REPEATED MEASURES ANALYSIS ON PERFOMANCE OF TWO SETS OF DAIRY CALVES FED ON MAIZE COWPEA GRUEL AND FED ON MILK

By

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DEDICATION

I dedicate this project to my mother Grace for supporting me in a special way. To my wife Mary and my son Raul, thank you for being there when I needed you most.

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ABSTRACT

Data analysis of data sets containing repeated measures observations taken from animals (as the experimental units) assigned to different treatments over a period of time is a common design in animal feeding experiments. Conventionally, repeated measures data were either analyzed as univariate or contrasts. In recent times, the GLM procedure has become more appealing for analyzing repeated measures data. Advanced GLM methods such Proc Mixed Models and the Generalized Estimating Equations (GEEs) are used to analyze complex repeated measures data. These data sets are complex due to missing cases or unequal spacing. When repeated measures data is free of missing cases and is equally spaced, then the normal proc GLM procedure is sufficient for analysis. This is typically the case of this study.

The objective of this study is to provide a background understanding of the proc GLM model methodology and its use in repeated measures analysis on balanced repeated measures data to compare two treatment regiment groups and to document their effects on the performance of dairy calves from birth to weaning. The study capitalizes on the ability of the GLM procedure to use the method of least squares to fit general linear models and its application of vital statistical methods such as regression, ANOVA, ANCOVA, MANOVA and partial correlation to establish the usefulness of the covariate (chosen in this study) in the repeated measures ANOVA model and finally to help in the testing of hypotheses in Multivariate Analysis of Variance.

The Pillai's Trace, Wilks' Lambda, Hotelling-Lawleys' Trace and the Roy's Maximum Root are some of the multivariate procedures employed in this study to test for significance in differences between the treatment regiments, multivariate tests for no time effects, multivariate tests for no time*replication effects, multivariate for no time*treatment effects, between and within subject effects.

Key results indicate no difference between the treatment regiment groups and therefore the information is used to advise smallholder farmers on cheaper dairy calf feeding alternatives.

CHAPTER 1

INTRODUCTION

1.1 BACKGROUND INFORMATION

As the population of Kenya continues to increase and land sizes decrease due to land subdivision the cost of milk production has significantly soared, it is therefore imperative for farmers to opt for cheaper calf feeding alternatives in order to save on production costs. In this case we wish to compare the performance of dairy calves by feeding them with milk as compared to feeding them on maize/cow pea's gruel and milk on a half-half basis.

From birth to weaning it is recommended that a calf consumes 406 litres of milk. In the coastal region where milk retails for up to 40/-per litre, this translates to about 16,600/-. This is too expensive to a smallholder farmer and as such many calves are neglected.

In Central Kenya it has been shown that farmers can save 2-3 litres per calf per day by feeding maize/beans gruel without affecting calf performance. The cost of beans is also quite high, therefore to try and minimize costs as much as possible we propose to adapt the use of cowpeas instead of beans.

The aim of this case study is to compare the effectiveness of the use of the Maize-cowpeas gruel with that of milk and to check whether the economic returns observed with milk are retained when maize-cowpea gruel is used.

During the experimental period the average cost of maize flour was KES 25 kg^{-1} and cowpea flour KES 71.50 kg^{-1}. So the cost of one of litre gruel (150g of

maize flour and 150g of cowpea flour) was KES 14.85. The cost of milk was KES 40 litre^{-1}. A single calf weighing 20 kg at birth required 406 litres of milk from week 3 to weaning (week 20). The same calf would need 203 litres milk and 203 litres gruel for the same period.

For the farmer to be able to produce 203 litres of gruel they require 58 KGs of a combination of maize and cowpeas whose cost is about KES. 5597. Adding this to the cost of 203 litres of milk, brings the total cost of this combination to about KES. 13717. This figure is less by a significant amount when equated to the cost of feeding dairy calves purely on milk.

1.2 LITERATURE REVIEW

The approach of analysis used to analyze this data is the repeated measures analysis. A review of what repeated measures analysis is and the cases in which it has been used, brings to light the justification for its use on this data set.

Researchers are often interested in analyzing data that results from longitudinal studies. Estimating equations for generalized linear modeling of longitudinal data have attracted a great deal of attention over the last decade. Liang and Zeger (1986) presented an approach to these problems involving generalized estimating equations (GEEs) extended from generalized linear models (GLMs) into a regression setting with correlated observations within subjects .

The class of generalized linear models is an extension of traditional linear models that allow the mean of a population to depend on a linear predictor through a nonlinear link function and allows the probability distribution of the response to be any member of an exponential family of distributions. This family was first introduced by Nelder and Wedderburn (1972) and consists of normal error linear regression models and a nonlinear exponential, Poisson regression models, logistic and probit models for binary data, as well as many other models, such as log-linear models for the categorical data. Refer to McCullagh and Nelder (1989) for a thorough account of statistical modeling using generalized linear models. However, frequently researchers are interested in analyzing data that results from a longitudinal period or a repeated measure design with a correlation existing between the observations on a specific subject.

Correlated data can arise from longitudinal studies, in which multiple measurements are taken on the same subject at different points in time. Longitudinal data can be defined as data collected from the observations of subjects on a number of variables over time. The main advantage of a longitudinal study is

its effectiveness for studying change over time. In fact, we speak of longitudinal data whenever we have observed some occurrence more than once. Longitudinal data correlation must be considered for any appropriate analysis method. Liang and Zeger (1986) formalized an approach to this problem using Generalized Estimating Equations (GEEs) to extend Generalized Linear Models (GLMs) into a regression setting with correlated observations within subjects. For details on the GEEs method, refer to Liang and Zeger (1986), Zeger and Liang (1986), and Diggle, Liang and Zeger (1994). In this study we will only review and use the GLM procedure because it is sufficient for the results that the study has interests in. Repeated measures analysis has widely been used in animal feeding experiments. Feed costs represent approximately one-half of the total cost of production for most classes of livestock (Kennedy et al., 1993), and it is the largest expense in most commercial beef operations (Arthur et al., 2004). Improvement of feed efficiency should be a major consideration in most livestock feeding experiments (Kennedy et al., 1993). These similar statements can be echoed in our study because it aims at reducing costs of feeding calves while keeping the efficiency of the feed.

In 2006, (Z. Wang et al.,) used repeated measures analysis to test for growth, feed intake, and feed efficiency in cattle using the Grow Safe System. Data were collected using the Grow Safe System at the University of Alberta Kinsella Research Station. The changes and relative changes among data from shortened test durations were used to determine the optimum test duration for 4 traits. The traits were fitted to a model with repeated measures using SAS.

Other publications that have employed repeated measures analysis in exploring performance of animals in animal feeding experiments include;

P.F. Arthur et al., 2008 who used repeated measures analysis to explore the optimum duration of performance tests for evaluating growing pigs for growth and feed efficiency traits,

M.F. Rosario et al., 2007 modeled the covariance structure to estimate and to predict feed conversion in broiler chickens from one experiment under repeated measures. Eight treatments that consisted in a combination of four strains (Arbor, Ag Ross 308, Cobb and RX) and two sexes were evaluated at six ages (7, 14, 21, 28, 35, and 42 d) in two blocks with three replicates per block. Feed conversion was subjected to a mixed model, MIXED procedure in SAS® software, where was modeled covariance structure using ten types.

Wang Z. and Goonewardene L. A. 2004. published 'the use of mixed models in the analysis of animal experiments with repeated measures data. The objective of the paper was to provide a mixed model methodology in a repeated measures analysis and use a balanced steer data from a growth study to illustrate the use of PROC MIXED in the SAS system using five covariance structures. The justification by these two for the use of the mixed model was that it is not affected by the presence of unequally spaced and/or missing data. In our case this threat is not anticipated because there are no missing cases and data is equally spaced in terms of time, therefore the GLM procedure can comfortably be used without affecting the output or results of the model.

1.2.1 REPEATED MEASURES ANALYSIS

When measurements are taken on the same experimental unit, the measurements tend to be co-related with each other. When the measurements represent qualitatively different things, such as weight, length, and width, this co-relation is taken into account by use of multivariate methods, such as multivariate analysis of variance. When the measurements can be thought of as responses to levels of an experimental

factor of interest, such as time, treatment, or dose, the correlation can be taken into account by performing a repeated measures analysis of variance which is a multivariate method.

Traditionally people used to analyze each variable by variable. Statistical packages like SAS and Genstat provide both the univariate and multivariate tests for repeated measures for one response.

1.2.2 USES OF REPEATED MEASURES DESIGN

- Conduct an experiment when few participants are available: The repeated measures design reduces the variance of estimates of treatment- effects, allowing statistical inference to be made with fewer subjects.
- Conduct experiment more efficiently: Repeated measures designs allow many experiments to be completed more quickly, as only a few groups need to be trained to complete an entire experiment.
- Study changes in participants' behavior over time: Repeated measures designs allow researchers to monitor how the participants change over the passage of time, both in the case of long-term situations like longitudinal studies and in the much shorter-term case of practice effect.

1.2.4 ADVANTAGES OF REPEATED MEASURES

The primary strengths of the repeated measures design is that it makes an experiment more efficient and helps keep the variability low. This helps to keep the validity of the results higher, while still allowing for smaller than usual number of subject groups.

1.3 PROBLEM STATEMENT

As the price of milk goes up and also its cost of production soars against other alternatives it is important for farmers to explore other alternatives that can be used as its substitute or complement in feeding dairy calves. This study focuses on

establishing the effect of feeding dairy calves on a combination of milk and Maize-cowpea gruel when equated to feeding entirely on milk. We wish to explore the possibility of entirely substituting the calves' milk diet with a cheaper alternative or partly substituting the milk ration with a cheaper alternative. In this case we are considering Maize-cowpea gruel.

1.4 BROAD OBJECTIVE

The broad objective of this study is to establish economically viable alternatives of feeding dairy calves without adversely affecting their performance. In this case maize-cowpea gruel is used as an alternative to milk.

1.5 SPECIFIC OBJECTIVES

- To determine the performance of dairy calves fed on maize-cowpea gruel as part of their ration in terms of growth rates
- To determine the economic viability of feeding dairy calves on maize-cowpea gruel to substitute part of their milk ration.

1.6 HYPOTHESES

- Dairy calves fed on maize-cowpea-gruel as part of their ration gained weight at a rate equal to that of those fed on milk
- It is cheaper to substitute part of dairy calves milk ration with maize-cowpea gruel without necessarily affecting their performance

1.7 SIGNIFICANCE OF THE STUDY

This study aims to inform farmers on economical feeding alternatives of dairy calves. It compares the effect on performance of dairy calves by feeding them on two treatments namely;

1. Milk
2. Maize-cowpea gruel and Milk

The study involves feeding these calves on the two treatments and monitoring them for weight changes over a period of 20 weeks.

The results obtained from this study will be used by smallholder dairy farmers to inform them on substituting part of the calves' ration with Maize-cowpea gruel which is a cheap alternative.

It is anticipated that the use of this combination will save the farmer 3-4 litres of milk. The milk so saved can be sold to improve the farmers' income from milk sales.

1.8 METHODOLOGY

1.8.1 Study Area

The study was carried out at the Kenya Agricultural Research Institute in Mtwapa, Mombasa-Kenya which is located at the coastal region of Kenya. The area is located 20 km North of Mombasa in Kilifi District along Mombasa - Malindi road.

1.8.2 Experimental Material and Units

Carefully considering problems and pitfalls in animal dietary experiments (DH Bake, 1986), sixteen dairy calves of approximately the same weight, age and body composition were selected to constitute the experimental units.

The sixteen dairy calves were tagged as follows: with Z5, Z13, Z15, Z4, Z9, Z7, Z11, and Z3 being fed on milk and Z14, Z6, Z8, Z10, Z16, Z12, Z17 and Z18 fed on maize-cowpea gruel. The first set of dairy calves was taken to be under treatment group 1 while the second set was taken to be under treatment group 2.

Body-weight measurements

Following a 14-day acclimatization period, each dairy calf was weighed at the beginning of the experiment (initial body weight, IBW) and every

successive seven-day thereafter. All calves were weighed during morning hours after overnight fasting using suspended weighing scale having a sensitivity of 100 grams. The experiment was initiated in April and ended in September 2008.

1.8.3 Treatment Allocation

The dairy calves were enclosed in a field and made to go through a crush. As the calves went through the crush, they were tagged with tags representing either milk or maize-cowpea gruel in an alternating manner. Eight dairy calves were allocated to be fed on maize-cowpea gruel and another set of eight dairy calves were allocated to be fed on milk. Treatment group 1 was taken to be the set of dairy calves that were fed on milk while treatment group 2 was taken to be the set of dairy calves that were fed on maize-cowpea gruel.

