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2025
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Maboea, Selloane . (2025). A reassessment of single long bone dimensions to estimate sex in adult South African skeletal remains [Master`s dissertation, University of the Witwatersrand, Johannesburg]. WIReDSpace. https://hdl.handle.net/10539/48263

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A reassessment of single long bone dimensions to estimate sex in adult South African skeletal remains.

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Plagiarism declaration

I, Selloane Kgadi Maboea, declare that this Dissertation Report is my own, unaided work. It is being submitted for the Degree of Master of Science in Medicine (Dissertation) at the University of the Witwatersrand, Johannesburg. It has not been submitted before for any degree or examination at any other University.



(Signature of candidate)

27th day of May 2025 in Bassonia, Johannesburg

Abstract

The use of postcraniometrics has been popularised in forensic anthropology to find landmark measurements and methods that provide high classification rates, high reliability, and repeatability in estimating demographic parameters. In 2000, Loth and İşcan utilised bony landmarks from the humerus, tibia and femur to develop univariate sectioning points to estimate sex in South African Black and White populations. The accuracy of the Loth and İşcan (2000) method has, however, not been validated. This study, therefore, aimed to validate the accuracy of the Loth and İşcan (2000) sectioning points on a Black and White South African sample. Given the small sample size of the Loth and İşcan (2000) study, this study further aimed at developing new sectioning points using a much larger sample of South African Black and White individuals, as well as adding sectioning points for South African Coloured individuals. In addition to creating new sectioning points, this study aimed to develop multivariate formulae utilising only the measurements defined in Loth and İşcan (2000) by employing flexible discriminant analysis (FDA) and stepwise discriminant function analyses (DFA). Applying the Loth and İşcan (2000) sectioning points to the current sample reduced accuracy to 80,75% for Black South Africans and 78,63% for White South Africans. Tibial distal breadth (TDB) misclassified all Black females and correctly classified only 2,00% of White females. The newly developed sectioning points outperformed the original ones. In multivariate analysis, both FDA and DFA performed well, with FDA performing slightly better. FDA accuracies ranged from 87,4% to 90,9%, while DFA ranged from 86,9% to 91,25%, with the highest accuracy for Black South Africans. Overall, the Loth and İşcan (2000) method showed reduced accuracy when applied to a larger South African sample, particularly for females. This study enhanced sex estimation by refining sectioning points and introducing multivariate formulae, achieving classification rates of 88,50–94,00% for Black, 84,50–90,50% for White, and 84,20–90,79% for Coloured South Africans.

Acknowledgements

I would like to extend my deepest gratitude to my supervisors, Dr Anja Meyer and Mr Okuhle Sapo, for their guidance and support through this journey. Thank you to Dr Brendon Billings and Mr Mashudu Mulaudzi for their help at the Raymond A. Dart Collection of Human Skeletons, they made data collection an absolute joy, thank you both for your kindness, humour, and the space you allowed for me to vent, and sometimes even cry. I would also like to extend my heartfelt thanks to Dr Mandi Albas for granting me access to the Kirstenbosch Skeletal Collection and reminding me that cool people still exist. The University of the Witwatersrand, Johannesburg, South Africa, for their financial assistance with the Postgraduate Merit Award and the J.J.J Smieszek Bursary. I am equally grateful to my family for their love, patience, and understanding, which has sustained me through the challenges and triumphs of this project. Their constant belief in me has been my greatest source of strength, and this accomplishment is as much theirs as it is mine. Thank you all for being my unwavering pillars. To my father, who passed in February of 2024: Through the pain, I was able to finish, a testament to the spirit you instilled within me. I dedicate this work to you.

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1. Introduction

Forensic anthropologists play a crucial role in estimating the presumptive identity of unknown individuals based on skeletal remains, often recovered from murder scenes and mass fatality disasters (Ousley *et al*., 2009). This is achieved by estimating a biological profile, which consists of specific demographic parameters such as age-at-death, stature, ancestry, and sex (Spradley, 2016; Siwan *et al.,* 2025). These profiles are constructed using various morphometric methods, which are typically population-specific (Krishan *et al*., 2016). Research has shown that demographic parameter estimation performs better when population-specific methods are employed (Spradley, 2016). Demographic parameters play an essential role in identifying unknown persons; for example, determining sex narrows down search parameters by approximately 50% (Spradley, 2016; Klales and Lesciotto, 2025).

Traditional methods, such as sex estimation using the pelvis proposed by Phenice, (1969) and Klales *et al.* (2012), and sex estimation utilising the cranium proposed by Walker, (2008), have often yielded accurate results but present certain limitations, including high subjectivity and ill-defined scoring criteria (Spradley and Jantz, 2011; Lottering, 2020; Braun *et al.,* 2023; Flaherty *et al.,* 2023). To ensure the scientific validity of methodologies, the Daubert criteria are commonly applied. These criteria require that a methodology has been previously tested, possesses defined standards for application, has undergone peer review and publication, has a known error rate, and is generally accepted within the relevant scientific field (Lesciotto, 2023).

In South Africa, violent crimes, body dumping resulting in specific taphonomic factors such as scavenger activity and displacement, deliberate or accidental burning of remains, resulting in severe fragmentation, and, less commonly, body mutilation frequently result in the

recovery of fragmentary human remains (Asala *et al.,* 2004; Lottering, 2020). As a result, methods designed for the analysis of well-preserved skeletal remains are often unsuitable in certain forensic contexts. Given the critical role of sex estimation in the identification process (Nakahashi and Nagai, 1986), the application of methods requiring fewer measurements becomes essential in cases involving incomplete remains. One such development is the study by Loth and İşcan (2000), which proposed the use of single long bone measurements for sex estimation, thereby facilitating the analysis of fragmentary or incomplete skeletal remains. Similarly, other postcranial studies (Steyn and İşcan, 1997, 1999; Barrier and L'Abbé, 2008; Spradley and Jantz, 2011; Moore *et al.,* 2016) have employed comparable approaches in single long bone sex estimation. However, these studies notably lack representation of the Coloured South African population.

Despite its contribution to the field, the study by Loth and İşcan (2000) was developed using a relatively small sample comprising 37 Black males, 44 Black females, 44 White males, and 42 White females. Furthermore, the study exclusively analysed and presented results for the South African Black and White population groups. The utilised sample was vaguely described as a "modern twentieth-century" sample, raising the possibility that its findings may be susceptible to the effects of secular change, potentially influencing the accuracy and applicability of the method over time. It is therefore recommended that the method be reassessed using a larger, more representative sample. Secular change is defined as non-genetic variation occurring over successive generations (Albanese, 2008) and is typically associated with shifts in living conditions, environmental factors, and socioeconomic status. These changes are often reflected in population means when analysing growth and development trends (Roche, 1979; Albanese, 2008). Consequently, secular change is recognised as a critical factor in most morphometric studies (Jantz, 1992; Gonçalves, 2014). However, due to the imprecise description of the age of the collection used by Loth and İşcan

(2000), some chronological overlap may exist. As the twentieth century spans from 1901 to 2000, and the sample employed in the present study dates from 1948 to 2014, the potential impact of secular change may be limited.

1.1 Aims and Objectives

The current study aimed to validate and evaluate the accuracy of the original Loth and İşcan (2000) sex estimation method. Secondly, it determined whether new sectioning points and accuracies can be obtained when a larger sample more representative of the current South African population is used. Thirdly, to try and improve on the original Loth and İşcan (2000) method by incorporating multivariate methods that may be useful in presenting higher accuracy rates in cases where more than one of the skeletal elements used in the Loth and İşcan (2000) method is available. To fulfil these aims, the following objectives have been met:

- Test the intra- and inter-observer repeatability of the Loth and İşcan (2000) measurements on a subsample.
- Test the accuracy of the original Loth and İşcan (2000) study on a sample of recent adult South African individuals of known sex.
- Utilising a larger sample of South African Black, White and Coloured individuals, develop new univariate sectioning points for each single long bone dimension for males and females.
- Develop multivariate flexible discriminate functions (FDAs) utilising different combinations of the single bone dimensions used in Loth and İşcan (2000).
- Develop multivariate discriminate functions (DFAs) utilising different combinations of the single bone dimensions used in Loth and İşcan (2000).
- Assess whether FDA or DFA functions produce higher classification accuracies.

2. Literature Review

2.1 Sexual dimorphism

Sex is biologically categorised as male or female and should not be confused with gender, which refers to an individual's self-identity and social role, predominantly shaped by cultural, environmental, and psychosocial factors (Armelagos, 1998; Torgrimson and Minson, 2005; Kirchengast, 2014). In contrast, sex pertains to the biological differences between males and females, determined by the presence of X and Y chromosomes, various genes, and the influence of hormones that regulate the establishment and maintenance of sexually dimorphic characteristics from embryonic and foetal development through to adulthood (Armelagos, 1998; Kirchengast, 2014).

Sexual dimorphism refers to the morphological differences observed between the sexes, classified into primary and secondary sexual dimorphism (Ralls and Mesnick, 2009; Kirchengast, 2014). Primary sexual dimorphism is directly associated with reproductive function and includes differences in the size and structure of gametes (sperm and ova), the configuration of reproductive organs, and the morphology of pelvic structures, which are adapted for parturition (Leong, 2006; Söder, 2007; Kirchengast, 2014).

Secondary sexual dimorphism pertains to phenotypic traits that develop in response to sex hormones such as androgens, oestrogens, and progestins, particularly during adolescence and puberty (Kirchengast, 2014). In childhood, differences in growth velocity between the sexes contribute to early sexual dimorphism (Greil, 2006), with these distinctions becoming most pronounced in young adulthood (18 to 26 years of age) before diminishing in later life (Greil, 2006). Observable characteristics associated with secondary sexual dimorphism include the

development of facial hair, breast tissue formation, variations in body size and height, voice changes, and other somatic traits. These differences are not only externally visible but are also morphologically and osteologically distinguishable, particularly once skeletal maturity has been attained.

During puberty, bone size differences between the sexes become established, primarily due to accelerated periosteal apposition and comparatively less endocortical expansion in males (Seeman, 2001). This process results in increased bone diameter, thicker cortical bone, and a larger medullary cavity in males. The thickening of cortical bone is driven by periosteal apposition, a process regulated by testosterone acting via the androgen receptor, as well as by growth hormone (GH) and insulin-like growth factor 1 (IGF-1) (Yeh *et al*., 1996; Zhang *et al*., 1999; Seeman, 2001; Mosekilde *et al.,* 2013).

Testosterone exerts a direct and positive influence on the human skeleton, particularly in relation to appositional growth — a process characterised by an increase in bone diameter through osteoblastic activity (Mosekilde *et al*., 2013). Osteoblasts, the cells responsible for bone formation, express androgen receptors, the distribution of which varies with age, with a higher receptor density present in younger bone compared to senescent bone (Notelovitz, 2002; Clarke and Khosla, 2009). Furthermore, a greater concentration of androgen receptors is found in cortical bone relative to trabecular bone. As cortical bone constitutes the outer surface of long bones, this differential receptor expression contributes to variations in bone shape and size (Notelovitz, 2002; Clarke and Khosla, 2009). Testosterone acts directly on osteoblasts through these androgen receptors, promoting bone formation by enhancing receptor expression and subsequent osteoblastic activity (Shigehara *et al*., 2021).

In addition to its role in appositional growth, testosterone also influences interstitial growth by stimulating the proliferation of chondrocytes. Interstitial growth refers to the increase in

bone length through the development of cartilage and its replacement by bone tissue. The extent of both appositional and interstitial growth is modulated by circulating testosterone levels. Androgens such as testosterone contribute significantly to bone strength through increased periosteal bone formation, ultimately resulting in larger overall bone dimensions in males (Seeman, 2001; Clarke and Khosla, 2009).

In contrast, female pubertal development is characterised by endocortical bone formation, increased cortical thickness, and a reduction in the size of the medullary cavity (Seeman, 2001). During this period, oestrogen inhibits periosteal apposition in females (Seeman, 2001; Clarke and Khosla, 2009). Oestrogens are well-documented for their role in the closure of epiphyseal growth plates during late puberty (Väänänen and Härkönen, 1996; Mosekilde *et al*., 2013) and are essential for the maintenance of trabecular bone volume and skeletal strength in both sexes (Mosekilde *et al.,* 2013). Notably, oestrogen demonstrates a biphasic effect on epiphyseal growth: at low concentrations , typically present in males , it stimulates growth, whereas higher concentrations , as observed in females , are associated with the cessation of bone growth (Chen *et al.,* 2019).

Although bone development processes differ between the sexes, cortical thickness is relatively comparable. However, measurable differences persist. The primary distinction lies in the predominance of periosteal apposition in males versus endocortical apposition in females (Seeman, 2001; Singh *et al.,* 2010). Greater periosteal bone formation in males leads to spatial differences in bone architecture, notably an increase in the medullary cavity area and, consequently, greater overall bone dimensions (Kontulainen *et al.,* 2005; Singh, 2010). The enlargement of the medullary cavity results in an expanded external bone perimeter. In simplified terms, male bone growth predominantly occurs outward (periosteal), while in females, it occurs inward (endocortical), contributing to observable sex-based size and shape differences (Seeman, 2001; Singh *et al.,* 2010).

Differences in long bone length between the sexes are also attributed to a prolonged prepubertal growth period in males compared to females (Cameron *et al*., 1982; Parfitt *et al.,* 2000; Seeman, 2001; Nieves *et al.,* 2005). Males typically experience a delayed onset of puberty, resulting in approximately one to two additional years of prepubertal growth relative to females (Cadogan *et al.,* 1998; Seeman, 2001; Singh *et al.,* 2010; Abacı and Besci, 2024). During this prepubertal stage, the appendicular skeleton undergoes rapid growth, with the lower limbs experiencing a faster growth rate than axial skeletal elements such as the spine (Bass *et al.,* 1999). As puberty commences, the growth rate of the appendicular skeleton decelerates, while axial skeletal growth accelerates (Gasser *et al.,* 1991; Bass *et al.,* 1999; Seeman, 2001; Iuliano-Burns *et al.,* 2009). Additionally, the pubertal growth spurt lasts longer in males than in females (Singh *et al.,* 2010; Scheffler and Hermanussen, 2018; Umbraško *et al.,* 2024), which further contributes to greater adult stature and larger bone size in males (Singh *et al.,* 2010).

Sexual dimorphism has also been shown to vary between populations (Black III, 1978; Brown, 1981; MacLaughlin and Bruce, 1986; González *et al.,* 2007; Crook, 2017; Ubelaker and DeGaglia, 2017; Padmakaran and Srivastava, 2023). This population specificity is attributed primarily to two interrelated factors: genetics and environmental influences (Ubelaker and DeGaglia, 2017). Genetics shape the degree of sexual dimorphism through selective pressures and genetic adaptations (Frayer and Wolpoff, 1985; Franklin *et al.,* 2008), while environmental factors encompass a broader range of influences, including nutrition, social roles, and disease burden (Frayer and Wolpoff, 1985; Ubelaker and DeGaglia, 2017). According to Ubelaker and DeGaglia (2017), population variability in the expression and measurable extent of sexual dimorphism across various aspects of the human skeleton results from the interaction of these genetic and environmental forces throughout growth and development.

Furthermore, Ubelaker and DeGaglia (2017) note that global research on sexual dimorphism has increasingly demonstrated the necessity of representing diverse population groups, particularly in size-based analyses. This underscores the importance of developing and applying population-specific sex estimation methods. The significance of such tailored standards is further illustrated in a study by Krüger *et al.* (2014), which evaluated the applicability of Walker's (2008) cranial sex estimation method , originally developed using a North American sample , on South African crania. When applied to this context, the highest classification accuracies were achieved for White South African males (94–97%), while the lowest were recorded for White South African females, with accuracies ranging from 31% to 62%. Black South African males showed classification rates of 84–92%, and Black South African females ranged between 55% and 90%. The notably lower accuracies, particularly among females, reveal population differences in cranial morphology (Krüger *et al*., 2015), reinforcing the necessity for population-specific sex estimation standards.

2.2 Sex estimation methods

Sex estimation in skeletal remains can be conducted using either morphological or metric assessments of shape and size. Morphological methods involve the macroscopic evaluation of bone shape, size, and configuration, focusing on features that typically differ between males and females (Loth and İşcan, 2000). These approaches frequently assess characteristics such as the greater robusticity seen in male skeletal remains and the relative gracility observed in females (Geller, 2005; Ubelaker and DeGaglia, 2017). Among skeletal elements, the os coxae is widely considered the most sexually diagnostic bone (Phenice, 1969; Tague, 1992; Patriquin *et al*., 2003; DeSilva and Rosenberg, 2017), followed in accuracy by long bones (Steyn and İşcan, 1997, 1999; France, 1998; Spradley and Jantz, 2011; Krüger *et al.,* 2017;

Liebenberg *et al.,* 2019), and lastly, the cranium (Bass, 2005; Franklin *et al.,* 2008; Pickering and Bachman, 2009; Krüger *et al*., 2015; Lottering, 2020).

Historically, sex estimation has largely focused on cranial and mandibular morphoscopic traits and osteometric measurements (Hrdlička, 1952; Krogman and İşcan, 1986; Bass, 2005; Pickering and Bachman, 2009). Morphoscopic features typically assessed include the development of the supraorbital ridge (Buikstra and Ubelaker, 1994; Steyn and İşcan, 1998; Dayal *et al*., 2008; Walker, 2008; Krüger *et al.,* 2015; Nikita and Michopoulou, 2018; Bertsatos *et al*., 2020; Gupta, 2023), the slope of the frontal bone (Buikstra and Ubelaker, 1994; Petaros *et al*., 2017), gonial flaring (Buikstra and Ubelaker, 1994; Oettlé *et al.,* 2009; Saini, 2017; Malek, 2022), mastoid size (Buikstra and Ubelaker, 1994; Steyn and İşcan, 1998; Dayal *et al.,* 2008; Walker, 2008; Krüger *et al.,* 2015; Nikita and Michopoulou, 2018; Bertsatos *et al*., 2020; Gupta, 2023), thickness of the supraorbital margins (Buikstra and Ubelaker, 1994; Steyn and İşcan, 1998; Dayal *et al.,* 2008; Walker, 2008; Krüger *et al.,* 2015; Nikita and Michopoulou, 2018; Bertsatos *et al.,* 2020; Gupta, 2023), projection of the mental eminence (Buikstra and Ubelaker, 1994; Steyn and İşcan, 1998; Dayal *et al.,* 2008; Walker, 2008; Krüger *et al.,* 2015; Nikita and Michopoulou, 2018; Braun *et al.,* 2022), and the expression of the nuchal crest (Buikstra and Ubelaker, 1994; Steyn and İşcan, 1998; Dayal *et al.,* 2008; Walker, 2008; Krüger *et al.,* 2015).

However, the cranium tends to be less reliable for sex estimation compared to postcranial measurements, as cranial morphology is often more influenced by population-specific genetic variation than by hormonal factors associated with biological sex (Maat *et al.,* 1997; Murail *et al*., 1999; Kjellström, 2004; Đurić *et al*., 2005; Garvin *et al*., 2014; Krüger *et al.,* 2015; Liebenberg *et al.,* 2019).

Considerable research has also focused on the pelvis for sex estimation, examining morphological traits such as the shape of the pelvic inlet, presence of a ventral arc (Phenice,

1969; Klales *et al.,* 2012; Chovalopoulou *et al.,* 2022; Hamzah *et al.,* 2023), the preauricular sulcus (Rogers and Saunders, 1994; Karsten, 2018; Inskip *et al.,* 2019), pubic bone robusticity (Kenyhercz, 2012; Klales *et al.,* 2012; Blake and Hartnett-McCann, 2018), the iliac crest (Fernandez Camacho *et al.,* 1993; Vetter and Moore-Jansen, 2009; Monge Calleja *et al.,* 2023), the size and position of the acetabulum (Macaluso Jr, 2010; Bubalo *et al.,* 2019; Warrier and San-Millán, 2024), auricular surface dimensions (Wescott, 2015), sacral width and curvature (Krüger *et al.,* 2017; Etli *et al., ,* 2019; Krenn *et al.,* 2022), subpubic angle (Klales *et al*., 2012; Ali *et al*., 2020; Ghafoor *et al*., 2023), greater sciatic notch dimensions (Buikstra and Ubelaker, 1994; Walker, 2005; Kilmer and Garvin, 2020; Knecht *et al*., 2021), and the morphology of the ischiopubic ramus (Phenice, 1969; Bruzek, 2002; Patriquin *et al*., 2003; Klales *et al*., 2012). Despite this, not all skeletal remains present with distinct morphological indicators of sexual dimorphism (Loth and İşcan, 2000).

As noted, the degree of sexual dimorphism expressed in skeletal morphology is shaped by a range of intrinsic and extrinsic factors, including environmental conditions, population affinity, social status, and varying levels of sex hormones such as testosterone and oestrogen (Kirchengast, 2014; Kleisner *et al*., 2021; Lassek and Gaulin, 2022; Muraro *et al*., 2022). Intrinsic factors encompass inherited biological variables such as genetics, hormonal levels, and developmental timing. For example, in males, intrinsic influences may manifest through strength and competitive behaviors linked to testosterone levels (Mabweazara *et al*., 2019). Conversely, extrinsic factors refer to environmental or cultural influences that affect phenotypic expression, such as body weight management trends impacting female physique (Mabweazara *et al*., 2019).

Given the complex interplay of intrinsic and extrinsic factors influencing sexual dimorphism, morphological sex estimation relies on the consistent expression of sexually dimorphic traits within a population for accurate classification. In contrast, metric analyses offer greater

objectivity and consistency, as growth patterns, skeletal development, and overall size are also shaped by the same variables affecting sexual dimorphism (Roche, 1979; Albanese, 2008). This highlights the particular value of metric analysis in the assessment of sexual dimorphism. Additionally, morphological methods remain highly subjective, requiring metric analysis to reduce observer bias and increase reliability (Ramsthaler *et al*., 2007; Curto *et al*., 2023). Metric methods are especially useful when the morphology of traits is ambiguous or when sex differences are primarily size-related (Loth and İşcan, 2000). However, the most robust results are often achieved when both morphological and metric methods are employed together to maximise accuracy and reliability.

Metric sex estimation holds several advantages: it minimises subjectivity, requires less observer experience (Spradley and Jantz, 2011), is easily repeatable, and most methods provide classification accuracies and statistical probabilities that strengthen their utility in medico-legal contexts (Spradley and Jantz, 2011). Metric analysis can involve the use of a single measurement (univariate) or multiple measurements (multivariate). Multivariate analyses typically produce higher classification accuracy rates than univariate analyses (Jiménez-Arenas and Esquivel, 2013). However, multivariate methods require a greater level of skeletal completeness, which limits their applicability in cases involving incomplete or fragmentary remains (Jiménez-Arenas and Esquivel, 2013). In contrast, univariate analysis is valuable because it can accurately classify sex using fewer measurements, making it especially practical in situations involving fragmentary remains, a common challenge in forensic cases (Steyn and İşcan, 1999; Asala, 2001). Consequently, univariate dimensions remain an important and effective option for sex estimation when skeletal material is limited (Steyn and İşcan, 1999).

Well-known and widely applied metric analysis methods in biological anthropology include discriminant function analysis (DFA), also referred to as linear discriminant analysis (LDA).

This technique is frequently used alongside software programs with built-in population databases, such as FORDISC (Jantz and Ousley, 2005), which provide classification accuracies and probabilities based on specific population groups. DFA is primarily applied when the dependent variable is categorical, the independent variables are continuous, and several statistical assumptions are met. These assumptions include the independence of observations, homogeneity of variance-covariance matrices, linearity, and multivariate normality (Krüger *et al*., 2017).

DFA is a well-established technique and has been applied to a wide range of skeletal elements, including the pelvis (Dibennardo and Taylor, 1983; Luo, 1995; Patriquin *et al*., 2003; Dixit *et al*., 2007; Steyn and İşcan, 2008; Macaluso Jr, 2010; Gómez-Valdés *et al*., 2011), cranium (Birkby, 1966; Franklin *et al*., 2005; Franklin *et al*., 2008; Walker, 2008; Dayal *et al*., 2009; Gapert *et al*., 2009; Robinson and Bidmos, 2009; Spradley and Jantz, 2011; Marinescu *et al*., 2014), femur (Dibennardo and Taylor, 1983; Loth and İşcan, 2000; Wrobel *et al*., 2002; Spradley and Jantz, 2011; Krüger *et al*., 2017; Banyeh *et al*., 2022), and humerus (Loth and İşcan, 2000; Mall *et al*., 2001; Wrobel *et al*., 2002; Spradley and Jantz, 2011; Krüger *et al*., 2017). Additional elements analysed with DFA include the ulna (Mall *et al*., 2001; Wrobel *et al*., 2002; Barrier and L'abbé, 2008; Spradley and Jantz, 2011; Krüger *et al*., 2017; Banyeh *et al*., 2022), radius (Mall *et al*., 2001; Wrobel *et al*., 2002; Barrier and L'abbé, 2008; Spradley and Jantz, 2011; Krüger *et al*., 2017; Ngidi *et al*., 2023), sacrum (Spradley and Jantz, 2011; Krüger *et al*., 2017), tibia (Loth and İşcan, 2000; Spradley and Jantz, 2011; Krüger *et al*., 2017), calcaneus (Spradley and Jantz, 2011; DiMichele and Spradley, 2012), vertebrae (Ostrofsky and Churchill, 2015), and ribs (Navadijo *et al*., 2023). In South African populations, DFA classification accuracies generally range between 85,00 – 95,00% for these skeletal elements. However, lower accuracies have been reported for specific elements such as the radius (Barrier and L'Abbé, 2008), ulna (Barrier and L'Abbé,

2008; Banyeh *et al*., 2022), and femur (Banyeh *et al*., 2022), where accuracy rates fall below 85%.

