Addis Ababa University
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Faculty of Science
Department of Statistics

MODELING GENOTYPE X ENVIRONMENT INTERACTION AND YIELD STABILITY IN MULTI-ENVIRONMENT MAIZE (*ZEA MAYS* L.) YIELD TRIAL

By
Belachew Mekbibe

A THESIS SUBMITTED TO THE OFFICE OF GRADUATE PROGRAMMES OF ADDIS ABABA UNIVERSITY, IN PARTIAL FULFILLMENT FOR THE AWARD OF MASTER OF SCIENCE IN STATISTICS

June 2008

DECLARATION

I, the undersigned, declare that the thesis is my original work, has not been submitted to any university anywhere for the award of any academic degrees and all sources of material used for the thesis have been duly acknowledged.

Name: Belachew Mekbibe

Signature: .....

Place: Faculty of Science, Addis Ababa University

Date: June 2008

This thesis has been submitted for examination with my approval as a University advisor.

.....

Girma Taye, Ph.D.

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This thesis is dedicated to my parents, Mekbibe and Yesharge. It is also dedicated to Luelae, Habtish, Mekdi, Dagi and GG for their understanding support.

TABLE OF CONTENTS

TABLE OF CONTENTS (*continued*)

LIST OF ABBREVIATIONS

AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis of Variance
CIMMYT	International Maize and Wheat Improvement Center
CSA	Central Statistical Agency
CV	Coefficient of Variation
DF	Degrees of Freedom
EIAR	Ethiopian Institute of Agricultural Research
EMA	Ethiopian Mapping Authority
GxE	Genotype x Environment Interaction
IRRI	International Rice Research Institute
LR	Linear Regression
MET	Multi-environment Trial
MS	Mean Square

LIST OF ABBREVIATIONS (*continued*)

NID	Normally and Independently Distributed
PCA	Principal Components Analysis
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System
SS	Sum of Squares
SV	Singular Value
SVD	Singular Value Decomposition

LIST OF TABLES

LIST OF TABLES (*continued*)

LIST OF FIGURES

ABSTRACT

Multi-environment trials (MET) play an important role to develop an understanding of how genotypes of an agricultural crop perform under different growing conditions. In a MET, a number of genotypes are tested in a number of environments using designs that involve several replications per environment. Plant breeders conduct multi-environment trials primarily to make cultivar evaluation and recommendation for a target region. However, this task is not generally easy due to the frequent presence of genotype x environment interaction. Genotype x environment interaction (GxE) is differential genotypic expression across environments. A significant GxE for a quantitative trait such as yield can seriously limit efforts in selecting superior genotypes for both new crop introduction and improved cultivar development. A number of methods and models have been proposed to cope with the presence of GxE in multi-environment trials.

Traditional statistical analyses of multi-environment trials provide little or no insight into the particular pattern or structure of the GxE. The additive main effects and multiplicative interaction (AMMI) model incorporates both additive and multiplicative components of the two-way data structure which account more effectively for the underlying interaction patterns. The least squares estimates of the main effect parameters for an orthogonal AMMI model are identical with the least squares estimates of the parameters for the model reduced to its additive part whereas the estimates of the multiplicative parameters are the leading terms of the singular value decomposition of the matrix residual to the additive part. In practice the series of multiplicative terms is truncated at some point beyond which further terms are believed to have little statistical significance. Results from AMMI analysis presented in biplots underpin better informed decisions on variety selection and recommendation in plant breeding research programs. A breeding trial for 15 genotypes of maize (*Zea mays* L.) grown in 8 location-year environments serves as an example.

In our study, standard ANOVA analysis showed a significant genotype x environment interaction effect for grain yield, in addition to the main effects. The environment effect accounted for more than 80% of the variability in the observed yield response. The magnitude of genotype x environment interaction sum of squares was larger than the genotype sum of squares. From a breeding viewpoint, this result gives some indication of the possible challenge in selecting superior genotypes. Generally, the larger the magnitude of the interaction term relative to the genotype effect, the more complex the problem of identifying broadly adapted genotypes.

In an attempt to explain the GxE of grain yield in the maize data, we subsequently fitted a regression on the mean model and an AMMI model. Results suggest that the AMMI model with two dimensions for the interaction (AMMI-2) was preferable to the more familiar ANOVA and linear regression procedures. Based on the selected AMMI model, genotypes G14, G1 and G2 were found to be relatively more stable varieties. Moreover, genotype G1 was identified as a more desirable variety. Interaction patterns revealed by AMMI biplots indicated that these maize genotypes are narrowly adapted because no genotype has superior performance (both high mean yield and high stability) in all environments. Among the 8 location-year environments Arsinegelle in 2004, Areka in 2004, Goffa in 2005 and Areka in 2005 exhibited larger interactions and were more discriminating of genotypes, whereas Awassa in 2004 exhibited negligible interaction and was the least discriminating of genotypes. In the current study, Goffa was identified as a location that was highly predictable in year-to-year interaction with genotypes (making specific cultivar recommendation more reliable). In contrast, Awassa, Arsinegelle and Areka were less predictable. Finally, it is recommended that future data collection should include information on external environmental and/or genotypic variables.

CHAPTER ONE
INTRODUCTION

1.1 The Crop

Maize (*Zea mays* L.) is a member of the grass family, *Gramineae*. It is believed that the crop was originated in Mexico and introduced to West Africa in the early 1500s by Portuguese traders (Dowswell et al., 1996). It was brought to Ethiopia during the 1600s to 1700s (Haffanagel, 1961). Maize is one of the most important food crops worldwide. It has the highest average yield per hectare and is third after wheat and rice in area and total production in the world. It is grown in most parts of the world over a wide range of environmental conditions, ranging between 50^0 latitude north and south of the equator. It also grows from sea level to over 3000 meters above sea level. Maize is used in many ways than any other cereal. It is used as a human food, feed for livestock and industrial purposes (Dowswell et al., 1996). Millions of people depend on maize for their daily food in Sub-Saharan Africa (Pixley & Bjarnason, 2002).

In Ethiopia, maize grows from moisture stress areas to high rainfall areas and from low lands to high lands. Maize is the staple food and one of the main sources of calorie in the major maize producing regions (Kebede et al., 1993). It is one of the important cereal crops grown in the country. It was cultivated on about 1.2 million hectares accounting for 19.3 percent of the estimated 6 million hectares of land allocated to all cereals. It stands first in total national production and yield per hectare (CSA, 1996/97).

Maize breeding in Ethiopia started about half a century ago. In the late 1960s and early 1970s several promising hybrids and composite varieties of East African origin were introduced, evaluated at different locations, and recommended for maize producing regions of Ethiopia. However, most of these maize varieties have been replaced by locally developed and better performing varieties. The superiority of these varieties was due to better interaction with variable environmental conditions (Benti, 1988).

Among the unique features of the Ethiopian environmental conditions is the variation experienced both from season to season and from place to place in the same season over relatively small areas. It is a country of great environmental variations (EMA, 1988). According to the Ministry of Agriculture categories of agro-ecologies, Ethiopia has 18 major agro-ecological zones and 47 sub agro-ecologies (MOA, 2000).

1.2 Multi-environment Yield Trials

A major task in many plant-breeding programs is to assess the suitability of individual crop genotypes for agricultural purposes across a range of agro-ecological conditions. To this purpose breeders perform so-called multi-environment trials (MET). In multi-environment trial, a set of genotypes is evaluated across a number of environments. These trials produce genotype by environment data (van Eeuwijk et al., 2004).

According to Crossa (1990), data from such trials have three main objectives: (a) to estimate accurately a given trait or multiple traits based on limited experimental data; (b) to determine stability and the pattern of response of genotypes for a given trait or set of traits across environments; and (c) to provide reliable guidance for selecting the best genotypes for planting in future years and at new sites. The author pointed out that data collected in MET are intrinsically complex having three fundamental aspects: structural patterns, non-structural noise, and relationships among genotypes, environments, and genotypes & environments considered jointly. Pattern implies that a number of genotypes respond to certain environments in a systematic, significant and interpretable manner, whereas noise suggests that the responses are unpredictable and un-interpretable.

When the performance of genotypes is compared across environments, several genotype attributes are considered, of which grain yield is one of the most important. The measured yield of each genotype in each test environment is a mixture of environment main effect (E), genotype main effect (G), and genotype x environment interaction (GxE). In normal METs, E explains most (up to 80% or higher) of the total yield variation, and G and GxE

are usually small (Gauch & Zobel, 1996; Vargas et al., 1999; Yan et al., 2000; Yan, 2002).

Yield trial research, aimed at selecting superior genotypes in a breeding program faces two fundamental problems: interaction and noise (Gauch & Zobel, 1996). Were there no interaction, a single variety of wheat (*Triticum aestivum* L.) or corn (*Zea mays* L.) or any other crop would yield the most the world over, and furthermore the variety trial need be conducted at only one location to provide universal results. And were there no noise, experimental results would be exact, identifying the best variety without error, and there would be no need for replication. So, one replicate at one location would identify that one best maize variety that flourishes worldwide. Returning now to reality, however, one genotype may perform well under specific environmental conditions and may give a poor performance under other conditions.

When assessing grain yield of a set of genotypes in a multi-environment trial, changes are commonly observed in the relative yield performance of genotypes with respect to each other across environments. This differential yield response of genotypes from one environment to another is called genotype x environment interaction (GxE) and can be studied, described and interpreted by statistical models (Crossa, 1990).

1.3 Problem Statement

Multi-environment yield trials produce quantities of data and finding the useful information within that data has been a major challenge of plant breeding. Most plant breeders develop knowledge of their genotypes and environments either from detailed field observations (often by visual comparison of new cultivars to check varieties in many locations, in what frequently appears to be an intuitive process) or based on results obtained from traditional approaches to data analysis (such as ANOVA or linear regression, which are flawed in one respect or another with regard to a given data set).

However, we believe that other efficient statistical assessment of multi-environment yield trial data is needed, aiming not to disregard breeders' impressions, but to enable them get effective insight into their research material. We want to emphasize that it is essential that agro-ecological understanding of the genotypes and the environments runs parallel with efficient statistical analysis of MET data.

1.4 Objectives of the Study

Several statistical procedures have been proposed to analyze multi-environment yield trial data and assess yield stability. The most commonly used statistical technique for analyzing genotype x environment interaction is the two-way cross classification analysis of variance (ANOVA). Linear regression (LR) techniques have been proposed which are based on some measure of the environment, usually an environmental index (mean). Multiplicative statistical models can also be used in analyzing genotype by environment data.

The present study considers several statistical approaches for the analysis of multi-environment yield trials in the context of plant breeding. In particular, the objectives of this study are to:

(i) compare genotype x environment interaction models used in multi-environment yield trials and choose the best one for the current data;

(ii) determine yield stability and classify genotypes based on similarity of response patterns; and

(iii) identify stable and high yielding genotypes.

Empirical results are illustrated with reference to a maize (*Zea mays* L.) variety trial.

The remainder of this thesis is organized as follows. Chapter 2 provides a review of related literature on genotype x environment interactions and phenotypic stability in agricultural crop variety trials. After data description, a number of GxE models and stability statistics are discussed in Chapter 3. Chapter 4 applies the methods typically employed in Chapter 3 to a real maize data set. Included in Chapter 4 is a discussion on

the results obtained. Some conclusions and recommendations are presented in the final Chapter. The appendixes contain SAS programs and diagnostic checks.

CHAPTER TWO
LITERATURE REVIEW

2.1 Basic Concepts

Quantitative Genetic Theory states that an individual's phenotype (P) is the product of the genotype (G) of the individual, the environment (E) that the individual is exposed to, and the interaction that occurs between the genotype of the individual and the environment (GxE) (Lee et al., 2003).

Genotypes refer to the set of genes possessed by individuals that are important for the expression of traits under investigation. The environment is usually defined as all non-genetic factors that influence expression of traits and may include locations, years, management practices or a combination of these factors that influence the growth and development of individuals and thereby influencing expression of traits (Basford & Cooper, 1998). Allard and Bradshaw (1964) classified environmental variables as unpredictable and predictable factors. The unpredictable variations include the fluctuating features of the location such as rainfall, relative humidity, temperature, etc., whereas the predictable variations are those factors which are under human control which include planting date, row spacing, plant population and rates of nutrient application. Both conditions provide a greater range of environmental condition to test genotypes (Eberhart & Russell, 1966).

Genotype by environment interactions by definition involves both genotypes and environments. The presence of genotype x environment interaction (GxE) in agriculture is expressed either as inconsistent responses of some genotypes relative to others due to genotypic rank change or as changes in the absolute differences between genotypes without rank change. The contribution of predictable environmental fluctuations to GxE can be reduced by allocating specific cultivars to specific environments. Unpredictable environmental variation is more difficult and often leads to large interactions (Allard &

Bradshaw, 1964). Large GxE effects tend to be viewed as problematic in breeding because the lack of predictable response hinders progress from selection (Dudley & Moll, 1969).

Yield trials generate observations of yield, ordinarily replicated, for a number of genotypes grown in a number of environments (location-year combinations). The measured yield of each cultivar in each test environment is a mixture of environment main effect (E), genotype main effect (G), and genotype x environment interaction (GxE).

According to Gauch and Zobel (1988) three options exist for increasing the usefulness of yield data:

1. *Improved experimental techniques*. Accuracy can be increased by larger plots, selection of sites with more uniform soil and more uniform management (application of seed, herbicide, fertilizer and so on). Also, more precise duplication of farmer's fields and management procedures can increase the pertinence of experimental results.
2. *More replicates or more sophisticated layout of the replicates*. The accuracy of a mean improves, for the completely randomized experimental design, with the square root of the number of replicates (Snedecor & Cochran, 1980). For more sophisticated experimental designs, such as the randomized complete block or randomized incomplete block designs, the rate of improvement may be somewhat different.
3. *Better statistical analyses.*

Plant breeders use yield trials to identify promising genotypes on the basis of phenotypic stability in different environments. However, this depends on the level of yield estimates and magnitude of GxE (Gauch, 1988).

To reduce the complications that the GxE creates when selecting superior genotypes, many attempts have been made to (i) understand the environmental components causing

the GxE (Epinat-Le Signor et al., 2001), (ii) examine the GxE biometrically (Lin et al., 1986; Zobel et al., 1988; Finlay & Wilkinson, 1963; Yan et al., 2001), (iii) develop selection strategies that involve stability parameter (Magari & Kang, 1993).

Instability of yield is one of the several factors that limit maize production, because for quantitative characters such as yield the relative performance of cultivars often changes from one environment to another. Most plant breeding programs aim at selecting genotypes that are consistently high yielding over the range of environments that occur in different locations or seasons. However, a significant genotype by environment interaction creates difficulty in identifying a superior variety (Eberhart & Russell, 1966). Information on the interaction of genotypes with environment is crucial in developing new cultivars for production in diverse environments. Such information guides the breeder in choice of selection methods and test sites for optimal character expression.

Allard and Bradshaw (1964) recommended extensive testing to identify cultivars that show minimum interaction with environments, or possess greatest yield stability. Among the test materials, an ideal genotype would be adapted to a wide growing conditions in a given production area. Therefore, identifying genotypes that show minimum interaction with environment or posses greatest yield stability is an important consideration particularly in regions where environmental fluctuations are considerable.

2.2 Understanding Genotype x Environment Interaction

When assessing grain yield of set of cultivars in a MET, changes are commonly observed in the relative yield performance of cultivars with respect to each other across sites. This differential yield response of cultivars from one environment to another is called genotype x environment interaction (GxE) and can be studied, described, and interpreted by statistical models (Crossa, 1990).

Statistically, GxE is detected as a significantly different pattern of responses among the genotype across environments. In biological terms, this will occur when the contributions

(or level of expression) of the genes regulating the trait differ among environments (Basford & Cooper, 1998).

Developing crop cultivars that perform well across a wide range of environmental conditions has long been a major challenge to plant breeders. In practice, genotype by environment interaction complicates the identification of superior genotypes (Allard & Bradshaw, 1964). GxE interaction is a major concern in plant breeding for two main reasons: it reduces progress from selection, and secondly, it makes cultivar recommendation difficult. GxE occurs both in short-term (less than five years testing at a location) and long-term (several years at various locations) crop performance trials (Eberhart & Russell, 1966).

Identification of causal factors of the GxE effect and quantification of unexplained variation are of prime importance for selecting or to recommend environmentally specific varieties (Epinat-Le Signor et al., 2001). An understanding of environmental and genotypic causes of GxE is important at all stages of plant breeding, including ideotype design, parent selection based on traits, and selection based on yield. Understanding of the cause of GxE can be used to establish breeding objectives, identify ideal test conditions, and formulate recommendations for areas of optimal cultivar adaptation (Yan & Hunt, 1998).

The study of GxE is particularly relevant for countries that have diversified agro-ecologies. Under such diversified agro-ecological conditions, the breeder should be able to select desirable genotypes without losing valuable germplasm and other vital resources. Hence, agro-ecological diversity could complicate breeding and testing of improved varieties with adequate adaptation, but it could also permit identification of extreme environmental conditions that might offer selection pressure from different stresses (Romagosa & Fox, 1993).

Selection of genotypes is based on the assessment of their phenotypic value in varying environments. GxE, which is associated with the differential performance of genetic

materials, tested at different locations and in different years and its influence on the selection and recommendation of genotypes has long been recognized (Lin et al., 1986; Becker & Léon, 1988; Crossa, 1990). Evaluation of genotypic performance at a number of locations provides useful information to determine their adaptation and stability (Crossa, 1990). Bilbro and Ray (1976) indicated that a successful breeding program should focus efforts on genotype yield level (average yield compared to standards), adaptation (what environment does the genotype best perform in), and stability (how consistent does the genotype yield compared to others). Measuring GxE helps to determine an optimum breeding strategy, to breed for specific or general adaptation, which depends on the expression of stability under a limited or wide range (Crossa, 1990; Romagosa & Fox, 1993).

The knowledge of GxE can help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine-tuning the programme (Shaffi et al., 1992; Kang & Magari, 1996). The presence of a large GxE interaction may necessitate establishment of additional testing sizes, thus increasing the cost of developing commercially important varieties. Thus, GxE relates to sustainable agricultures as it affects efficiency of breeding programme and allocation of limited resources (Shaffi et al., 1992).

Another important part of the genotype evaluation process is selecting the appropriate field trial locations that best represent the target environments for which the breeding program is directed toward. The term mega-environment describes the separation of a crop growing area into different target zones (Gauch & Zobel, 1997). Gauch and Zobel (1997) contend that subdividing a crop-growing region into several mega-environments implies higher heritabilities and faster progress for plant breeders, potentially stronger competitiveness for seed producers and higher yields for growers.

2.3 Some Concepts of Stability

In earlier years, a major concern in agricultural research has been to develop high yielding crop cultivars. Lately, however, stable and sustainable yields under varying environmental conditions have constantly been gaining importance over increased yields. Stable yields play a major role in the developing countries. A main strategy among small-scale subsistence farmers, particularly in marginal areas, is risk-minimization. In these areas, stable yields are the key to sustainable food supplies (Piepho, 1996).

In agricultural research, different concepts and definitions of stability have been developed mainly for application in plant breeding programs and in the evaluation of yield trials. The interest of plant breeders in stability stems from the need to develop well-buffered cultivars. The term stability refers to the behavior of a crop in varying environments. The breeders' aim is to develop cultivars that are stable across a range of environments. Environments may be locations or years or combinations of both. However, the concept of stability is by no means unambiguous; it is defined in many ways depending on how the investigator wishes to look at the problem while the procedures that measure these various concepts are also numerous (Lin et al., 1986; Becker & Léon, 1988; Delacy et al., 1996).

In a critical literature review of stability, Lin et al. (1986) classified the conventional stability concept into three types.

Type one: A genotype is considered to be stable if its among-environment variance is small. A stable genotype possesses an unchanged performance regardless of any variation of the environmental conditions. This concept of stability is useful for quality traits, disease resistance, or for stress characters like winter hardiness. Methods used to describe this type of stability are coefficient of variability for each genotype used by Francis and Kannenberg (1978) and the genotypic variances across environments.

Type two: A genotype is considered stable if its response to environments is parallel to the mean response of all genotypes in the trial. A stable genotype has no deviations from the general response to environments and thus permits a predictable response to environments. Wricke's (1962) ecovalence and Shukla's (1972) stability variance can be used to measure type 2 stability.

Type three: A genotype is considered to be stable if the residual mean square from the regression model on the environmental index is small. The environmental index implicates the mean yield of all the genotypes in each location minus the grand mean of all the genotypes in all locations. Eberhart and Russell (1966) deviation from regression can describe type 3 stability.

Lin et al. (1986) concluded that among these three types of stability, type 3 is the most problematic, because the residual MS from a regression model is merely an indication of goodness of fit, and cannot be considered as a stability parameter. Their reason was that the regression model is a data-based descriptive model (not a predictive model based on external variables), and thus the residuals do not have a deterministic property that can be associated with genotypes. Since type 2 stability uses the mean response as the standard, a stable genotype by this definition implies stability only with respect to the other genotypes in the test and it cannot be generalized. In contrast to both types 2 and 3, type 1 is a biologically meaningful parameter: it measures a genotype's homeostatic property to resist environmental change. However, this parameter has practical disadvantages. A breeder would like to find a genotype not only with good type 1 stability but also with high yield. However, type 1 stability is often associated with a relatively poor response in environments where other genotypes have high yields. Furthermore, although a high level of performance under a wide range of environments is desirable, this is difficult to achieve in practice. Even if it can be achieved, the effort is not entirely necessary, because several less widely adapted genotypes can be bred and then grown separately in different environments to achieve maximum production. Thus, the usefulness of type 1 depends largely on the range of environments under which the experiment is conducted.

Becker and Léon (1988) have suggested two different approaches to assess stability: the static concept and the dynamic concept. According to the static concept (type one in Lin et al., 1986), maximum stability occurs when the yield of the genotype under consideration is constant across environments, i.e., stability in the sense of homeostasis. On the other hand, according to the dynamic concept (type two in Lin et al., 1986), a genotype is regarded as stable if its performance in different environments is close to what can be expected from the potentials of those environments. Maximum stability occurs if the difference between a genotype's yield and the environmental index, commonly defined as the mean of all tested genotypes, is constant across environments. Whenever this difference is not the same in all environments, the corresponding genotype is said to interact with environments. Hence, if a breeder prefers the dynamic concept, the goal of breeding stable genotypes may be translated as the goal of minimizing genotype x environment interactions. The dynamic approach regards interactions as random unpredictable fluctuation (noise).

In certain cases, however, one may seek to further analyze the interactions and extract predictable information from it (pattern). This leads to the regression approach first suggested by Yates and Cochran (1938) and further elaborated by Finlay and Wilkinson (1963) and Eberhart and Russell (1966). Recent developments comprise application of a multiplicative interaction model, which was first introduced by Gollob (1968) and Mandel (1971) and has been introduced in the agricultural context as AMMI (Additive Main Effects and Multiplicative Interaction) model (Gauch, 1988, 1992).

2.4 General Statistical Considerations

Within plant breeding, a tradition exists to describe phenotypic responses across environments in terms of statistical parameters that have well defined statistical properties. The dominant quantitative genetic paradigm in plant breeding dictates models for phenotypic expression to consist of sums of terms that are indexed by either genotypes, environments, or combinations of both (Lee et al., 2003; van Eeuwijk et al., 2004).

The simplest model for the description of phenotypic responses across environments, the additive model, contains only single indexed terms. For the phenotypic response of genotype i in environment j, y_{ij}, we write $y_{ij} = \mu + G_i + E_j + random\ \ error$. The additive model merely states that we might try to describe the phenotypic responses for a set of genotypes as a set of parallel straight lines, where the differences between the responses are given by the differences between the genotypic main effects. To illustrate this, we consider the increase in the mean response for a genotype i, when going from environment j to j^*, where we assume that j^* represent the better environment, or, $E_{j^*} > E_j : y_{ij^*} - y_{ij} = E_{j^*} - E_j$. It is obvious that all genotypes will show the same increase in phenotypic response, when going from j to j^*. When the environmental main effect is interpreted as an indicator of environmental quality, we might say that all genotypes exhibit the same sensitivity to the environment.

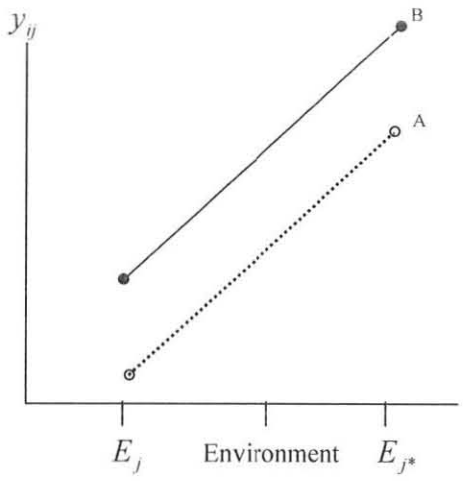
The main purpose of the additive model is to interpret phenotypic differences in terms of differences between the levels of the genotypic factor on the one hand and between levels of the environmental factor on the other hand for the included sets of genotypes and environments. This result from the reduction of a function of two variables, y_{ij}, into two functions of a single variable each, G_i and E_j (Mandel, 1961, 1971).

The additive model is an elementary model that is more important as a didactical tool to introduce statistical models for genotype by environment data than a serious description of such data. The additive model provides a null model against which to test models that are more complicated with terms for genotype by environment interaction. Genotype by environment interaction occurs whenever genotypes react differently to environmental changes. So, whenever the difference in phenotypic performance between two environments j and j^* varies between two genotypes i and i^*, i.e. $y_{ij^*} - y_{ij} \neq y_{i^*j^*} - y_{i^*j}$, the additive model will be inadequate and a more elaborate model should be formulated. Presence of GxE rules out simple interpretative models that have only additive main

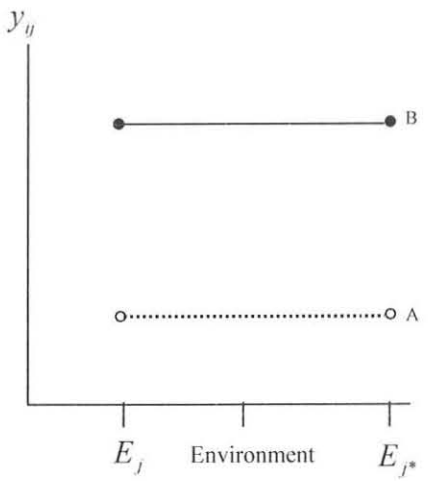
effects of genotypes and environments (Mandel, 1971; Crossa, 1990; Kang & Magari, 1996).

Traditionally, the additive model is extended to a full interaction model with double indexed genotype by environment terms for each combination of genotype and environment $y_{ij} = \mu + G_i + E_j + (GxE)_{ij} + random \quad error$. In the full interaction model there are as many independent parameters as genotype by environment combinations and from the point of view of parsimony little has been accomplished by fitting this model to the data. Predictions of phenotypic responses for environments that were not in the set of trial environments are impossible, as there will be no estimates for the particular $(GxE)_{ij}$ terms. Compare this with the situations for which the additive model provides a good fit. In those cases rough predictions are possible as long as the quality of the new environment can be ranked as being in between two environments that were part of the multi-environment trial.