1.8.5 Data Collection

The data on weights of calves fed on the two treatments over a period of 10 weeks was recorded. This raw data was then digitized into MS Excel and verified against the original data sheets. The weights data was expressed in kilograms

1.8.6 Data Analysis

Data analysis was done using SAS, R, SPSS (17.0) statistical data analysis software and Excel.

1.8.8 Assumptions of Multivariate Analysis of Variance

Some assumptions have to be met before carrying out multivariate analysis of variance. These assumptions include:

1. The data from group i has common mean vector μ_i
2. The data from all groups have common variance-covariance matrix Σ.
3. *Independence*: The subjects are independently sampled.

4. *Normality*: The data are multivariate normally distributed.

NB: According to Chuong B. Do (2008) a vector-valued random variable $X = [X_1 \ldots . X_n]^T$ has a multivariate normal distribution with mean $\mu \in R^n$ and a covariance matrix $\sum \in S_{++}^n$, if its probability density function is given by

$$p(x; \mu, \Sigma) = \frac{1}{(2\pi)^{n/2}|\Sigma|^{1/2}} \exp\left(-\frac{1}{2}(x-\mu)^T\Sigma^{-1}(x-\mu)\right). \qquad 1.1$$

We write this as $X \sim N(\mu, \Sigma)$.

CHAPTER 2

EXPLORATORY DATA ANALYSIS (EDA)

2.1 INTRODUCTION

It is a key thing to ensure that the data conforms to the underlying assumptions e.g.; Multivariate normality assumptions before carrying out any analyses or fitting any models to the data.

Exploratory data analysis, EDA (John Tukey, 1978) is an approach to analyzing data for the purpose of formulating hypothesis worth testing, complementing the tools of conventional statistics for testing hypothesis.

The objectives of carrying the EDA were to:

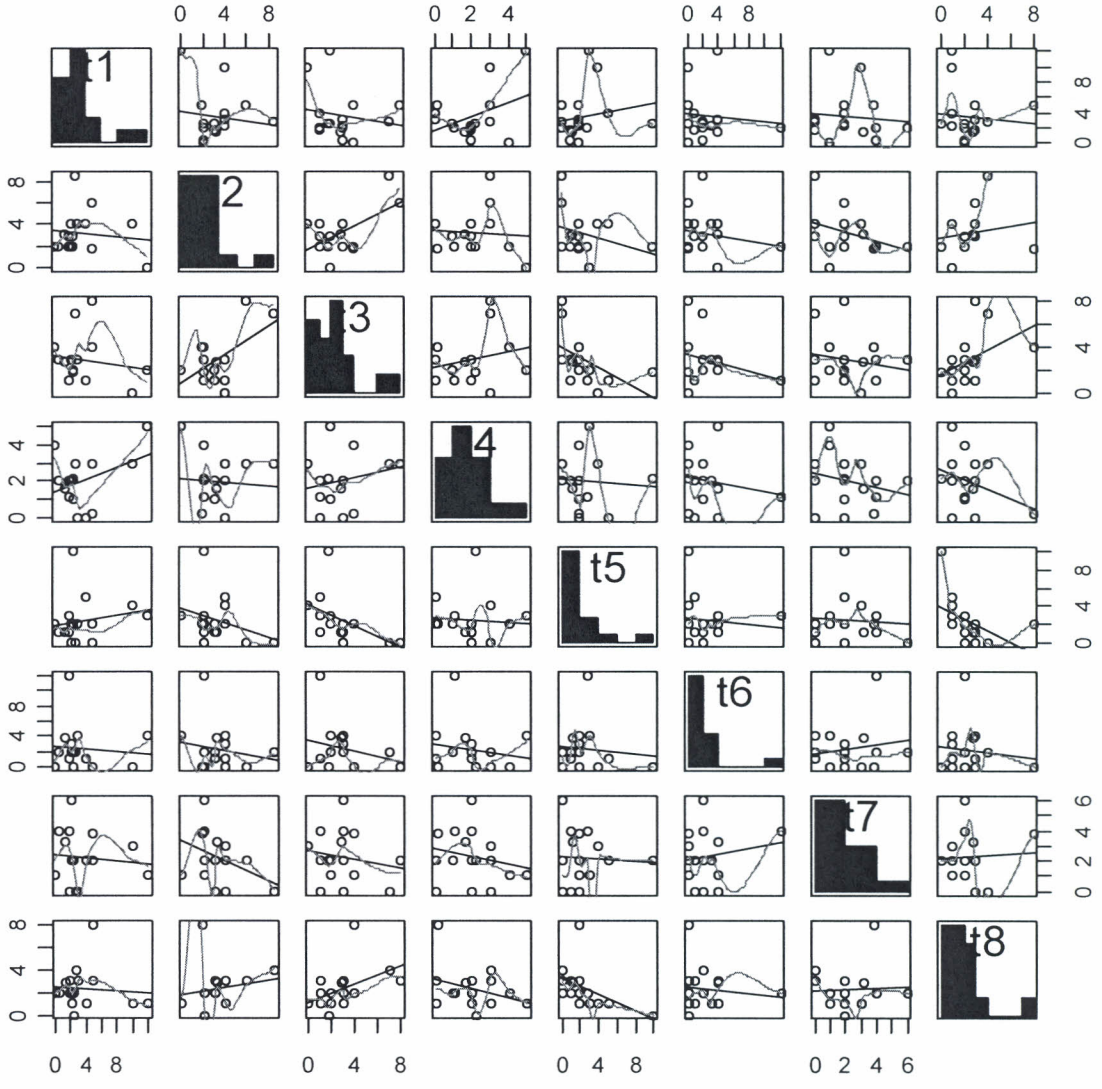
- Suggest hypothesis to be tested
- Assess the assumptions on which statistical inference would be based
- Support the selection of appropriate statistical tools and techniques
- Provide a basis for further data collection through surveys or experiments

EDA employs both graphical and quantitative techniques to give insight into the data set allowing the data to reveal its structure, detect outliers and anomalies and suggests a possible model to be fitted to the data. The techniques used are run-sequential plots, histograms, normal probability plots, scatter plots and the box whisker plots.

2.1.1 Histograms

Histograms were plotted for all the differences of the weights from week 1-20. There the number of variables considered as such for this multivariate EDA using histograms were n-1 i.e. 20-1.

Figure 1: scatter plot matrix of the data showing distributions and correlations of the variables.



Looking at this scatter plot, it is clear from the histograms that the variables of this data indicate skewness to the right and therefore there is need to think of transforming the data, but before that a few more tests can be done.

In some cases relationships between subsequent variables can be observed. Through this it can be observed that some variables have positive

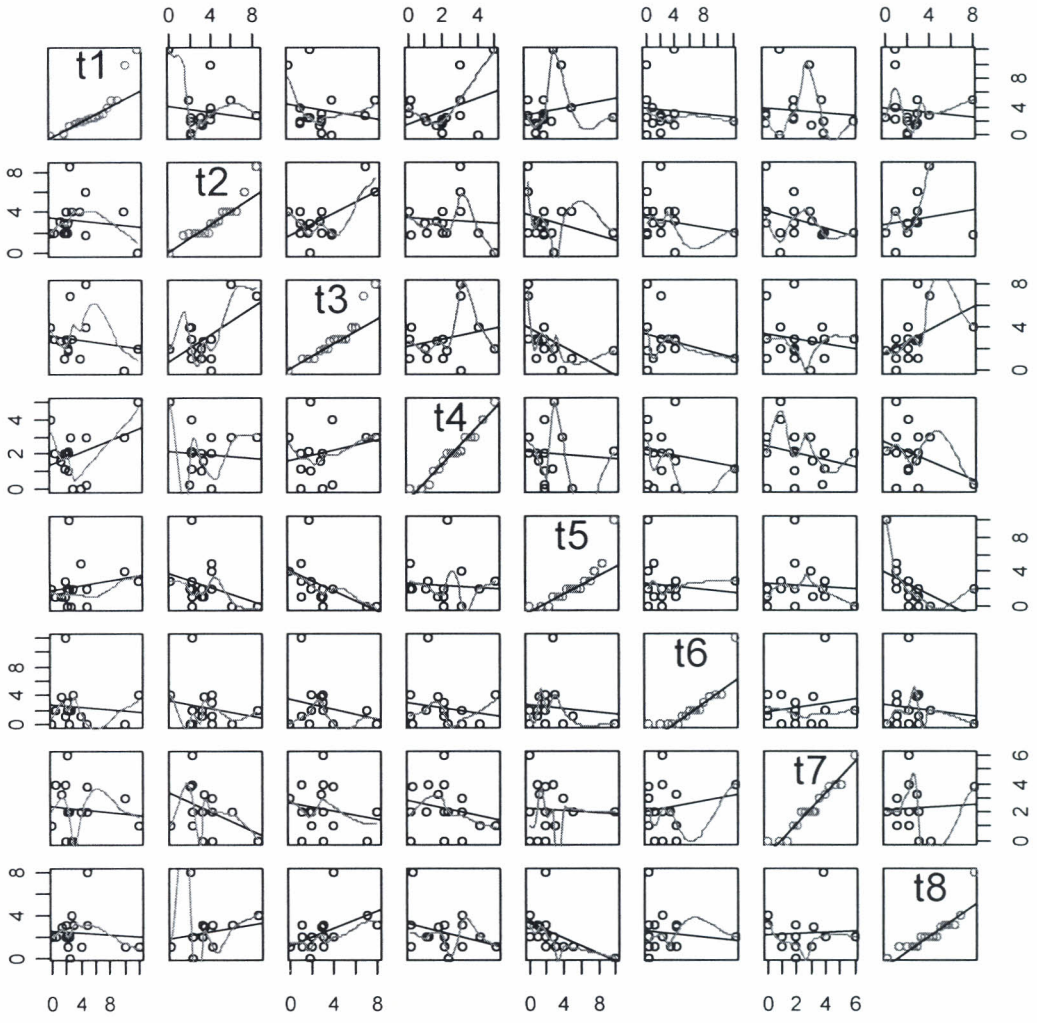
relationships and others have negative relationships. In a few cases however, there no clear definition of relationships between subsequent variables.

2.1.2 Normal QQ Plots

In statistics, a **Q-Q plot** ("Q" stands for quantile) is a probability plot, which is a graphical method for comparing two probability distributions by plotting their quantiles against each other.

A Q-Q plot is used to compare the shapes of distributions, providing a graphical view of how properties such as location, scale, and skewness are similar or different in the two distributions. Q-Q plots can be used to compare collections of data, or theoretical distributions. The use of Q-Q plots to compare two samples of data can be viewed as a non-parametric approach to comparing their underlying distributions. A Q-Q plot is generally a more powerful approach to doing this than the common technique of comparing histograms of the two samples, but requires more skill to interpret

