2338-0128

PROCEEDINGS BOOK THE 8th ANNUAL BASIC SCIENCE INTERNATIONAL CONFERENCE

6-7 March 2018 Ijen Suites Hotel Resort & Convention Malang, Indonesia

Convergence of Basic Sciences, Toward the World's Sustainability Challenges

Topics

Energy
Environmental Science and Technology
Instrumentation and Measurement
Material Science and Technology
Mathematics, Statistics, and Modelling
Molecular and Health Science
Science and Technology Education





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GGE Interaction Biplot in the RCIM Model and the Evaluation for the Outlying Observations

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Abstract. Multilocation experiment is an experiment frequently used in the case of plant breeding for determining the variety of some future lines. In this case, genotype (G) is applied on the different environments. We know that the evaluation would be difficult when genotype by environment interaction (GEI) appeared. Statistical methods have been developed in order to determine the diversity of genotype on the different environments, e.g. modelling graph of genotype and genotype by environment interaction biplot $(GGE \ Biplot)$. In the case of $GGE \ Biplot$, the main factor of $GGE \ Biplot$ is generated as the main examiner effect or environment (E) is deleted, while the main entry effect (G) and the interaction genotype and environment (GE) entry is kept and combined. Therefore, biplot based on the centered data contains only G + GE. in addition, $GGE \ Biplot$ method is a development of AMMI method. subsequently, the main purpose of this research is to analyze biplot of $GE \$ and $GGE \$ by applying RCIM model in order to overcome the outliers. Here, the simulation is applied on the data using single environment outliers technique to evaluate biplot characteristics in the case of the appearance of outliers. We now will focus on the data visualization of the interaction and the effect of an outlying observations

INTRODUCTION

Genotype interaction with the environment is a matter of concern in plant breeding. Plants with the same genotype when planted in different environments will result in different crop production depending on the environment, as well as plants with different genotypes when planted in the same environment then the production will also differ depending on the genotype. Therefore, by utilizing the adaptation and stability of good crops and their components in the genotype, it is possible to develop or identify superior varieties and adapt well. The development of high yield cultivars with extensive adaptability is the ultimate goal in agriculture. Evaluation becomes difficult when there is an interaction between genotype × environment (genotype by environment interaction, GEI). GEI is caused by differential responses of genotypes to environmental variables (Kang et al., 2002). Two frequently used statistical analyzes are the main additive effects and multiplicative interaction models (AMMI) and the major genotype effects and genotype interaction effects model (GGE) (Gauch, 2006). These two statistical analyzes have broader relevance for agricultural researchers because they refer to the two-way data matrix that often arises from different types of experiments. The biplot GGE technique can be used to compare the appearance of different genotypes in an environment, compare the appearance of one genotype in different environments, compare the appearance of two genotypes in all environments, find out the highest-powered genotypes in different environments, know genotypes and ideal environments, compare genotypes based on multiple nature, and knowing of genotypes with some appropriate traits (Yan and Kang, 2002). The AMMI model combines genotype variance analysis and major environmental effects with GEI main component analysis into an integrated approach (Gauch and Zobel 1996). The biplot GGE method is a further development of the AMMI method. This method uses several functions of the AMMI method together. It allows visual testing of the relationship between the test environment, genotype and GEI.

The difference from AMMI is that GGE biplot analysis is based on environmentally-focused PCAs, whereas AMMI analysis refers to PCAs centered over long distances. For research purposes to describe the mega-environment, AMMI and GGE are appropriate, and the comparison so far shows similar results, as expected. For research purposes the accuracy, AMMI and GGE (as well as multiplicative models shifted, etc.). The GGE biplot model (the main genotype model) (G) plus G x E), provides a more complete developer and visual evaluation of all aspects of data by creating biplot which simultaneously represents average performance and stability, as well as identifying mega environments (Ding et al., 2007; Kang, 1993; Yan, 2001; Yan and Kang, 2003). GGE biplot can be useful for displaying which data patterns can be won, to identify high crop and stable cultivars and a discriminatory and representative test environment (Yan et al., 2001). The objective of this study was to evaluate the interaction of G x E by using AMMI and GGE biplot analysis for crop yields from wheat crosses, obtained from diallele cross, to identify stable hybrids under stress and non-stress conditions.

GGE METHOD

GGE technique is a GEI analysis technique that involves the influence of genotype (G) and genotype × environment (GE). The most common use of biplot GGE bases itself on the regression linear-bilinear (SREG) regression model (Samonte et al., 2005; Cornelius et al., 1996). The biplot GGE technique can be used to compare the appearance of different genotypes in an environment, compare the appearance of one genotype in different environments, compare the appearance of two genotypes in all environments, find out the highest-powered genotypes in different environments, know genotypes and ideal environments, compare genotypes based on multiple nature, and knowing of genotypes with appropriate traits (Yan Kang, The GGE (Genotype + Genotip by Environment) technique has been widely used for genotype × environmental interaction analysis. The GGE technique has several advantages over the AMMI (Additive Main Effects and Multiplicative Interaction) which are: (1) GGE biplot graphics for the which-won-wherel superior than AMMI1 graph for mega-environment analysis, (2) GGE biplot- the average versus stability is superior to the AMMI biplot in selecting genotypes because it explains G + GE, and (3) on the AMMI technique is not evaluated the test environment (Yan et al., 2007).

The basic model of GGEcan be written as: $Y_{ij} - \overline{Y}_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$

$$Y_{ii} - \overline{Y}_i = \lambda_1 \xi_{i1} \eta_{i1} + \lambda_2 \xi_{i2} \eta_{i2} + \varepsilon_i$$

Where:

 Y_{ij} is the average of the observed value of the i-th genotype and the j-th environment

 \overline{Y}_i is the average of the observed value for all genotype and environment

 λ_1 and λ_2 are the singular value of PC1 and PC2

 ξ_{i1} and ξ_{i2} are the score of PC1 and PC2 for the i-th genotype

 η_{i1} and η_{i2} are the score of PC1 and PC2 for the j-th environment

 ε_{ij} is the residuals

EXPERIMENTAL DETAILS

The simulated data is generated by the R program. The data of this table uses two-way table data where the data is normally distributed. Data were obtained by simulating randomly generated two-way tables with sizes of n = 50 genotypes (rows) and p = 8 environments (columns). Genotype \times environmental interactions are described by two multiplicative rates.

The method used to analyze the data in this study is to use RCIM which will be interpreted using GGE Biplot. To simplify the calculation process used the help of one software in statistics that is R. To analyze the data using RCIM assisted with the packages available on R ie VGAM package. This package provides functions for GLM vectors and other additive models such as VGLM and VGAM.

RESULTS AND DISCUSSION

The MSE was inflated became higher than before in the original data without outlier. There was different influence correspond to the GE or the GGE model, the outlier was seen to affect the inflation of the MSE of the GE model higher than of the GGE model. Generally, either for the GE or the GGE model, there was a tendency that the higher value of outlier the higher MSE we got. Specifically, for the GE model, the more number of outliers in the data the larger values of MSE, either of scattered outlier or single environment outliers. We can say here that both the GE and the GGE model still facing the vulnerability of scattered outliers.

ACKNOWLEDGEMENT

We would also like to show our gratitude to the committee of the 8th Annual Basic Science International Conference 2018 for accepting our manuscript to be published in this conference proceeding.

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