Because of differences cells weight , dimension of success is not nested as usual for the AMMI model with the same cell weight.
Error for diagnostic goal, after convergence, can be obtained from the row regression as well as column regression. Errors of row and column regressions will deviate just a little from the others, because computing of row regression errors assumes column parameters more known than parameters estimate. While for column regression error, estimating of row parameters is also not necessary to be known. Other possibility is to make regressor of parameters result of row and column interactions in the same way as one degree of freedom test for additiveness which gives a regression interpretation, and fits the model with their main effect and regressors. Error of this model is a compromised result between row regression and column regression errors.
Diagnostic error done to assess goodness of fit model is adopted from the GLM. Goodness of fit model can be informally investigated by plotting errors versus fitted values. Generally, for assessment goodness of fit model is suggested to use standardized deviance error and plot it versus linear predictor, or versus fitted values transformed to information scale constant of error distribution. Transformations of fitted value for some errors distribution are $\hat{\mu}$ for normally distributed error; $2\sin^{-1}\sqrt{\hat{\mu}}$ for

Binomial error; $2\sqrt{\hat{\mu}}$ for Poisson error;

$2\log(\hat{\mu})$ for Gamma error, and soon.

Goodness of fit model is showed by pattern of errors that spread randomly with constant shift at zero mean. Systemic deviation on this plot is to be in forms: (i) curve form, or (ii) existence of shift change as fitted value change. Curve form can be caused by one of link function use. So, if the plot contain no deviation, we may clime that the link function used is appropriate (model is appropriate). The same thing can also be obtained from errors plot versus linear predictors. Note that this plot is meaningless for binary data. Some other errors plots is used to investigate variance function and link function which are used (McChullagh & Nelder 1989).

Plot absolute value of error versus fitted value gives informal investigation about properness variance function assumed. This properness is showed by spreading around of points horizontally, and no indication of trends or certain pattern. Improperness of variance function is showed by trend on mean, i.e., positive trend shows that that variance function currently used is gradually increase as increasing of mean and vice versa. Informal investigation about link function used can be done by investigating plot working variate versus linear predictor, but it is not general and meaningless, especially for Binomial distribution.

Visualization interactions by using biplot GAMMI models

Biplot is very good to show multiplicative interaction in AMMI models. In Biplot, rows and columns are represented by points in two or three dimension spaces. Coordinate of points are obtained from rows and columns scores. Singular values are placed to rows and columns scores in different ways based on what interest, i.e., the relationships among rows, columns, or among rows and columns. By plotting rows scores $\gamma_{ik}^r = \gamma_{ik}\sqrt{\lambda_k}$, the distances among rows points are proportional to the number of rows interactions. Plotting $\delta_{kj}^c = \delta_{kj}\sqrt{\lambda_k}$ transforms this relationship to column points. By assuming row and column point as terminal point of vector started at initial point, simple-geometrically can be showed that the number of interactions, or non-additive, between a row and column can be approached by inner-product among vectors in Biplot. This inner-product can be obtained by projecting one of row or column vectors to each other, and then multiplying between length of vector and

length of vector where the projection occurs. For the wide class of GAMMI model, it is probable to visualize interaction by using Biplot, but its interpretation depends on certain link function.

Log-bilinear gammi models

Here we give an other special example of GAMMI model which is to be row x column Goodman's model (RC Goodman's model) for two ways frequencies table I x J. The model assumes that each cell I x J are independent and has Poisson distribution. P_{ij} is probability of observations placed in i^{th} row and j^{th} column,

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

where α_i^+ and β_j^+ are positive parameters.

As an identification constrain of multiplicative interaction part, we use same constrain as AMMI model constrain. By taking logarithm, that model is equivalent to log-bilinear model:

$$\eta_{ij} = \log(P_{ij}) = \mu + \alpha_i + \beta_j + \sum_{k=1}^{K} \sqrt{\lambda_k}\,\gamma_{ki}\,\delta_{kj}$$

and known as generalized AMMI model with logarithm as link function, where the μ, α_i and β_j are the logarithmic form of α_i^+ and β_j^+.

Non-independent form is more relevant to association row x column model than non-additive form. Goodman defined two forms of non-independent as follows.
The first is,

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

and the second is Log Odds Ratio :

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

It is defined for cells in rows i and s ; and columns j and t. Scaled row parameter $\gamma_{ki}^r = \gamma_{ki}\sqrt{\lambda_k}$ can be interpreted as slope of a weighted linear regression of non-independent measure ω_{ij} on column score δ_{kj} :

$$\sum_{j=1}^{J} \omega_{ij}\,\delta_{kj} = \gamma_{ki}^r$$

When δ_{kj} are used as coordinate of row points in biplot, squared distance between two row points tends to non-independent between two rows, because

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

The same relationship can be obtain deductively for γ_{ki} and δ_{kj}^{ξ}. Therefore, Goodman recommended to visualize from row points and column points by using $\gamma'_{ki} = \gamma_{ki}\sqrt{\lambda_k}$ and $\delta_{kj}^{\xi} = \delta_{kj}\sqrt{\lambda_k}$, respectively.