Another valuable technique is flexible discriminant analysis (FDA), a nonparametric adaptation of DFA that replaces the linear regression model with a nonparametric regression approach. This adjustment enables FDA to function as a more flexible classifier, particularly in cases where the assumptions of DFA are violated (Liebenberg, 2014; Liebenberg *et al*., 2015; Krüger *et al*., 2017; Stull *et al*., 2017; Coelho and Curate, 2019; Liebenberg *et al*., 2019; Knecht *et al*., 2021; Nogueira *et al*., 2023). In South Africa, FDA has been primarily employed in ancestry and sex estimation research (Liebenberg, 2014; Liebenberg *et al*., 2015; Liebenberg *et al*., 2019; Bothma, 2023). Notable studies have applied FDA for sex estimation based on the pelvis (Coelho and Curate, 2019) and long bones (Krüger *et al*., 2017; Stull *et al*., 2017; Liebenberg *et al*., 2019; Nogueira *et al*., 2023). In South African contexts, FDA classification accuracies for sex estimation have ranged from 75,00% to 98,00% (Krüger *et al*., 2017; Stull *et al*., 2017; Liebenberg *et al*., 2019).

2.3 Postcranial sex estimation

Pearson (1915) was the first to propose that sex could be estimated using postcranial metrics, a suggestion that has since been supported by numerous studies (Berrizbeitia, 1989; Steyn & İşcan, 1999; Loth and İşcan, 2000; Barrier and L'Abbé, 2008; Spradley & Jantz, 2011; Krüger *et al.,* 2017; Liebenberg *et al*., 2019). Differences in testosterone and oestrogen levels between sexes contribute to variations in the shape and size of long bones, which underpins the use of these bones in sex estimation (Seeman, 2001; Clarke and Khosla, 2009). Consequently, long bone dimensions have shown considerable promise for accurately estimating an individual's sex.

One of the earliest studies employing postcranial measurements was conducted by Berrizbeitia (1989), who used sectioning points on the radial head diameter to estimate sex. The sample comprised radii from Black and White North American individuals in the Terry Collection at the Smithsonian Institution. Classification accuracy ranged from 92,00% for the left radius, 94,00% for the right radius, and 96,00% when both radii were used.

Subsequent studies, such as Brown *et al*. (2007), applied Purkait's triangle method to the proximal femur in a sample of 200 Indo-European and African American adult femora from the Terry Collection. The Purkait triangle involves measuring the sides of a triangle defined by three anatomical landmarks on the femur. Discriminant function analysis revealed that the distance between the greater and lesser trochanters produced accuracy rates of 85,50%, while the maximum vertical diameter of the femoral head yielded 87,00%. When both measurements were used in a multivariate model, classification accuracy improved to 90,00%.

Similarly, Albanese *et al*. (2008) employed population-independent metric ratios and logistic regression to estimate sex from the proximal femur, achieving classification accuracies of 90,60% to 95,00%, particularly when analysing the neck angle at the greater trochanter. Albanese (2013) later developed additional population-independent equations to estimate sex from the clavicle, humerus, radius, and ulna. When tested on the Grant Collection sample, these equations produced accuracy rates ranging from 87,40% to 97,50%, depending on the bone and sample.

Several prominent South African studies have also used postcranial elements, including the tibia, femur, humerus, radius, ulna, clavicle, fibula, innominate, sacrum, and calcaneus, to estimate sex in South African Black and White populations, achieving classification accuracies between 76,00% and 98,00% (Steyn & İşcan, 1997, 1999; Loth & İşcan, 2000; Barrier and L'Abbé, 2008; Krüger *et al*., 2017).

For example, Steyn and İşcan (1997) studied a White South African sample, taking multiple femoral measurements (e.g., maximum length, head diameter, midshaft circumference and diameter, and epicondylar breadth) and tibial measurements (e.g., physiological length, proximal and distal epiphyseal breadths, diameter and circumference at the nutrient foramen, and distal shaft circumference). Using both univariate and multivariate discriminant function analyses (DFAs), they reported classification accuracies between 86,00% and 91,00%, with multivariate models performing best.

In a follow-up study, Steyn and İşcan (1999) examined the humerus in Black and White South Africans using multivariate and stepwise DFAs, achieving classification accuracies of 95,00% and 96,00%, respectively.

Barrier and L'Abbé (2008) analysed various metric dimensions of the radius and ulna. For the radius, measurements included maximum length, distal breadth, midshaft sagittal and transverse diameters, vertical head height, minimum and maximum head diameters, and circumferences at the head and tuberosity. For the ulna, variables included maximum length, anterior-posterior and medial-lateral diameters, minimum circumference, olecranon breadth, minimum olecranon breadth, and olecranon height. Using both univariate and multivariate DFAs, they achieved classification accuracies of 76,00% and 86,00%.

Krüger *et al*. (2017) employed 39 osteometric measurements from 11 postcranial bones, the clavicle, scapula, humerus, radius, ulna, sacrum, innominate, femur, tibia, fibula, and calcaneus, in a sample of 360 South African individuals (Black, White, and Coloured). They used linear discriminant analysis (LDA) and flexible discriminant analysis (FDA) to classify sex and ancestry. In univariate models, the anteroposterior diameter of the radius yielded the highest accuracy for both LDA and FDA. LDA-based univariate accuracies ranged from 56% to 89,00%, while FDA ranged from 60,00% to 89,00%.

For bone-specific models, LDA accuracies ranged from 75,00% to 90,00%, with the radius being most accurate and the sacrum and fibula least accurate. FDA results were similar, ranging from 75,00% to 91,00%, with the clavicle outperforming other bones and the fibula again being the poorest performer.

In multivariate subset analyses, LDA achieved accuracies of 90,00% to 98,00%, particularly when combining bones from the hip and lower limbs. FDA models yielded similar accuracies of 90,00% to 97,00%, with the best performance observed when all variables were included in the analysis.

2.4 Loth and İşcan (2000) method

In 2000, Loth and İşcan demonstrated that, within the Black South African population, the measurements with the highest classification accuracies were the femoral head diameter (92,00%) and the humeral head diameter (91,00%) (Loth and İşcan, 2000; Barrier and L'Abbé, 2008). In contrast, for the White South African population, the femoral distal breadth yielded the highest classification accuracy at 90,50%.

Loth and İşcan (2000) employed eight univariate measurements defined by Buikstra and Ubelaker (1994): humeral head diameter (HHD), humeral epicondylar breadth (HEB), femoral head diameter (FHD), femoral midshaft circumference (FMC), femoral distal breadth (FDB), tibial proximal breadth (TPB), tibial circumference at the nutrient foramen (TCN), and tibial distal breadth (TDB). These measurements were taken from the humerus, femur, and tibia of South African individuals, 81 Black and 86 White.

Using these univariate dimensions, the study reported classification accuracies ranging from 74,30% to 91,90%. In the White South African sample, FMC yielded the lowest accuracy (74,30%), while in the Black South African sample, TCN had the lowest accuracy (83,50%). Despite being the least accurate in their respective groups, both metrics still produced relatively high classification rates.

Importantly, Loth and İşcan (2000) focused on long bone measurements from skeletal elements that are commonly recovered at crime scenes or mass graves, even when remains are fragmented. As such, their method provides forensic anthropologists with a practical approach to estimating sex in the absence of the pelvis or when dealing with incomplete remains.

Their study applied univariate discriminant function analysis to determine whether a measurement fell within the male or female range, using average values or sectioning points specific to each population group. While numerous studies have cited this work (Kranioti, 2009; Bidmos *et al*., 2010; Blau, 2014; Krüger *et al*., 2015; Kiskira *et al*., 2022), none have validated the method or developed multivariate formulas using the same set of measurements.

3. Materials and methods

The samples used in this study were obtained from the Raymond A. Dart Collection of Modern Human Skeletons (University of the Witwatersrand), the Pretoria Bone Collection (University of Pretoria), and the Kirsten Skeletal Collection (University of Stellenbosch) (Table 1) (Dayal *et al*., 2009; Alblas *et al*., 2018; L'Abbé *et al*., 2021). The sample comprised of adult individuals, and the ages at death ranged between 24 and 89 years.

The collections present a cross-section of the population of South Africa (Steyn and İşcan, 1999; Baliso *et al.*, 2024) and consist of unclaimed and donated remains (Krüger *et al.,* 2017). The skeletal remains used in this study belong to 476 South African Black, White, and Coloured individuals. One hundred were Black males, 100 were Black females, 100 were White males, 100 were White females, 56 were Coloured males, and 20 were Coloured females. In total, only 30 individuals were analysed from the Kirsten Skeletal Collection. The

limited sample analysed from the skeletal collection was a result of the collection only allowing access to remains for which consent had been granted at the time.

Table 1: Shows a breakdown of the sample and where the remains are housed

	Raymond A. Dart Collection of Modern Human Skeletons		Pretoria Bone Collection		Kirsten Skeletal Collection		**Total**
	Males	Females	Males	Females	Males	Females	
Black South African	80	80	20	20	-	-	200
White South African	80	80	20	20	-	-	200
Coloured South African	26	7	9	4	21	9	76
Total	186	167	49	44	21	9	476

Out of the 476 individuals, 200 of the Black and White individuals were utilised to test for the accuracy of the original sectioning points of the Loth and İşcan (2000) method.

After that, the same eight measurements utilised in the Loth and İşcan (2000) method were collected for the 476 individuals, including Coloured individuals. These included the humeral head diameter (HHD), humeral epicondylar breadth (HEB), femoral head diameter (FHD), femoral midshaft circumference (FMC), femoral distal breadth (FDB), tibial proximal breadth (TPB), tibial circumference at the nutrient foramen (TCN), and the tibia distal breadth (TDB). Measurement definitions from Buikstra and Ubelaker (1994) were also used by Loth and İşcan (2000). Figures 1 to 3 below describe each measurement and the instrument used. All measurements were taken in millimetres (mm).



Figure 1: The left humerus, anterior view (Taken from Buikstra and Ubelaker,1994: Page 80)

Term	*Definition*
Humeral head diameter (42)	The distance between the most superior and inferior points on the border of the articular surface. Measured using a sliding calliper.
Humeral epicondylar breadth (41)	Distance of the most laterally protruding point on the lateral epicondyle from the corresponding projection of the medial epicondyle. Measured using a sliding calliper.

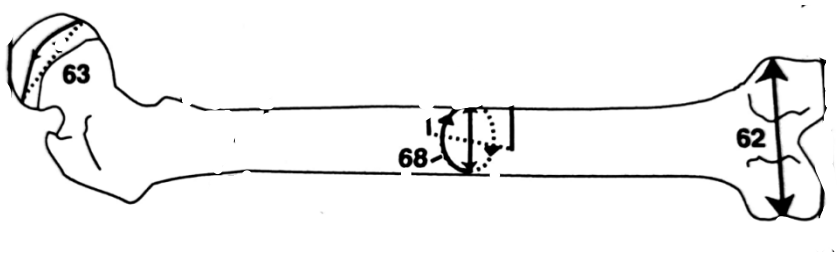


Figure 2: The left femur, posterior view (Taken from Buikstra and Ubelaker, 1994: Page 83)

Term	*Definition*
Femoral head diameter (63)	The maximum diameter of the femur head. Measured using a sliding calliper.
Femoral midshaft circumference (68)	Circumference measured at the diaphysis's midpoint, at the Linea aspera's highest elevation. Measured using tailor tape.
Femoral distal breadth (62)	distance between the two most laterally projecting points on the epicondyles. Measured using a sliding calliper.

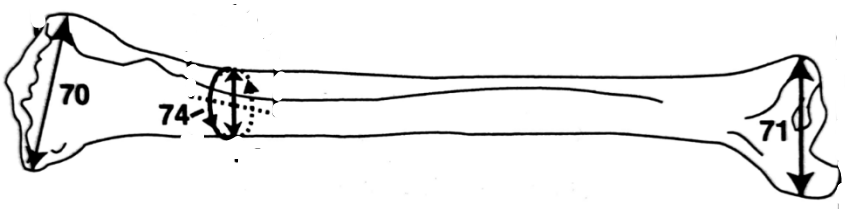


Figure 3: The left tibia, anterior view (Taken from Buikstra and Ubelaker, 1994:Page 83)

Term	*Definition*
Tibial proximal breadth (70)	Maximum distance between the two most laterally projecting points on the medial and lateral condyles of the proximal articular region (epiphysis). Measured using a sliding calliper.

Tibial circumference at the nutrient foramen (74)	Circumference measured at the level of the nutrient foramen. Measured using tailor tape.
Tibial distal breadth (71)	Maximum distance between the two most laterally projecting points on the medial malleolus and the lateral surface of the distal articular region (epiphysis). Measured using a sliding calliper.

Each measurement was recorded three times at approximately five-minute intervals. For the intra and inter-observer comparison, the same protocol was followed, with measurements taken in triplicate and comparable time intervals between recordings. The average between the three measurements obtained was used as a final measurement to account for possible intra- and -interrater error. Measurements were taken from the left side unless it was absent. The individual was excluded from the sample if both the left and the right tibia, humerus, and/or femur were missing or damaged to such an extent that the measurement could not be taken.

3.1 Statistics

All data was analysed using IBM SPSS version 29 (IBM Corp., 2023) and R Studio (RStudio Team, 2024). The intra- and inter-observer errors were calculated using Technical Error of Measurement (TEM). A technical error of measurement (TEM) was calculated on a subsample (n = 40) to assess the degree of repeatability. The percentage of technical error of measurement (%TEM) was calculated, and the desired result would have been less than 2% to account for the intra-and inter-observer error. The %TEM was calculated for both males and females within the Black and White populations to determine whether measurements were equally repeatable across all groups. Furthermore, the overall %TEM for each landmark measurement was calculated. To calculate the %TEM for both inter- and intra-observer error, the average of the triplicate values for each observer was subtracted from the individual

triplicate measurements. The differences were then squared and summed for all measurements. This total was divided by twice the number of individuals in the sample subset to obtain the TEM value.

$$TEM = \sqrt{\frac{\sum(X_1 - X_2)^2}{3N}}$$

Finally, the TEM was divided by the mean of the measurements taken and multiplied by 100 to express the technical error as a percentage (%TEM) (Langley *et al.*, 2018).

$$\%TEM = (\frac{TEM}{mean\ of\ all\ measureements}) \times 100$$

The sample's descriptive statistics were then analysed using IBM SPSS version 29 (IBM Corp., 2023). Descriptive analysis began with the entire sample, followed by analysis by sex, and finally by population and sex. Following this, a Shapiro Wilk was used to determine the normality of the sample. Thereafter, a Kruskal-Wallis test was employed to analyse whether there was a statistical difference between the measurements of the different groups, the difference when sex was pooled, and the difference for when the measurements were pooled for both population and sex. Afterwards, a pairwise comparison of Dunn's test with Bonferroni correction for multiple comparisons was utilised to determine whether intergroup differences were present in the sample.

To test the accuracy of the original Loth and İşcan (2000) method; 50 Black males, 50 Black females, 50 White males and 50 White females were classified utilising the original Loth and İşcan (2000) sectioning points. Thereafter, the sensitivity and specificity of the Loth and İşcan (2000) the method was calculated. The sensitivity measures how well the model performs when testing true positives (Shreffler and Huecker, 2024). It indicates the proportion of positive results predicted compared to how many should have been predicted. The formula used was the number of predicted positives divided by the number of actual positives within the sample.

$$sensitivity = (no.of\ predicted\ positives)/(no.of\ actual\ positives)$$

Results between 80% and 100% indicate high sensitivity and that the method sufficiently classifies accurately positives (Plante and Vance, 1994; Lalkhen and McCluskey, 2008). Specificity measures how well the model classifies true negatives. It indicates the proportion of true negatives predicted to the number of negatives that should have been predicted (Shreffler and Huecker, 2024). The formula is the number of predicted negatives over the number of actual negatives within the sample.

$$specificity = (no.of\ predicted\ negatives)/(no.of\ actual\ negatives)$$

Similar to the sensitivity, 80 - 100% indicates that the method effectively classifies the negatives. Results for both sensitivity and specificity were visually represented using Receiver Operating Characteristic (ROC) curves.

To establish if new univariate sectioning points on a larger sample would provide better accuracy, all the measurements of all eight landmarks were taken from the individuals within a specific population (e.g., Black, White or Coloured). A simple data summary indicated each measurement's mean, median, minimum, maximum, and standard deviation. Given the larger sample size, new sectioning points and classification accuracy rates were established. For univariate estimation, the sectioning points were determined for measurements of a specific landmark (e.g., the humeral head diameter) by adding the overall mean ($\bar{x}_t$) for both males ($\bar{x}_m$) and females ($\bar{x}_f$) within one population (e.g., black South Africans) and divided into two.

The equation to calculate the overall mean:

$$\bar{x}_t = \frac{\bar{x}_m + \bar{x}_f}{2}$$

Following this, the sectioning point of each univariate landmark measurement was established by dividing the overall mean ($\bar{x}_t$) by 2.

$$sectioning\ point = \frac{\bar{x}_t}{2}$$

To establish the accuracy of the original Loth and İşcan (2000) sectioning points, the number of individuals within the total sample for whom sex was correctly estimated (CE) was determined by comparing the size of the relevant landmark to the sectioning points. Thereafter, the classification accuracies of each sectioning points belonging to a specific landmark were determined by dividing the number of correct estimates by sex over the total number of individuals. After that, a percentage was calculated (Spradley and Jantz, 2011). The formula(s) for classification accuracy is as follows:

$$Classification\ accuracy = \frac{CE_{males}}{total\ no.of\ male\ individuals\ in\ the\ sample} \times 100$$

$$Classification\ accuracy = \frac{CE_{females}}{total\ no.of\ female\ individuals\ in\ the\ sample} \times 100$$

After analysing the univariate data and the normality of the data, a flexible discriminant analysis (FDA) was run using R Studio (RStudio Team, 2024), as certain measurements were non-parametric. Flexible discriminant analysis (FDA) is a nonparametric version of discriminant analysis that substitutes linear regression with a nonparametric regression method (Hastie *et al.,* 2000; Stull *et al.*, 2017). The analysis was completed using R Studio (RStudio Team, 2024). The packages used in R Studio were foreign, caret, ROSE, haven, dpylr, earth, and mda. The packages were used to retrieve coefficients to formulate multivariate formulas with different variables, obtain sectioning points for the relevant formulas and calculate the predicted group memberships. All measurements were initially input into the FDA, followed by separate analyses using only the humeral, femoral, and tibial measurements. The package ROSE will be used to upsample and balance the data as the sample sizes of the populations are unbalanced. ROSE will do so by increasing the number of individuals in the smaller groups (the Coloured population) by duplicating existing data or generating synthetic data. Finally, a stepwise discriminant function analysis (DFA) was run

using IBM SPSS version 29 (IBM Corp., 2023), similar to the FDA, all measurements were input into the DFA. The DFA then identified the combination of measurements that produced the highest classification accuracies. Henceforth, the accuracies were compared to those obtained by FDA.

3.2 Ethics

The samples that were used in this study were obtained from the Raymond A. Dart Collection of Modern Human Skeletons (University of the Witwatersrand), the Pretoria Bone Collection (University of Pretoria) and the Kirstenbosch Collection (University of Stellenbosch). An application for access to skeletal remains was submitted to all these collections as well as an application for an ethics clearance waiver. Access to the ethics clearance waiver (W-CBP-220504-01) at the University of the Witwatersrand was obtained, and ethics approval (39/2024) was obtained from the University of Pretoria.

4. Results

4.1 Inter- and intra-observer

The technical error of measurement (TEM) for all measurements from both Black and White South African samples taken by the intra-observer fell under the acceptable 1,5% and inter-observer values fell below 2% as proposed by Perini *et al.* (2005) and Langley *et al.* (2018), suggesting that the measurements are adequately repeatable (Table 2). When accounting for sex and population affinity, the following trends were noticed when tested for intra-and interobserver repeatability.

For Black males, the humeral epicondylar breadth (HEB) (intraobserver error = 0,13%) and femoral head diameter (FHD) (interobserver error = 0,72%) were most repeatable. In contrast, the tibial proximal breadth (TPB), the tibial distal breadth (TDB) (interobserver

error = 1,58%), and the humeral head diameter (HHD) (intraobserver error = 1,55%) had the highest error margins, indicating that these measurements were the least repeatable.

Similarly, HEB was the most repeatable (intraobserver error = 0,02%) in Black females, followed by HHD (interobserver error = 0,42%). The measurements with greater error margins for intraobserver were FMC (intraobserver error = 0,55%) and FHD had the greatest interobserver error margin (interobserver error = 1,98%).

HHD (intraobserver rate = 0%) and FMC (interobserver error = 0,29%) were the most repeatable in White males, while tibial circumference at the nutrient foramen (TCN) had the highest error margins for both intra- and interobserver (intraobserver error = 0,32%; interobserver error = 1,86%).

In White females, HEB and FMC had the lowest %TEM indicating that these measurements were highly repeatable (intraobserver error = 0,01%; interobserver error = 0,43%), whereas HHD and FHD had higher error margins for intraobserver analysis (intraobserver error = 1,05%) and FDB and TCN had greater error margins for interobserver (interobserver error = 1,63%).

Table 2: The %TEM of Blacks and White samples.

		Black (n = 100)		White (n = 100)	
		Male (n = 50)	Female (n = 50)	Male (n = 50)	Female (n = 50)
		%TEM	**%TEM**	**%TEM**	**%TEM**
HHD	Intra	1,04	0,04	0	1,05
	Inter	1,55	0,42	1,01	1,29
HEB	Intra	0,13	0,02	0,01	0,01
	Inter	1,61	1,83	0,85	0,43
FHD	Intra	0,2	0,09	0,08	1,05
	Inter	0,72	1,98	1,79	1,29
FMC	Intra	0,67	0,55	0,26	0,01
	Inter	1,31	0,69	0,29	0,43
FDB	Intra	0,18	0,24	0,03	0,07
	Inter	1,21	1,48	0,85	1,63
TPB	Intra	0,25	0,13	0,03	0,06
	Inter	1,58	0,86	0,72	1,56
TCN	Intra	0,18	0,24	0,32	0,07
	Inter	1,21	1,48	1,86	1,63
TDB	Intra	0,25	0,13	0,09	0,06
	Inter	1,58	0,86	1,17	1,56

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth

Table 3 shows the intra- and interobserver of all populations and sexes pooled. HEB had the highest intraobserver repeatability (intraobserver error = 0,08%) and FMC had the highest interobserver repeatability (interobserver error = 0,28%). Humeral head diameter (HHD) presented with the highest intraobserver %TEM value (intraobserver error = 0,32%) and FHD had the highest interobserver %TEM (interobserver error = 0,54%) indicating that the measurements are slightly less repeatable than the other measurements however, still indicating high repeatability.

Table 3: Intra-observer and Intra-observer TEM and %TEM

Measurements	Intra-observer TEM (mm)	Intra-observer %TEM	Inter-observer TEM (mm)	Inter-observer %TEM
HHD	0,141	0,32	0,198	0,45
HEB	0,046	0,08	0,243	0,41
FHD	0,080	0,18	0,240	0,54
FMC	0,178	0,21	0,243	0,28
FDB	0,090	0,12	0,286	0,38
TPB	0,083	0,11	0,266	0,37
TCN	0,211	0,24	0,337	0,38
TDB	0,094	0,18	0,266	0,52

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth

4.2 Descriptive statistics

The following section outlines a simple summary of the data. Looking at the overall sample (n = 476). TCN showed the most variance (SD = 10,152), and it indicated a greater difference between the minimum (49,62 mm) and maximum (124 mm) values (range = 74,38 mm). In contrast, TDB had the lowest SD (4,24) and the lowest difference between the maximum (62,01 mm) and minimum (41,06 mm) values (Range = 20,95 mm) (Table 4).

Table 4: Descriptive statistics of all measurements for all 476 individuals within the sample.