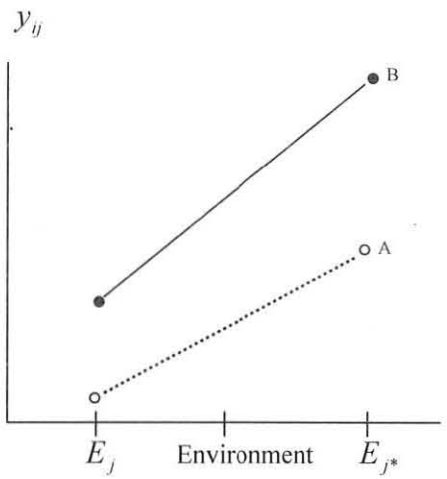
Figure 2.1 displays four hypothetical cases for the mean responses of two genotypes (A and B) in two environments (E_j and E_{j*}). Cases (a) and (b) depict a lack of an interaction effect. Note that in both graphs the lines are parallel. Cases (c) and (d) indicate an interaction effect. Here we see that the lines are not parallel. In Case (c) the interaction is of a non-crossover type; genotype B can be recommended for both E_j and E_{j*}. In Case (d) the interaction is of a crossover type. In plant breeding, the most important type of GxE is crossover or qualitative, which implies changes in the rankings of genotypes across environments. Crossover GxE complicates breeding, testing and selection of superior genotypes. In general, when different lines or cultivars of a given crop are evaluated in a sufficiently wide range of environments, genotype x environment interactions of crossover type seem to be very common (Ceccarelli, 1989; Annicchiarico, 2002).



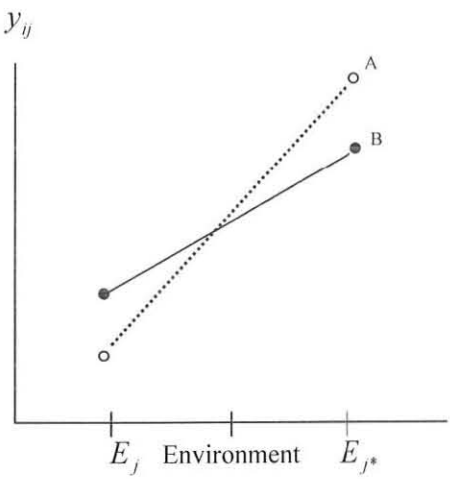
(a) Null genotype x environment interaction (GxE) effect.



(b) Null GxE effect.



(c) Non-crossover GxE.



(d) Crossover GxE.

Figure 2.1 Patterns of the genotype behaviors in different environments outlining the two fundamental types of interaction, considering only a simple case of two genotypes and two environments.

Source: Annicchiarico, 2002.

Although the ANOVA can partition the total variation into that due to the main effects and that due to the interaction, it fails to exhaustively analyze the nonadditive GxE. The first attempt to extract more information from the GxE term was the use of linear regression. The regression approach partitions GxE into a pattern component attributable to heterogeneity among the linear response of genotypes to varying yield potential of environments and a residual based on deviations from regressions (Sneller et al., 1997). This approach has been extensively used in genetics, plant breeding and agronomy for determining yield stability of different genotypes or agronomic treatments (Crossa, 1990). It was first proposed by Yates and Cochran (1938) in their analysis of a barely yield trial. Yates and Cochran (1938) introduced the model in which the GxE term is linearly related to the environmental effect. This approach was later used by Finlay and Wilkinson (1963) and slightly modified by Eberhart and Russell (1966).

The regression on the environmental mean model partitions the genotypes x environment interaction into a component due to linear regression of the i^{th} genotype on the environmental mean and a residual. The philosophy behind this model is that in the absence of explicit physical or meteorological characterization of an environment, a good approximation to the biological quality of an environment is given by the average phenotypic performance across the genotypes. The phenotypic responses of individual genotypes are then regressed on the average performance and the genotype by environment interaction GxE expresses itself by differences in the slopes between the genotypes (Vargas et al., 1999; van Eeuwijk et al., 2004).

The statistical success of the regression on the mean model depends on the proportion of GxE that is described by the differential environmental sensitivity of the genotypes, or, equivalently, by the quality of the environmental effect as a reflection of the environmental forces that causes phenotypic differences between genotypes. The regression on the mean model provides only limited flexibility for describing GxE, because of its rather specific, one-dimensional incorporation of the environmental factors affecting the phenotypic responses.

Part of the genotype's performance across environments or genotypes stability is expressed in terms of three empirical parameters: the mean performance, the slope of the regression line, and the sum of squares deviation. An ideal genotype possesses high yield performance; regression coefficient equal to unity; and small sum of squares of deviations (Eberhart & Russell, 1966). Many authors—Crossa (1988), for example—have recognized the difficulty to reach a fair compromise between the mean, the slope and the deviation from regression that will allow the breeder to make a correct decision as to the superiority of the varieties. Lin et al. (1986) suggested the main reason for the difficulty in trying to reconcile these stability parameters in a unified conclusion: even though the genotype's response to environments is multivariate, the regression approach tries to transform it into a univariate problem.

In the literature some other definitions for the regression coefficient and the deviations are proposed which are merely linear transformations. For example, the regression coefficients are diminished by one to get a mean of zero (Perkins & Jinks, 1968).When attention is focused on environments; the converse analysis may be performed by regressing each environment yields on the genotype means.

The regression method has received criticism from the scientific community (Becker & Léon, 1988; Lin et al., 1986; Crossa, 1990). The first statistical criticism of regression analysis is that the genotype mean is not independent of the marginal means of the environment. Regressing one set of variables on another that is not independent violates one of the assumptions of regression analysis. This interdependence may be a major problem for small numbers but not when the number of genotypes is large (say 15 to 20). If the standard set for stable yield is based on very few genotypes (say 4), each estimated stability coefficient involves regressing one genotype on an average to which it contributes one – fourth.

The second statistical problem is that it assumes a linear relationship between interaction and environmental means. When this assumption is violated, the effectiveness of the analysis is reduced, and results may be misleading. In fact, the analysis requires that a

high proportion of the genotype by environment effects should be attributable to linear regression.

A major biological problem pointed out by Crossa (1990) is when only a few low or high yielding environments are included in the analysis. The genotype fit may be determined largely by its performance in a few extreme environments, which in turn generates misleading results and thus regression analysis should be used with caution when the data set includes results from only a few high or low yielding environments.

Another biological criticism of the regression method is that relative stability of any two genotypes depends not only on the particular set of environments included in the analysis but also on the other genotypes that are included in the regression calculation. It has been shown that a stability of a genotype depends on the mean performance of the group with which that entry is being compared. Furthermore, it is possible that the ranking of two genotypes stability coefficients may be reversed when they are being compared with two other sets of genotypes.

Most of the data collected in agricultural experiments are multivariate in nature because several attributes are measured on each of the individuals included in the experiments, i.e., genotypes, agronomic treatments, etc. Such data can be arranged in a matrix Y, where the $(i, j)th$ element represents the value observed for the j^{th} attribute measured on the i^{th} individual (case) in the sample. Common multivariate techniques used to analyze such data include principal component analysis (PCA) if there is no a priori grouping of either individuals or variables; canonical variate or discriminant analysis if the individuals in the sample form a priori groups; and cluster analysis if some partitioning of the sample is sought (Dias & Krzanowski, 2003).

According to Crossa (1990) multivariate analysis has three main purposes: a) to eliminate noise from the data pattern (i.e. to distinguish systematic from non-systematic variations; b) to summarize the data; and c) to reveal a structure in the data. In contrast with classic

statistical methods, the function of multivariate analysis is to elucidate the internal structure of the data from which hypotheses can be generated and later tested by statistical methods (Williams & Gillard, 1971, cited by Crossa, 1990). A typical example of a matrix Y arises in the analysis of MET, in which the rows of Y are the genotypes and the columns are the environments where the genotypes are tested. A genotype grown in different environments will frequently show significant fluctuation in yield performance relative to other genotypes. Yield response of m genotypes tested in n environments can be regarded as m points in n-dimensional space (Lin et al., 1986; Crossa, 1990).

Recent studies have shown the additive main effects and multiplicative interaction (AMMI) model to be useful for analyzing yield trial data (Gauch, 1988; Zobel et al., 1988; Gauch & Zobel, 1988, 1989, 1996). The AMMI model combines analysis of variance for the genotype and environment main effects with principal components analysis of the genotype x environment interaction (GxE).

A significant feature of multivariate models, including AMMI analysis, is that they account for a large proportion of pattern in the first few dimensions with subsequent dimensions accounting for a diminishing percentage of pattern and an increasing percentage of noise (Gauch, 1988).

Zobel et al. (1988) compared the traditional statistical analyses (analysis of variance, linear regression, and principal components analysis) with AMMI analysis, and showed that the traditional analyses were not always effective in analyzing the MET data structure. The ANOVA model describes main effects effectively and determine if GxE is a significant source of variation, but it does not provide insight into the patterns of genotypes or environments that give rise to the interaction. The LR method uses environmental means, which are frequently poor estimates of environments, such that the fitted lines in most cases account for a small fraction of the total GxE variation. PCA is a multiplicative model that contains no sources of variation for additive genotype and environment main effects and does not analyze the interaction effectively (Zobel et al., 1988). AMMI analysis has been shown to be effective because it captures a large portion

of the GxE sum of squares, it cleanly separates main and interaction effects that present agricultural researchers with different kinds of opportunities, and the model often provides biologically meaningful interpretation of the data (Zobel et al., 1988; Ebdon & Gauch, 2002).

AMMI has proven effective for a variety of purposes:

1) Better understanding of GxE is facilitated by the genotype and environment PCA scores, particularly as presented graphically in a biplot (Zobel et al., 1988).
2) More accurate yield estimates (Gauch, 1988; Gauch & Zobel, 1988).
3) Greater accuracy translates into new options to create experimental designs with fewer replications or with more genotypes and/or environments (Gauch & Zobel, 1989; Gauch, 1990).
4) Greater accuracy also improves success in selecting truly superior material. In a typical plant breeding scenario, the selection gain requiring 3 years without AMMI could be achieved in only 2 years with AMMI (Gauch & Zobel, 1989).
5) Ultimately the better understanding of interactions and the greater accuracy of yield estimates makes possible more reliable variety recommendations and more rapid advancement in breeding programs (Gauch & Zobel, 1989).

AMMI can also be useful for model diagnosis (Bradu & Gabriel, 1974, 1978). It may identify other models or sub cases as most appropriate for a given data set. If only the additive or only the multiplicative portions of the AMMI model are significant, then the ANOVA or PCA sub cases are indicated. Furthermore, if the PCA axes in AMMI are ineffective in concentrating the interaction SS into a few axes, then the interaction is probably highly complex, and consequently it may be difficult or impossible to find any parsimonious or reduced model; hence, the ANOVA composite test for interaction is then appropriate for diagnosing the general means model. Indeed, unless one at least tries AMMI, in many cases it will be difficult to justify or to discover the more appropriate model (Gauch, 1988).

Williams (1952) was the first author to link the fixed effects two-way model with principal component analysis (PCA). Gollob (1968) and Mandel (1971) extended Williams' (1952) work by considering the GxE as the sum of multiplicative terms. AMMI has gone under a host of names, including FANOVA (factor analysis of variance), MI (multiplicative interaction), doubly centered PCA, and biplot analysis (although this last name is a misnomer since "biplot" refers to a type of graph, not to a particular model). Historically, the first motivation for using AMMI, clearly reflected in the influential paper by Bradu and Gabriel (1978), was dimensionality reduction: to produce a parsimonious, low-dimensional summary of complex, high-dimensional data. But Huber (1985) show that PCA–related analyses can effectively separate pattern from noise. Accordingly, a second motivation for using AMMI, first reported in Gauch (1988) and Gauch and Zobel (1988), was noise reduction: to distinguish pattern from idiosyncratic variations in the data, thereby gaining accuracy and improving decisions.

AMMI analysis of yield data is supplied with no environmental data—just yield data. Nevertheless, significant AMMI parameters (for both main and interaction effects) ordinarily reflect identifiable causal factors. By various informal or formal means, the pattern in AMMI parameters or biplots can usually be interpreted clearly in terms of evident environmental or genetic causal factors (Gauch & Zobel, 1996).

The AMMI algorithm has two parts: ANOVA and PCA. The first part of AMMI analysis uses ANOVA to partition the total variation into three orthogonal sources: Genotypes (G), environments (E), and genotype x environment interactions (GxE). The second part of AMMI analysis uses PCA to partition the genotype x environment interaction (GxE) into several orthogonal interaction axes. After fitting the genotype and environment main effects in the model, a crucial step in the analysis is the determination of the amount of pattern, namely the portion of GxE variation representing real responses to genotypes and environments, and of noise, i.e. the random variation effecting GxE effects. Ideally, only pattern is included in the selected AMMI model by retaining in its multiplicative term the statistically significant genotype x environment interaction PCA axes (Annicchiarico, 1997). However, one aspect that has not been fully resolved concerns the determination

of the multiplicative components to be retained in the model to adequately explain the pattern in the interaction. Some proposals have been put forward by, among others, Gollob (1968), Mandel (1971), Gauch and Zobel (1988).

Yield data from MET are usually quite large, and it is difficult to grasp the general pattern of the data without some kind of graphical presentation (Yan, 2002). The biplot technique (Gabriel, 1971) provides a powerful solution to this problem. The biplot facility available from AMMI allows visual inspection and interpretation of the underlying structure and causes of interaction (Gauch, 1988; Zobel et al., 1988; Shafii & Price, 1998; Vargas et al., 1999; Ebdon & Gauch, 2002). A biplot consists of PCA scores plotted against each other (e.g., component 1 versus component 2) or PCA scores plotted against genotypic and environmental means.

One disadvantage of the AMMI biplot is if the number of components retained in the model is large (say > 3), it is difficult to describe the behavior of the GxE due to the impossibility of obtaining graphs in more than three dimensions. It is possible to plot all pairs of components but, in this case, each component accounts only for a small portion of the total GxE variation.

AMMI can be combined with classifications by circling groups of points in a biplot, or equivalently, by using different symbols for different groups. The classification may come from a clustering algorithm applied to the yield data to classify genotypes or environments or both, or it may come from intrinsic, known factors, such as the pedigrees of the genotypes or the geographical locations of the environments (Crossa et al., 1991; Gauch & Zobel, 1996).

The remainder of this section focuses on reviewing studies reported by researchers at the Ethiopian Institute of Agricultural Research, particularly in relation to statistical analysis of genotype by environment interactions in agricultural variety trials. We want to emphasize that most of these studies used traditional statistical approaches developed to describe and interpret genotype by environment data. A comprehensive discussion of the

numerous studies is not possible here, but some of the studies may be reviewed in few details.

Mosisa et al. (2001) studied the interaction of 20 maize (*Zea mays* L.) genotypes of East African and CIMMYT origins in 9 locations, using linear regression analysis. The authors reported that none of the tested genotypes exhibited broad adaptability. Gelana et al. (2001) calculated Eberhart and Russell's stability statistics for 20 maize (*Zea mays* L.) genotypes tested in 18 location-year environments and recommended cultivars for drought stressed areas of Ethiopia. Regression analysis has also been used by Adugna and Elias (1994), Fekadu (1994), Fetien (1997), Asrat and Daniel (2004), among others.

Elias and Assefa (1999) applied Duncan's multiple range test and regression analysis to evaluate dry pod yield performance in elite ground nut (*Arachis hypogaea* L.) variety trials conducted in North Omo zone. Their study found highly significant genotype x environment interaction for dry pod yield, and picked two Virginia bunch types as winning genotypes. In Geremew et al. (2001), average linkage cluster analysis and regression analysis were performed to investigate the diversity and explore yield stability of 64 sorghum [*Sorghum bicolor* (L.) Moench] cultivars collected from Gambella area and evaluated at 3 locations. Despite the fact that the composite test of interaction failed to reject the null hypothesis that interaction is not present, the authors took the approach of continuing with further analysis of the interaction. They argued that, in a case where some genotypes contributed more to the interaction sum of squares than the others, failure of the composite test of interaction should not be regarded as a stopping rule. Consequently, they clustered the tested genotypes into three groups and also selected eight 'representative' genotypes to be used in future improvement program.

Interesting studies in the area of genotype by environment interactions in agricultural experiments have been carried out by Girma (1997) and Girma et al. (2000). Girma (1997) discussed in a statistical sense a subset of methods from the array of available techniques for analyzing GxE, emphasizing the AMMI model and single-DF interaction contrasts. The author concluded that no single model can be preferred to be used at all

times. Also, the cited paper suggested that, depending on the type of data set and research purpose, models can be 'complementary rather than being competitive'.

In analyzing yield trial data for 36 field pea (*Pisum sativum* L.) genotypes and 8 environments, Girma et al. (2000) used AMMI analysis to partition the genotype x environment interaction matrix into individual genotypic & environmental scores and came to the conclusion that AMMI-2 tends to be the best model for extracting patterns and rejecting noise from the data. Girma and colleagues further compared AMMI score-based analysis and observed values for clustering environments and field pea cultivars into homogeneous subsets. They indicated that cluster analysis following the AMMI modeling of GxE effects has the theoretical advantage of assessing similarity after separating the pattern from the noise portion of GxE variation and therefore suggested using the expected yields of genotype-environment combinations according to the selected AMMI model, rather than the observed yield values. Using the results from AMMI plus cluster analysis, the authors identified few varieties presenting good yield and stability for the target areas.

CHAPTER THREE
MATERIALS AND METHODS

3.1 Setting of Field Trial and the Data

The data being considered here are obtained from trials conducted by Awassa National Maize Research Project of Ethiopian Institute of Agricultural Research (EIAR). Grain yield data of fifteen maize genotypes (Table 3.1) evaluated from 2004-2005 in eight location-year environments (Table 3.2) was used in this study. An "environment" is defined here as a location-year combination. Environments are considered as random effects whereas genotypes are considered as fixed effects.

Table 3.1 List of maize genotypes used in the study.

No.	Genotype code
1	G1
2	G2
3	G3
4	G4
5	G5
6	G6
7	G7
8	G8
9	G9
10	G10
11	G11
12	G12
13	G13
14	G14
15	G15

The experimental design used in each trial was a randomized complete block design (RCBD) with three replicates. Each genotype (entry) was grown in a four-row plot 5.1m long with 75cm spacing between rows and 30 cm spacing between plants. Plots were managed conventionally and followed the established local practices. The experiment was performed under rain fed conditions and fertilizers were not applied. In each plot, the

central two rows were harvested manually after eliminating the border areas. Grain yields are expressed in qt/ha at 12.5 moisture content.

An important consideration in the analysis of genotype-by-environment data is whether environments are considered as fixed or random. If interest is in performance of genotypes in the particular testing environments, environments are usually regarded as fixed. In this case, inferences pertain to specific genotypes and specific environments rather than some population of genotypes and environments. If environments can be regarded as a random sample from a population of environments, it is appropriate to regard environmental and interaction effects as random.

Table 3.2 Description of environments included in the study.

Location code	Name	Altitude (m)	Soil type	Year *	
				2004	2005
1	Awassa	1700	Andosol	E1	E5
2	Arsinegelle	1960	Andosol	E2	E6
3	Areka	1800	Nitosol	E3	E7
4	Goffa	1300	Acrisol	E4	E8

* Environment code is given in this column.

Multi-environment data can be analyzed either as replicate data or as genotype-environment means. If trials at different environments were laid out in complete blocks with the same number of replications and the error variance does not vary among trials, genotype-environment means are conditionally independent and are measured with equal precision. In this case, analysis based on means is valid, even when some genotype-environment combinations are missing (Piepho, 1999).

Table 3.3 displays the general form of genotype-environment means observed from the evaluation of m genotypes in n environments. In Table 3.3, entry y_{ij} is the empirical mean response of the i^{th} genotype in the j^{th} environment, $\bar{y}_{i.}$ is the marginal mean of genotype i, $\bar{y}_{.j}$ is the marginal mean of environment j, and $\bar{y}_{..}$ is the overall mean.

Table 3.3 Data structure for genotype-by-environment means of a multi-environment trial.

Genotype	Environment						Marginal mean $(\bar{y}_{i.})$
	1	2	.	.	.	n	
1	y_{11}	y_{12}	.	.	.	y_{1n}	$\bar{y}_{1.}$
2	y_{21}	y_{22}	.	.	.	y_{2n}	$\bar{y}_{2.}$
.	.	.				.	.
.	.	.				.	.
.	.	.				.	.
m	y_{m1}	y_{m2}	.	.	.	y_{mn}	$\bar{y}_{m.}$
Marginal mean $(\bar{y}_{.j})$	$\bar{y}_{.1}$	$\bar{y}_{.2}$	.	.	.	$\bar{y}_{.n}$	$\bar{y}_{..}$

3.2 Statistical Methods

The analysis of multi-environment yield trials is usually complicated by the presence of genotype x environment interaction (GxE). Genotype x environment interaction has been studied, described, and interpreted by means of several statistical models (Crossa, 1990). The next sections discuss various approaches for the analysis of phenotypic stability by modeling the genotype x environment interaction. The method receiving primary attention is the additive main effects and multiplicative interaction (AMMI) model.

3.2.1 The Interaction Model in ANOVA

The most commonly used statistical technique for analyzing genotype x environment interaction (GxE) in multi-environment yield trials is the conventional analysis of variance (ANOVA). Consider a trial in which the yield of m genotypes measured in n environments (location-year combinations) each with r replications, totaling mnr observations. The classic model for analyzing the total yield variation contained in mnr observations is the analysis of variance.

In analyzing data from such a multi-environment yield trial, the initial analysis is a separate analysis of variance (ANOVA) for each environment. If the individual experiments are laid out as randomized complete block designs (RCBD), separate ANOVA structure for each environment is

Genotypes or Entries	$(m-1)$ DF
Replicates or Blocks	$(r-1)$ DF
Error	$(m-1)(r-1)$ DF

Replicates serve to estimate the error variance within environments, reduce bias and improve accuracy. At this stage we should assess for homogeneity of error variances across environments. If error variance is homogeneous across environments, a combined analysis of variance (ANOVA) for a complete set of experiments could be carried out.

A combined ANOVA can be performed using either plot values or data of genotypes in individual environments that have been averaged across experiment replicates (i.e. genotype-environment cell means). To convert the results of an ANOVA performed on a cell mean basis into results on a plot basis, for a constant number experiment replicates (r), the sum of squares (SS) of effects must be multiplied by r (Cochran & Cox, 1957).

Combined ANOVAs have advantages such as: (a) verification of the occurrence (i.e. significance) of different effects (main & interaction); (b) estimation and comparison of mean values for levels of fixed factors; and (c) estimation of the variance components. The ANOVA may also represent one step in the analysis of adaptation or in the assessment of yield stability measures (Annicchiarico, 2002).

In multi-environment yield trials of m genotypes $(i = 1,2,...,m)$, n environments $(j = 1,2,...,n)$, and r replicates $(l = 1,2,...,r)$ arranged in RCBD, the linear model for the conventional analysis of variance (ANOVA) is

$$y_{ijl} = \mu + \tau_i + \delta_j + \xi_{l(j)} + (\tau\delta)_{ij} + \varepsilon_{ijl} \qquad (3.1)$$

where

y_{ijl} is the observed yield response of the i^{th} genotype in the j^{th} environment of the l^{th} replicate;

μ is the grand mean overall genotypes and environments;

τ_i is the additive main effect of the i^{th} genotype, with $\sum_{i=1}^{m}\tau_i = 0$;

δ_j is the additive main effect of the j^{th} environment, assumed to be NID$\left(0,\sigma_\delta^2\right)$;

$\xi_{l(j)}$ is the l^{th} block effect in the j^{th} environment, assumed to be NID$\left(0,\sigma_\xi^2\right)$;

$(\tau\delta)_{ij}$ is the non-additive interaction (GxE) of the i^{th} genotype in the j^{th} environment, assumed to be NID$\left(0,\sigma_{\tau\delta}^2\right)$; and

ε_{ijl} is an experimental error term corresponding to y_{ijl}, assumed to be NID$\left(0,\sigma^2\right)$.

The within-environment residual mean square measures the genotype means due to differences in soil fertility and other factors, such as shading and competition from one plot to another (Crossa, 1990). The pooled error MS (MS_e) to be inserted in the ANOVA can be estimated from the experimental errors of individual trials. If there is little variation in residual mean squares from one environment to another and for trials with the same number of replicates, the pooled error variance (MS_e) is found by averaging the residual mean squares of all environments:

$$MS_e = \frac{\sum_{j=1}^{n} MS_{e(j)}}{n} \qquad (3.2)$$

where

$MS_{e(j)}$ is the residual mean square (MS) for the j^{th} $(j = 1,2,...,n)$environment.

Table 3.4 The general analysis of variance (ANOVA).

Source of variation	DF	Mean square
Environment (E)	$n-1$	MS_E
Replicate within environment (R/E)	$n(r-1)$	$MS_{R/E}$
Genotype (G)	$m-1$	MS_G
Genotype x environment interaction (GxE)	$(m-1)(n-1)$	MS_{GxE}
Experimental error (e)	$n(m-1)(r-1)$	MS_e
Total	$mnr-1$	

As mentioned above, analysis of variance of multi-environment trials is useful for estimating variance components related to different sources of variation. For balanced multi-environment trials, that is, those with the same number of genotypes observed per environment, estimation of the variance component can be accomplished using the "analysis of variance method". Each of the mean squares is known to estimate a function of the variance components defined in the model. These functions are called expected mean squares. Denoting an expected value by the symbol **E**, it may be shown that the expected mean squares for the ANOVA model in equation (3.1) are

$$\mathbf{E}\ (MS_E) = \sigma^2 + r\sigma^2_{\tau\delta} + m\sigma^2_{\xi} + mr\sigma^2_{\delta}$$

$$\mathbf{E}\ (MS_{R/E}) = \sigma^2 + m\sigma^2_{\xi}$$

$$\mathbf{E}\ (MS_G) = \sigma^2 + r\sigma^2_{\tau\delta} + nr\frac{\sum_{i=1}^{m}\tau_i^2}{m-1} \qquad (3.3)$$

$$\mathbf{E}\ (MS_{GxE}) = \sigma^2 + r\sigma^2_{\tau\delta}$$

$$\mathbf{E}\ (MS_e) = \sigma^2$$

The method consists of equating the expected mean squares to their observed values in the analysis of variance and solving for the variance components. In equating observed and expected mean squares we obtain

$$MS_E = \sigma^2 + r\sigma^2_{\tau\delta} + m\sigma^2_{\xi} + mr\sigma^2_{\delta}$$

$$MS_{R/E} = \sigma^2 + m\sigma^2_{\xi}$$

$$MS_{GxE} = \sigma^2 + r\sigma^2_{\tau\delta} \qquad (3.4)$$

and

$$MS_e = \sigma^2 .$$

Therefore, the estimators of the variance components are

$$\hat{\sigma}^2 = MS_e$$

$$\hat{\sigma}^2_{\tau\delta} = \frac{MS_{GxE} - MS_e}{r}$$

$$\hat{\sigma}^2_{\xi} = \frac{MS_{R/E} - MS_e}{m} \qquad (3.5)$$

and

$$\hat{\sigma}^2_{\delta} = \frac{MS_E + MS_e - MS_{GxE} - MS_{R/E}}{mr} .$$

The analysis of variance method of variance component estimation does not require the normality assumption. It does yield estimators of the variance components that are best quadratic unbiased (i.e., of all unbiased quadratic functions of the observations, these estimators have minimum variance). This method is limited to balanced data and occasionally produces a negative estimate of a variance component. Clearly, variance components are by definition non-negative, so a negative estimate of a variance component is viewed with some concern. A good discussion of variance component estimation is given by Searle (1971).