For simultaneously visualize, he recommended to use $\gamma_{ki}^* = \gamma_{ki}\lambda_k^{0.5(1-c)}$ and $\delta_{kj}^* = \delta_{kj}\lambda_k^{0.5c}$, $(0 \leq c \leq 1)$, where the choice of c depends on its weighted-point in row or column. The inner-product between row and column points in simultaneous biplot tends to non-independent measure ω_{ij} where γ and δ are scaled to γ^* and δ^* as follows :

$$\omega_{ij} = \log\left(\frac{P_{ij}}{\alpha_i^? \beta_j^?}\right) = \sum_{k=1}^{K} \sqrt{\lambda_k}\gamma_{ki}\delta_{kj}$$

$$\omega_{ij} = \sum_{k=1}^{K} \gamma_{ki}^* \delta_{kj}^* = |\gamma_i^*||\delta_j^*|\cos(\gamma_i^*, \delta_j^*)$$

where γ_i^* and δ_j^* represent as vector of length K. In the same biplot, inner-product between difference of row points and difference of column points tends to log odds ratio :

$$\pi_{ij} = \log\left(\frac{P_{ij} P_{st}}{P_{it} P_{sj}}\right)$$

$$\pi_{ij} = \sum_{k=1}^{K} \sqrt{\lambda_k}(\gamma_{ki} - \gamma_{ks})(\delta_{kj} - \delta_{kt})$$

$$\pi_{ij} = \sum_{k=1}^{K} (\gamma_{ki}^* - \gamma_{ks}^*)(\delta_{kj}^* - \delta_{kt}^*)$$

$$\pi_{ij} = |\gamma_i^* - \gamma_s^*||\delta_j^* - \delta_t^*|\cos(\gamma_i^* - \gamma_s^*, \ \delta_j^* - \delta_t^*)$$

where γ_i^*, γ_s^*, δ_j^* and δ_t^* are vectors of length K. Simultaneous biplot provides a very good tool to visualize non-independence in two way table of computing analyzed by association row × column. For other GAMMI model, interpretation of relationship biplot still must be investigated. In addition, distance between points of one of rows or columns will indicate some non-additive or non-independent forms. Simultaneously visualize must be interpreted more carefully, but the inner-product of row or column points still tends to non-additive at linear predictor scale.

Especially, for Poisson data case (log-bilinear model), biplot provides two important informations. Firstly, information about dependence between rows or columns which are showed by distance (square) between rows or between columns on biplot. And the second is information about ratio of two probabilities events (odds ratio).

This information is to be geometrical interpretation that uses vector projection properties. Odds is ratio of two probabilities events. From the two ways table genotype x population of pests can be obtained information about ratio of probabilities. We define x_{ij} as i^{th} row and j^{th} column cells values, and $P_{ij} = x_{ij}/\sum_{ij}x_{ij}$ is probability of ith row and j^{th} column events such that we can compute probability ratio of two genotypes, for instance, i^{th} and s^{th} genotypes are attacked by pests, say, j^{th} pest, as P_{ij}/P_{sj}.

Odds ratio
Ratio of two odds', for example, ratio between odds of jth pest on i^{th} genotype and s^{th} genotype, and odds of tth pest on same, is given as follows :

$$\frac{P_{ij}/P_{it}}{P_{st}/P_{sj}}$$

This odds ratio can be understood by seeing Figure 1B and considering ratio of difference length between a and b by c and d. Note that if vectors that connect two pests and connect two genotypes are perpendicular each other (orthogonal, $\alpha = 90^o$) then this ratio will be equal to 1, and logarithm of it is equal to zero. According to log-bilinear model (GAMMI log-link) odds ratio can be obtained logarithm scale:

$$\pi_{ij} = \log\left(\frac{P_{ij} P_{sh}}{P_{ih} P_{sj}}\right) = \sum_{k=1}^{K} \sqrt{\lambda_k}(\gamma_{ki} - \gamma_{ks})(\delta_{kj} - \delta_{kh})$$

by taking derivation of formula, and gives :

$$\pi_{ij} = \sum_{k=1}^{K} (\gamma_{ki}^* - \gamma_{ks}^*)(\delta_{kj}^* - \delta_{kt}^*)$$

$$\pi_{ij} = |\gamma_i^* - \gamma_s^*||\delta_j^* - \delta_t^*|\cos(\gamma_i^* - \gamma_s^*, \ \delta_j^* - \delta_t^*)$$

$$log\left(\frac{P_{ij}}{P_{sj}}\right) \approx a - b$$

$$log\left(\frac{P_{ij}P_{st}}{P_{it}P_{sj}}\right) \approx log\left(\frac{a/b}{c/d}\right) = log\left(\frac{a \cdot d}{b \cdot c}\right)$$

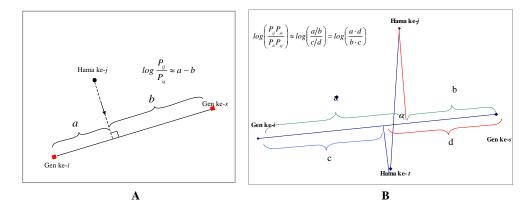| A	B

Figure 1. Geometrical visualization of Odds (A) and Odds Ratio (B).

