

**KWAME NKRUMAH UNIVERSITY OF SCIENCE AND
TECHNOLOGY**



**Morphological characterisation of breeds of sheep: A discriminant
analysis approach**

By

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Declaration

I hereby declare that this submission is my own work towards the award of the M. Phil degree and that, to the best of my knowledge, it contains no material previously published by another person nor material which had been accepted for the award of any other degree of the university, except where due acknowledgement had been made in the text.

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Dedication

To my wife Elizabeth Agyarko and children

KNUST



Abstract

In this study the characterisation and separation or discrimination of three sheep breeds (crosses, West African Dwarfs (WAD) and West African Long Legged (WALL) based on their physical traits (morphological characterisation) was investigated extensively with the application of discriminant analysis. The study's main objective was specifically based on developing a variable selection criterion that can discriminate best among the three sheep breeds as well as obtain a reliable mathematical function or equation (discriminant function) for provision of maximum separation among the three known sheep breeds. Data from College of Education, Mampong animal farms on various breeds of sheep (hybrid/crossed breed, Sahell or WALL and Djallonke or WAD) were used. Factor Analysis was employed as a variable selection criterion for selecting six sheep traits that can discriminate best among the sheep breeds. Canonical discriminant function was derived for the eight variable data set and was compared with the derived Quadratic Discriminant Functions (QDF) using the six extracted sheep traits. The six variable QDF distance classifier provided maximum separation after cross validation than the 8-variable canonical discriminant functions. The derived mathematical functions (QDFs) were able to provide maximum separation among the three known sheep breeds with a correct classification rate of 0.86. The study recommended the use of a Quadratic Discriminant Function for discrimination and classification of breeds of animal since it gives more accurate results than other classifiers such as Linear Discriminant Function.

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Chapter 1

INTRODUCTION

The assignment or allocation of individuals or observations to the various known groups with their respective mean vectors and distinguishing characteristics has been a major concern for years and research is ongoing to obtain the best function to ensure maximum separation. This study considered the separation or classification of sheep into their respective groups (cross breed, hybrid and local breed (WAD)) based on their measured physical characteristics by using two classification functions and the evaluation of the performance of the classification functions using several error estimators. This chapter takes a look at the background of the study, the statement of the problem, research questions and objectives, research methodology, justification of the study as well as the organisation of the study.

1.1 Background of the Study

Characterization of animal genetic resource (AnGR) encompasses all activities associated with the identification, quantitative and qualitative description of breed populations and the natural habitat and production systems to which they are or not adapted. Thousands of farm animal breeds have been developed over millennia to thrive in specific locations. Today, many countries are losing these genetic resources which are critical for both food security and sustainable development. The Food and Agricultural Organisation (FAO) report estimates that, industrial livestock operations are growing twice as fast as traditional mixed farming systems and six times as fast as traditional grazing systems. As a result, only a limited number of species and breeds now provide most of the world's livestock products, (FAO,2007) . Domestication of livestock by man introduced a

major cultural revolution. Hominids and early man were hunters and gatherers for millions of years. The climatic fluctuations which followed the end of the glacial period some 14000 years ago may have been instrumental in forcing man to domesticate animals. Records of the domestication of sheep dates back as early as 700 BC in the Near East.

The population bureau, 2011 has the world's population figure to be over 6 billion and that of Ghana to be 24.23 million (Ghana Statistical Board, 2011). Since this figure increases on daily basis, the quantity of food and other products must increase. Not only should diversity be maintained for practical purposes, but also for cultural reasons. A community's domestic animals can enhance the environment as a living system, thus also enhancing the humans inhabitant's quality of life. One of the areas being exploited to help remedy this situation is ruminant production enterprise. Small ruminant production is now exploited on a large scale because they do not compete with humans for cereals instead they depend solely on grasses, legumes and forbs which abound in Ghana. The three northern regions of Ghana, constituting about 47 percent of the total land area are of vast natural grassland comprising Sudan and guinea savanna which creates suitable environment for cattle, goat and more importantly sheep (Alhassan and Barnes, 1993) and also holds about 74 percent of the total livestock population. African sheep breeds migrated with various nations from Asia, Arabia and the Middle East into North Africa. Epstein (1971) stated that a number of nomadic black and coloured tribes inhabited North Africa many years ago. A tsetse fly breakout stretching along the equator across the whole of Africa restricted these nations from migrating southwards. According to archaeological records. Sheep migrated to the cape as recently as 2000 years ago Sheep seem to have received the least attention in all aspect of management, nutrition breeding and health in spite of the fact that they have many merits over some other classes of livestock and are found in all towns and villages in Ghana. (Koney, 2004). In Ghana sheep

are often seem to roam about to fend for themselves during the day in many rural areas with animals from different households mixing together of unknown records. Normally, sheep meant for breeding purposes are selected based on good farm records, proper health conditions, performance of ancestors and aesthetic traits. It is pertinent to house sheep to enhance means of measuring heritable differences among them so that farmers can select animals that can pass on superior characteristics to subsequent generations. Indigenous and locally developed sheep breeds are an important asset for many reasons, but particularly because, overtime, they have developed unique combinations of adaptive traits such as; tolerance or resistance to various diseases, tolerance to fluctuations in availability and quality of feed resources and water supply, adaptation to low capacity management conditions.

1.2 Statement of the Problem

The problem of statistical discrimination involving three multivariate normal distributions with known or unknown population centroids and with equal (or unequal) covariance matrices has been considered by many researchers. Some other researchers have applied the concept of discriminant analysis which also serve as a classificatory rule in allocating observations or objects into their known groups. Researchers including Fisher (1936), Lachenbruch (1975), Krzanowski(1997), Desu and Geisser (1973) have used discriminant analysis extensively in various fields where mostly linear discriminant function (LDF) was the main classification function obtained for classifying the known observations. Other researchers such as (Asamoah-Boaheng et al, (2014)) and (B. Xu et al,(2011)) used Quadratic discriminant Function (QDF) as well as the comparison of LDF and QDF. Notwithstanding these enormous application of discriminant analysis in health, education, social sciences, humanities, not much extensive work has been focused on the application of discriminant analysis in classifying

or separating breeds of sheep. Also most of the classification procedures normally keep silence on the variable selection criterion. In as much as it has limited application in the agriculture sector, the application of certain classifications methods including Euclidean Distance Function (EDF) are yet to be used to provide maximum separation among the various breeds of sheep.

1.3 Objectives of the study

The main objective of the study is to develop a mathematical algorithm for discriminating/separating the three breeds of sheep based on certain measured anthropometric characteristics.

1.3.1 Specific objectives

1. To perform variable selection criterion for discriminating best among the three known breeds of sheep.
2. To obtain discriminant functions for providing maximum separation among the breeds of sheep.

1.4 Methodology

The study was based on classifying breeds of sheep by employing discriminant analysis approach in developing a mathematical equation/function in providing maximum separation. Data from College of Education, Mampong animal farms on various breeds of sheep (hybrid/crossed breed, Sahell/WALL and Djallonke/WAD) was used. The data was composed of nine (9) anthropometric characteristics of a total of 61 sheep including their weight(Wt), height (Ht), Length

(Lgth), Ear length, TL-Lgt, CHST, HK LGTH, HK LTH-T LTH and age. Factor Analysis with the application of Principal Component Analysis (PCA) method was used as the main method for variable selection and six (6) variables were selected from the nine (9) variables. Discriminant analysis was employed after the variable selection criterion was used to select the variables that will provide maximum separation among the various breeds of sheep. Discriminant functions as well as classification rules for the 9 variables as well as the six (6) extracted variables were obtained and compared based on their misclassified observations.

1.4.1 Data

Secondary data based on nine anthropometric characteristics of three breeds of sheep was used for the study.

1.4.2 Analytical software used

R console version 2.15.1 as well as STATA version 12 were the main statistical analytical software's employed in analysing the data.

1.5 Justification of Work

This study will contribute immensely to knowledge since equal mean discrimination is one of the interesting aspects of discriminant analysis. The study would therefore provide the needed statistical evidence to justify the best classification rule based on the derived discriminant functions.

Chapter 2

LITERATURE REVIEW

This section presents reviews of existing literature of the various breeds of sheep in and around Ghana, the application of discriminant analysis in separating known groups of animals and some summary of abstract relating to the study.

2.1 Sheep farming in Ghana

Ghana's agriculture is predominantly smallholder, traditional and rain fed. About 136000 km^2 of land covering approximately 57% of the country's total land area of 238539 km^2 is classified as agricultural land area out of which 58000 km^2 (24.4 percent) is under cultivation and 11000 hectares (hc) under irrigation. About 60 percent of all farms in the country are less than 1.2 hc, 25 percent are between 1.2-2.0 hc with a mere 15 percent above 2.0 hc and the mean farm size is less than 1.6 hc (Oppong-Anane, 2006). Although the majority of rural household keep some sort of livestock, livestock farming is adjunct to crop farming. Poultry predominate in the South while cattle production is concentrated in the Savanna Zones. Livestock production is a major feature in Ghana's agriculture and contributes largely towards meeting food needs, providing drought power, manure to maintain soil fertility and structure and cash income, particularly for farmers in the northern part of the country (Oppong-Anane, 2006).

The ruminant industry is composed largely of small scale enterprises in the rearing of cattle, sheep and goat. Sheep production is generally widespread in the country (MOFA, 1998). Their distribution in Ghana remains universal. Production was formerly restricted to the Savanna Zones of Northern Ghana and the Coastal Grassland area of Southern Ghana. The Northern sector holds greater percentage of the National (Koney, 2004). The high population pressure, increasing urbanization, deepening land fragmentation, erratic rainfall distribution and increasing need for food and meat to feed the growing

population put the nation in perpetual need to adjust the food security equation (FAO,1995). As a result, livestock development has seen appreciable improvement providing farmers with an opportunity to diversify and add value.

2.1.1 Sheep breeds in Ghana

FAO, (2007) defined a breed as either a homogeneous, sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species, or a homogeneous group for which geographical separation from phenotypically similar groups has led to general acceptance of its separate entity. The requirement for effective management for conservation at the country level for each species includes identifying and listing the breeds. Furthermore, their description and characterization is important to understand their unique qualities and their potential contributions.

2.1.2 The West African Dwarf Sheep (Djallonke)

The West African Dwarf Sheep also known as Djallonke inhabit the area South of latitude 14°N including the Coastal area of West and Central Africa of which Ghana is inclusive (Ngere,1973). They are generally white coloured although usually spotted with black or red colours. Tan with black belly is also common. They have a wither height of 40-60 cm and a body weight of 20-30 kg; these measurement indicate their characteristics small size, Domestic Animal Genetic Resource Information System. The horns of rams are crescent shaped with angular cross sections; the ewes are polled or have tiny scars. The eyes are large, their backs is straight; their tails is fairly thick at the root growing thinner till it terminates at the hock. The Djallonke sheep are known for their adaptation to the tropical hot and humid environment of West Africa and considered tolerant to typanosomiasis infection. The population for Djallonke is estimated at 1.8 million

in Ghana (Domestic Animal Diversity- Information System (DAD-IS)). The Djallonke sheep are used for meat. They have good reproductive capacity: age at first lambing is 18.8 months and lambing interval of 10 months. Average litter size is 1.22 kids, ranging from 1.0 -1.7 kids depending on variety. The average lambing interval from literature report is 257.95 days ranging from 191-344 days. Birth weight ranging from 1.04 kg -1.64 kg was reported in Nigeria and 1.06 kg - 1.4 kg in Ghana by Wilson (1991). Tuah et al. (1999) reported birth weight ranging between 1.5 kg and 2.1 kg depending on dam's nutrition level in Ghana.