In general, variance component methodology is important in multi-environment trials, since errors in measuring the yield performance of a genotype arises largely from

genotype x environment interaction. Therefore, knowledge of the size of this interaction is required to (a) obtain efficient estimates of genotype effects and (b) determine optimum resource allocations, that is, the number of plots and environments to be included in future trials. In a breeding program, variance component methodology is used to measure genetic variability and to estimate the heritability and predicted gain of a trait under selection (Crossa, 1990).

Equivalent expression for the ANOVA model based on cell-means is

$$y_{ij} = \mu + \tau_i + \delta_j + (\tau\delta)_{ij} + \bar{\varepsilon}_{ij} \tag{3.6}$$

where

y_{ij} is the empirical mean response of the i^{th} genotype in the j^{th} environment;

μ, τ_i, δ_j and $(\tau\delta)_{ij}$ are as in model (3.1);

and

$\bar{\varepsilon}_{ij}$ is the mean error related to y_{ij}, assumed to be $NID\left(0, \frac{\sigma^2}{r}\right)$ (where σ^2 is the within-environment error variance, assumed to be constant and r is the number of replications associated to the yield mean y_{ij}).

In model (3.6), after removing replicate effect when combining the data the mn observations are partitioned into two sources: (a) additive main effects for genotypes and environments, and (b) non-additive effect due to genotype x environment interaction. This model is appropriate for the analysis of means from equally replicated data with homoscedastic errors (Piepho, 1997).

The ANOVA model is not parsimonious, because each genotype x environment interaction (GxE) cell has its own interaction parameter, and uninformative, because the independent interaction parameters are complicated and difficult to interpret (Dias & Krzanowski, 2003).

The conventional ANOVA is useful in identifying and testing sources of variability, it does not discern patterns of the underlying interaction. That is, it does not explore any underlying structure within the observed non-additive (GxE). The analysis of variance fails to determine the pattern of response of genotypes and environments. The valuable information contained in $(m-1)(n-1)$degrees of freedom is particularly wasted if no further analysis is done. Since the non-additive structure of the data matrix has a non-random (pattern) and random (noise) component, the advantage of the additive model is lost if the pattern component of the non-additive structure is not further partitioned into functions of one variable each (Crossa, 1990).

The additive nature of the ordinary ANOVA model allows adequate description of main effects; however, the interaction (residual from the additive model) is non additive and requires other techniques to identify interaction relationships.

3.2.2 The Environmental Variance

For the specific case of evaluating phenotypic stability by using the static concept Römer (1917), as explained in Lin et al. (1986); Weber et al. (1996), proposed the use of the variance of each genotype over the environments. Thus, to measure the static phenotype stability of the i^{th} genotype across a set of environments, the following could be used:

$$S_i^2 = \frac{\sum_{j=1}^{n}\left(y_{ij} - \bar{y}_{i.}\right)^2}{n-1} \qquad i = 1,2,...,m \qquad (3.7)$$

where

y_{ij} is the mean yield of the i^{th} genotype in the j^{th} environment, and

$\bar{y}_{i.}$ is the marginal mean of genotype i.

A stable genotype has a small variance. A problem with this method is that, in general, genotypes with high phenotypic stability measured through the environmental variance show low yield. In consequence, plant breeders do not use this method to evaluate yield stability across environments, or other related random variables. Derived quantities

include $S_i = \sqrt{S_i^2}$ and the coefficient of variation $\left(CV_i = S_i / \bar{y}_{i.}\right)$ (Lin et al., 1986; Weber et al., 1996).

3.2.3 Ecovalence

The simplest method to evaluate phenotypic stability using the dynamic concept is due to Wricke (1962)*. Wricke (1962) considered stability in terms of minimum genotype x environment interaction or minimum possible variability of a genotype over environments.

Wricke's (1962) ecovalence is given by

$$W_i = \sum_{j=1}^{n} \left(y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..} \right)^2 \qquad i = 1,2,...,m \qquad (3.8)$$

where

y_{ij} is the empirical mean response of the i^{th} genotype in the j^{th} environment,

$\bar{y}_{i.}$ is the marginal mean of genotype i,

$\bar{y}_{.j}$ is the marginal mean of environment j, and

$\bar{y}_{..}$ is the overall mean.

The ecovalence $\left(W_i\right)$ corresponding to the i^{th} genotype represents the contribution of this genotype to the genotype x environment interaction sum of squares (SS_{GxE}). Genotypes with low ecovalence have smaller fluctuations from the mean across different environments and are therefore considered relatively more stable. The ecovalence strongly depends on the environments included in the analysis and the breeder can manipulate the ecovalence by choosing specific locations (Weber et al., 1996).

*abridged from Piepho (1996) and Weber et al. (1996).

3.2.4 Shukla's Stability Variance

Shukla (1972) proposed a measure which he called "stability variance" of genotype $i\ (i = 1,2,...,m)$ as its variance across environments after environmental main effects have been removed. Since the genotype main effect is by definition a constant value for a given genotype over a wide range of environments, the stability variance is based on the residual $\left[(\tau\delta)_{ij} + \bar{\varepsilon}_{ij}\right]$ matrix.

Shukla's stability variance model may be written as

$$y_{ij} = \mu + \tau_i + \delta_j + \vartheta_{ij} \tag{3.9}$$

where $\vartheta_{ij} = (\tau\delta)_{ij} + \bar{\varepsilon}_{ij}$ with variance $Var(\vartheta_{ij}) = \sigma_i^2$ for every i. The variance σ_i^2 may be regarded as a measure of stability (stability variance) of the i^{th} genotype. Shukla (1972) assumes that errors are homoscedastic and the number of replications is the same in each environment, such that the analysis can be based on means y_{ij} and heterogeneity in σ_i^2 indicates heterogeneity in interaction variances.

A genotype is regarded as stable, if it has a small variance of the effects ϑ_{ij}, i.e., a small "stability variance". This term for $\sigma_i^2 = Var(\vartheta_{ij})$ was coined by Shukla (1972). If we assume that all genotypes have a common error variance $Var(\varepsilon_{ijl}) = \sigma^2$, stability differences results merely from differences of a genotype's interaction variance $\theta_i^2 = Var\left[(\tau\delta)_{ij}\right]$. The stability variance can then be expressed as $\sigma_i^2 = \theta_i^2 + \frac{\sigma^2}{r}$.

Maximum stability occurs when $\theta_i^2 = 0$ and hence $\sigma_i^2 = \frac{\sigma^2}{r}$, i.e., when the variability of ϑ_{ij} effects is minimal. The experimental design has an influence on the magnitude of σ^2 and hence of σ_i^2 (σ^2 and σ_i^2 will tend to be smaller for RCBD design than a completely randomized design), but it does not influence contrasts among the stability variances of any two genotypes. Clearly,

$$\sigma_i^2 - \sigma_{i'}^2 = \theta_i^2 - \theta_{i'}^2 \qquad \text{for } i \neq i' = 1,2,\ldots,m$$

which is independent of σ^2.

Shukla's unbiased estimator of σ_i^2 is

$$\hat{\sigma}_i^2 = \frac{m}{(m-2)(n-1)} \sum_{j=1}^{n} \left(y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..} \right)^2 - \frac{\sum_{i=1}^{m} \sum_{j=1}^{n} \left(y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..} \right)^2}{(m-1)(m-2)(n-1)} . \qquad (3.10)$$

This estimator is a MINQUE (Minimum Norm Quadratic Unbiased estimator) of σ_i^2 (Rao, 1970).

Since $W_i = \sum_{j=1}^{n} \left(y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..} \right)^2$ and $MS_{GxE} = \frac{\sum_{i=1}^{m} \sum_{j=1}^{n} \left(y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..} \right)^2}{(m-1)(n-1)}$

$\hat{\sigma}_i^2$ can be rewritten as

$$\hat{\sigma}_i^2 = \frac{m}{(m-2)(n-1)} W_i - \frac{MS_{GxE}}{(m-2)} \qquad (3.11)$$

or, equivalently,

$$\hat{\sigma}_i^2 = \frac{m}{(m-2)(n-1)} W_i - \frac{\sum_{i=1}^{m} W_i}{(m-1)(m-2)(n-1)} \qquad (3.12)$$

where

W_i is Wricke's ecovalence.

A genotype possessing relatively small stability variance $\left(\hat{\sigma}_i^2\right)$ is considered to have greater stability, whereas relatively large values of $\hat{\sigma}_i^2$ indicate greater instability. A drawback of the stability analysis under consideration is the possibility of obtaining negative estimates. The MINQUE is a linear combination of W_i, and therefore both W_i and $\hat{\sigma}_i^2$ are equivalent for ranking purposes (Lin et al., 1986; Weber et al., 1996).

3.2.5 Linear Regression

Another important method for analyzing and interpreting the non-additive structure (genotype x environment interaction) of two-way classification data is the linear regression on the environmental mean model. The basic idea consists of regressing genotypic responses against environmental index (mean) through a linear model (Yates & Cochran, 1938; Finlay & Wilkinson, 1963; Eberhart & Russell, 1966).

The regression model (frequently termed as joint regression) partitions the genotype x environment interaction term, $(\tau\delta)_{ij}$, in part due to linear regression (ϕ_i) on the environmental main effect and a deviation (d_{ij}) :

$$(\tau\delta)_{ij} = \phi_i \delta_j + d_{ij} \tag{3.13}$$

An elaborate way to write the regression model, that shows the relation with the full interaction analysis of variance model in equation (3.1), is

$$y_{ijl} = \mu + \tau_i + \delta_j + \xi_{i(j)} + \phi_i \delta_j + d_{ij} + \varepsilon_{ijl} \tag{3.14}$$

This model partitions the interaction (relative to ANOVA model in Table 3.4) into $(m-1)$ DF for heterogeneity of genotype regressions and the residual $(m-1)(n-2)$ DF for deviations from regression.

Table 3.5 The general analysis of variance for the regression model.

Source of variation	DF
Environment (E)	$n-1$
Replicate within environment (R/E)	$n(r-1)$
Genotype (G)	$m-1$
Genotype x environment interaction (GxE)	$(m-1)(n-1)$
Regression	$m-1$
Residual	$(m-1)(n-2)$
Experimental error (e)	$n(m-1)(r-1)$
Total	$mnr-1$

Model (3.14) may be rewritten as

$$y_{ijl} = \mu + \tau_i + \xi_{l(j)} + (1+\phi_i)\delta_j + d_{ij} + \varepsilon_{ijl} = \mu + \tau_i + \xi_{l(j)} + \beta_{1i}\delta_j + d_{ij} + \varepsilon_{ijl}, \qquad (3.15)$$

where $\beta_{1i} = 1 + \phi_i$ (subject to the estimability constraint $\frac{1}{m}\sum_{i=1}^{m}\beta_{1i} = 1$) is a regression coefficient corresponding to the i^{th} genotype. Note that when all ϕ_i are zero, or all β_{1i} are one, the regression model reduces to the additive model. Alternatively, the regression model will be equivalent to the full interaction model when $(\tau\delta)_{ij} = \phi_i\delta_j$ for all genotype by environment combinations.

Usually the environmental main effect δ_j is set equal to the environment mean $(\bar{y}_{.j})$, so that the mean yield response of the i^{th} genotype in the j^{th} environment (Yates & Cochran, 1938; Finlay & Wilkinson, 1963; Eberhart & Russell, 1966) can be written

$$y_{ij} = \beta_{oi} + \beta_{1i}\bar{y}_{.j} + d_{ij} \qquad i = 1,2,...,m \text{ and } j = 1,2,...,n \qquad (3.16)$$

where β_{oi} and β_{1i} are, respectively, the intercept and slope of the i^{th} genotype; and d_{ij} is a random deviation. It is assumed that the random term d_{ij} is independently normally distributed with zero mean and variance σ_d^2 (Finlay & Wilkinson, 1963).

This model uses the marginal means of the environments as independent variables in the regression analysis and restricts the interaction to a multiplicative form. The philosophy behind this model is that in the absence of explicit physical or meteorological characterization of an environment, a good approximation to the biological quality of an environment is given by the average phenotypic performance across the genotypes. The phenotypic responses of individual genotypes are then regressed on the average performance and the genotype by environment interaction (GxE) expresses itself by differences in the slopes between the genotypes (Vargas et al., 1999; van Eeuwijk et al., 2004).

The least squares function, L, of equation (3.16) is

$$L = \sum_{j=1}^{n} d_{ij}^2 = \sum_{j=1}^{n} \left(y_{ij} - \beta_{0i} - \beta_{1i} \bar{y}_{.j} \right)^2 \tag{3.17}$$

Minimizing the least squares function is simplified if $\bar{y}_{.j}$ in equation (3.16) is replaced by I_j to give

$$y_{ij} = \beta'_{0i} + \beta_{1i} I_j + d_{ij} \qquad i = 1,2,...,m \text{ and } j = 1,2,...,n \tag{3.18}$$

where

$$I_j = \bar{y}_{.j} - \bar{y}_{..} \qquad j = 1,2,...,n \qquad \left(\sum_{j=1}^{n} I_j = 0 \right)$$

and

$$\beta'_{0i} = \beta_{0i} + \beta_{1i} \bar{y}_{..} \qquad i = 1,2,...,m$$

Equation (3.18) is frequently called the transformed model. In Equation (3.18) the regressor variable is corrected for its average, resulting in a transformation on the intercept. By employing the transformed model the least squares function becomes

$$L = \sum_{j=1}^{n} \left(y_{ij} - \beta'_{0i} - \beta_{1i} I_j \right)^2 \tag{3.19}$$

The least squares estimators of β'_{0i} and β_{1i}, say $\hat{\beta}'_{0i}$ and $\hat{\beta}_{1i}$, must satisfy

$$\frac{\partial L}{\partial \beta'_{0i}} = -2 \sum_{j=1}^{n} \left(y_{ij} - \hat{\beta}'_{0i} - \hat{\beta}_{1i} I_j \right) = 0$$

$$\frac{\partial L}{\partial \beta_{1i}} = -2 \sum_{j=1}^{n} \left(y_{ij} - \hat{\beta}'_{0i} - \hat{\beta}_{1i} I_j \right) I_j = 0 \tag{3.20}$$

Simplifying these two equations yields

$$n \hat{\beta}'_{0i} = \sum_{j=1}^{n} y_{ij}$$

$$\hat{\beta}_{1i} \sum_{j=1}^{n} I_j^2 = \sum_{j=1}^{n} y_{ij} I_j \tag{3.21}$$

Equations (3.21) are called the least squares normal equations. Their Solutions are

$$\hat{\beta}'_{0i} = \frac{1}{n}\sum_{j=1}^{n} y_{ij} = \bar{y}_{i.} \qquad i = 1,2,...,m \tag{3.22}$$

$$\hat{\beta}_{1i} = \frac{\sum_{j=1}^{n} y_{ij} I_j}{\sum_{j=1}^{n} I_j^2} \qquad i = 1,2,...,m \tag{3.23}$$

Thus, $\hat{\beta}'_{0i}$ and $\hat{\beta}_{1i}$ are the least squares estimators of the intercept and slope, respectively. The fitted linear regression model is

$$\hat{y}_{ij} = \hat{\beta}'_{0i} + \hat{\beta}_{1i} I_j \tag{3.24}$$

If we wish to present our results in terms of the original intercept's, β_{0i}, then

$$\hat{\beta}_{0i} = \hat{\beta}'_{0i} - \hat{\beta}_{1i}\bar{y}_{..} \tag{3.25}$$

and the fitted model is

$$\hat{y}_{ij} = \hat{\beta}_{0i} + \hat{\beta}_{1i}\bar{y}_{.j} \tag{3.26}$$

The estimates of the regression coefficients β_{1i} are used as measures of the stability of the different genotypes (Finlay & Wilkinson, 1963).

- If $\hat{\beta}_{1i} > 1$, the genotype is said to be responsive to improvement in the environmental conditions and can be recommended for favorable environments.
- If $\hat{\beta}_{1i} < 1$, the genotype is said to be non-responsive to improvement in the environmental conditions and can be recommended for unfavorable environments.
- If $\hat{\beta}_{1i} = 1$, the genotype is said to be more stable relative to the other genotypes tested and can be recommended for most environmental conditions.

Many plant breeders might not understand the reason why responsive genotypes are only recommended for favorable environments. To answer this question, it is necessary to observe that a genotype possessing $\hat{\beta}_{1i} > 1$ may potentially provide lower yields as the environmental conditions worsen. Therefore, the risk of poor performance is high when a genotype that is classified as responsive is chosen for unfavorable environments. In the same way a genotype with $\hat{\beta}_{1i} < 1$, classified as non-responsive, is not recommended for favorable environments because this genotype may not respond very positively to improved environmental conditions.

A regression based procedure to evaluate the relative stability of a set of genotypes across a variety of environments is outlined by Eberhart and Russell (1966). Eberhart and Russell (1966) advocated the mean square deviation (error) from the regression of the i^{th} genotype against environmental mean $\left(s_{di}^2\right)$ as a measure of the stability of the i^{th} genotype. A genotype with minimum deviations from regression has been considered as most stable.

In many applications, a genotype response observed across a series of environments is expressed in terms of three empirical measures: the mean performance, the slope of the regression line and the deviation from the linear response. An ideal genotype should have:

- highest mean performance;
- $\hat{\beta}_{1i} = 1$; and
- $s_{di}^2 = 0$.

Lin et al. (1986) and Crossa (1990) noted that in trying to determine which genotypes is superior with the regression approach, plant breeders have difficulty reaching a compromise between mean performance, slope of the regression and deviation from regression, because the genotypes response to environments is intrinsically multivariate whereas regression tries to transform it into a univariate problem.

3.2.6 The Additive Main Effects and Multiplicative Interaction (AMMI)

A hybrid statistical model which incorporates both the additive and multiplicative components of the two-way data structure is the additive main effects and multiplicative interaction (AMMI) model. In this model the additive portion of the variance is separated from the multiplicative variance (interaction) by ANOVA. Principal components analysis (PCA) is then applied to the interaction (residual) portion from the additive ANOVA model to extract a new set of coordinate axes which account more effectively for the interaction patterns. It has proven useful for understanding complex genotype x environment interactions. AMMI results presented in biplots can be used to provide insightful interpretation of data from large, complex experiments. Estimation is accomplished according to the least squares principles (Gollob, 1968; Mandel, 1971; Bradu & Gabriel, 1978; Gabriel, 1978; Gauch, 1988; Zobel et al., 1988; Shaffi & Price, 1998; Vargas et al., 1999; Ebdon & Gauch, 2002).

3.2.6.1 The Model

AMMI combines ANOVA and PCA into a single model with linear (additive) and bilinear (multiplicative) parameters. We write the full/saturated AMMI model with t multiplicative terms (AMMI-t , say) in the form

$$y_{ij} = \mu + \tau_i + \delta_j + \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} \qquad i = 1,2,..,m \qquad j = 1,2,...,n \quad (3.27)$$

where

y_{ij} is the cell mean of the i^{th} genotype in the j^{th} environment;

μ is the grand mean;

τ_i is the main effect of the i^{th} genotype;

δ_j is the main effect of the j^{th} environment;

t is the number of multiplicative (bilinear) terms, $t \leq \min(m-1, n-1)$;

λ_k is the singular value (square root of the eigenvalue) of the k^{th} multiplicative component that is ordered $\lambda_1 \geq \lambda_2 \geq ... \geq \lambda_t > 0$;

α_{ik} is the i^{th} element of the k^{th} left singular vector associated with genotypes;

and

γ_{jk} is the j^{th} element of the k^{th} right singular vector associated with environments.

The additive parameters are μ, τ_i and δ_j. The multiplicative parameters are λ_k, α_{ik} and γ_{jk}. The α_{ik} are genotype interaction parameters that measure genotype sensitivity to hypothetical environmental factors denoted by environmental interaction parameters γ_{jk}. Orthonormality constraints for the genotype and environmental interaction parameters are

$$\sum_i \alpha_{ik} = \sum_j \gamma_{jk} = 0$$

$$\sum_i \alpha_{ik}^2 = \sum_j \gamma_{jk}^2 = 1$$

and

$$\sum_i \alpha_{ik}\alpha_{ik'} = \sum_j \gamma_{jk}\gamma_{jk'} = 0 \quad \text{for } k \neq k'$$

Thus, the bilinear GxE term (interaction effect) in model (3.27) is represented by

$$(\tau\delta)_{ij} = \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk} . \tag{3.28}$$

The main advantage of the additive model, i.e., the possibility of expressing a function of two variables in terms of functions of a single variable, is retained by the AMMI model since all α terms are functions of i only and all γ terms are functions of j only (Mandel, 1971).

Model (3.27) can be written in matrix notation, using a superior T to denote a transpose of a matrix or a vector, as:

$$Y = \mu 1_m 1_n^T + \tau 1_n^T + 1_m \delta^T + \mathrm{A}\Lambda\Gamma^T \tag{3.29}$$

where

$$\underset{(mxn)}{Y} = \begin{bmatrix} y_{11} & y_{12} & . & . & . & y_{1n} \\ y_{21} & y_{22} & . & . & . & y_{2n} \\ . & . & . & & & . \\ . & . & & . & & . \\ . & . & & & . & . \\ y_{m1} & y_{m2} & . & . & . & y_{mn} \end{bmatrix}$$

is the data matrix of dimension mxn of grain yield of m genotypes in n environments;

μ is a scalar representing the grand mean;

1_m and 1_n are $mx1$ and $nx1$ vectors with all elements equal to one, respectively;

$$\underset{(mx1)}{\tau} = \begin{bmatrix} \tau_1 \\ \tau_2 \\ . \\ . \\ . \\ \tau_m \end{bmatrix}$$ is a $mx1$ vector of main effects of genotypes;

$$\underset{(nx1)}{\delta} = \begin{bmatrix} \delta_1 \\ \delta_2 \\ . \\ . \\ . \\ \delta_n \end{bmatrix}$$ is a $nx1$ vector of main effects of environments;

$\Lambda = diag[\lambda_1 \quad \lambda_2 \quad . \quad . \quad . \quad \lambda_t]$ is a txt diagonal matrix such that $\lambda_1 \geq \lambda_2 \geq ... \geq \lambda_t > 0$;

$$\underset{(mxt)}{A} = \begin{bmatrix} \alpha_{11} & \alpha_{12} & . & . & . & \alpha_{1t} \\ \alpha_{21} & \alpha_{22} & . & . & . & \alpha_{2t} \\ . & . & . & & & . \\ . & . & & . & & . \\ . & . & & & . & . \\ \alpha_{m1} & \alpha_{m2} & . & . & . & \alpha_{mt} \end{bmatrix} = \begin{bmatrix} \underset{(mx1)}{\alpha_1} & \underset{(mx1)}{\alpha_2} & . & . & . & \underset{(mx1)}{\alpha_t} \end{bmatrix}$$

is a mxt matrix of genotype interaction parameters; and

$$\underset{(nxt)}{\Gamma} = \begin{bmatrix} \gamma_{11} & \gamma_{12} & . & . & . & \gamma_{1t} \\ \gamma_{21} & \gamma_{22} & . & . & . & \gamma_{2t} \\ . & . & . & & & . \\ . & . & & . & & . \\ . & . & & & . & . \\ \gamma_{n1} & \gamma_{n2} & . & . & . & \gamma_{nt} \end{bmatrix} = \begin{bmatrix} \underset{(nx1)}{\gamma_1} & \underset{(nx1)}{\gamma_2} & . & . & . & \underset{(nx1)}{\gamma_t} \end{bmatrix}$$

is a nxt matrix of environmental interaction parameters. The normalization and orthogonality constraints are

$$1_m^T \mathrm{A} = 1_n^T \Gamma = \underset{(1xt)}{0} \text{ (where } \underset{(1xt)}{0} \text{ is a } 1xt \text{ vector of zeros) and}$$

$$\mathrm{A}^T \mathrm{A} = \Gamma^T \Gamma = I_t .$$

Correspondences between singular value decomposition (SVD) and principal components analysis (PCA) are as follows: Define X to be mxn matrix

$$\underset{(mxn)}{\mathrm{X}} = \begin{bmatrix} (\tau\delta)_{11} & (\tau\delta)_{12} & . & . & . & (\tau\delta)_{1n} \\ (\tau\delta)_{21} & (\tau\delta)_{22} & . & . & . & (\tau\delta)_{2n} \\ . & . & . & & & . \\ . & . & & . & & . \\ . & . & & & . & . \\ (\tau\delta)_{m1} & (\tau\delta)_{m2} & . & . & . & (\tau\delta)_{mn} \end{bmatrix}$$

where each element of the matrix specifies the interaction effect for the i^{th} genotype in the j^{th} environment. The X matrix, of rank $t \le \min(m-1, n-1)$, is submitted to singular value decomposition (SVD) in the following way:

$$\mathrm{X} = \mathrm{A}\Lambda\Gamma^T \tag{3.30}$$

Denoting the k^{th} column of A and Γ, respectively, by α_k and γ_k, matrix X can be expressed as

$$\mathrm{X} = \mathrm{A}\Lambda\Gamma^T = \sum_{k=1}^{t} \lambda_k \alpha_k \gamma_k^T \tag{3.31}$$

As is well known, the values $\lambda_k^2, k = 1,2,...,t$ are the non-null eigenvalues of XX^T and of $\mathrm{X}^T\mathrm{X}$. It further follows that

$$XX^T = A\Lambda^2 A^T = \sum_{k=1}^{t} \lambda_k^2 \alpha_k \alpha_k^T$$

and (3.32)

$$X^T X = \Gamma\Lambda^2\Gamma^T = \sum_{k=1}^{t} \lambda_k^2 \gamma_k \gamma_k^T$$

That is, the α_k's are eigenvectors of XX^T with eigenvalues $\lambda_1^2, \lambda_2^2, ..., \lambda_t^2$ and γ_k's are eigenvectors of $X^T X$ with the same eigenvalues. The vectors $\alpha_1, \alpha_2, ..., \alpha_t$ are orthonormal and so are $\gamma_1, \gamma_2, ..., \gamma_t$ (Good, 1969).