METHODS

The data is experimental data of leaf pest control on variety of soybean endure that is hybrid result of BALITKABI, Malang, East Java. This experiment involves four varieties of soybean endure resulted by hybrid (Wilis, IAC-100, IAC-80-596-2 and W/80-2-4-20). This research uses leaf pest population data at 14 days old after planting.

Research steps to obtain information about stableness genotype endure are as follows :

1. **Identifying of distribution and handling of experiment data.** Leaf pest population data identified has Poisson distribution. While, percentage of rice-grain and total of grain data identified has binomial distribution. These two sets of data are arranged into two ways table I x J, genotype versus type of leaf pest, and genotype versus location, where cells contain means of replication/block.
2. **Fitting GAMMI Model.** Fitting GAMMI model algorithm is complicated enough, because it is to be a criss-cross regression or alternating regression between row and column regressions, where each regression includes GLM class that is done iteratively by using iterative reweighted least square (IRLS). Therefore, this algorithm involves three types of convergence, i.e., in row regression, in column regression, and in alternating regression. It is complexity of this modeling algorithm. However, basic idea of this algorithm seems easy to be understood. This algorithm is given in Van Eeuwijk, 1995. Fitting model is done by using software GENSTAT 7th edition or more expand. Poisson distribution data is modeled by using link function logarithm
3. **Analysis of Deviance.** If in AMMI model (ANOVA in general) we test effect of factors by using sum of square then in GAMMI model (GLM in general) we use deviance. We use F-test to determine multiplicative axis/component by comparing ratio between mean deviance

component tested and error mean deviance to F-table value.

4. **Appropriateness Model.** We investigate appropriateness model by using errors diagnostic visually, i.e., errors plot.
5. **Analysis of Stableness Genotype Endure.** Information about stableness genotype endure can be obtained through biplot GAMMI2 configuration. Biplot GAMMI2 gives row and column scores plot (in this case, genotype x pest population or genotype x location) simultaneously. By considering whole biplot, nearness between row and column points shows interaction and dependence (association) of them. Association parameter is given by singular value (generalized). Nearness between certain row point (genotype) and certain column point (pest population or location) indicates association between genotype and certain pest population or location. Small singular value for ith GAMMI axis indicates meaningless of the axis.

RESULTS AND DISCUSSION

Endurance of soybean to leaf pest

Four genotypes of soybean gave different leaf endurance responses on five types of leaf pest. Table 2 provides population mean of five pests found on four soybean varieties at 14 days old after planting. Based on the algorithm of Eeuwijk (1995) GAMMI model was using link function natural logarithm and Poisson distribution. Analysis of deviance is given in Table 3. It shows that the mean of error deviance is 0.0134; and computation of error based on Pearson's Chi-square is 0.0135. Table 3 shows that GAMMI2 model is appropriate because mean deviance ratio of axis 2 is significant at p-value $< 0.0541 = F_{4;2}$. Singular value of axis 1 and axis 2 are 1.739 and 0.5927,

respectively. Plotting of errors deviance versus fitted values and linear predictors shows that there is no anomaly. Plotting of working variate versus linear predictor can indicate improperness link function usage, if the plot is non linear. Also, the plot shows that there is no anomaly (Figure 2). So that GAMMI2 model which has log-link and has Poisson distribution fits data well. Biplot GAMMI2 provides information about interaction genotype × pest (Figure 3). Genotype W/80 shows tendency to be variety candidate that has endurance to all types of leaf pests unless to Emproasca, comparing with variety IAC-100 that specifically susceptible to Agromyza.

Biplot of interaction in log-bilinear model can be used well to find pairs of soybean genotypes and pairs of pest types population which has odds ratio equal to one or log odds ratio equal to zero. On our data, we find that these pairs are genotypes W/80 and IAC-80, and the Bemisia and the Agromyza. Delivery line of genotypes is "almost" perpendicular to its of pests. It means that log odds ratio "tends" to zero. Table 2 can verify that odds ratio between both of them tends to 1. It means that W/80 and IAC-80 has the same thing, and W/80 and IAC-80 more tend to be attacked by Bemisia than the Agromyza in the same scale.