2.1.3 Sahelian breed of sheep

This breed, which is also known as the West African Long- Legged (WALL) is found throughout the Sahel and Savanna zones of Tropical Africa. In Senegal, Niger basin, Chad and Cameroon, they are tall and meaty. The matured ram of this breed has the height of 75-85 cm at withers and weighs between 40 kg and 70 kg while the ewes weigh 30.41 kg (Williamson and Payne, 1987). The Sahelian sheep is good meat animal and three main types are recognized in Nigeria (Combs, 1981). They are the Uda, Yankasa and Belami. Many variations of the local sheep belong to the Fulani breed including the Uda (most numerous), Yankasa, ornu and fellata. The Uda types are mostly found in the Northern part of West Africa. They have short hair and a convex face. Their ears are long and pendulous. They are generally white in colour from the tail to the middle of the body, then either brown or black from this point to the head. Uda are tall, standing about 65 cm at the shoulders (Withers) and weigh about 40 kg. The Yankasa have short head, a short neck and non-pendulous ears. They are white in colour with black patches on the face especially around the eye (Abbey et al., 2008).

2.2 Definition of characterization

Characterization of Animal Genetic Resource (AnGR) encompasses all activities associated with the identification, quantitative and qualitative description of

breed populations and the natural habitat and production systems to which they are or not adapted (Rege, 1992). Characterization means the distillation of all knowledge which contributes to the reliable prediction of genetic performance of an animal genetic resource in a defined environment and provides a basis for the distinguishing between AnGR and for assessing available diversity. Characterization thus includes a clear definition of the genetic attributes of an animal genetic resource and the environment to which it is adapted or known to be partially or not adapted to at all. It should include the population size of the animal genetic resource, its physical description, adaptation, uses, prevalent breeding systems, population trends, predominant production systems, description of environment in which it is predominantly found, indication of performance level (growth, reproduction, meat etc.), genetic parameters of the performance traits and information in genetic distinctiveness of the animal genetic resources in the species (FAO, 2007). Characterization must be presented and undertaken in a broader context of utilization. A thorough review of, and synthesis of data from the (conventional and grey) literature should be a first step in any breed characterization work (Barker, 1992).

2.2.1 Types of characterization

Phenotypic characterization

This includes such characteristics as presence and absence of horns, coat colour, body length, withers height, heart girth, tail length, fur type (wool versus hair) etc. Some of these (e.g. Presence or absence of horn) have simple Mendelian inheritance and have been studied extensively at least in temperate livestock. Others such as height at withers, heart girth and body length are obviously quantitative in nature. Physical characteristics are arguably the most commonly used criteria for breed or strain definitions. For this reason attempts have been made to use these traits in classifying hitherto uncharacterized population. One

of such example is multivariate analysis of physical characteristics, International Committee for Animal Recording (ICAR, 2000). Farm Africa (1996) reported workings in which various measurements both qualitative (e.g. Presence or absence of beard, wattle, ruff etc.) and quantitative (e.g. height, body length, chest girth etc.) were subjected to multivariate analysis to classify heterogeneous, previously unclassified indigenous Ethiopian goats population into taxonomically distinct, relatively similar entities or groups.

Morphological characterization

Morphological characterization entails the description and documentation of the physical traits of a breed. The first step of the characterization of local genetic resource is based on the knowledge of variation in the morphological traits (Delgado et al., 2001). Multifactorial analysis of morphological traits has been proved to be suitable in assessing the variation within a population and can discriminate different population types when all measured morphological variables are considered simultaneously. These kinds of studies are commonly reported in goats (Dossa et al., 2007). However multivariate analyses on morphological traits are rarely reported in sheep (Riva et al., 2004). Physical description of a breed should focus on characters which, in the view of keepers of the breed and local experts, facilitate identification of animals as being members of the breed or strain. These should include coat colour (common and/or special colours and colour combinations); horn shape and size; and presence or absence of hair/wool, hump (including relative size), tail type, dewlap and other specific visible characteristics. Physical or morphological characteristics can be particularly useful in the classification of populations/strains/breeds within a species. This approach is recommended as a first step in the classification of heterogeneous previously uncharacterized populations.

2.3 Genetic Characterisation

Genetic characterization entails describing and classifying livestock breed and species at molecular level using techniques for DNA analysis. The need for conservation comes from the potential rate of decrease of genetic variation. The loss of genetic variation between and within breed is detrimental not only from the perspective of culture and conservation but also utility since lost genes may be of future economic interest. Within breeds, high rate of loss of genetic variation leads to reduced chances of breed survival due to decreased fitness through inbreeding depression. These breeds become subject to faster changes in gene frequencies, greater rate of loss of genes and genetic constitutions (haplotypes). These are all due to small, ineffective population sizes, or equivalent high rate of inbreeding. Once animal genetic has been lost, it cannot be replaced. Advances in biotechnology offer possibilities of improving, utilizing and conserving present domestic animal diversity. The economic implications of maintaining existing farm animal genetic resource in their natural environment are negligible as compared to the cost involved in biotechnology development (FAO, 2007).

Genetic characterization at the molecular level explores polymorphism in selected protein molecules and DNA markers in order to measure genetic variation at the population level. Because of the low level of polymorphism observed in proteins and hence limited applicability in diversity studies, DNA-level polymorphism are the markers of choice for molecular genetics characterization. The process of genetic characterization at the molecular level comprises of field sampling of biological materials often blood or hair root samples, laboratory extraction of DNA, DNA storage, laboratory assaying (e.g. genotyping or sequencing, data analysis, report writing and maintenance of a molecular genetic information). Sampling for molecular analysis may be

combined with surveying and/or monitoring as molecular information on its own cannot be used for utilization and conservation decisions (Hannotte et al., 2005).

2.4 Morphological traits of sheep

2.4.1 Body Colour

The body of the West African Dwarf is generally black piebald on white. They are generally white coloured although usually spotted with black or red colours. Tan with black belly is also common. The Uda type of the Sahelian breed is generally white in colour from the tail to the middle of the body, with either brown or black neck. The Yankasa are white in colour with black patches, while the Belami are generally all white (Abbey et al., 2008).

2.4.2 Head Colour

The head colour of the WAD sheep is generally white, black spotted or brown. The Uda is black or brown headed, the Yankasa is white with black patches on the face especially around the eye, while the Belami is all white. (Abbey et al., 2008).

2.4.3 Muzzle

Sheep usually have black muzzle. The Yankasa, White Maure and the Barbados blackbelly sheep show a black muzzle colour.

2.4.4 Hoof

The hoofs of all the three breeds of sheep are usually brown, black or white. Animals with solid colours usually have their hoofs being same in colour as the body.

2.4.5 Body Measurements

Body measurements are considered as qualitative growth indicators which reflect the conformational changes occurring during the life span of animals. Linear body measurements are divided into skeletal and tissue measurements. The height at withers is part of the skeletal measurements, whereas the heart girth is part of the tissue measurements. Indices using body measurements have been used to estimate shape which is usually difficult to quantify due to its subjectivity in comparison with size. Through principal component analysis of body measurements, it could be possible to identify a relatively small number of factors that can be used to describe relationship among sets of several interrelated variables (Arthur et al., 1989). Factors developed through such techniques could also help to contrast animals of different shapes and sizes (Brown et al., 1973).

2.4.6 Body Length

This is the distance between the crown and the sacrococcygeal joint. It is also one of the morphometric body measurements which are directly related to the size and weight of animal. It is not affected by an animal's condition but is affected by the type of breed and age of an animal. The Fulani sheep of Senegal has a medium size of 65- 75 cm (Bradford, 1983) while the Mossi an early cross between the Sahelian (Toronke) and Djallonke has a small size of 50- 60 cm (Wilson, 1991).

2.4.7 Horn Length

This is the distance of the horns attachment to the tip. It is one of the traits used in the phenotypic characterization of animals (Rege, 2006). It is shorter in some breeds and longer in other breeds of sheep. For instance, the West African

Dwarf sheep breed is noted to have a short horn length generally (ILCA, 2006). The Black Maure (Sahel) from Mali has a horn length of 30 cm (Wilson, 1991) while the Vogan has a horn length of 30-40 cm.

2.5 Application of Discriminant Analysis to separation of breeds of animals/sheep and other Agric Data

A research paper published in the International Journal of Biodiversity and Conservation, volume 5 on Morphometric characterization of Nigerian indigenous sheep using multifactorial discriminant analysis was investigated by Yunusa et al. (2013). Data comprising a total number of 1195 animals with 380 Yankasa sheep, 414 Uda sheep, 224 Balami sheep and 177 West African Dwarf (WAD) sheep in South Western Nigeria was used for data analyses. The study measured 17 morphometric characters to study their phenotypic variations. Shoulder width (SW), neck circumference (NC), head length (HeL), head width (HW), horn length (HL) and hock length (HoL) were among the measurements taken from the various breeds of sheep. In coming out of the trait or characteristic that best differentiate the Nigerian sheep, a stepwise multifactorial discriminant analysis was explored. Among the eight (8) distinguishing traits found, their length of tail was found to be the most discriminating character. The computed Euclidean distances gave the longest genetic distance being found between WAD and Uda sheep while the closest breeds were Balami and Uda. The largest Euclidean distance obtained for genetic gap between Uda and WAD sheep gives prospect for improvement if they are cross-breed.

A multivariate analysis of phenotype differentiation in Bunaji and Sokoto Gudali cattle was investigated by Yakubu et al. (2010). The main objective of their study was based on the application of multi-factorial discriminant analyses using ten

morphological traits in examining morphometric differentiation in two Nigerian breeds of cattle. Some of the measured morphological traits considered in their study were withers height, rump height, chest circumference, body length, face length, tail length, rump length, head width, rump width and shoulder width) of 224 Bunaji and 87 Sokoto Gudali cattle. They subjected some of the breeds of cattle aged within 2.5-3.6 years to an extensive management system. After the application of the stepwise discriminant analysis, only three variables, rump width, withers height and face length were found to be the best variables or trait for providing maximum discrimination or separation among the two cattle breeds. Also the Mahalanobis distance of 7.19 observed between the two cattle populations was high and significant, which is an indication that they belong to genetically different groups. Also Nearest Neighbour Discriminant Analysis was employed and 85.48 percent Bunaji cattle were classified into their source population while 96.55 percent of their Sokoto Gudali counterparts were correctly assigned into their source genetic group.

Herrera et al. (1996) studied an application of a multifactorial discriminant analysis in the morpho-structural differentiation of Andalusian caprine breeds in Spain. Different types of discriminant analysis including simple; canonical; and stepwise, were applied in the analysis of the data. After the computation of the Mahalanobis distance in simple discriminant analysis approach, the greatest distance was between Florida and Malaga breeds (26.329) and the least between Malaga and Granada (2.042). The canonical discriminant analysis and stepwise discriminant analysis determined the differences between the breeds, where their head length was identified as the most discriminated variable in all the breeds. Shin circumference and rump length were also identified as the most discriminant variables in groups based on productive ability and cephalic profile.

Yakubu et al. (2010a) conducted a study by applying the concept of discriminant analysis on morphometric differentiation in West African Dwarf and Red Sokoto goats. Their study was aimed mainly at evaluating the usefulness of morphometric characteristics in distinguishing between two important local goat breeds in Nigeria. Data based on fifteen measured morphometric traits on 160 West African Dwarfs (WAD) and 142 Red Sokoto (RS) goats that ranged in age of up to 19 months was used for data analysis. A univariate analysis was conducted and all the body measurements for RS goats were significant higher than that of WAD. Results from Canonical Discriminant Analysis indicated that, only seven external morphological characteristics of strong discriminating power were extracted. The variables that discriminated best between the two goat populations were rump height, followed in order by body length, horn length, face length, chest girth, neck circumference and head width. The derived discriminant function correctly classified 100 percent of individuals goats into their respective populations. The performance of the classification function was evaluated through the cross validation method using the split-sample method and 99.7 percent correct classification was achieved (i.e 99.4 percent of WAD goats and 100 percent of RS goats were correctly assigned to their source genetic group).

Leotta (2004) researched into the use of linear discriminant analysis to characterise three dairy cattle breeds on the basis of several milk characteristics. Leotta performed a Fishers Linear Discriminant Analysis (FLDA) on fourteen (14) milk production traits of milk samples made up of 199 cows of different breeds. The analysis performed on the 14 measured variables from the three cattle breeds allowed us to identify 10 of these as variables useful for discrimination. From the results, it was observed that, Fat and TS were identified as the most important variables for first canonical variate and SNF, Lactose as well Protein were also identified as the second canonical variates.