If the $i^{th}(i = 1,2,...,m)$ element of the vector $\alpha_k (k = 1,2,...,t)$ is denoted by α_{ik} and the $j^{th}(j = 1,2,...,n)$ element of the vector $\gamma_k (k = 1,2,...,t)$ is denoted by γ_{jk}, decomposition (3.31) has its element wise representation

$$(\tau\delta)_{ij} = \sum_{k=1}^{t} \lambda_k \alpha_{ik} \gamma_{jk}$$

with the restrictions $$\sum_{i=1}^{m} \alpha_{ik} = \sum_{j=1}^{n} \gamma_{jk} = 0$$

$$\sum_{i=1}^{m} \alpha_{ik}^2 = \sum_{j=1}^{n} \gamma_{jk}^2 = 1$$

and

$$\sum_{i=1}^{m} \alpha_{ik} \alpha_{ik'} = \sum_{j=1}^{n} \gamma_{jk} \gamma_{jk'} = 0 \quad \text{for} \quad k \neq k' = 1,2,...,t$$

The rank of X is $t \leq \min(m-1, n-1)$, so that the index k in the sum of multiplicative components can run from 1 to t.

A part of the interaction may well be random error or otherwise unsuitable for bilinear modeling. Consequently, the partitioning of the interaction into multiplicative terms is carried out only partially; i.e., only a few multiplicative terms of the $\lambda_k \alpha_{ik} \gamma_{jk}$ type (typically, one or two or three such terms) are retained ; the remaining terms are pooled

together and considered as random residual error, producing a reduced model (Mandel, 1971; Aastveit & Martens, 1986 ; Gauch & Zobel, 1996).

In a more general setting, $s < t$ non-null eigenvalues are kept producing a reduced/truncated AMMI model (denoted by AMMI-s) given by

$$y_{ij} = \mu + \tau_i + \delta_j + \sum_{k=1}^{s} \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij} \quad i = 1,2,...,m \quad j = 1,2,...,n \qquad (3.33)$$

where

s indicates the number of multiplicative terms necessary for an adequate description of the GxE;

ρ_{ij} is the residual not accounted for by retained multiplicative terms for the GxE.

Thus the interaction of genotype i with environment j is described by $\sum_{k=1}^{s} \lambda_k \alpha_{ik} \gamma_{jk}$, discarding the noise given by $\rho_{ij} = \sum_{k=s+1}^{t} \lambda_k \alpha_{ik} \gamma_{jk}$. The s hypothetical environmental/genotypic variables are expected to have the property of discriminating maximally between genotypes/environments.

The AMMI model with s multiplicative terms for replicated data may be written as

$$y_{ijl} = \mu + \tau_i + \delta_j + \xi_{l(j)} + \sum_{k=1}^{s} \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij} + \varepsilon_{ijl},$$

$$i = 1,2,...,m \quad j = 1,2,...,n \quad l = 1,2,...,r \qquad (3.34)$$

where $y_{ijl}, \mu, \tau_i, \delta_j, \xi_{l(j)}, \varepsilon_{ijl}$ are as in model (3.1).

The simplest AMMI model (AMMI-0), $y_{ijl} = \mu + \tau_i + \delta_j + \xi_{l(j)} + \varepsilon_{ijl}$, estimates the additive main effects (i.e., genotypes & environments) without considering interaction. AMMI-1, $y_{ijl} = \mu + \tau_i + \delta_j + \xi_{l(j)} + \lambda_1 \alpha_{i1} \gamma_{j1} + \rho_{ij} + \varepsilon_{ijl}$, combines the main effects from AMMI-0 with interaction effects estimated from the first multiplicative term. AMMI-2, $y_{ijl} = \mu + \tau_i + \delta_j + \xi_{l(j)} + \lambda_1 \alpha_{i1} \gamma_{j1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \rho_{ij} + \varepsilon_{ijl}$, considers main effects plus the first two multiplicative terms. AMMI-3 to AMMI-t (the full AMMI model) includes,

sequentially, one more multiplicative term each. ρ_{ij} is of course different for each of these different AMMI models. Gauch and Zobel (1996) concluded that an intermediate model (often AMMI-1 or AMMI-2) is most appropriate for yield trials, with simpler models under fitting real patterns, and with more complex models over fitting spurious noise.

We now turn to equation (3.27) and concern ourselves with the estimation of the parameters. Denoting estimates by a caret (^) placed over the symbols of the parameters, the estimation is accomplished by application of the method of least squares (Gollob, 1968; Mandel, 1971; Gabriel, 1978). The least-square fit to this model for balanced data (equal replications and no missing observations) is obtained in two steps. First the additive main effects (μ, τ_i and δ_j) are fitted using the ordinary calculation for two-way analysis of variance. The variance not captured by this additive model remains in its residual namely the interaction. Second, the multiplicative interaction effects (λ_k, α_{ik} and γ_{jk}) are fitted using principal components analysis (PCA). Note that PCA is applied here to the interaction, that is, to the residual from the additive model, rather than to the original data.

The Least square estimators of μ, τ_i and δ_j are

$$\hat{\mu} = \bar{y}_{..} \tag{3.35}$$

$$\hat{\tau}_i = \bar{y}_{i.} - \bar{y}_{..} \qquad i = 1,2,...,m \tag{3.36}$$

$$\hat{\delta}_j = \bar{y}_{.j} - \bar{y}_{..} \qquad j = 1,2,...,n \tag{3.37}$$

The parameters λ_k, α_{ik} and γ_{jk} for all values of k are estimated entirely from the matrix of residuals, namely

$$\underset{(mxn)}{Z} = \lfloor z_{ij} \rfloor$$

where

$$z_{ij} = y_{ij} - \bar{y}_{..} - (\bar{y}_{i.} - \bar{y}_{..}) - (\bar{y}_{.j} - \bar{y}_{..}) = y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..}$$

This is the usual matrix of residuals in the analysis of variance of two-way table of means corrected for genotype and environmental main effects (residual from additivity). From SVD the matrix Z , rank $(Z)=t$, can be expressed as

$$\underset{(mxn)}{Z} = \hat{A}\hat{\Lambda}\hat{\Gamma}^{T}$$

where $\hat{\Lambda}$ is a diagonal matrix with positive numbers, $\hat{\lambda}_k$, on the diagonal, and $\hat{A}$ & $\hat{\Gamma}$ are such that

$$1_m^T \hat{A} = 1_n^T \hat{\Gamma} = \underset{(1xt)}{0}$$

$$\hat{A}^T \hat{A} = \hat{\Gamma}^T \hat{\Gamma} = I_t .$$

Denoting the k^{th} column of $\hat{A}$ and $\hat{\Gamma}$, respectively, by $\hat{\alpha}_k$ and $\hat{\gamma}_k$, matrix Z can be expressed as

$$\underset{(mxn)}{Z} = \hat{A}\hat{\Lambda}\hat{\Gamma}^{T} = \sum_{k=1}^{t} \hat{\lambda}_k \hat{\alpha}_k \hat{\gamma}_k^{T} \tag{3.38}$$

and an individual element of Z as

$$z_{ij} = \sum_{k=1}^{t} \hat{\lambda}_k \hat{\alpha}_{ik} \hat{\gamma}_{jk} \tag{3.39}$$

The quantities $\hat{\lambda}_k$, $\hat{\alpha}_{ik}$, $\hat{\gamma}_{ik}$ for $k = 1,2,...,t$ are the least squares estimates of our model parameters λ_k , α_{ik} , γ_{jk}.

In short, least squares fitting of an AMMI-t model to two-way layout of genotype by environment data is a process of $t+2$ steps, the first two steps for fitting the additive terms, the next t for fitting the multiplicative terms, each of these being fitted to the residuals from all preceding fits. It is important to note that the order of fitting is not reversible: If the bilinear terms are fitted before the linear ones, the least squares fit is not obtained.

3.2.6.2 Determining Optimal Number of Multiplicative Terms in the AMMI Model

After fitting the genotype and environment main effects in the model, a crucial step in AMMI analysis is the determination of the amount of pattern, namely the portion of GxE

variation representing real responses to genotypes and environments. To achieve this, a truncated AMMI model should be used and thus criteria for determining the number of components needed to explain the pattern in the GxE term have been the objects of some research (Gollob, 1968; Mandel, 1971; Gauch & Zobel, 1988).

Two basic approaches have involved to determine the optimal number of multiplicative terms to be retained in the GxE component. One approach uses a cross-validation method in which the data are randomly split into modelling data and validation data. AMMI is fitted to the modelling data and the mean squared errors of prediction (expressed as the root mean squared predictive difference, RMSPD) are determined from the validation data. The other approach for determining the best predictive truncated model is to use tests of hypotheses about the k^{th} component, $H_{0k} : \lambda_k = 0$, using the complete data set (and not a subset like in the cross-validation approach). These tests are based on the sequential sum of squares explained by the multiplicative terms. In the sequel we present a brief heuristic discussion of the latter approach. For the former, the reader is referred to Gauch and Zobel (1988) and the references contained therein.

Consider the identity from cell-means:

$$SS_{GxE} = \sum_{i=1}^{m}\sum_{j=1}^{n}\left(y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..}\right)^2 = trace\left(\mathrm{ZZ}^T\right) = trace\left(\mathrm{Z}^T\mathrm{Z}\right) \qquad (3.40)$$

where

$$\underset{(mxn)}{\mathrm{Z}} = \left[z_{ij}\right] = \left[y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..}\right].$$

From SVD and property of the trace of matrix, we have

$$trace\left(\mathrm{ZZ}^T\right) = trace\left(\hat{\mathrm{A}}\hat{\Lambda}^2\hat{\mathrm{A}}^T\right) = trace\left(\hat{\Lambda}^2\hat{\mathrm{A}}^T\hat{\mathrm{A}}\right)$$

$$= trace\left(\hat{\Lambda}^2 I_t\right) \qquad (\text{Since } \hat{\mathrm{A}}^T\hat{\mathrm{A}} = I_t)$$

$$= trace\left(\hat{\Lambda}^2\right) = \sum_{k=1}^{t}\hat{\lambda}_k^2$$

By a similar argument, it follows that

$$trace\left(\mathrm{Z}^{T}\mathrm{Z}\right)=\sum_{k=1}^{t}\hat{\lambda}_{k}^{2}\ .$$

Hence,

$$SS_{GxE}=\sum_{k=1}^{t}\hat{\lambda}_{k}^{2} \tag{3.41}$$

The sequential sum of squares of the AMMI model for the k^{th} component, S_k, is given by

$$\begin{aligned} S_k &= \sum_{i=1}^{m}\sum_{j=1}^{n}\left(\hat{\lambda}_k\hat{\alpha}_{ik}\hat{\gamma}_{jk}\right)^2 = \hat{\lambda}_k^2\sum_{i=1}^{m}\sum_{j=1}^{n}\left(\hat{\alpha}_{ik}^2\hat{\gamma}_{jk}^2\right) \\ &= \hat{\lambda}_k^2\left(\sum_{i=1}^{m}\hat{\alpha}_{ik}^2\right)\left(\sum_{j=1}^{n}\hat{\gamma}_{jk}^2\right) \\ &= \hat{\lambda}_k^2 \qquad \text{for} \quad k=1,2,...,rank(\mathrm{Z}) \end{aligned} \tag{3.42}$$

Obviously, the sum of squares for interaction Z was divided into individual sums of squares which correspond to the different terms $\hat{\lambda}_k\hat{\alpha}_k\hat{\gamma}_k^T$.

The test criteria involve, at least indirectly, the ratio of the accumulated sum of squares for the first s components to the total SS_{GxE} i.e.,

$$\frac{\sum_{k=1}^{s}\hat{\lambda}_k^2}{SS_{GxE}} \tag{3.43}$$

One of the usual procedures consists of determining the degrees of freedom associated with a particular component of SS_{GxE} for each member of the family of AMMI models. This enables mean squares to be computed for each component, together with an error mean square. Since we have an orthogonal partition of the interaction sum of squares, the ratio of the mean square of any interaction component to the error mean square is then assumed to follow an F distribution with the corresponding degrees of freedom. This implicitly assumes a normal distribution for the original response variable, and enables individual interaction components to be subjected to significance tests. Selection of the

optimal model is based on F tests for the successive terms of the interaction, the number of included terms corresponding to the number of significant components.

Two systems for assigning DF in the AMMI model, those of Gollob (1968) and Mandel (1971), are particularly popular (Gauch & Zobel, 1996). However, the authors warn that, unfortunately, there are disagreements between these methods. Choosing one requires both theoretical and practical considerations. The approach of Gollob (1968) is very easily applied, since the number of degrees of freedom for component k (ν_k) of the interaction is simply defined to be

$$\nu_k = (m-1)+(n-1)-(2k-1) = m+n-1-2k \tag{3.44}$$

Mandel (1971) defines the number of degrees of freedom for component k (ν_k) to be

$$\nu_k = \mathbf{E}\,(\hat{\lambda}_k^2/\sigma^2) \tag{3.45}$$

where σ^2 is the error variance. However, simulations then have to be conducted to evaluate the number of degrees of freedom in particular cases. Mandel gives some tables derived from such simulations for a limited set of conditions. These tables, however, are not exhaustive and this reduces the practical utility of the method.

For some years, the degrees of freedom have been obtained by Mandel's (1971) proposal, which was considered exact and therefore correct. However, this proposal has received much criticisms recently (e.g., Gauch, 1992), and it is now felt to be less appropriate than the approach of Gollob (1968). The reason for this criticism centres on the assumptions made by Mandel in his simulations that the matrix contains only noise and not signals, whereas the presence of signal affects the component patterns substantially.

Gauch (1992) discusses the question of obtaining the degrees of freedom for the multiplicative components of an AMMI model. He concludes that rigorous simulations seem unnecessary or impractical, and generally recommends the use of Gollob's system when one is using an F-test approach. Therefore by Gollob's system, the full joint analysis of variance has the structure as shown in Table 3.6. For integration with

ANOVA results (such as in Table 3.4), S_k values must be multiplied by r (no of replicates).

Table 3.6 The general analysis of variance for the AMMI model.

Source of variation	DF	Sum of squares
Environment (E)	$n-1$	SS_E
Rep within environment (R/E)	$n(r-1)$	$SS_{R/E}$
Genotype (G)	$m-1$	SS_G
Genotype x environment interaction (GxE)	$(m-1)(n-1)$	SS_{GxE}
PCA-1	$v_1 = m+n-1-(2x1)$	$r\hat{\lambda}_1^2$
PCA-2	$v_2 = m+n-1-(2x2)$	$r\hat{\lambda}_2^2$
.	.	.
.	.	.
.	.	.
PCA-s	$v_s = m+n-1-(2xs)$	$r\hat{\lambda}_s^2$
Residual	$(m-1)(n-1)-\sum_{k=1}^{s} v_k$	$SS_{GxE} - r\sum_{k=1}^{s}\hat{\lambda}_k^2$
Experimental error (e)	$n(m-1)(r-1)$	SS_e
Total	$mnr-1$	

3.2.6.3 The Theory of Biplot

The concept of biplot was developed by Gabriel (1971) to graphically display a rank-two matrix. The significance of this concept is that if a two-way data set can be sufficiently approximated by a rank-two matrix, then it can be graphically displayed and investigated. Bradu and Gabriel (1978) explored the use of biplot as a diagnostic tool for choosing an appropriate model for the analysis of two-way data. We now present some theoretical

discussion about a biplot of a matrix using the generic terminology "row markers" and "column markers" of Bradu and Gabriel (1978).

Any matrix of rank-two can be displayed as a biplot which consists of a vector for each row and a vector for each column, chosen so that any element of the matrix is exactly the inner product of the vectors corresponding to its row and to its column. If a matrix is of higher rank, one may display it approximately by a biplot of a matrix of rank-two which approximates the original matrix. The biplot provides a useful tool of data analysis and allows the visual appraisal of the structure of large data matrices (Gabriel, 1971; Bradu & Gabriel, 1978).

If $\underset{(mxn)}{Y}$ is of rank-two, then there is an infinity of ways to factor it in the form

$$Y = GH^T \tag{3.46}$$

where each of the matrices

$$G = \begin{bmatrix} g_1^T \\ g_2^T \\ \cdot \\ \cdot \\ \cdot \\ g_m^T \end{bmatrix} \quad , \; H = \begin{bmatrix} h_1^T \\ h_2^T \\ \cdot \\ \cdot \\ \cdot \\ h_n^T \end{bmatrix}$$

has two columns. Of course, $V(Y) = V(G)$, $V(Y^T) = V(H)$, where $V(Y)$ denotes the space spanned by the columns of matrix Y, and thus $V(Y^T)$ denotes the space spanned by the rows of Y.

The biplot consists of markers (vectors) which are displayed with respect to some system of rectangular coordinates: $g_1, g_2, ..., g_m$ denote the row markers and $h_1, h_2, ..., h_n$ denote the column markers. Relation (3.46) is equivalent to

$$y_{ij} = g_i^T h_j \qquad (i = 1,2,...,m; j = 1,2,...,n), \tag{3.47}$$

and this yields the following immediate interpretation of the biplot: each element of the matrix is the scalar product of the corresponding row and column markers.

A scalar product of two vectors is well known to be the signed product of the length of the projection of either one of them onto the other by the length of the other, the sign being positive if any only if the projection and the vector projected upon are in the same direction. Applying this length factorization to representation (3.47) we note the following. In the i^{th} row, the elements $y_{ij}\,(j=1,2,...,n)$ are ordered in size exactly like the projections of column markers $h_j\,(j=1,2,...,n)$ onto i^{th} row marker g_i. Similarly, the ordering of elements $y_{ij}\,(i=1,2,...,m)$ in the j^{th} column is the same as that of the projections of row markers $g_i\,(i=1,2,...,m)$ onto the j^{th} column marker h_j.

Linear combinations of rows and columns can also be represented on the biplot. In particular, one may plot the average row marker

$$g_{\cdot} = \frac{1}{m}\sum_{i=1}^{m} g_i \tag{3.48}$$

and the average column marker

$$h_{\cdot} = \frac{1}{n}\sum_{j=1}^{n} h_j \tag{3.49}$$

and use these for the following scalar product representations:

average of a column $\quad \bar{y}_{\cdot j} = g_{\cdot}^{T} h_j \quad ,$ (3.50)

average of a row $\quad \bar{y}_{i\cdot} = g_i^{T} h_{\cdot} \quad ,$ (3.51)

and the overall average $\quad \bar{y}_{\cdot\cdot} = g_{\cdot}^{T} h_{\cdot}$ (3.52)

Again, the factorization of these scalar products shows that column averages $\bar{y}_{\cdot j}$ $(j=1,2,...,n)$ are ordered as the projections of column marker h_j onto the average row marker $g_{\cdot}$. Similarly, row averages $\bar{y}_{i\cdot}$ $(i=1,2,..,m)$ are ordered as projections of row markers g_i onto the average marker $h_{\cdot}$.

One may also represent row and column effects and interaction residuals by scalar products in the following way:

column effect as $\bar{y}_{.j} - \bar{y}_{..} = g_{.}^{T}\left(h_j - h_{.}\right)$, (3.53)

row effect as $\bar{y}_{i.} - \bar{y}_{..} = \left(g_i - g_{.}\right)^{T} h_{.}$, (3.54)

and residuals as $y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..} = \left(g_i - g_{.}\right)^{T}\left(h_j - h_{.}\right)$. (3.55)

Decomposition (3.46) is not unique. In fact, there are infinitely much such decompositions and their displays differ in many ways. Yet the above scalar product representations properties hold equally for all such decompositions and are thus relevant for any biplot.

A matrix Y of rank greater than two cannot be biplotted exactly. However, it may be approximated by a rank-two matrix $Y_{[2]}$ and that approximation can be biplotted. A systematic way to find a rank-two approximation of a matrix Y is given by the singular value decomposition (SVD) of a matrix. The SVD is the representation of a matrix Y of rank-t in the form

$$Y = P\Lambda Q^{T} = \sum_{k=1}^{t} \lambda_k p_k q_k^{T}$$

where

$\Lambda = diag\left[\lambda_1 \quad \lambda_2 \quad . \quad . \quad . \quad \lambda_t\right]$, $\quad \lambda_1 \geq \lambda_2 \geq \ldots \geq \lambda_t > 0$,

$\underset{(mxt)}{P} = \left[p_1 \quad p_2 \quad . \quad . \quad . \quad p_t\right]$ is a particular orthonormal basis of $V(Y)$,

$\underset{(nxt)}{Q} = \left[q_1 \quad q_2 \quad . \quad . \quad . \quad q_t\right]$ is a particular orthonormal basis of $V\left(Y^{T}\right)$.

The values λ_k^2, $k = 1,2,\ldots,t$ are the non-null eigenvalues of YY^{T} and of $Y^{T}Y$. It further follows that

$$YY^{T} = P\Lambda^2 P^{T} = \sum_{k=1}^{t} \lambda_k^2 p_k p_k^{T}$$

and $$Y^{T}Y = Q\Lambda^2 Q^{T} = \sum_{k=1}^{t} \lambda_k^2 q_k q_k^{T}$$

and that the relation

$$Yq_k = \lambda_k p_k \qquad \text{for } \forall k = 1,2,...,t$$

and $$Y^T p_k = \lambda_k q_k \qquad \text{for } \forall k = 1,2,...,t$$

hold.

The following property of the SVD is relevant for the present purposes. Matrices

$$Y_{[1]} = \lambda_1 p_1 q_1^T$$

and

$$Y_{[2]} = \lambda_1 p_1 q_1^T + \lambda_2 p_2 q_2^T = \begin{bmatrix} p_1 & p_2 \end{bmatrix} \begin{bmatrix} \lambda_1 & 0 \\ 0 & \lambda_2 \end{bmatrix} \begin{bmatrix} q_1^T \\ q_2^T \end{bmatrix}$$

are, respectively, the least squares (Euclidean) rank-one and rank-two (or less) approximations of Y (Householder &Young, 1938).

The approximate biplot of Y is then the exact biplot of

$$Y_{[2]} = \begin{bmatrix} p_1 & p_2 \end{bmatrix} \begin{bmatrix} \lambda_1 & 0 \\ 0 & \lambda_2 \end{bmatrix} \begin{bmatrix} q_1^T \\ q_2^T \end{bmatrix} \tag{3.56}$$

and its goodness of fit is measured by

$$\rho_2^{(2)} = \left(\lambda_1^2 + \lambda_2^2\right) \Big/ \sum_{k=1}^{t} \lambda_k^2 \tag{3.57}$$

If $\rho_2^{(2)}$ is near to one, such a biplot will give a good approximation of Y. In choosing, as in (3.46), factors G and H of $Y_{[2]}$ for biploting, one may use the factorization provided by the singular decomposition (3.47). Writing

$$p_i = \begin{bmatrix} p_{1i}, & p_{2i}, & . & . & . & p_{mi} \end{bmatrix}^T \quad , \qquad q_j = \begin{bmatrix} q_{1j}, & q_{2j}, & . & . & . & q_{nj} \end{bmatrix}^T$$

one obtains

$$Y_{[2]} = \begin{bmatrix} p_{11} & p_{12} \\ . & . \\ . & . \\ . & . \\ p_{m1} & p_{m2} \end{bmatrix} \begin{bmatrix} \lambda_1 & 0 \\ 0 & \lambda_2 \end{bmatrix} \begin{bmatrix} q_{11} & . & . & . & q_{n1} \\ q_{12} & . & . & . & q_{n2} \end{bmatrix}.$$

One choice of G and H would be

$$g_i^T = \left[\sqrt{\lambda_1}p_{i1} \quad \sqrt{\lambda_2}p_{i2}\right] \qquad (i = 1,2,...,m),$$

$$h_j^T = \left[\sqrt{\lambda_1}q_{j1} \quad \sqrt{\lambda_2}q_{j2}\right] \qquad (j = 1,2,...,n). \tag{3.58}$$

Other choices of G and H are obtained by defining

$$g_i^T = \left[p_{i1} \quad p_{i2}\right] \qquad (i = 1,2,...,m)$$

$$h_j^T = \left[\lambda_1 q_{j1} \quad \lambda_2 q_{j2}\right] \qquad (j = 1,2,...,n) \tag{3.59}$$

or

$$g_i^T = \left[\lambda_1 p_{i1} \quad \lambda_2 p_{i2}\right] \qquad (i = 1,2,...,m)$$

$$h_j^T = \left[q_{j1} \quad q_{j2}\right] \qquad (j = 1,2,...,n). \tag{3.60}$$

It should be understood that the biplot is not in itself a model for the data. It is merely an approximate display based on the model which may help the investigator benefit from such a display. Other aspects of the biplot are discussed elsewhere (Gabriel, 1971, 1972; Corsten & Gabriel, 1976; Bradu & Gabriel, 1978; Gabriel, 1978; Daigle & Rivest, 1992).

3.2.6.4 AMMI Model and the Biplot

To generate a biplot that can be used in visual analysis of MET data, the SVs have to be partitioned into the genotype and environment eigenvectors so that equation (3.33) can be written in the form

$$y_{ij} = \mu + \tau_i + \delta_j + \sum_{k=1}^{s} \alpha_{ik}^* \gamma_{jk}^* + \rho_{ij} \tag{3.61}$$

where α_{ik}^* and γ_{jk}^* are called interaction PCA axis k scores for genotype i and environment j, respectively. In a biplot, genotype i is displayed as a point defined by all α_{ik}^* values, and environment j is displayed as a point defined by all γ_{jk}^* values (k = 1 and 2 for a two- dimensional biplot). Singular-value partitioning is implemented by

$$\alpha_{ik}^{*} = \lambda_k^{f_k}\alpha_{ik} \quad \text{and} \quad \gamma_{jk}^{*} = \lambda_k^{1-f_k}\gamma_{jk} \tag{3.62}$$

where f_k is the partition factor for PCA axis k. As mentioned above; f_k can be anything between 0 and 1 $(0 \le f_k \le 1)$, leading to numerous ways to construct a biplot. The influence of different partitioning factors on a biplot has rarely been documented, except in Yan (2002). Three special scaling methods will be reviewed in some detail below.

a) Environment-focused scaling. It is referred to as environment-focused scaling if $f_k = 0$, i.e., if the SV is completely partitioned into the environment eigenvectors so that $\alpha_{ik}^{*} = \alpha_{ik}$ and $\gamma_{jk}^{*} = \lambda_k\gamma_{jk}$. In this scaling, the environmental scores are in the original unit of yield (qt/ha), and the genotype scores are normalized (unit less). Because all of the SV is partitioned into the environment scores, the range of the environment scores is likely many times greater than that of the genotypes, and when directly plotted, the genotypes are likely to be crowded in the biplot. Therefore, a biplot based on environment-focused scaling is most suitable for visualizing the interrelationship among the environments but not for that of genotypes. To generate a biplot in which the ranges of the genotypes and the environments are comparable, the genotype scores for both axes can be multiplied by an arbitrary number. Multiplying both axes of the genotype scores with a positive number is equivalent to multiplying such a number to each element of the residual data matrix and will not alter the genotype x environment pattern of the data.

b) Genotype-focused scaling. It is referred to as genotype-focused scaling when $f_k = 1$, i.e., when the SV is partitioned entirely into the genotype eigenvectors so that $\alpha_{ik}^{*} = \lambda_k\alpha_{ik}$ and $\gamma_{jk}^{*} = \gamma_{jk}$. In this scaling, the unit of the genotype scores (α_{ik}^{*}) is the original unit of yield, and the environment scores (γ_{jk}^{*}) are unit less. Because all of the SV is partitioned into the genotype scores, the range of the genotype scores are likely to be many times greater than that of the environment scores. As a result, the environments in the biplot are likely to be crowded relative to the genotypes. Therefore, a biplot based on genotype-focused scaling is suitable for evaluating the genotypes but not the environments. To generate a biplot in which the ranges of the genotypes and the

environments are comparable, the environment scores of both axes can be multiplied by an arbitrary factor.

c) Symmetric scaling. It is called symmetrical scaling when f_k takes the value of 0.5 so that $\alpha_{ik}^{*} = \lambda_k^{0.5}\alpha_{ik}$ and $\gamma_{jk}^{*} = \lambda_k^{0.5}\gamma_{jk}$. This type of scaling has the unique property that genotype scores and environmental scores have the same unit for both PCA axis 1 and PCA axis 2, which is the square root of the original unit $\left[(qt/ha)^{0.5}\right]$. This property makes it possible to visualize the relative magnitude of genotype variation and environment variation for both axes. This is the scaling method used in AMMI analysis (Gauch, 1988). It is intermediate between the environment-focused scaling and the genotype-focused scaling in all aspects.

