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FACULTY OF SCIENCE AND TECHNOLOGY
Department of Applied Mathematics and Statistics

RESEARCH TOPIC

Morphological characterization of autochthonous sheep breeds at
Matopos Research Station : A Markov Chain Monte Carlo
Algorithm Approach.

BY

CHIPINDU LOVEMORE

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GWERU,ZIMBABWE

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SUPERVISOR : MR M. DAMBAZA

MIDLANDS STATE UNIVERSITY
FACULTY OF SCIENCE AND TECHNOLOGY
DEPARTMENT OF APPLIED MATHEMATICS AND STATISTICS

APPROVAL FORM

The undersigned certify that they have supervised ,read and recommended the Midlands State University to accept a research project entitled , **Morphological characterization of autochthonous sheep breeds at Matopos Research Station : A Markov Chain Monte Carlo Algorithm Approach** by Chipindu Lovemore submitted in partial fulfillment of the Bachelor of Science in Applied Statistics Honours Degree at the Midlands State University.

STUDENT..... DATE

SUPERVISOR..... DATE

CHAIRPERSON..... DATE

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Abstract

Failure to characterize autochthonous sheep breeds may result to the extinction of the important natural resource which can easily adapt to the local variation in climate change. Environmental factors and some human practices especially artificial insemination is leading to the evolving of different pedigrees. Price determination is an important aspect in designing pricing models, but what really contributes to the weight of autochthonous sheep breed remains as the major question which needs to be addressed. By merely looking at a sheep is it possible to deduce its body weight another question of interest arises again. This project addressed several issues associated with the characterization of autochthonous sheep by establishing the relationship between morphological traits and the body weight of an animal. The relationship was further addressed through the application of several methods namely the principal component analysis, generalized linear models, WinBugs model programming and the Markov Chain Monte Carlo Algorithm Approach. The major reason behind this project was to come up with conducive way which saves resource limited farmers of sheep in being charged exorbitant prices in trying to use the more advanced technology such as (DNA) in characterizing indigenous sheep.

Acknowledgments

"If there were no God , it would have been necessary to invent him" (Francois Marie Arouet)

First, i would like to thank the Almighty God, may his name be exalted and hallowed above all.It was not an easy road but the God in the Mountain remained also the God in the valley, he remained by my side whispering the words" go as far as you can see when you get there you will be able to see more". Special mention goes to Mr G.Sisito (Biometrician) and the Matopos Research Station staff, during my work related learning they made me to redefine the word success as being able to do more especially to those who depend on you. In brief i am what i am because of them.

My father H. Chipindu does not deserve my appreciation or acknowledgment as his son but the Lord Almighty will reward him, he made my dream to come true. The Musoko family deserves also a special mention their input to my academic achievement was superb.

Obviously the whole story can be concluded by appreciating the encouragement i got from my academic supervisor Mr M.Dambaza,may the Lord continue to hover over him and his family.

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1 CHAPTER ONE

1.1 INTRODUCTION

1.2 Background Of The Study

Over the years sheep production has been one of the major means of transforming rural livelihoods especially of resource limited livestock keepers, in order to reduce poverty and attaining sustainable agriculture and universal food security . The relative contribution of livestock to agricultural gross domestic product (GDP) is higher in developed regions but the trend has been slightly downwards over the past 30 years, whereas in most developing regions, there has been a rise in the importance of livestock (FAO, 2011).The characterization of livestock resources is usually meant to serve the purpose of developing conservation and utilization programs. Characterization of Farm Animal Genetic Resources[FAGR] encompasses all activities associated with the identification , quantitative and qualitative description and documentation of breed population characteristics and natural habitats and production system to which they are or not adapted. Besides the classification , morphological characters together with geographical distributions there is need also to physically identify, describe, and recognize a distinct animal genetically.

Constituents of morphological characterization involve collecting a number of different kinds of data which include the following according to Commission of Genetic Resource For Food and Agriculture, 2011: (The draft guidelines

on phenotypic characterization of animal genetic resources)

- the breeds geographical distribution and if possible their population sizes and structures;
- the breeds phenotypic characteristics,, including physical features and appearance, economic traits (e.g. growth, reproduction and product yield/quality) and some measures (e.g. range) of variation in these traits the focus is generally on the productive and adaptive attributes of the breeds;
- images of typical adult males and females, as well as herds or flocks in their typical production environments;
- information on the breeds origin and development;
- any known functional and genetic relationships with other breeds within or outside the country;
- biophysical and management environment(s) in which the breeds are maintained;
- responses of the breeds to environmental stressors, such as disease and parasite challenge, extremes of climate and poor feed quality, and any other special characteristics of the population in terms of adaptation; and

- relevant indigenous knowledge (including but not limited to gender specific knowledge) of traditional management strategies used by communities to utilize the genetic diversity in their livestock.

While most of these data elements can be collected directly during field work as shown,

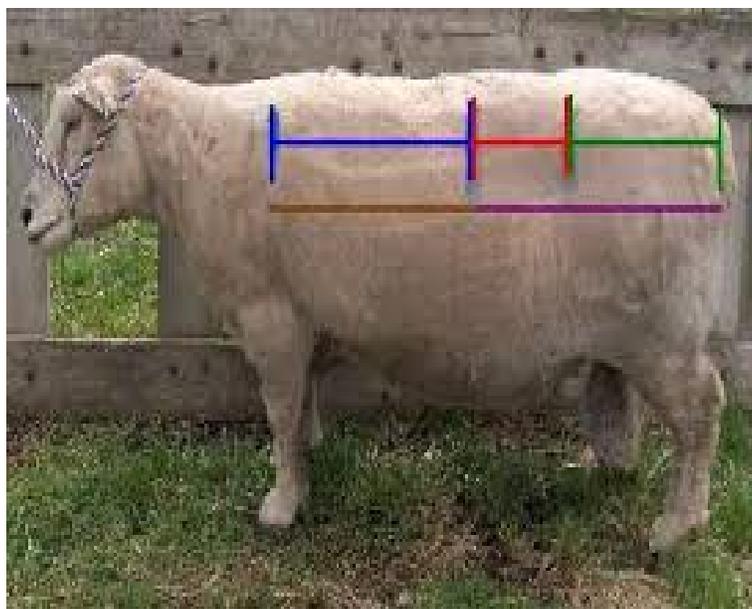


Figure 1: Morphological traits measurements.

valuable information may also be obtained from secondary sources in the published and unpublished literature (including electronic datasets related to aspects of the production environment). In this study the data pertaining to morphological traits was extracted from secondary sources that is the indigenous register for sheep at Matopos Research Station. Genetic resources conservation especially of indigenous breeds is one of the key aspects in

addressing climate change negative impact on livestock and this is one of the major role of organizations like European Association of Animal Production (EAAP) and African Union. The documentation of existing genetic resources, including the description of the population phenotypic characteristics, cultural importance and genetic uniqueness is one of the main areas of the livestock conservation activities (Ducher and Groeneveld, 2005).

Within the livestock industry small ruminants(eg. goats and sheep) represent a very important national resource. Sheep are reared primarily for meat, skin as well as hair and play a significant socio-economic roles in the lives of resource limited farmers, rural dwellers and commercial farmers as well. Indigenous sheep are important and adaptable domesticated animals which need to be conserved as different pedigrees of sheep are now evolving due to climate change and other factors. In order to characterize the indigenous sheep the association between the body weight and other morphological traits must be utilized.Body weight is considered to be the major parameter of interest in different pricing policies and models of sheep. Body measurements can also be used in weight estimation and commercial selection programmes based on its utility in determining breed evolution trends (Araujo et al.; 2006). The body weight of sheep is used for mating decisions, pricing, health assessment, the effectiveness of a certain feed or diet.