Aziz and Al-Hur (2013) applied Size-free Canonical Discriminant Analysis in differentiating between three Saudi goat types. They utilised body weight and 16 body measurements randomly selected from the three Saudi goats and was used to discriminate between 188 animals. After conducting a size free discriminant analysis on the data.

Bagherian and Rahmani (2009) studied morphological discrimination between two populations of shemaya, *Chalcalburnus chalcoides* (Actinopterygii, Cyprinidae), using a truss network and was published in Animal Biodiversity and Conservation journal volume 32. A morphometric differentiations between two populations and sexes of shemaya fishes using a truss network was studied. Measurements of truss distances between 15 landmarks of 66 specimens were taken. Assessment of the size adjustment transformations were made by dividing characters (truss distance) by centroid size of specimen. Multivariate analysis of variance (MANOVA), principal component analysis and discrimination analysis were performed to investigate distinction and patterns of morphological variations between populations and sexes. Results from the MANOVA (Wilks test) indicated a significant difference for mean vectors between populations. Also results from the discriminant analysis indicated 97 and 89.4 percent of correct classification of samples to their original groups for population and sex respectively.

Gonzalez et al (2014) investigated into the usefulness of discriminant analysis in the morpho-functional classification of Spanish dog breeds. Their study was aimed at determining whether the classification of local Spanish breeds of dogs, based on morphological traits, matches or differs from the classification based on the dogs' breeding goals. A total number 1365 dogs comprising 709 females and 656 males were used for then study and 15 biometric measurements and 10

functional indices were obtained in the 1365 dogs with 16 different breeds. They therefore evaluated the morphological characteristics of spanish dog breeds and FCI groups. From their results, they found that the chosen set of morphometric traits were suitable for characterizing individual dogs and for differentiating between several dog breeds.

Traorea et al (2008) investigated into multivariate characterization of morphological traits in Burkina Faso sheep. Their study was based on 6440 female sheep from Burkina Faso and seven body measurements were taken as well as four qualitative morphological traits. Their study sample also included three main environmental areas and sheep breeds of Burkina Faso namely the Sahel area

(Burkina-Sahel sheep), the Sudan-Sahel area (Mossi sheep) and the Sudan area (Djallonké sheep). Results from the Canonical analysis showed that, there exist small differences in the recorded body measurements of Sudan and the Sudan-Sahel sheep even though most body traits showed higher average values in the Burkina-Sahel sheep. Mahalanobis distance was used to measure the shortest distance between the Sudan and the Sudan-Sahel sheep. Discriminant analysis performed in classifying the various sheep breeds showed that most Sudan (Djallonké) individuals representing approximately 61 percent were classified as being Sudan Sahel (Mossi) individuals while whilst most Burkina-Sahel individuals were classified into their environmental area of sampling representing 89.46 percent correct classification rate.

Ebegbulem et al (2011) researched into the morphometric differentiation of West African Dwarf Goats in southeastern Nigeria using discriminant Analysis. One Hundred and twenty One (121) West African Dwarf (WAD) goats aged between less than year and 4 years sampled from local farmers from Nigeria were used for the study. The 121 goats were grouped into three classes based on their Withers height (WH). The discriminant analysis approached discovered six variables as

the major determinants of classification. Among the six variables, Rump height (RH) was discovered as the major discriminator, followed by Bodyweight, Heart girth, Body length, and Foreleg length in that order. After the application of discriminant 83.5 percent of correct classification of goats were achieved. The high percentage was attributed to the fact that WAD goats can be classified into three strains.

Morphological and micro-satellite DNA diversity of Nigerian indigenous sheep was studied by Agaviezor et al (2012). Ten Morphological traits measured on 402 animals and 15 microsatellite DNA markers. Results from stepwise discriminant analysis indicated tail length, rump height, chest girth, ear length and chest depth as the most discriminating variables for classification.

2.6 Other Applications of Discriminant Analysis

Comparing the performance of zero mean classification functions under unequal misclassification cost was investigated by Asamoah-Boaheng et al. (2014) and was published in the American Journal of Applied mathematics and statistics. In their study, the performance of two zero mean classification functions namely the Minimum Expected Cost of Misclassification (MECM) method and Quadratic Discriminant Function (QDF) were compared by evaluating their performance using Balanced Error Rate and Cross Validation Methods. Female liked sex 10 variate data extracted from the Stocks twin data was used for validation purposes. From the results of their study, the performance of the two functions were compared and evaluated under the following misclassification cost ratios; 1:1, 1:2, 1:3 and 1:4. The result revealed that the QDF performed better than MECM in providing maximum separation between the two groups (mono and dizygotic

twins). Again, it indicated that the two classification rules were sensitive to misclassification cost ratios above 1:2.

Genetic diversity of living organisms is the baseline for their survivability in a wide array of environments. Morphological conformation appraisal of livestock is probably the oldest way of information and it played a key role in many breeding associations and has been used with great success over the years (Janssens and Vandepitte, 2004). Morphological description of farm animals is largely influenced by the environmental factors, but this influence is reduced with good sampling technique and the use of adequate sample size. Also visual appraisal is affected by individual biases and differences among observers, therefore, the results obtained from morphological description may be complemented with both biochemical and DNA analysis. Body measurements have also been widely used for estimating animal's live weight especially when there is no access to weighing equipment. It is widely used to predict the weight of cattle with great success but not popularly used in sheep Lawrence and Fowler (2002). Several parts of animal body have been measured for use but those parts that are directly related to bone development find more use because of lesser influence the environment have on them.

Silva et al. (2014) applied discriminant analysis based on echocardiography in classifying congestive heart failure in dogs with myxomatous mitral value disease (MMVD). MMVD is one of the most common cardiac abnormalities in dog that can lead to cardiac heart failure (CHF). The study was conducted on dog population which was divided into three (3) groups. All the dogs first received a physical examination and thoracic radiographs to evaluate them for the signs of CHF. Group I consisted of the healthy animal (control) group II of animals with MVD but no CHF and group III animals with MVD signs of CHF. Echocardiography was also performed in all the dogs together with clinical evaluation. The variables

measured on the three groups for the analysis were weight , body surface area, aortic diameter, the ratio of the left atrium or aortic diameters, the ratio between the mitral regurgitation jet area and left atrial area, vena contracta diameter and mitral value proximal isovelocity surface area. They established a linear discriminant function for each of the three groups and the classification method proposed resulted in classifying 34 out of a total of 81 dogs used in the study into group II. 27 in group III and the rest in group I. 6/34 of animals classified in group II should have been classified as group III and 3/27 of animals classified in group III should have been classified as group II. Their study showed 90.4 with only 9.6 misclassified .They concluded that despite some limitations, the statistical model could be used as an auxiliary method to identify cardiac heart failure (CFH) in dogs with MMVD.

Gwary et al . (2012) developed three (3) discriminant functions or models to study and evaluate the influence farmer's socio-economic characteristics on their participation in research and extension approach (PREA). 605 farmers comprising 393 males and 212 females were used for the study. The farmers were grouped into four (4) as the dependant variables according to level of their participation in PREA. The different levels of participation were no, low, moderate and high participation designated as group 1, 2, 3 and 4 respectively .The predictors or the discriminating variables measured on the respondent were educational status, family size, farming experience (years), ownership of personal farm, marital status, farm size, gender, extensive contact, production motive and land tenure system . Analysis of the collective data indicate that contact point with the extension agent and ownership status and years of farming experience were the highest discriminating variables that made significant contribution as discriminators between the different level of participation in PREA. They recommended in their research that, there is the need to improve on the level of farmers' education, ensured steady access to extension service and more

equitable land tenure arrangement. In the field of poultry, different multivariate approaches such as principal components analysis, cluster analysis and multi-trait techniques have been used by researchers regarding the growth performance and the genetic breeding of chicken.

Rosario et al .(2008) were among the few scholars who have employed discriminant analysis in this field. In their study on "Canonical Discriminant Analysis Applied to Broiler Chicken Performance" canonical discriminant analysis was used to evaluate the performance of broiler chicken. They used 1920 chicks equal number of males and females from three commercial broiler stains (Arbor Acres, AgRoss308 and Cobb 500) and an experimental strain (RX) constituting eight (8) treatments for the study, housing them in 48 pens with 40 animals per pen. During the experimental period from 1 to 42 days, they regulated feeding, water, temperature, humidity and light evenly distributed in the pens and measurements on the average feed intake, average live weight, feed conversion and carcass, breast and leg weights were obtained for the analysis. SAS CANDISC procedure was to implement the canonical discriminant analysis, where differences between treatments were obtained by F-test over the squared Mahalanobis distances. The researchers used discriminant analysis in order to reduce the number of the original traits and allow the discrimination and classification of treatment. The result of the study showed that average live weight and carcass weight were the most important traits to discriminate treatments and the contrast between the average feed intake and average live weight plus feed conversion were used to classify them. Their result also indicated a clear variation between sexes where males were better than females. They recommended the use of canonical discrimination as suitable for evaluating broiler chicken performance because the method reduced the number of original traits to very few for classification.

Rigby (1997) researched into Bayesian discrimination between two multivariate normal populations with equal covariance matrices and his study was published in the Journal of the American Statistical Association, volume 92. Rigby compared the Bayesian and Classical estimates of P , the probability that, a new observation/object/individual belongs of the two multivariate normal populations with equal variance covariance matrices. The study showed the regions of location of a new observation for which the estimates differ. In other words the estimates differed greatly in a dimensionally reduced transformed space. Based on the results, it was realised that the Bayesian estimates generally provides a less extreme and more estimates of P .

A research article titled "Exact Misclassification Probabilities for Plug-In Normal Quadratic Discriminant Functions; The Equal-Means Case", and published in the Journal of Multivariate Analysis was investigated by McFarland (2001). McFarland studied the problem of discrimination by discriminating between two independent multivariate normal populations $N_p(\mu, \Sigma_1)$ and $N_p(\mu, \Sigma_2)$ with common means vectors μ (zero mean difference) and unequal covariance matrices Σ_1, Σ_2 using random training samples. A stochastic representation for the exact distribution of the plug-in quadratic discriminant function was derieved using the Bassel functions of the second kind of matrix for classifying a newly obtained observation.

An efficient method for simulating the discriminant functions and estimating the corresponding probabilities of misclassification was obtained since the stochastic representation involved only chi-square and F-distributions. For each application an estimate of the exact probabilities of misclassification was obtained with the application of the Stocks twin data.

Rausch and Kenkelley (2009) investigated into the comparison of linear and mixture models for discriminant analysis under non-normality. Through Monte-

Carlo simulation, methods for discriminant analysis were compared with respect to classification accuracy under non-normality. The following methods were compared and they are ; discriminant analyses based both on raw scores and on ranks; linear logistic discrimination; and mixture discriminant analysis. Linear discriminant analysis based on ranks yielded the highest rates of classification accuracy in only a limited number of situations and did not produce a practically important advantage over competing methods. Mixture discriminant analysis, with a relatively small number of components in each group, attained relatively high rates of classification accuracy and was most useful for conditions in which skewed predictors had relatively small values of kurtosis.

Srivastava (2006) studied the problem of classifying a new observation vector into one of the known two groups, $\Pi_i, i = 1, 2$ which are distributed under multivariate normal with common variance covariance matrices. From the study, it was realised that the total number of observation vectors from the two groups were less than the dimension of the observation vectors. The researcher further introduced Moore-Penrose inverse to compute the sample-squared distance between the two groups. A classification rule was developed based on the minimum distance to classification an observation observation vector into two or several groups. The researcher further developed for error of misclassification for large p and n as $n = O(p^\delta), 0 < \delta < 1$ and was used to assess the performance of the classification functions and rules.

Chapter 3

METHODOLOGY

3.0.1 Introduction

This part of the study explains in details the various methods and methodology employed in the analysis of the data. The method of analysis looks at discriminant analysis approach in general and factor analysis as a criterion for variable selection (i.e data reduction tool).