Variables	*Entire Sample combined*			
	Mean (x̄)*	**SD***	**Min***	**Max***
HHD	43,5696	4,31899	32,79	55,51
HEB	59,4029	5,26031	46,89	75,89
FHD	44,6924	7,98948	34,58	55,46
FMC	88,1499	8,26862	64,33	117
FDB	77,1084	6,32758	60,86	96,19
TPD	73,1666	5,67885	59,25	89,79
TCN	94,5255	10,15210	85	124
TDB	52,0741	4,24318	41,06	62,01

All measurements are in mm
Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
SD: Standard deviation
Min: Minimum
Max: Maximum

The mean values for each landmark measurement differed for both male and female groups. The means for all male measurements were noticeably higher than for females (Table 4). In both sexes, the measurements that indicated the greatest standard deviation was TCN (Male SD = 8,58 mm; Female SD = 7,32 mm), followed by FMC (Male SD = 7,01 mm; Female SD = 5,76 mm). The landmark that presented with the lowest variance in size was TDB (Male SD = 3,19 mm; Female SD = 3,18 mm). As expected, TCN had the largest bone dimensions (Male mean = 100,29 mm; Female mean = 70 mm) in both sexes and HHD presents with the lowest mean dimensions (Male mean = 45,88 mm; Female mean = 32,79 mm). Males consistently exhibited slightly higher standard deviations than females for all eight measurements, potentially reflecting greater morphological variation within the male sample. This may, in part, be influenced by the slightly larger male sample size (n = 256) compared to females (n = 220) (Table 5).

Table 5: Descriptive statistics of each landmark measurement with the sample split by the two sexes.

Variables	*Males (N = 256)*				*Females (N = 220)*			
	Mean*	**SD***	**Min***	**Max***	**Mean***	**SD***	**Min***	**Max***
HHD	45,88	3,68	33,52	55,51	32,79	3,34	32,79	52,28
HEB	62,68	3,99	50,87	75,89	46,89	3,78	46,89	69,36
FHD	46,76	5,76	36,80	55,46	34,58	2,94	34,58	51,26
FMC	92,93	7,01	74,00	117,00	64,33	5,76	64,33	101,00
FDB	80,85	4,97	65,82	96,19	60,86	4,76	60,86	91,15
TPD	76,81	4,12	63,78	89,79	59,25	4,08	59,25	83,08
TCN	100,29	8,58	85,00	124,00	70,00	7,32	70,00	112,33
TDB	54,67	3,19	46,42	62,01	41,06	3,18	41,06	61,00

All measurements are in mm
Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
SD: Standard deviation
Min: Minimum
Max: Maximum

Differences were depicted when the sample was split into their various population groups and further into their sexes (Table 6). The general trend indicates that males from each population generally have larger long bone dimensions on average than females, as shown in Table 6, with the means of all the males of each population being greater than the female means. White South African males exhibited the highest mean values for all measurements compared to the other male groups, followed by Black South African males and then Coloured South African males across all eight measurements. Similarly, White South African females displayed the highest mean values, followed by Black South African females and Coloured South African females. Both Black and White South African males presented with higher standard deviations than their female counterparts for all eight measurements. However, among the Coloured South African group, males only showed higher standard deviations for FMC (Male SD = 6,93) and TCN (Male SD = 7,67).

Table 6: Descriptive statistics of all three population groups split into the two sexes

White South African*								
Variables	*Males (n = 100)*				*Females (n = 100)*			
	Mean	**SD**	**Min**	**Max**	**Mean**	**SD**	**Min**	**Max**
HHD	49,19	2,58	41,41	55,51	43,37	2,50	38,15	52,28
HEB	64,76	3,82	53,03	75,89	56,53	3,96	46,89	69,36
FHD	48,96	2,55	43,12	55,46	43,34	2,61	37,99	50,36
FMC	94,72	6,058	75,67	117,00	85,08	5,32	74,00	101,00
FDB	84,33	4,30	75,35	96,19	75,43	4,09	67,39	91,15
TPD	78,97	3,84	71,00	89,79	70,58	3,90	62,77	82,26
TCN	100,57	9,07	85,00	120,67	88,65	7,24	70,00	112,33
TDB	55,89	2,81	49,27	62,01	50,25	3,03	44,26	59,35
Black South African*								
Variables	*Males (n = 100)*				*Females (n = 100)*			
	Mean	**SD**	**Min**	**Max**	**Mean**	**SD**	**Min**	**Max**
HHD	43,71	2,21	38,94	49,68	38,82	2,057	34,65	44,59
HEB	61,91	3,13	55,44	72,31	55,11	3,15	48,50	65,81
FHD	45,64	2,26	40,52	51,87	40,31	2,12	35,16	45,53
FMC	94,11	6,93	79,00	110,00	81,11	5,04	70,00	94,00
FDB	79,06	3,74	69,88	90,54	70,67	3,64	62,82	80,08
TPD	76,03	3,51	67,70	85,19	67,84	3,40	60,90	75,89
TCN	102,27	7,85	84,33	124,00	87,81	7,25	73,33	104,00
TDB	53,40	2,91	47,46	60,56	48,27	2,70	41,06	54,27
Coloured South African*								
Variables	*Males (n = 56)*				*Females (n = 20)*			
	Mean	**SD**	**Min**	**Max**	**Mean**	**SD**	**Min**	**Max**
HHD	43,85	3,09	33,52	50,61	38,78	3,79	32,79	50,48
HEB	60,34	3,95	50,87	68,05	53,34	4,50	48,60	67,37
FHD	44,81	2,61	36,80	49,66	39,62	3,34	34,58	51,26
FMC	87,65	6,22	74,00	109,00	77,50	5,59	64,33	92,00
FDB	77,82	4,35	65,82	89,35	69,84	6,00	60,86	88,73
TPD	74,35	3,76	63,78	82,24	66,08	4,85	59,25	83,08
TCN	96,28	7,67	82,00	119,67	83,62	6,98	72,00	101,00
TDB	52,75	2,72	46,42	58,02	46,92	3,84	41,31	61,00

All measurements are in mm

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
SD: Standard deviation
Min: Minimum
Max: Maximum

4.3 Normality

Thereafter, the normality of the data was analysed using a Shapiro-Wilks test. The results depicted differences in normality for each population for each landmark. All the population samples were normally distributed for HEB, FHD, FMC, FDB (Appendix 1). All population samples were normally distributed for HHD except for Coloured females ($p < 0,001$). For TCN, White males ($p < 0,001$) were not normally distributed, and finally, for TDB, Coloured females were also not normally distributed; as some of the data was not normally distributed, to analyse the data, non-parametric tests were used.

4.4 Kruskal-Wallis and Post hoc test

4.4.1 Differences between measurements when for sex and population groups are pooled (Kruskal-Wallis)

To analyse whether there were differences in the measurements when control both sex and population groups are pooled, a non-parametric Kruskal-Wallis test was run (Appendix 1). The output of the Kruskal-Wallis test (Table 7) shows that the different groups (e.g., White males, White females, Black Males, Black females, Coloured males and Coloured females) have a statistically significant difference for all landmark measurement values as the p-value is less than 0,05 ($p < 0,01$).

Table 7: Output for the Kruskal-Wallis test for comparing the different groups.

	HHD	HEB	FHD	FMC	FDB	TPB	TCN	TDB
Kruskal-Wallis H	311,93	265,47	295,72	249,42	284,41	280,76	218,40	266,15
df	5	5	5	5	5	5	5	5
p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth

In addition, the landmark size difference between population groups (sexes pooled) (i.e., Black, White and Coloured) was tested for significance. In Table 8, the Kruskal-Wallis output indicates that the population samples have a statistically significant difference in measurement sizes for all eight dimensions ($p < 0,001$).

Table 8: Result of the Kruskal-Wallis test between population groups (sexes pooled).

	HHD	HEB	FHD	FMC	FDB	TPB	TCN	TDB
Kruskal-Wallis H	136,58	16,19	64,05	22,25	59,95	24,12	2,39	28,54
df	2	2	2	2	2	2	2	2
p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth

Furthermore, a Kruskal-Wallis test was administered to test the significance of the differences in measurements between sexes (pooled population groups). Table 9 shows that males and females have statistically significant differences in the measurements of all eight landmarks ($p < 0,001$), as females presented with smaller dimensions.

Table 9: Results from the Kruskal-Wallis test comparing males and females.

	HHD	HEB	FHD	FMC	FDB	TPB	TCN	TDB
Kruskal-Wallis H	162,01	233,26	214,51	198,13	208,33	241,40	200,56	220,77
df	1	1	1	1	1	1	1	1
p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth

4.4.2 Differences between measurements when sex and population groups are pooled (Dunn's test)

Following that, a pairwise comparisons Dunn's post hoc test was performed to further break down the intergroup differences. Each population sample was compared with another population sample included in the study. When comparing the population sample, TCN is the only landmark measurement that had dimensions that did not show a statistically significant difference between all three populations (White vs Black: p = 0,801; Coloured vs White: p = 0,185; Black vs Coloured: p = 0,131) (Table 10). Besides TCN, the Black and White population samples displayed a statistically significant difference for all other measurements; similarly, the comparisons of Coloured and White population samples indicated that all measurements, except measurements for TCN displayed significant intergroup differences. In contrast, Black and Coloured population samples displayed a statistically significant difference for HHD (p = 0,008) and FMC (p = 0,034) and were not statistically different for HEB, FHD, FMC, FDB, TPB, TCN, and TDB (Table 10).

Table 10: Output of the Pairwise comparison results that compared the three different population samples.

		HHD	HEB	FHD	FMC	FDB	TPB	TCN	TDB
White vs Black**	Test statistic	158,885	52,218	106,790	43,018	103,703	64,913	-3,458	69,223
	p-value	<0,001	0,008	<0,001	0,002	<0,001	<0,001	**0,801***	<0,001
Coloured vs White**	Test statistic	110,054	49,071	86,840	82,254	82,220	55,841	24,537	65,465
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	0,003	**0,185***	<0,001
Black vs Coloured**	Test statistic	-48,831	-3,146	-19,950	39,236	-21,483	-9,071	27,995	-3,757
	p-value	0,008	**0,865***	**0,282***	0,034	**0,246***	**0,625***	**0,131***	**0,839***

p-values are not statistically significant
****South Africans***
Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth

Further analysis was performed to ascertain which of the measurements differed significantly between population samples using a pairwise comparison post hoc test (Appendix 2 and table 10). Groups that showed a statistically significant intergroup difference ($p < 0,05$) for all eight measurements were White males and Coloured males, White males and White females, White males and Black females, White males and Coloured females, Black males and Black females, Black males and Coloured females, Coloured males and Black females, Coloured males and Coloured females, and White females and Coloured females.

White males and Black males did not show statistically significant differences for FMC ($p = 0,423$) and TCN ($p = 0,350$). Black males and Coloured Males were not statistically significantly different for almost all eight dimensions, namely for, HHD ($p = 0,668$) , HEB ($p = 0,053$), FHD ($p = 0,179$), FDB ($p = 0,181$), TPB ($p = 0,064$), TCN ($p = 0,060$). Black males and White females were generally significantly different for all dimensions except HHD ($p = 0,562$) (Table 11). Similarly, Black females and White females had one landmark measurement that had dimensions that were not statistically significant (TCN; $p = 0,562$). Coloured males and White females did not show a statistically significant difference for HHD ($p = 0,358$). Finally, Black females and Coloured females did not show a statistically significant difference for any of the dimensions of the eight measurements.

Table 11: Output of the pairwise comparison result of the different groups.

		HHD	HEB	FHD	FMC	FDB	TPB	TCN	TDB
WM and BM	Test statistic	162,07	66,17	105,60	15,57	104,40	65,34	-18,19	75,37
	p-value	<0,001	<0,001	<0,001	**0,423***	<0,001	<0,001	**0,350***	<0,001
WM and CM	Test statistic	152,22	110,53	136,48	122,84	135,12	107,86	66,93	118,57
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
WM and WF	Test statistic	173,34	219,03	195,94	167,97	195,99	207,47	175,65	205,37
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
WM and BF	Test statistic	329,04	257,30	303,93	238,44	299,00	271,96	186,93	268,45
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
WM and CF	Test statistic	7321,33	293,14	320,13	287,74	306,50	304,38	239,57	306,97
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
BM and CM	Test statistic	-9,85	44,36	30,89	107,28	30,72	42,53	85,12	43,20
	p-value	**0,668***	**0,053***	**0,179***	<0,001	**0,181***	**0,064***	<0,001	**0,060***
BM and WF	Test statistic	11,27	152,86	90,35	152,40	91,60	142,14	193,84	130,00
	p-value	**0,562***	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
BM and BF	Test statistic	166,97	191,13	198,33	222,87	194,61	206,63	205,12	193,08
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
BM and CF	Test statistic	159,26	226,97	214,53	272,18	202,10	239,04	257,76	231,61
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
CM and WF	Test statistic	21,18	108,50	59,46	45,12	60,88	99,61	108,72	86,80
	p-value	0,358	<0,001	0,010	0,049	0,008	<0,001	<0,001	<0,001
CM and BF	Test statistic	176,82	146,76	167,44	115,59	163,89	164,10	119,99	149,877
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
CM and CF	Test statistic	169,10	182,61	183,65	164,90	171,38	196,51	172,63	188,402
	p-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001

WF and BF	Test statistic	155,70	38,27	107,99	70,87	103,01	64,49	11,28	63,08
	p-value	<0,001	0,049	<0,001	<0,001	<0,001	<0,001	**0,562***	0,001
WF and CF	Test statistic	147,99	74,11	124,19	119,78	110,51	96,91	63,92	101,61
	p-value	<0,001	0,028	<0,001	<0,001	0,001	0,004	<0,001	0,003
BF and CF	Test statistic	-7,72	35,85	16,21	49,31	7,50	32,42	52,64	38,53
	p-value	**0,819***	**0,287***	**0,631***	**0,143***	**0,824***	**0,336***	**0,118***	**0,253***

***p-values are not statistically significant**
Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
WM: White males
BM: Black males
CM: Coloured males
WF: White females
BF: Black females
CF: Coloured females

4.5 Analysis of Loth and İşcan (2000)

Using the original sectioning points from the Loth and İşcan (2000) method, classification accuracies (CA) were calculated for each of the eight measurements in a sample of 50 Black males, 50 Black females, 50 White males, 50 White females (Table 6 and Figure 4). The overall classification accuracy obtained for the Black sample was 80,75%, which was lower than the proposed Loth and İşcan (2000) accuracy of 88,31%. Similarly, the classification accuracy for the South African White sample was also found to be lower (79,63%) than that reported by the original authors (84,28%) (Table 12). Looking at the CA for males and females, we see that the males overall presented with higher CA's than females, with the Black males presenting with the highest CA (93,75%) followed by the White males (86,00%). Females obtained much lower classification accuracies when using the Loth and İşcan (2000) sectioning points, with the White females presenting with a CA of 71,25% and the Black females a much lower CA of 67,75%. These discrepancies can be explained by the very low CAs obtained for some of the individual measurements, with the tibial distal breath

(TDB) for females, presenting with a CA of 0,00% for Black females and 2% for White females. Overall, the sectioning points produced good classification accuracies for Black males, with most of the measurements falling in the 90,00 – 100,00% classification range. The population sample with the least accurate classification rates was Black South African females, with none of the measurements producing classification accuracies above 85,00%. With Loth and İşcan's (2000) classification accuracies considered, most of the accuracies decreased. There was, however, an increase in the accuracy of TCN for the Black South African population sample from 83,50% (Loth and İşcan, 2000) to 87,00% (current study), and an increase in HEB in the White South African sample from 88,40% (Loth and İşcan, 2000) to 89,00% (current study). In Black males, TCN and TDB performed the best with 100,00% classification accuracy utilising the original Loth and İşcan (2000) sectioning points in this study and FDB had the lowest classification accuracy of 82,00%. In Black females, the landmark measurement with the poorest accuracy was TDB (0,00%), and FHD and FDB had the greatest classification accuracy of 84,00%. Similar to Black males, TDB was the landmark measurement with the highest accuracy in White males with 100,00% and FDB with the lowest (76,00%). In White females, TDB presented the lowest accuracy rate of 2,00%, and HEB had the highest with 90,00%.

Table 12: A comparison of classification accuracies (CA) obtained using Loth and İşcan (2000) sectioning points in this study and those reported by Loth and İşcan (2000).

	BM CA (%)	BF CA (%)	Total CA (%)	Original Loth and İşcan (2000)'s CA (%)	WM CA (%)	WF CA (%)	Total CA (%)	Original Loth and İşcan (2000)'s CA (%)
HHD	90,00	76,00	83,00	90,90	82,00	86,00	84,00	84,60
HEB	90,00	68,00	79,00	88,90	88,00	90,00	89,00	88,40
FHD	92,00	84,00	88,00	91,90	88,00	80,00	84,00	85,90
FMC	98,00	80,00	89,00	89,90	86,00	74,00	80,00	74,30
FDB	82,00	84,00	83,00	86,40	76,00	84,00	80,00	90,50
TPB	98,00	76,00	87,00	87,50	88,00	80,00	84,00	87,70
TCN	100,00	74,00	87,00	83,50	80,00	74,00	77,00	82,10
TDB	100,00	0,00	50,00	87,50	100,00	2,00	51,00	80,70
OVERALL ACCURACY %	93,75	67,75	80,75	88,31	86,00	71,25	78,63	84,28

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
WM: White males
BM: Black males
CM: Coloured males
WF: White females
BF: Black females
CF: Coloured females
CA: Classification Accuracy

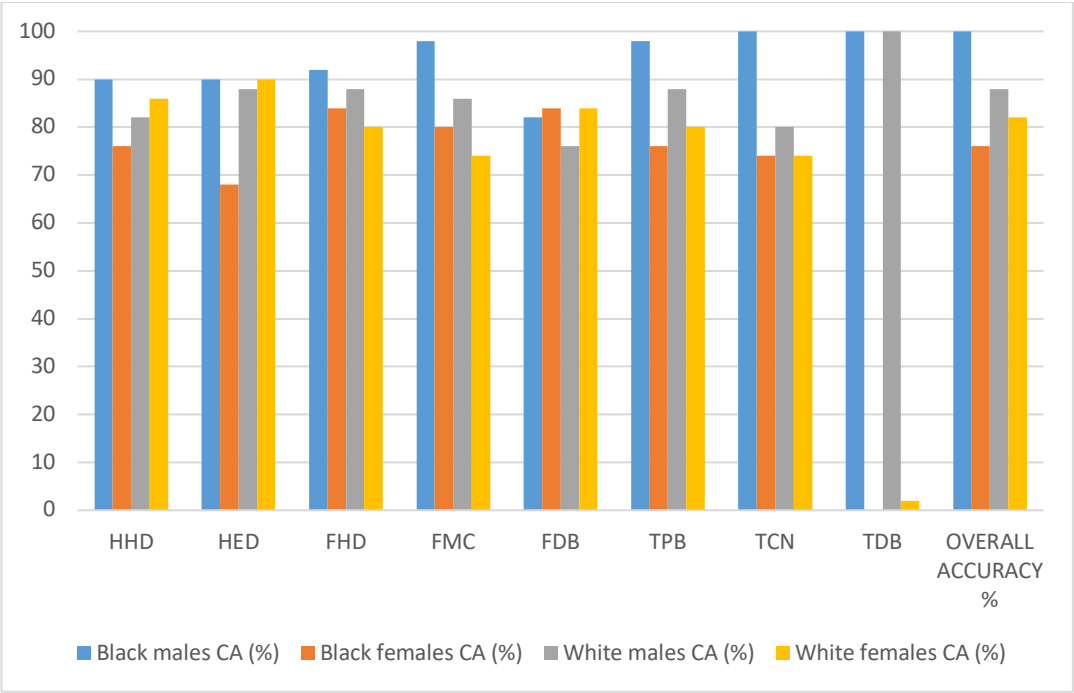


Figure 4: A bar graph illustrating the classification accuracies obtained in this study when using the original Loth and Isçan (2000) sectioning points.

The classification accuracies of each landmark measurement were further analysed utilising on ROC curves (Appendix 3). The measurements that presented with the greatest area under the curve (AUC) were for the tibial circumference at the nutrient foramen (TCN) (AUC = 0,99) (Fig. 5 and Table 13) and FMC (AUC = 0,99) (Fig. 6 and Table 13). The lowest AUC was obtained for HHD (AUC = 0,86) (Fig. 7 and Table 12), which is still relatively high. The AUC of all measurements were all very close to 1,00, indicating almost perfect classification using the Loth and İşcan (2000) univariate sectioning points. This entails that the dimensions are highly sexually dimorphic and are good predictors of sex. The landmark dimension with the best sensitivity and specificity is TCN (sensitivity = 97,40%, specificity = 95,00%) (Table 13). This indicates that TCN produces low false negative and low false positive classifications and thus is effective in distinguishing between sexes with minimal misclassification. In contrast, TDB had the lowest specificity of 0,00%, showing that the sectioning point has a high rate of false positives classification.

Table 13: Sensitivity and specificity of the sectioning points proposed by Loth and İşcan (2000).

Measurements	AUC*	Sensitivity (%)	Specificity (%)
HHD	0,86	99,10	53,30
HEB	0,98	99,10	80,60
FHD	0,97	100,00	59,60
FMC	0,99	100,00	75,90
FDB	0,94	98,00	66,00
TPB	0,97	100,00	73,80
TCN	0,99	97,40	95,00
TDB	0,99	100,00	0,00

******Area under the curve*
Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
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TDB: Tibial distal breadth

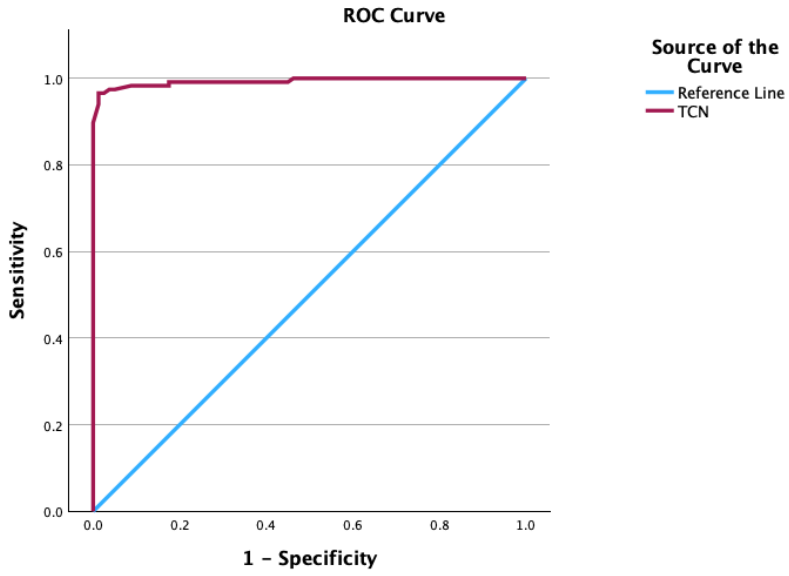


Figure 5: ROC curve of TCN

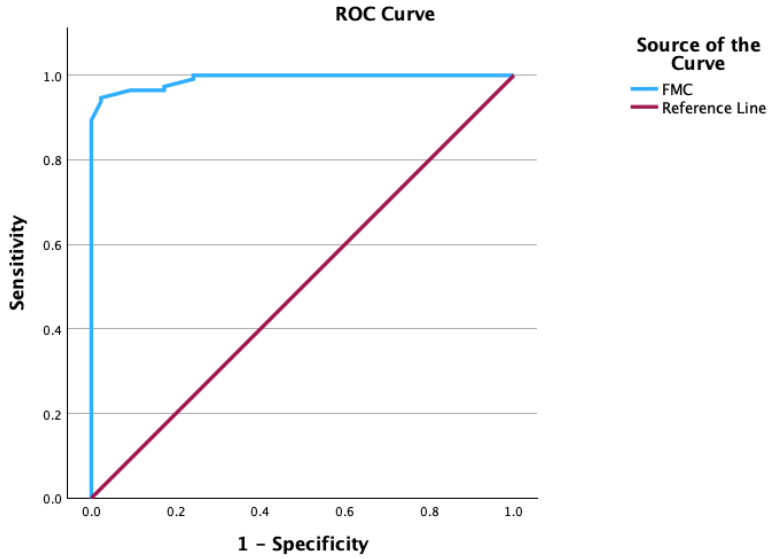


Figure 6: ROC curve of FMC

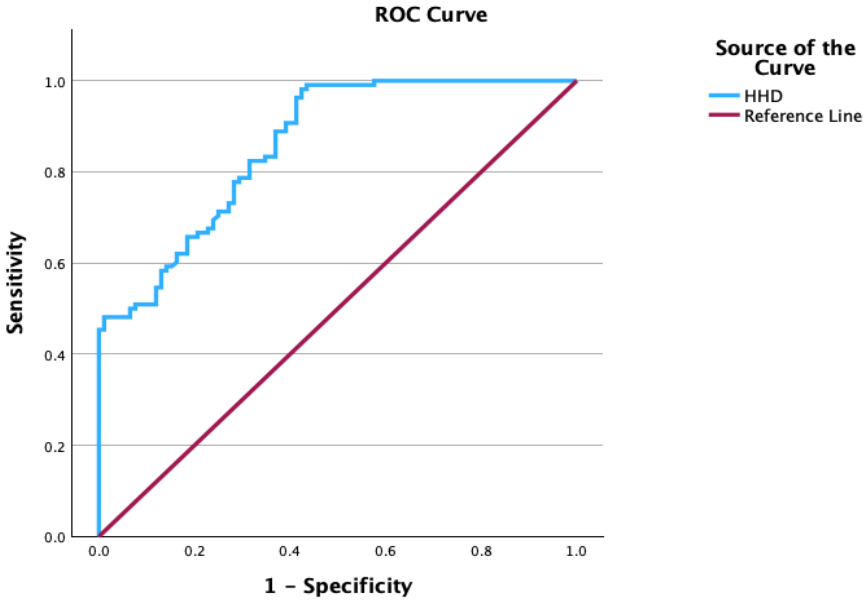


Figure 7: ROC curve of HHD

4.6 Sectioning points obtained

Table 14 shows the newly calculated sectioning points obtained by dividing the sum of each populations' male and female means.. The sectioning points were established using a sample comprising South African Black (n = 100), White (n = 100) and Coloured (n = 76). The means and sectioning points were compared to the original Loth and İşcan (2000) means and sectioning points for the Black (n = 81) and White (n = 86) populations. When comparing the sectioning points, HHD had the most similar sectioning points when comparing the Loth and İşcan (2000) sectioning points to the more recent sectioning points for both populations. In contrast, TDB had the biggest difference in sectioning points, and the points increased.