The results of AMMI analysis can be presented graphically in the form of biplots (Gauch, 1988; Zobel et al., 1988; Shaffi & Price, 1998; Vargas et al., 1999; Ebdon & Gauch, 2002) in which the genotype and environment scores of the first two or three bilinear (multiplicative) terms are represented by vectors in a space, with starting points at the origin and end points determined by the scores. Usually the environmental and genotypic scores of the first and second bilinear terms are plotted. The distance between two genotype vectors (their end points) is indicative of the amount of interaction between the genotypes. The cosine of the angle between two genotype (or environment) vectors approximates the correlation between the genotypes (or environments) with respect to their interaction. Acute angles indicate positive correlation, with parallel vectors (in exactly the same directions) representing a correlation of 1. Obtuse angles represent negative correlations, with opposite directions indicating a correlation of -1. Perpendicularity of directions indicates a correlation of 0. The relative amounts of interaction for a particular genotype over environments can be obtained from orthogonal projections of the environmental vectors on the line determined by the direction of the corresponding genotype vector. Environmental vectors having the same direction as the genotype vectors have positive interactions (that is, these environments favoured these genotypes), where as vectors in the opposite directions have negative interactions.

To visualize main effects and interaction, a biplot of interaction PCA 1 scores against genotypic and environmental means is used in AMMI analysis. Figure 3.1 illustrates a biplot of genotypic scores for interaction PCA axis 1 against genotypic means. An ideal cultivar should have the highest mean performance and be absolutely stable. Such an ideal cultivar with superior performance in all environments (both favorable and unfavorable) is so represented in the AMMI biplot (Figure 3.1) by the dot with an arrow pointing to it. Although such an ideal cultivar may not exist in reality, it can be used as a reference for cultivar evaluation. A genotype is more desirable if it is located closer to the ideal cultivar.

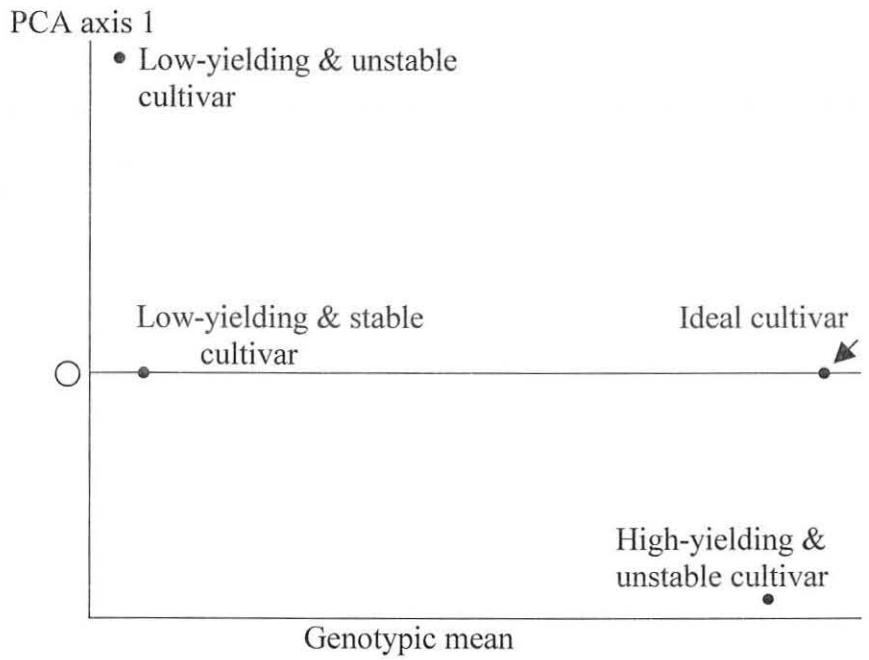


Figure 3.1 Illustration of a biplot of interaction PCA axis 1 versus genotypic means, presenting the main types of genotypes and patterns of stability and adaptation.

Source: Ebdon and Gauch, 2002.

CHAPTER FOUR
RESULTS AND DISCUSSION

4.1 Introductory Remarks

Replicated grain yield data (qt/ha) of 15 maize genotypes grown during 2004 and 2005 from 4 locations was used in this study. In the analysis, each combination between the 4 locations and 2 years was considered as an environment, making a total of 8 environments. The experimental layout at each environment was a randomized complete block design with 3 replicates.

The software IRRISTAT, released by the International Rice Research Institute (IRRI) of Manila, Philippines, was used for the Gollob's F-test. All other analyses described in this thesis were performed using SAS. In particular, the environmental variance, Wricke's ecovalence and Shukla's stability variance were performed by SAS MACRO developed by Hussein et al. (2000). The SAS program statements for individual ANOVAs for each environments, the combined ANOVA across environments, LR analysis and AMMI analysis were written by the author and are deferred to Appendix 1.

The usual diagnostic plots—including a normal probability plot of residuals, a histogram of residuals, plot of residuals versus fitted values, plot of residuals versus levels of regressor variable—and formal statistical procedures to assess model assumptions for the individual ANOVAs (i.e. for yield data at each environment), the combined ANOVA across environments (i.e. for the entire yield data), and the separate LR models (for each genotype yield) were performed. Examination of the results do not reveal any serious violations of the assumptions that errors are normally and independently distributed with mean zero and constant variance, nor is there any evidence pointing to possible outliers. As an illustration, SAS output for the ANOVA model for the yield data in E2 (Arsinegelle-2004) & E5 (Awassa-2005), the combined ANOVA model for the entire yield data and the LR model for the yield data of G4 and G12 are presented in Appendix 2.

Separate analyses of variance (ANOVA) were first done with the classical RCBD model with random blocks at each environment. Summary of results of the separate analyses is given in Table 4.1. As suggested by Dagnelie (1975), cited by Annicchiarico (2002), homogeneity of experimental errors among test environments in MET yield trials can easily be assessed by regressing error mean square on mean yield of the trials, with both terms expressed on a logarithmic scale. Such a procedure can reveal whether transformation is required or not before combining results over environments. (Regression slope (b): $b \approx 2$ suggests a logarithmic transformation of the complete data set; $b \approx 1$ suggests a square root transformation; and $b \approx 0$ discourages any data transformation).

Table 4.1 Summary of experiment error and experiment mean yield, obtained from ANOVAs for individual trials (i.e. environments), and their logarithmic transformation.

Environment	Experimental error in the j^{th} environment $\lfloor MS_{e(j)} \rfloor$	Mean grain yield (qt/ha) in the j^{th} environment $(\bar{y}_{.j})$	$\log\lfloor MS_{e(j)} \rfloor$	$\log(\bar{y}_{.j})$
E1(Awassa-2004)	32.5641	38.6911	1.51274	1.58761
E2 (Arsinegelle-2004)	82.2848	61.6980	1.91532	1.79027
E3 (Areka-2004)	22.4999	53.4704	1.35218	1.72811
E4 (Goffa-2004)	81.5356	45.1049	1.91135	1.65422
E5 (Awassa-2005)	64.2862	79.5767	1.80812	1.90079
E6 (Arsinegelle-2005)	33.6214	67.0251	1.52662	1.82624
E7 (Areka-2005)	46.9730	54.4653	1.67185	1.73612
E8 (Goffa-2005)	92.9974	56.9542	1.96847	1.75553

For our data set, result from regression on log-transformed values of both variables ($b = 0.4$) discouraged any data transformation. In addition, a plot of residuals against mean yield of environments (see Appendix 2) indicated no heterogeneity of experimental errors among trials. Therefore, a combined analysis of variance (ANOVA) was performed on the original (untransformed) yield data for the complete set of trials. Genotypes were considered fixed effects, while environments and replicates within environments as random effects.

4.2 Analysis of Variance of MET Maize Yield Trial

Table 4.2 shows the analysis of variance (ANOVA) for the entire maize yield trial, consisting of 360 yield observations on 15 genotypes in 8 environments each with 3 replicates. These data have a total of 359 DF. The experimental error, calculated from the whole experiment, has a sum of squares of 12789.34368 associated with 224 degrees of freedom. The grand mean is 57.12 qt/ha.

The ANOVA model partitions the treatment (combinations of 8 environments and 15 genotypes) DF and SS into three sources: additive environment effects, additive genotype effects and the genotype x environment interaction (that is, the non-additive residual from the additive ANOVA model). The analysis of variance across environments showed significant effects for environment ($P < 0.0001$), genotype ($P<0.0001$), and genotype x environment interaction ($P=0.0375$) for grain yield. These sources contain 81.8%, 6.1% and 12.1% of the treatment SS, respectively. These percentages are typical in multi-environment yield trials (see, for instance, Gauch & Zobel, 1996). The magnitude of the sum of squares (SS) for GxE was large, i.e., about two times the genotype main effect SS, and significant when tested against the pooled error variance.

One feature of the ANOVA in Table 4.2 merits clarification. The interaction mean square (MS_{GxE}) is lower than the genotype mean square (MS_G). However, the interaction SS is almost two times as large as the genotype SS. This disparity between MS and SS view points arise because the genotype and interaction sources have 14 and 98 DF, respectively, thus differing in DF by an enormous factor of 7.

In the maize yield trial, large main effects for environments indicate that the testing environments were different in yield potential. This can be explained by the fact that environment grain yields (averaged across genotypes) ranged from 38.69qt/ha at Awassa in 2004 to 79.58 qt/ha at Awassa in 2005. Also, significant effect for genotype reveals that there were differences among cultivars for grain yield. Genotype grain yields (averaged across environments) ranged from 50.40 qt/ha for G13 to 64.24 qt/ha for G3.

The significant genotype x environment interaction effect implies that genotypes reacted dissimilarly to changing environments for grain yield. An indication of the presence of genotype x environment interaction (GxE) is the differential yield ranking of genotypes across environments. In this study, different genotypes produced the highest grain yields at different environments. Genotype G10 was the highest yielder at the highest yielding environment (E5), while G6 was the highest yielder at the lowest yielding environment (E1). As to the remaining environments, genotype G3 was the highest yielding cultivar at environments E2 & E6, G11 at E3, G1 at E4 and G7 at environment E8 (results not shown).

Table 4.2 Analysis of variance for grain yield (qt/ha) of the 15 maize genotypes grown in 8 environments.

Source of variation	DF	Sum of squares	Mean square	F value
Total	359	79235.73446		
Rep within environment	16	4404.32592	275.27037	
Treatment	119	62042.06487	521.36189	
Environment (E)	7	50748.83724	7249.83389	126.98**
Genotype (G)	14	3768.55680	269.18263	4.71**
Genotype x Environment interaction (G x E)	98	7524.67083	76.78236	1.34*
Error	224	12789.34368	57.09528	

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.
Trial mean: 57.12 qt/ha; coefficient of variation (%), 19.4

Estimated variance component due to environment $\left(\hat{\sigma}_{\delta}^{2} = 154.55281\right)$ made the greater contribution to the total estimated variance for grain yield. Genotype x environment interaction and residual components of variance were $\hat{\sigma}_{\tau\delta}^{2} = 6.56236$ and $\hat{\sigma}^{2} = 57.09528$, respectively.

The relative performance of genotypes based on the mean grain yield over environments is presented in Table 4.3. The three highest yielding varieties over 8 environments were G3 (64.24 qt/ha), G7 (60.83 qt/ha), and G6 (59.78 qt/ha). The two lowest yielding varieties were G13 (50.40 qt/ha) and G12 (52.74 qt/ha). Means across environments are adequate indicators of genotypic performance only in the absence of GxE. If GxE is

present, use of means across environments ignores that genotypes differ in relative performance over environments.

Table 4.3 Mean grain yield (qt/ha) of 15 (G1-G15) maize genotypes over 8 test environments.

Genotype	Mean grain yield (qt/ha)
G1	57.30
G2	55.48
G3	64.24
G4	54.94
G5	58.33
G6	59.78
G7	60.83
G8	57.80
G9	56.38
G10	56.02
G11	58.36
G12	52.74
G13	50.40
G14	55.06
G15	59.18

A large genotype x environment interaction for yield of these 15 maize genotypes was found. Owing to the large genotype x environment interaction, a study needs to be made on yield stability.

4.3 The Environmental Variance

Yield stability usually refers to a genotype's ability to perform consistently across a range of environments. As discussed more thoroughly in Section 2.3, most stability measures relate to either of two contrasting concepts of stability: static (type 1) and dynamic (type 2) (Lin et al., 1986; Becker & Léon, 1988). Static stability is analogous to the biological concept of homeostasis: a stable genotype tends to maintain a constant yield across environments. Dynamic stability implies for a stable genotype a yield response in each

environment that is always parallel to the mean response of the tested genotypes, i.e., zero GxE.

The environmental variance (S_i^2) is one of the major stability measures for the static stability concept (type 1 stability), i.e., the variance of genotype yields recorded across test environments. The smaller the S_i^2, the more stable the i^{th} genotype. Derived stability measure includes its coefficient of variation.

Table 4.4 Genotype mean grain yield, environmental variance (S_i^2), and coefficient of variation (CV_i) for the 15 maize varieties.

Genotype	Mean grain yield (qt/ha)	Environmental variance (S_i^2)	Coefficient of variation $(CV_i\%)$
G1	57.30	144.57	20.98
G2	55.48	108.96	18.81
G3	64.24	245.79	24.41
G4	54.94	104.46	18.60
G5	58.33	182.47	23.16
G6	59.78	217.97	24.70
G7	60.83	210.95	23.88
G8	57.80	175.12	22.89
G9	56.38	199.54	25.05
G10	56.02	245.67	27.98
G11	58.36	196.36	24.01
G12	52.74	231.84	28.87
G13	50.40	162.76	25.31
G14	55.06	159.95	22.97
G15	59.18	188.63	23.21

Genotype's variance across environments and coefficient of variation are listed in Table 4.4. Based on these two measures, genotypes G4, G2 and G1 can be considered relatively more stable. Genotypes G4 and G2 have mean grain yield of 54.94 qt/ha and 55.48 qt/ha, respectively, which are below the grand mean, while genotype G1 have mean yield of 57.30 qt/ha which is slightly above the grand mean (57.12 qt/ha). By contrast, genotypes G12 and G10 can be regarded as unstable varieties (see also the plot in Figure 4.1).

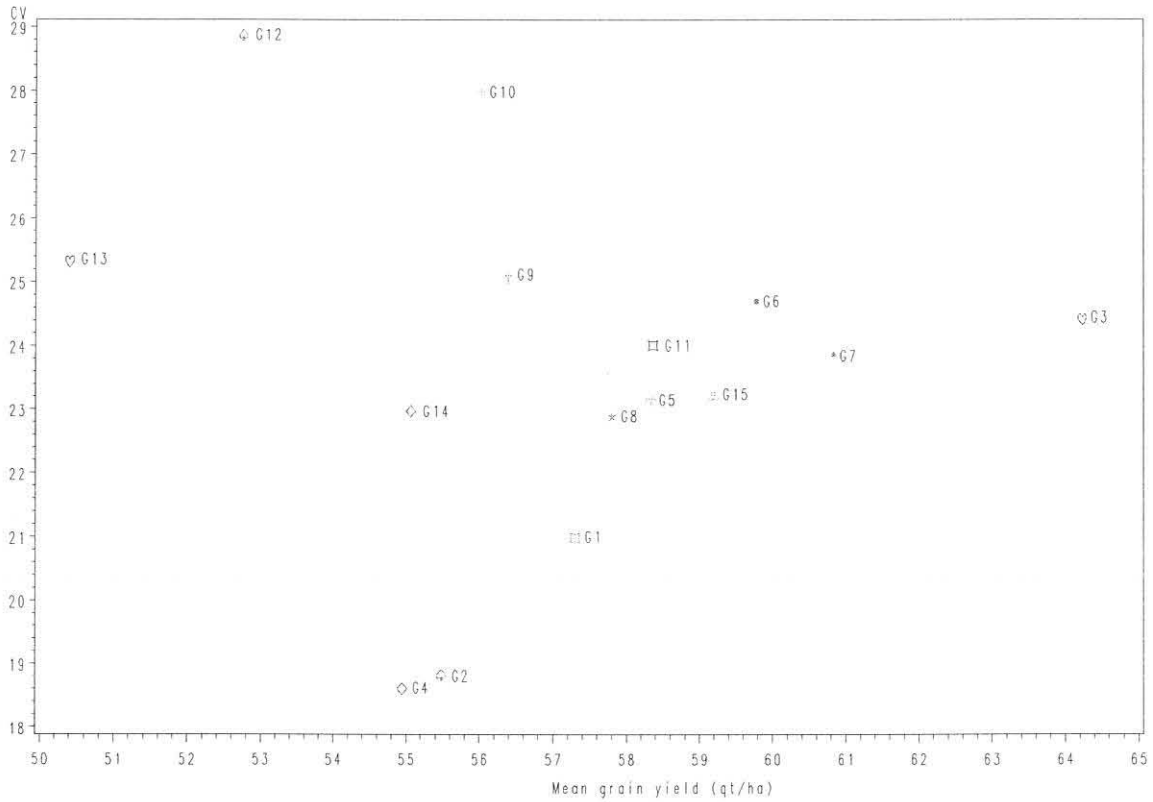


Figure 4.1 Plot of CV versus mean grain yield for 15 maize genotypes.

The GxE effect contributing to yield stability can be either:

- exploited, by breeding and growing genotypes that are stable according to the static concept (i.e. with a better response in unfavorable environments); or
- minimized, by using material that is stable according to the dynamic concept.

4.4 Wricke's Ecovalence

Wricke (1962) defined the concept of ecovalence as the contribution of each genotype to the genotype x environment interaction sum of squares. The ecovalence (W_i) or stability of the i^{th} genotype is its interaction with environments, squared and summed across environments. Accordingly, genotypes with low ecovalence have smaller fluctuations from the mean across different environments and are therefore more stable.

The amount of interaction displayed by each genotype (ecovalence) (Wricke, 1962) is given in Table 4.5. The most interactive genotype was G10 followed by genotypes G6 and G12. Genotypes G1, G14 and G9 have low ecovalence and are thus more stable. However, these varieties were not best for mean yield. Considering yield stability in conjunction with mean yield, it seems that variety G15 has relatively good yield and maintained its yield stability.

Table 4.5 Genotype mean grain yield, ecovalence (W_i), and contribution (%) of genotypes to genotype x environment sum of squares (SS_{GxE}) for the 15 maize varieties.

Genotype	Mean grain yield (qt/ha)	Ecovalence (W_i)	$\%SS_{GxE}$
G1	57.30	31.50	1.3
G2	55.48	77.60	3.1
G3	64.24	193.87	7.7
G4	54.94	155.85	6.2
G5	58.33	110.04	4.4
G6	59.78	382.87	15.3
G7	60.83	124.89	5.0
G8	57.80	95.83	3.8
G9	56.38	75.95	3.0
G10	56.02	385.88	15.4
G11	58.36	168.82	6.7
G12	52.74	314.75	12.5
G13	50.40	245.53	9.8
G14	55.06	42.67	1.7
G15	59.18	102.13	4.1

4.5 Shukla's Stability Variance

Shukla (1972) proposed a stability statistic, $\hat{\sigma}_i^2$, that is based on the partitioning of the GxE sum of squares into components attributable to individual genotypes. With $\hat{\sigma}_i^2$, a genotype has stable trait expression when its contribution to the GxE is small. The $\hat{\sigma}_i^2$ encompasses both GxE pattern and residual, or noise.

Table 4.6 shows estimates of stability variances (σ_i^2). Thus, genotypes G1, G14 and G9 can be regarded as relatively more stable cultivars. On the contrary, genotypes G10, G6, and G12 can be judged unstable. Joint examination of Tables 4.5 and 4.6 reveals that Wricke's ecovalence and Shukla's stability variance are equivalent for assessment of yield stability of the genotypes. Our result on the concurrence of W_i and $\hat{\sigma}_i^2$ was similar to other studies (Lin et al., 1986; Piepho, 1996; Weber et al., 1996; Sneller et al., 1997). To avoid redundancy, we suggest that the ecovalence and stability variance should not be used side by side for assessment of yield stability in multi-environment trials.

Table 4.6 Genotype mean grain yield and Shukla's stability variance $(\hat{\sigma}_i^2)$ for the 15 maize varieties.

Genotype	Mean grain yield (qt/ha)	Stability variance ($\hat{\sigma}_i^2$)
G1	57.30	3.22
G2	55.48	10.82
G3	64.24	29.99
G4	54.94	23.72
G5	58.33	16.17
G6	59.78	61.14
G7	60.83	18.62
G8	57.80	13.83
G9	56.38	10.55
G10	56.02	61.64
G11	58.36	25.86
G12	52.74	49.91
G13	50.40	38.50
G14	55.06	5.06
G15	59.18	14.87

Whereas the static stability concept considers G4, G2, G1 relatively more stable, the dynamic concept regards G1, G14, G9 as more stable among the 15 maize varieties. Note that genotype G1 was classified as relatively stable in both approaches.

Further approaches to examine genotype x environment interaction attempt to dissect the information included in the GxE term. For plant breeding, the recovery of pattern might be considered the principal objective of analysis. The exploration of GxE starts by using linear regression (LR).

4.6 Regression analysis

Another procedure for modeling statistical interaction is the linear regression of the genotype performance on the environment mean (Yates & Cochran, 1938; Finlay & Wilkinson, 1963; Eberhart & Russell, 1966). This model can be depicted in a set of straight lines with different slopes, one for each genotype, and the heterogeneity of slopes accounts for the interaction.

The analysis of variance (ANOVA) decomposition (Table 4.2) confirms that interactions can not be ignored. To that end, the genotype x environment interaction (G x E) was analyzed (Table 4.7) using the linear regression technique. In Table 4.7, the genotype x environment interaction (GxE) is partitioned into two components: heterogeneity of genotype regressions; and the deviations from regressions.

The regression of each genotype's yields on the environmental means partitioned this maize data set's 98 DF for genotype x environment interaction with a sum of squares (SS) of 7524.67083 into: heterogeneity of genotype regressions with 14 DF and a SS of 610.13637 and the residual 84 DF for deviations from regressions and a SS of 6914.53445. It is noteworthy that the sum of squares (SS) of regression accounted for only 8.1% of the genotype x environment interaction SS, and the remaining 91.9% was accounted for by the SS of the regression residual. The argument that heterogeneity of slopes generally explains only a small proportion of the interaction is supported by this data.

The SS proportion accounted for by heterogeneity (model R^2) may be obtained by summing up the model SS across separate regression analyses of GxE effects performed for each individual genotype, and calculating the proportion in the total SS in the regressions. The complement to one of this value indicates the proportion of GxE variation accounted for by deviations from regressions.

The genotype regressions term was tested for significance using an F-ratio with deviations from regressions MS as the error term. The deviations from regressions MS were tested for significance using the error term for overall genotype x environment interaction (GxE) in the ANOVA. The genotype regressions have a mean square (MS) of 43.58117 with 14 DF, giving an insignificant F-ratio of 0.53. The resulting residual with 84 DF has a larger MS than does the interaction itself, and its F-ratio of 1.44 is significant at the 5% level. For a model to produce a residual more significant than the source from which the residual is taken constitutes the ultimate in model failure. In conclusion, the linear regression analysis is ineffective for this data set.

Table 4.7 Joint regression partitioning of the genotype x environment interaction (GxE) for grain yield (qt/ha) of 15 genotypes grown in 8 environments.

Source of variation	DF	Sum of squares	Mean square	F value
Total	359	79235.73446		
Rep within environment	16	4404.32592	275.27037	
Treatment	119	62042.06487	521.36189	
Environment (E)	7	50748.83724	7249.83389	126.98**
Genotype (G)	14	3768.55680	269.18263	4.71**
Genotype x Environment interaction (G x E)	98	7524.67083	76.78236	1.34*
Regression	14	610.13637	43.58117	0.53 ns
Residual	84	6914.53445	82.31589	1.44*
Error	224	12789.34368	57.09528	

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.

ns Not significant.

Trial mean: 57.12 qt/ha; coefficient of variation (%): 13.22779; $R^2 = 0.838591$.

Table 4.8 shows the results of separate regression analyses for the 15 maize genotypes. Again, each β_{1i} coefficient was tested for difference to unity using the deviation from regression of the individual genotype as an error term, as provided by separate regression analyses for the individual genotypes. As was anticipated, none of the $\hat{\beta}_{1i}$ values was significantly different from $1 (p > 0.05)$. For this particular maize data set, slope estimates ranged from 0.75496 (G4) to 1.17673 (G3) for grain yield. It can be concluded

that the regression slope is unable to detect any difference in yield stability of the genotypes.

Table 4.8 Genotype mean grain yield and results from regression of genotypic responses against environmental mean.

Genotype	Mean grain yield (qt/ha)	$\hat{\beta}_{1i}$	F for $H_0 : \beta_{1i} = 1$	$pr > F$	s^2_{di}	P-value for the lack of fit test	R^2
G1	57.30	0.93467	0.22	0.6415	64.803155	0.9842	0.6746
G2	55.48	0.80381	3.02	0.0963	43.150955	0.9156	0.6972
G3	64.24	1.17673	1.16	0.2931	91.065993	0.5630	0.7005
G4	54.94	0.75496	4.00	0.0581	50.847325	0.5669	0.6329
G5	58.33	1.01755	0.01	0.9081	76.389580	0.6908	0.6758
G6	59.78	1.00674	0.00	0.9671	88.489773	0.0146	0.6379
G7	60.83	1.09927	0.28	0.6005	118.057643	0.8661	0.6115
G8	57.80	1.00110	0.00	0.9917	37.155717	0.2574	0.8058
G9	56.38	1.08565	0.43	0.5195	57.901344	0.7951	0.7579
G10	56.02	1.09133	0.30	0.5885	93.627217	0.0280	0.6617
G11	58.36	1.03441	0.06	0.8104	67.948336	0.2929	0.7077
G12	52.74	1.07991	0.17	0.6798	123.445333	0.2843	0.5923
G13	50.40	0.89635	0.46	0.5068	79.803960	0.1692	0.6076
G14	55.06	0.97750	0.03	0.8678	60.419448	0.9379	0.7086
G15	59.18	1.04003	0.13	0.7251	42.721677	0.3306	0.7957

The analysis of variance for the regression model (Table 4.7) shows that the β_{1i}'s are homogeneous among genotypes. Moreover, the residual MS is substantially larger than the error MS indicating heterogeneity of residuals among genotypes. Therefore, stability for these maize genotypes was evaluated by considering deviation from regression. Eberhart and Russell (1966) advocated using the mean square deviation from regression of i^{th} genotype against environmental mean, s^2_{di}, to evaluate the relative stability of a set of genotypes across a variety of environments. According to the s^2_{di} values, G8, G15 and G12 can be regarded as more stable varieties. Of these, genotype G15 can be considered best, judging from its mean yield (59.18qt/ha) and deviation from regression ($s^2_{di} = 42.721677$). On the contrary, G12, G7 and G3 can be classified as unstable varieties.