3.1 The concept of Discrimination and Classification

Discriminant Analysis (DA) is a set of methods used to distinguish among groups in the data and to allocate new observations into the existing groups. DA is used in situations where the clusters are known a priori. The aim of discriminant analysis is to classify an observation, or several observations, into these known groups (Härdle and Simar, 2007). For instance, in credit scoring, a bank knows from past experience that there are good customers (who repay their loan without any problems) and bad customers (who showed difficulties in repaying their loan). When a new customer asks for a loan, the bank has to decide whether or not to give the loan.

While classification is to sort objects (observations) into two or more labelled classes with the emphasis on deriving a rule that can be used to optimally assign new objects to the labelled classes (that is allocation), (Johnson and Wichern, 2007). The idea of discrimination and classification frequently overlap, and the distinction between separation and allocation becomes blurred but they are always applied together in discriminant analysis.

3.2 Allocation rules for known distributions

Discriminant analysis is a set of methods and tools used to distinguish between groups of populations, Π_j and to determine how to allocate new observations into groups. In general we have populations $\Pi_j, j = 1, 2, \dots, J$ and we have to allocate an observation x to one of these groups.

A discriminant rule is a separation of the sample space (in general R^p) into some sets R_j such that $x \in R_j$ and its identified as a member of population/group Π_j . The main aim of discriminant analysis here is to find good regions R_j such that the error of misclassification is small and such rules are described when the population distributions are known (Härdle and Simar, 2007).

3.3 Maximum Likelihood discriminant rule

Let the probability density functions of each known population Π_j be $f_j(x)$. The maximum likelihood discriminant (ML rule) rule is given by allocating x to Π_j thereby maximizing the likelihood $L_j(x) = f_j(x) = \max_i f_i(x)$. mathematically, the sets R_j given by the ML discriminant rule are defined as

$$R_j = \{x : L_j(x) > L_i(x) \forall i = 1, \dots, J, i \neq j\} \quad (3.1)$$

When classifying an observation into a certain group, it is possible for one to encounter a misclassification error. For $J = 2$ group, the probability of assigning x into group 2 when actually they originally comes from population 1 can be calculated as

$$p_{21} = P(X \in R_2 | \Pi_1) = \int_{R_2} f_1(x) dx \quad (3.2)$$

In a similar pattern, the conditional probability of classifying an object as belonging to the 1st population Π_1 although it actually comes from population 2 Π_2 is

$$p_{12} = P(X \in R_1 | \Pi_2) = \int_{R_1}^Z f_2(x) dx \quad (3.3)$$

Whenever observations are misclassified, they create a cost $C(i|j)$ when a Π_j observations is assigned to R_i . Hence a cost matrix can be explained in the table below.

Table 3.1: The cost matrix

<i>True Pop.</i>	<i>Classified population</i>	
	Π_1	Π_2
Π_1	0	$C(2 1)$
Π_2	$C(1 2)$	0

Let π_j be the prior probability of population Π_j where 'prior' means a priori probability that an individual selected belongs to Π_j . Prior probabilities should be considered if its is clear ahead of time that an observation is more likely to stem from a certain population Π_j .

The Expected Cost of Misclassification (ECM) is given by

$$ECM = C(2|1)p_{21}\pi_1 + C(1|2)p_{12}\pi_2 \quad (3.4)$$

The classification rule that keeps the ECM small or minimize it over a class of rules will be of a particular interest in the study. The discriminant rule minimizing the ECM in 3.3 for the two population is been derived in the theorem below.

Theorem 3.3.1 *For two given populations, the rule use for minimizing the ECM is given by:*

$$R_1 = \left\{ x : \frac{f_1(x)}{f_2(x)} \geq \left(\frac{C(1|2)}{C(2|1)} \right) \left(\frac{\pi_2}{\pi_1} \right) \right\}$$

$$R_2 = \left\{ x : \frac{f_1(x)}{f_2(x)} < \left(\frac{C(1|2)}{C(2|1)} \right) \left(\frac{\pi_2}{\pi_1} \right) \right\}$$

Hence the ML discriminant rule is a special case of the ECM rule for the case of equal misclassification costs and equal prior probabilities. For simplicity, we assume a unit misclassification cost, $C(1|2) = C(2|1) = 1$ and equal prior probabilities, $\pi_1 = \pi_2$. Hardle and Simar (2007)."

Theorem 3.3.2 Suppose $\Pi_i = N_p(\mu_i, \Sigma)$

(a) The ML rule allocates x to Π_j , where $j \in 1, \dots, J$ is the value minimizing the square Mahalanobis distance between x and μ_i : $\delta(x, \mu_i) = (x - \mu_i)' \Sigma^{-1} (x - \mu_i)$, $i = 1, \dots, J$

(b) In the case of $J = 2$, $x \in R_1$ then $\alpha' (x - \mu) \geq 0$, where $\alpha = \Sigma^{-1}(\mu_1 - \mu_2)$ and $\mu = \frac{1}{2}(\mu_1 + \mu_2)$

Proof

Part (a) of the theorem follows directly from comparison of the likelihoods. For $J = 2$, part (a) says that x is allocated to Π_1 if

$$(x - \mu_1)' \Sigma^{-1} (x - \mu_1) \leq (x - \mu_2)' \Sigma^{-1} (x - \mu_2) \text{ By}$$

rearrangement of terms, it leads to :

$$-2\mu_1' \Sigma^{-1} x + 2\mu_2' \Sigma^{-1} x + \mu_1' \Sigma^{-1} \mu_1 - \mu_2' \Sigma^{-1} \mu_2 \leq 0$$

Which is equivalent to

$$2(\mu_2 - \mu_1)' \Sigma^{-1} x + (\mu_1 - \mu_2)' \Sigma^{-1} (\mu_1 + \mu_2) \leq 0$$

$$(\mu_1 - \mu_2)' \Sigma^{-1} \left\{ x - \frac{1}{2}(\mu_1 + \mu_2) \right\} \geq 0$$

$$\alpha' (x - \mu) \geq 0$$

3.4 Bayes Discriminant Rule

Let the prior probability of population Π_j be π_j and note that $\sum_{j=1}^J \pi_j = 1$. The Bayes rule of discrimination assigns x to Π_j that gives the largest value of $\pi_j f_j(x)$, $\pi_j f_j(x) = \max_i \pi_i f_i(x)$. Therefore the Bayes discriminant rule is defined by the region $R_j = \{x : \pi_j f_j(x) \geq \pi_i f_i(x) \forall i = 1, \dots, J\}$. However, the Bayes rule of discrimination becomes identical to Maximum Likelihood discriminant rule for $\pi_j = 1/J$.

3.5 The Probability of Misclassification for the ML rule ($J = 2$)

Consider a multivariate normal distribution with mean vectors μ_i and common variance covariance matrix Σ , then for the case of two groups, it is difficult to derive the probabilities of misclassifications for the ML discriminant rule. Considering $p_{12} = P(x \in R_1 | \Pi_2)$ and making reference to part (b) in the proof section we have $p_{12} = P\{\alpha^0(x - \mu) > 0 | \Pi_2\}$. The probability of being classified into population 1

Π_1 although x stems from population 2 Π_2 is equal to $p_{12} = \Phi\left(-\frac{1}{2}\delta\right)$. Similarly, the probability of being classified into population 2 although x stems from population 1 is equal to $p_{21} = \Phi\left(-\frac{1}{2}\delta\right)$. (Hardle and Simar, 2007)."

3.6 Cost of Misclassification

According to Krzanowski (1988) another aspect of classification is cost. A rule that ignores costs may cause problems. The cost associated with each of these mistakes are $c(1|1), c(1|2), c(2|2)$ and $c(2|1)$ respectively. The costs are zero for correct classification, so the expected or average cost of misclassification is given by

$$\begin{aligned}
ECM &= c(2|1)P(2|1)p_1 + c(1|2)P(1|2)p_2 \\
&= \int_{R_2} c(2|1)p_1 f_1(\mathbf{x})d\mathbf{x} + \int_{R_1} c(1|2)p_2 f_2(\mathbf{x})d\mathbf{x} \quad (3.5)
\end{aligned}$$

The best classification rule is the one that yields minimum expected cost due to misclassification, and this rule will be obtained by finding the region R_1 and R_2 minimizing ECM in 3.5 allocate \mathbf{x}

$$R_1 : \frac{f_1(x)}{f_2(x)} \geq \left(\frac{c(1|2)}{c(2|1)} \right) \left(\frac{p_2}{p_1} \right) \quad (3.6)$$

$$R_2 : \frac{f_1(x)}{f_2(x)} < \left(\frac{c(1|2)}{c(2|1)} \right) \left(\frac{p_2}{p_1} \right) \quad (3.7)$$

The right hand side of 3.6 and 3.7 known as the cut-off point is denoted by \mathbf{k} . It is clear from 3.5 that the implementation of the minimum ECM rule requires (1) the density function ratio evaluated at a new observation \mathbf{x}_0 , (2) the cost ratio, and (3) the prior probability ratio. The appearance of ratios in the definition of the optimal classification regions is significant (Johnson and Wichern, 2007).

The likelihood ratio discriminant rule is thus a special case of the *ECM* rule for equal misclassification costs and equal prior probabilities. Other special cases of Minimum Expected Cost Regions are:

(a) $p_2/p_1 = 1$ (equal prior probabilities); $k = c(1|2)/c(2|1)$

$$R_1 : \frac{f_1(\mathbf{x})}{f_2(\mathbf{x})} \geq \frac{c(1|2)}{c(2|1)} \quad R_2 : \frac{f_1(\mathbf{x})}{f_2(\mathbf{x})} < \frac{c(1|2)}{c(2|1)}$$

(b) $c(1|2)/c(2|1) = 1$ (equal costs of misclassification); $k = p_2/p_1$

$$R_1 : \frac{f_1(\mathbf{x})}{f_2(\mathbf{x})} \geq \frac{p_2}{p_1} \quad R_2 : \frac{f_1(\mathbf{x})}{f_2(\mathbf{x})} < \frac{p_2}{p_1}$$

When the prior probabilities are unknown, they are often considered to be equal. Similarly, the costs of misclassification are also often taken to equal when they are unknown.

3.7 Total Probability of Misclassification

Criteria other than the ECM can be used to "optimal" classification procedures.

One might ignore cost of misclassification and choose R_1 and R_2 to minimize the total probability of misclassification (TMP).

$$\begin{aligned}
 \text{TMP} &= P(\text{misclassifying a } \Pi_1 \text{ observation or misclassifying a } \Pi_2 \text{ observation}) \\
 &= P(\text{observation comes from } \Pi_1 \text{ and is misclassified}) \\
 &\quad + P(\text{observation comes from } \Pi_2 \text{ and is misclassified}) \\
 &= p_1 \int_{R_2} f_1(\mathbf{x}) d\mathbf{x} + p_2 \int_{R_1} f_2(\mathbf{x}) d\mathbf{x}
 \end{aligned}$$

Mathematically, this problem equivalent to minimizing the expected/average cost of misclassification when the cost of misclassification are equal.

The rule **(b)** could have been derived equivalently by minimizing TPM , where

$$TPM = P(2|1)p_1 + P(1|2)p_2 \quad (3.8)$$

is given by ECM of (2.2) but with $c(2|1)$ and $c(1|2)$ removed. It is worth mention that the rule **(b)** is equivalent to the allocation rule derived by maximizing the posterior probability of population membership.

3.8 Classification with equal covariance matrices ($\Sigma_i =$

$$\Sigma_j = \Sigma)$$

The density of population π_i ($i = 1, 2$) is now given by;

$$f_i(x) = \frac{1}{(2\pi)^{p/2} \det(\Sigma)^{1/2}} \exp -\frac{1}{2}(x - \mu_i)^T \Sigma^{-1}(x - \mu_i) \quad (3.9)$$

If the populations π_1 and π_2 both have multivariate normal densities with equal covariance matrices, then the classification rule corresponding to minimizing ECM becomes: classify x_0 as π_1 if

$$(\mu_1 - \mu_2)^T \Sigma^{-1} x_0 - \frac{1}{2}(\mu_1 - \mu_2)^T \Sigma^{-1}(\mu_1 + \mu_2) \geq \left[\ln \left(\frac{c(1|2)}{c(2|1)} \right) \left(\frac{p_2}{p_1} \right) \right] \quad (3.10)$$

and classify x_0 as π_2 otherwise.