Table 14: The original Loth and İşcan (2000) sectioning points compared to the estimated sectioning points acquired from the sample utilised in this study.

	Loth and İşcan (2000) means	Loth and İşcan (2000)'s original sectioning points	Newly calculated means	Calculated sectioning points	Loth and İşcan (2000) means	Loth and İşcan (2000)'s original sectioning points	Newly calculated means	Calculated sectioning points
	Black South Africans				**White South Africans**			
HHD	**M:** 43,80 **F:** 37,70	40,50	**M:** 43,71 **F:** 38,82	41,30	**M:** 49,00 **F:** 43,00	46,10	**M:** 49,19 **F:** 43,37	46,30
HED	**M:** 61,30 **F:** 53,50	57,00	**M:** 61,91 **F:** 55,11	58,40	**M:** 63,60 **F:**55,70	59,70	**M:** 64,75 **F:** 56,52	60,40
FHD	**M:** 45,30 **F:** 39,20	42,00	**M:** 45,64 **F:** 40,31	43,70	**M:**48,40 **F:** 43,10	45,80	**M:** 48,96 **F:** 43,34	46,20
FMC	**M:** 90,00 **F:** 78,80	84,00	**M:** 94,11 **F:** 81,11	87,60	**M**: 92,00 **F:** 84,50	88,30	**M**: 94,72 **F:** 85,08	89,90
FDB	**M**: 79,20 **F:** 69,60	74,00	**M:** 79,06 **F:** 70,67	74,90	**M**: 84,00 **F:** 75,20	79,70	**M:** 84,33 **F:** 75,43	79,90
TPB	**M:** 74,90 **F**: 64,90	69,50	**M:** 76,03 **F:** 67,84	71,90	**M:**78,20 **F:** 69,80	74,10	**M**: 78,97 **F:** 70,58	74,80
TCN	**M:** 98,40 **F:** 85,10	91,20	**M:**102,27 **F:** 87,81	94,70	**M:** 97,30 **F:** 87,20	92,40	**M:** 100,57 **F:** 88,65	94,60
TDB	**M:** 45,40 **F:** 39,90	42,40	**M:** 53,40 **F:** 48,27	51,10	**M:** 46,80 **F:** 41,90	44,40	**M:** 55,89 **F:** 50,25	53,40

Abbreviation key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath

TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
M: Male ; **F** = Female

Thereafter, completely new sectioning points for the Coloured South African population were established and shown in Table 15, as this population group was not included in the Loth and İşcan (2000) study. The sectioning points obtained for the Coloured South African population are similar to the newly developed sectioning points obtained for the Black South African population, measurements such as HHD are the same for both populations with 41,31 (Table 15) in Coloured South Africans and 41,30 (Table 15) in Black South Africans. White South Africans consistently had the highest sectioning points (Table 14) compared to both Black and Coloured South African populations.

Table 15: The newly calculated sectioning points obtained for the Coloured South African population.

Coloured South Africans		
	Means	**Sectioning points**
HHD	**M:** 43,85 **F:** 38,78	41,31
HED	**M:** 60,35 **F:** 53,34	56,84
FHD	**M:** 44,81 **F:** 39,62	42,21
FMC	**M:** 87,65 **F:** 77,5	82,57
FDB	**M:** 77,82 **F:** 69,84	73,83
TPB	**M:** 74,35 **F:** 66,08	70,22
TCN	**M:** 96,28 **F:** 83,62	89,95
TDB	**M:** 52,75 **F:** 46,92	49,83

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth

4.7 Flexible Discriminant analysis (FDA)

Initially, FDA was utilised to classify the sex by considering all six groups at one time with all eight measurements included in the analysis. FDA is a non-parametric discriminant analysis model that utilises non-linear regressions to classify and hence offers a level of flexibility compare to DFA. The expectation was that by sex estimating all six groups, the FDA would be able to perform sex estimation while considering ancestry in a single step.Therefore, individuals were classified into one of six groups: White males, Black males, Coloured males, White females, Black females, or Coloured females (Fig. 8). When using FDA, it is affected by unequal sample sizes and thus balancing techniques were utilised such as upsampling the minority class, which in this case, was the Coloured South African sample. This resulted in all the populations having a balanced number of individuals in the population thus making the sample size 600 individuals in total (100 for each group). The group that presented with the highest classification was the White South African males with 81 individuals being correctly classified, followed by White South African females with 71 individuals being accurately classified. 21 Black males were classified as Coloured males, and 20 Coloured males were classified as Black males. Similarly, 20 Black females were classified as Coloured females, and 22 Coloured females were classified as Black female. The classification accuracies for Black South African males (61 individuals were correctly classified), Black South African females (64 individuals were correctly classified), Coloured South African males (51 individuals were correctly classified), and Coloured South African females (65 individuals were correctly classified) are relatively low due to the misclassifications as the FDA was taking sex and ancestry into account.

Figure 8: The confusion matrix of an FDA classifying individuals into groups.

		True						Total individual classified
		White male	**Black male**	**Coloured male**	**White female**	**Black female**	**Coloured female**	
Prediction	**White male**	81	5	6	5	0	4	101
	Black male	6	61	20	3	4	0	94
	Coloured male	4	26	51	6	8	0	95
	White female	9	5	11	71	4	9	109
	Black female	0	3	9	6	64	22	104
	Coloured female	0	0	3	9	20	65	97
Total number of individuals classified		100	100	100	100	100	100	**600**

Subsequently, classification was performed per population, first using all eight measurements, and then separately with humeral, femoral, and tibial measurements. Table 16 (Appendix 5(1)) shows the FDA output for Black South Africans. The output includes four different multivariate discriminant functions. The discriminant function number 1 consider all eight measurements from all three bones, the second is a function formed utilising humeral measurements, the third utilises femoral, and the fourth utilises tibial measurements. All four functions have the same sectioning point of 0,00. When analysing the centroids, it is shown that males have lower centroids than females; thus, when classifying using the sectioning points, values less than 0 would be male and values above zero would be classified as female. The classification accuracies of the discriminant functions for Black South Africans ranged from 88,50 to 92,50%. The first function, which includes all eight measurements, had the greatest classification accuracy of 92,50%, whereas Function 4, which utilises the tibial measurements, had the lowest accuracy (88,50%).

Table 16: The coefficients and variables used to develop multivariate formulas and the sectioning points related to each formula for the Black South African population.

Black South Africans					
	Functions and variables	Coefficients	Centroids	Sectioning points	Classification accuracy
1.	HHD HEB FHD FMC FDB TPB TCN TDB **CONSTANT**	-0,069899480 -0,041502430 -0,037058999 -0,035595825 0,005984064 -0,047955172 0,004116396 0,032972729 **10,947683168**	**M:** -1,49 **F:** 1,49	0,00	92,50%
2.	HHD HEB **CONSTANT**	-0,14254106 -0,08154416 **10,65277561**	**M:** -1,29 **F:** 1,29	0,00	91,50%
3.	FHD FMC FDB **CONSTANT**	-0,09669018 -0,03683215 -0,03864001 **10,27258356**	**M:** -1,38 **F:** 1,38	0,00	91,00%
4.	TPB TCN TDB **CONSTANT**	-0,103124660 -0,024450068 -0,005402141 **10,018448955**	**M:** -1,26 **F:** 1,26	0,00	88,50%
Average classification					90,90%

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
M: Male
F: Female

For White South Africans, the accuracies of the multivariate formulae created by FDA, ranged from 84,50% to 89,00% (Table 17 and Appendix 5 (2)). The lowest classification accuracies were seen for the femoral measurements (84,50%) and the highest for all eight measurements (89,00%) and the humeral measurements (89,00%). White South Africans presented with lower accuracy rates compared to Black and Coloured South Africans when utilising FDA analysis. Similarly, the male centroids were below the female centroids; therefore, values below the sectioning points will be classified as male.

Table 17: The coefficients and variables used to develop multivariate formulas and the sectioning points related to each formula for the White South African population.

White South Africans					
	Functions and variables	Coefficients	Centroids	Sectioning points	Classification accuracy
1.	HHD HEB FHD FMC FDB TPB TCN TDB **CONSTANT**	-0,0840216408 -0,0373269409 -0,0300981885 -0,0023698278 0,0426239723 -0,0418808390 -0,0001594921 -0,0471218043 **10,0095864567**	**M:** -1,30 **F:** 1,27	-0,01	89,00%
2.	HHD HEB **CONSTANT**	-0,124134463 -0,05878847 **9,30932071**	**M:** -1,234406 **F:** 1,209963	-0,01	89,00%
3.	FHD FMC FDB **CONSTANT**	-0,10300049 -0,01661080 -0,04427385 **9,78327436**	**M:** -1,138236 **F:** 1,115697	-0,01	84,50%
4.	TPB TCN TDB **CONSTANT**	-0,070404096 -0,002616215 -0,084004746 **9,993456419**	**M:** -1,160838 **F:** 1,137851	-0,01	87,00%
Average classification					87,40%

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
M: Male
F: Female

The overall accuracies for the multivariate formulae produced by FDA for Coloured South Africans were between 88,16% and 90,79%. Similarly, the highest classification accuracy for the discriminant functions of Coloured South Africans was when all eight measurements were considered (90,79%) (Table 18). The lowest classification accuracy was for both humeral landmarks (88,16%) and femoral landmarks (88,16%). Again, male centroids are less than female centroids; thus, discriminant score less than the sectioning points presented in Table 18 (Appendix 5 (3)) will be classified as male.

Table 18: The coefficients and variables used to develop multivariate formulas and the sectioning points related to each formula for the Coloured South African population.

Coloured South Africans					
	Functions and variables	Coefficients	Centroids	Sectioning points	Classification accuracy
1.	HHD HEB FHD FMC FDB TPB TCN TDB **CONSTANT**	0,039376541 -0,025079813 -0,049997209 -0,002180596 0,063862894 -0,130092314 -0,018828679 -0,014657377 **9,204653809**	**M:** -0,60 **F:** 1,69	0,54	90,79%
2.	HHD HEB **CONSTANT**	-0,05343267 -0,08529639 **7,26187285**	**M:** -0,47 **F:** 1,32	0,42	88,16%
3.	FHD FMC FDB **CONSTANT**	-0,09610574 -0,03423705 -0,01774498 **8,42847048**	**M:** -0,52 **F:** 1,47	0,47	88,16%
4.	TPB TCN TDB **CONSTANT**	-0,06850882 -0,02310555 -0,04107422 **9,19556209**	**M:** -0,58 **F:** 1,62	0,52	89,47%
Average classification					89,2%

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TCN: Tibial circumference at the nutrient foramen
TDB: Tibial distal breadth
M: Male
F: Female

4.8 Discriminant function analysis (DFA)

Compared to FDA, another analysis method was utilised to create multivariate formulae. DFA is a parametric discriminant model that uses linear regressions to classify. In DFA analysis, the output produced a formula with landmark measurement combinations with the highest classification accuracies by utilising stepwise variable selection. Classification accuracies for DFA functions for Black South Africans ranged between 94,00% to 88,50%. Again function 1 utilising all measurements provided the highest classification accuracy

(94,00%) (Table 19 and Appendix 6 (2)). Similar to the FDA outputs, the sectioning point for Black South Africans is 0,00. Any value below zero will be classified as female, and any value above it will be classified as male.

Table 19: The coefficients, sectioning points and classification accuracies of the discriminant functions produced by stepwise DFA

Black South Africans					
	Functions and variables	Coefficients	Centroids	Sectioning point	Classification accuracy (%)
1.	HHD HEB FMC TPB **CONSTANT**	0,166 0,085 0,070 0,076 **-23,475**	**M:** 1,47 **F:** -1,47	0,00	94,00%
2.	HHD HEB **CONSTANT**	0,293 0,168 **-21,904**	**M:** 1,29 **F:** -1,29	0,00	91,50%
3.	FHD FMC FDB **CONSTANT**	0,203 0,077 0,081 **-21,534**	**M:** 1,38 **F:** - 1,38	0,00	91,00%
4.	TPB TCN **CONSTANT**	0,217 0,051 **-20,441**	**M:** 1,26 **F:** - 1,26	0,00	88,50%
Average classification					91,25%

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FMC: Femoral midshaft circumference
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TDB: Tibial distal breadth
M: Male
F: Female

In White South Africans, classification accuracies for DFA functions ranged between 90,50% and 86,00% (Table 20). The highest classification accuracy was obtained for function 1, which including the humeral head diameter, the humeral epicondylar breadth, and the tibial distal breath (Table 20 and Appendix 6 (1)). The combination of these measurements results in a classification accuracy of 90,50%. The male centroid was larger than the female centroid; thus, any value greater than the sectioning point will be classified as male.

Table 20: The coefficients, sectioning points and classification accuracies of the discriminant functions produced by stepwise DFA.

White South Africans					
	Functions and variables	Coefficients	Centroids	Sectioning point	Classification accuracy
1.	HHD HEB TDB **CONSTANT**	0,198 0,080 0,115 **-20,140**	**M:** 1,27 **F:** -1,24	0,013	90,50%
2.	HHD HEB **CONSTANT**	0,252 0,119 **-18,899**	**M:** 1,23 **F:** -1,20	0,01	89,50%
3.	FHD FDB **CONSTANT**	0,213 0,118 **-19,238**	**M:** 1,12 **F:** -1,10	0,01	86,00%
4.	TPB TDB **CONSTANT**	0,147 0,171 **-20,122**	**M:** 1,15 **F:** -1,13	0,01	87,50%
Average classification					88,40%

Abbreviation Key:
HHD: Humeral head diameter
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
FDB: Femoral distal breath
TPB: Tibial proximal breadth
TDB: Tibial distal breadth
M: Male
F: Female

In Coloured South Africans, both the tibial proximal breath and femoral head diameter produced accuracies of 88,20%. Similar to all other DFA outputs, the male centroids were larger than females (Table 21 and Appendix 6 (3)).

Table 21: **The coefficients, sectioning points and classification accuracies of the discriminant functions produced by stepwise DFA**

Coloured South Africans				
Functions and variables	Coefficients	Centroids	Sectioning point	Classification accuracy (%)
HEB **CONSTANT**	0,244 **-14,290**	**M:** 0,45 **F:** -1,26	-0,41	84,20%
FHD **CONSTANT**	0,356 **-15,453**	**M:** 0,49 **F:** -1,36	-0,44	88,20%
TPB **CONSTANT**	0,246 **-17,762**	**M:** 0,54 **F:** -1,50	-0,48	88,20%
Average classification				86,90%

Abbreviation Key:
TPB: Tibial proximal breadth
HEB: Humeral epicondylar breadth
FHD: Femoral head diameter
M: Male

F: Female

4.9 Flexible Discriminant Analysis (FDA) vs Discriminant Function Analysis (DFA)

When comparing the average classification accuracies of FDA and DFA. Overall, Black South Africans had the greatest average classification accuracies (FDA: 90,90% ; DFA: 91,25%) (Table 22 and Fig. 8). For Black South Africans, DFA produced a higher classification accuracy (91,25%) than FDA (90,90%). Similarly, the average accuracy of White South Africans is greater for DFA (88,40%) than for FDA (87,40%). The Coloured South African population, however, has greater average classification accuracy for FDA (89,20%) compared to the average accuracy of the DFA discriminant functions (86,90%). FDA slightly outperformed DFA (Table 22).

Table 22: Average classification accuracies of the average classification accuracies of the discriminant functions produced by FDA vs DFA for each population group.

Statistical method	Populations	Average Accuracy (%)	Overall accuracy (%)
FDA	Black South African	90,90	89,17%
	White South African	87,40	
	Coloured South African	89,20	
DFA	Black South African	91,25	88,85%
	White South African	88,40	
	Coloured South African	86,90	

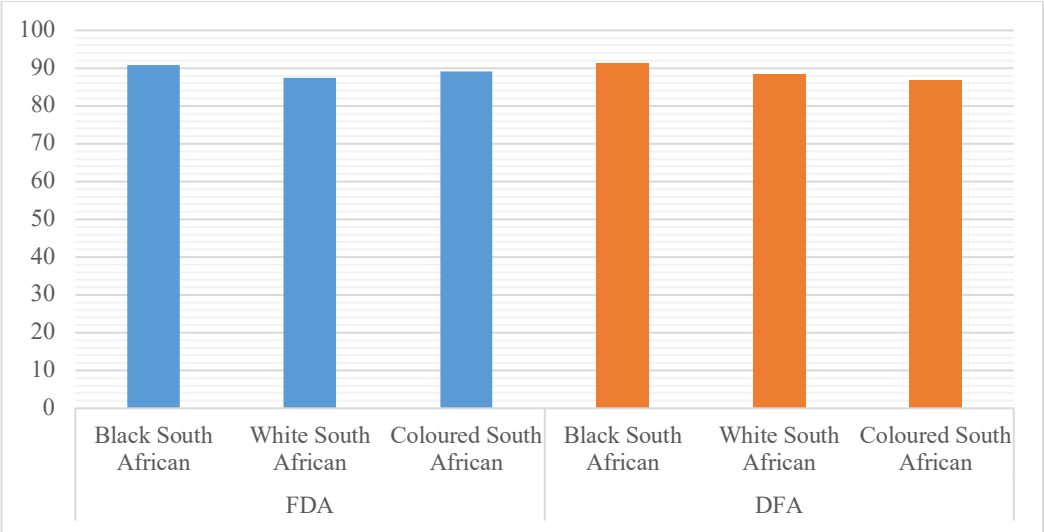


Figure 9: Bar graph comparing the average classification accuracies of the discriminant functions produced by FDA vs. DFA for each population group.

5. Discussion

This study aimed to evaluate the accuracy of the Loth and İşcan (2000) sex estimation method, known for univariate sectioning points using eight measurements (HHD, HEB, FHD, FMC, FDB, TPB, TCN, and TDB) from three long bones, the humerus, tibia, and femur, in South African Black and White populations. Furthermore, this study aimed to establish new univariate sectioning points using a larger sample that better represents the current South African population by incorporating the Coloured population. Additionally, it sought to develop multivariate functions with higher accuracy rates by employing both flexible discriminant analysis (FDA) and discriminant function analysis (DFA) to determine which method yields the highest classification accuracies.

5.1 Repeatability of Loth and İşcan's (2000) measurements

Intra- and inter-observer error rate measurements are important, given the need for valid, reliable and repeatable methods (Byrnes *et al.*, 2017). The reliability of a method is determined by whether the method produces the same results when utilised by two or more observers (Adams and Byrd, 2002). Low intra- and interobserver error rates determine higher reliability (Adams and Byrd, 2002). This study showed high repeatability rates, with all %TEM values falling below 1,50% and below 2% for inter-observer, suggesting high repeatability for intra- and inter-observer measurements (Ulijaszek and Kerr, 1999; Perini *et al.,* 2005; White *et al.,* 2011; Langley *et al.,* 2018). Interobserver error rates were slightly higher than intraobserver error rates (Table 2). Higher interobserver error may be due to a multitude of reasons, including a difference in observer judgement where this concerns bony landmark associated with specific measurements, the difference in the use of the measuring tool, i.e. sliding calliper and tailor tape, and the differences in observer training and

experience (Sutherland and Suchey, 1991; Adams and Byrd, 2002; Bruzek, 2002; L'Abbé *et al.,* 2005; Spradley and Jantz, 2011).

5.2 Accuracy of the Loth and İşcan (2000) sectioning points in a sample of SA Black and White individuals

A general decrease in the accuracies was seen in this study compared to the classification accuracies reported by Loth and İşcan (2000). For Black South Africans, the accuracy percentage went from 88,31% (Loth and İşcan, 2000) to 80,75% (current study) and for White South Africans, it went from 84,28% (Loth and İşcan, 2000) to 78,63% (current study). This can be a result of numerous influences including secular change, the sample size, and the inconsistencies of tibial landmarks.

5.2.1 Secular Change

Loth and İşcan (2000) developed their method using a 20th-century South African sample spanning 1901–2000, whereas the current study's sample ranges from 1948 to 2014. Their smaller sample size (n = 167) and earlier timeline may not have captured the biological variation introduced by secular change, long-term shifts in body size and proportions driven by environmental, nutritional, and socio-economic factors (Roche, 1979; Bogin, 2020). Numerous studies have documented these changes in postcranial dimensions, shaped by both improved and adverse living conditions over time (Vance *et al*., 2010; Grine *et al*., 2020; Bidmos *et al*., 2024).

Importantly, the early 20th century in South Africa was marked by profound socio-political upheavals, including the South African War (1899–1902), World War I (1914–1918), the Great Depression (1929–late 1930s), and World War II (1939–1945). These events brought economic downturns, widespread poverty, limited healthcare access, food scarcity, and high disease burdens, affecting both Black and White South Africans, though with stark racial disparities in how communities recovered (Minnaar, 1990, 1994; Seekings, 2011). Black

South Africans endured sustained systemic exclusion, forced labour, poor living conditions, malnutrition, and overcrowding, conditions known to impair skeletal growth, especially during critical developmental windows like puberty (Garn and Bailey, 1978; Bogin, 2020).

In this study, higher landmark measurement means were recorded for both Black and White males and females compared to those reported by Loth and İşcan (2000). From a secular change perspective, this likely reflects physiological responses to improved socio-economic conditions in the decades following these historical crises. Since the 1960s, Black South Africans began to experience incremental gains in nutrition, healthcare, and earlier maturation (Hawley *et al*., 2009; Cardoso *et al*., 2019), with evidence of reduced stunting and increased stature (Armstrong *et al*., 2011; Said-Mohamed *et al*., 2015). In line with this, a significant portion of the Black individuals in this study died after 1962, representing populations benefitting from these post-war improvements.

White South Africans, while historically advantaged, were nonetheless affected by the broader socio-economic hardships of the early 20th century, including the South African War, World Wars, and the Great Depression, all of which temporarily suppressed living standards, nutrition, and healthcare access (Minnaar, 1990, 1994; Seekings, 2011). However, in contrast to Black South Africans, White communities were able to recover more rapidly from these events due to systemic privileges under colonial and apartheid systems. From the mid-20th century onward, White South Africans experienced improvements in living conditions, urbanization, medical care, and consistent access to nutrient-dense diets, factors strongly associated with positive secular changes in body size and proportions (Bogin, 2020; Steckel, 2009).

The increase in measurements observed in White males and females in this study reflects these long-term secular trends, consistent with patterns seen in other industrialized

populations, where gradual gains in stature and skeletal dimensions have been linked to enhanced socio-economic stability, public health, and reduced disease burden over successive generations (Eveleth and Tanner, 1990; Komlos and Lauderdale, 2007). These changes likely resulted in larger long bones in later-born individuals within this group, contributing to higher sectioning points in the present study compared to Loth and İşcan (2000). Their earlier sample, which included individuals who lived through periods of significant economic and social instability between 1901 and 1948, would naturally exhibit smaller skeletal dimensions reflective of constrained growth conditions during those decades.

These overlapping historical, environmental, and socio-economic factors provide context for the higher sectioning points developed in this study and explain the decreased accuracy of the Loth and İşcan (2000) values in a contemporary context. Their sectioning points were calibrated to a population whose growth and skeletal development were constrained by harsh early 20th-century conditions, whereas the present study's sample reflects secular improvements in body size and proportions within both racial groups.

5.2.2 Sample size

Another point to consider is that Loth and İşcan (2000) utilised a relatively small sample size and hence, could result in the inflated accuracies. Loth and İşcan (2000) utilised a sample made up of 37 Black males, 44 Black females, 44 White males and 42 White females. This study utilised 100 Black males, 100 Black females, 100 White males, and 100 White females. The increased sample size results in increased precision and accuracy (Bartholdy *et al.*, 2020). By having more data, the model picks up on subtle differences between groups and establishes a clear, defined pattern for classification. Moreover, it reduces noise by accounting for the influence of outliers such as individuals which have smaller or larger long bone dimensions than expected and captures more variability within the population (Faber

and Fonseca, 2014). The use of a larger datas*et al*lows for the representation of population heterogeneity and accounts for a broader range of variation (Faber and Fonseca, 2014). Using a smaller sample size increases sampling error by relying on skeletal remains that may not accurately represent the broader population (e.g., outliers). It also reduces statistical power, leading to inaccurate sectioning points, and produces less robust cross-validation due to overfitting. This was observed in this study, as classification accuracies decreased when the Loth and İşcan (2000) sectioning points were applied to a different sample but produced greater classification rates when used by Loth and İşcan (2000). Ultimately, the small sample size introduced bias (Faber and Fonseca, 2014) as it contains inflated accuracies as it performed relatively well on training data.