There is need to adopt more practical and reliable characterization approaches to assist in the development of sound management and pricing policies. To handle more complex scenarios in characterizing the autochthonous sheep

breeds the Markov Chain Monte Carlo (MCMC) algorithm can be implemented utilizing the relationship between weight and other morphological traits.

1.3 Problem statement

The variation in gene pool and influence of varied climatic condition have given rise to different local population of sheep which are preservation of unique genes that should be conserved for local and international future benefits (Adebambo, 2004). The general resource limited farmers always find it difficult to adopt advanced technological approaches such as biopolymer of deoxyribonucleic acid tests (DNA) in the characterization of indigenous sheep as it is associated with exorbitant prices, which they can not afford. The failure to characterize the local breed of sheep has accordingly been recognized as neglecting the sustainable use of animal genetic resource which will lead to some extent unreasonable economic indicators and pricing models.

1.4 Justification of the problem statement

Phenotypic variation present in a population of sheep arises due to genotypic and environmental effects and the magnitude of phenotypic variability differs under different environmental conditions (M Okpeku et al), therefore the purpose of this study is to objectively describe the linear type traits of extensively managed mature indigenous sheep at Matopos Research Station and to predict body weight from their orthogonal shape characteristic. Efforts

have been made in differentiating morphometric of sheep breeds but restricted to the use of analysis of variance which to a certain extent may fail to handle complex situations or scenarios, therefore the application of the Markov Chain Monte Carlo (MCMC) algorithm which the system and traces its convergence to a target distribution.

1.5 Research Questions

- How does the characterization of autochthonous sheep breeds according to their morphological traits facilitate to proper management principles or policies?
- How best can sheep pricing be modeled and what could be some major parameters to be considered by farmers and key actors in the industry?
- Considering the association /relationship between the body weight of sheep and its morphological characteristics, how can this be utilized in explaining sheep pricing models.
- How best can the Markov Chain Monte Carlo algorithm (MCMC) approach be implemented in explaining the relationship between weight and morphological traits and in predicting weight from morphological characteristics?

1.6 Aim of the study

The study aims to design a tool to aid management decisions of indigenous sheep breeds for commercial purposes and breeding programs utilizing the genetic resource.

1.7 Objectives

- To determine the linear type traits of extensively managed mature autochthonous sheep breeds at Matopos Research Station.
- To determine the major morphological variables to be taken into consideration by farmers and key actors in the industry when designing sheep pricing models.
- To verify and validate the relationship between body weight and morphological traits using the Markov Chain Monte Carlo (MCMC) algorithm.

1.8 Research Hypothesis

- There is an association between the body weight of sheep and its morphological traits.
- The morphetric differentiation of indigenous sheep breeds can be used to deduce the best explanatory parameters of sheep pricing models.
- The relationship involving body weight and morphological traits may be different when orthogonal conformation traits derived from the MCMC

algorithm are used instead of the inter-correlated original morphological variables.

1.9 Assumption

The sex (male or female) and generational differences of sheep does not have an impact on the morphological characterization.

1.10 Delimitation

The study will be based on Matopos Research Institution only as it is the biggest livestock research institution in Zimbabwe located in the semi-arid regions. This is because it has the mandate to carry out researches and disseminate the findings to its stakeholders (general public, farmers, academic institutions, non-governmental organizations and etc).

1.11 Significance of the study

The findings of this study will redound to the benefit of stakeholders of Matopos Research Institution especially resource limited and commercial farmers who are or who want to venture into sheep production. Correct characterization of indigenous sheep breeds will lead to the formulation of sound conservative measures and pricing policies of our own native land breeds. This will enhance the contribution of sheep to the Gross Domestic Products (GDP) of the country within the livestock sector and reasonable

economic indicators.

1.12 Definition of terms

1. Morphological characterization - is a scientific study of form and structure without regard to function in order to depict something in a particular way.
2. Autochthonous breeds - these are indigenous breeds adaptable to native land climatic and environmental conditions.
3. Phenotypic variations - is any observable characteristic of an organism such as its morphological, developmental, biochemical or physiological properties or behavior.
4. Markov Chain Monte Carlo Algorithm - is simply a tool for estimating model parameters that has been proven to be effective for handling complex problems.

2 CHAPTER TWO

LITERATURE REVIEW

2.1 Introduction

This chapter consists of an evaluation report of information found in the literature related to this study area. The review will describe, summarize, evaluate and clarify the related literature that is autochthonous sheep breeds in Zimbabwe, morphological characterization of breeds, markov chain idea, monte carlo principle and markov chain monte carlo algorithm approach . It will give a theoretical base for the research and help to determine the nature of the research.

2.2 Autochthonous Sheep Breeds In Zimbabwe

The term autochthonous is thus contradictory since it refers to creatures originating in the place where found. Wherever these animals came from, there must have been considerable dynamism in their emergence and modifications under the pressures of various natural and cultural environments (University of Edinburgh, 2001). In addition to documentary and iconographic sources, the ancient history of domesticates is studied on the basis of the direct evidence of their bones. Archaeozoology is the identification, analysis and scientific as well as socio-cultural interpretation of animal remains from

archaeological sites. According to *ZimFieldGuide.com* for Livestock, Cultural and Wildlife information for Zimbabwe, the history and origin of the sabi/save sheep breeds in Zimbabwe can be traced back to the Rozvi people who first lived along the Save river and trading with the Arabs.



Figure 2: Save River

The figure above shows the picture of Save River where the Rozvi people first lived practicing their agriculture especially the rearing of Sabi sheep.

2.2.1 Distribution of the Sabi sheep

The exact and pure distribution of the Sabi sheep breed in Zimbabwe is not clearly known. However, populations of the breed are found and scattered mainly in the dry areas of the country, such as Binga, Sabi valley and Gokwe. Some of the sheep have been crossbred and are no longer true to the original Sabi type and have been continually infused with Blackhead Persian blood as reported by Matika et al. (2003). According to Sikosana (pers. comm.),



Figure 1: sabi



Figure 2: sabi

the only known pure breed Sabi population is at Matopos Research Institute which has approximately 300 breeding ewes (nucleus) as well as at Makoholi and Henderson Research Institutes. The nucleus and main flock at Matopos has been closed since the original flock which was established at the then Makoholi Experiment Station in 1951. The foundation stock was reportedly obtained from two main sources, Gokwe in North-west Zimbabwe and the Sabi River valley in South-western Zimbabwe. The status of the breed elsewhere in Zimbabwe is not accurately known or recorded. . The small flocks established at Makoholi and Henderson Research Institutes represent a strategic reserve for the conservation of this important sheep breed.

The breed is threatened with extinction. According to the Country Report on the State of the *World Animal Genetic Resources* published in 2004, The Sabi / Save sheep is the most common indigenous sheep in Zimbabwe. Sabi sheep are found throughout Zimbabwe, particularly in the communal

areas. It is fat-tailed with a hairy coat. Save sheep range in colour from black through all shades of brown to pure white. Their ears can be very small- almost non- existent in some cases in certain families, and quite big in others. They have a wide, swinging fat – tail which would seem to function as a food reserve for periods of nutritional stress. Save sheep are small in size and are relatively slow growing. However, Save sheep are hardly and fecund under adverse conditions and, in addition, they are resistant to most of the local diseases.