In practice, the population parameters μ_1 and μ_2 and Σ are unknown and have to be estimated from the data. Suppose we have n_1 objects belonging to π_1 (denoted as $x_1^{(1)}, \dots, x_{n_1}^{(1)}$) and n_2 objects from π_2 (denoted as $x_1^{(2)}, \dots, x_{n_2}^{(2)}$)

with $n_1 + n_2 = n$ the total sample size. The sample mean vectors and covariance matrices of both groups are estimated using their sample estimators. Since both populations have the same covariance matrix Σ we combine the two sample covariance matrices S_1 and S_2 to obtain a more precise estimate of Σ . Replacing μ_1 , μ_2 and Σ with \bar{x}_1 , \bar{x}_2 and S_{pooled} in equation (3.6), then the sample classification rule is obtained as ; classify x_0 as π_1 if

$$(\bar{x}_1 - \bar{x}_2)^T S_{pooled}^{-1} x_0 - \frac{1}{2}(\bar{x}_1 - \bar{x}_2)^T S_{pooled}^{-1}(\bar{x}_1 + \bar{x}_2) \geq \left[\ln \left(\frac{c(1|2)}{c(2|1)} \right) \left(\frac{p_2}{p_1} \right) \right] \quad (3.11)$$

and classify x_0 as π_2 otherwise.

Below gives the special case of equation (3.7) where the prior probabilities and the misclassification cost are equal:

$$\left[\ln \left(\frac{c(1|2)}{c(2|1)} \right) \left(\frac{p_2}{p_1} \right) \right] = \ln(1) = 0 \quad (3.12)$$

such that we assign x_0 to π_1 if

$$(\bar{x}_1 - \bar{x}_2)^T S_{pooled}^{-1} x_0 \geq \frac{1}{2} (\bar{x}_1 - \bar{x}_2)^T S_{pooled}^{-1} (\bar{x}_1 + \bar{x}_2) \quad (3.13)$$

Denote $a = S_{pooled}^{-1} (\bar{x}_1 - \bar{x}_2) \in \mathbb{R}^p$ and the above equation can be rewritten as;
 $a^T x_0 \geq \frac{1}{2} (a^T \bar{x}_1 + a^T \bar{x}_2)$ (Johnson and Wichern, 2007).

3.9 Distance Based Classification

We now turn our attention to classification rules for several groups based on the distance between x and the discriminating groups. We consider the case where x is multivariate normal in $\Pi_i, i = 1, 2, \dots, g$. The Mahalanobis squared distance between x and Π_i is defined as

$$\Delta_i^2 = (x - \mu_i)^T \Sigma_i^{-1} (x - \mu_i) \quad (3.14)$$

The allocation rule is allocate x to the group for which Δ_i^2 is smallest.

3.10 The Quadratic Classifier ($\Sigma_1 \neq \Sigma_2$)

Suppose that the joint densities of $X^0 = [X_1, X_2, \dots, X_p]$ for population Π_1 and Π_2 are given by

$$f_i(x) = \frac{1}{(2\pi)^{p/2} |\Sigma_i|^{1/2}} \exp \left[-\frac{1}{2} (x - \mu_i)^T \Sigma_i^{-1} (x - \mu_i) \right] \quad (3.15)$$

The covariance matrices as well as the mean vectors are different from one another for the two populations. The regions of minimum expected cost misclassification (ECM) and minimum total probability of misclassification (TPM) depends on the ratio of the densities, $(f_1(\mathbf{x}))/f_2(\mathbf{x})$, or equivalently, the natural logarithm of the density ratio, $\ln[(f_1(\mathbf{x}))/f_2(\mathbf{x})] = \ln[f_1(\mathbf{x})] - \ln[f_2(\mathbf{x})]$ when the multivariate normal densities have different covariance structures, the terms in the density ratio involving $|\Sigma_i^{1/2}|$ do not cancel as they do when we have equal covariance matrices and also the quadratic forms in the exponents of $f_i(\mathbf{x})$ do not combine. Therefore substituting multivariate normal densities with different covariance matrices into 3.6 and 3.7 and after taking the natural logarithms and simplifying, the likelihood of the density ratios gives the quadratic function in

$\mathbf{x} \in \Pi_1$ if

$$-\frac{1}{2}\mathbf{x}'(\Sigma_1^{-1} - \Sigma_2^{-1})\mathbf{x} + (\mu_1'\Sigma_1^{-1} - \mu_2'\Sigma_2^{-1})\mathbf{x} - k \geq \ln \left[\left(\frac{c(1|2)}{c(2|1)} \right) \left(\frac{p_2}{p_1} \right) \right],$$

where

$$k = \frac{1}{2} \ln \left(\frac{|\Sigma_1|}{|\Sigma_2|} \right) + \frac{1}{2} (\mu_1'\Sigma_1^{-1}\mu_1 - \mu_2'\Sigma_2^{-1}\mu_2) \quad (3.16)$$

otherwise, $\mathbf{x} \in \Pi_1$. Considering the Mahalanobis distance, the function is sometimes written as

$$f(\mathbf{x}) = D_1^2(\mathbf{x}) - D_2^2(\mathbf{x}) + \ln \left[\frac{|\Sigma_1|}{|\Sigma_2|} \right] - 2 \ln \left(\frac{p_1}{p_2} \right) \quad (3.17)$$

The quantity $D_i^2(\mathbf{x}) = (\mathbf{x} - \mu_i)'\Sigma_i^{-1}(\mathbf{x} - \mu_i)$ is the Mahalanobis Square Distance. When $\Sigma_1 = \Sigma_2$ the function reduces to linear classifier rule (Adebanji and Nokoe, 2004)

In many applications, the distributions of the populations of interest may not be multivariate normal. If the data are not multivariate normal, transformation of the data to more nearly normal and a test for equality of covariance matrix can be conducted to see whether the linear rule or the quadratic rule is appropriate. This transformation is done before testing is carried out. we can also use the linear or quadratic rule without worrying about the form of the parent population and

hope that it will work reasonably well. Studies have shown that there are nonnormal cases where LDF performs poorly, even though the population covariance matrices are the same. The moral is to always check the performance of any classification procedure (Johnson and Winchurn, 2007).

3.10.1 Classification into Several Populations

Generalization of classification procedure for more than two discriminating groups (ie from 2 to $g \geq 2$) is straight forward. However, not much is known about the properties corresponding sample classification function, and in particular, their error rates have not been fully investigated. Therefore, we focus only on the Minimum ECM Classification with equal misclassification cost and Minimum TPM for multivariate normal population with unequal covariance matrices (Quadratic discriminant analysis).

Minimum ECM Classification with Equal Misclassification Cost

Allocate \mathbf{x}_0 to Π_k if

$$p_k f_k(\mathbf{x}) > p_i f_i(\mathbf{x}) \quad \text{for all } i \neq k \quad (3.18)$$

or, equivalently, Allocate \mathbf{x}_0 to Π_k if

$$\ln p_k f_k(\mathbf{x}) > \ln p_i f_i(\mathbf{x}) \quad \text{for all } i \neq k \quad (3.19)$$

Note that the classification rule in 3.18 is identical to the one that maximizes the posterior probability $P(\Pi_i|\mathbf{x}) = P(\mathbf{x} \text{ comes from } \Pi_i \text{ given that } \mathbf{x} \text{ is observed})$ where

$$P(\Pi_i|\mathbf{x}) = \frac{p_i f_i(\mathbf{x})}{\sum_{i=1}^g p_i f_i(\mathbf{x})} = \frac{(\text{prior}) \times (\text{likelihood})}{\sum [(\text{prior}) \times (\text{likelihood})]} \quad (3.20)$$

Therefore, one should keep in mind that in general minimum ECM rule must have the prior probability, misclassification cost and density function before it can be implemented.

Minimum TPM Rule for Unequal-Covariance Normal Populations

Suppose that the Π_i are multivariate normal populations, with different mean vectors μ_i and covariance matrices Σ_i ($i = 1, \dots, g$). An important special case occurs when the

$$f_i(\mathbf{x}) = \frac{1}{(2\pi)^{p/2} |\Sigma_i|^{\frac{1}{2}}} \exp\left\{-\frac{1}{2}(\mathbf{x} - \mu_i)' \Sigma_i^{-1} (\mathbf{x} - \mu_i)\right\}$$

with $c(i | i) = 1, c(k | i) = 0, k \neq i$ then

$$\begin{aligned} \ln p_k f_k(\mathbf{x}) &= \ln p_k - \left(\frac{p}{2}\right) \ln\{(2\pi)\} - \frac{1}{2} \ln |\Sigma_k| - \frac{1}{2} (\mathbf{x} - \mu_k)' \Sigma_k^{-1} (\mathbf{x} - \mu_k) \\ &= \max_i \ln\{p_i f_i(\mathbf{x})\} \end{aligned} \quad (3.21)$$

The constant $(p/2)\ln(2\pi)$ can be ignored in 3.21, since it is the same for all population. Therefore, quadratic discriminant score for i th population is defined as

$$d_i^Q(\mathbf{x}) = -\frac{1}{2} \ln |\Sigma_i| - \frac{1}{2} (\mathbf{x} - \mu_i)' \Sigma_i^{-1} (\mathbf{x} - \mu_i) + \ln p_i \quad (3.22)$$

The quadratic score $d_i^Q(\mathbf{x})$ is composed of contributions from the generalized variance $|\Sigma_i|$, the prior probability p_i , and the square of the distance from \mathbf{x} to the population mean μ_i .

Allocate \mathbf{x} to Π_k if the quadratic score

$$d_k^Q(\mathbf{x}) = \text{largest of } d_1^Q(\mathbf{x}), d_2^Q(\mathbf{x}), \dots, d_g^Q(\mathbf{x}). \quad (3.23)$$

In practice, the μ_i and Σ_i are unknown, but a training set of correctly classified observations is often available for the construction of estimates. The relevant sample quantities for population Π_i are the sample mean vector, $\bar{\mathbf{x}}_i$, sample covariance matrix, S_i and sample size, n_i . The estimate of the quadratic discriminant score 3.23 is then

$$\hat{d}_i^Q(\mathbf{x}) = -\frac{1}{2} \ln |\mathbf{S}_i| - \frac{1}{2}(\mathbf{x} - \bar{\mathbf{x}}_i)' \mathbf{S}_i^{-1}(\mathbf{x} - \bar{\mathbf{x}}_i) + \ln p_i \quad \text{for} \quad i = 1, 2, \dots, g \quad (3.24)$$

3.11 Factor Analysis as a variable selection criterion

The major aim of factor analysis is the orderly simplification of a large number of intercorrelated measures to a few representative constructs or factors (Johnson and Wichern, 2007).

3.11.1 Orthogonal factor model

The aim of factor analysis is to explain the outcome of p variables in the data matrix X using fewer variables (i.e. the so-called factors). Ideally all the information in X can be reproduced by a smaller number of factors. These factors are interpreted as latent (unobserved) common characteristics of the observed $x \in R^p$. The case just described occurs when every observed $x = (x_1, \dots, x_p)^0$ can be written as

$$x_j = \sum_{\ell=1}^k q_{j\ell} f_{\ell} + \mu_j, j = 1, \dots, p. \quad (3.25)$$

where f_{ℓ} for $\ell = 1, \dots, k$ denotes the factors. It is therefore expected that, the number of factors k should always be much smaller than p . However it is possible to create a representation of the observations that is similar to the one in equation 3.25 by means of principal components, but only if the last $p - k$ eigenvalues corresponding to the covariance matrix are equal to zero.

Consider a p -dimensional random vector X with mean μ and covariance matrix $\text{Var}(X) = \Sigma$. A model similar to equation 3.25 can be written for X in matrix notation as

$$X = \phi F + \mu \quad (3.26)$$

where F is the k -dimensional vector of the k factors. when equation 3.26 is used, it is often assumed that, the factors F are centered, uncorrelated and standardised: $E(F) = 0$ and $Var(F) = I_k$

If the last $p-k$ eigenvalues of Σ are equal to zero, X can be expressed as a factor model as shown in equation 3.26.