Figure 2: Normal QQ-plots

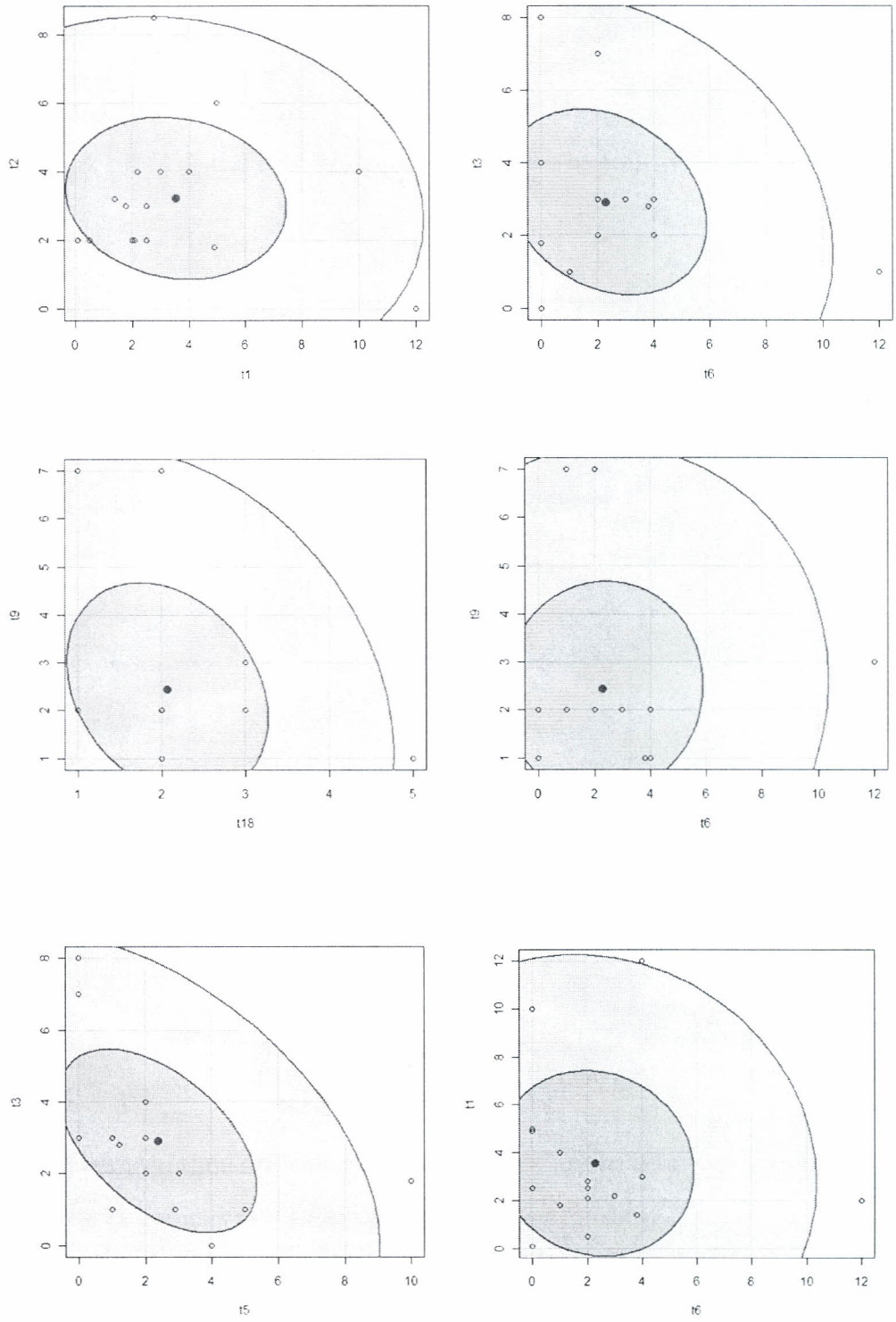

t1
t2
t3
t4
t5
t6
t7
t8

Looking at these scatter plots and focusing on individual variables, the QQ-plots confirm what was indicated by the histograms above. Majority of the variables clearly indicate a departure from normality.

The relationships between variables remain the same as indicated above under histograms.

The following variables seem contain values that can be termed as outliers; t1, t2, t3, t5, t6, t8, t9 and t19, but to be sure that they are indeed outliers we can plot some ellipses for these particular variables.

Figure 3: Ellipses of untransformed data

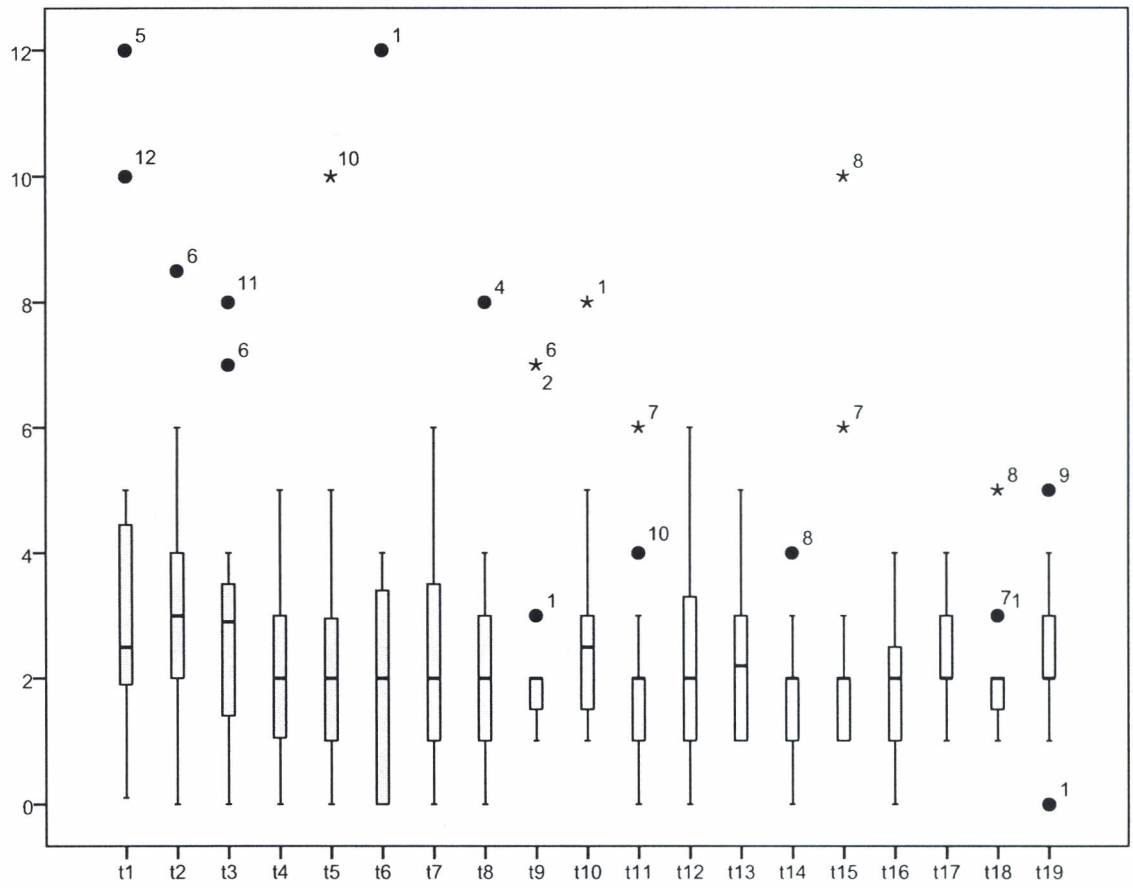


From these ellipses our suspicions are confirmed. There are indeed outliers and therefore we need to deal them appropriately.

2.1.3 Box Plots

The box plots of the untransformed data are as follow.

Figure 4: Box Plots of untransformed data



This plot confirms our suspicion that there are several outliers in this data set. The skewness in all the variables is also evident. Therefore, without any further testing for multivariate normality and sphericity of data set we conclude that the untransformed data negates sphericity assumptions and is

not multivariate normal. There is therefore a need to transform the data for it to be useful in statistical inference.

2.2 DATA TRANSFORMATION

There are several methods for transforming data sets to meet multivariate assumptions:

The logarithm and square root transformations are commonly used for positive data, and the multiplicative inverse (reciprocal) transformation can be used for non-zero data. The power transform is a family of transformations parameterized by a non-negative value λ that includes the logarithm, square root, and multiplicative inverse as special cases. To approach data transformation systematically, it is possible to use statistical estimation techniques to estimate the parameter λ in the power transform, thereby identifying the transform that is approximately the most appropriate in a given setting. Since the power transform family also includes the identity transform, this approach can also indicate whether it would be best to analyze the data without a transformation. In regression analysis, this approach is known as the *Box-Cox technique*.

The reciprocal and some power transformations can be meaningfully applied to data that include both positive and negative values (the power transform is invertible over all real numbers if λ is an odd integer). However when both negative and positive values are observed, it is more common to begin by adding a constant to all values, producing a set of non-negative data to which any power transform can be applied.

A common situation where a data transformation is applied is when a value of interest ranges over several orders of magnitude. Many physical and social phenomena exhibit such behavior — incomes, species populations, galaxy sizes, and rainfall volumes, to name a few. Power transforms, and in particular the logarithm, can often be used to induce symmetry in such data. The logarithm is often favored because it is easy to interpret its result in terms of "fold changes."

The logarithm also has a useful effect on ratios. If we are comparing positive quantities X and Y using the ratio X / Y, then if $X < Y$, the ratio is in the unit interval (0,1), whereas if $X > Y$, the ratio is in the half-line $(1,\infty)$, where the ratio of 1 corresponds to equality. In an analysis where X and Y are treated symmetrically, the log-ratio $\log(X / Y)$ is zero in the case of equality, and it has the property that if X is K times greater than Y, the log-ratio is the equidistant from zero as in the situation where Y is K times greater than X (the log-ratios are $\log(K)$ and $-\log(K)$ in these two situations).

If values are naturally restricted to be in the range 0 to 1, not including the end-points, then a logic transformation may be appropriate: this yields values in the range $(-\infty, \infty)$.

In our case we used the square root transformation. In addition, since we had some values as zero and we cannot obtain square roots for zero, we modified the square root function to take the form:

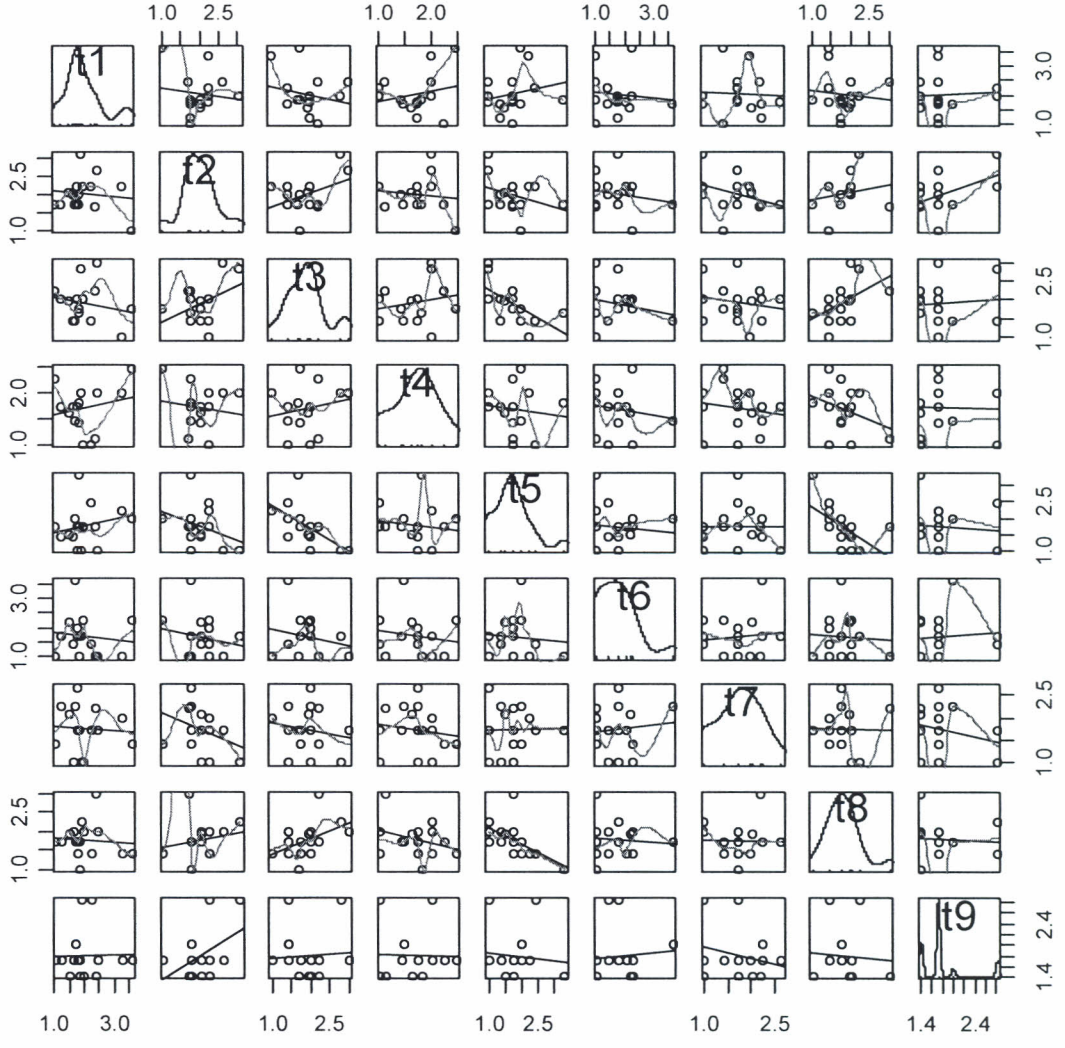
$$f(x) = \sqrt{(x + 1)} \qquad 2.1$$

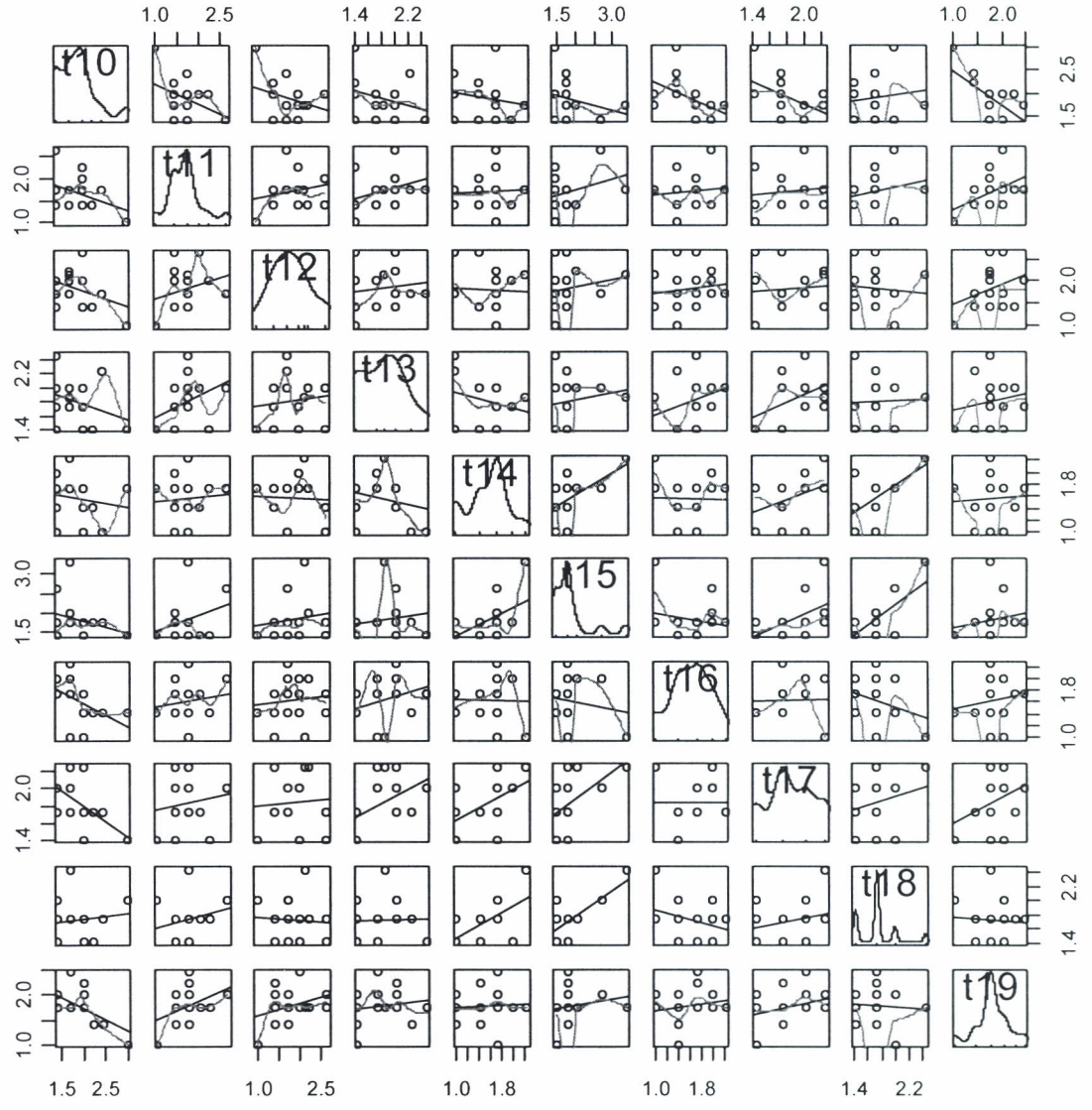
Where, x is the change in weight between subsequent weeks.

Upon transformation the data is now multivariate normal. This is the data set that was used to carry out statistical analysis. Just to verify this, we carry out a normality test.

2.2.1 Scatter plot Matrix with Density Plots for each Variable

Figure 5: Density Plots of the transformed data

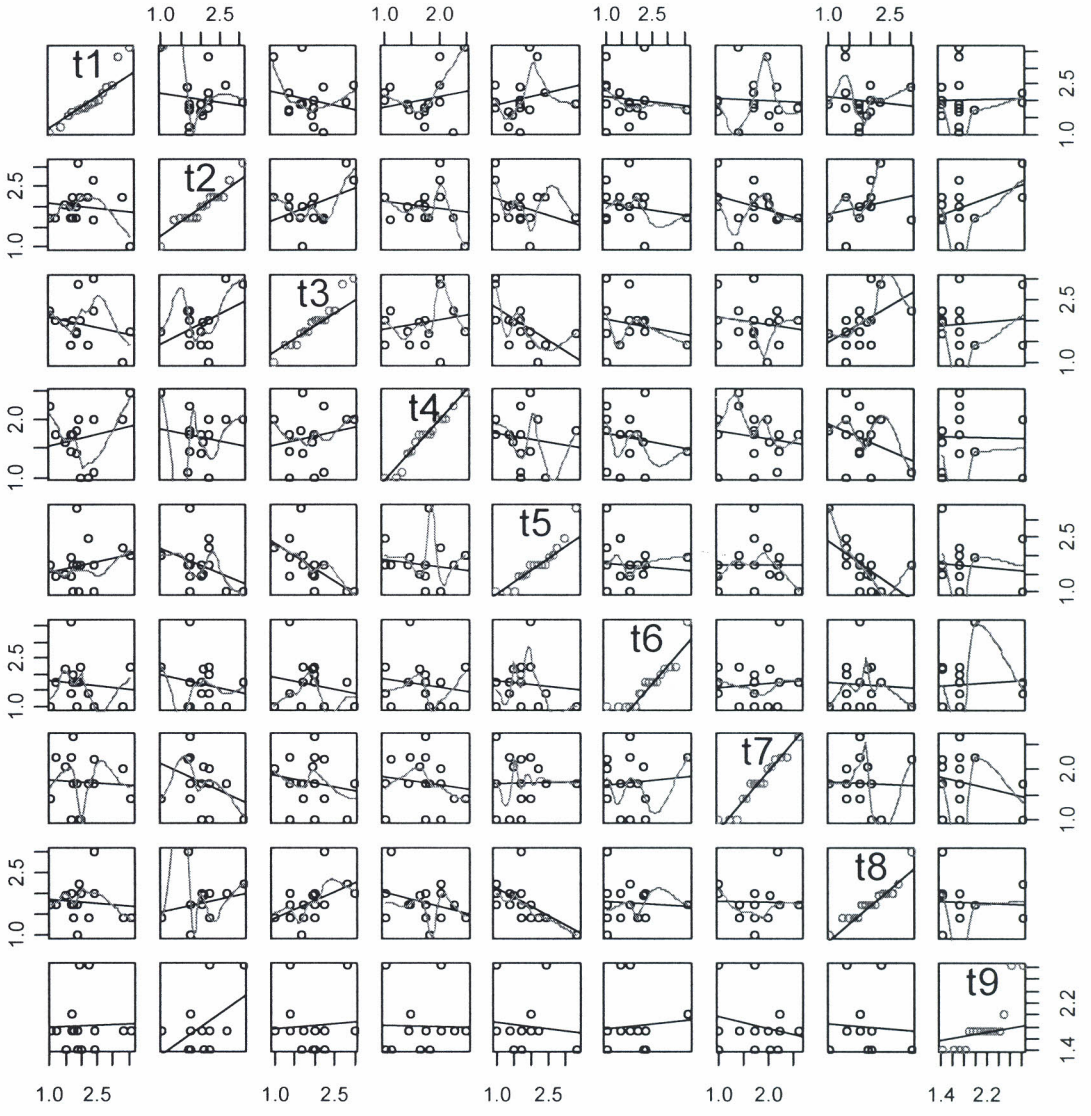


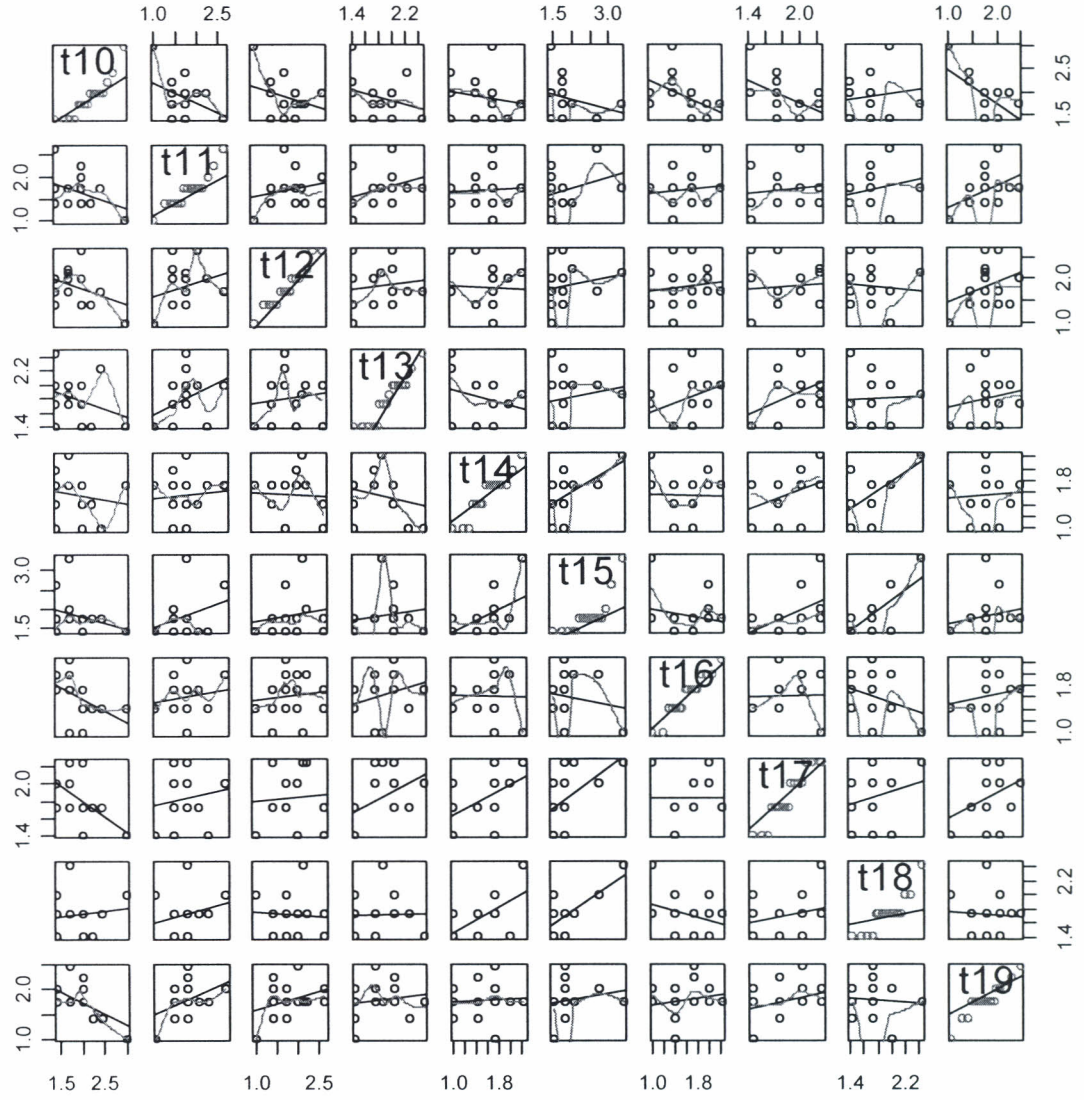


Looking at the density plots along the main diagonal for the variables, we can observe that these density plots follow the normal distribution. Since majority of these variables follow this distribution, we conclude that the transformed data is multivariate normal.

2.2.2 Normal QQ plots

Figure 6: Normal QQ of the transformed data





The quantile - quantile plots plotted above also confirm the conclusions made from density plots and therefore with certainty we can conclude that our data set is multivariate normal. Hence we can carry out statistical analysis and infer on this data set as it.

CHAPTER 3

ANALYSIS OF COVARIANCE

3.1 INTRODUCTION

3.1.1 Definition of Covariance Analysis

Analysis of covariance is a combination of analysis of variance (ANOVA) and linear regression that accounts for intergroup variance when performing ANOVA. Including a continuous variable (the covariate) in an ANOVA model will account for known variance not related to the treatment. Covariates are variables not controlled for in the experiment that still affect the dependent variable

Analysis of covariance requires measurement of the character of primary interest plus the measurement of one or more variables known as the covariate. In our experiment the covariate is the initial birth weight of the calves. It is used with the dependent variable to define a regression model for the weights data.

The covariance technique is effective for controlling experimental error caused by use of different calves in the experiment. The covariance analysis removes the effect of different birth of the calves that were used in the experiment.

It is well known that in designed experiments the ability to detect existing differences among treatment increases as the size of the experimental error decreases, a good experiment attempts to incorporate all possible means of

minimizing the experimental error. Besides proper experimentation, a proper data analysis also helps in controlling experimental error. In institutions where blocking alone may not be able to achieve adequate control of experimental error, proper choice of data analysis may help a great deal. By measuring one or more covariates, the characters whose functional relationships to the character of primary interest are known - the analysis of covariance can reduce the variability among experimental units by adjusting their values to a common value of the covariate. For example, in our case here - which a typical animal feeding experiment, the initial body weights of the animal usually differs. Using this initial body weight as a covariate, the final weights recorded after the animals have been subjected to various physiological feeds (treatments) can be adjusted to the values that would have been obtained had there been no variation in the initial body weights of the animals at the start of the experiment.