The importance of sheep varies between regions and ethnic groups. While farmers in most parts of the country rear sheep primarily for meat production, some ethnic groups keep sheep mainly for socio-cultural purposes. In an effort to conserve the indigenous Sabi breed, nucleus flocks are maintained on government research stations and the University of Zimbabwe.

2.2.2 Sabi Characteristics and Physical Traits

The Sabi sheep breed offers Zimbabwe and the Southern African region an opportunity to benefit from its unique and outstanding qualities as an adapted indigenous breed. Indeed the trans boundary nature of the Sabi which is also found in parts of Zambia, Botswana and South Africa provides Southern Africa with a breed that can withstand the elements and vagaries of climate change and considered a breed for the future (Donkin D. J. 2000). The important characteristics and physical traits of Sabi sheep in Zimbabwe can be best summarized by the table below according to Matopos Journal

for Indigenous breeds 2001:

Physical Trait	Description
Coat colour:	Multi-color (white, brown, tan, combinations)
Coat description:	Hair
Hair type:	Straight
Hair length:	Short, Long
Face profile:	Convex, Flat
Muzzle color:	Pigmented, (not pigmented in young)
Throat ruff:	Absent
Toggles:	Absent
Horns:	Present, polled
Horns (number):	2
Horn shape:	Spiral, Curved
Horn length:	Medium to Long
Horn orientation:	Backwards, drooping
Ear size:	Medium to Large
Ear orientation:	Drooping
Body frame:	Medium to large
Back profile:	Straight
Rump profile:	Sloping
Legs:	Long
Hoof colour:	Dark, Striped
Tail length:	Long
Tail thickness:	Fat, Fat-rumped

Table 1: Breed characteristics and physical traits

2.3 Morphological Characterization Of Breeds

The term “morphological characterization” in this study is used to refer to the process of identifying distinct breed populations and describing their

physical characteristics in relation to weight and those of their production environments. In this context, the term “production environment” is taken to include not only the “natural” environment but also management practices and the common uses to which the animals are put, as well as social and economic factors such as market orientation, niche and marketing opportunities.

The geographical distribution of breed populations is here considered to be an integral part of morphological characterization. Complementary procedures used to unravel the genetic basis of the phenotypes of breeds, their patterns of inheritance from one generation to the next, and to establish relationships between breeds are referred to as molecular genetic characterization (FAO, 2010b). Phenotypic and molecular genetic characterization of breeds are used to measure and describe genetic diversity in these resources as a basis for understanding them and utilizing them sustainably. The guidelines distinguish between two phases or levels of characterization. The term “primary characterization” is used to refer to activities that can be carried out in a single visit to the field (e.g. measurement of animals’ morphological features, interviews with livestock keepers, observation and measurement of some aspects of the production environment, mapping of geographical distribution) (Capote et al., 1998; Dossa et al., 2007; Herrera et al;1996; Jordana et al;1993; Zaitoun et al., 2005). The term “advanced characterization” is used to describe activities that require repeated visits. These include the measurement of productive (e.g. growth rate, milk production) and adaptive (e.g. resistance or tolerance to specific diseases) capacities of breeds in specified production

environments(Duchev and Groeneveld, 2006; Duchev et al; 2006).However, multivariate analysis on morphological traits are rarely reported in sheep (Riva et al;2004).

The breed characterization can be best categorized into two major groups, quantitative and qualitative traits description. Qualitative traits can be recorded either as discrete categories of expression (e.g. color of hair or feathers) or binary variables (e.g. presence or absence of wattles). Collection, management and analysis of data on qualitative traits are therefore different from the equivalent procedures for quantitative traits. Quantitative traits are measures of the size and dimension of animals' bodies or body parts and are more directly correlated to production traits than qualitative traits are. For instance, body weight and chest girth are directly related to body size and associated production traits. Typically, these variables have a continuous expression.

2.3.1 WinBUGS Software Model Programming



WinBUGS implements various MCMC algorithms to generate simulated observations from the posterior distribution of the unknown quantities (parameters or nodes) in the statistical model (I Ntzoufras, 2011).The idea is that with

sufficiently many simulated observations, it is possible to get an accurate picture of the distribution.

WinBUGS analysis — model specification, data, initial values, and output is contained in a single compound document. Analytic tools are available as pull down menus and dialog boxes. Data files are entered as lists (or can be embedded as sub documents). Output is listed in a separate window but can be embedded in the compound document to help maintain a paper trail of the analysis. Any part of the compound document can be folded out of sight to make the document easier to work with. Data can be expressed in list structures or as rectangular tables in plain text format; however, WinBUGS cannot read data from an external file.

2.4 Markov Chain Idea

Markov chains are a relatively simple but very interesting and useful class of random processes. A Markov chain describes a system whose state changes over time. The changes are not completely predictable, but rather are governed by probability distributions. These probability distributions incorporate a simple sort of dependence structure, where the conditional distribution of future states of the system, given some information about past states, depends only on the most recent piece of information (Jim Albert;2011). That is, what matters in predicting the future of the system is its present state, and not the path by which the system got to its present state. Markov chains illustrate many of the important ideas of stochastic processes in an

elementary setting. This classical subject is still very much alive, with important developments in both theory and applications coming at an accelerating pace in recent decades. Mathematically a Markov Chain can be defined as a sequence $(X_1, X_2, X_3, \dots, X_n)$ of random variables that has the “Markov property”.

2.5 Monte Carlo Methods

Credit for inventing the Monte Carlo method often goes to Stanislaw Ulam, a Polish born mathematician who worked for John von Neumann on the United States Manhattan Project during World War II [N. Metropolis and S. Ulam. 1949.].He invented the Monte Carlo method in 1946 while pondering the probabilities of winning a card game of solitaire.

Monte Carlo methods are a broad class of computational algorithms that rely on repeated random sampling to obtain numerical results(Jim Albert;2011). Their essential idea is using randomness to solve problems that might be deterministic in principle.In general terms, the Monte Carlo method (or Monte Carlo simulation) can be used to describe any technique that approximates solutions to quantitative problems through statistical sampling.Monte Carlo simulation is more specifically used to describe a method for propagating (translating) uncertainties in model inputs into uncertainties in model outputs (results) (C Andrieu, 2003) . Hence, it is a type of simulation that explicitly and quantitatively represents uncertainties. Monte Carlo simulation relies on the process of explicitly representing uncertainties by specifying inputs as

probability distributions. If the inputs describing a system are uncertain, the prediction of future performance is necessarily uncertain. That is, the result of any analysis based on inputs represented by probability distributions is itself a probability distribution.

2.6 Markov Chain Monte Carlo Algorithm Approach

In statistics, Markov chain Monte Carlo (MCMC) methods are a class of algorithms for sampling from a probability distribution based on constructing a Markov chain that has the desired distribution as its equilibrium distribution (A Doucet and M Jordan; 2003). The state of the chain after a number of steps is then used as a sample of the desired distribution. The quality of the sample improves as a function of the number of steps. In Bayesian statistics, the recent development of MCMC methods has been a key step in making it possible to compute large hierarchical models that require integrations over hundreds or even thousands of unknown parameters (S. Richardson D.J. Spiegelhalter; 200). They are also used for generating samples that gradually populate the rare failure region in rare event sampling. MCMC methods are primarily used for calculating numerical approximations of multi-dimensional integrals, for example in Bayesian statistics, computational physics, computational biology and computational linguistics. Markov Chain Monte Carlo Algorithm Approach can be achieved by incorporating the Gibbs and Metropolis Hastings algorithms.