Alternatively, the differences in classification accuracies observed between the two studies may stem from the fact that the Loth and İşcan (2000) reports model accuracies derived from the training sample without validation on an independent dataset. This lack of external validation leaves the generalizability and potential biases of the sectioning points untested. Hartley *et al*. (2022) emphasise that without such validation, sex estimation methods are susceptible to cognitive biases, particularly when contextual information influences metric analyses. Furthermore, adherence to evidentiary standards in forensic anthropology necessitates that methods be replicated and validated across diverse populations to ensure reliability and applicability in varied forensic contexts (Christensen and Crowder, 2009). The absence of validation on independent samples raises concerns about the robustness and forensic utility of the developed sectioning points, highlighting the need for comprehensive testing to establish their accuracy and generalizability.

5.2.3 The underperformance of TDB and the problematic nature of the tibial measurements.

An additional factor contributing to the decrease in classification accuracies of the Black and White South African populations using the original Loth and İşcan (2000) sectioning points is the landmark measurement that performed the poorest; the tibial distal breadth (TDB), classified at an accuracy of 87,5% in Black South Africans and 87,7 % in White South Africans in the original Loth and İşcan (2000) papers and decreased to 50% in the Black South African sample and 51% in the White South African sample. The drop in accuracy of TDB was mainly due to the poor classification of females in both Black (0%) and White (2%) populations. Furthermore, when analysing the sensitivity and specificity of each landmark measurement, TDB presented with the lowest specificity, implying that the measurements do not correctly reject non-cases i.e. false positives: for example, it classifies females as males. In contrast, TDB has a high sensitivity, which entails that it can classify true positives correctly, thus classifying males as males, hence the high classification accuracy. Similar findings were seen in a study conducted by Dangar *et al.* (2015), where the distal tibial epiphyseal breadth or TDB classified 0% of the females in the sample for both left and right tibiae and classified 1,89% of males using the right tibia and 0% of males using the left tibiae. The poor classification of TDB can be attributed to numerous reasons, such as the problematic nature of obtaining consistent tibial measurements. This is evident in a study conducted by Adams and Byrd (2002) and Robinson and Bidmos (2011), in which it was shown that the tibia was notoriously problematic for osteometric analysis due to its asymmetric morphology and difficulty in measuring tibial distal epiphyseal breadths. As aforementioned, the accuracy of TDB was particularly inadequate for females; a possible reason for this is the potential overlap in bone measurements between males and females. The TDB may thus be less sexually dimorphic in South African Black and White individuals

(Steyn and İşcan, 1999; Barrier and L'Abbé, 2008; Wallace *et al.*, 2020). This was highlighted when analysing the descriptive statistics of the entire sample and when the sample was split by sex. TDB presented with low standard deviations (SD_{males}= 3,19248 mm; $SD_{females}$ = 3,17741 mm) and a small difference in the maximum and minimum values ($range_{males}$ = 15,59 mm; $range_{females}$ = 19,94 mm) when the whole sample was considered and when the samples were split by sex, this indicated low variability and thus showed the consistency of the measurement despite the sex considered compared to the other measurements (Sikka and Jain, 2016) in this case, the measurements were consistently classified as male. Another possible explanation is differences in the interpretation of landmark measurement definitions (Langley *et al*., 2018). In the current study, the newly developed sectioning points were larger for both Black and White South African populations, increasing from 42,40 (Loth and İşcan, 2000) to 51,10 for Black South Africans, and from 44,40 (Loth and İşcan, 2000) to 53,40 for White South Africans, despite the use of a similarly dated sample. Similarly, the mean values for the TDB measurement in Black and White South African males and females in the current study were notably larger than those reported by Loth and İşcan (2000). This discrepancy could potentially be attributed to differences in the interpretation of the measurement definitions (such as those outlined by Buikstra and Ubelaker, 1994), instrumental factors, and variations in observer experience between the two studies (Smith and Boaks, 2014). Although consistently low intra- and inter-observer error rates suggest that observer inconsistency was minimal within the current study, it remains possible that these factors, particularly differences in systematic setup between the two studies, may have influenced the variations observed in measurement values (Adams and Byrd, 2002; Langley *et al*., 2016).

Another unclear tibial landmark measurement was TCN. In the Kruskal-Wallis test, TCN was the only landmark measurement that was not statistically significant in all populations; the

wide variability of TCN could explain this as it had the largest SD (SD = 10,15210 mm) and the largest range (range = 74,38) potentially encompassing measurements for all three populations. When analysing the ROC curve of TCN, it had the greatest AUC of 0,993, indicating that it is a good predictor of sex and is highly sexually dimorphic. However, the classification accuracies of the landmark measurement were highly variable. The landmark measurement often did not present with the highest or second highest classification accuracies for both this study and the original Loth and İşcan (2000) study. A potential reason for the wide variability in the size of TCN is the potential presence of overlapping distributions and because TCN was not normally distributed for White males. Additionally, the variability may be influenced by differences in the position of the nutrient foramen (Roy *et al*., 2020; Jabeen *et al*., 2023). Since the TCN measurement is typically taken in proximity to the nutrient foramen, variations in its anatomical position along the tibial shaft can alter the measurement location and result in increased variance in recorded values hence affecting the classification accuracy of the measurement for different populations.

5.3 The overlap between Black and Coloured populations

Another notable observation in the Kruskal-Wallis test is that the Black and Coloured populations were not significantly different in the sizes of all eight measurements and the newly developed sectioning points for both the populations were similar. Studies such as Liebenberg *et al.* (2019) showed considerable overlap in the postcranial skeletal measurements of Black and Coloured South Africans, making it difficult to distinguish between the two groups and similar outcomes have been seen in other articles as well (Liebenberg, 2014; Liebenberg *et al.*, 2015; Bothma, 2023). A plausible explanation for this phenomenon might involve a study conducted by Quintana-Murci *et al.* (2010) that shows that Coloured South African individuals have five different parental populations: KhoeSan,

Bantu-speaking populations, Europeans, Indians, and Southeast Asians. The study shows that the two major parental contributions are European and African (KhoeSan and Bantu-speaking populations). The maternal European contribution was ~5%. However, the paternal contribution (32,4%) had greater contribution with almost equal contribution from the African population (~40%); the maternal contribution of the African population contributed almost double that of paternal contribution (79%) (Quintana-Murci *et al.*, 2010). This could potentially explain why there are no significant differences between the measurements between the two populations. It also highlights the Bantu-speaking and KhoeSan people's considerable genetic contribution to Coloured South African's genetics, furthermore, other studies such as Wood *et al.* (2005) and Petersen *et al.* (2013) show that KhoeSan and Bantu-speaking individuals have a history of intermarriage before Apartheid , and thus, similarities are seen between Black and Coloured individuals. The misclassification of Black South Africans as Coloured South Africans and vice versa in the FDA output further supports these claims of intermixture and, thus, overlap between the two populations.

Furthermore, genetics also plays a role in the size and shape of long bones (Macho, 1991; Siddiqi, 2013). During skeletal development, genetic information is expressed morphologically by different codes dictating growth, development and allometry processes (Liebenberg *et al.*, 2015). This ultimately influences the variation seen between individuals. Human variation is multifactorial and is affected by different evolutionary mechanisms and population-specific historical contingencies. In South Africa, variation between populations is a result of differences in geographical origins, population history brought on by different socio-political factors, and positive assortative mating (Relethford, 2009; Stull *et al.,* 2014; Liebenberg *et al.,* 2015; McDowell *et al.,* 2015). As aforementioned, Coloured South Africans have significant genetic contributions from various population groups, including the

KhoeSan populations, commonly characterised by their small size (Wells, 1934). However, the effects of genetics or environmental influences differ somewhat (Stull, 2013). In childhood, environmental factors are shown to have a significantly larger impact on growth and development than genetics (Garn and Bailey, 1978; Stull, 2013); thus, the shared lived experience of the Black and Coloured populations has had a more significant effect on long bone dimensions (Macho, 1991; Siddiqi, 2013).

Since the introduction of colonisation, African individuals suffered major disparity. In South Africa, the disparity persisted through the transition from a colonial state to an apartheid government (Piotrowski, 2019). The effects of colonisation directly affected both Black and Coloured people similarly. Colonisation introduced concepts such as land ownership disparity, slavery, forced labour, land confiscation, massacres, and cultural suppression (Piotrowski, 2019). Numerous conflicts occurred between the Dutch and the KhoeSan individuals in the Cape, and as a result, the KhoeSan population in the Cape Colony was almost entirely eradicated. Subsequently, followed the introduction of Apartheid policies that further enforced the socioeconomic marginalisation of Black and Coloured individuals, and these policies resulted in a deeply entrenched poverty that continues to affect future generations post-apartheid (Chtourou *et al.*, n.d). As previously mentioned, these conditions ultimately led to the disparities in nutritional access, poor standards of living, and poor healthcare, thus resulting in the stunted growth of these individuals. Studies such as Hoppa (1992) show the effects of lower socioeconomic backgrounds on development. Hoppa (1992) showed that children from higher socioeconomic backgrounds were typically heavier and taller than children from lower socioeconomic backgrounds, indicating a difference in bodily dimensions and, thus, bone dimensions. Furthermore, nutritional deficiencies due to the lack of access to nutritious food delay the onset of puberty and result in slower development over

a long period of time, resulting in stunted growth (Kuzawa and Bragg, 2012). Although, Black and Coloured South Africans have different ancestral backgrounds, the typical environmental and socio-cultural conditions that these populations have experienced throughout their lifetime may result in similarities in their postcranial skeletal dimensions (Bateson *et al.,* 2014; Lea *et al.*, 2018).

Due to the overlap observed in measurements between the Black and Coloured South African populations in this study, it may be worthwhile for forensic anthropologists to consider applying the sectioning points developed for Black South Africans to classify Coloured individuals. Alternatively, these two groups could potentially be combined into a single population category when developing new sectioning points. Given the biological and historical factors contributing to this morphological similarity, it would be valuable to test the sectioning points proposed by Loth and İşcan (2000) for Black South Africans on the Coloured population to determine whether they yield comparable classification accuracies. If these sectioning points produce high accuracies when applied to the Coloured population, their use in forensic contexts could be considered, particularly in cases where population affinity is uncertain or when dedicated sectioning points for Coloured South Africans are unavailable.

5.4 The development of multivariate functions and the comparison between FDA and DFA

In the current study, multivariate landmark measurement combinations incorporating landmarks from all three long bones (humerus, femur, and tibia) consistently produced higher classification accuracies than models constructed from landmark combinations within a single bone. This outcome highlights the value of integrating multiple skeletal regions when estimating sex, as it captures a broader expression of sexual dimorphism distributed across

the postcranial skeleton. Single bone models, while useful, are limited in that they rely on isolated aspects of skeletal morphology, which may not sufficiently account for overlapping male and female ranges or inter-individual variation within a population. By combining landmarks from different bones, multivariate models are able to leverage the complementary nature of sexually dimorphic traits and reduce the influence of measurement error or localized bone-specific variation (Spradley and Jantz, 2011; Kranioti *et al.,* 2019). Additionally, these multivariate approaches consider the interrelationships between measurements, improving the model's ability to discriminate between sexes by analysing patterns of covariation rather than relying on individual traits in isolation (Langley *et al*., 2016). This finding underscores the importance of a holistic skeletal approach in forensic and biological anthropology, particularly in diverse and heterogeneous populations such as those in South Africa, where patterns of sexual dimorphism may manifest differently across skeletal elements (Bidmos and Asala, 2004; Dayal *et al.,* 2008).

Furthermore, the prevalence of both parametric and non-parametric data led to the use of two distinct discriminant methods: FDA and stepwise DFA (LDA). In both analyses, Black South Africans exhibited the highest classification accuracies, ranging from 88,50% to 92,50% for FDA and 88,50% to 94,00% for DFA, indicating a higher degree of sexual dimorphism. In contrast, White South Africans showed the lowest classification accuracies for FDA, ranging from 84,50% to 89,00%, which aligns with findings by Krüger (2014) that White South Africans are the least sexually dimorphic among the three populations studied. This lack of sexual dimorphism in White South Africans could be attributed to limited gene flow and a lack of environmental variability. According to Hedrick (2007), differential selection, gene flow, and genetic drift in the two sexes can cause significant differences in allele frequencies between males and females. Moreover, limited gene flow can lead to more rapid evolutionary

changes and stronger selective pressures, particularly when specific genes have sex-limited expression, thereby influencing the evolutionary shifts in traits that distinguish males from females. Coloured South Africans, on the other hand, had the lowest classification accuracy for DFA, ranging from 84,20% to 86,90%. Due to the Coloured South African sample having nonparametric data, likely as a result of the small sample size (Klecka, 1980; Tabachnick and Fidell, 2019), hampered its performance under DFA and contributed to the decreased accuracy.

Overall FDA produced greater classification accuracy of 89,17% compared to DFA, which obtained accuracy of 88,85%. This not an anomaly as similar results have been obtained in studies such as Liebenberg *et al.* (2015) which compared Discriminant Function Analysis (DFA, also known as Linear Discriminant Analysis or LDA) and Flexible Discriminant Analysis (FDA). FDA marginally outperformed LDA, which aligns with the findings of this study, as the FDA performed better than DFA by 0,32%. A similar trend of FDA outperforming DFA was seen in a study conducted by Stull *et al.* (2017) that looked at sex estimation of subadults utilising diaphyseal dimensions by employing LDA, FDA, and logistic regression models. Stull *et al.* (2017) highlight that logistic regression and FDA achieve higher classification rates than DFA in the results. In contrast, other studies, such as the one conducted by Knecht *et al.* (2021) that looked at sex estimation from the greater sciatic notch, utilising six statistical models, including LDA and FDA. In the Stull *et al.* (2017) study, two groups were created, the first group (group 1) included measurements that were specific to the greater sciatic notch, and the second group included all other variables that were measurements that concerned the relation of the depth of the greater sciatic notch to structures such as the pubis, the ischial ramus, etc. Knecht *et al.* (2021) obtained similar results for FDA and LDA, with 92% and 93% accuracy rates, respectively, for group 1. In group 2, the study opted for a stepwise LDA and obtained perfect classification accuracy,

slightly outperforming the FDA. Similarly, Krüger *et al.* (2017) estimated sex using various long bones in a South African population and like Knecht *et al.* (2021), LDA and FDA resulted in similar classification accuracies. However, unlike in the Knecht *et al.* (2021) study, the FDA achieved slightly better results. To further expand on the comparison, a study by Nogueira *et al.* (2023) analysed the radii in a French sample using six statistical models, including LDA and FDA. The study obtained accuracies greater than 96% for LDA and accuracies lower than 90% for FDA.

Due to contrasting data on which statistical model produces the most accurate classifications, additional factors must be considered, including what are the advantages and disadvantages of applying one statistical method over the other. Despite FDA and logistic regression obtaining high classification accuracies in the Stull *et al.* (2017) study, Stull *et al.* (2017) states that none of the models offer practical applicability, and this could be due to reasons such as the complexity of the models and whether they can be used in a forensic setting. Additionally, the study highlights that the FDA has larger confidence intervals and thus may be less precise and more variable than DFA. Furthermore, Krüger *et al.* (2017) highlighted that another limitation to the use of FDA is that FDA is limited to R studio, and other statistical programs cannot perform FDA, thus shifting preference to the use of DFA as it is more accessible and has lower computational complexity. While FDA has its limitations, it also has its advantages. The most significant benefit that FDA offers is that it allows for nonlinear relationships and interactions between variables and effectively manages multiple variables from different skeletal elements at one time (Friedman, 1989; Krüger *et al.*, 2017; Stull *et al.,* 2017). Liebenberg *et al.* (2015) further highlights another advantage of FDA, which involves fewer assumptions about the data and this is evident as FDA yielded classification accuracies of 88,16 – 90,79% for the Coloured South African population

despite the small sample size and the non-parametric nature of the data and thus making FDA are strong alternative when the assumptions of DFA are not met. DFA assumes linear relationships and multivariate normality, and this may not be the case for all datasets, including some that were represented in this study. However, DFA was still able to achieve high classification rates despite some of the data in the study not being normally distributed. This may be attributed to the Central Limit Theorem, which states that, regardless of the sample's original distribution, the distribution of the sample mean will approach normality as the sample size increases, provided the data comes from a distribution with finite mean and variance (Kwak and Kim, 2017). The Central Limit Theorem operates under certain conditions, such as having a sufficiently large sample size. It is an important consideration when choosing the most suitable analysis model for nonparametric data. However, DFA is often preferred due to its established reliability and relative ease of understanding (Liebenberg, 2014; Krüger *et al.,* 2017).

6. Limitations

A key limitation of this study lies in its inability to fully assess the extent of secular change, as the sample employed shares overlapping timelines with that of the Loth and İşcan (2000) study. This temporal overlap restricts the study's capacity to capture long-term biological trends and generational shifts in dimensions. Additionally, the sample size for the Coloured South African population was relatively small, which limited the development of robust multivariate formulas for this group. In several cases, formulae relied on a single landmark measurement, reducing the predictive power and generalizability of the models. The limited sample size also prevents a thorough and conclusive exploration of the relationship and potential overlap between the Black and Coloured populations, particularly in dimensions.

An important consideration is the impact of data upsampling on classification results, particularly for the Coloured population. The improved accuracy observed in the FDA models for this group may be partially attributable to the artificial duplication of individuals to increase sample size. While upsampling helps balance group sizes, it can introduce bias by reducing variability within the subsample, potentially inflating accuracy metrics and limiting the model's applicability to truly independent data.

Another significant limitation is that the classification accuracies reported in this study, similar to that of Loth and İşcan (2000), represent model accuracies derived from the training sample and were not validated on independent test samples. This means that the reported accuracies may be overestimated, as the models have not been tested for generalizability to new, unseen data.

Additionally, the influence of model assumptions on classification accuracy must be considered. While the comparison between Flexible Discriminant Analysis (FDA) and Discriminant Function Analysis (DFA) offered valuable insights into the practical strengths and limitations of each method, deviations from statistical assumptions, such as linearity, multivariate normality, and homogeneity of variance-covariance matrices, can significantly impact model performance on independent test samples. This is especially critical for DFA, which is highly sensitive to these assumptions. If the model is poorly suited to the population structure, it may perform well on the training data yet fail to generalize to new cases. FDA offers greater flexibility in this regard, as it accommodates non-linear relationships and is potentially more robust when handling complex data structures.

7. Conclusion

This study aimed to validate the accuracy of the original Loth and İşcan (2000) sex estimation method by applying their univariate sectioning points to a contemporary South African skeletal sample. The results confirmed that while the original sectioning points still yield relatively high accuracies for certain measurements, particularly among South African males, overall accuracy decreased when compared to the figures reported by Loth and İşcan (2000). This decline is likely influenced by secular changes over time, differences in sample size, and the absence of testing the sectioning points on an independent sample, as well as the inconsistencies in the measurement of specific tibial landmarks. These findings highlight the necessity for the periodic re-evaluation and refinement of sex estimation methods as population structures evolve and become increasingly diverse more especially, with the growing availability and acceptance of hormone therapies and gender-affirming procedures. It is crucial to consider how such interventions may alter skeletal morphology, potentially complicating traditional binary sex estimation approaches. This underscores the importance of developing inclusive, flexible forensic techniques capable of adapting to a broader spectrum of biological variation. Furthermore, the study emphasises the critical need to test newly developed sectioning points on independent samples to ensure their reliability and applicability in real-world forensic contexts.

The study also sought to develop new univariate sectioning points using a larger, more representative sample, which notably included the previously excluded Coloured South African population. The newly derived sectioning points were generally larger than those proposed by Loth and İşcan (2000) for both Black and White South Africans, a difference potentially attributed to secular growth trends and sample composition. The inclusion of the Coloured population facilitated the development of new, population-specific sectioning points, while simultaneously revealing a significant overlap in measurements between the

Black and Coloured populations. This overlap likely reflects shared lived experiences, gene flow, and historical patterns of admixture, emphasizing the importance of context-specific forensic standards.

Furthermore, by incorporating multivariate analyses, this study demonstrated how combining multiple measurements can enhance classification accuracy. The multivariate functions developed using flexible discriminant analysis (FDA) achieved high classification rates, while also outperforming traditional discriminant function analysis (DFA) in scenarios where assumptions of normality and homogeneity of variance-covariance matrices may be violated.

8. Future Research

Building on these findings, several avenues for future research are recommended. Firstly, it would be valuable to test both the newly developed univariate and multivariate formulae against independent validation samples to assess their generalisability and forensic applicability. Additionally, given the observed overlap in measurements between the Black and Coloured South African populations, future work should explore whether the sectioning points established for Black South Africans could be reliably applied to Coloured individuals. If high classification accuracies are achieved, it may be appropriate to consider merging these groups for certain forensic applications or developing combined sectioning points.

Moreover, future studies should prioritise increasing the Coloured population sample size to strengthen the statistical power and precision of both univariate and multivariate models. Repeating the study on individuals born after 1994 would also allow for a more accurate assessment of the full impact of secular change on long bone morphology and its implications for sex estimation methods.

An important methodological consideration for future work is addressing the potential bias introduced by upsampling smaller subsamples, as was necessary for the Coloured population in this study. This process may artificially reduce variability and inflate classification accuracy, so future studies should avoid or statistically correct for this where possible. Lastly, future research should investigate the effects of modern hormone therapies and gender-affirming surgical procedures on skeletal morphology, to ensure forensic anthropological practices remain relevant and inclusive in increasingly diverse social and biological contexts.