The orthogonal factor model is given by

$$X = \phi F + U + \mu \quad (3.27)$$

Where μ_j is the mean of the variable j , U_j is the j -th specific factor, F is the j -th common factor and ϕ_j is the loading of the j -th variable on the j -th factor. The random vectors F and U are unobservable and uncorrelated.

X is a vector with dimension $p \times 1$, ϕ is a matrix with dimension, $p \times k$, F with dimension $k \times 1$, and μ is a vector with dimension $p \times 1$. It is assumed that the factor variables F are uncorrelated random vectors and that the specific factors are uncorrelated and have zero covariance with the common factors. More precisely, it is assumed that, $E(F) = 0$, $var(F) = I_k$, $E(U) = 0$, $Cov(U_i, U_j) = 0$ for $i \neq j$, $Cov(F, U) = 0$.

The generalised factor model in equation 3.27 together with the above assumptions constitute the orthogonal factor model below. Equation 3.27 implies for the components of $X = (X_1, \dots, X_p)$ that

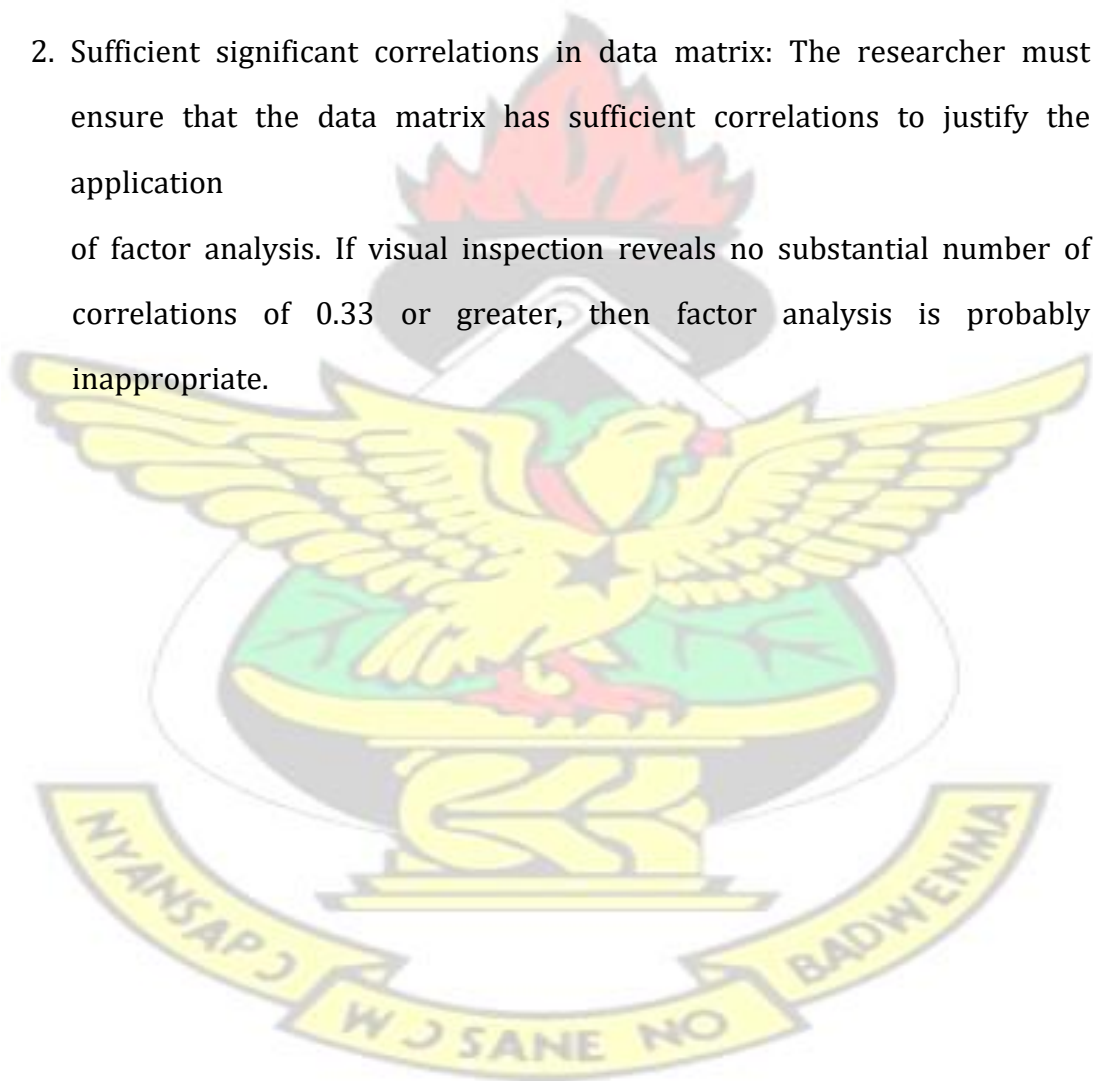
$$X_j = \sum_{k=1}^k \phi_{jk} F_k + U_j + \mu_j, \forall j = 1, \dots, p. \quad (3.28)$$

The factor model explains the variations of X by a small number of latent factors F common to its p components and it entirely explains all the correlation structure between its components together with "noise" or random walk U which normally allows specific variations of each component to enter.

3.11.2 Assumptions

The assumptions underlying factor analysis can be classified as statistical and conceptual. Statistical assumptions include normality and linearity and sufficient significant correlations in data matrix.

1. Normality and linearity: Departures from normality and linearity can diminish the observed correlation between measured variables and thus degrade the factor solution.
2. Sufficient significant correlations in data matrix: The researcher must ensure that the data matrix has sufficient correlations to justify the application of factor analysis. If visual inspection reveals no substantial number of correlations of 0.33 or greater, then factor analysis is probably inappropriate.



Chapter 4

RESULTS and DISCUSSION

4.1 Introduction

This Chapter presents the results of the analysed data and extensive discussion of the results and their relation to existing literature. This section is in two parts. First and foremost, descriptives statistics consisting mainly of measures of central tendencies were employed in the preliminary analysis. The second part comprises the use of factor analysis as a variable selection criterion and Discriminant analysis for deriving classification functions to ensuring maximum separation between the known breeds of sheep.

4.2 Preliminary Analysis

Descriptive statistics mainly the measures of central tendencies such as the mean and the standard deviation of the various traits for each of the three breeds were computed and are shown in Table 4.1. The various traits of the various sheep breeds considered were their HEIGHT, LENGTH, EAR LTH (Ear Length), WT (Weight), CHST (Chest Size), HK LGTH (Hook Length), TL-LTH (Tail Length) and HK LTH-TLTH (Difference between Hook length and Tail length). From Table 4.1, the computed means and their respective standard deviations shows some differences in the measured traits across the three breeds. Next is to check whether there is significance difference among the groups means of all the eight measured traits considered in the study.

Test of significance was conducted to test statistically whether there are differences among the group means of the measured traits for the various breeds

of sheep. F-test was computed to justify whether there is indeed a significant difference or not.

Table 4.1: Group and descriptive statistics of the traits of sheep breeds

Group Statistics				
Breed Type	Traits	Mean	Std. Deviation	N
	HEIGHT	52.70	4.150	23
	LENGTH	54.04	4.724	23
	EAR LTH	9.30	.703	23
	TL-LTH	24.52	2.745	23
	WT	20.09	4.935	23
	CHST	67.09	5.477	23
	HK LGTH	27.57	1.973	23
	HK LTH-T LTH	3.09	2.043	23
	HEIGHT	62.56	9.221	9
	LENGTH	57.89	7.491	9
	EAR LTH	12.22	1.394	9
	TL-LTH	33.22	3.528	9
	WT	23.44	10.382	9
	CHST	69.56	10.933	9
	HK LGTH	30.11	4.885	9
	HK LTH-T LTH	-3.11	2.369	9
	HEIGHT	52.69	4.907	29
	LENGTH	53.86	5.848	29
	EAR LTH	9.52	.688	29
	TL-LTH	26.72	3.337	29
	WT	20.79	7.153	29
	CHST	66.48	8.412	29
	HK LGTH	27.10	2.807	29
	HK LTH-T LTH	.28	1.998	29
	HEIGHT	54.15	6.429	61
	LENGTH	54.52	5.798	61
	EAR LTH	9.84	1.293	61
	TL-LTH	26.85	4.218	61
	WT	20.92	6.958	61
	CHST	67.16	7.813	61
	HK LGTH	27.72	3.056	61
	HK LTH-T LTH	.84	2.928	61

Table 4.2 show the results obtained as a result of the significance test conducted for mean difference of the measured traits.

Table 4.2: Tests of Equality of Group Means, (Significance level(α) = 0.05)

Traits	Wilks' Lambda	F-test	df1	df2	P-value
HEIGHT	.699	12.488	2	58	.000
LENGTH	.941	1.833	2	58	.169
EAR LTH	.395	44.373	2	58	.000
TL-LTH	.541	24.653	2	58	.000
WT	.975	.756	2	58	.474
CHST	.982	.525	2	58	.595
HK LGTH	.887	3.676	2	58	.031
HK LTH-T LTH	.483	31.024	2	58	.000

From Table 4.2, *Wilks lambda* as well as *F-test* were computed for each of the eight traits/characteristics for the three groups combined. From the table, the *p-values* for HEIGHT, EAR LTH, TL LTH, HK LGTH and HK LTH-TLTH were all recorded as 0.000. By rule since $p - value = 0.000 < \alpha = 0.05$, we reject the null hypothesis of test of no difference among the traits of the breeds and conclude that, there exist significant difference of the following measured traits (*HEIGHT, EAR LTH, TL LTH, HK LGTH and HK LTH-TLTH*) among the three breeds. Also the test discovered the following traits of the breeds (*LENGTH, WT, CHST*) as being equal across the three breeds of sheep and hence there exist no significance difference between the sheep LENGTH, WT and CHST with recorded *p-values* of 0.169, 0.474 and 0.595 respectively.

4.3 Further Analysis

This section of the study focuses on extensive analysis of the data with some robust and complex methods as well as detailed discussion of the gathered results. Factor analysis was employed to select/identify the variables that best provide maximum separation among the three sheep breeds.

First and foremost, the equality of the variance covariance matrices for the three sheep breeds were tested with Box M test of covariance matrices. The log determinants of the three covariance matrices for two groups were found from the table as almost equal with the other one slightly apart from the other two.

The hypothesis for testing the equality of covariance matrices was stated as:

$H_0: \Sigma_1 = \Sigma_2 = \Sigma_3$ vrs $H_1 = \Sigma_i \neq \Sigma_j$, for some $i \neq j$, where $i, j = 1, 2, 3$.

From Box M table, we observed a *p* – value of 0.141, and since the observed *p* – value is greater than the significance (α) of 5 percent, we fail to reject the null hypothesis of no difference and conclude that, all the three variance covariance matrices are equal. Based on this results, all discriminant as well as the classifications function assumed a linear approach.

Table 4.3: Test for equality of covariance matrices

Log Determinants		Test Results	
Breed Type	Rank	Log Determinant	
			54.842
Djallonke/WAD	8	6.742	Approx. 1.256
Sahel/WALL	7		df1 36
Crosses	8	10.582	df2 7506.655
Pooled within-groups	8	10.597	P-value. .141

4.3.1 Factor Analysis

The major aim of factor analysis is the orderly simplification of a large number of intercorrelated measures to a few representative constructs or factors. The primary function of factor analysis is to identify these clusters of high intercorrelations as independent factors. The main steps involved in factor analysis are ; Computation of the correlation matrix, extraction of initial factors, determining the number of factors to be extracted and rotation Methods.

In following the steps of factor analysis, the correlation coefficients forming the correlation matrix were computed for all the eight physical traits of the three sheep breeds as shown in Table 4.4.