2.7 Conclusion

It is evident from the related literature that the Markov Chain and Monte Carlo integration can be implemented in simulating and estimation of parameters in complex models. Since the characterization of autochthonous sheep breeds basing on the relationship between weight and other measurable physical characteristics involves a pool of random variables with different parameters that needs to be estimated, the Markov Chain Monte Carlo Algorithm can be used. A chain of morphological random variables is created which is markovian and simulated using the Monte Carlo approach.

3 CHAPTER THREE

RESEARCH METHODOLOGY

3.1 Introduction

This chapter will address approaches and methods that were used to answer the objectives. Model development and formulation is the major focus of this section. The following procedures are going to be discussed; general description of the study site, data collection procedures, morphological variables measured, how the principal component analysis was used to justify variables in model building, model development, Win-Bugs model formulation, Markov Chain Monte Carlo Algorithm and model validation and verification.

3.2 Study Site

The study was carried out at Matopos Research Institute. Matopos Research Institute is the biggest livestock research institution located in the semi arid areas of Zimbabwe that is in Matebeleland South Province. The Institution is government owned and its major agricultural activity is livestock production and agricultural related scientific researches to assist its stockholders.

Matopos Research Station is situated 30 kilometers south of Bulawayo on the boarder of the Rhodes Matobo National Park. It is situated at longitude 28°30'E, latitude 20°23' at altitude of 1340m above sea level. It is one of the largest four Livestock Research Institutes in the Department of Research and

Specialist Services (DRSS) under the Ministry of Agriculture, Mechanization and Irrigation Development (AMID). The work of the station is primarily extensive and semi- extensive land use in an environment where rainfall is particularly variable. Research is directed towards developing technologies for sustainable livestock production, within a semi-arid environment, using rangeland and other feedstuffs. The Institute seeks to establish facts that will allow increased efficiency and output in livestock production to provide basis for sound policies with respect to land use and agricultural administration.

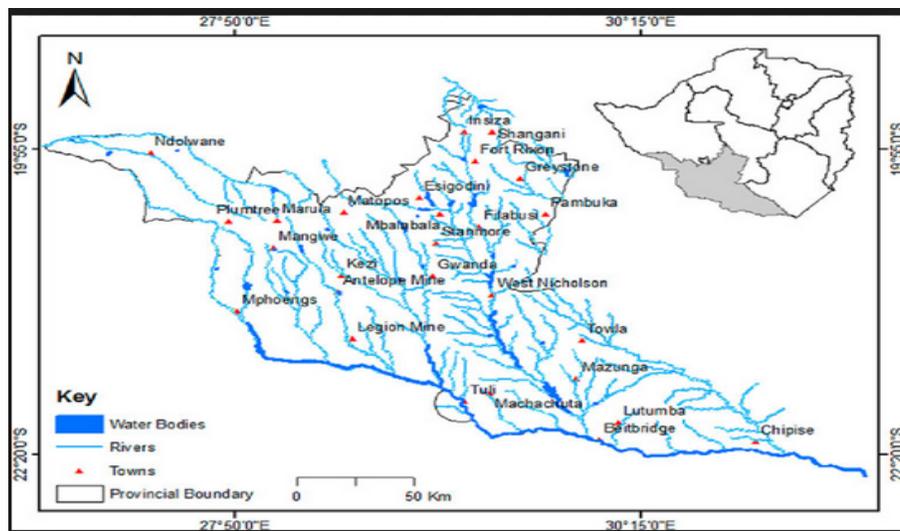


Figure 5 : The geographical location map of Matopos.

The geographical map above shows the location of Matopos in Matebeland South. In the area rainfall is highly variable and on average the annual is about 600mm between October and April. The area experiences temperatures from 20.9 to 29.4 degrees Celsius in October.

3.3 Sampling Method and Data Collection Procedure

The population of mature indigenous sheep at Matopos is Eighty five comprising of 50 males and 30 females. For the purposes of research , experimental accuracy and academic purposes only 25 sheep were randomly selected irregardless of their generational differences and sex. The animals should be 24 months old as determined by dentition as described by Wilson and Durkin (1999). A simple random sample was implemented to select a sample of 25 sheep and their morphological traits were measured. The sampling procedure was carried out basing on the registration numbers of sheep. The identification of which sheep to be included in the sample was determined by the tag registration number randomly selected. Kaiser-Meyer-Olkin measure of sampling adequacy was used to justify the sample size with the given classification below.

Variable	Classification	Comment
1	0.00-0.49	unacceptable
2	0.50-0.59	miserable
3	0.60-0.69	mediocre
4	0.70-0.79	middling
5	0.80-0.89	meritorious
6	0.90-1.00	marvelous

Table 2: The Kaiser-Meyer-Olkin measure of sampling adequacy

3.4 Morphological Variables Measured

The morphological traits measured were; Body weight[BW] , Withers length[WL], Rump height[RH], Face length[FL], Shoulder width [SW], Rump length[RL], Tail length[TL], Chest circumference[CC], Head width[HW], Rump width[RW], Height at withers[HW] , Body length[BL] .The weight measurement(cm) was done using a graduated measuring stick. Animals were placed on a flat ground and held by two field assistants in order to achieve this. The length and circumference measurements (cm) were effected using a tape rule while the width measurements (cm) were taken using a calibrated wooden caliper. Measurements are were taken before the animals were released for grazing .To avoid inter-individual variations and bias all measurements were carried out by the same person.

3.5 Model Development/Formulation

The general linear model was considered to be the best to describe the relationship between the body weight of indigenous sheep and its morphological traits. The model is given by the formula:

$$\mathbf{Y} = \boldsymbol{\beta}\mathbf{X} + \boldsymbol{\epsilon}.$$

where :

\mathbf{Y} is a column vector of body weight.

$\boldsymbol{\epsilon}$ is a column vector of random error terms.

$\boldsymbol{\beta}$ is a vector of parameters; $\boldsymbol{\beta} = [\beta_0, \beta_1, \beta_2 + \dots + \beta_n]^T$.

\mathbf{X} is a vector of morphological traits.

3.5.1 Principal Component Analysis.

The morphological traits were measured on objects with similar characteristics and as a result multicollinearity was present in the data which lead to redundancy of traits which could be possibly important in terms explaining the relationship . In order to resolve this the researcher opted to use the principal component analysis for variable selection. By definition the principal component is a reduction tool that can be used to reduce a large set of variables into a small set that still contains most of the information in large set. According to [4] it is a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated

variables. First the principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability. The advantages of this multivariate procedure can be summarized as follows:

- identify how different variables work together to create the dynamics of the system.
- reduce the dimensionality of the data.
- decrease redundancy in the data.
- filter some of the noise in the data.
- compress the data.
- prepare the data for further analysis using other techniques.

3.5.2 WinBugs Software Model Programming



The final model was programmed using the Bugs language as it is a powerful software for Bayesian and Markov Chain Monte Carlo methods. This enables the researcher to use the R2WinBugs package in R for model

simulation and parameter estimation as this package accommodates the Bugs language for further analysis. R2WinBUGS package provides possibility to call a BUGS model, summarize inferences and convergence in a table and graph, and save the simulations in arrays for easy access in R / S-PLUS. The listed procedures below were followed in WinBugs:

- checking the model if it is syntactically correct.
- loading the data in vector form.
- specifying the number of Markov Chain Monte Chains.
- model compilation.
- loading initial values.
- generating burn-in value.
- defining and specifying parameters to be monitored.
- performing the sampling to generate posteriors.
- checking convergence and displaying of results.