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10. Appendices

Appendix 1: Normality

Tests of Normality

		Kolmogorov-Smirnov[a]			Shapiro-Wilk		
	Groups	Statistic	df	Sig.	Statistic	df	Sig.
HHD	White Males	,071	100	,200*	,989	100	,618
	Black Males	,088	100	,055	,979	100	,113
	Coloured Males	,097	56	,200*	,972	56	,223
	White females	,064	100	,200*	,984	100	,250
	Black females	,081	100	,109	,978	100	,086
	Coloured females	,261	20	<,001	,855	20	,006
HED	White Males	,071	100	,200*	,984	100	,261
	Black Males	,068	100	,200*	,983	100	,234
	Coloured Males	,092	56	,200*	,979	56	,420
	White females	,087	100	,058	,962	100	,006
	Black females	,049	100	,200*	,984	100	,281
	Coloured females	,166	20	,151	,824	20	,002
FHD	White Males	,070	100	,200*	,989	100	,568
	Black Males	,067	100	,200*	,983	100	,221
	Coloured Males	,061	56	,200*	,979	56	,417
	White females	,060	100	,200*	,985	100	,341
	Black females	,076	100	,169	,988	100	,493
	Coloured females	,168	20	,140	,796	20	<,001
FMC	White Males	,070	100	,200*	,979	100	,111
	Black Males	,069	100	,200*	,986	100	,405
	Coloured Males	,103	56	,200*	,961	56	,066
	White females	,070	100	,200*	,986	100	,369
	Black females	,061	100	,200*	,987	100	,406
	Coloured females	,136	20	,200*	,947	20	,326
FDB	White Males	,044	100	,200*	,989	100	,566
	Black Males	,081	100	,108	,980	100	,134
	Coloured Males	,079	56	,200*	,986	56	,755
	White females	,063	100	,200*	,969	100	,019
	Black females	,076	100	,167	,980	100	,130
	Coloured females	,149	20	,200*	,889	20	,026
TPD	White Males	,056	100	,200*	,985	100	,311
	Black Males	,077	100	,145	,990	100	,690
	Coloured Males	,117	56	,053	,970	56	,179
	White females	,082	100	,093	,972	100	,030

	Black females	,079	100	,130	,977	100	,081
	Coloured females	,219	20	,013	,790	20	<,001
TCN	White Males	,071	100	,200*	,893	100	<,001
	Black Males	,098	100	,019	,987	100	,446
	Coloured Males	,160	56	,001	,917	56	<,001
	White females	,053	100	,200*	,984	100	,269
	Black females	,073	100	,200*	,973	100	,040
	Coloured females	,192	20	,053	,956	20	,460
TDB	White Males	,075	100	,180	,978	100	,101
	Black Males	,064	100	,200*	,987	100	,423
	Coloured Males	,104	56	,198	,970	56	,173
	White females	,085	100	,072	,985	100	,316
	Black females	,054	100	,200*	,994	100	,956
	Coloured females	,238	20	,004	,727	20	<,001

*. This is a lower bound of the true significance.

a. Lilliefors Significance Correction

Appendix 2: Kruskal-Wallis test

i. Groups

Ranks

	Groups	N	Mean Rank
HHD	White Males	100	409,50
	Black Males	100	247,43
	Coloured Males	56	257,28
	White females	100	236,16
	Black females	100	80,46
	Coloured females	20	88,18
	Total	476	
HED	White Males	100	377,79
	Black Males	100	311,62
	Coloured Males	56	267,26
	White females	100	158,76
	Black females	100	120,50
	Coloured females	20	84,65
	Total	476	
FHD	White Males	100	395,21
	Black Males	100	289,61
	Coloured Males	56	258,72
	White females	100	199,27
	Black females	100	91,28
	Coloured females	20	75,08
	Total	476	
FMC	White Males	100	353,69
	Black Males	100	338,13
	Coloured Males	56	230,85
	White females	100	185,73
	Black females	100	115,26
	Coloured females	20	65,95
	Total	476	
FDB	White Males	100	393,20
	Black Males	100	288,80
	Coloured Males	56	258,08
	White females	100	197,21
	Black females	100	94,20
	Coloured females	20	86,70
	Total	476	
TPD	White Males	100	378,43
	Black Males	100	313,09
	Coloured Males	56	270,56

Ranks

	Groups	N	Mean Rank
	White females	100	170,96
	Black females	100	106,47
	Coloured females	20	74,05
	Total	476	
TCN	White Males	100	328,79
	Black Males	100	346,98
	Coloured Males	56	261,86
	White females	100	153,14
	Black females	100	141,87
	Coloured females	20	89,23
	Total	476	
TDB	White Males	100	380,72
	Black Males	100	305,36
	Coloured Males	56	262,15
	White females	100	175,36
	Black females	100	112,28
	Coloured females	20	73,75
	Total	476	

Test Statistics[a,b]

	HHD	HED	FHD	FMC	FDB	TPD	TCN
Kruskal-Wallis H	311,928	265,467	295,716	249,415	284,410	280,761	218,404
df	5	5	5	5	5	5	5
Asymp. Sig.	<,001	<,001	<,001	<,001	<,001	<,001	<,001

Test Statistics[a,b]

	TDB
Kruskal-Wallis H	266,149
df	5
Asymp. Sig.	<,001

a. Kruskal Wallis Test

b. Grouping Variable: Groups

ii. Sex

Ranks

	sex	N	Mean Rank
HHD	Male	256	312,89
	Female	220	151,93
	Total	476	
HED	Male	256	327,76
	Female	220	134,63
	Total	476	
FHD	Male	256	324,10
	Female	220	138,89
	Total	476	
FMC	Male	256	320,74
	Female	220	142,80
	Total	476	
FDB	Male	256	322,86
	Female	220	140,34
	Total	476	
TPD	Male	256	329,31
	Female	220	132,83
	Total	476	
TCN	Male	256	321,25
	Female	220	142,20
	Total	476	
TDB	Male	256	325,34
	Female	220	137,45
	Total	476	

Test Statistics[a,b]

	HHD	HED	FHD	FMC	FDB	TPD	TCN	TDB
Kruskal-Wallis H	162,009	233,255	214,508	198,134	208,328	241,398	200,557	220,779
df	1	1	1	1	1	1	1	1
Asymp. Sig.	<,001	<,001	<,001	<,001	<,001	<,001	<,001	<,001

a. Kruskal Wallis Test

b. Grouping Variable: sex

iii. Population

Ranks

	Population	N	Mean Rank
HHD	White	200	322,83
	Black	200	163,95
	Coloured	76	212,78
	Total	476	
HED	White	200	268,28
	Black	200	216,06
	Coloured	76	219,20
	Total	476	
FHD	White	200	297,24
	Black	200	190,45
	Coloured	76	210,39
	Total	476	
FMC	White	200	269,71
	Black	200	226,69
	Coloured	76	187,45
	Total	476	
FDB	White	200	295,20
	Black	200	191,50
	Coloured	76	212,98
	Total	476	
TPD	White	200	274,69
	Black	200	209,78
	Coloured	76	218,85
	Total	476	
TCN	White	200	240,97
	Black	200	244,42
	Coloured	76	216,43
	Total	476	
TDB	White	200	278,04
	Black	200	208,82
	Coloured	76	212,57
	Total	476	

Test Statistics[a,b]

	HHD	HED	FHD	FMC	FDB	TPD	TCN	TDB
Kruskal-Wallis H	136,583	16,191	64,048	22,252	59,950	24,116	2,393	28,538
df	2	2	2	2	2	2	2	2
Asymp. Sig.	<,001	<,001	<,001	<,001	<,001	<,001	,302	<,001

a. Kruskal Wallis Test

b. Grouping Variable: Population

Appendix 3: Posthoc test output

1. Groups
   i. HHD

Pairwise Comparisons of Groups

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Black females-Coloured females	-7,715	33,694	-,229	,819	1,000
Black females-White females	155,700	19,453	8,004	<,001	,000
Black females-Black Males	166,970	19,453	8,583	<,001	,000
Black females-Coloured Males	176,817	22,958	7,702	<,001	,000
Black females-White Males	329,040	19,453	16,915	<,001	,000
Coloured females-White females	147,985	33,694	4,392	<,001	,000
Coloured females-Black Males	159,255	33,694	4,727	<,001	,000
Coloured females-Coloured Males	169,102	35,832	4,719	<,001	,000
Coloured females-White Males	321,325	33,694	9,537	<,001	,000
White females-Black Males	11,270	19,453	,579	,562	1,000
White females-Coloured Males	21,117	22,958	,920	,358	1,000
White females-White Males	173,340	19,453	8,911	<,001	,000
Black Males-Coloured Males	-9,847	22,958	-,429	,668	1,000
Black Males-White Males	162,070	19,453	8,331	<,001	,000
Coloured Males-White Males	152,223	22,958	6,630	<,001	,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

ii. HEB

Pairwise Comparisons of Groups

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured females-Black females	35,845	33,694	1,064	,287	1,000
Coloured females-White females	74,110	33,694	2,200	,028	,418
Coloured females-Coloured Males	182,609	35,832	5,096	<,001	,000
Coloured females-Black Males	226,970	33,694	6,736	<,001	,000
Coloured females-White Males	293,140	33,694	8,700	<,001	,000
Black females-White females	38,265	19,453	1,967	,049	,738
Black females-Coloured Males	146,764	22,958	6,393	<,001	,000
Black females-Black Males	191,125	19,453	9,825	<,001	,000
Black females-White Males	257,295	19,453	13,226	<,001	,000
White females-Coloured Males	108,499	22,958	4,726	<,001	,000
White females-Black Males	152,860	19,453	7,858	<,001	,000
White females-White Males	219,030	19,453	11,259	<,001	,000
Coloured Males-Black Males	44,361	22,958	1,932	,053	,800
Coloured Males-White Males	110,531	22,958	4,814	<,001	,000
Black Males-White Males	66,170	19,453	3,402	<,001	,010

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

iii. FHD

Pairwise Comparisons of Groups

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured females-Black females	16,205	33,694	,481	,631	1,000
Coloured females-White females	124,190	33,694	3,686	<,001	,003
Coloured females-Coloured Males	183,648	35,832	5,125	<,001	,000
Coloured females-Black Males	214,535	33,694	6,367	<,001	,000
Coloured females-White Males	320,130	33,694	9,501	<,001	,000
Black females-White females	107,985	19,453	5,551	<,001	,000
Black females-Coloured Males	167,443	22,958	7,293	<,001	,000
Black females-Black Males	198,330	19,453	10,195	<,001	,000
Black females-White Males	303,925	19,453	15,624	<,001	,000
White females-Coloured Males	59,458	22,958	2,590	,010	,144
White females-Black Males	90,345	19,453	4,644	<,001	,000
White females-White Males	195,940	19,453	10,072	<,001	,000
Coloured Males-Black Males	30,887	22,958	1,345	,179	1,000
Coloured Males-White Males	136,482	22,958	5,945	<,001	,000
Black Males-White Males	105,595	19,453	5,428	<,001	,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

iv. FMC

Pairwise Comparisons of Groups

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured females-Black females	49,305	33,681	1,464	,143	1,000
Coloured females-White females	119,775	33,681	3,556	<,001	,006
Coloured females-Coloured Males	164,898	35,818	4,604	<,001	,000
Coloured females-Black Males	272,175	33,681	8,081	<,001	,000
Coloured females-White Males	287,740	33,681	8,543	<,001	,000
Black females-White females	70,470	19,446	3,624	<,001	,004
Black females-Coloured Males	115,593	22,950	5,037	<,001	,000
Black females-Black Males	222,870	19,446	11,461	<,001	,000
Black females-White Males	238,435	19,446	12,262	<,001	,000
White females-Coloured Males	45,123	22,950	1,966	,049	,739
White females-Black Males	152,400	19,446	7,837	<,001	,000
White females-White Males	167,965	19,446	8,638	<,001	,000
Coloured Males-Black Males	107,277	22,950	4,674	<,001	,000
Coloured Males-White Males	122,842	22,950	5,353	<,001	,000
Black Males-White Males	15,565	19,446	,800	,423	1,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

v. FDB

Pairwise Comparisons of Groups

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured females-Black females	7,495	33,694	,222	,824	1,000
Coloured females-White females	110,505	33,694	3,280	,001	,016
Coloured females-Coloured Males	171,380	35,832	4,783	<,001	,000
Coloured females-Black Males	202,100	33,694	5,998	<,001	,000
Coloured females-White Males	306,495	33,694	9,097	<,001	,000
Black females-White females	103,010	19,453	5,295	<,001	,000
Black females-Coloured Males	163,885	22,958	7,138	<,001	,000
Black females-Black Males	194,605	19,453	10,004	<,001	,000
Black females-White Males	299,000	19,453	15,370	<,001	,000
White females-Coloured Males	60,875	22,958	2,652	,008	,120
White females-Black Males	91,595	19,453	4,709	<,001	,000
White females-White Males	195,990	19,453	10,075	<,001	,000
Coloured Males-Black Males	30,720	22,958	1,338	,181	1,000
Coloured Males-White Males	135,115	22,958	5,885	<,001	,000
Black Males-White Males	104,395	19,453	5,367	<,001	,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

vi. TPB

Pairwise Comparisons of Groups

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured females-Black females	32,415	33,694	,962	,336	1,000
Coloured females-White females	96,905	33,694	2,876	,004	,060
Coloured females-Coloured Males	196,513	35,832	5,484	<,001	,000
Coloured females-Black Males	239,040	33,694	7,095	<,001	,000
Coloured females-White Males	304,375	33,694	9,034	<,001	,000
Black females-White females	64,490	19,453	3,315	<,001	,014
Black females-Coloured Males	164,098	22,958	7,148	<,001	,000
Black females-Black Males	206,625	19,453	10,622	<,001	,000
Black females-White Males	271,960	19,453	13,980	<,001	,000
White females-Coloured Males	99,608	22,958	4,339	<,001	,000
White females-Black Males	142,135	19,453	7,307	<,001	,000
White females-White Males	207,470	19,453	10,665	<,001	,000
Coloured Males-Black Males	42,528	22,958	1,852	,064	,960
Coloured Males-White Males	107,863	22,958	4,698	<,001	,000
Black Males-White Males	65,335	19,453	3,359	<,001	,012

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

vii. TCN

Pairwise Comparisons of Groups

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured females-Black females	52,640	33,687	1,563	,118	1,000
Coloured females-White females	63,915	33,687	1,897	,058	,867
Coloured females-Coloured Males	172,632	35,824	4,819	<,001	,000
Coloured females-White Males	239,565	33,687	7,112	<,001	,000
Coloured females-Black Males	257,755	33,687	7,652	<,001	,000
Black females-White females	11,275	19,449	,580	,562	1,000
Black females-Coloured Males	119,992	22,954	5,228	<,001	,000
Black females-White Males	186,925	19,449	9,611	<,001	,000
Black females-Black Males	205,115	19,449	10,546	<,001	,000
White females-Coloured Males	108,717	22,954	4,736	<,001	,000
White females-White Males	175,650	19,449	9,031	<,001	,000
White females-Black Males	193,840	19,449	9,967	<,001	,000
Coloured Males-White Males	66,933	22,954	2,916	,004	,053
Coloured Males-Black Males	85,123	22,954	3,708	<,001	,003
White Males-Black Males	-18,190	19,449	-,935	,350	1,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

viii. TDB

Pairwise Comparisons of Groups

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured females-Black females	38,525	33,694	1,143	,253	1,000
Coloured females-White females	101,605	33,694	3,016	,003	,038
Coloured females-Coloured Males	188,402	35,832	5,258	<,001	,000
Coloured females-Black Males	231,605	33,694	6,874	<,001	,000
Coloured females-White Males	306,970	33,694	9,111	<,001	,000
Black females-White females	63,080	19,453	3,243	,001	,018
Black females-Coloured Males	149,877	22,958	6,528	<,001	,000
Black females-Black Males	193,080	19,453	9,925	<,001	,000
Black females-White Males	268,445	19,453	13,800	<,001	,000
White females-Coloured Males	86,797	22,958	3,781	<,001	,002
White females-Black Males	130,000	19,453	6,683	<,001	,000
White females-White Males	205,365	19,453	10,557	<,001	,000
Coloured Males-Black Males	43,203	22,958	1,882	,060	,898
Coloured Males-White Males	118,568	22,958	5,164	<,001	,000
Black Males-White Males	75,365	19,453	3,874	<,001	,002

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

2. Populations

i. HHD

Pairwise Comparisons of Population

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Black-Coloured	-48,831	18,536	-2,634	,008	,025
Black-White	158,885	13,755	11,551	<,001	,000
Coloured-White	110,054	18,536	5,937	<,001	,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.

Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.

a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

ii. HEB

Pairwise Comparisons of Population

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Black-Coloured	-3,146	18,536	-,170	,865	1,000
Black-White	52,218	13,755	3,796	<,001	,000
Coloured-White	49,071	18,536	2,647	,008	,024

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.

Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.

a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

iii. FHD

Pairwise Comparisons of Population

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Black-Coloured	-19,950	18,536	-1,076	,282	,845
Black-White	106,790	13,755	7,764	<,001	,000
Coloured-White	86,840	18,536	4,685	<,001	,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

iv. FMC

Pairwise Comparisons of Population

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured-Black	39,236	18,528	2,118	,034	,103
Coloured-White	82,254	18,528	4,439	<,001	,000
Black-White	43,018	13,750	3,129	,002	,005

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

v. FDB

Pairwise Comparisons of Population

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Black-Coloured	-21,483	18,536	-1,159	,246	,739
Black-White	103,703	13,755	7,539	<,001	,000
Coloured-White	82,220	18,536	4,436	<,001	,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

vi. TPB

Pairwise Comparisons of Population

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Black-Coloured	-9,071	18,536	-,489	,625	1,000
Black-White	64,913	13,755	4,719	<,001	,000
Coloured-White	55,841	18,536	3,013	,003	,008

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

vii. TCN

Pairwise Comparisons of Population

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Coloured-White	24,537	18,532	1,324	,185	,556
Coloured-Black	27,995	18,532	1,511	,131	,393
White-Black	-3,458	13,752	-,251	,801	1,000

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

viii. TDB

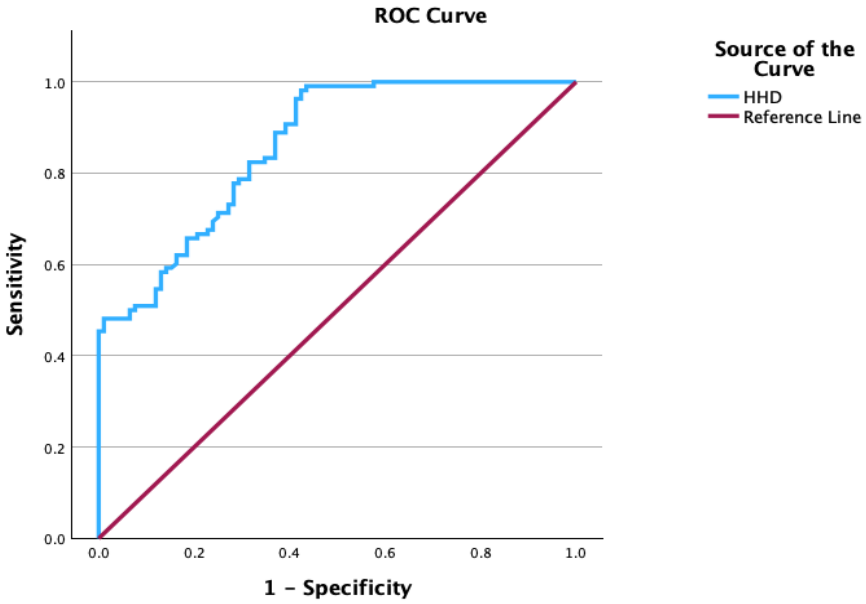
Pairwise Comparisons of Population

Sample 1-Sample 2	Test Statistic	Std. Error	Std. Test Statistic	Sig.	Adj. Sig.[a]
Black-Coloured	-3,757	18,536	-,203	,839	1,000
Black-White	69,223	13,755	5,032	<,001	,000
Coloured-White	65,465	18,536	3,532	<,001	,001

Each row tests the null hypothesis that the Sample 1 and Sample 2 distributions are the same.
Asymptotic significances (2-sided tests) are displayed. The significance level is ,050.
a. Significance values have been adjusted by the Bonferroni correction for multiple tests.

Appendix 4: ROC curves

i. HHD



Area Under the ROC Curve

Test Result Variable(s): HHD

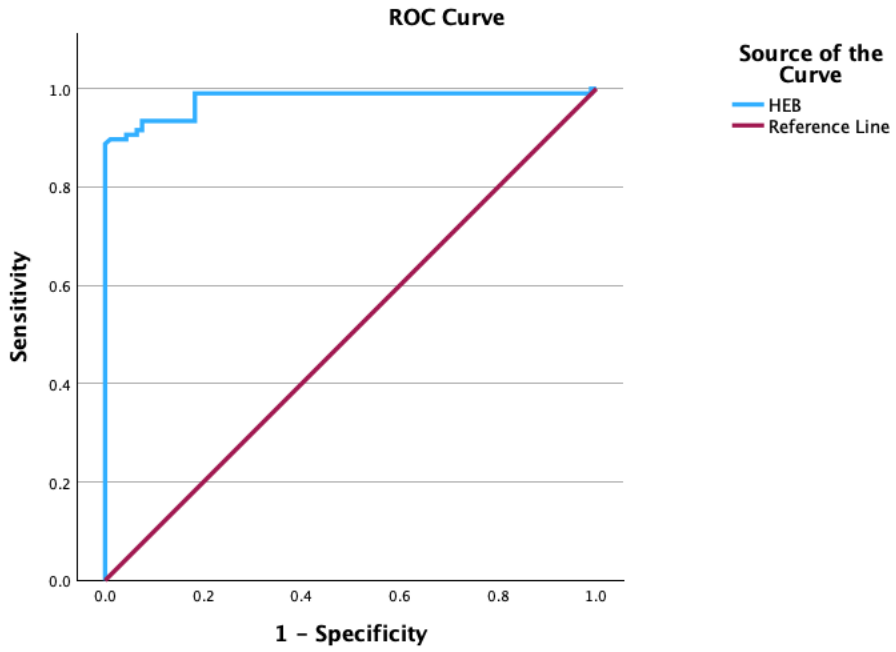
Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.859	.025	.000	.810	.908

The test result variable(s): HHD has at least one tie between the positive actual state group and the negative actual state group. Statistics may be biased.

a. Under the nonparametric assumption

b. Null hypothesis: true area = 0.5

ii. HEB



Area Under the ROC Curve

Test Result Variable(s): HEB

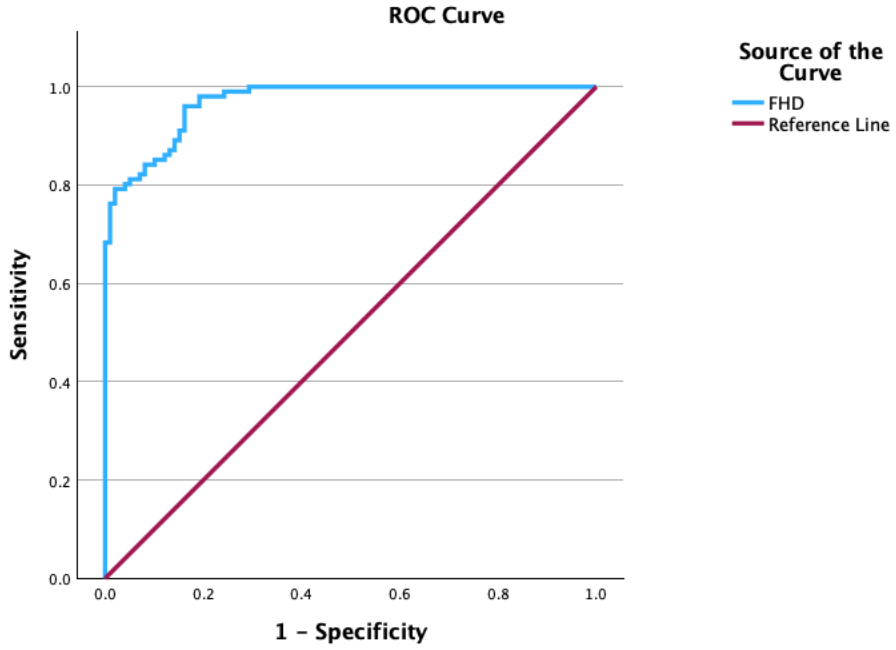
Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.978	.010	.000	.958	.999

The test result variable(s): HEB has at least one tie between the positive actual state group and the negative actual state group. Statistics may be biased.

a. Under the nonparametric assumption

b. Null hypothesis: true area = 0.5

iii. FHD



Area Under the ROC Curve

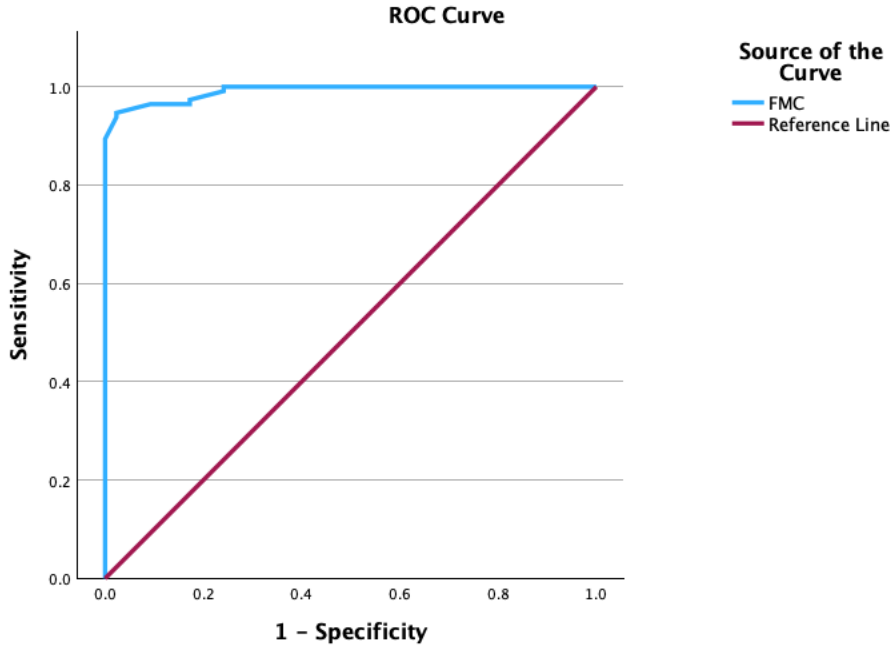
Test Result Variable(s): FHD

Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.969	.009	.000	.951	.987

a. Under the nonparametric assumption

b. Null hypothesis: true area = 0.5

iv. FMC



Area Under the ROC Curve

Test Result Variable(s): FMC

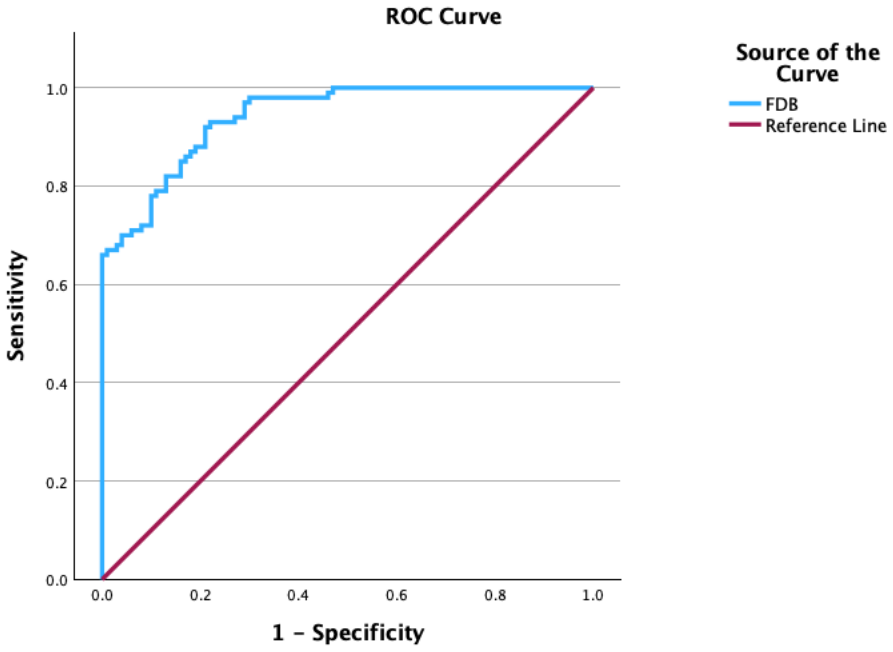
Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.991	.004	.000	.983	.999