3.1.1 Uses of Covariance Analysis in Agricultural Research

According to Rajender Parsad and V.K. Gupta (2008), there are several uses of covariance analysis in agricultural research. Some of the most important ones are:

1. To control experimental error and to adjust treatment means.
2. To aid in the interpretation of the experimental results.
3. To estimate missing data.

3.1.1.1. Error control and Adjustment of Treatment Means

It is now well known that the size of the experimental error is closely related to the variability between experimental units. It is also known that proper blocking can reduce experimental error by maximizing the differences within blocks. Blocking however, cannot cope with certain types of variability.

Use of covariance analysis should be considered in experiments in which blocking couldn't adequately reduce the experimental error (for instance in our case). By measuring an additional variable (e.g., initial birth weight) that is known to be linearly related to the primary variable weight change, the source of variation associated with the covariate can be deducted from experimental error. This adjusts the primary variable weight change linearly upward or downward, depending on the relative size of its respective covariate. The adjustment accomplishes two important improvements:

1. The treatment mean is adjusted to a value that it would have had; had there been no differences in values of the covariate.
2. The experimental error is reduced and the precision for comparing treatment means is increased.

Although blocking and covariance techniques are both used to reduce experimental error, the differences between the two techniques are such that they are usually not interchangeable. Analysis of covariance can be used only when the covariate representing the heterogeneity among the experimental units can be measured quantitatively. However, that is not a necessary condition for blocking. In addition, because blocking is done prior to the start of the experiment, it can be used only to cope with sources of variation that occur during the experiment. Thus, covariance analysis is useful, as a supplementary procedure to take care of sources of variation that cannot be accounted for by blocking.

3.1.1.2. Aid in Interpretation of Experimental Results

The covariance technique can assist in the interpretation and characterization of the treatment effects on the primary character of interest weight change, in much the same way that the regression and correlation analysis is used. By examining the primary character of interest weight change together with

other characters whose functional relationships to the weight change are known, the biological processes governing the treatment effects on the weight change can be characterized more clearly.

The major difference between the use of covariance analysis for error control and for assisting in interpretation of results is in the type of covariate used. For error control, the covariate should not be influenced by the treatments being tested; but for the interpretation of results, the covariate should be closely associated with the treatment effects.

3.1.1.3. Missing Data

The only difference between use of covariance analysis for error control and that for analysis of missing data is the manner in which the values of the covariate are assigned. When covariance analysis is used to control error and to adjust treatment means, the covariate is measured along with the weight change for each experimental unit. But when covariance analysis is used to analyze the missing data, the covariate is not measured but is assigned, one each, to the missing observation. We will leave this discussion at that because we do not have missing data in our case.

3.1.2 Assumptions of ANCOVA

ANCOVA has the same assumptions as ANOVA except there are two important additional considerations (Andy Field, 2008): (1) independence of the covariate and treatment effects, and (2) homogeneity of regression slopes. The first one basically means that the covariate should not be different across the groups in the analysis (in other words, if you did an ANOVA or t-test using the groups as the independent variable and the covariate as the outcome, this analysis should be non-significant). For details on this assumption we refer you to Miller and Chapman (2001).

When ANCOVA is conducted we look at the overall relationship between the outcome (dependent variable) and the covariate: we fit a regression line to the entire data set, ignoring to which group a unit belongs. In fitting this overall model we, therefore, assume that this overall relationship is true for all groups of participants. For example, if there is a positive relationship between the covariate and the outcome of one group, we assume that there is a positive relationship in all the other groups too. If however, the relationship between the outcome (dependent variable) and covariate differs across the groups then the overall regression model is inaccurate (it does not represent all the groups). This assumption is very important and is called the assumption of homogeneity of regression slopes.

3.1.3. Rules for Determining Expected Mean Squares for Balanced Data

An expected mean square is a weighted sum of variances, with each variance multiplied by a coefficient. For random effects, the variances are given implicitly (Neter J. and Wasserman W. (1974)). For example, for a set of 'I' fixed treatment effects, $\alpha_1, \alpha_2, \ldots\ldots, \alpha_I$, the variance is

$$\sigma_\alpha^2 = \frac{[\Sigma_i \alpha_i^2]}{(I-1)} \qquad 3.1$$

It is always the sum of squared effects divided by the number of degrees of freedom in the effects.

The following rules come in two parts. Part A is used to determine which variance components should be included. Part B is then used to determine the coefficients of these included variance components.

Part A

1. Always include σ_e^2, the variance of chance error terms
2. List of set of variance components in the model whose subscripts contain all the factors included in the desired mean square. For a main effect, this

includes all interactions containing this main effect. For an interaction effect, this includes all higher order interactions between this interaction and other effects or interactions, but not any lower interactions.

3. From the list in step 2, delete any interaction variance component for which the additional factors beyond those in the desired expected mean square are not all random.

Part B

1. The coefficient of σ_e^2 is always 1.
2. The coefficient of any other variance component is the number of replicates of each of the treatments times the product of the numbers of factor levels that do not appear in the subscript of the variance component. (Remember the number of replicates of each treatment is assumed to be constant).

The test used for the presence of treatment main effects depends on whether the main effects are random or fixed.

3.1.4 Defining Variance Components

It has been demonstrated by Janssen (2006) how different variance components describe at different levels the variability in observations with mixed model structure. The variance - covariance matrix of Y is;

$$y_{ij} = constant + \alpha_i + \beta x_{ij} + \varepsilon_{ij}$$

$$yij = \mu + \alpha_i + \beta(x_{ij} - \bar{x}) + \varepsilon_{ij} \qquad 3.21$$

where;

α_i is the effect of factor A (groups or treatments)

β is pooled (across groups) regression slope b/w Y and X

x_{ij} is value of covariate for jth observation in ith group

ε_{ij} is variation in Y not explained by either factor A or Covariate X

The first part of the model,$X\beta$, does not contribute to the variance of y as it only contains fixed effects. Furthermore, the assumptions are made such that each element ul in the vector u is a random effect which comes from a normal distribution with mean 0 and variance σ_{ul}, and that the elements are independent from each other and that the covariances among the elements of u are thus zero. The variance - covariance matrix of u is thus given by a diagonal matrix$D(\underline{u})$. All the elements in the vector u are assumed to be independent form the elements of e. We further have that the elements in e are also normally distributed with mean u and standard variance σ^2 and are independent from each other. Given the assumptions, the variance - covariance matrix of Y is given by;

$$D(Y) = D(Zu) + D(e) = ZD(u)Z^T + \sigma^2 I_N \qquad 3.3$$

Fitting the Model;

The GLM procedure was used in fitting the model. The dependent variable was the weight change and the initial weight was used as the covariate. Overall, the model was found to fit very well ($p<0.001$).

The ANOVA table is as follows.

Table 1: Analysis of Covariance Table

Source	DF	Type III SS	Mean Square	F value	Pr > F
Initial weight	1	3.374	3.374	0.26	0.6212
Treatments	1	350.38	350.38	26.61	0.0002

The covariate is not significant in this model ($p=0.2612$) but it still explains some variation in the dependent variable. Therefore we can as well decide to keep it in the repeated measures analysis.

The treatment effects are highly significant ($p<0.001$). It is therefore imperative to check whether there is a significant difference between the two treatment means.

CHAPTER 4

REPEATED MEASURES ANALYSIS OF VARIANCE

4.1 INTRODUCTION

Repeated measurements, as the name suggests, are observations of the same characteristic, which are made several times. What distinguishes such observations from those in more traditional statistical data modeling is that the same variable is measured on the same observational unit more than once. The responses are not independent as in the usual regression analysis and more than one observational unit is involved. The responses do not form a simple time series. To many animal scientists, a mention of the term repeated measurements evokes the idea of either the fisheries study of growth curves or split plot designs. However, once one begins to delve into the subject, one realizes that these two subjects, in no way, completely cover the field of repeated observations. In fact, repeated measurements are very frequent not only in animal science experiments but also in almost all scientific fields where statistical models are used

Few animals may be available (or few used, because of complex technique) in experiments with non-random repeated measurement (e.g. p animals in each of r treatment groups, each measured in p periods). In such cases, the use of summary statistics for each animal to eliminate the time factor, or ordinary univariate split-plot tests of the treatment means or multivariate analysis is inadvisable, because comparison of the treatments are not sufficiently sensitive for any of those procedures. The problem is that main

effects of treatments must be tested by the mean square for the animals within treatments, which is inflated by positive correlations among repeated observations. Even conditional tests (e.g. comparisons of treatments within periods), as well as tests of means of summary statistics, cannot be very sensitive; because, with low replication, the standard errors of mean differences are not much smaller than the ordinary (error) standard deviation among animals treated alike, without the influence of correlations induced by repeated measurement. In severe restriction of numbers of animals leaves few degrees of freedom for error, either reducing statistical power drastically or preventing multivariate analysis entirely. In such cases, the primary benefit of a Repeated Measures Design (RMD) is statistical power relative to sample size, which is important in many real researches. RMD use the same subjects throughout different treatments and thus, require fewer subjects overall. Because the subjects are constant, the variance due to subjects can be partitioned into the error variance term, thereby making any statistical test more powerful.

According to Ozkan GORGULU and Suati SAHINLER (2008), RMDs are quite versatile, and researchers use many different designs and call the designs by many different names. For example, a one way repeated measures ANOVA may be considered as a one-factor within subjects ANOVA. Two way repeated measures ANOVA may be referred to as a two-way within subjects ANOVA. These designs are called related samples models, matched samples models, longitudinal studies and within-subject designs. In RMDs, total variation consists of two parts as Between-Subject Factor(s) (BSF) or non-repeated factor(s) and Within-Subject Factor(s) (WSF) or repeated factor(s), and an error terms are computed for each source of variation. Having effect of animal within treatment removed from experimental error reduces experimental error; this provides having the researchers make a more reliable decision. A BSF is a non-repeated or

grouping factor, such as race or experimental group, for which subjects will appear in only one level. A WSF is repeated factors for which subjects will participate in each level e.g. subjects participate in both experimental conditions, albeit at different times. In repeated measures experimental design the following assumptions should be validated; the measurement errors are independent, and identically normally distributed with mean 0 and the same variance. The subjects are considered to be a random sample from the subject population of interest, so that the subject effect is random.

Measurements from the same subject will be positively correlated. It is assumed that the variance of the difference between the estimated means for any two different factor levels will be the same. This property is called sphericity. A slightly more restrictive assumption is that the covariance between observations within any be the same for any two different factor levels. This property is called compound symmetry. Compound symmetry is a special case of more general property, sphericity. If compound symmetry exists, then sphericity also exists, but it is possible for sphericity to exist when compound symmetry does not. Alternative analytic techniques are available when assumptions validity is dubious. These include an ε adjustment procedure based on Geisser and Greenhouse (1958) and a multivariate analysis using Hotelling's T 2 statistic.

4.2 ONE WAY REPEATED MEASURES DESIGN

It is the simplest design among the RMDs. There is one factor in this design and all of the experimental units are taken into experiment within the factor levels. A repeated factor might be different time points (periods), different treatments or the different levels of the same treatment.

The model of the design is,

$y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}$ i =1,2,3,. . . ,n ; j =1,2,3,. . ., p, 4.1

Where μ is overall mean, α_i is the effect of ith animal, β_j, is the effect of jth period or treatmentε_{ij} is error term. Table 1 presents a general illustration of one-way repeated measures designs with n subject and p treatments or periods (repeated measures). In one-way RMD, the sources of total variation are the between subject and within subject variations, and the aim is to test the differences among the periods or treatments. The sources of within subject variation are also variation among the treatments and error. Thus,

$$SS_{TOTAL} = SS_{BETWEEN-SUBJECT} + SS_{WITHIN-SUBJECT} \quad 4.2$$

$$= SS_{BETWEEN-SUBJECT} + SS_{TREATMENT} + SS_E$$

All sources of variations are computes as follows;

$$CT = \left[\sum_{i=1}^{n}\sum_{j=1}^{p} y_{ij}\right]^2/np, \quad 4.3$$

$$SS_{TOTAL} = \sum_{i=1}^{n}\sum_{j=1}^{p}(y_{ij} - \bar{y})^2 = \sum_{i=1}^{n}\sum_{j=1}^{p} y_{ij}^2 - CT, \quad 4.4$$

$$SS_{TREATMENT} = p\sum_{i=1}^{n}(\bar{y}_i - \bar{y})^2 = \sum_{i=1}^{n}\frac{y_i^2}{p} - CT, \quad 4.5$$

$$SS_{BETWEEN-SUBJECT} = \frac{\sum_{j=1}^{p} y_j^2}{n} - CT, \quad 4.6$$

$$SS_{WITHIN-SUBJECT} = SS_{TOTAL} - SS_{TOTAL-SUBJECT}, \quad 4.7$$

$$SS_E = SS_{TOTAL} - SS_{BETWEEN-SUBJECT} - SS_{TREATMENT} = SS_{WITHIN-SUBJECT} - SS_{TREATMENT} \quad 4.8$$

Table 2 presents analysis of variance (ANOVA) summary table contains the results of all computations in general.