3.6 Markov Chain Monte Carlo Algorithm

There are basically two conceptually distinct parts in Markov chain Monte Carlo (MCMC) that is a sampler is designed for simulating a Markov Chain and then an estimator is constructed on the Markov chain for computing

integrals of interest. The major focus of its application in this research is finding good sampling algorithm, diagnosing convergence in MCMC and making good inferences given a good model. Basically they are two major approaches to MCMC algorithm the Gibbs sampling, where the chain has a joint stationary distribution and Metropolis-Hastings sampling but the researcher used the hybrid approach that is the combination of the two.

Let $m(x)$ be a nonnegative function on a state space χ and its integral $W = \int m(x) d\mu_0$ is analytically intractable with respect to a baseline measure μ_0 . A Markov Chain Monte Carlo algorithm can be applied to simulate a Markov chain (x_1, \dots, x_n) converging to the probability distribution with density

$$p(x) = \frac{m(x)}{W},$$

without requiring the value of its normalizing constant W . Then a common approach is that, if n is sufficiently large, these points are used as an approximate and dependent sample from the distribution $p(x)$ for Monte Carlo integration.

3.6.1 The Markov Chain Monte Carlo (MCMC) idea

Markov Chain Monte Carlo algorithm provides a manageable route by which to obtain estimates of parameters for the distribution. It is a stochastic procedure that repeatedly generates random samples that characterize the distribution of parameters of interest. The process of generating the random samples is the role of the Markov Chain and that of generating summary

statistics from random samples is the role of Monte Carlo. Design a Markov Chain on finite state space:

$$\text{state space : } x^{(i)} \in \{x_1, x_2, \dots, x_s\}$$

$$\text{Markov property : } p(x^{(i)} | x^{(i-1)}, \dots, x^{(1)}) = T(x^{(i)} | x^{(i-1)})$$

Such that when simulating a trajectory of states from it, it will explore the state space spending more time in the most important regions (i.e. where $p(x)$ is large) and defined as follows:

3.6.2 The Monte Carlo principle

Let $p(x)$ be a target density defined over a high-dimensional space (e.g. the space of all possible configurations of morphological traits under study). The idea of Monte Carlo techniques is to draw a set of (*iid*) samples x_1, \dots, x_N from p in order to approximate p with the empirical distribution:

$$I(f) = \int f(x) p(x) dx \approx \frac{1}{N} \sum_{i=1}^N f(x^{(i)}) \xrightarrow{N \rightarrow \infty} I(f)$$

Using these samples we can approximate integrals $I(f)$ (or v large sums) with tractable sums that converge (as the number of samples grows) to $I(f)$

and $I(f)$ is given by :

$$I(f) = \int f(x) p(x) dx \approx \frac{1}{N} \sum_{i=1}^N f(x^{(i)}) \xrightarrow{N \rightarrow \infty} I(f)$$

The MCMC process is summarized below :

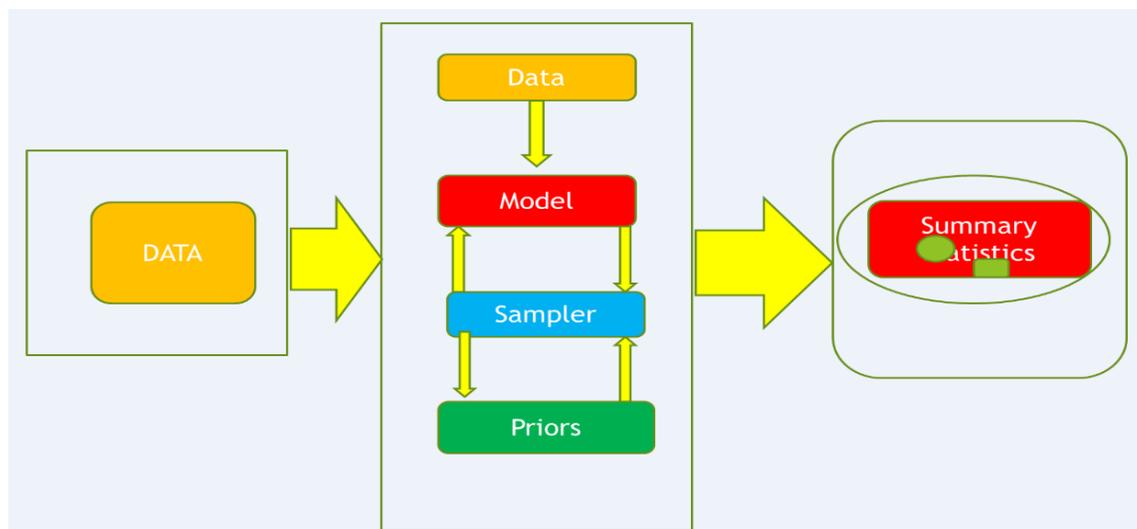


Figure 6: The Markov Chain Monte Carlo Algorithm Process.

The morphological traits data was used for model development. The model was simulated in order to produce random samples and priors and finally the summary statistics were obtained from the process.

3.7 Model Validation and Verification.

The other vital statistical procedures that were considered and implemented by the researcher model validation and verification. The Markov Chain Monte Carlo algorithm provides a convenient way of validating and verifying the model; as the model should converge to a target distribution.

Verification is like debugging—it is intended to ensure that the model does what it is intended to do. Models, especially simulation models, are often large computer programs. Therefore all techniques that can help develop, debug or maintain large computer programs are also useful for models. Listed below are some of the verification procedures that the MCMC algorithm can do:

- Continuity testing.
- Degeneracy testing to see if it works for extreme values.
- Seed independency (simulation only).
- Animation (simulation only).
- Deterministic model (simulation only).
- Tracing (simulation only).

Validation is the task of demonstrating that the model is a reasonable representation of the actual system: that it reproduces system behavior with enough fidelity to satisfy analysis objectives. For most models there are three separate

aspects which should be considered during model validation: assumptions, input parameter values and distributions and output values and conclusions. In MCMC algorithm the following are the validation procedure that are available:

- Expert intuition.
- Real system measurement.
- Theoretical results /measurements.

The procedure of model verification and validation can be best summarized by the diagram below:

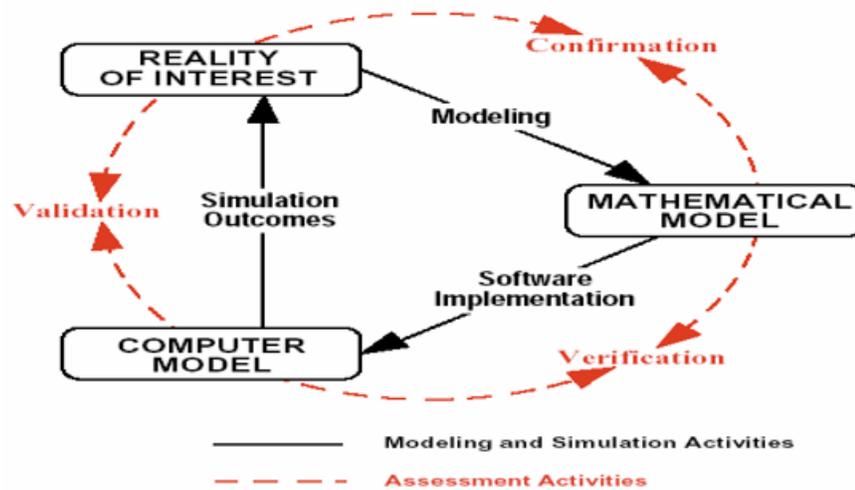


Figure 7 :The Conceptual Frame Work Of Modeling and Simulation Activities.