Table 4.4: Correlation matrix for traits of sheep breeds

	HEIGHT	LENGTH	EAR LTH	TL-LTH	WT/kg	CHST	HK LGTH	HKLTH -T LTH
HEIGHT	1.000	.746	.574	.698	.692	.745	.733	-.235
LENGTH	.746	1.000	.276	.498	.776	.845	.656	-.018
EAR LTH	.574	.276	1.000	.613	.187	.214	.456	-.395
TL-LTH	.698	.498	.613	1.000	.498	.502	.718	-.685
WT	.692	.776	.187	.498	1.000	.895	.600	-.078
CHST	.745	.845	.214	.502	.895	1.000	.671	-.006
HK LGTH	.733	.656	.456	.718	.600	.671	1.000	.010
HK LTH -T LTH	-.235	-.018	-.395	-.685	-.078	-.006	.010	1.000

By observation from the Table 4.4, mostly any two of the traits of sheep were generally found to be highly correlated or are highly intercorrelated. In order to ensure that, all the variables are highly intercorrelated, KMO and Bartlett test was conducted to ensure that all the variables put together are highly intercorrelated. Table 4.5 below shows the KMO and Bartlett test for checking the adequacy of the computed correlation matrix to ensure whether the traits/variables are inter-correlated or not or whether they are dependent on each other or not.

Table 4.5: KMO and Bartlett's Test Sphericity

Approx. Chi-Square	614.706
df	28
P-value	.000

The following hypothesis was tested for the above test. H_0 : All the eight variables or traits are not highly intercorrelated

H_1 : All the eight variables or traits are highly intercorrelated.

From Table 4.5, the p -value of 0.000 was recorded and by rule, since the p -value is less than the significance level (α) of 0.05, we rejected the null hypothesis and concluded that all the eight variables, in general are fairly highly intercorrelated with each other. By this test, the assumption of factor analysis is satisfied and

hence factor analysis was conducted for the selection of variables that would provide maximum separation among the three known sheep breeds.

Table 4.6 shows the communalities of each of the eight traits or in other words the proportion of variance in each variable/trait accounted for by the common factors. Thus the proportion of variance accounted for by the common factors, or the communality of a variable is 1 for all the variables.

Table 4.6: Communalities

Traits	Initial	Extraction
HEIGHT	1.000	.836
LENGTH	1.000	.829
EAR LTH	1.000	.630
TL-LTH	1.000	.916
WT	1.000	.806
CHST	1.000	.899
HK LGTH	1.000	.712
HK LTH-T LTH	1.000	.766

The second step in factor analysis is basically about the extraction of factors to explain the known variables.

Table 4.7 shows the Total Variance explained which presents the number of common factors computed, the eigenvalues associated with these factors, the percentage of total variance accounted for by each factor, and the cumulative percentage of total variance accounted for by the factors. Although eight factors have been computed, it is therefore obvious that, not all the eight will be useful in representing the list of eight variables/traits. In deciding the number of factors to be extracted to explain the eight variables, the computed eigen values with the factors was shown in Table 4.7 to help the researcher decide on the number of factors to extract. As a rule, a criterion was developed to retain only factors with eigenvalues of 1 or greater. Hence from Table 4.7, only two factors were found to be having eigenvalues of at least 1. Hence these two factors will be responsible for explaining all the eight (8) of the sheep breeds identified. These two factors

accounted for 59.28% and 20.65% of the total variance, respectively. That is, almost 79.93% of the total variance is attributable to these two extracted factors.

Table 4.7: Total Variance Explained

	Initial Eigenvalues		Extraction Sums of Squared Loadings		
	Total	% of Variance	Total	% of Variance	Cum. %
1	4.74	59.28	4.74	59.28	59.28
2	1.65	20.65	1.65	20.65	79.94
3	.73	9.08			
4	.39	4.99			
5	.22	2.72			
6	.172	2.151			
7	.087	1.087			
8	.003	.032			

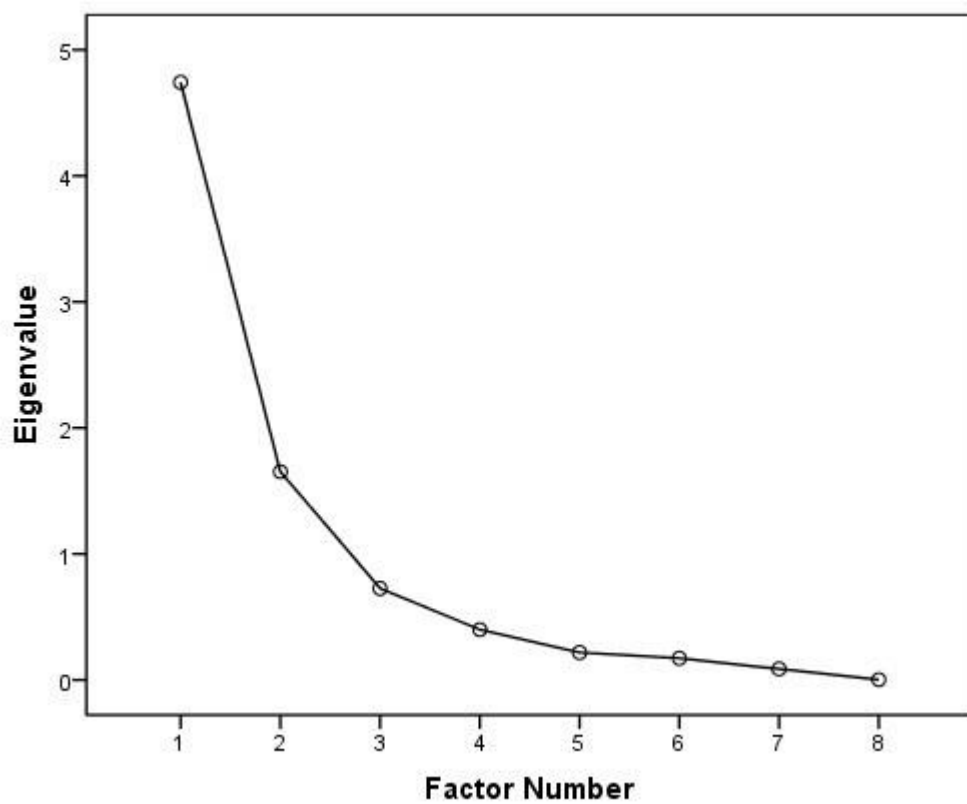


Figure 4.1: Scree plot for factor/component extraction The scree plot (Figure 4.1) again appears that a two-factor model should be sufficient to represent the data set since the curve turns first on factor number two (2). Thus a model with two factors may be adequate to represent the data. Table 4.8 shows the component matrix of the variables which represents the unrotated component analysis factor matrix and it shows the correlations relating the variables or traits to the three extracted factors. The observed coefficients or correlations are called factor loadings and therefore indicate how closely the variables are related to each factor.

Since factors are extracted on the basis of proportion of total variance explained under factor unrotation, there is a high possibility of occurrence of significant cross-loadings. From Table 4.8, majority of the traits of sheep by observation has loaded highly under factor 1 and 2. The LENGTH variable is loaded by factors 1 and 2 at the same time, as well as EAR LTH, TL-LTH, WT, CHST, HK LGTH and HK LTH-TLTH.

Table 4.8: Component matrix

	Factor/Component	
	1	2
HEIGHT	.914	
LENGTH	.847	.335
EAR LTH	.559	-.564
TL-LTH	.814	-.504
WT	.828	.348
CHST	.863	.393
HK LGTH	.839	
HK LTH-T LTH		.827

Since five of the eight variables are cross loaded, there is the need to rotate the variables under VARIMAX rotation method in order to maximize the relationship or correlation between the factors and each of the eight sheep traits. The rotated

matrix in Table 4.9 presents the two extracted factors for the eight sheep traits under VARIMAX rotation. To identify what these factors represent, it would be necessary to consider what items loaded on each of the two factors. The clustering of the sheep traits in each factor offer best clue as to the meaning of that factor. After the application of VARIMAX rotation as shown in Table 4.9, two variables or two of the sheep traits namely HEIGHT and TL-LTH were cross loaded (i.e. a variable having relationship with more than one factor at the same time) and hence by, rule they were deleted leaving behind six variables.

Table 4.9: Rotated Component Matrix

	Factor	
	1	2
HEIGHT	.799	.445
LENGTH	.906	
EAR LTH		.757
TL-LTH	.492	.821
WT	.895	
CHST	.947	
HK LGTH	.788	
HK LTH-T LTH		-
		.866

4.3.2 Discriminant functions and classifications

This section of the study focusses on the derivation of discriminant functions as well as classification rules for classifying three breeds of sheep into their known groups. First and foremost an 8 variable classification functions was derived for classification followed by a six (6) variable discriminant function.

Canonical Discriminant Analysis

First an eight variable canonical discriminant functions were derived based on the fact that, the major assumption of discriminant analysis was not violated (equal covariance matrices across the three groups).

In order to determine whether the functions to be derived are significant or not, there was the need for the researcher to know the number of functions needed for the separation purposes. Hence the number of functions equals the number of groups or sheep breeds minus one. In this case, we have three groups (WAD, WALL and hybrid or crosses), thus we have $3 - 1 = 2$ possible functions needed for separation purposes. This is evident in Table 4.10 and 4.11 where the first function (function 1) explains 93.1% of the variance and has a small lambda (0.166) and it is significant with p-value of 0.000. The second function explains only 6.9% of the variance in the data, with a recorded p-value of 0.066. Therefore, the second function does not contribute much significantly in the discrimination process as compared to that of the first function. In other words, this factor does not help much in discriminating the groups

Table 4.10: Table of eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	3.734	93.1	93.1	.888
2	.275	6.9	100.0	.465

Table 4.11: Wilks lambda test

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1 through 2	.166	97.987	16	.000
2	.784	13.256	7	.066

In conducting the discriminant analysis, the entire data was standardised due to different measurement scales used for the various breed traits to assume a unit variance or dispersion, under the standard normal distribution. The two derived canonical discriminant functions are :

$$\begin{aligned}
 Discscore1 = & 9.56 - 0.11Ht - 0.07LTH - 0.88EL + 0.37TL - 0.04Wt \\
 & + 0.13CHST - 0.35HK + 0.71HKL - TLt
 \end{aligned}
 \tag{4.1}$$

$$\begin{aligned}
 Discscore2 = & -6.74 + 0.14Ht - 0.031LTH - 0.23EL + 1.63TL - 0.07Wt \\
 & - 0.01CHST - 1.61HK + 1.93HKL - TLt
 \end{aligned}
 \tag{4.2}$$

After computing the discriminant scores using the above two equations, the following proportion of correct classification and misclassifications were recorded and being presented in Table 4.12. Observations were classified into their desired group through the computation of each of the groups prior probabilities.

Table 4.12: Classification Results

Breed Type	Predicted,Group Membership			
	Djallonke/WAD	Sahel/WALL	Crosses	Total
Djallonke/WAD	15	0	8	23
Sahel/WALL	0	8	1	9
Crosses	5	0	24	29
Djallonke/WAD	65.2	0	34.8	100.0
Sahel/WALL	0	88.9	11.1	100.0
Crosses	17.2	0	82.8	100.0
Djallonke/WAD	15	0	8	23
Sahel/WALL	0	8	1	9
Crosses	6	0	23	29
Djallonke/WAD	65.2	0	34.8	100.0
Sahel/WALL	0	88.9	11.1	100.0
Crosses	20.7	0	79.3	100.0

After computation of the discriminant scores using the two canonical discriminant functions derived based on the original variables, the proportion of correct classification as well as misclassified observations were recorded as shown in Table 4.12. Also the same table presents the proportion of correct

classification and misclassification of the cross-validated observations. The cross validated observations means that, observations or sheep breeds were taken out, one after the other, and discriminant functions were derived without the inclusion of the left out observations, but the new derived function was used to classify the left out sheep breeds or observations. From Table 4.12, 65.2% of the original observations from the *Djallonke/WAD* sheep group were correctly classified, with the remaining 34.8% being misclassified into the sheep crosses group.