Table 2. Population means of five types of leaf pest on four genotypes of soybean.

Genotipe	Types of leaf pest				
	Bemissia	*Emproosca*	*Agromyza*	*Lamprosema*	*Longitarsaus*
IAC-100	0.50	1.75	2.25	0.50	1.75
IAC-80	3.00	2.75	1.00	1.75	3.25
W/80	3.50	4.00	1.25	2.00	2.00
Wilis	4.00	3.00	1.00	1.75	4.00

Table 3. Analysis of Deviance for leaf pest population data.

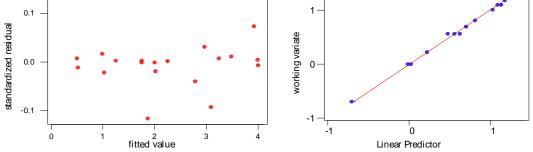| Source	DF	Deviance	Deviance Mean	Deviance Mean Ratio	p-value
Leaf pest	4	4.1845	1.0461	78.38	0.0126
Genotype	3	2.8359	0.9453	70.83	0.0139
GAMMI 1	6	3.6709	0.6118	45.84	0.0215
GAMMI 2	4	0.9477	0.2369	17.75	0.0541
Error	2	0.0267	0.0133		
Total	19	11.6656	0.6140		

Figure 2. Error plot for soybean pest data: Standardized error versus fitted value GAMMI2 log link model (left); Working variate versus linear predictor plot (right).
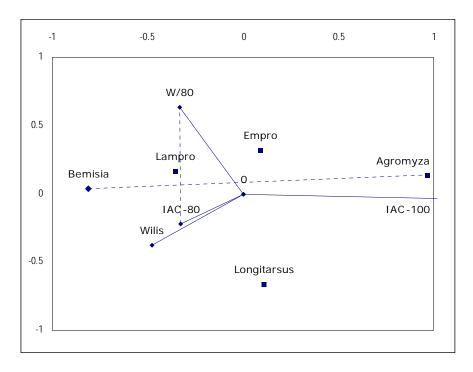
Figure 3. Biplot GAMMI2 for leaf pest data with logarithm link function.

CONCLUSION

Generalized AMMI (GAMMI) model accommodates data non-normally distributed to obtain completely interaction decomposition by modeling probability of events. In agronomy, it has benefit to test stability/adaptability of genotype on indicator variables that are non-normally distributed, but their distribution have been known to be in exponential family, for examples, Poisson, Binomial, and Gamma. Biplot of Poisson GAMMI model with link function logarithm gives addition information about odds ratio. In study on endurance of soybean genotype on leaf pest, the GAMMI2 model has described well that genotype W/80 is to be variety candidate which is endure to almost all types of leaf pest. In addition, IAC-100 is endure to the fly. The log-odds ratio of genotypes W/80 and IAC-100 to both Bemisia and Agromyza pests tend to zero.

REFERENCES

Falguerolles de A. 1996. Generalized Linear-Bilinear Models. An Abstract. Society of Computational Economics. 2nd International Conference on Computing and Finance. Genewa, Switzerland, 26–28 June 1996. http://www.unige.ch/ ce/ce96/defalgue/

Gabriel KR. 1998. Generalised Bilinear Regression. *Biometrika*. **85** (3):689-700.

Gollob HF. 1968. A Statistical Model which Combines Features of Factor Analytic and Analysis of Variance Techniques. *Psychometrika*. **33**:73-116.

Hadi AF & Sa'diyah H. 2004. AMMI Model untuk Analisis Interaksi Genotipe × Lokasi. *Jurnal Ilmu Dasar*. **5**(1):33-41

Hadi AF, Sa'diyah H, Sumertajaya IM. 2007. Penanganan Ketaknormalan Data pada Model AMMI menggunakan Transformasi Box-Cox. *Jurnal Ilmu Dasar*. **8**(2): 165-174.

Mattjik AA. & Sumertajaya IM. 2002. *Perancangan Percobaan dengan Aplikasi SAS dan MINITAB*. 2nd Ed. IPB Press. Bogor.

Mattjik AA. 2005. *Interaksi Genotipe dan Lingkungan dalam Penyediaan Suumberdaya Unggul.* Naskah Orasi Ilmiah Guru Besar Biometrika. Fakultas Matematika dan Ilmu Pengetahuan Alam Institut Pertanian Bogor. Bogor.

McCullagh P & Nelder JA. 1989. *Generalized Linear Models.* 2nd ed. Chapman and Hall, London.

Nelder JA & Wedderburn RWM. 1972. Generalized Linear Models. *J. Royal Stat. Soc.* Series A (General). **135**(3): 370-384.

Van Eeuwijk FA. 1995. Multiplicative Interaction in Generalized Linear Models. *Biometrics,* **51,** 1017–1032.