4 CHAPTER FOUR

DATA PRESENTATION AND RESULTS ANALYSIS

4.1 Introduction

The previous chapter discussed the methodology that the researcher used in morphological characterization of autochthonous breeds. In this chapter results and data obtained from the research are presented and analyzed. The results are based on the data obtained from the data base of autochthonous sheep at Matopos Research Institution.

WinBugs and R softwares were employed to come up with results from the gathered data. The results displayed in this chapter were valid and relevant interpretations are made. This chapter deals with the results from the Principal Component, WinBugs programmed model and Markov Chain Monte Carlo Algorithm in R (R2WinBugs MCMC package).

4.2 Results from the Principal Component Analysis

The summary statistics of morphological traits calculated include the mean, median, maximum, minimum, first quartile range and the third quartile range. The figure below shows the summary statistics of the measured morphological traits.

Body.weight	chest.circumference	Heart.girth	Body.length		
Min. :13.11	Min. :12.50	Min. :20.00	Min. :46.50		
1st Qu.:16.50	1st Qu.:16.00	1st Qu.:23.00	1st Qu.:48.50		
Median :17.78	Median :18.00	Median :24.00	Median :52.50		
Mean :18.56	Mean :18.74	Mean :23.86	Mean :52.38		
3rd Qu.:20.83	3rd Qu.:21.00	3rd Qu.:25.50	3rd Qu.:55.00		
Max. :25.44	Max. :25.50	Max. :27.00	Max. :62.00		
tail. Circumference	Height of withers	Leg length	rump.width	rump.height	
Min. :17.00	Min. :51.00	Min. :16.00	Min. :23.00	Min. :17.00	
1st Qu.:26.00	1st Qu.:56.00	1st Qu.:18.00	1st Qu.:24.00	1st Qu.:19.00	
Median :28.00	Median :57.00	Median :19.00	Median :24.50	Median :22.10	
Mean :27.86	Mean :57.28	Mean :19.32	Mean :24.74	Mean :21.53	
3rd Qu.:30.00	3rd Qu.:60.00	3rd Qu.:20.00	3rd Qu.:25.50	3rd Qu.:23.20	
Max. :34.00	Max. :65.00	Max. :29.00	Max. :27.00	Max. :26.50	
face.length	shoulder.width				
Min. :12.00	Min. :14.70				
1st Qu.:14.00	1st Qu.:19.50				
Median :16.40	Median :22.00				
Mean :16.82	Mean :21.03				
3rd Qu.:19.00	3rd Qu.:23.00				
Max. :22.00	Max. :25.00				

Table 3: Summary Statistics

4.2.1 Sampling Adequacy

Variable	kmo
Bodyweight	0.7755
chestcircum-e	0.7899
Heartgirth	0.7643
Bodylength	0.7722
tailCircum-e	0.3004
Heightofwi~s	0.7579
Leglength	0.8496
rumpwidth	0.8082
rumpheight	0.7447
facelength	0.8693
shoulderwi~h	0.5106
Overall	0.7555

Table 4: The Kaiser-Meyer-Olkin measure of sampling adequacy

The leg length, rump width and face length KMO values are between (0.80-0.89) classified as meritorious whilst the rest of the variable are in the middling class that is within the range (0.70-0.79). The overall KMO (Kaiser-Meyer-Olkin) value

falls in the range(0.70-0.79) which is classified as middling.

4.2.2 The correlation matrix

	Bodywe-t	chestc-e	Heartg-h	Bodyle-h	tailCi-e	Height-s	Leglen-h	rumpwi-h	rumphe-t	facele-h	should-h
Bodyweight	1.0000										
chestcircu-e	0.9692	1.0000									
Heartgirth	0.6181	0.5745	1.0000								
Bodylength	0.7082	0.7070	0.4025	1.0000							
tailCircum-e	-0.0265	0.0604	-0.1683	-0.0744	1.0000						
Heightofwi-s	0.6398	0.6705	0.4453	0.5633	0.5379	1.0000					
Leglength	0.4847	0.5043	0.3497	0.5796	0.1042	0.5523	1.0000				
rumpwidth	0.8071	0.7866	0.4898	0.6098	0.1420	0.7128	0.4085	1.0000			
rumpheight	0.3455	0.3644	0.0111	0.2186	0.1403	0.2801	0.0224	0.4828	1.0000		
facelength	-0.6202	-0.6450	-0.4375	-0.5416	0.0471	-0.4120	-0.4608	-0.3976	-0.2889	1.0000	
shoulderwi-h	0.2446	0.2858	0.0272	-0.0230	0.2071	0.2962	0.1469	0.4739	0.3977	-0.1187	1.0000

Table 5: Correlation Matrix

The table above shows the Correlation Matrix of the morphological traits. This was used as a technique to assess the relationship between the variables to be incorporated into the final model. Most of the variables in the data set were positively correlated as the measurements were taken on sheep with similar characteristics. The procedure created a platform for the application of principal component analysis to reduce the dimensionality of the data collected.

4.2.3 Principal Component analysis Loadings

Loadings:					
	PC1	PC2	PC3	PC4	PC5
Body.weight	0.928	-0.139	-0.134		0.114
chest.circumference	0.936				
Heart.girth	0.627	-0.409		0.491	0.198
Body.length	0.777	-0.301		-0.305	
tail. circumference	0.136	0.719	0.598		0.202
Height of withers	0.804	0.293	0.407		0.135
Leg length	0.641	-0.155	0.418	-0.101	-0.528
rump.width	0.867	0.213	-0.157	0.169	
rump.height	0.427	0.490	-0.532	-0.390	0.158
face.length	-0.692	0.238		0.321	0.157
shoulder.width	0.349	0.639	-0.328	0.336	-0.462
	PC1	PC2	PC3	PC4	PC5
SS loadings	5.343	1.660	1.156	0.755	0.670
Proportion var	0.486	0.151	0.105	0.069	0.061
Cumulative var	0.486	0.637	0.742	0.810	0.871

Table 6:Principal Component Loadings

The table above shows the the principal component loadings for each and every morphological trait from component one to component 5.Only 5 components were considered, as the highest proportion of variability is contained in them. According to the principal component rule variables with the highest loadings must be considered in the model. Body weight, chest circumference,heart girth,body length,height of withers,leg length and rump with have highest loadings as indicated in the table. These variables were used in building a model taking the body weight as a dependent variable.