The lack of fit test was significant for genotypes G6 and G10 $(p < 0.05)$. This suggests that the LR model appears to be inadequate for these two cultivars. The separate regression analyses for the other genotypes indicated no lack of fit. The coefficient of determination (R^2), computed from separate regression analyses, ranged from 0.5923 to 0.8058. The coefficient of determination were relatively large for varieties G8 (0.8058) and G15 (0.7957).

There is considerable disagreement in assessing yield stability among the methods presented so far. Results from a simple variance or CV of the genotype across environments identified G4, G2 and G1 as more stable varieties. Based on the contribution of genotype's to genotype x environment interaction, varieties G1, G14 and G9 were classified as more stable. The slopes resulting from regressing on environmental mean proved unfruitful to detect any difference in stability pattern for the varieties analyzed in this study. Finally, varieties G8, G15 and G12 were considered more stable from Eberhart and Russell's deviation from regression. Essentially, it is difficult to reconcile all of these assessments into a unified conclusion.

Although the LR happen not to partition useful sources from the interaction, this large interaction SS should simulate other attempts to partition this interaction. A generalization of the regression on the environmental mean model is the multiplicative model also called Principal Component Analysis of the GxE or Additive Main Effects and Multiplicative Interaction (AMMI) model (Gollob, 1968; Mandel, 1971; Gauch, 1988).

4.7 Additive Main Effects and Multiplicative Interaction (AMMI) Analysis and Biplot Representation

In AMMI, the interaction $(\tau\delta)_{ij}$ is partitioned into successive multiplicative terms or products of the form $\alpha_i^* \gamma_j^*$, where α_i^* can be interpreted as the genotypic sensitivity of genotype i to a hypothetical environmental variable γ^*, which has value γ_j^* in

environment j. Alternatively, γ_j^* can be interpreted as the environmental potentiality of environment j to a hypothetical genotypic variable α^*, which takes value α_i^* for genotype i.

The application of AMMI to the maize yield data set is shown in Table 4.9. The genotype and environment main effects are identical with ANOVA and have the usual interpretations of overall yield or productivity. Using the full AMMI model, the GxE was partitioned into seven interaction PCA axes. AMMI partitions the 98 DF in the genotype x environment interaction, producing a first interaction PCA axis with 20 DF containing 54.6% of the interaction SS, giving a MS of 205.3185 and a significant F-ratio of 3.60. Similarly, the second interaction PCA axis explained 14.7% of the interaction SS with 18 DF, giving a MS of 61.3050 and a significant F-ratio of 1.07. The remaining interaction PCA axes have F-ratios of less than 1, so they may be combined into a residual with 60 DF, a MS of 38.5790 and an F-ratio 0.68. Consequently, the partitioning of the interaction SS by AMMI is extremely effective in finding structure within the interaction.

The SS of the first two interaction PCA axes is almost 1.4 times as large as is the SS for genotypes. Also, the first interaction PCA axis alone has a higher SS than the genotype SS. Note in Table 4.9 that the SS for axis 2 is only one-fourth that of axis 1. Clearly any realistic or accurate analysis of these maize yield data must consider this large interaction.

The first two bilinear interaction terms of the AMMI analysis of variance accounted for 69.3% of the genotype x environment interaction sum of squares, indicating that with only 38 DF, from the 98 DF contained in the analysis of variance for genotype x environment interaction, a considerable amount of GxE was explained (Tables 4.9 and 4.10). Hence, the AMMI-2 model is selected for this particular yield trial. This partitions the treatment SS and DF into a model with a SS of 59727.25404 in 59 DF and a residual with a SS of 2314.74 in 60 DF. Overall, this model contains 96.3% of the treatment SS.

Table 4.9 Additive main effects and multiplicative interaction (AMMI) partitioning of the genotype x environment interaction (G x E) for grain yield (qt/ha) of 15 genotypes grown in 8 environments.

Source of variation	DF	Sum of squares	Mean square
Total	359	79235.73446	
Rep within environment	16	4404.32592	275.27037
Treatment	119	62042.06487	521.36189
Genotype (G)	14	3768.55680	269.18263 **
Environment (E)	7	50748.83724	7249.83389 **
Genotype x Environment interaction (G x E)	98	7524.67083	76.78236 *
PCA-1	20	4106.37	205.3185 **
PCA-2	18	1103.49	61.3050 *
PCA-3	16	826.68	51.6675 ns
PCA-4	14	671.55	47.9679 ns
PCA-5	12	411.78	34.3150 ns
PCA-6	10	306.75	30.6750 ns
PCA-7	8	97.98	12.2475 ns
Error	224	12789.34368	57.09528

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.
ns Not significant.

These results show that AMMI-2 is more parsimonious and effective than the original ANOVA model, i.e. it requires fewer DF for an adequate description of the interaction and excludes most of its actual noise. We would tend to exclude the 3rd and later axes from the AMMI model. The ANOVA interaction is then replaced by the first two multiplicative terms.

The sum of squares (SS) of the first two significant interaction PCA axes and the SS of PCA axis 1 were higher than the SS of regression by 8.5 and 6.7 fold, respectively. These results demonstrate the effectiveness of the AMMI model in capturing and partitioning the SS of genotype x environment interaction in comparison to the linear regression

technique. The superiority of AMMI over joint regression analysis for describing GxE was also revealed in the works of Nachit et al. (1992) and Annicchiarico et al. (2005).

Table 4.10 Eigenvalues and associated variance proportions for yield of 15 maize genotypes grown in 8 environments.

PCA	Eigenvalue	Variance proportion (%)	
		Component	Cumulative
PCA-1	4106.37	54.6	54.6
PCA-2	1103.49	14.7	69.3
PCA-3	826.68	11.0	80.3
PCA-4	671.55	8.9	89.2
PCA-5	411.78	5.5	94.7
PCA-6	306.75	4.1	98.8
PCA-7	97.98	1.3	100

Estimates for the environmental and genotypic scores of AMMI-2 (i.e. of interaction PCA axis 1 and axis 2) are given in Tables 4.11 and 4.12, respectively. The PCA scores of a genotype from AMMI analysis indicate the stability or adaptation of a genotype across environments. The larger the PCA scores, either positive or negative, the more specifically adapted a genotype is to certain environments. The closer the PCA scores near zero, the more stable or adapted a genotype is over all test environments. Environment scores from AMMI analysis relating to interaction also have meaningful interpretation. Environments with large PCA scores are more discriminating of genotypes, while environments with PCA scores near zero exhibit little interaction across genotypes and low discrimination among genotypes.

Genotype and environment combinations with PCA scores of same signs produce positive specific interaction effects, whereas combinations of opposite signs have negative specific interactions. For example, Arsinegelle-2004(E2) and genotype G6 or

G5 have positive specific interaction effects whereas genotype G12 or G13 and Arsinegelle-2004(E2) have negative specific interaction effects. Environments which have same signs of interaction PCA scores discriminate genotypes similarly, for example Goffa-2005(E8) & Goffa-2004(E4) or Areka-2004(E3) & Awassa-2005(E5); and environments with opposite sign of interaction scores discriminate genotypes differently, for example Areka-2004(E3) & Arsinegelle-2004(E2). It is worth to note that obtaining information from Tables 4.11 and 4.12 is not as immediate and quick.

Table 4.11 Estimates for the environmental scores of AMMI-2.

Environment	Mean grain yield (qt/ha)	$\hat{\lambda}_1^{1/2}\hat{\gamma}_{j1}$	$\hat{\lambda}_2^{1/2}\hat{\gamma}_{j2}$
Awassa-2004 (E1)	38.69	0.09567	-0.06623
Arsinegelle-2004 (E2)	61.70	4.38464	1.05489
Areka-2004 (E3)	53.47	-1.14365	-1.94329
Goffa-2004 (E4)	45.10	-1.74944	1.55912
Awassa-2005 (E5)	79.58	-2.31702	-0.64108
Arsinegelle-2005 (E6)	67.03	2.21686	-0.27249
Areka-2005 (E7)	54.47	0.25792	-2.22470
Goffa-2005 (E8)	56.95	-1.74498	2.53379

The results of AMMI analysis can easily be visualized on the basis of two AMMI biplots: a biplot of PCA axis 1 versus PCA axis 2 for both genotypes & environments (Figure 4.2) and a biplot of PCA axis 1 versus mean yield of both genotypes & environments (Figure 4.3).

In Figure 4.2 genotypes and environments are depicted as points on a plane. The position of the point for genotype i is given by the estimates for the genotypic scores $\left(\lambda_2^{1/2}\alpha_{i2}, \lambda_1^{1/2}\alpha_{i1}\right)$; similarly, the point coordinates for environment j originate from the estimates for the environmental scores $\left(\lambda_2^{1/2}\gamma_{j2}, \lambda_1^{1/2}\gamma_{j1}\right)$. In a vector representation, the

genotype and environment point determine lines starting at the origin (0,0). The interaction effect of genotype i in environment j is approximated by projecting the genotype point $\left(\lambda_2^{1/2}\alpha_{i2}, \lambda_1^{1/2}\alpha_{i1}\right)$ onto the line determined by the environmental vector, which has a slope $\lambda_1^{1/2}\gamma_{j1}/\lambda_2^{1/2}\gamma_{j2}$, where distance from the origin provides information about the magnitude of the interaction. The angle between the vectors of genotype i and environment j tells us something about its nature: the interaction is positive for acute angles, negligible for right angles, and negative for obtuse angles. The abscissa shows the PCA-2 scores and the ordinate shows the PCA-1 scores, and thus genotypes/environments that appear almost on a vertical line have similar interaction pattern for PCA-2, and those that fall almost on a horizontal line have similar interaction pattern with PCA-1. Genotypes/environments that fall in the bottom left quadrant have a negative interaction along both axes, and those that fall in the top right quadrant have positive interaction with both axes, while the others have different signs of interactions for both axes. Genotypes with large PCA-1 or PCA-2 or both (either positive or negative) have high interactions, whereas genotypes with PCA-1 or PCA-2 scores near zero have small interactions for the corresponding axis. Since PCA-2 is more exposed to noise than PCA-1, genotypes that have large negative or positive values along the latter axis have stronger interaction than those along the former axis. Points representing genotypes and environments that are close to the origin contribute little to the interaction and can be well approximated by additive terms alone. A biplot of PCA axis 1 versus PCA axis 2 depicts the level of interaction inherent in the data; it does not present a contrast of interaction and main effects. To investigate main effects and interaction a biplot of PCA axis 1 versus genotype and environment yield means is presented in Figure 4.3.

The AMMI biplot in Figure 4.3 shows contemporarily main effects (genotypes and environments average yields) and interaction, as PCA-1 scores. The ordinates are the PCA-1 scores, and the abscissas are the means for genotypes & environments. The grand mean is indicated as a vertical, solid line. In this biplot, displacement along the abscissa reflects differences in main effects, whereas displacement along the ordinate indicates

differences in interaction effects. In both AMMI biplots open circles represent genotypes whereas closed circles represent environments.

Let's now examine the distribution of genotypes and environments in Figure 4.2. Note that the biplot captures 69.3% of the interaction SS. Because the GxE component of the AMMI model is based on the product of interaction PCA scores, it follows that genotypes or environments with small interactions (smaller scores) will appear close to the center of the axes. Genotypes G14, G1 and G2 exhibit this trait, and therefore are relatively more stable. Conversely, genotypes such as G6, G13, G12 and G10 are further from the center and, thus, show strong interaction effects. For genotypes with interaction scores near zero (these genotypes do not interact much with environments), mean yield is consistent across environments (both favorable and unfavorable) and overall ranking were fairly reliable; whereas for genotypes with large interaction mean yield was highly variable across environments and overall ranking were less reliable.

Among the 8 location-year environments Arsinegelle-2004(E2), Goffa-2005(E8), Areka-2004(E3) and Areka-2005(E7) exhibited larger interactions and were more discriminating of genotypes, whereas the environment Awassa-2004(E1) exhibited negligible interaction and low discrimination. The nearly additive behavior of E1 indicates that genotypic yields in that environment were highly correlated with the overall genotypic means across environments.

The direction of the genotypes and environments from the axes' center also contain important information on the interaction. As an example, genotype G13 and environment Arsinegelle-2004(E2) appear opposite from each other indicating their contributions to the interaction was in opposing directions (e.g., they are negatively correlated). By contrast, genotype G10 and environment Goffa-2005(E8) both have the same relative direction, so that both contribute positively to the interaction. Indeed, the best genotype with respect to Arsinegelle-2004(E2) was variety G6. For environments Goffa-2004(E4) and Goffa-2005(E8) the best genotype was G10. Likewise, genotype G13 was best for Awassa-2005(E5); G4 was best for Areka-2004(E3); G7 was best for Areka-2005(E7)

and G3 was best for Arsinegelle-2005(E6). Thus, the biplot can give information on relative stability, as well as suggesting trends of similar or dissimilar genotypes and environments.

Table 4.12 Estimates for the genotypic scores of AMMI-2.

Genotype	Mean grain yield (qt/ha)	$\hat{\lambda}_1^{1/2}\hat{\alpha}_{i1}$	$\hat{\lambda}_2^{1/2}\hat{\alpha}_{i2}$
G1	57.30	-0.31893	-0.35921
G2	55.48	0.47921	-0.04796
G3	64.24	1.89746	-0.17596
G4	54.94	-0.96587	-1.17939
G5	58.33	1.29554	0.78112
G6	59.78	3.01407	0.95777
G7	60.83	0.36848	-2.02470
G8	57.80	1.16259	0.53931
G9	56.38	0.00964	-1.09645
G10	56.02	-2.52220	2.14937
G11	58.36	-0.01756	2.07426
G12	52.74	-2.63350	-0.09962
G13	50.40	-2.41456	-0.61214
G14	55.06	-0.19985	0.17452
G15	59.18	0.84549	-1.08091

The second biplot (Figure 4.3) is of interaction PCA axis 1 versus mean yield of both genotypes and environments. This graph is relevant as it accounts for 94.5% of the treatment SS due to main effects and interaction associated with 120 genotype-environment combinations. This figure illustrates the wide discrepancy between the variability of environments and genotypes. Genotypes are represented as a narrow band at or around 57.12 qt/ha, while environments cover a larger yield range. As before, the position of genotypes or environments is important, with those appearing closer to the vertical reference line at PCA1 = 0 exhibit little or no interaction indicating a greater relative stability. The AMMI biplot (Figure 4.3) separates the high yielding genotypes & environments, at the right-hand side, from the low yielding genotypes & environments, at its left-hand side.

In the case of genotypes, the first PCA axis was dominated by varieties G6, G12, G10, G13 and G3, suggesting that these cultivars exhibit a high degree of influence over the GxE. Genotypes G9, G11, G14, G1, G7 and G2 with interaction scores near zero (Figure 4.3) do not interact much with environments, and therefore their rank orders are relatively stable.

A pattern clearly indicated in Figure 4.3 is the linear relationship between interaction scores and main effects for genotypes. More specifically, the top yielding and bottom yielding genotypes have opposite interaction scores. For example, genotype G3 (the highest yielding) and the lowest yielding genotype G13, differ markedly in their interaction. G3 has a large positive interaction score (1.89746) while G13 has a large negative score (-2.41456). Consequently, the top yielding and bottom yielding genotypes are adapted to different environments. Their relative rank order varies greatly with environment, so these genotypes are narrowly adapted.

PCA axis1 for environments showed sizable scores for Arsinegelle-2004 (E2), Awassa-2005(E5) and Arsinegelle-2005(E6). Environments Goffa-2004(E4) and Goffa-2005(E8) differ in main effect but not in interaction, whereas Areka-2004(E3) and Areka-2005(E7) have nearly similar main effect but are distinctly different and opposite in their interaction with genotypes. Environments Awassa-2004(E1) and Awassa-2005(E5) differ in both main effect and interaction. Awassa-2004(E1) represents an environment with small main effect and small interaction, whereas Awassa-2005(E5) could be described as having a large main effect and large interaction. Environments Awassa-2005 (E5) and Arsinegelle-2005(E6) generally produce higher yields compared to environments Awassa-2004(E1) and Goffa-2004(E4).

The relative ranking of genotypes at Goffa is relatively stable from year-to-year, as indicated by similar year-to-year interaction scores, although between years there is much variation in grain yields. It is important to recognize that year-to-year variations in main effect have no effect on genotype rankings, but interaction variations do. Conversely, Awassa shows high variability in both main effect and interaction (PCA-1 scores) from

year-to-year, making specific cultivar recommendation for such location more difficult compared with Goffa. Other locations with low predictability included Arsinegelle and Areka.

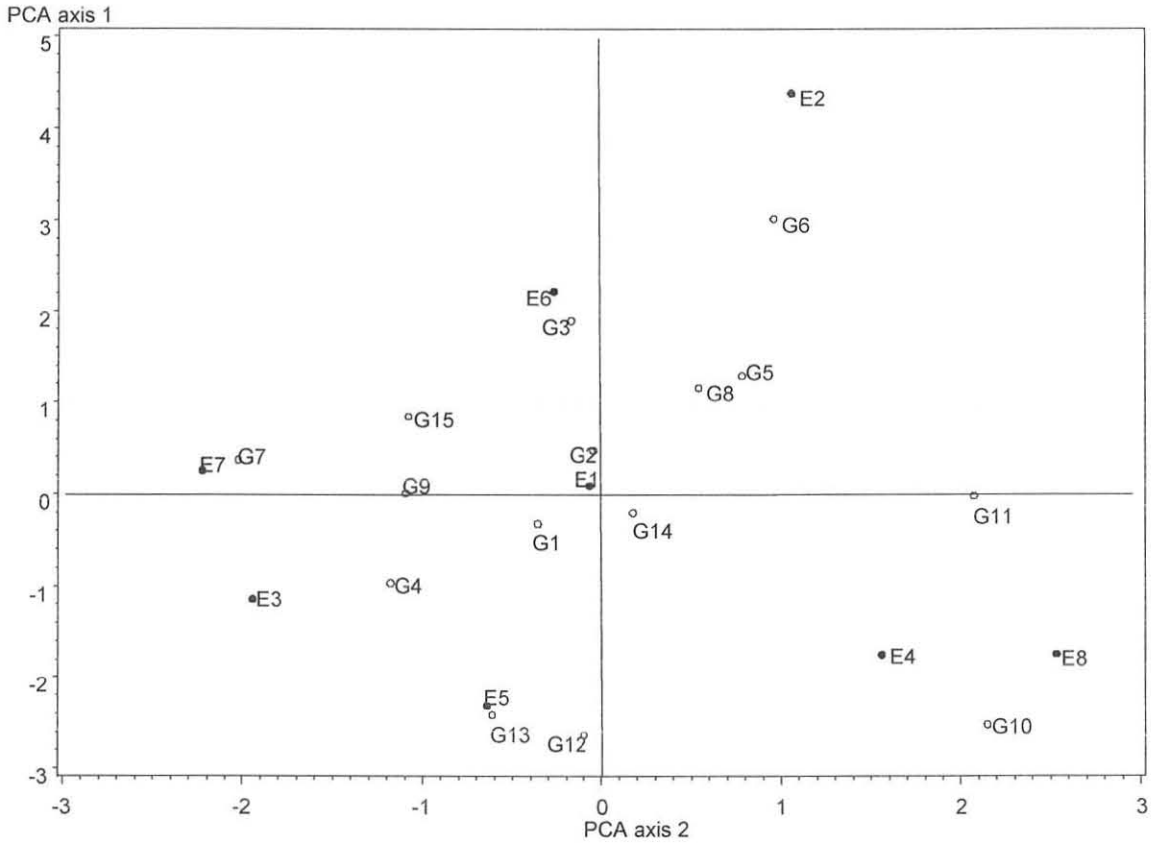


Figure 4.2 Biplot of interaction principal components analysis (PCA) axis 1 versus axis 2 for grain yield (qt/ha) for 15 maize genotypes grown in 8 environments. The horizontal line is PCA axis 1 = 0 and the vertical line is PCA axis 2 = 0.

Grain yield performance is better for genotypes growing in environments with large scores of the same sign, whereas poorer yield performance is expected with large scores of opposite sign. Therefore a genotype such as G6 with a large positive score (3.01407) performs better in environments like Arsinegelle in 2004 (score = 4.38464) having a score of the same sign because this combination results in a large positive interaction. G6 performs poorer in environments such as Awassa in 2005 with a large negative score

(-2.31702) because this combination results in a large negative interaction. The opposite is the case for genotype G12 with a large negative score (-2.63350); G12 performs better in environments with a large negative score (for instance, Awassa in 2005).

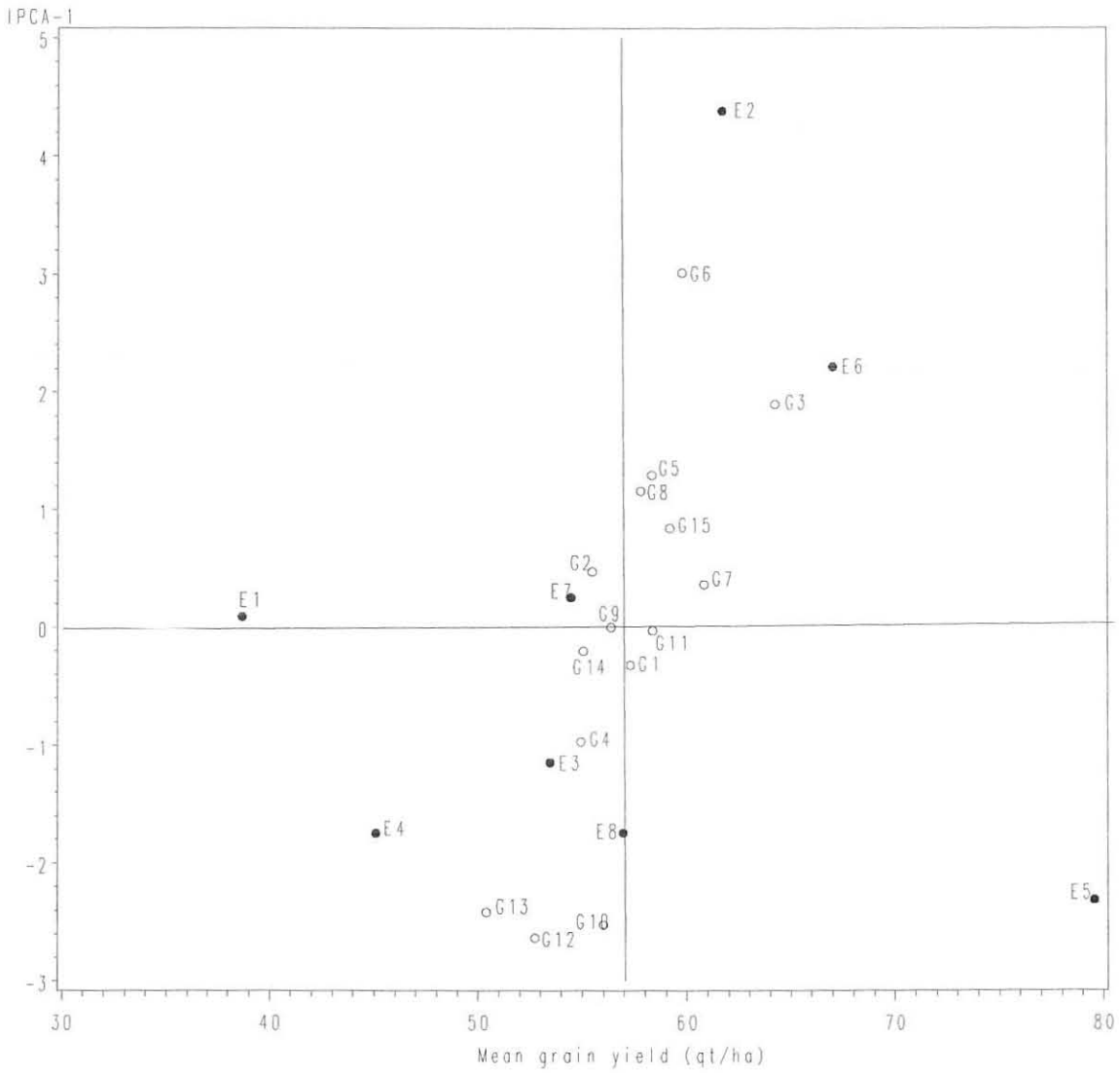


Figure 4.3 Biplot of interaction principal components analysis (PCA) axis 1 versus mean yield (qt/ha) for 15 maize genotypes grown in 8 environments. The vertical line represents the grand mean of the experiment. The horizontal line is PCA axis 1 = 0.

In general, maize genotypes that had PCA-1 scores > 0 responded positively (adaptable) to environments that had PCA-1 scores > 0 (i.e., their interaction is positive) but

responded negatively to environments that had PCA-1 scores < 0. The reverse applies for maize genotypes that had PCA-1 scores < 0. Hence, genotypes G6, G3, G5, G8 and G15 were adapted to Arsinegelle (2004 & 2005). In contrast, genotypes G12, G10, G13 and G4 were adapted to Awassa (2005), Goffa (2004 & 2005) and Areka (2004). Hence, these biplots are useful in determining genotypic stability and range of performance as well as providing insight into the causes of the underlying interaction.

The AMMI-1 estimated yield for any genotype in any environment may be calculated from the biplot (Figure 4.3), as described by Zobel et al.(1988). For any genotype-environment combination, the additive (main effects) of the AMMI model equals the genotype mean plus the environment mean minus the grand mean, and the multiplicative part (interaction effect) is the product of genotype and environment PCA-1 scores. For example, genotype G2 at Areka in 2005 (E7) has an additive effect 55.48 + 54.47 - 57.12 = 52.83 qt/ha, an interaction effect of 0.47921 x 0.25792 = 0.12 qt/ha. Therefore, the AMMI-1 model gives a yield estimation for G2 in Areka-2005 of 52.83 + 0.12 = 52.95 qt/ha. In comparison, the yield estimated by the ANOVA model was 53.24 qt/ha.

