A new computerized program for grain yield stability analysis in wheat

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Abstract. Advanced statistical codes we present in MINITAB statistical environment, produces comprehensive computational and graphical outputs for the best stability analysis, additive main and multiplicative interaction effect (AMMI). The experiment comprised of a population of doubled-haploid wheat lines at 2006-2009 ys. As lattice designs. The results of AMMI analysis of grain yield showed the significant ($P<0.01$) effect of years, lines, and their interaction effect, along with 49.1, 7.80 & 20.63% of the total variation, respectively. Also the written macro partitioned the GEI effect to three IPCA scores, accounted for 40.70, 35.32 & 23.96% of the GEI, respectively. The results of the cross-validation with FR (Cornelius) indicated the appropriateness of AMMI2 model, whereby the biplots of genotypes & years drawn, by which the stable genotypes were chosen. This program provided useful computations such as: principal component analysis, cluster analysis, Finlay-Wilkinson stability regression analysis and so on. In general, this program has a high potential for AMMI yield (etc) stability analyses, following estimating their parameters and could be applied by researchers working with stability analysis in plant breeding programs to obtain the most tolerant/resistant cultivars during multienvironment trials.

Key words: MINITAB statistical software, wheat (*Triticum aestivum* L.), yield stability analysis.

Introduction

Genotype by environment interaction plays an important role in various fields of biology and agriculture, especially plant breeding and refers to different interactions of genetic materials at different environments. Additive main and multiplicative interaction method (AMMI) seems to be the best and the most applicable stability method. It combines the ANOVA and principal component analysis (PCA) (Zobel et al., 1988) and is more efficient than GGEBiplot (Gauch et al., 2008; Yan et al., 2007). AMMI method has many applications in plant breeding, e.g. for designing the breeding programs and specific adaptability and selection of proper environment. Following to AMMI analysis, IPCA scores are achieved helping to draw biplots to identify resistant and sensitive genotypes. The best model of AMMI, i.e. AMMI1 or AMMI2, etc. can be determined by some ways such as RMSPD parameter with MATMODEL software (Gauch and Furnas, 1991), by cross-validation method (Gauch, 1992), test of FR (Cornelius, 1993). In an AMMI model nominal or estimated yields are retained in the model which are more validated and more being used.

Many researchers utilized the AMMI method to evaluation the agronomic and physiologic traits in plants like wheat. Taghouti et al. (2010) using AMMI, studied qualitative traits of 12 wheat genotypes, at 3 growth seasons, and 5 locations and reported that environments, genotypes and their interaction effect had significant effects on qualitative traits and MMI3 model was the appropriate model with 3 PC scores accounted for the most contribution of the variation of GEI.

This study was conducted to show the potential, strength and various applications of the written macro called "AMMI.MAC" in MINITAB statistical software along with its utilization in a real dataset and experiment in the field at four years.

Materials and Methods

An AMMI macro written in MINITAB statistical software covering 2300 lines of programming tested on a real experiment conducted. The experiments were conducted at the research farm of Shahrekord University, Iran on a clay loam soil (21% sand, 35% silt, 40% clay) located at N 32°21' E 50°49', 2125 m a.s.l. A set of 103 DH lines, their parents and 5 local genotypes were applied in rectangular lattice designs.

In AMMI analysis, the PCA is conducted on the residual matrix following by obtaining some IPCA scores, which are tested based on their F parameter in an ANOVA model. The mathematical model of AMMI is as: $Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$.

where Y_{ger} is the yield of genotype g in environment e for replicate r, μ is the grand mean, α_g is the genotype g mean deviation (genotype mean minus grand mean), β_e is the environment e mean deviation, λ_n is the singular value for IPCA axis n, γ_{gn} is the genotype g eigenvector value for IPCA axis n, δ_{en} is the environment e eigenvector value for IPCA axis n, ρ_{ge} is the residual, and ε_{ger} is the error.

In this research, MINITAB v.13 (Http://www.minitab.com) was applied to data normalization, study the homogeneity of variances, combined or joint regression analysis and AMMI analysis following by Biplot designing. The AMMMI macro discussed here should be put within the "macros" folder of MINITAB main folder. For operating the macro, the user should refer to the complete guidance mentioned in Arminian et al. (2008). It is important to note that this macro works in different cases: 1) the user has in hand a dataset arrayed in a two-way matrix of genotype by environment, 2) the dataset arrayed in 3 columns of genotype, environment and the trait under study, 3) in case 3 there is another column called replication as G, E, R and the trait. It is worthy to note that our macro responds well to conditions where some of the observations or even treatments (here genotypes) are missed. For prompting the macro to operate suppose one has a dataset of G, E, R and yield, respectively within the columns of C11-C14. For this, the command line is activated by clicking within the session page of MINITAB and then through Editor>Enable commands. Then, type in front of the command line editor MTB> as: %AMMI c11-c14. The macro then asks some questions, which should be responded well to it operate goodly. Although the macro depicts the cluster analyses and biplots, but it is suggested that draw given diagrams by MINITAB macro after achieving the IPCA scores and nominal means from Graph>plot pathway.