4.3 The Final model

The generalized linear model was suggested by the researcher to model the relationship between body weight and other morphological traits. The results from the principal component analysis were used to build the model with the exact traits that registers the highest principal component loadings. The output from R programming software is shown below:

```
Call:
glm(formula = Body.weight ~ chest.circumference + Heart.girth +
  Body.length + `Height of withers` + rump.width + `Leg length`,
  data = morpho)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5491 -0.3805  0.1027  0.4067  1.2338

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -5.705949   4.854792  -1.175  0.0005***
chest. Circumference|  0.756352   0.090973   8.314 1.41e-07 ***
Heart.girth    0.163409   0.112055   1.458  0.002**
Body.length    0.037706   0.060363   0.625  0.0040 **
`Height of withers` -0.075998   0.075470  -1.007  0.00027***
rump.width     0.352845   0.229657   1.536  0.0012***
`Leg length`   -0.008037   0.085241  -0.094  0.0026**
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.5951177)

    Null deviance: 228.766  on 24  degrees of freedom
Residual deviance:  10.712  on 18  degrees of freedom
AIC: 65.759

Number of Fisher Scoring iterations: 2
```

Table 7: Final Model

From the R output all the morphological traits suggested by the principal component analysis were significant as their p-values were less than 0.05. The generalized linear model that describes the relationship was as follows:

$$\begin{aligned} \text{Body.weight} = & -5.705949 + 0.756352\text{chest.circumference} + \\ & 0.163409\text{heart.girth} + 0.0337706\text{body.lengt} - 0.075998\text{heartofwithers} + \\ & 0.352845\text{rump.width} - 0.008037\text{leg.length} \end{aligned}$$

4.4 WinBugs Programmed Model

The final model above was programmed using the WinBugs software which also supports R programming language. The major reason for this was to accommodate the application of the Markov Chain Monte Carlo Algorithm in simulating the model and estimation of parameters. All the morphological traits were normally distributed and the prior distribution was defined in relation to this important aspect. The parameters were also defined in the model programming to allow a simple approach of assessing and investigating their behavior as the sample size increases. The syntax for the model is shown in the figure below:

```

## Morphological Characterisation Model.
model{
  for(i in 1:morpho){
    y[i]~dnorm(mu[i],tau)
    mu[i]<-beta0+beta1*chest.circumference+beta2*Heart.girth+
      beta3*Shoulder.width+beta4*Tail.circumference+Rumb.width
  }
  ## prior distribution
  beta0~dnorm(0.0,1.0E-4)
  beta1~dnorm(0.0,1.0E-4)
  beta2~dnorm(0.0,1.0E-4)
  beta3~dnorm(0.0,1.0E-4)
  beta4~dnorm(0.0,1.0E-4)
  beta5~dnorm(0.0,1.0E-4)
  tau~dgamma(0.01,0.01)
}

##Data and initial value specification
##units
list(beta0=0,beta1=0,beta3=0,beta4=0,beta5=0,tau=1)

##DATA
list((n=25,
      Body.weight=c(),
      chest.circumference=c(),
      Heart.girth=c(),
      Shoulder.width=c(),
      Tail.circumference=c(),
      Rumb.width=c()))

```

Figure 8: WinBugs programmed Model

4.5 Results from the Markov Chain Monte Carlo Algorithm

Application of the Markov Chain Monte Carlo Algorithm to the final programmed model in WinBugs yielded the results below. The algorithm usually retains the parameters as nodes, mean, standard deviation, median, Monte Carlo error and the sample size..

node	mean	sd	MC error	2.50%	median	97.50%	start	sample
beta_0	106.6	3.625	0.03477	99.32	106.6	113.6	1001	10000
beta_1	618.5	0.1068	0.01354	597.9	6.184	639.8	1001	10000
beta_2	608.2	0.4714	0.07308	524.8	6.052	709.3	1001	10000
beta_3	536.7	0.08526	0.01663	426	0.6016	755.4	1001	10000
beta_4	548.9	0.08526	0.01663	244.7	0.3984	574.1	1001	10000
beta_5	376.8	0.9265	0.02124	535	536.7	538.6	1001	10000
beta_6	536.7	0.256	0.0314	546.3	548.9	551.2	1001	10000

Table 8 : A 1000 update burn in followed by a further 10000 updates gave the parameter estimates

From the results above the point of interest is the MC error, they are supposed to be approximately equal to zero as we simulate the model. The results were based on 1000 update burn in followed by a further 10000 iteration or updates. Monte Carlo errors were maintained at approximately equal to zero. This ensures how accurate and efficient the approach is. As we increase the number of iterations the model estimates must converge to a target distribution. If the Monte Carlo errors remains at zero then there is assurance that the estimated statistics will converge to the distribution of interest.

In this project the researcher decided to use the high breed approach to Markov Chain Monte Carlo Algorithm that is the combination of the Gibbs and Metropolis Hastings Algorithms. The table below shows the results of the comparison of estimators of $\log Z$.

	$n = 500$		$n = 1000$		$n = 2500$		$n = 5000$	
	Chib	Lik	Chib	Lik	Chib	Lik	Chib	Lik
Time Ratio	<.01	2.2	<.01	3.5	<.01	7.8	<.01	15.8
Bias	-.0042	-.013	-.0024	-.0063	-.00093	-.0025	-.00082	-.0012
Std Dev	.113	.0108	.0807	.00459	.0513	.00167	.0363	.000803
Sqrt MSE	.113	.0167	.0807	.00777	.0513	.00299	.0363	.00148
Approx Err	NA	.0124	NA	.00607	NA	.00244	NA	.00125

Table 9: Comparison of estimators of $\log Z$.

The results in the table are based on R programming language through the use of R2WinBugs package designed to support the Bugs language in R. The distributions are normally distributed and during the 5000 simulations the Gibbs sampler is started at (0,0) and run for n iterations. The Chib's estimator and the likelihood estimator $\log Z$ are compared in the above table. For n=5000, the mean square error of the likelihood estimator is smaller as compared to that of the Chib's estimator by a factor of $(0.0363/0.001480)^2$, but the total computational time of the likelihood estimator is 16.8 times as large as compared to that of the Chib's estimator. The absolute bias and standard deviation of the likelihood estimator appear to decrease at n^{-1} rate. Relative to the standard deviation the bias becomes appreciable.

4.6 Model Validation and Verification Results

4.6.1 Convergence for Markov Chain Monte Carlo

As a way of validating and verifying the results from the Markov Chain Monte Carlo, it must converge to a target distribution. In this case the target distribution was the normal. The figure below shows the parameter estimates as the sample size increases from zero to 1000.

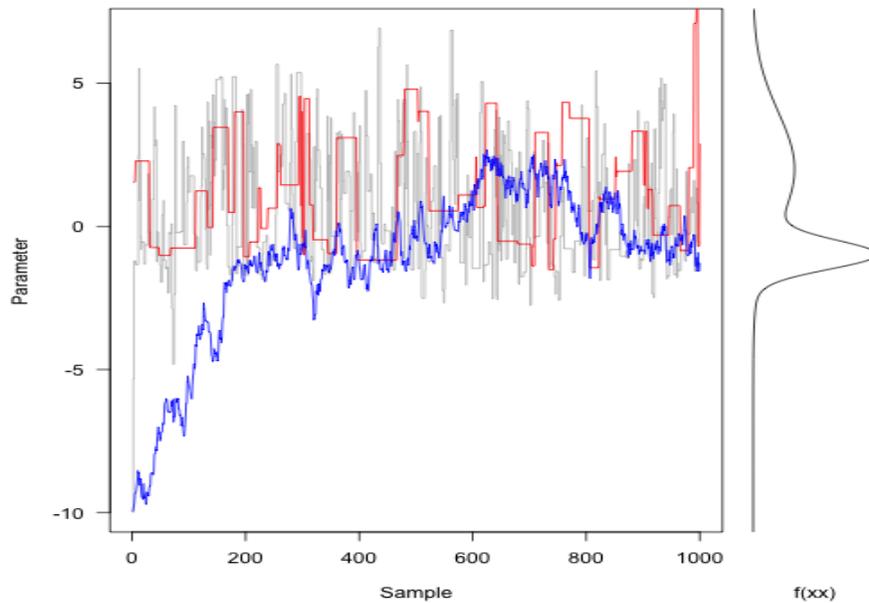


Figure 9 : Parameter estimation plots as the sample increases to 1000.

As we increase the sample size the degree of precision is reached. The sample size was increased to 1000 and all the estimates of parameters were given and tend to follow a particular pattern as the sample increases. The approach does not begin with the precision but the precision is achieved as we increase the sample size.