The general ANOVA table with one way repeated measures differs from one way independent samples ANOVA table such that, the row for subjects acts as another factor and the residual or error term is the interaction between

subjects and treatments, not real error (The real error is the differences among the experimental units, which subject to same treatment). This difference arises because subjects are constant through the treatments and; thus, subject effects may be partitioned out of the error variance. There is still only one effect of interest, treatments, with only one test statistic.

4.3 TWO WAY REPEATED MEASURES DESIGN

There are two factors, one of them BSF (A) and the other is WSF (B) in this designs. Because the experimental units were classified as one inside the other with factor levels of A but as factorial with factor levels of B, interaction between experimental units and factor A could not be considered.

In a two-way RMD, the sources of total variation are separated in two parts as the between subject (SSBETWEEN-SUBJECT) and within subject variations (SSWITHIN-SUBJECT).

Therefore,

$$SS_{BETWEEN-SUBJECT} = SS_A + SS_{E1} \; and \; SS_{WITHIN-SUBJECT} = SS_B + SS_{AxB} + SS_{E2} \qquad 4.9$$

Thus, the model of the design is,

$$y_{ij} = \mu + \alpha_i + \gamma_{(i)k} + \beta_j + (\alpha\beta)_{ij} + \varepsilon_{(i)jk} \qquad 4.10$$

$$i = 1,2,\dots,n; j = 1,2,\dots.,p; k = 1,2,\dots.,q$$

Where μ is overall mean, α_i is the effect of the ith level of factor A, β_j is the effect of jth period or treatment, $(\alpha\beta)_{ij}$ is the interaction effect of A and B, $\gamma_{(i)k}$ is the effect of kth experimental unit in ith level of the A factor (Error 1) and $\varepsilon_{(i)jk}$ is error term (Error 2).

Table 3 presents a general illustration for two-way repeated measures designs with n levels of BSF, q subjects and p treatments or periods

(repeated measures). As seen in Table 3, while the measurements are taken from different experimental units in each levels of BSF (A), they are taken from the same experimental unit in all levels of WSF (B).

All sources of variations are calculated as follows;

$$CT = \left[\sum_{i=1}^{n}\sum_{j=1}^{p}\sum_{k=1}^{r} y_{ijk}\right]^2 / npr, \quad 4.11$$

$$SS_{TOTAL} = \sum_{i=1}^{n}\sum_{j=1}^{p}\sum_{k=1}^{q} y_{ijk}^2 - CT, \quad 4.12$$

$$SS_{BETWEEN-SUBJECTS} = \frac{\sum_{i=1}^{n}\sum_{k=1}^{q} y_{i.k}^2}{p} - CT, \quad 4.13$$

$$SS_A = \frac{\sum_{i=1}^{n} y_{i..}^2}{pq} - CT, \quad 4.14$$

$$SS_{E1} = SS_{BETWEEN-SUBJECT} - SS_A, \quad 4.15$$

$$SS_{WITHIN-SUBJECTS} = SS_{TOTAL} - SS_{BETWEEN-SUBJECT}, \quad 4.16$$

$$SS_B = \frac{\sum_{j=1}^{p} y_{.j.}^2}{nq} - CT, \quad 4.17$$

$$SS_{AxB} = \left[\frac{\sum_{i=1}^{n}\sum_{j=1}^{p} y_{ij}^2}{q}\right] - CT - SS_A - SS_B, \quad 4.18$$

$$SS_{E2} = SS_{WITHIN-SUBJECT} - SS_B - SS_{AxB}. \quad 4.19$$

Table 4 presents analysis of variance (ANOVA) summary table contains the results of all computations for general.

Error 1 is used to test factor A, and Error 2 is used to test B and AxB [14]. Testing AxB interaction effect is more as than comparing the main effects (A and B). ρ in Table 4 is coefficient of correlation which denotes the total correlation between two levels of factor that come to one after another and contain repeated measurement [2,14], and computed as;

$$\rho = [MS_{E1} - MS_{E2}]/p\sigma^2 \quad 4.20$$

Where p is the number of periods or treatments, σ^2 is the variation among the experimental units which are in the same treatment and $\sigma^2 = [MS_{E1} + (p-1)MS_{E2}]/p$. If the measurements are taken from different experimental units, $\rho = 0$.

4.4 HYPOTHESIS TESTING IN MANOVA

All current MANOVA tests are made on **A** = **E**-1**H**. There are four different multivariate tests that are made on **E**-1**H**. Each of the four test statistics has its own associated *F* ratio. In some cases the four tests give an exact *F* ratio for testing the null hypothesis and in other cases the *F* ratio is approximated. The reason for four different statistics and for approximations is that the mathematics of MANOVA get so complicated in some cases that no one has ever been able to solve them.

To understand MANOVA, it is not necessary to understand the derivation of the statistics. Here, all that is mentioned is their names and some properties. In terms of notation, assume that there are q dependent variables in the MANOVA, and let λ_i denote the ith Eigen-value of matrix **A** which, of course, equalsHE^{-1}.

The first statistic is *Pillai's trace*. Some statisticians consider it to be the most powerful and most robust of the four statistics. The formula is

$$Pillai's trace = trace[H(H+E)^{-1}] = \sum_{i=1}^{q} \frac{\lambda_i}{1+\lambda_i} \qquad 4.21$$

The second test statistic is *Hotelling-Lawley's trace*.

$$Hotelling - Lawley's trace = trace(A) = trace(HE^{-1}) = \sum_{i=1}^{q} \lambda_i \qquad 4.23$$

The third is *Wilk's lambda* (Λ). (Here, the upper case, Greek Λ is used for Wilk's lambda to avoid confusion with the lower case, Greek λ often used to denote an Eigen-value. However, many texts use the lower case lambda as the notation for Wilk's lambda.) Wilk's Λ was the first MANOVA test statistic developed and is very important for several multivariate procedures in addition to MANOVA.

$$Wilk's\ lambda = \Lambda = \frac{|E|}{|H+E|} = \prod_{i=1}^{q} \frac{1}{1+\lambda_i} \qquad 4.24$$

The quantity (1 - Λ) is often interpreted as the proportion of variance in the dependent variables explained by the model effect. However, this quantity is not unbiased and can be quite misleading in small samples.

The fourth and last statistic is *Roy's largest root*. This gives an upper bound for the *F* statistic.

$$Roy's\ largest\ root = \max(\lambda_i) \qquad 4.25$$

or the maximum Eigen-value of $\boldsymbol{A} = \boldsymbol{HE^{-1}}$. (Recall that a "root" is another name for an Eigen-value.) Hence, this statistic could also be called Roy's largest Eigen-value.

Note how all the formula in equations are based on the Eigen-values of $\boldsymbol{A} = \boldsymbol{HE^{-1}}$. This is the major reason why statistical programs such as SAS print out the Eigen-values and eigenvectors of $\boldsymbol{A} = \boldsymbol{HE^{-1}}$.

Once these statistics are obtained, they are translated into *F*-statistics in order to test the null hypothesis. The reason for this translation is identical to the reason for converting Hotelling's T^2--the easy availability of published tables of the *F* distribution. The important issue to recognize is that in some cases, the *F* statistic is exact and in other cases it is approximate. Good statistical packages will inform you whether the *F* is exact or approximate.

In some cases, the four will generate identical *F* statistics and identical probabilities. In other's they will differ. When they differ, Pillai's trace is often used because it is the most powerful and robust. Because Roy's largest root is an upper bound on *F*, it will give a lower bound estimate of the probability of *F*. Thus, Roy's largest root is generally disregarded when it is significant but the others are not significant

In our case, the weights data is such that we can only observe significant weight change after five weeks. Therefore, our analyses consider a five week interval for the repeated measures analysis.

The GLM procedure was used for the analyses with results from the SAS output indicating significance of the model ($p<0.05$).

The type III SS ANOVA table is as follows.

Table 2: Repeated Measures Analysis of Variance

Source	DF	Type III SS	Mean Square	F-value	Pr>F
Initial Weight	1	27.8829	27.8292	2.2	0.18
Replication	7	96.1446	13.7349	1.1	0.4623
Treatments	1	358.0743	358.0743	28.6	0.0017

Manova Test Criteria and Exact F Statistics for the Hypothesis is of no Time Effect

H=Type III SSCP Matrix for Time

E=Error SSCP Matrix

S=1 M=1 N=1

Table 3: Multivariate Tests-No time effect

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilk's Lambda	0.607	0.65	4	4	0.6581
Pillai's Trace	0.3929	0.65	4	4	0.6581
Hotelling-Lawley Trace	0.6473	0.65	4	4	0.6581
Roy's Greatest Root	0.6473	0.65	4	4	0.6581

Manova Test Criteria and F approximations for the Hypothesis of no Time*rep Effect

H=Type III SSCP Matrix for Time*rep

E=Error SSCP Matrix

S=4 M=1 N=1

Table 4: Multivariate Tests- No time*rep effect

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilk's Lambda	0.0404	0.81	28	15.8	0.6947
Pillai's Trace	1.9616	0.96	28	28	0.5401
Hotelling-Lawley Trace	6.3938	0.57	28	10	0.8821
Roy's Greatest Root	4.1192	0.12	7	7	0.0408

NB: the F-statistic for Roy's Greatest Root is an upper bound.

Manova Test Criteria and Exact F statistics for the Hypothesis of no Time*treat Effect

H=Type III SSCP Matrix for Time*treat

E=Error SSCP Matrix

Table 5: Multivariate Tests – No Time*Treat effect

Statistic	Value	F Value	Num DF	Den DF	Pr > F
Wilk's Lambda	0.5046	0.98	4	4	0.507
Pillai's Trace	0.4953	0.98	4	4	0.507
Hotelling-Lawley Trace	0.9815	0.98	4	4	0.507
Roy's Greatest Root	0.9815	0.98	4	4	0.507

The GLM Procedure

Repeated Measures Analysis of Variance

Tests of Hypotheses for Between Subjects Effects

Table 6: Between Subject Effects

Source	DF	Type III SS	Mean Square	F-value	Pr>F
Replication	7	1.5213	0.2173	2.66	0.1105
Treatments	1	0.2253	0.2253	2.75	0.141
Error	1	0.5729	0.0818		

The GLM procedure

Repeated Measures Analysis of Variance

Univariate Tests of Hypotheses for Within Subjects Effects

Table 7: Within Subject Effects

						Adj. Pr > F	
Source	DF	Type III SS	Mean Square	F-value	Pr>F	G-G	H-F
Time	4	0.852	0.213	0.75	0.566	0.5328	0.566
Time*rep	28	9.3031	0.3322	1.17	0.3397	0.3614	0.3397
Time*Treatments	4	0.7345	0.2837	0.65	0.6336	0.5917	0.6336
Error(Time)	28	7.9456	0.2837				

Greenhouse-Geisser Epsilon	0.7405
Huyh-Feldt Epsilon	2.8100

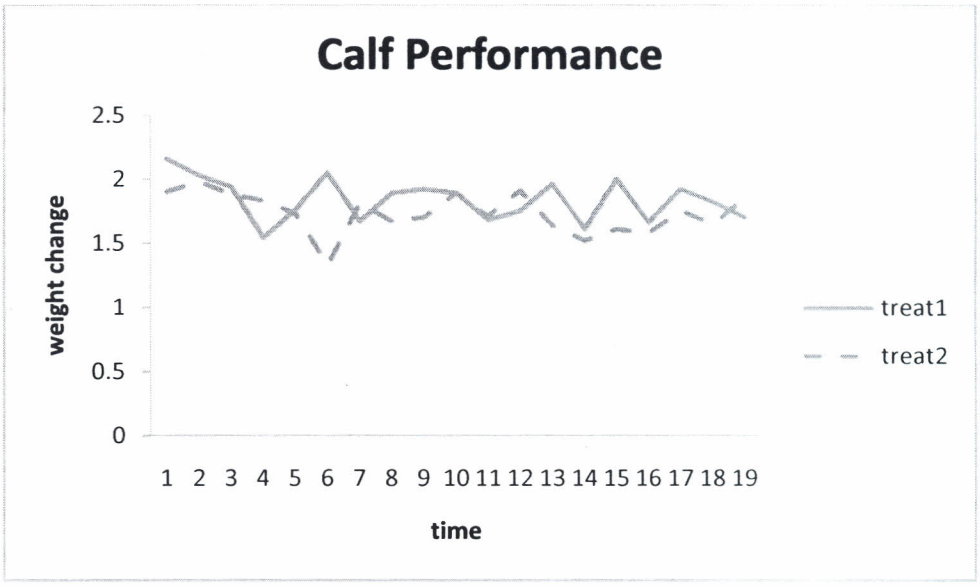
The Greenhouse and Geisser epsilon measures by how much the sphericity assumption is violated. The epsilon is then used to adjust for the potential bias in the F-statistic. The epsilon can be 1, which means that the sphericity assumption is met perfectly. An epsilon smaller that 1 means that the sphericity assumption is violated. The further it deviates from 1, the worse the violation; it can be as low as epsilon=1(1-k), which produces the lower bound of the epsilon (the worst case scenario). The worst case scenario depends on k, the number of levels in the repeated measures factor. In real life is rarely exactly 1-which is indeed the case we have in this data. If it is not much smaller than 1, then we feel comfortable with the results of the ANOVA. The Greenhouse and Geisser epsilon is derived from the variance-covariance matrix of the data. For its evaluation we need to first calculate the variance covariance matrix o the variables (S). The diagonal entries are the variances and the off diagonal entries are the covariances. From this variance-covariance matrix, the epsilon can be estimated. Also we need the mean of the main diagonal entries of S, the mean of all entries, the mean of all entries in row I of S, and the individual entries in the variance-covariance matrix. The epsilon procedure was proposed by Greenhouse and Geisser (1959).