Results and Discussion

The present macro outputs have many results, including: printing the original data, ANOVA table, treatments (genotypes) mean, standard deviations (SD) and effects, CV of design, residuals of genotypes, environments mean and SD and their effects, the central part of AMMI or ANOVA table covering Gollob F (Gollob, 1968), and also Cornelius F or FR (Cornelius 1993, Dias and Krzanowski, 2003). Other than Gollob F, the FR test is an alternative to cross-validation tests and according to Gauch (personal communications) could be an alternative to it. The ANOVA table of AMMI model for 4 ys. Of grain yield is shown in Table 1. It can be seen from the Table 1 that years, genotypes, and their interaction effects were significant and accounted for 49.1, 7.80 & 20.63% of the total variation, respectively. Furthermore, the written macro partitioned the GEI effect to three IPCA scores, accounted for 40.70, 35.32 & 23.96% of the GEI, respectively. The macro also drew a biplot containing years and genotypes against IPCA1 and IPCA2 scores. As shown from the Figure 1, year 2009 is the most stable year among all the years. Moreover, the genotypes located in the center of the Biplot are the most stable ones. And also e.g. genotypes "g72" and "g89" and "g76" is sample most sensitive genotypes in this experiment.

Another issue in this experiment is choosing six of all genotypes within each environment, which is an efficiency of this macro compared to other softwares like GENSTAT or IRISTAT. Furthermore, in our written macro for MINITAB, the Finlay-Wilkinson regression analysis is possible to fit the linear regression the mean of each treatment to all genotype's means and compute the regression equation. Of course many possibilities are possible and computable in these macros which are not discussed here.

Some advantages of our macro compared to other softwares doing AMMI analysis:

Our program has many applications in various fields of sciences. Some of its efficiencies are comparatively as: 1) Simplicity and ease of use, 2) having potential color graphical representation, especially for biplots, 3) applying the F or FR test for cross-validation instead of RMSPD, which is very tedious and hard in other windows-based softwares, 4) applicable when some observations and even treatments are missed, 5) evolving some important valuable statistical models like PCA, factor analysis, cluster categorization, 6) extracting 6 of the stable genotypes within each environment, 7) performing the Finlay-Wilkinson regression fitting for each genotype as discussed, 8) performing supplementary genotype analysis compared to other programs for the first time among AMMI analysis

programs. In whole, this macro is suggested for selection the stable and high yielding materials in stability analysis of biological and agricultural materials to whom want to apply AMMI analysis easier and faster with vast analyses.

Table 1. ANOVA table of wheat grain yield of 103 DH lines, their parents and 5 Iranian varieties at 2006-2009 ys. G and C denote Gollob and Cornelius, respectively.

SOV	R	SS	MS	P-value
Years (Y)	3	36.27	12.09	0.000
R(E)	8	1.49	0.19	0.000
Genotype (G)	100	5.76	0.06	0.000
G*Y	300	15.23	0.05	0.000
IPCA1-G	102	6.20	0.06	0.000
IPCA1-C	198	9.03	0.05	0.000
IPCA2-G	100	5.38	0.05	0.000
IPCA2-C	98	3.65	0.04	0.000
IPCA3-G	98	3.65	0.04	0.000
IPCA3-C	-	-	-	-
Error	800	15.10	0.02	-

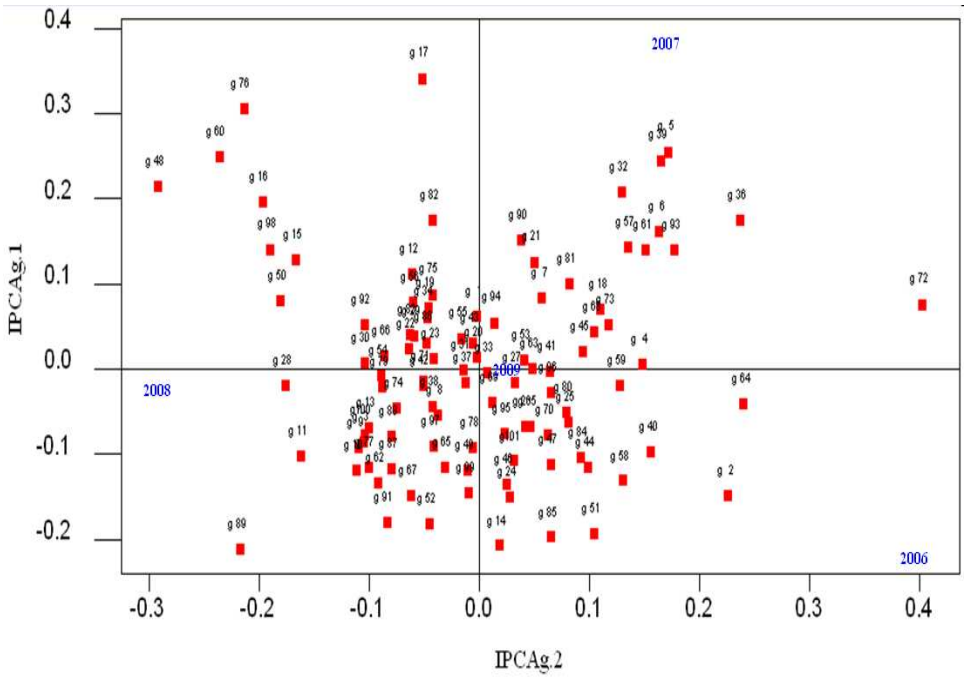

Figure 1. Biplot of IPCA1 and IPCA2 for genetypes and years at 2006-2009.

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