The diagram below show the behavior of the dependent variable y at different iterations . As the iteration increases the behavior of y is expected to follow a constant pattern.

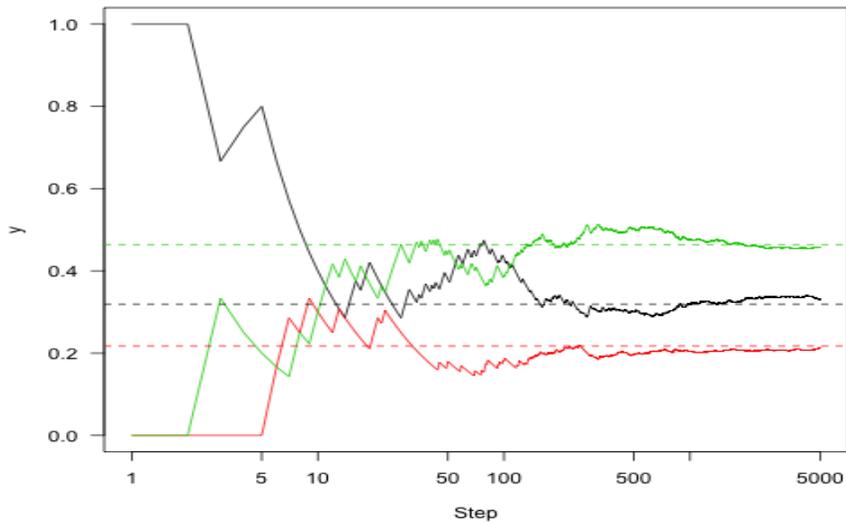


Figure 10: Behavior of y at different iterations.

It can be noted that as the iterations increases then the estimated values of y tend to follow a certain pattern. This is a clear indication that they will obviously converge to a target distribution.

Since the target distribution is normal then the cumulative mean(s) must converge to zero as we continue to increase the iterations. The figure below shows the behavior of the cumulative mean as the iterations were extended to 10000.

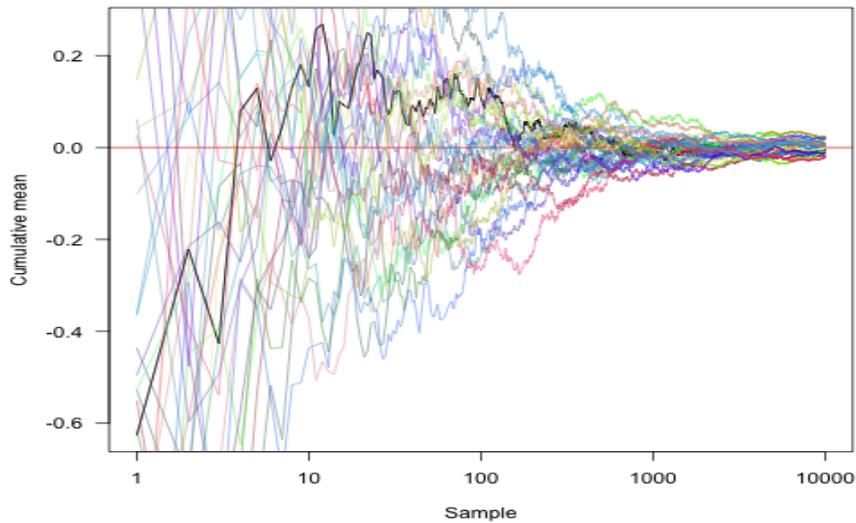


Figure 11: Convergence of the cumulative mean as the iterations extended to 10000.

If the target distribution is normal then the cumulative mean is supposed to converge to zero. The figure above shows that as the iterations reaches the range (1000-10000) then it automatically converges to zero. This implies that the process is successful and can be implemented without doubt.

As a confirmation approach the diagram below was plotted considering the y values and the x values.

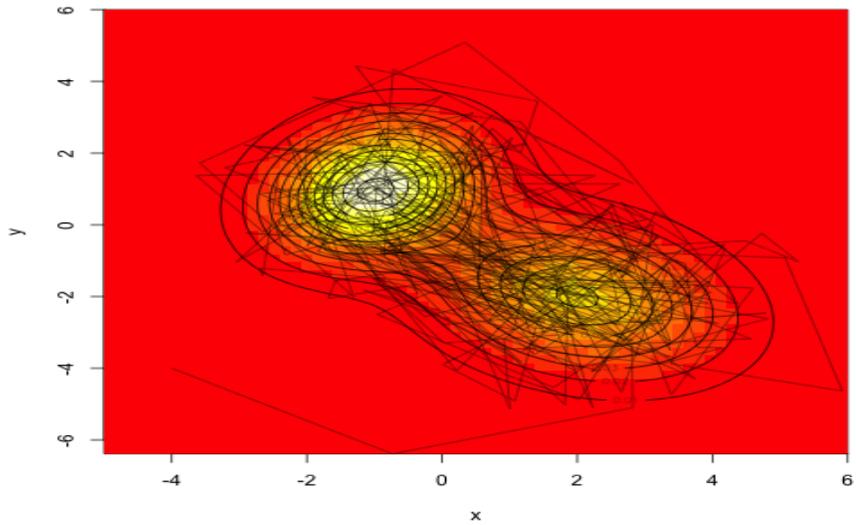


Figure 12: Convergence of the y and x to zero.

All the other points are scattered around zero confirming that the distribution can accurately identified as the normal distribution.

5 CHAPTER FIVE

5.1 CONCLUSION AND RECOMMENDATIONS

5.1.1 Conclusion

The linear type traits of extensively managed mature autochthonous sheep breeds at Matopos Research Station were identified to be Body weight [BW], Height at withers [HW], Rump height [RH], Body length [BL], Face Length [FL], Shoulder width [SW], Rump length [RL], Tail length [TL], Chest circumference [CC], Leg length [L.L] and Rump Width [RW].

Out of all the above mentioned morphological traits the body weight was best explained by Height at withers [HW], Chest circumference [CC], Rump Width [RW], Height at withers [HW], Leg length [L.L] and Heart girth. The relationship was confirmed by the principal component analysis and the generalized linear model.

WinBugs model programming facilitate to proper and convenient way of implementing the Markov Chain Monte Carlo Algorithm in simulating the model and estimation of parameters.

Implementing the Markov Chain Monte Carlo Algorithm all the morphological traits parameter estimates converges to a target distribution.

As we increase the sample size then the greater the precision of estimates that best characterize the autochthonous sheep breeds.

5.1.2 Recommendations

The recommendations are directed to the stakeholders of Matopos Research Station specifically to those resource limited farmers who are into sheep production. Resource limited farmers and all those who are actively involved in sheep production need to consider the previously mentioned morphological traits when designing sheep pricing models, in order. The major component to consider when pricing sheep is its weight but the question addressed in the research is what really contributes to the weight of the animal. This obviously will be facilitated to the convenient way and cheaper method of physically identifying the morphological traits in relation to its weight without the application of expensive approaches.

To reduce high costs associated with advanced technological approaches such as the (biopolymer of deoxyribonucleic acid) DNA test, those actively involved in sheep production need to consider the morphological characterization. The approach can really work as it was tested and verified through the application of the Markov Chain Monte Carlo Algorithm.

Correct characterization of autochthonous sheep breed will enhance the contribution of livestock to the Gross Domestic Product (GDP). Autochthonous sheep breeds can easily adapt to local climatic changes.

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