Therefore based on this procedure we conclude that our epsilon suggest that the ANOVA results can be interpreted comfortably.

A paired t-test was carried out to test for differences in means between the two treatments. A two tailed test of hypothesis was used in this case with the following statement of the null hypothesis.

$$H_0: \mu_1 = \mu_2$$

Figure 7: Treatment means profiles



The paired t-test results (p=0.06) indicate that we fail to reject H_0. This means that there is no significance difference between the two means. We can therefore that conclude that the two treatment effects are the same. That is, the two treatments (milk and maize-cowpea gruel) when administered to dairy calves under similar environmental conditions have the same effect on their performance.

CHAPTER 5

TEST OF PARALLELISM BY USE OF REGRESSION

5.1 INTRODUCTION

By using dummy variables, we can broaden the application of regression analysis. In particular dummy variables allow us to employ regression analysis to produce the same information obtained by such seemingly distinct analytical procedures as analysis of covariance and analysis of variance (David G. Kleinbaum, Lawrence L. Kupper, Keith E. Muller (2007)).

There are three basic questions to consider when comparing two straight-line regression equations:

1. Are the two slopes the same or different (regardless of whether the intercepts are different)?
2. Are the two intercepts the same or different (regardless of whether the slopes are different)?
3. Are the two lines coincident (that is, the same), or do they differ in slope and /or intercept?

There are two general approaches to answering the earlier three questions related to comparing two straight lines.

Method I

Treat treatment 1 and treatment 2 data separately by fitting the two separate regression equations

$$Y_{t1} = \beta_{0t1} + \beta_{1t1} + \varepsilon_{t1} \qquad 5.1$$

And

$$Y_{t2} = \beta_{0t2} + \beta_{1t2} + \varepsilon_{t2} \quad 5.2$$

And then conduct appropriate two-sample t tests

Method II

Define dummy variable Z to be 0 if treatment 1 and 1 if treatment 2. Thus, for the n_{t1} means on t1, Z=0; and for the n_{t2} means on t2, Z=1. Our data will then be of the form:

$$\text{T1: } (X_{1t1}, Y_{1t1}, 0), (X_{2t1}, Y_{2t1}, 0), \ldots\ldots, (X_{nt1}, Y_{nt1}, 0) \quad 5.3$$

$$\text{T2: } (X_{1t2}, Y_{1t2}, 0), (X_{2t2}, Y_{2t2}, 0), \ldots\ldots, (X_{nt2}, Y_{nt2}, 0) \quad 5.4$$

Then, for the combined data above, the single multiple regression model

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \varepsilon \ (*) \quad 5.5$$

Yields the following two models for the two values of Z;

$$\begin{cases} Z = 0: Y_{t1} = \beta_0 + \beta_1 X + \varepsilon \\ Z = 1: Y_{t2} = (\beta_0 + \beta_2) + (\beta_1 + \beta_3) X + \varepsilon \end{cases}$$

5.6

This allows us to write the regression coefficients for the separate models for the method I in terms of the coefficients of model (*) above as follows:

$$\beta_{0t1} = \beta_0, \quad \beta_{0t2} = \beta_0 + \beta_2, \quad \beta_{1t1} = \beta_1, \quad \beta_{1t2} = \beta_1 + \beta_3 \quad 5.7$$

Thus, model (*) incorporates the two separate regression equations with within a single model and allows for different slopes (β_1 for t1 and $\beta_1 + \beta_3$ for t2) and different intercepts (β_0 for t1 and $\beta_0 + \beta_2$ for t2).

In our case here we adopt method II.

5.2 Comparing Two Straight lines using a Single Regression Equation

Comparing regression equations by this approach uses a single multiple regression model that contains one or more dummy variables to distinguish the groups being compared. When comparing two straight lines, the model is given by

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \varepsilon \quad 5.8$$

Where Y=weight change, and X=initial birth weight, and Z is a dummy variable indicating treatments allocated (1 if treatment 2, 0 if treatment 1). For our data ($n_{t1} = n_{t2} = 19$), the fitted model is

$$Y = 1.93 - 0.0094X - 0.11Z - 0.00015XZ \quad 5.9$$

This yields the following separate straight-lines equations:

$$Z = 0: \hat{Y}_{t1} = 1.93 + 0.0094X \quad 5.10$$

$$Z = 1: \hat{Y}_{t2} = 1.24 + 0.95X$$

These two straight-line equations are exactly the same as obtained by fitting separate regressions

5.3 Test of Parallelism: Single Model Approach

Referring again to the above dummy variable model, the null hypothesis that the two regression lines are parallel is equivalent to $H_0: \beta_3 = 0$. If the slope for t2, $\beta_{1t2} = \beta_1 + \beta_3$, simplifies to β_1, which is the slope for t2 (i.e., the two lines are parallel). The test statistic for testing $H_0: \beta_3 = 0$ is the partial F statistic (or equivalent t test) for the significance of the addition of the variable XZ to a model already containing X and Z.

In our case, this test statistic is computed as follows;

$$F(XZ|X,Z) = \frac{regression\ SS(X,XZ) - regression\ SS(X,Z)}{MS\ residual\ (X,Z,XZ)} \quad 5.11$$

$$= 0.007 \quad (p = 0.987)$$

The F statistic obtained as such is so small (p is large); so we do not reject the null hypothesis and therefore have no statistical basis for believing that the two lines are not parallel. This was the same decision made on the basis of separate regression fits. In fact, the F computed here is (theoretically) the square of the corresponding T computed using the separate straight-line fits, although the numerical answers may not agree due to round off errors.

5.4 Test of Equal Intercepts: Single Model Approach

The hypothesis that the two intercepts are equal, allowing for unequal slopes, is the equivalent to H_0: $\beta_2 = 0$ for the overall model. The test compares the overall model

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \varepsilon \quad 5.12$$

to the reduced model

$$Y = \beta_0 + \beta_1 X + \beta_2 \beta_3 XZ + \varepsilon \quad 5.13$$

This is a variables-added-last test considering Z, the treatment group dummy variable. Another approach involves a variables-added-in-order test comparing

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \varepsilon \quad 5.14$$

to the reduced model

$$Y = \beta_0 + \beta_1 X + \varepsilon \qquad 5.15$$

Note that this latter test presumes equal slopes, so it is essentially a test for coincidence, assuming parallelism

5.5 Test of Coincidence: Single Model Approach

The hypothesis that the two regression lines are coincident is H_0: $\beta_2 = \beta_3 = 0$. When both β_2 and β_3 are 0, the model for t2, $Y_{t2} = (\beta_0 + \beta_2) + (\beta_1 + \beta_3)X + \varepsilon$, reduces to $Y_{t1} = \beta_0 + \beta_1 X + \varepsilon$ for t1 (i.e., the two lines are coincident). The test of H_0: $\beta_2 = \beta_3 = 0$ is thus a multiple partial F test, since it concerns a subset of regression coefficients. The two models being compared are therefore

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \varepsilon \qquad 5.16$$

and

$$Y = \beta_0 + \beta_1 X + \varepsilon \qquad 5.17$$

The computation from our data:

$$F(XZ, Z|X) = \frac{\frac{[regression\ SS(X,Z,XZ) - regession\ SS(X)]}{2}}{MS\ residual\ (X,Z,XZ)} \qquad 5.18$$

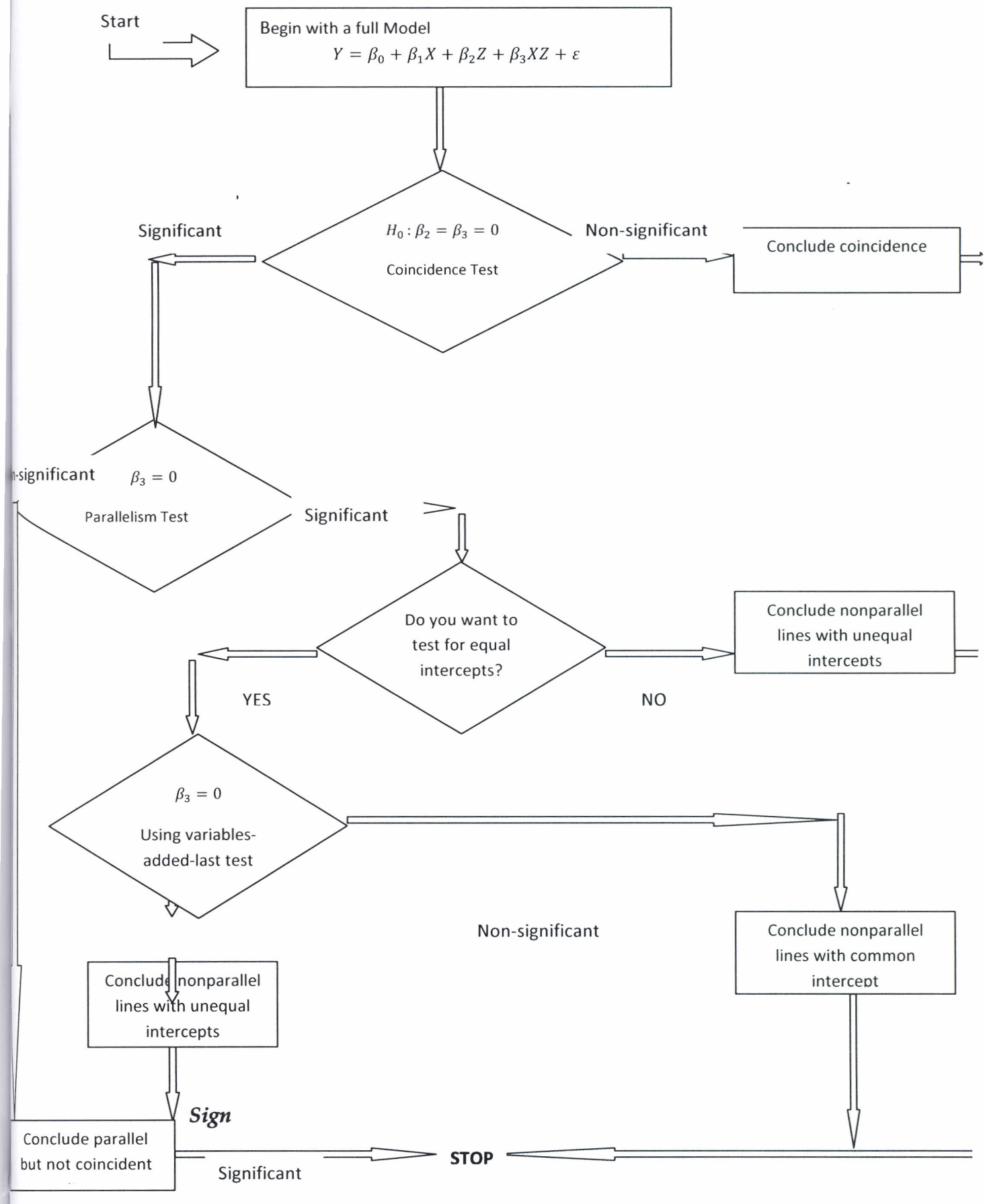
$= 19.1$

Comparing this F with $F_{1,18,0.999} = 7.72$, we reject H_0 with p<0.001 and conclude that there is very strong evidence that the two lines are not coincident. This conclusion contradicts our earlier conclusion using the results from separate tests for equal slopes and equal intercepts.