The test result variable(s): FMC has at least one tie between the positive actual state group and the negative actual state group. Statistics may be biased.

a. Under the nonparametric assumption

b. Null hypothesis: true area = 0.5

v. FDB



Area Under the ROC Curve

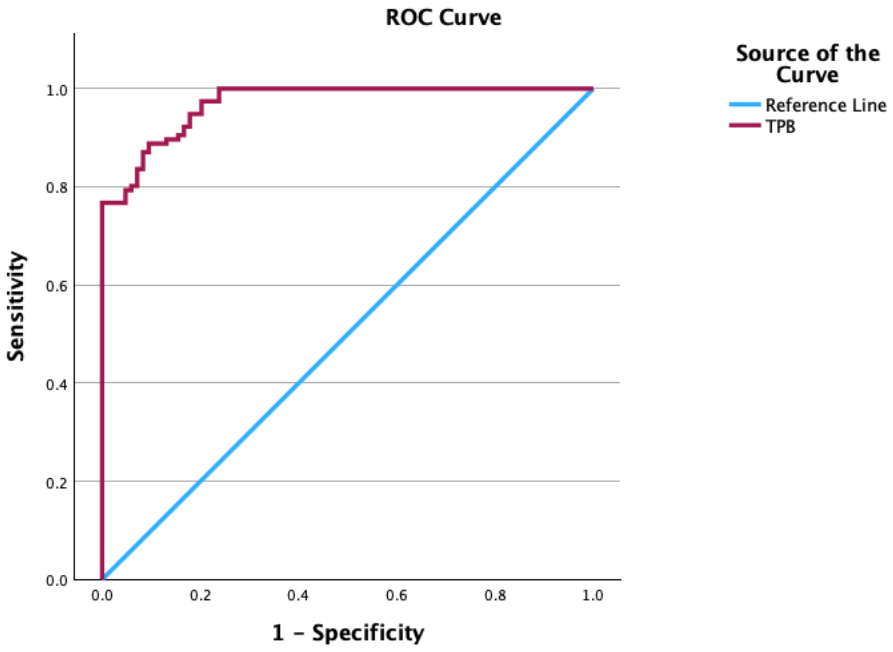
Test Result Variable(s): FDB

Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.942	.014	.000	.914	.970

a. Under the nonparametric assumption

b. Null hypothesis: true area = 0.5

vi. TPB



Area Under the ROC Curve

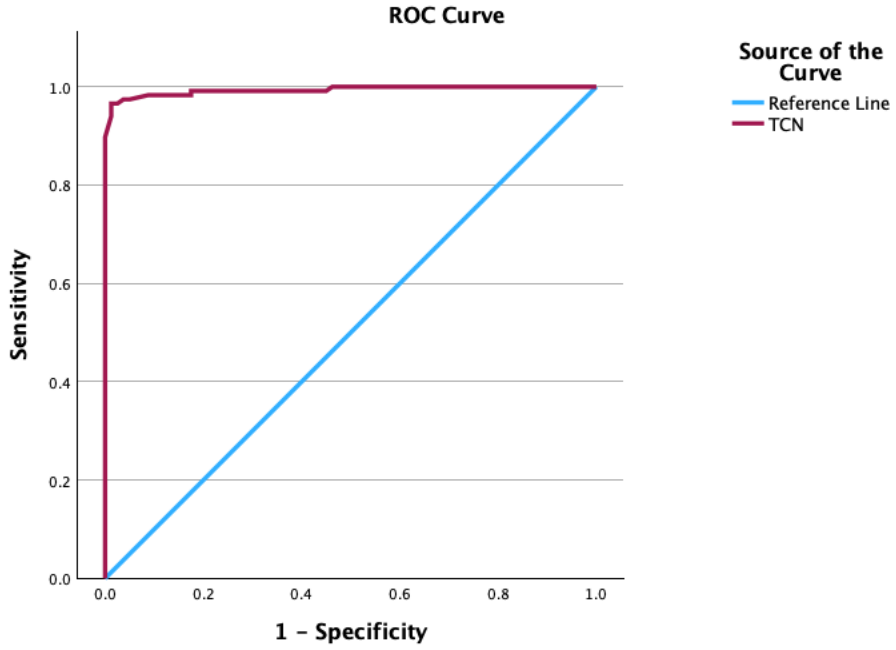
Test Result Variable(s): TPB

Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.970	.009	.000	.952	.988

a. Under the nonparametric assumption

b. Null hypothesis: true area = 0.5

vii. TCN



Area Under the ROC Curve

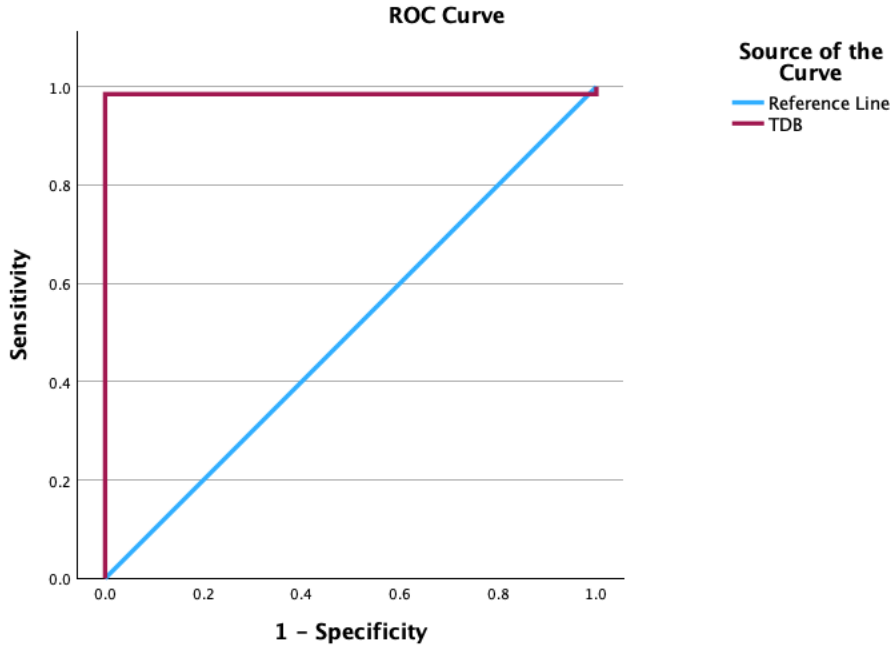
Test Result Variable(s): TCN

Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.993	.004	.000	.984	1.002

The test result variable(s): TCN has at least one tie between the positive actual state group and the negative actual state group. Statistics may be biased.

a. Under the nonparametric assumption
b. Null hypothesis: true area = 0.5

viii. TDB



Area Under the ROC Curve

Test Result Variable(s): TDB

Area	Std. Error[a]	Asymptotic Sig.[b]	Asymptotic 95% Confidence Interval	
			Lower Bound	Upper Bound
.985	.009	.000	.968	1.002

a. Under the nonparametric assumption

b. Null hypothesis: true area = 0.5

Appendix 5: FDA output

1. FDA output for Black South Africans

i. Humerus, tibia and femur

```
> library(foreign)
> library(caret)
Loading required package: ggplot2
Loading required package: lattice
> library(ROSE)
Loaded ROSE 0.0-4
> library(haven)
> library(dplyr)

Attaching package: ‘dplyr’

The following objects are masked from ‘package:stats’:

    filter, lag

The following objects are masked from ‘package:base’:

    intersect, setdiff, setequal, union

> library(earth)
Loading required package: Formula
Loading required package: plotmo
Loading required package: plotrix
> library(mda)
Loading required package: class
Loaded mda 0.5-5
> landmark_data<-read_sav ("C:/Users/Puseletso Maboea/Documents/Masters/Blac
k population data1.sav")
> print(landmark_data)
> fda_model <- fda(sex ~ HHD + HEB + FHD + FMC + FDB + TPB + TCN + TD
B, data =
+landmark_data)
> colnames(landmark_data) <-
+         c("HHD","HEB","FHD","FMC","FDB","TPB","TCN","TDB","sex")
> landmark_data$HHD <- as.numeric(landmark_data$HHD)
> landmark_data$HEB <- as.numeric(landmark_data$HEB)
> landmark_data$FHD <- as.numeric(landmark_data$FHD)
> landmark_data$FMC <- as.numeric(landmark_data$FMC)
> landmark_data$FDB <- as.numeric(landmark_data$FDB)
> landmark_data$TCN <- as.numeric(landmark_data$TCN)
> landmark_data$TPB <- as.numeric(landmark_data$TPB)
> landmark_data$TDB <- as.numeric(landmark_data$TDB)
> fda_model <- fda(sex ~ HHD + HEB + FHD + FMC + FDB + TPB + TCN + TD
B, data =
+                                                landmark_data)
> print(fda_model)
Call:
fda(formula = sex ~ HHD + HEB + FHD + FMC + FDB + TPB + TCN +
    TDB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
```

```
 v1
100

Degrees of Freedom (per dimension): 9

Training Misclassification Error: 0.075 ( N = 200 )
> predictions <- as.factor(predictions)
> landmark_data$sex <- as.factor(landmark_data$sex)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 92  7
         2  8 93

               Accuracy : 0.925
                 95% CI : (0.8793, 0.9574)
    No Information Rate : 0.5
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.85

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.9200
            Specificity : 0.9300
         Pos Pred Value : 0.9293
         Neg Pred Value : 0.9208
             Prevalence : 0.5000
         Detection Rate : 0.4600
   Detection Prevalence : 0.4950
      Balanced Accuracy : 0.9250

       'Positive' Class : 1

> fda_model$fit
$fitted.values
         [,1]
1 -0.97197226
1 -1.19038173
1 -1.06689802
1 -1.60131615
1 -0.77220456
1 -0.39856999
1 -0.39592430
1 -0.98757567
1 -1.58270342
1 -1.03449256
1 -0.61099951
1 -0.67915452
1 -1.01956661
1 -1.48154764
1 -0.87599171
1 -0.03402774
1 -0.48062149
1  0.06276627
1 -1.18238874
1 -0.93351062
1 -0.70022052
```

1 -0.42293970
1 -1.48886756
1 -0.65986763
1 -0.43157416
1 -0.68744951
1 0.09650827
1 0.10138201
1 -1.35543599
1 -0.38912939
1 -1.29705198
1 -0.77037735
1 -0.14788335
1 -0.66063568
1 -0.26318376
1 -0.29408688
1 -0.40198454
1 -0.17951295
1 -0.90356932
1 -0.15537321
1 0.41710826
1 -1.20427741
1 -1.32258945
1 -0.43025918
1 -0.21411889
1 0.17214463
1 -1.66647461
1 -0.17978685
1 -0.54549974
1 -0.85076357
1 -0.50736127
1 -0.79404517
1 -0.88754363
1 -0.66857262
1 -0.66238483
1 -0.38885165
1 -0.65504630
1 -0.25349067
1 -0.56365177
1 0.03099871
1 -0.92494563
1 -1.77096977
1 -0.67711475
1 -0.47739793
1 -0.77193189
1 -1.22597624
1 -0.92430726
1 -0.28757080
1 -0.99100495
1 -0.48127333
1 -1.27448862
1 -0.69578049
1 -0.49877319
1 -0.86866309
1 -0.89955588
1 -0.80451915
1 -0.01266611
1 -1.13786943
1 -0.77801557
1 -0.62737677
1 0.11076234

1 -1.02730017
1 0.27414065
1 -0.70346852
1 -1.02010623
1 -0.63596600
1 -0.49783183
1 -1.29607221
1 -0.84753785
1 -1.19749604
1 -0.59213726
1 -0.67813317
1 -1.01115137
1 -0.69366161
1 -0.43171879
1 -0.28760130
1 -0.76193383
1 -0.23944105
1 -0.91972349
1 -0.87997436
2 1.23467440
2 0.95526339
2 1.06715209
2 -0.19622831
2 0.43447484
2 -0.48098319
2 0.14115877
2 1.01380149
2 1.23288582
2 1.00940690
2 0.25494192
2 0.83277695
2 0.75033086
2 1.10651641
2 1.14037128
2 0.82668308
2 0.40019765
2 1.15471619
2 0.67655351
2 1.43130476
2 0.26604524
2 1.44498067
2 0.59871609
2 -0.82623582
2 0.55282398
2 0.91232487
2 1.40549754
2 0.06716820
2 0.78385688
2 -0.03661516
2 0.34582226
2 1.04988516
2 0.85583501
2 0.87161791
2 0.62148061
2 1.14120757
2 1.06506983
2 1.04803592
2 1.05614710
2 1.26150659
2 0.01949250

2 0.60251159
2 1.02204328
2 0.50007487
2 0.34071200
2 1.07901502
2 0.69817988
2 0.09471784
2 0.36083657
2 0.20001309
2 0.77176165
2 0.12176107
2 1.36363861
2 0.50598099
2 1.35265504
2 1.16188603
2 0.40649830
2 0.35717554
2 0.26365777
2 1.21035684
2 0.94545755
2 0.05837539
2 1.02424085
2 1.25331220
2 -0.13417040
2 0.95839484
2 1.02029388
2 -0.27904807
2 1.06186482
2 0.94561747
2 0.30424064
2 1.32985805
2 1.39721727
2 0.94974858
2 0.16909119
2 0.23300353
2 0.41555319
2 0.59894417
2 1.12862700
2 0.76187371
2 0.15751501
2 1.37527020
2 1.15235080
2 0.52322426
2 0.67724045
2 0.83273806
2 0.68884115
2 0.91378428
2 0.82001981
2 0.40516442
2 0.51573097
2 1.43430702
2 0.13761185
2 0.37379992
2 0.31433389
2 0.39044189
2 1.03801887
2 0.29051227
2 -0.16430843
2 0.96612284

```
$coefficients
                [,1]
Intercept 10.947683168
HHD       -0.069899480
HEB       -0.041502430
FHD       -0.037058999
FMC       -0.035595825
FDB        0.005984064
TPB       -0.047955172
TCN        0.004116396
TDB        0.032972729

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 9

attr(,"class")
[1] "polyreg"

> b<-coefficients[,1]
> centroids<-aggregate(cbind(HHD,HEB,FHD,FMC,FDB,TPB,TCN,TDB)~sex,dat
a =
+landmark_data,FUN=mean)
>
> centroids<-fda_model$means
> print(centroids)
         v1
1 -1.488064
2  1.488064
attr(,"scaled:scale")
[1] 0.6720142
```

ii. Humerus

```
> fda_model <- fda(sex ~ HHD + HEB, data =
+ landmark_data)
> print(fda_model)
Call:
fda(formula = sex ~ HHD + HEB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 3

Training Misclassification Error: 0.085 ( N = 200 )
> predictions <- as.factor(predictions)
> landmark_data$sex <- as.factor(landmark_data$sex)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 92  9
         2  8 91

               Accuracy : 0.915
                 95% CI : (0.8674, 0.9497)
    No Information Rate : 0.5
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.83

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.9200
            Specificity : 0.9100
         Pos Pred Value : 0.9109
         Neg Pred Value : 0.9192
             Prevalence : 0.5000
         Detection Rate : 0.4600
   Detection Prevalence : 0.5050
      Balanced Accuracy : 0.9150

       'Positive' Class : 1

> fda_model$fit
$fitted.values
          [,1]
1 -0.528655779
1 -0.601853909
1 -0.621122832
1 -1.140426594
1 -0.315456307
1  0.237032923
1 -0.379943793
1 -0.586061057
1 -1.735423460
```

1 -0.861173539
1 -0.738350510
1 -0.535007936
1 -1.003656560
1 -1.234294154
1 -0.567501815
1 -0.041706533
1 -0.596011284
1 0.115708690
1 -1.117988209
1 -0.455361874
1 -0.098673217
1 -0.186556639
1 -0.719157718
1 -0.914055972
1 -0.489608549
1 -0.642111201
1 0.141491422
1 -0.040592886
1 -1.461244352
1 -0.457552624
1 -1.571110964
1 -0.853094361
1 -0.479278089
1 -0.768876905
1 -0.068147781
1 -0.411422909
1 -0.217931613
1 -0.794378562
1 -0.823250428
1 -0.241532193
1 -0.019154645
1 -1.078662141
1 -1.414241155
1 -0.360659162
1 0.107044147
1 0.175078409
1 -1.731505689
1 -0.152469677
1 -0.740241863
1 -0.711764044
1 -0.359482515
1 -0.854402797
1 -1.293950734
1 -0.897758781
1 -0.279014497
1 -0.436485676
1 -1.041786698
1 -0.142633381
1 -0.320337613
1 -0.185134932
1 -1.179544080
1 -2.272179136
1 -0.440021406
1 -0.557910942
1 -0.944305294
1 -1.286366700
1 -1.353555062
1 -0.819307158
1 -1.136428559

1 -0.251866313
1 -1.622429682
1 -0.402337566
1 -0.809907604
1 -1.013703883
1 -0.702390351
1 -0.319619087
1 -0.164340691
1 -0.624487483
1 -0.635107571
1 -0.595797808
1 0.084173684
1 -0.736947918
1 0.515436076
1 -0.827811073
1 -1.007714421
1 -0.590111213
1 -0.358537434
1 -1.328667375
1 -0.568728500
1 -0.761841393
1 -0.271093266
1 -0.339037773
1 -0.859898306
1 -0.502867558
1 -0.083943677
1 0.131336020
1 -0.407772289
1 -0.325509782
1 -0.921909372
1 -0.751037031
2 0.845020733
2 1.125835221
2 0.911033406
2 0.079174147
2 0.446302322
2 -0.478513941
2 0.175313977
2 0.977869524
2 1.035495918
2 1.177676070
2 0.074570211
2 0.942298153
2 0.635619247
2 1.038715287
2 0.717533577
2 1.081571296
2 -0.211326095
2 1.021890772
2 0.368092353
2 1.145265730
2 0.070948197
2 1.200057606
2 0.667041579
2 -1.070026735
2 0.591820670
2 1.403371936
2 1.384072490
2 -0.118115433
2 0.728587959

2 -0.117038033
2 0.213290764
2 1.132520871
2 0.929158057
2 1.085431027
2 0.478425438
2 0.718840096
2 0.987590632
2 0.841571584
2 0.962825475
2 1.331212811
2 0.080925113
2 0.514541396
2 0.881986164
2 0.040027692
2 0.133236270
2 1.221951637
2 0.525473843
2 0.028032891
2 0.267044231
2 0.153975745
2 0.783457156
2 0.071967558
2 1.040395910
2 0.696622297
2 1.206995127
2 1.042462045
2 0.294329760
2 0.400170392
2 0.319442565
2 1.224721665
2 0.941807671
2 0.317050642
2 0.637114108
2 1.113164641
2 -0.245344929
2 0.883768778
2 0.846101837
2 -0.339704294
2 1.140286433
2 0.769033228
2 0.092648760
2 1.420276286
2 1.434441000
2 0.987222978
2 -0.003964056
2 0.069056546
2 0.644001228
2 0.290583300
2 1.014929539
2 0.363149666
2 0.125348112
2 0.995095790
2 0.889360128
2 0.243546006
2 1.050270601
2 1.070301885
2 0.523620588
2 0.866537320
2 0.672723577

```
2  0.554018897
2  0.405980475
2  0.887178573
2  0.351461372
2  0.497730076
2  0.507165877
2  0.677013600
2  0.948361299
2  0.641309546
2 -0.186256879
2  1.030817932

$coefficients
                [,1]
Intercept 10.65277561
HHD       -0.14254106
HEB       -0.08154416

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 3

attr(,"class")
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(HHD,HEB)~sex,data =
+                                                    landmark_data,FUN=mean)
>
> centroids<-fda_model$means
> print(centroids)
         v1
1 -1.293366
2  1.293366
attr(,"scaled:scale")
[1] 0.7731763
```

iii. Femur

```
fda_model <- fda(sex ~ FHD + FMC + FDB, data =
+landmark_data)

> print(fda_model)
Call:
fda(formula = sex ~ FHD + FMC + FDB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 4

Training Misclassification Error: 0.09 ( N = 200 )
> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 91  9
         2  9 91

               Accuracy : 0.91
                 95% CI : (0.8615, 0.9458)
    No Information Rate : 0.5
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.82

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.910
            Specificity : 0.910
         Pos Pred Value : 0.910
         Neg Pred Value : 0.910
             Prevalence : 0.500
         Detection Rate : 0.455
   Detection Prevalence : 0.500
      Balanced Accuracy : 0.910

       'Positive' Class : 1

> fda_model$fit
$fitted.values
          [,1]
1 -1.17196609
1 -1.30919619
1 -0.87176361
1 -1.57170040
1 -0.82230879
1 -0.67819328
1 -0.13928027
```

1 -1.22029463
1 -1.41867713
1 -0.88719299
1 -0.52238180
1 -0.54942447
1 -1.14075520
1 -1.77855407
1 -0.97876942
1 0.15055355
1 -0.26360346
1 -0.22496490
1 -1.11818847
1 -1.09824737
1 -0.97253916
1 -0.44442164
1 -1.58432117
1 -0.49825302
1 -0.28740189
1 -0.36470721
1 0.03646080
1 -0.13385425
1 -1.33374551
1 -0.46764410
1 -1.26425012
1 -0.78605449
1 0.04991297
1 -0.43439761
1 -0.46500475
1 -0.16841938
1 -0.52649979
1 -0.07947126
1 -1.03820966
1 -0.03540367
1 0.48430669
1 -1.23357261
1 -1.54254670
1 -0.47178193
1 -0.36751334
1 0.48741964
1 -1.37913895
1 -0.10199257
1 -0.62714414
1 -0.83553804
1 -0.53263325
1 -0.64130432
1 -0.89342939
1 -0.67589914
1 -0.82818723
1 -0.31944002
1 -0.51187187
1 -0.32768844
1 -0.58390423
1 -0.21359401
1 -0.64032757
1 -1.50887210
1 -0.75978631
1 -0.34396265
1 -0.52211314
1 -1.31200278

1 -0.61188382
1 -0.28973742
1 -0.70275847
1 -0.09184051
1 -0.77433973
1 -0.69178368
1 -0.17628545
1 -0.56759914
1 -0.97201374
1 -1.13484290
1 0.09970992
1 -1.43739588
1 -0.72450016
1 -0.34138048
1 0.23630318
1 -1.03605604
1 0.10635998
1 -0.72189461
1 -0.73053448
1 -0.45712700
1 -0.44805440
1 -1.09490402
1 -0.81414174
1 -1.32654820
1 -0.53032403
1 -0.99461211
1 -0.94950888
1 -0.66768927
1 -0.34881857
1 -0.25364882
1 -0.79311187
1 0.02842484
1 -1.10210120
1 -0.78742932
2 1.16170625
2 0.82261809
2 1.21816199
2 -0.36043409
2 0.40085294
2 -0.32069842
2 0.08538384
2 0.93158564
2 0.88580407
2 0.82594774
2 0.37072442
2 1.05647054
2 0.79187635
2 1.03089390
2 1.13856877
2 0.64943100
2 0.55780397
2 1.16759763
2 0.43786706
2 1.37624799
2 0.16032755
2 1.28142631
2 0.50797040
2 -0.40633125
2 0.66110145

2 0.76550827
2 1.06067075
2 -0.00681144
2 0.54309952
2 0.08112185
2 0.29554240
2 0.90811621
2 0.79140875
2 0.59328837
2 0.63859442
2 1.04477989
2 1.09362486
2 1.02007760
2 0.99463128
2 1.19199485
2 -0.01534297
2 0.58869651
2 1.13551192
2 0.91173304
2 0.47696610
2 0.76547709
2 0.66940785
2 0.34200088
2 0.40646136
2 0.01409379
2 0.39776657
2 0.06230023
2 1.25953505
2 0.43470271
2 1.33484415
2 1.26183879
2 0.39863541
2 0.39428663
2 0.06904532
2 1.17032565
2 0.71893505
2 -0.01652772
2 1.57843234
2 0.99774006
2 0.05127515
2 0.85444642
2 0.76844365
2 -0.45277080
2 0.94897285
2 1.07497708
2 0.37542007
2 1.36092429
2 1.54359993
2 1.07876271
2 -0.03396758
2 0.24649514
2 0.52782994
2 0.57997366
2 1.01766198
2 0.91531746
2 0.15144844
2 1.73860545
2 1.06786334
2 0.64939742

```
2  0.27306329
2  0.79571882
2  0.98643972
2  0.89276660
2  0.74247789
2  0.25481678
2  0.54388825
2  1.32234883
2  0.18494006
2  0.26451499
2  0.12331225
2  0.28639991
2  1.03175059
2  0.24376763
2 -0.17028969
2  0.67171032

$coefficients
              [,1]
Intercept 10.27258356
FHD       -0.09669018
FMC       -0.03683215
FDB       -0.03864001

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 4

attr(,"class")
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(FHD,FMC,FDB)~sex,data =
+                                                  landmark_data,FUN=mean)
>
> centroids<-fda_model$means
> print(centroids)
        v1
1 -1.384543
2  1.384543
attr(,"scaled:scale")
[1] 0.7222601
```

iv. Tibia

```
fda_model <- fda(sex ~ TPB + TCN + TDB, data =
+                                          landmark_data)
>
> print(fda_model)
Call:
fda(formula = sex ~ TPB + TCN + TDB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 4

Training Misclassification Error: 0.115 ( N = 200 )
> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 89 12
         2 11 88

               Accuracy : 0.885
                 95% CI : (0.8325, 0.9257)
    No Information Rate : 0.5
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.77

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.8900
            Specificity : 0.8800
         Pos Pred Value : 0.8812
         Neg Pred Value : 0.8889
             Prevalence : 0.5000
         Detection Rate : 0.4450
   Detection Prevalence : 0.5050
      Balanced Accuracy : 0.8850

       'Positive' Class : 1


> fda_model$fit
$fitted.values
          [,1]
1 -0.82176944
1 -0.97893065
1 -0.70961370
1 -1.60160784
1 -0.73164703
1 -0.90148112
1 -0.41118056
1 -1.03344688
```