Additionally, the AMMI-1 model predicts its mean yield close to that of the AMMI-0 model (main effect model) in environments with PCA-1 score near zero (Awassa-2004 or Areka-2005), very large yield than that is obtained with AMMI-0 model in environments with positive PCA-1 score (Arsinegelle-2004 or Arsinegelle-2005), and very small yield than the AMMI-0 model in environments with negative PCA-1 score (Awassa-2005, Goffa-2004, Goffa-2005 or Areka-2003).

In summary, interaction patterns revealed by AMMI model biplot analyses indicate that genotypes G14, G1 and G2 exhibit smaller interactions with environments and are therefore more stable as observed across both interaction axes. Because of its moderately-high yield and stable performance across environments, G1 was identified as the most desirable genotype among the 15 genotypes tested. No genotype has superior performance in all environments (highest yield and stable performance). Maize breeders

should aim for a cultivar with a stable yield performance (similar to that of G1), yet capable of out-yielding G3.

CHAPTER FIVE
CONCLUSIONS AND RECOMMENDATIONS

5.1 Conclusions

The objectives of the study were to: (1) compare genotype x environment interaction models used in multi-environment yield trials & choose the best one for the current data (2) determine yield stability & classify genotypes based on similarity of response patterns and (3) identify stable & high yielding genotypes. Grain yield data (qt/ha) of 15 genotypes of maize (*Zea mays* L.) grown during the years 2004 and 2005 at 4 locations was used in the study.

The conventional analysis of variance showed significant effects for environment ($P < 0.0001$), genotype ($P<0.0001$), and genotype x environment interaction ($P=0.0375$) for grain yield and accounted for 81.8%, 6.1%, and 12.1% of the treatment combinations SS, respectively. Environments were a much larger source of variability than genotypes. The interaction is important, having a SS which is twice as large as the genotype SS. It is precisely the existence of genotype x environment interaction (GxE) that causes genotype rankings to vary from environment to environment, and causes yield estimates based upon only additive effects to be inaccurate and unreliable. In other words, presence of GxE does not permit to define an overall ranking of varieties across environments.

Joint regression and AMMI models were compared for capacity of describing the GxE and for assessment of the relative stability of the genotypes across environments. The environmental variance, Wricke's (1962) ecovalence and Shukla's (1972) stability variance were considered in addition. It is noteworthy that these stability measures are based on the ANOVA interaction, whereas the use of LR or AMMI allows to evaluate stability after reduction of the noise from the interaction term.

One should recognize the importance of both a large amount of explained variation and a low number of degrees of freedom as desirable features of a model. Also, the model that adequately describes the interaction generally provides reliable assessment of relative stability of a set of genotypes across a variety of environments.

The regression of each genotype's yields on the environment means partitioned the interaction into 14 DF for genotype regressions and the residual 84 DF for deviations from regressions. While the LR model accounted for less degrees of freedom, it was unable to explain a large proportion of interaction variation. Moreover, the fit was mediocre as indicated by a significant residual. For this maize data set it seems that the ANOVA model is better than the LR model.

In accordance with the AMMI model, principal component analysis was used to decompose the GxE into seven (nonzero) components of which the first two were deemed significant. These two components accounted for over 69% of the variability (interaction sum of squares) while using less than half of the degrees of freedom. Overall, the AMMI model accounted for 96.3% of the treatment SS with 59 DF (14 for genotypes, 7 for environments, and 38 for the first two dimensions of the interaction). The AMMI model discards the non-interpretable random variation (noise) and use then information from all test genotypes and environments to identify the trial functional patterns. The results of this maize multi-environment yield trial show that the AMMI model is parsimonious than the conventional analysis of variance model in describing genotype x environment interaction and is superior to the regression on the environmental mean in modeling and interpreting GxE.

A successful model captures as much of the treatment SS as possible with as few DF as possible. This constraint of parsimony is required because otherwise the winner is always the trivial ANOVA model having $(mn-1)$ DF. Model success requires accuracy and parsimony.

The AMMI model provides a useful technique in diagnosing genotype x environment interaction patterns. It enables clustering of genotypes based on similarity of response characteristics and identifying potential trends across environments. The model is most effective when the rank of the interaction matrix is two or three or, ideally, when it can be closely approximated as such. Thus, the number of PCA axes retained for most applications is usually $s \leq 3$, which is intended to reduce the dimension of the system and provide a more parsimonious description of the underlying interaction structure. It is also an appropriate diagnostic tool in situation where a significant GxE is accompanied by non-significant genotype and environment main effects. The AMMI model provides easily interpretable information on the stability of genotypes and trends of environments, as well as the correlation between a genotype and environment.

The following major findings emerged for the multi-environment yield trial data set analyzed here.

- Significant variation existed for environment, genotype, and genotype x environment interaction.
- A bi-dimensional AMMI model was adequate for describing GxE variation.
- The AMMI model was preferable to ANOVA and regression on environmental mean model.
- Genotypes G14, G1 and G2 were more stable, whereas G6, G13, G12 and G10 were unstable varieties.
- Genotype G1 was the most desirable among the 15 genotypes tested.
- Goffa was highly predictable in year-to-year interaction with genotypes (making cultivar recommendations more predictable and reliable), whereas Awassa, Arsinegelle and Areka were less predictable.

By considering the factors discussed in this paper, it is suggested that plant-breeding research to analyze GxE and assess yield stability in MET trials should include AMMI analysis. AMMI models could extract more information from the GxE, thereby aiding researchers in identifying specific cultivars with competitive yields across diverse

environments. AMMI can help agricultural researchers get more information out of expensive yield trial data, enabling breeding to progress more quickly, and making variety recommendations more reliable.

5.2 Recommendations

Two recommendations seem worthwhile.

- First, the promising results with AMMI presented here are not to be understood as a general recommendation of AMMI for all yield trial data sets, although it is expected that AMMI is best for a majority of yield trials having a significant interaction.
- Second, future data collection should include information on external environmental variables (such as precipitation, temperature, soil, etc) or external cultivar variables (such as physiology, maturity, disease reaction, genetic markers, etc) or both. When information on external environmental (or genotypic) variables is available, these variables can be correlated to or regressed on the environmental (genotypic) scores estimated by AMMI. Information from these regressions can be superimposed on the AMMI biplot along with cultivar and environmental scores so that better explanation of the grain yield GxE is possible. Also, when additional information is available, other statistical models including factorial regression models and partial least squares regression can be used to determine which of these external environmental or cultivar variables influence GxE of grain yield.

The use of appropriate biometrical methods is necessary for finding useful information within quantities of data produced in plant breeding trials, where the high costs and the time spent in assays are powerful justifications to search for improved methods.

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APPENDIX 1

Most statistical analyses presented in this thesis were done using SAS software. The most relevant SAS program statements are presented below, with classification variables for genotypes, environments and blocks labeled as **gen**, **env**, and **rep**, respectively. To draw attention to some procedures in SAS, PROC GLM was used for different ANOVAs. Variance components were estimated by the 'analysis of variance method' via PROC VARCOMP. Regression analysis was done using PROC REG, while PROC RSREG was implemented for the lack of fit test. The AMMI analysis was performed by PROC IML (Interactive Matrix Language).

A) SAS codes for separate ANOVAs

```
options nodate;
data belachew;
input env rep gen yield;
cards;
. . . .
;
run;
proc sort;
by env rep;
run;
proc glm outstat= temp;
by env;
class rep gen;
model yield=rep gen /ss3;
random rep/test;
lsmeans gen /stderr pdiff;
title 'analysis of variance for individual experiments';
output out=bel1 rstudent=res1 p=pred;
run;
proc univariate plot normal data=bel1;
var res1;
by env;
run;
proc plot data=bel1;
plot res1*pred= '*';
by env;
run;
proc plot data=bel1;
plot res1*env= '*';
run;
proc means data=belachew;
by env;
output out=bel2 mean=envmn;
var yield;
run;
data bel3;
```

```
merge bel1 bel2;
by env;
proc plot data=bel3;
plot res1*envmn= '*';
run;
```

B) SAS codes for combined ANOVA

```
options nodate;
data belachew;
input env rep gen yield;
cards;
. . . .
;
run;
proc glm;
class env rep gen;
model yield = env rep(env) gen env*gen /ss3;
random env rep(env) env*gen /test;
lsmeans gen;
title 'analysis of variance for a complete set of experiments';
output out=bel1 rstudent=res1 p=pred;
run;
proc print data=bel1;
run;
proc univariate plot normal data=bel1;
var res1;
run;
proc plot data=bel1;
plot res1*pred = '*';
run;
proc varcomp method=MIVQUE0;
class env rep gen;
model yield=gen env rep(env) env*gen/fixed=1;
title 'estimation of variance components';
run;
```

C) SAS codes for regression analysis

```
options nodate;
data belachew;
input env rep gen yield;
cards;
. . . .
;
run;
proc sort data=belachew;
by env;
run;
proc means noprint;
by env;
output out=bel mean=envmn;
var yield;
```

```
run;
data b;
merge belachew bel;
by env;
proc print data=b;
run;
proc glm data=b;
class env gen rep;
model yield = env rep(env) gen env*gen /ss1;
random env rep(env) env*gen;
run;
proc glm data=b;
class env gen rep;
model yield = env rep(env) gen envmn*gen env*gen /ss1;
test h=envmn*gen e=env*gen / htype=1 etype=1;
output out=bel1 rstudent= res1 p=pred1;
run;
proc print data=bel1;
run;
proc univariate plot normal data=bel1;
var res1;
run;
proc plot data=bel1;
plot res1*pred1='*';
run;
proc sort data=b;
by gen;
run;
proc reg data=b;
by gen;
model yield=envmn /alpha=.05 influence;
test envmn=1;
output out=bel2 rstudent=res2 p=pred2 cookd=cookyld lcl=lowyld
ucl=higyld;
run;
proc print data=bel2;
run;
proc univariate plot normal data=bel2;
by gen ;
var res2;
run;
proc plot data=bel2;
by gen;
plot res2*pred2='*';
run;
proc plot data=bel2;
by gen;
plot res2*envmn= '*';
run;
proc rsreg data=b;
by gen;
model yield=envmn/lackfit covar=1 noopt;
title 'results from regression of yield on environment mean';
run;
```

D) SAS codes for AMMI analysis

```
options nodate;
DATA belachew;
INPUT env rep gen yield;
CARDS;
. . . .
;
RUN;
PROC SORT ;
BY env gen;
RUN;
PROC MEANS;
VAR yield;
OUTPUT out=avgyld mean=ylda;
BY env gen;
RUN;
PROC GLM ;
CLASS gen env;
MODEL ylda=env gen;
OUTPUT out=residual r=r_yield;
RUN;
PROC IML;
USE residual;
READ ALL VAR{env gen r_yield};
READ ALL VAR _NUM_ INTO x;
r_yield=x[,3];
m=15;
n=8;
resid = shape (r_yield,m,n);
CALL SVD (u,q,v,resid);
axes = 'Axis-1':'Axis-8';
b=q#q;
SUMb= SUM(b);
e=(b/SUMb)*100;
sqq=SQRT(q);
d=DIAG(sqq);
uq=u*d;
vq=v*d;
score= 'SCORE 1': 'SCORE 8';
PRINT 'Eigen Values', b[ROWNAME=axes COLNAME='SS' FORMAT=12.4];
PRINT '%SS Explained by Each Axis',e[ROWNAME=axes COLNAME='%SS'
FORMAT=12.2];
PRINT 'Genotypic Scores' , uq[ROWNAME= 'gen' COLNAME= 'score'
FORMAT=12.4];
PRINT 'Environmental Scores', vq[ROWNAME='env' COLNAME='score'
FORMAT=12.4];
QUIT;
RUN;
```

APPENDIX 2

A) Residual analysis for the ANOVA model for the maize yield data at Arsinegelle in 2004 (E2).

The UNIVARIATE Procedure
Variable: residual

Moments

N	45	Sum Weights	45
Mean	0.00232552	Sum Observations	0.10464831
Std Deviation	1.0371493	Variance	1.07567866
Skewness	0.15207611	Kurtosis	-0.4601547
Uncorrected SS	47.3301045	Corrected SS	47.3298611
Coeff Variation	44598.6343	Std Error Mean	0.15460909

Basic Statistical Measures

Location		Variability	
Mean	0.002326	Std Deviation	1.03715
Median	0.227023	Variance	1.07568
Mode	.	Range	4.77393
		Interquartile Range	1.60784

Tests for Location: Mu0=0

Test	-Statistic-		-----p Value------	
Student's t	t	0.015041	Pr > |t|	0.9881
Sign	M	0.5	Pr >= |M|	1.0000
Signed Rank	S	-18.5	Pr >= |S|	0.8373

Tests for Normality

Test	--Statistic---		-----p Value------	
Shapiro-Wilk	W	0.973936	Pr < W	0.3988
Kolmogorov-Smirnov	D	0.116139	Pr > D	0.1300
Cramer-von Mises	W-Sq	0.101103	Pr > W-Sq	0.1068
Anderson-Darling	A-Sq	0.556541	Pr > A-Sq	0.1461

The UNIVARIATE Procedure
Variable: residual

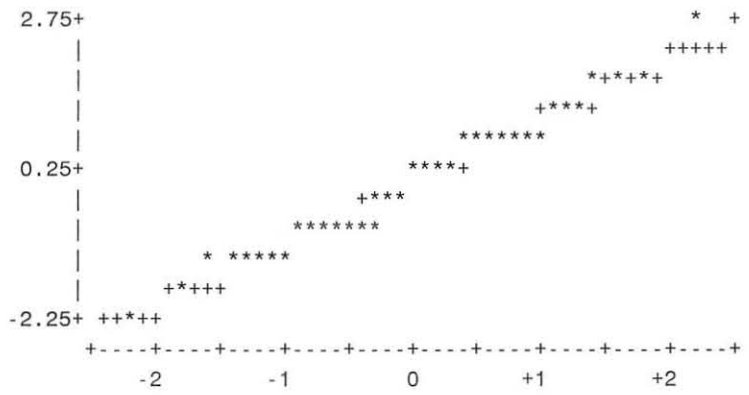
Quantiles (Definition 5)

Quantile	Estimate
100% Max	2.611642
99%	2.611642
95%	1.587057
90%	1.288166
75% Q3	0.698917
50% Median	0.227023
25% Q1	-0.908927
10%	-1.237709
5%	-1.396328
1%	-2.162288
0% Min	-2.162288

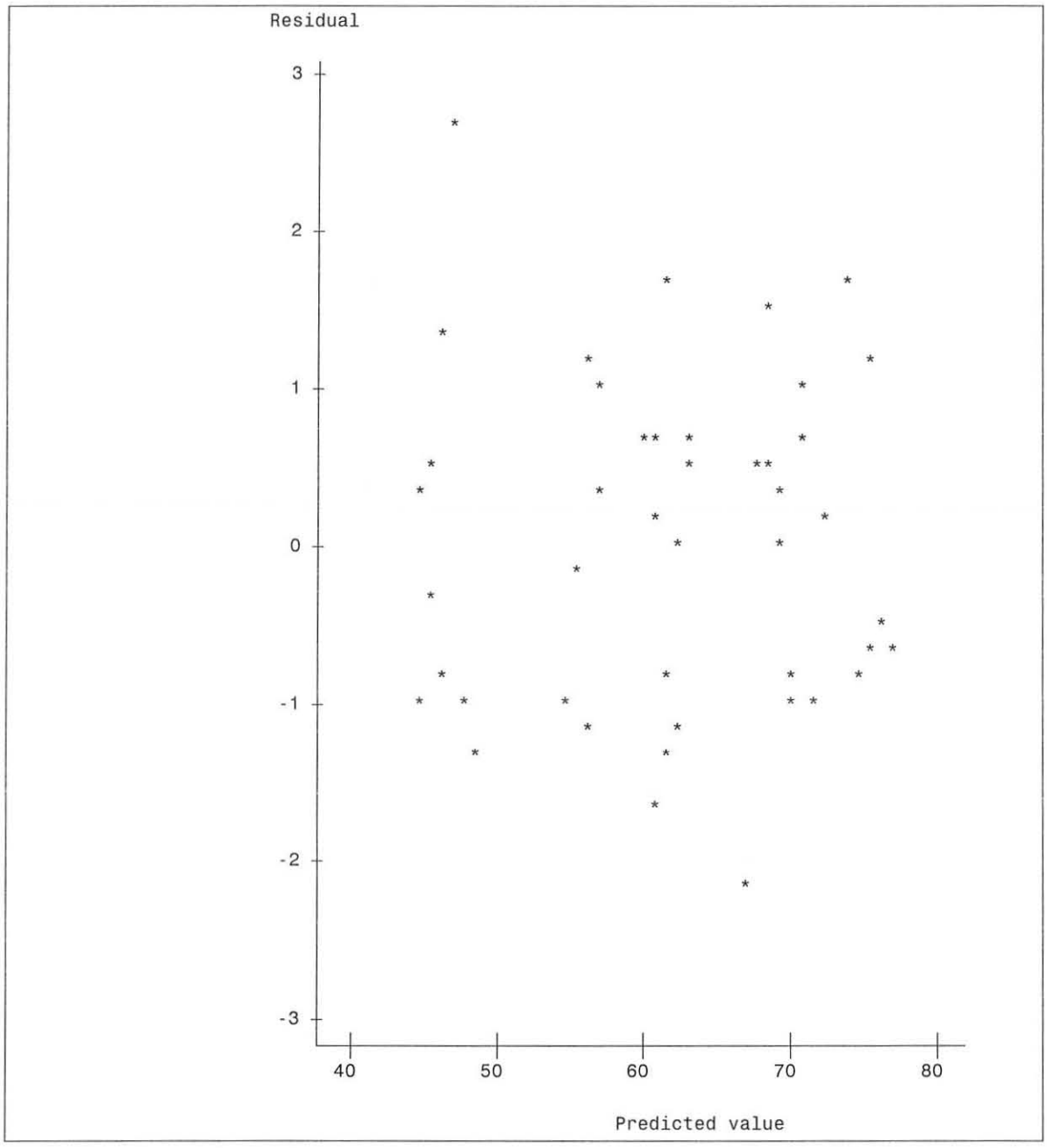
Extreme Observations

------Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
-2.16229	43	1.28817	15
-1.61378	31	1.53768	6
-1.39633	12	1.58706	35
-1.35279	1	1.63736	18
-1.23771	45	2.61164	39

Normal Probability Plot



Plot of residuals versus fitted values.



B) Residual analysis for the ANOVA model for the maize yield data at Awassa in 2005 (E5).

The UNIVARIATE Procedure
Variable: residual

Moments

N	45	Sum Weights	45
Mean	0.00538959	Sum Observations	0.24253164
Std Deviation	1.04329487	Variance	1.08846419
Skewness	0.31912104	Kurtosis	-0.1759985
Uncorrected SS	47.8937313	Corrected SS	47.8924242
Coeff Variation	19357.5851	Std Error Mean	0.15552522

Basic Statistical Measures

Location		Variability	
Mean	0.005390	Std Deviation	1.04329
Median	0.037989	Variance	1.08846
Mode	.	Range	4.11464
		Interquartile Range	1.13372

Tests for Location: Mu0=0

Test	-Statistic-		-----p Value------	
Student's t	t	0.034654	Pr > |t|	0.9725
Sign	M	2.5	Pr >= |M|	0.5515
Signed Rank	S	-5.5	Pr >= |S|	0.9513

Tests for Normality

Test	--Statistic---		-----p Value------	
Shapiro-Wilk	W	0.970952	Pr < W	0.3134
Kolmogorov-Smirnov	D	0.068044	Pr > D	>0.1500
Cramer-von Mises	W-Sq	0.0339	Pr > W-Sq	>0.2500
Anderson-Darling	A-Sq	0.293407	Pr > A-Sq	>0.2500

Extreme Observations

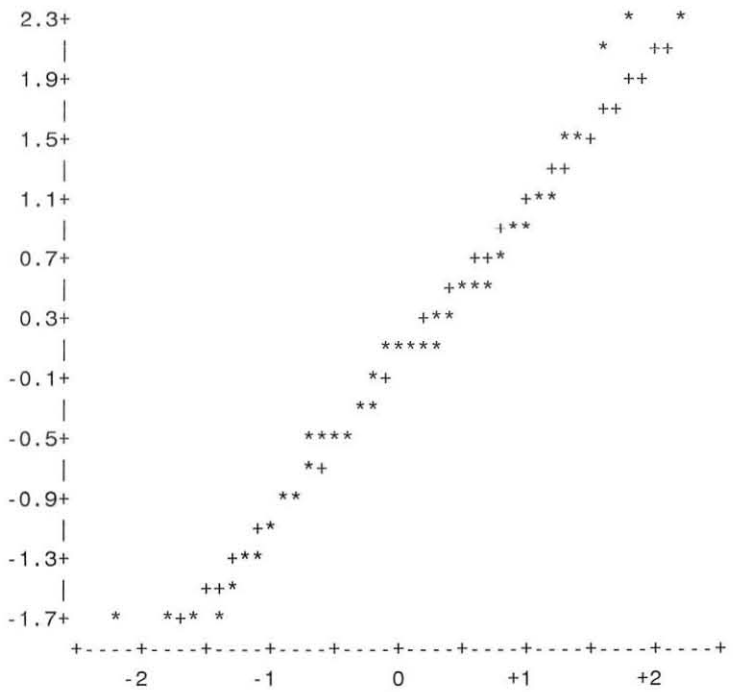
------Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
-1.77995	35	1.55734	33
-1.63067	7	1.55875	24
-1.62078	34	2.05978	27
-1.61638	18	2.31089	4
-1.45581	41	2.33469	25

The UNIVARIATE Procedure
Variable: residual

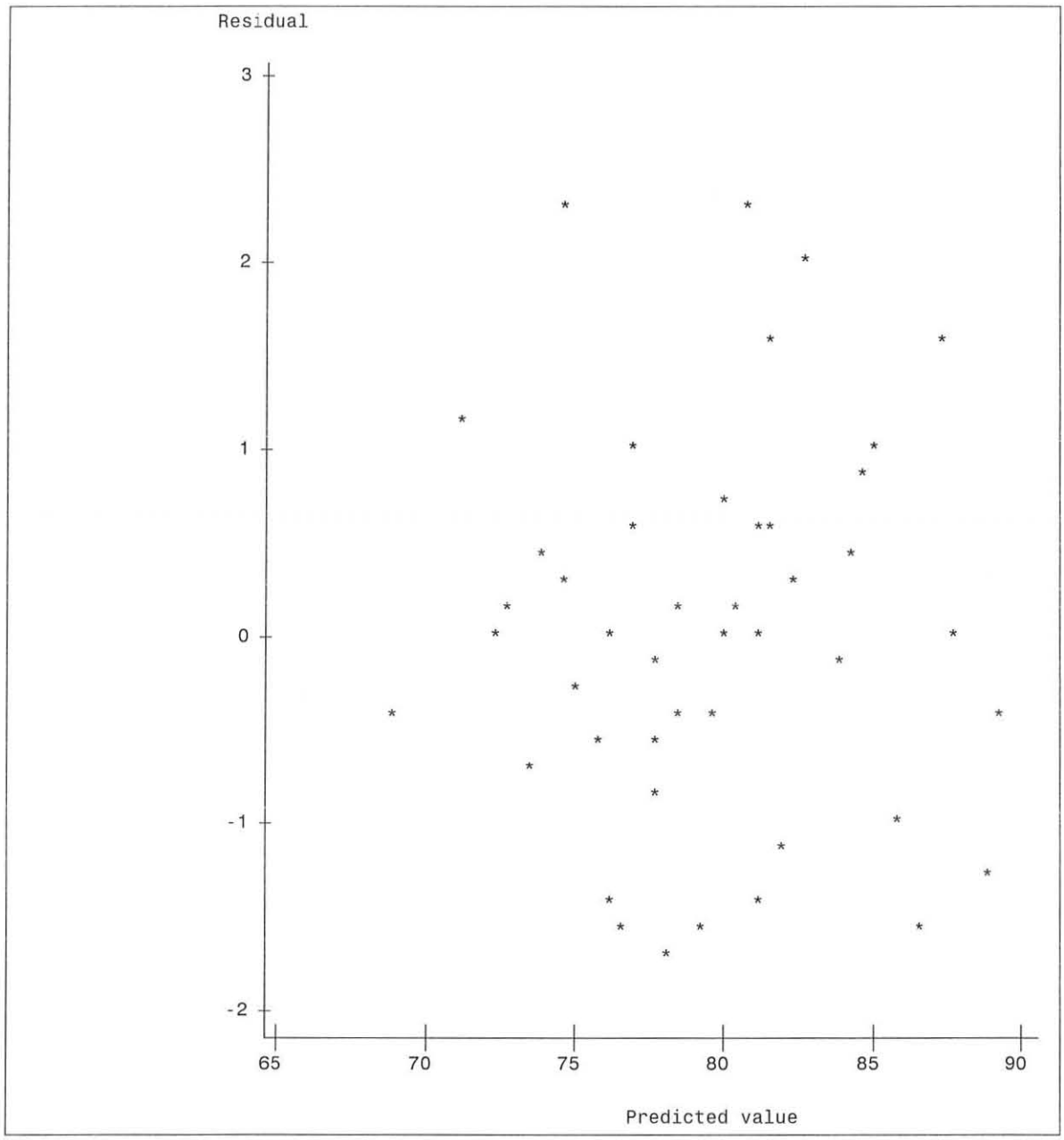
Quantiles (Definition 5)

Quantile	Estimate
100% Max	2.334692
99%	2.334692
95%	2.059779
90%	1.557338
75% Q3	0.547684
50% Median	0.037989
25% Q1	-0.586036
10%	-1.455808
5%	-1.620782
1%	-1.779947
0% Min	-1.779947

Normal Probability Plot

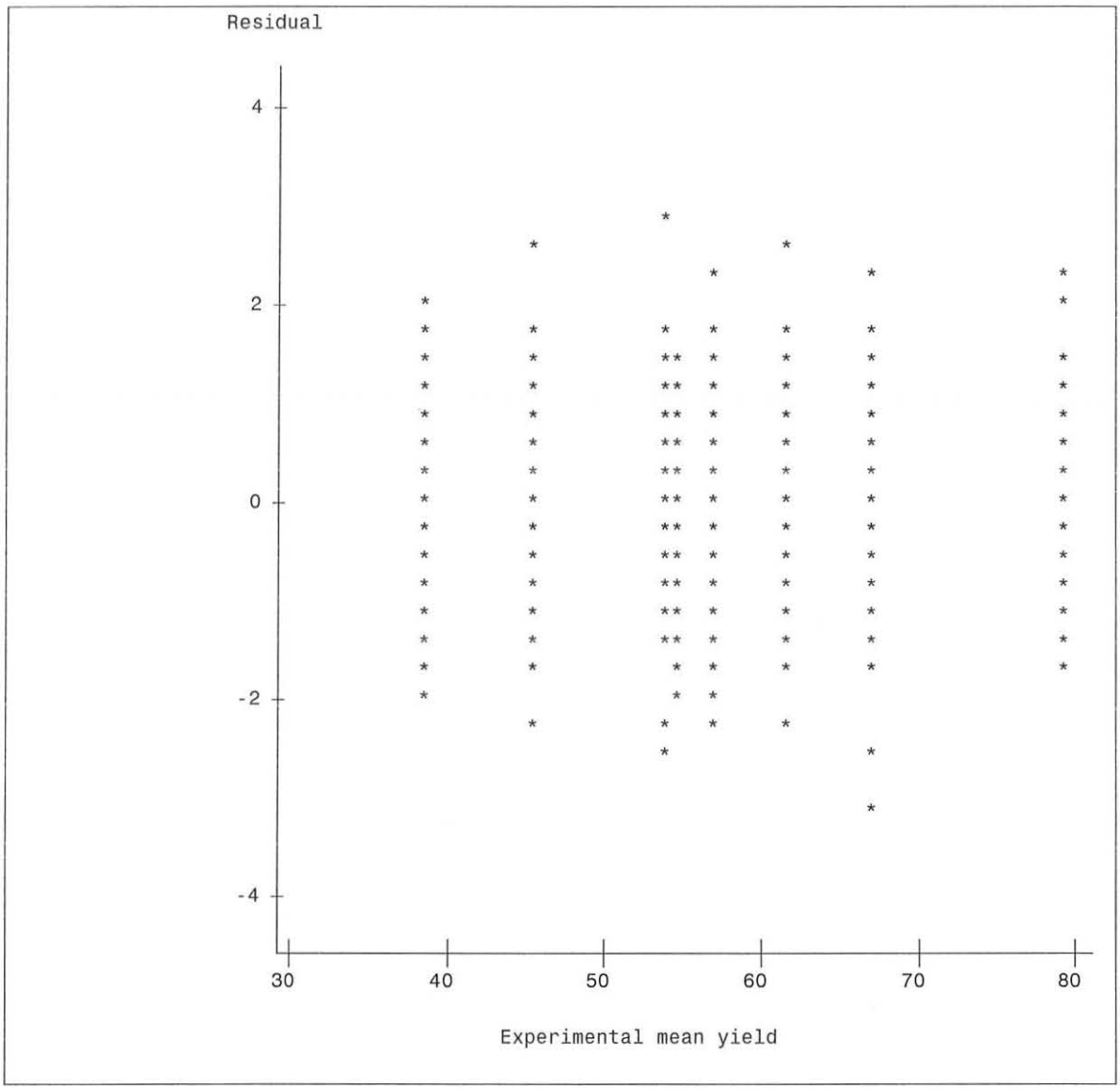


Plot of residuals versus fitted values.