5.6 Testing strategies and Interpretation: Comparing Two Straight Lines

Several strategies can be used to a best model for comparing two straight lines. Strategies for more general situations can be found in chapter 16 of (David G. Kleinbaum, Lawrence L. Kupper, Keith E. Muller (2007)).

Here we prefer a backward strategy that is, starting with the largest model of interest and then trying to reduce the model through a sequence of hypothesis tests. A flow diagram of this strategy for comparing two straight lines is given below.


Start
Begin with a full Model
$Y = \beta_0 + \beta_1 X + \beta_2 Z + \beta_3 XZ + \varepsilon$
Significant
$H_0 : \beta_2 = \beta_3 = 0$
Coincidence Test
Non-significant
Conclude coincidence
-significant
$\beta_3 = 0$
Parallelism Test
Significant
Do you want to test for equal intercepts?
Conclude nonparallel lines with unequal intercepts
YES
NO
$\beta_3 = 0$
Using variables-added-last test
Non-significant
Conclude nonparallel lines with common intercept
Conclude nonparallel lines with unequal intercepts
Sign
Conclude parallel but not coincident
Significant
STOP

In our case the model to be considered is the model (*) above, which contains X, Z, and XZ as independent variables. To reduce the model, we performed tests for coincidence, then for parallelism and then for equal intercepts;

1. If the test for coincidence is non-significant, we stop further testing and conclude that the best model is

   $Y = \beta_0 + \beta_1 X + \varepsilon$ 5.19

2. If test for coincidence is significant and the test for parallelism is non-significant, then the data argue for parallel but non-coincident lines
3. If the test for coincidence is significant and test for parallelism is significant, then we might not even be interested in the test for equal intercepts; if we are, however, the appropriate test procedure would involve the variables-added-last statistic F(Z | X,XZ), which does not assume parallel lines.

Applying this strategy to the weights data, we would conclude, based on the tests reported above, that the test for coincidence is significant and the test for parallelism is non-significant, so that our overall conclusion is that the best model has the form

$$Y = \beta_0 + \beta_1 X + \beta_2 Z + \varepsilon \qquad 5.20$$

In other words, we assume parallel lines (and non-coincidental) lines.

5.7 CONCLUSIONS AND RECOMMENDATIONS

For us to draw our conclusions it is imperative to glance back at the profile curves in chapter 4 that indicate the calves' performance as a result of the treatment intervention.

These curves show that the weight change caused by the two treatments over time fluctuates around the same regions with weight gain ranging between 1.54 - 2.13 kg for the calves fed exclusively on milk whereas the weight gain of those that were fed on the maize - cowpea gruel ranged between 1.52 kg and 1.9 kg.

The figures stated above almost average around the same neighbourhood. Moreover, the test of hypothesis results indicate that the two treatment means are not significantly different and therefore we can conclude that feeding dairy calves on milk plus maize cow-peas gruel lowers the cost of production without affecting the their growth or performance.

Recommendation

Based on the above conclusion and also looking at the cost benefit analysis carried out in the background information we would therefore recommend the use of maize-cowpea gruel as an alternative feed for dairy calves.

APPENDICES

Appendix 1

Dataset 1: Weekly weights

Calf Id	Z5	Z13	Z15	Z4	Z9	Z7	Z11	Z3	Z14	Z6	Z8	Z10	Z16	Z12	Z17	Z18
Rep	1	2	3	4	5	6	7	8	1	2	3	4	5	6	7	8
Trt_grp	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2
Birth_wt	18	18	18	21.3	19	16.7	23.8	21	12.9	16.5	16	21	24.2	20.9	22.5	20.5
WK1	20	22	21	26.2	31	19.5	26	22	13	19	21	31	26	23	23	23
WK2	22	26	25	28	31	28	30	25	15	21	27	35	29	25	25	26
WK3	23	27	28	32	33	35	33	28	19	22.8	35	35	30	28	28	28
WK4	24.1	27	28	32.2	38	38	35	30	23	25	38	38	32	30	30	29
WK5	27	32	30	34.2	41	38	37	31	25	35	38	42	33	30	31	31
WK6	39	33	34	34.2	45	40	40	35	25	35	38	42	34	32	33	33
WK7	43	35	34	38	46	40	42	38	26	37	40	45	34	38	37	35
WK8	45	46	37	46	47	44	43	41	28	37	43	46	37	40	39	37
WK9	48	43	38	47	49	51	45	42	30	38	45	48	39	42	41	39
WK10	56	46	40	52	50	52	46	44	32	41	49	49	41	45	44	42
WK11	56	48	41	54	52	53	52	46	34	45	50	50	43	47	47	43
WK12	56	49	45	56	54	56	54	49	37	48	51	51	45	48	53	49
WK13	57	52	48	60	59	58	57	52	39	49	52	52	48	50	56	50

WK14	59	53	50	60	59	61	59	56	41	51	53	53	50	52	57	50
WK15	60	55	53	62	60	63	65	66	43	52	55	54	52	54	58	52
WK16	61	57	56	63	62	66	68	66	45	53	56	56	56	54	60	53
WK17	62	59	60	65	65	69	71	70	48	54	58	58	58	58	62	54
WK18	65	61	62	67	66	70	74	75	50	56	59	60	60	60	64	55
WK19	65	65	64	68	68	72	77	77	55	58	60	62	62	63	66	58
WK20	67	67	68	70	70	75	78	80	57	59	63	63	64	65	68	60

Appendix 2

Dataset 2: Weight differences

Calf Id	Z5	Z13	Z15	Z4	Z9	Z7	Z11	Z3	Z14	Z6	Z8	Z10	Z16	Z12	Z17	Z18
REP	1.0	2.0	3.0	4.0	5.0	6.0	7.0	8.0	1.0	2.0	3.0	4.0	5.0	6.0	7.0	8.0
TREAT	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
INTWT	18.0	18.0	18.0	21.3	19.0	16.7	23.8	21.0	12.9	16.5	16.0	21.0	24.2	20.9	22.5	20.5
WTCHNGE	49.0	49.0	50.0	48.7	51.0	58.3	54.2	59.0	44.1	42.5	47.0	42.0	39.8	44.1	45.5	39.5
dw1	1.7	2.2	2.0	2.4	3.6	1.9	1.8	1.5	1.0	1.9	2.4	3.3	1.7	1.8	1.2	1.9
dw2	1.7	2.2	2.2	1.7	1.0	3.1	2.2	2.0	1.7	1.7	2.6	2.2	2.0	1.7	1.7	2.0
dwk3	1.4	1.4	2.0	2.2	1.7	2.8	2.0	1.9	2.2	1.7	3.0	1.0	1.4	2.0	2.0	1.7
dwk4	1.4	1.0	1.0	1.1	2.4	2.0	1.7	1.6	2.2	1.8	2.0	2.0	1.7	1.7	1.7	1.4
dwk5	2.0	2.4	1.7	1.7	2.0	1.0	1.7	1.5	1.7	3.3	1.0	2.2	1.4	1.0	1.4	1.7
dwk6	3.6	1.4	2.2	1.0	2.2	1.7	2.0	2.2	1.0	1.0	1.0	1.0	1.4	1.7	1.7	1.7
dwk7	2.2	1.7	1.0	2.2	1.4	1.0	1.7	2.0	1.4	1.7	1.7	2.0	1.0	2.6	2.2	1.7
dwk8	1.7	1.4	2.0	3.0	1.4	2.2	1.4	1.9	1.7	1.0	2.0	1.4	2.0	1.7	1.7	1.7
dwk9	2.0	2.8	1.4	1.4	1.7	2.8	1.7	1.4	1.7	1.4	1.7	1.7	1.7	1.7	1.7	1.7
dwk10	3.0	2.0	1.7	2.4	1.4	1.4	1.4	1.7	1.7	2.0	2.2	1.4	1.7	2.0	2.0	2.0
dwk11	1.0	1.7	1.4	1.7	1.7	1.4	2.6	1.7	1.7	2.2	1.4	1.4	1.7	1.7	2.0	1.4
dwk12	1.0	1.4	2.2	1.7	1.7	2.0	1.7	2.1	2.0	2.0	1.4	1.4	1.7	1.4	2.6	2.6
dwk13	1.4	2.0	2.0	2.2	2.4	1.7	2.0	1.8	1.7	1.4	1.4	1.4	2.0	1.7	2.0	1.4
dwk14	1.7	1.4	1.7	1.0	1.0	2.0	1.7	2.2	1.7	1.7	1.4	1.4	1.7	1.7	1.4	1.0
dwk15	1.4	1.7	2.0	1.7	1.4	1.7	2.6	3.3	1.7	1.4	1.7	1.4	1.7	1.7	1.4	1.7
dwk16	1.4	1.7	2.0	1.4	1.7	2.0	2.0	1.0	1.7	1.4	1.4	1.7	2.2	1.0	1.7	1.4
dwk17	1.4	1.7	2.2	1.7	2.0	2.0	2.0	2.2	2.0	1.4	1.7	1.7	1.7	2.2	1.7	1.4
dwk18	2.0	1.7	1.7	1.7	1.4	1.4	2.0	2.4	1.7	1.7	1.4	1.7	1.7	1.7	1.7	1.4
dwk19	1.0	2.2	1.7	1.4	1.7	1.7	2.0	1.7	2.4	1.7	1.4	1.7	1.7	2.0	1.7	2.0

Appendix 3

Dataset 3: Transformed weight differences

int wt	wtchange	t1	t2	t3	t4	t5	t6	t7	t8	t9	t10	t11	t12	t13	t14	t15	t16	t17	t18	t19
18	49	1.7	1.7	1.4	1.4	2.0	3.6	2.2	1.7	2.0	3.0	1.0	1.0	1.4	1.7	1.4	1.4	1.4	2.0	1.0
18	49	2.2	2.2	1.4	1.0	2.4	1.4	1.7	1.4	2.8	2.0	1.7	1.4	2.0	1.4	1.7	1.7	1.7	1.7	2.2
18	50	2.0	2.2	2.0	1.0	1.7	2.2	1.0	2.0	1.4	1.7	1.4	2.2	2.0	1.7	2.0	2.0	2.2	1.7	1.7
21.3	48.7	2.4	1.7	2.2	1.1	1.7	1.0	2.2	3.0	1.4	2.4	1.7	1.7	2.2	1.0	1.7	1.4	1.7	1.7	1.4
19	51	3.6	1.0	1.7	2.4	2.0	2.2	1.4	1.4	1.7	1.4	1.7	1.7	2.4	1.0	1.4	1.7	2.0	1.4	1.7
16.7	58.3	1.9	3.1	2.8	2.0	1.0	1.7	1.0	2.2	2.8	1.4	1.4	2.0	1.7	2.0	1.7	2.0	2.0	1.4	1.7
23.8	54.2	1.8	2.2	2.0	1.7	1.7	2.0	1.7	1.4	1.7	1.4	2.6	1.7	2.0	1.7	2.6	2.0	2.0	2.0	2.0
21	59	1.5	2.0	1.9	1.6	1.5	2.2	2.0	1.9	1.4	1.7	1.7	2.1	1.8	2.2	3.3	1.0	2.2	2.4	1.7
12.9	44.1	1.0	1.7	2.2	2.2	1.7	1.0	1.4	1.7	1.7	1.7	1.7	2.0	1.7	1.7	1.7	1.7	2.0	1.7	2.4
16.5	42.5	1.9	1.7	1.7	1.8	3.3	1.0	1.7	1.0	1.4	2.0	2.2	2.0	1.4	1.7	1.4	1.4	1.4	1.7	1.7
16	47	2.4	2.6	3.0	2.0	1.0	1.0	1.7	2.0	1.7	2.2	1.4	1.4	1.4	1.4	1.7	1.4	1.7	1.4	1.4
21	42	3.3	2.2	1.0	2.0	2.2	1.0	2.0	1.4	1.7	1.4	1.4	1.4	1.4	1.4	1.4	1.7	1.7	1.7	1.7
24.2	39.8	1.7	2.0	1.4	1.7	1.4	1.4	1.0	2.0	1.7	1.7	1.7	1.7	2.0	1.7	1.7	2.2	1.7	1.7	1.7
20.9	44.1	1.8	1.7	2.0	1.7	1.0	1.7	2.6	1.7	1.7	2.0	1.7	1.4	1.7	1.7	1.7	1.0	2.2	1.7	2.0
22.	45.5	1.	1.	2.	1.	1.	1.	2.	1.	1.	2.	2.	2.	2.	1.	1.	1.	1.	1.	1.

5		2	7	0	7	4	7	2	7	7	0	0	6	0	4	4	7	7	7	7
20.5	39.5	1.9	2.0	1.7	1.4	1.7	1.7	1.7	1.7	1.7	2.0	1.4	2.6	1.4	1.0	1.7	1.4	1.4	1.4	2.0

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