Also 88.9% of the *Sahel or WALL* sheep breed were correctly classified into their respective group, only one (1) representing 11.1% being misclassified into the *crosses* sheep breed. The functions derived was able to separate the cross sheep breed from the other breeds with 82.8% correct classification of the cross breed into their desired group with the remaining 17.2% being misclassified into the *Djallonke/WAD* sheep breed. In all 78.9 percent correct classification of the sheep breeds using the linear discriminant functions with eight variables or traits was achieved.

A six variable Discriminant function

After the application of the Factor Analysis, which was used to select the variables or breed traits, that would provide maximum separation among the three sheep groups, the following traits were identified as providing maximum separation among the various known groups. The six extracted breed traits includes;

LENGTH, EAR LTH, WT, CHST, HKL GTH and HKLTH-TLTH.

In checking the equality of the covariance matrices for the three groups using the new data (six variate data), Box M test was employed and the computed determinants for each of the three covariance matrices as well as the recorded p-value indicated that, the three covariance matrices of the sheep breeds are not equal, or at least one of the covariance matrices is not equal to the other. Hence,

since the covariance matrices are not equal, the appropriate discriminant function to be derived for classification of the sheep breeds is the Quadratic Discriminant Function (QDF). In this case, two discriminant functions were derived to classify the sheep breeds into their respective groups under unequal prior probability and equal misclassification cost. The two functions derived are as follows;

$$(x - \bar{x}_1)'S_1^{-1}(x - \bar{x}_1) - (x - \bar{x}_2)'S_2^{-1}(x - \bar{x}_2) \leq 0.377 \quad (4.3)$$

$$(x - \bar{x}_1)'S_1^{-1}(x - \bar{x}_3) - (x - \bar{x}_3)'S_3^{-1}(x - \bar{x}_3) \leq 0.148 \quad (4.4)$$

Based on the above quadratic discriminant functions, the various probabilities of correct classification were obtained and are presented in Table 4.13

Table 4.13: Probabilities of correct classifications and misclassification's

Classification			Probabilities		
Observations.	TRUE	Class.	Djallonke/WAD	Sahel/WALL	Crosses
1	Sahel/WALL	Sahel/WALL	0	1	0
2	Sahel/WALL	Sahel/WALL	0	1	0
3	Crosses	Crosses	0.0111	0.0013	0.9876
4	Sahel/WALL	Sahel/WALL	0	1	0
5	Crosses	Crosses	0.0727	0.1946	0.7327
6	Crosses	Crosses	0.0396	0	0.9604
7	Crosses	Crosses	0.0989	0.0012	0.8999
8	Sahel/WALL	Sahel/WALL	0	1	0
9	Sahel/WALL	Sahel/WALL	0	1	0
10	Crosses	Crosses	0	0	1
11	Sahel/WALL	Sahel/WALL	0	0.9998	0.0001
12	Sahel/WALL	Sahel/WALL	0	1	0
13	Crosses	Crosses	0.0155	0	0.9845
14	Sahel/WALL	Sahel/WALL	0	1	0
15	Sahel/WALL	Sahel/WALL	0.0567	0.6766	0.2667
16	Crosses	Crosses	0.2552	0	0.7448
17	Crosses	Crosses	0.409	0	0.591
18	Crosses	Crosses	0.3286	0.0003	0.6711
19	Crosses	Crosses	0.2602	0	0.7398

20	Crosses	Crosses	0.4336	0	0.5664
21	Crosses	Crosses	0.268	0	0.732
22	Crosses	Crosses	0.0426	0	0.9574
23	Crosses	Crosses	0.2697	0	0.7303
24	Crosses	Crosses	0	0	1
25	Crosses	Crosses	0.4503	0	0.5497
26	Crosses	Crosses	0.0774	0	0.9226

Table 4.14: Probabilities of classifications (Cont'd)

Observations.	Classification		Proportion		
	TRUE	Class.	Djallonke/WAD	Sahel/WALL	Crosses
27	Djallonke	Crosses*	0.4958	0	0.5042
28	Crosses	Crosses	0.0926	0	0.9074
29	Djallonke	Crosses*	0.439	0	0.561
30	Djallonke	Djallonke	0.6132	0	0.3868
31	Djallonke	Djallonke	0.6708	0	0.3292
32	Crosses	Crosses	0.2863	0	0.7137
33	Crosses	Djallonke *	0.5045	0	0.4954
34	Djallonke	Crosses*	0.4141	0	0.5859
35	Crosses	Crosses	0.4416	0	0.5584
36	Crosses	Djallonke *	0.627	0	0.373
37	Djallonke	Djallonke	0.5014	0	0.4986
38	Djallonke	Crosses*	0.1932	0	0.8068
39	Djallonke	Djallonke	0.9076	0	0.0924
40	Djallonke	Djallonke	0.7433	0	0.2567
41	Djallonke	Djallonke	0.9266	0	0.0734
42	Djallonke	Djallonke	0.5118	0	0.4882
43	Djallonke	Djallonke	0.9428	0	0.0572
44	Djallonke	Djallonke	0.7214	0	0.2786
45	Crosses	Djallonke *	0.6205	0	0.3795
46	Crosses	Crosses	0	0	1
47	Crosses	Djallonke *	0.875	0	0.125
48	Crosses	Djallonke *	0.6798	0	0.3202
49	Crosses	Djallonke *	0.72	0	0.28
50	Djallonke	Djallonke	0.9915	0	0.0085
51	Crosses	Djallonke *	0.5377	0	0.4623
52	Crosses	Crosses	0.365	0	0.635
53	Djallonke	Djallonke	0.9978	0	0.0022
54	Djallonke	Djallonke	0.8449	0	0.1551
55	Djallonke	Djallonke	0.7136	0	0.2864
56	Djallonke	Djallonke	0.9022	0	0.0978

57	Djallonke	Djallonke	0.9561	0	0.0439
58	Djallonke	Djallonke	0.9207	0	0.0793
59	Djallonke	Djallonke	0.9989	0	0.0011
60	Djallonke	Djallonke	0.9993	0	0.0007
61	Djallonke	Djallonke	0.9988	0	0.0012

* indicates misclassified observations

From Table 4.14, which shows the various probabilities of correct classification, for observation 27, the true population was found to be Djallonke sheep breed, but after the classification using the derived QDF, it was rather classified as cross breed with a probability of 0.5042, indicating a misclassified observation. Also observation 29 which was supposed to be a Djallonke sheep breed was misclassified as a cross breed with its associated probability of 0.561. Meaning observation 29 is more likely to be classified as a cross breed. Similarly observation 33 which comes from a cross sheep breed was misclassified into the Djallonke breed. Also observation 45 belonging to the cross breed was misclassified as a Djallonke sheep breed. In all four (4) Djallonke sheep breeds were misclassified into the cross sheep breeds, seven (7) observations were also misclassified from the cross breed to Djallonke sheep breed. In all eleven (11) sheep breeds were misclassified from either Djallonke or crosses sheep breed. None of the Sahel or WALL sheep breeds were misclassified into either Djallonke or crosses breed. In summary, out of the total sixty one (61) sheep breeds, fifty (50) of them were correctly classified into their respective sheep breed representing approximately 85 percent with eleven (11) being misclassified. The summary of classification and misclassification rates are presented in the confusion matrix table as shown in Table 4.15

Table 4.15: Confusion matrix for summary of classification

TRUE	CLASSIFIED			
	Djallonke/WAD	Sahel/WALL	Crosses	Total
Djallonke/WAD	19 82.61	0 0.00	4 17.39	23 100.00
Sahel/WALL	0 0	9 100	0 0	9 100.00
Crosses	7 24.14	0 0.00	22 75.86	29 100.00

Total	26	9	26	61
	42.62	14.75	42.62	100.00
Priors	0.3770	0.1475	0.4754	

From Table 4.15, 82.61 percent of correct classification of Djallonke/WAD sheep breeds were recorded, with a misclassification rate of 0.1739 into the crosses sheep breed. Also none of the Sahel/WALL sheep breeds were misclassified and a 100 percent correct classification was achieved. For the crosses breed, results from Table 4.15 shows 75.86 correct classification with only 24.14 percent of them being misclassified into the Djallonke/WAD sheep breed. In all 86.2 percent correct classification of sheep breed was achieved.

In evaluating the performance of the derived QDFs, the Leave-one-out method was employed and after the process the summary of correct and misclassified observations were recorded and are presented in Table 4.16.

As evident from the table, the classification of the Djallonke sheep breed saw approximately 61 percent correct classification of the sheep, similar correct classification rate of approximately 67 percent was recorded for classification of Sahel/WALL breed. The method under leave-one-out correctly classified 62.07 percent of the crosses sheep breed. In all the Sahel/WALL breed recorded the highest correct classification of 0.6667 under leave-one-out error rate estimator.

Table 4.16: Leave-one-out classification summary

TRUE	Classified			
	Djallonke/WAD	Sahel/WALL	Crosses	Total
Djallonke/WAD	14 60.87	0 0.00	9 39.13	23 100.00
Sahel/WALL	0 0.00	6 66.67	3 33.33	9 100.00
Crosses	11 37.93	0 0.00	18 62.07	29 100.00
Total	25 40.98	6 9.86	30 49.18	61 100.00
Priors	0.377	0.1475	0.4754	

Chapter 5

SUMMARY OF FINDING, CONCLUSIONS AND RECOMMENDATIONS

5.1 Introduction

This Chapter presents the summary of the results/findings, the concluding part of the study based on the summary of the results and possible recommendations to be suggested.

5.2 Summary

This study was based on the following two specific objectives;

1. To perform variable selection criterion for discriminating best among the three known breeds of sheep.
2. To obtain discriminant functions for providing maximum separation among the breeds of sheep.

The presentation and discussion of results of this study were categorised into two, namely the preliminary and further analysis. The preliminary analysis was mainly based on the computation of descriptive statistics specifically the measures of central tendencies such as the mean and the standard deviation of the various traits for each of the three breeds. The study observed some differences in the traits of sheep breeds based on their computed averages. Test of significance difference among the mean. The values of all the eight traits were tested using F-test. The study found significance difference among the following traits namely; HEIGHT, EAR LTH, TL LTH, HK LGTH and HK LTH-TLTH. However the following traits (LENGTH, WT, CHST) were discovered as having no significance difference among the three sheep breeds.

Based on further analysis carried out in the previous chapter, the following summarises of the results were obtained from the analysis.

- The equality of the three covariance matrices of the three sheep breeds were tested based on the eight variate data using Box's M test. Results from the test indicates that all the covariance matrices for the eight variate data are equal.
- Two Canonical/Linear discriminant functions were derived using the 8 variate data under the equal covariance condition.
- Using the two derived linear discriminant functions, the proportion of correct classification as well as misclassifications were recorded.
- Factor analysis was employed as a variable selection criterion to select the variables that provide better separation among sheep breeds in their respective groups/population.
- After satisfying all the assumptions of factor analysis, the eight variables separating the sheep breeds were reduced to a more simplified data of six (6) variate data.
- The six extracted sheep traits data was therefore used to compute the discriminant functions for provision of maximum separation. However, the covariance matrices of the three sheep breeds for were tested using the Box's M test.
- The Box M test indicated that, the six variate data have unequal covariance matrices across the three sheep groups.
- Two quadratic discriminant functions were derived for separation and classification purposes.
- In all approximately 87 percent of correct classification was achieved after cross validation process.

5.3 Conclusion

The study was aimed at establishing a separator or discriminating function for separating the three known sheep breeds (hybrid or crosses, WAD and WALL sheep breeds). The derived discriminant functions provided maximum separation among the three known breeds with an overall classification rate of 78.9 percent. However, factor analysis extracted six traits out of the eight variables and the derived discriminant functions with the six variables provided better separation than the eight variate discriminant equation (Canonical discriminant function). Quadratic discriminant functions were derived from the six variate data and 86.2 percent correct classification of sheep breeds were achieved. The study can therefore conclude that breeds of sheep and other animals can clearly be separated based on their physical traits with minimum error of misclassification.

5.4 Recommendation

The following are some recommendations made by the researcher according to the findings of the study.

1. One should consider adopting/using the quadratic discriminant function since it more appropriate in classifying known breeds of animals as compared to other classifiers.
2. Further studies should consider a data with large sample size as well as large dimension to really study the effect of these factors on classification.

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