C) Diagnostic plot to assess homogeneity of experimental errors among the trials.

Plot of residuals versus experiments mean yield.



D) Residual analysis for the combined ANOVA model for the entire maize yield trial data.

The UNIVARIATE Procedure
Variable: residual

Moments

N	360	Sum Weights	360
Mean	0.0001519	Sum Observations	0.05468365
Std Deviation	1.00598634	Variance	1.01200851
Skewness	0.0700554	Kurtosis	0.07396245
Uncorrected SS	363.311063	Corrected SS	363.311055
Coeff Variation	662273.073	Std Error Mean	0.05302014

Basic Statistical Measures

Location		Variability	
Mean	0.000152	Std Deviation	1.00599
Median	0.032494	Variance	1.01201
Mode	.	Range	5.84756
		Interquartile Range	1.25007

Tests for Location: Mu0=0

Test	-Statistic-		-----p Value------	
Student's t	t	0.002865	Pr > |t|	0.9977
Sign	M	6	Pr >= |M|	0.5621
Signed Rank	S	20	Pr >= |S|	0.9919

Tests for Normality

Test	--Statistic---		-----p Value------	
Shapiro-Wilk	W	0.997157	Pr < W	0.7892
Kolmogorov-Smirnov	D	0.027705	Pr > D	>0.1500
Cramer-von Mises	W-Sq	0.041412	Pr > W-Sq	>0.2500
Anderson-Darling	A-Sq	0.265138	Pr > A-Sq	>0.2500

Quantiles (Definition 5)

Quantile	Estimate
100% Max	3.0420577
99%	2.6862774
95%	1.6524992
90%	1.2218883
75% Q3	0.6302452
50% Median	0.0324943
25% Q1	-0.6198204
10%	-1.3366553
5%	-1.6647200
1%	-2.4674128
0% Min	-2.8055018

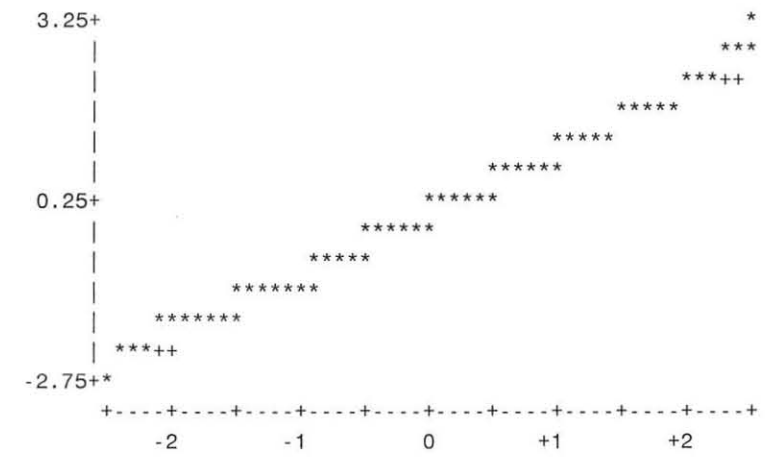
The UNIVARIATE Procedure
Variable: residual

Extreme Observations

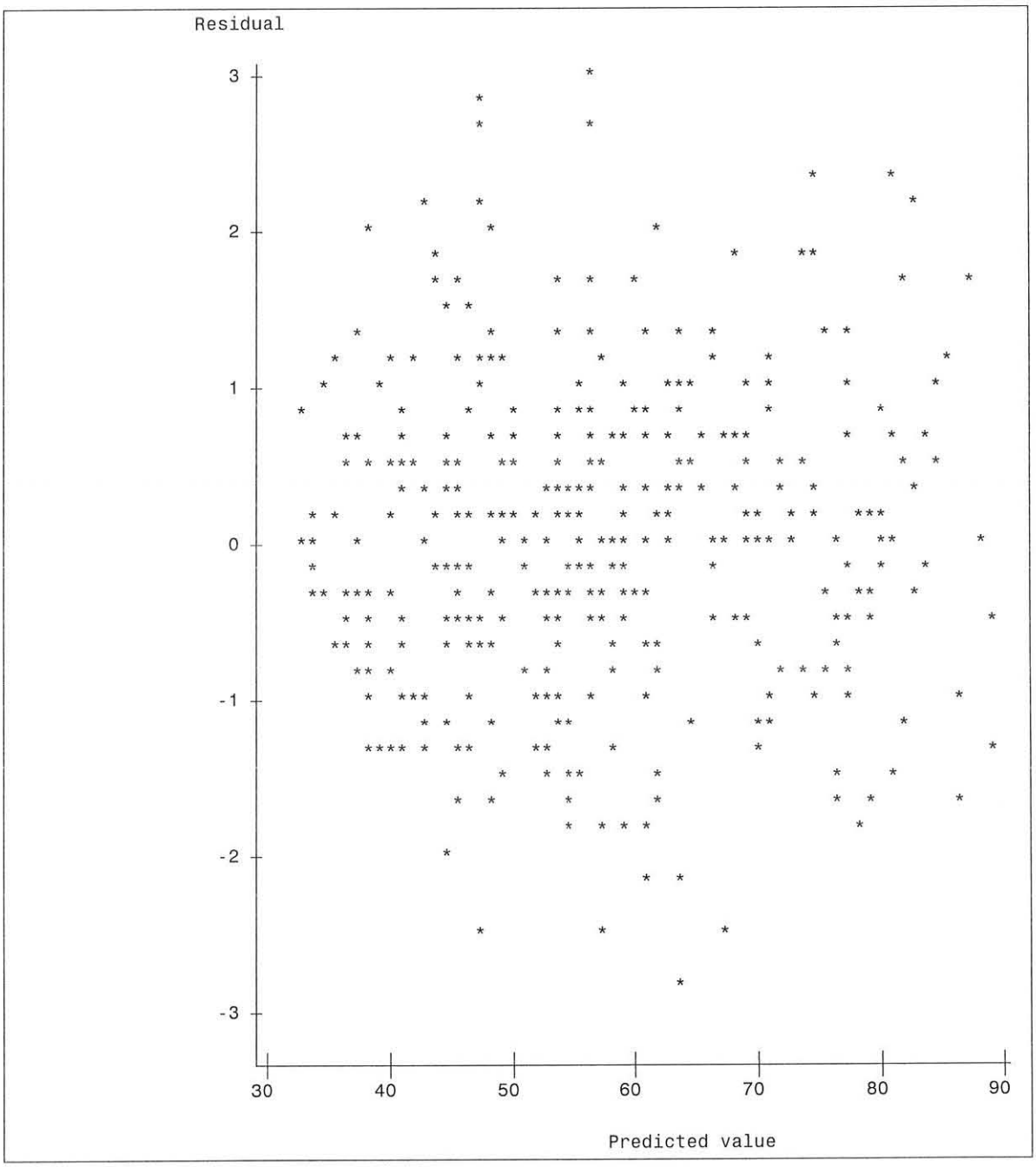
------Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
-2.80550	327	2.32369	205
-2.53896	359	2.68628	332
-2.46815	88	2.72915	177
-2.46741	167	2.89952	84
-2.15438	316	3.04206	311

```
                Histogram                    #          Boxplot
 3.25+*                                      1             0
     .**                                     3             0
     .***                                    5             |
     .*********                             17             |
     .***************                       29             |
     .**************************            54         +-----+
 0.25+**************************************  77         *--+--*
     .*******************************         64         |     |
     .************************              48         +-----+
     .*******************                   38             |
     .*********                             18             |
     .**                                     4             |
-2.75+*                                      2             0
     ----+----+----+----+----+----+----+----
     * may represent up to 2 counts
```

Normal Probability Plot



Plot of residuals versus fitted values.



E) Residual analysis for the regression on the environment mean model for G4.

The UNIVARIATE Procedure
Variable: residual

Moments

N	24	Sum Weights	24
Mean	0.00410003	Sum Observations	0.09840081
Std Deviation	1.05527367	Variance	1.11360253
Skewness	0.39025717	Kurtosis	0.03165855
Uncorrected SS	25.6132616	Corrected SS	25.6128582
Coeff Variation	25738.1715	Std Error Mean	0.21540684

Basic Statistical Measures

Location		Variability	
Mean	0.00410	Std Deviation	1.05527
Median	-0.02554	Variance	1.11360
Mode	.	Range	3.95564
		Interquartile Range	1.36159

Tests for Location: Mu0=0

Test	-Statistic-		-----p Value------	
Student's t	t	0.019034	Pr > |t|	0.9850
Sign	M	0	Pr >= |M|	1.0000
Signed Rank	S	-4	Pr >= |S|	0.9119

Tests for Normality

Test	--Statistic---		-----p Value------	
Shapiro-Wilk	W	0.965626	Pr < W	0.5612
Kolmogorov-Smirnov	D	0.090064	Pr > D	>0.1500
Cramer-von Mises	W-Sq	0.023883	Pr > W-Sq	>0.2500
Anderson-Darling	A-Sq	0.225973	Pr > A-Sq	>0.2500

The UNIVARIATE Procedure
Variable: residual

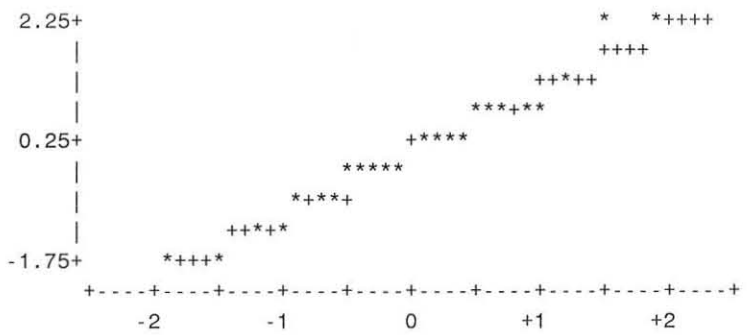
Quantiles (Definition 5)

Quantile	Estimate
100% Max	2.2544711
99%	2.2544711
95%	2.2006017
90%	1.1750436
75% Q3	0.6542329
50% Median	-0.0255432
25% Q1	-0.7073562
10%	-1.3457029
5%	-1.6665439
1%	-1.7011660
0% Min	-1.7011660

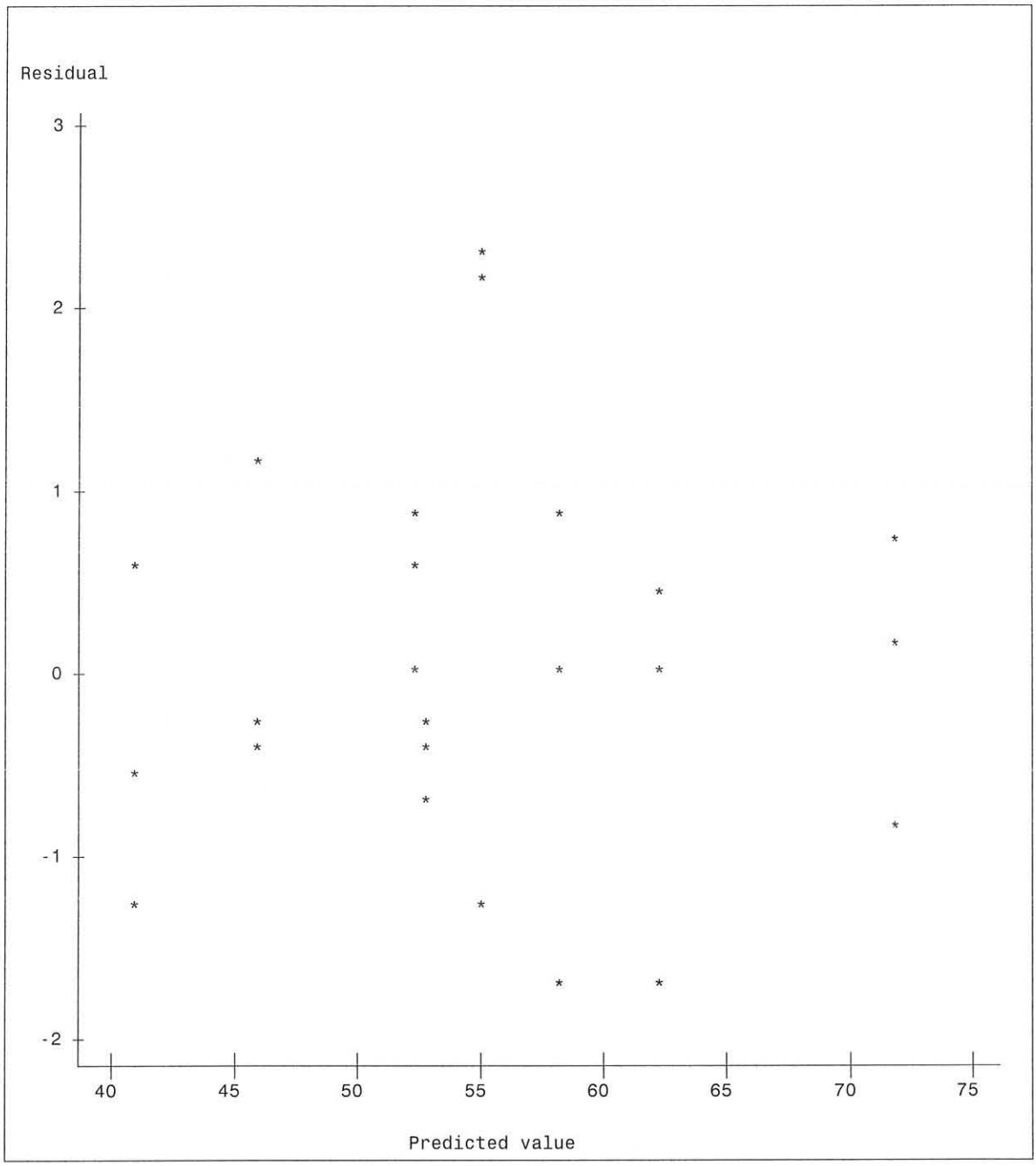
Extreme Observations

------Lowest------		------Highest-----	
Value	Obs	Value	Obs
-1.701166	6	0.792588	4
-1.666544	16	0.903964	7
-1.345703	3	1.175044	10
-1.295426	24	2.200602	22
-0.923751	13	2.254471	23

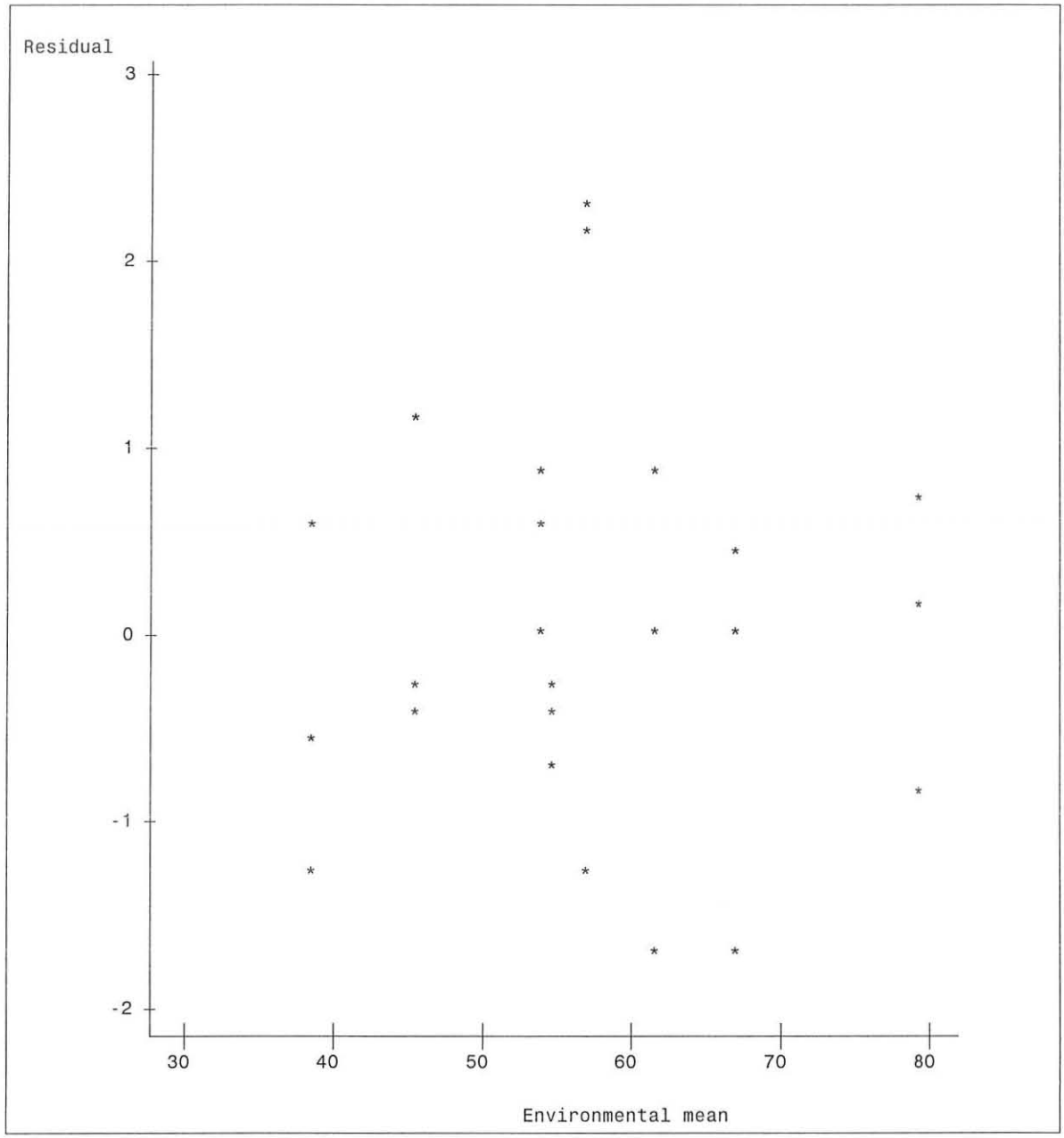
Normal Probability Plot



Plot of residuals versus fitted values.



Plot of residuals versus levels of the regressor variable.



F) Residual analysis for the regression on the environment mean model for G12.

The UNIVARIATE Procedure
Variable: residual

Moments

N	24	Sum Weights	24
Mean	0.01710222	Sum Observations	0.41045316
Std Deviation	1.0625154	Variance	1.12893897
Skewness	0.25240292	Kurtosis	-0.1385839
Uncorrected SS	25.9726159	Corrected SS	25.9655962
Coeff Variation	6212.73556	Std Error Mean	0.21688505

Basic Statistical Measures

Location		Variability	
Mean	0.01710	Std Deviation	1.06252
Median	-0.03766	Variance	1.12894
Mode	.	Range	4.03563
		Interquartile Range	1.08224

Tests for Location: Mu0=0

Test	-Statistic-		-----p Value------	
Student's t	t	0.078854	Pr > |t|	0.9378
Sign	M	0	Pr >= |M|	1.0000
Signed Rank	S	0	Pr >= |S|	1.0000

Tests for Normality

Test	--Statistic---		-----p Value------	
Shapiro-Wilk	W	0.97347	Pr < W	0.7524
Kolmogorov-Smirnov	D	0.091571	Pr > D	>0.1500
Cramer-von Mises	W-Sq	0.030605	Pr > W-Sq	>0.2500
Anderson-Darling	A-Sq	0.223709	Pr > A-Sq	>0.2500

The UNIVARIATE Procedure
Variable: residual

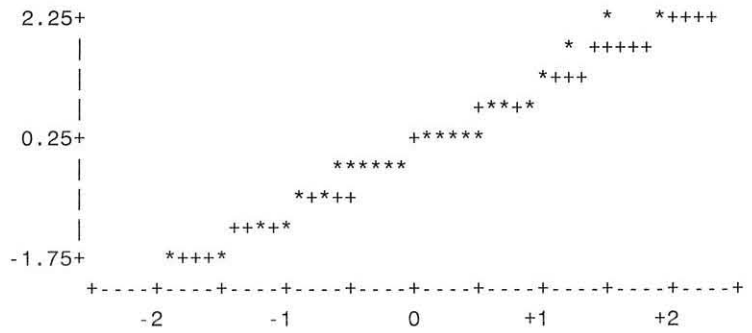
Quantiles (Definition 5)

Quantile	Estimate
100% Max	2.1745893
99%	2.1745893
95%	2.0105937
90%	1.5800371
75% Q3	0.5654021
50% Median	-0.0376598
25% Q1	-0.5168398
10%	-1.4458090
5%	-1.6388545
1%	-1.8610437
0% Min	-1.8610437

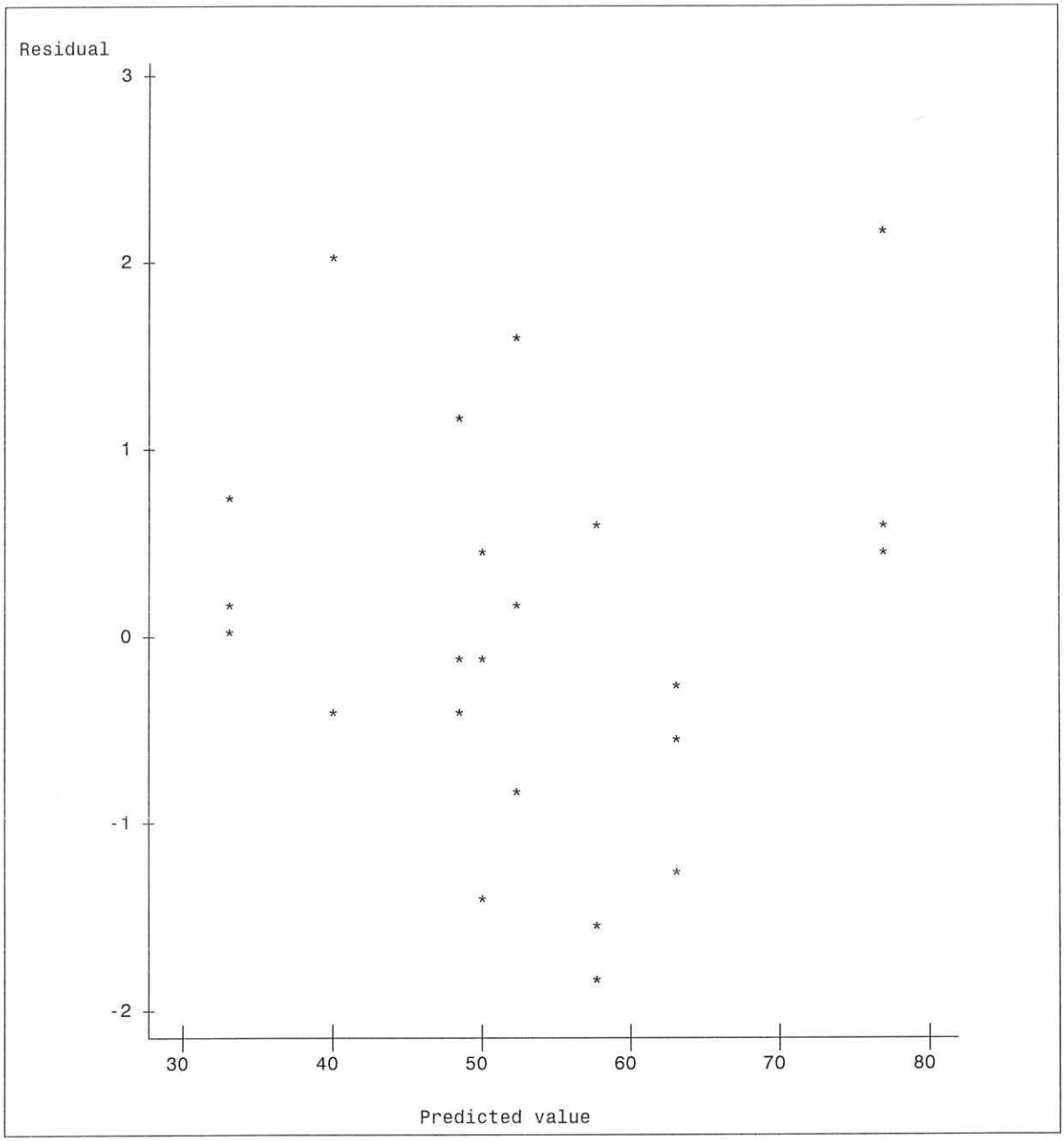
Extreme Observations

------Lowest------		------Highest-----	
Value	Obs	Value	Obs
-1.861044	4	0.750537	1
-1.638855	5	1.190516	7
-1.445809	21	1.580037	22
-1.324184	18	2.010594	12
-0.839313	24	2.174589	15

Normal Probability Plot



Plot of residuals versus fitted values.



Plot of residuals versus levels of the regressor variable.