1 -1.97230545
1 -1.04299069
1 -0.50423945
1 -0.53944287
1 -1.17312948
1 -1.15176769
1 -0.54360540
1 -0.29357036
1 -0.01633174
1 -0.36861930
1 -0.92463884
1 -1.00846072
1 -0.68113305
1 -0.26762702
1 -1.53996921
1 -0.62406670
1 -0.62891235
1 -0.93980483
1 0.15743528
1 -0.04612890
1 -1.28435325
1 -0.68134016
1 -0.92280298
1 -0.67274530
1 0.04224217
1 -0.62464435
1 -0.19487887
1 -0.33343685
1 -0.66871362
1 0.10737251
1 -1.10336129
1 0.20181563
1 0.66724784
1 -1.02216094
1 -1.53325902
1 -0.83311897
1 -0.55288108
1 0.34795196
1 -1.57983995
1 -0.25066680
1 -0.52891018
1 -0.78292412
1 -0.67102736
1 -0.59800700
1 -1.08712985
1 -0.73983987
1 -0.90488530
1 -0.48565322
1 -0.63413426
1 -0.37292212
1 -1.39794697
1 -0.21539113
1 -0.31694724
1 -1.18048364
1 -0.77169573
1 -0.63174677
1 -0.71162600
1 -1.24802927
1 -0.58301331

1 -0.42786475
1 -0.75367078
1 -0.03777080
1 -1.09352032
1 -0.57388619
1 -0.20730694
1 -1.17026825
1 -0.27293218
1 -0.96115414
1 0.03313484
1 -1.46156801
1 -0.48687515
1 -0.11688435
1 0.32364822
1 -0.82468960
1 -0.19218151
1 -0.39003368
1 -0.38511927
1 -0.62645577
1 -0.06992459
1 -0.88993592
1 -0.10096051
1 -1.26134359
1 -0.64106049
1 -0.69543508
1 -0.56165183
1 -0.68744827
1 0.04250748
1 0.11792327
1 -0.13867918
1 0.16379235
1 -0.50772981
1 -0.55938589
2 1.04644692
2 0.77579281
2 1.27005704
2 0.04611202
2 -0.03486749
2 -0.56690757
2 0.42315705
2 1.14084333
2 1.01558046
2 0.98549161
2 0.23579038
2 0.79057318
2 0.92497865
2 1.19065468
2 1.23900593
2 0.63590336
2 0.17266525
2 1.06393965
2 0.70537589
2 1.25968699
2 0.45396408
2 1.36756964
2 0.49919558
2 -0.55253874
2 0.52295654
2 0.94170174

2 1.27024245
2 -0.01575089
2 0.56108774
2 0.25060949
2 0.32421923
2 0.64352834
2 0.96907658
2 0.39223579
2 0.33203322
2 0.93284729
2 0.94277279
2 0.65759384
2 1.20419669
2 1.39914726
2 0.18206894
2 0.19050812
2 0.85039337
2 0.91477497
2 0.64109798
2 0.78210356
2 0.69077163
2 0.25433090
2 0.59662837
2 -0.09173440
2 0.47416993
2 0.17141911
2 1.29412946
2 0.35372639
2 1.41261964
2 1.36801860
2 0.28217469
2 0.13497552
2 -0.05080541
2 1.14389310
2 0.99709417
2 -0.06047790
2 1.31699497
2 0.91061288
2 -0.16878357
2 0.84470566
2 0.66577980
2 -0.62588774
2 0.75732650
2 1.04469196
2 0.14567675
2 0.82801357
2 1.16561269
2 0.55926480
2 -0.43525204
2 0.29638487
2 0.29712741
2 0.74181296
2 0.74144212
2 0.93105577
2 0.05749664
2 1.29711014
2 1.08089347
2 0.55334011
2 0.31180944

```
2  0.88713677
2  1.26496111
2  0.57863178
2  0.28993074
2 -0.05128097
2  0.91510507
2  1.57774709
2  0.06087968
2  0.31700035
2  0.06113296
2  0.48992984
2  0.85932154
2  0.21573695
2 -0.10683725
2  0.84212900

$coefficients
                [,1]
Intercept 10.018448955
TPB       -0.103124660
TCN       -0.024450068
TDB       -0.005402141

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 4

attr(,"class")
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(TPB,TCN,TDB)~sex,data =
+                                                    landmark_data,F
UN=mean)
>
> centroids<-fda_model$means
> print(centroids)
       v1
1 -1.26302
2  1.26302
attr(,"scaled:scale")
[1] 0.7917533
```

2. FDA output for White South Africans

i. Humerus, femur and tibia

```
> library(foreign)
> library(caret)
> library(ROSE)
> library(haven)
> landmark_data<-read_sav ("C:/Users/Puseletso Maboea/Documents/Masters/White
population data (REAL).sav")
> colnames(landmark_data) <-
+         c("HHD","HEB","FHD","FMC","FDB","TPB","TCN","TDB","sex")
>
> landmark_data$HHD <- as.numeric(landmark_data$HHD)
> landmark_data$HEB <- as.numeric(landmark_data$HEB)
> landmark_data$FHD <- as.numeric(landmark_data$FHD)
> landmark_data$FMC <- as.numeric(landmark_data$FMC)
> landmark_data$FDB <- as.numeric(landmark_data$FDB)
> landmark_data$TCN <- as.numeric(landmark_data$TCN)
> landmark_data$TPB <- as.numeric(landmark_data$TPB)
> landmark_data$TDB <- as.numeric(landmark_data$TDB)
> library(dplyr)
> library(earth
> library(earth)
> fda_model <- fda(sex ~ HHD + HEB + FHD + FMC + FDB + TPB + TCN + TDB,
data =
+landmark_data)
>
> print(fda_model)
Call:
fda(formula = sex ~ HHD + HEB + FHD + FMC + FDB + TPB + TCN +
    TDB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 9

Training Misclassification Error: 0.11 ( N = 200 )
> predictions <- as.factor(predictions)
> landmark_data$sex <- as.factor(landmark_data$sex)
> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 88 11
         2 11 90

               Accuracy : 0.89
                 95% CI : (0.8382, 0.9298)
    No Information Rate : 0.505
    P-Value [Acc > NIR] : <2e-16
```

```
               Kappa : 0.78

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.8889
            Specificity : 0.8911
         Pos Pred Value : 0.8889
         Neg Pred Value : 0.8911
             Prevalence : 0.4950
         Detection Rate : 0.4400
   Detection Prevalence : 0.4950
      Balanced Accuracy : 0.8900

       'Positive' Class : 1

> fda_model$fit
$fitted.values
         [,1]
1 -0.75520923
1  0.35858771
1 -0.61314557
1 -0.43460525
1 -1.22852602
1 -1.01907685
1 -0.39813820
1 -1.07816421
1 -0.00685535
1 -0.98341115
1 -0.53136162
1 -0.41252337
1 -0.83312589
1  0.55936992
1 -0.21049667
1 -0.89602183
1 -0.46202448
1 -0.14411611
1 -0.57499644
1 -1.07844855
1  0.51276261
1 -1.60298964
1 -0.57267657
1 -0.46351692
1 -0.31332279
1 -0.33976366
1 -1.11493224
1 -1.65471500
1 -0.38722889
1  0.29855508
1 -0.76920215
1 -0.52073571
1 -0.26889187
1 -0.02764148
1 -0.71441441
1 -0.91007484
1 -0.10742552
1 -0.34679921
1 -0.28552138
1 -0.69278494
1  0.01186499
```

1 -0.66913688
1 -0.60547840
1 -0.56590984
1 -0.99203138
1 -0.68313419
1 0.09238878
1 -0.23108871
1 -0.80538852
1 -0.50158048
1 -1.17931812
1 -1.14820154
1 -1.02785008
1 -0.92982757
1 -0.86727580
1 -0.51119740
1 -0.62444285
1 -0.51337558
1 0.23357263
1 -0.66557902
1 -1.06459919
1 0.05914967
1 -0.21817317
1 -0.63993349
1 -0.80171428
1 -0.48120428
1 0.14373878
1 -0.23101929
1 -0.51326899
1 -1.44833787
1 -0.85570924
1 -0.77585176
1 -0.70375312
1 -0.54749295
1 -0.53101187
1 -1.08967094
1 -1.22515808
1 -0.98715501
1 -0.31354074
1 -0.18599084
1 -1.28575018
1 -0.41136399
1 -0.72762322
1 -1.00909548
1 -0.84147602
1 -0.86468988
1 -1.28811036
1 -0.41225163
1 -1.04503788
1 0.20700374
1 -0.54887193
1 -1.35434110
1 -0.87337079
1 -0.82873739
1 -0.32844335
1 -1.52383707
1 -1.23802354
1 -0.94385726
1 -1.39203338
2 -0.35341657

2 0.59041939
2 0.44030297
2 1.05334781
2 -0.23854831
2 0.94495689
2 1.11655222
2 1.14245055
2 0.50736471
2 1.29379566
2 1.45926830
2 1.36168570
2 0.76698231
2 0.52763317
2 0.52404378
2 1.38582861
2 0.58057780
2 0.83811867
2 0.76117771
2 0.93167077
2 1.09975559
2 0.76320307
2 0.22332090
2 1.00506421
2 1.36441517
2 0.74769806
2 1.05864111
2 1.60711835
2 -0.28983275
2 0.18331221
2 0.27806783
2 0.10717572
2 0.88227658
2 0.14287264
2 -0.05200892
2 1.03880159
2 1.00863053
2 0.34705117
2 0.32519029
2 0.84445968
2 0.22174146
2 0.77440683
2 1.15335135
2 0.76431781
2 -0.09794756
2 0.58213034
2 0.52105589
2 0.84994965
2 0.01164999
2 0.41515195
2 0.84960404
2 0.38360161
2 0.79031011
2 0.62494530
2 0.94456875
2 0.41899591
2 -0.54518991
2 0.68421692
2 1.00309729
2 0.53690829

```
2  1.06852844
2  0.37626041
2  0.04117925
2  0.32802831
2 -1.01466359
2  0.70818774
2  0.02953876
2  0.46932840
2  1.06160112
2  1.64428793
2  0.19190639
2 -0.28611684
2  0.16883999
2 -0.52171828
2  1.65554741
2  0.62828161
2  0.49242698
2  1.38506347
2  0.49730322
2  1.13325067
2  0.07431103
2  1.16727826
2  0.84520852
2  0.48223311
2  0.60735776
2  0.92017132
2  0.98923873
2  0.51602288
2 -0.04184053
2  0.55822169
2  1.25631501
2 -0.11384925
2  0.49020516
2  1.06060496
2  0.33500791
2  0.31092029
2  0.75566258
2  0.63998302
2  1.03344557
2  0.76087728
2  0.41647815

$coefficients
                [,1]
Intercept 10.0095864567
HHD       -0.0840216408
HEB       -0.0373269409
FHD       -0.0300981885
FMC       -0.0023698278
FDB        0.0426239723
TPB       -0.0418808390
TCN       -0.0001594921
TDB       -0.0471218043

$degree
[1] 1

$monomial
[1] FALSE
```

```
$df
[1] 9

attr(,"class")
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(HHD,HEB,FHD,FMC,FDB,TPB,TCN,TDB)~sex,data
=
+                                                landmark_data,FUN=mean)
>
> centroids<-fda_model$means
> print(centroids)
        v1
1 -1.299262
2  1.273534
attr(,"scaled:scale")
[1] 0.7774031
```

ii. Humerus

```
fda_model <- fda(sex ~ HHD + HEB, data =
+                                          landmark_data)
> print(fda_model)
Call:
fda(formula = sex ~ HHD + HEB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 3

Training Misclassification Error: 0.105 ( N = 200 )
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 88 11
         2 11 90

               Accuracy : 0.89
                 95% CI : (0.8382, 0.9298)
    No Information Rate : 0.505
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.78

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.8889
            Specificity : 0.8911
         Pos Pred Value : 0.8889
         Neg Pred Value : 0.8911
```

```
          Prevalence : 0.4950
      Detection Rate : 0.4400
Detection Prevalence : 0.4950
   Balanced Accuracy : 0.8900

    'Positive' Class : 1

> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 88 10
         2 11 91

               Accuracy : 0.895
                 95% CI : (0.844, 0.9338)
    No Information Rate : 0.505
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.79

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.8889
            Specificity : 0.9010
         Pos Pred Value : 0.8980
         Neg Pred Value : 0.8922
             Prevalence : 0.4950
         Detection Rate : 0.4400
   Detection Prevalence : 0.4900
      Balanced Accuracy : 0.8949

       'Positive' Class : 1
> fda_model$fit
$fitted.values
          [,1]
1 -0.6633275407
1  0.3429919627
1 -0.4329951356
1 -0.4467024461
1 -1.1183297861
1 -1.0191159912
1 -0.1405421439
1 -1.1619739604
1  0.1144028911
1 -1.1343369037
1 -0.5626408588
1 -0.5552525264
1 -0.6477904269
1  0.6876264345
1 -0.0491226466
1 -0.8751795626
1 -0.4350655845
1 -0.0938249596
1 -0.5916749042
1 -1.2014851256
1  0.7673024766
```

1 -1.6131279356
1 -0.5207445080
1 -0.6488404267
1 -0.2323669624
1 -0.3021801183
1 -0.6750713897
1 -1.5030990119
1 -0.3176875563
1 0.1068844961
1 -0.8008579491
1 -0.2957383222
1 -0.2066141421
1 0.1226512901
1 -0.7924167904
1 -1.0346633012
1 -0.2680054939
1 -0.4763674500
1 -0.2530999827
1 -0.6272793950
1 -0.1384206073
1 -0.8187250648
1 -0.5532196420
1 -0.6263900998
1 -1.1713807598
1 -0.5807393900
1 0.1188739810
1 -0.2815024254
1 -0.9548448896
1 -0.2117576728
1 -1.1951256313
1 -0.8684842419
1 -1.0477462537
1 -0.8467646880
1 -1.0527104227
1 -0.5701106707
1 -0.6318320894
1 -0.4869823242
1 0.2401565011
1 -0.4579826416
1 -1.2180791618
1 -0.0476976456
1 -0.2184595942
1 -0.5042945047
1 -1.0205326564
1 -0.7005563929
1 0.1087771216
1 -0.1100172704
1 -0.5236523953
1 -1.3742089974
1 -0.6514811944
1 -0.6942897906
1 -0.4941944435
1 -0.4221737279
1 -0.6837792742
1 -0.7818210205
1 -0.9839104712
1 -0.9593112394
1 -0.3258551200
1 -0.0009533432

1 -1.2137170447
1 -0.5719597752
1 -0.5369000234
1 -0.9279396973
1 -0.6435805535
1 -0.8728235339
1 -1.1273483831
1 -0.3785410916
1 -1.2843731484
1 0.1787007169
1 -0.4776163630
1 -1.8731991323
1 -0.7342410150
1 -0.9409191863
1 -0.5155432891
1 -1.4399548996
1 -1.3252505885
1 -0.8798386003
1 -1.0312288131
2 -0.4147898140
2 0.3200872843
2 0.3509585026
2 1.2083722212
2 -0.1005900253
2 0.4634116616
2 0.9862515448
2 1.1415149635
2 0.5332583393
2 1.4337623164
2 1.6112115719
2 1.2396940171
2 0.7164488127
2 0.3847053029
2 0.3694153634
2 1.1201723964
2 0.5999605269
2 0.8517558845
2 0.8964505057
2 0.6715456010
2 1.1105681690
2 1.0095295611
2 0.2385221404
2 1.0622612362
2 1.3469314679
2 0.7280124056
2 1.0206637915
2 1.5142520057
2 -0.0485659761
2 0.0918879533
2 0.3341267724
2 -0.0148386022
2 0.8889122372
2 0.0408124979
2 0.0315073016
2 1.0481678339
2 0.8576508843
2 0.5946009109
2 0.2286569467
2 0.9975701991

2 0.4035790225
2 1.0162401403
2 0.9976771865
2 0.5984159096
2 -0.1503493274
2 0.5774988592
2 0.7212365715
2 0.6615354083
2 0.1204327655
2 0.6106206574
2 0.5920545017
2 0.2870945826
2 0.9714040439
2 0.3151883701
2 0.9002230747
2 0.2851391348
2 -0.6148488847
2 0.6291737371
2 0.8431124857
2 0.6359982262
2 0.9808757761
2 0.5062105806
2 0.1940577716
2 0.4297452495
2 -1.2241267272
2 0.6182945697
2 -0.1758370853
2 0.4672819159
2 1.1984917691
2 1.5761555409
2 0.2211520748
2 0.0179764012
2 0.2605932982
2 -0.6168399116
2 1.6655488262
2 0.7112670201
2 0.6736851507
2 1.1841497792
2 0.4196110758
2 1.2372749158
2 0.2370258562
2 1.1686558644
2 0.4228134511
2 0.3758320987
2 0.7502193323
2 0.7945919003
2 1.0689680947
2 0.4720098041
2 -0.0653503395
2 0.2880717609
2 1.0276780888
2 0.0937581476
2 0.4252225530
2 0.9133269200
2 0.1682689252
2 0.2822868252
2 0.4614152506
2 0.5491796845
2 0.8631669118

```
2  0.9951868020
2  0.3899671617

$coefficients
              [,1]
Intercept  9.30932071
HHD       -0.12413463
HEB       -0.05878847

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 3

attr(,"class")
[1] "polyreg"


> b<-coefficients[,1]
> centroids<-aggregate(cbind(HHD,HEB)~sex,data =
+                                                    landmark_data,FU
N=mean)
>
> centroids<-fda_model$means
> print(centroids)
        v1
1 -1.234406
2  1.209963
attr(,"scaled:scale")
[1] 0.8182479
```

iii. Femur

```
fda_model <- fda(sex ~ FHD + FMC + FDB, data =
+                                                landmark_data)

> print(fda_model)
Call:
fda(formula = sex ~ FHD + FMC + FDB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 4

Training Misclassification Error: 0.155 ( N = 200 )
> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics
```

```
          Reference
Prediction  1  2
         1 83 15
         2 16 86

               95% CI : (0.7873, 0.8922)
    No Information Rate : 0.505
    P-Value [Acc > NIR] : <2e-16

                  Kappa : 0.6899

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.8384
            Specificity : 0.8515
         Pos Pred Value : 0.8469
         Neg Pred Value : 0.8431
             Prevalence : 0.4950
         Detection Rate : 0.4150
   Detection Prevalence : 0.4900
      Balanced Accuracy : 0.8449

       'Positive' Class : 1

> b<-coefficients[,1]
> centroids<-aggregate(cbind(FHD,FMC,FDB)~sex,data =
+                                                                    lan
dmark_data,FUN=mean)
>
> centroids<-fda_model$means
> print(centroids)
         v1
1 -1.138236
2  1.115697
attr(,"scaled:scale")
[1] 0.887382
> fda_model$fit
$fitted.values
          [,1]
1 -0.848938862
1  0.262012072
1 -0.790023784
1 -0.646975585
1 -1.337340283
1 -0.839147816
1 -0.267573649
1 -1.238446205
1 -0.025806364
1 -0.537189509
1 -0.504609325
1 -0.223408045
1 -0.904609168
1  0.302825457
1 -0.131992974
1 -0.976284485
1 -0.341200682
1  0.062995541
1 -0.495502695
1 -0.981445400
```

1 0.125350850
1 -1.272565546
1 -0.427822969
1 0.043281202
1 -0.808998087
1 -0.473883519
1 -1.266246936
1 -1.874395141
1 -0.826320326
1 0.720982713
1 -0.199488626
1 -0.392397080
1 0.012805659
1 -0.791687109
1 -0.872959742
1 -0.160183358
1 -0.304976290
1 -0.300863042
1 -0.846107307
1 0.197997011
1 -0.484241389
1 -0.429810565
1 -0.421563709
1 -0.991103693
1 -0.338960851
1 0.095457048
1 -0.393862989
1 -0.613007656
1 -0.089778254
1 -1.092933929
1 -0.852481075
1 -1.268951138
1 -0.754306882
1 -0.400850107
1 -0.405280305
1 -0.498871005
1 -0.071323246
1 0.185186274
1 -0.372001075
1 -0.962212637
1 0.191370286
1 -0.484238818
1 -0.308000784
1 -0.626731557
1 -1.106954424
1 -0.150157177
1 0.245520262
1 -0.704255090
1 -1.721905049
1 -0.963366518
1 -1.177862971
1 -0.487377792
1 0.217638915
1 -0.799649720
1 -0.921786438
1 -1.262758046
1 -0.594208667
1 -0.330707963
1 0.046394610

1 -0.817104699
1 -0.239826558
1 -0.449572731
1 -1.115458978
1 -0.649276213
1 -0.918750142
1 -1.004964976
1 -0.545137599
1 -0.600759145
1 0.154657113
1 -0.984704267
1 -1.600617747
1 -1.036530767
1 -0.208331822
1 -0.429901013
1 -1.109042297
1 -0.838859974
1 -1.045203090
1 -1.367112022
2 -0.694519299
2 0.870743055
2 0.345439944
2 1.155356522
2 -0.317174985
2 0.713830890
2 0.891178919
2 1.165080049
2 0.252890467
2 1.055274646
2 1.185673237
2 1.205446977
2 0.937027906
2 0.348302671
2 0.586027400
2 1.110914821
2 0.385784055
2 0.683187319
2 0.778801996
2 0.580066381
2 1.101599086
2 0.597240408
2 0.322926907
2 0.834304231
2 1.521265742
2 0.140893580
2 0.634515725
2 1.376960621
2 -0.473841078
2 0.343944701
2 -0.181112462
2 -0.029841184
2 0.940166727
2 0.310554121
2 -0.156784751
2 0.775060789
2 0.705492220
2 -0.132079470
2 -0.039088412
2 0.905984652

2 0.321259548
2 0.265226271
2 1.176528939
2 0.599184687
2 -0.121928823
2 0.964239074
2 0.206328743
2 0.936833079
2 -0.166273595
2 0.370445225
2 0.920246199
2 0.428394051
2 0.455747082
2 0.887870763
2 0.918586134
2 0.651774318
2 -0.604967485
2 0.828744403
2 0.929869205
2 0.511783078
2 0.965288686
2 0.537440180
2 -0.008037670
2 0.169130456
2 -1.033685382
2 0.469309021
2 0.005205733
2 0.443214087
2 0.618772773
2 1.274090260
2 0.006963456
2 -0.304740584
2 0.345064721
2 -0.051935791
2 1.246547315
2 0.519348459
2 0.367384130
2 1.495100487
2 0.881124828
2 1.104704060
2 -0.057781852
2 1.147018215
2 1.056869137
2 0.669274442
2 0.777104173
2 0.880035290
2 0.865329580
2 0.567839521
2 0.260256693
2 0.508914360
2 1.279490444
2 0.113287686
2 0.512946282
2 0.551270510
2 0.668048469
2 0.584492328
2 0.466093766
2 0.322016229
2 1.127116781

```
2  1.072157967
2  0.303464285

$coefficients
              [,1]
Intercept  9.78327436
FHD       -0.10300049
FMC       -0.01661080
FDB       -0.04427385

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 4

attr(,"class")
[1] "polyreg
```

iv. Tibia

```
> fda_model <- fda(sex ~ TPB + TCN+ TDB, data =
+                                                    landmark_data)
>
> print(fda_model)
Call:
fda(formula = sex ~ TPB + TCN + TDB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 4

Training Misclassification Error: 0.13 ( N = 200 )
> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 86 13
         2 13 88

               Accuracy : 0.87
                 95% CI : (0.8153, 0.9133)
    No Information Rate : 0.505
    P-Value [Acc > NIR] : <2e-16
```

```
               Kappa : 0.74

 Mcnemar's Test P-Value : 1

            Sensitivity : 0.8687
            Specificity : 0.8713
         Pos Pred Value : 0.8687
         Neg Pred Value : 0.8713
             Prevalence : 0.4950
         Detection Rate : 0.4300
   Detection Prevalence : 0.4950
      Balanced Accuracy : 0.8700

       'Positive' Class : 1

> fda_model$fit
$fitted.values
          [,1]
1 -0.809650065
1  0.319118542
1 -0.814468543
1 -0.572052681
1 -1.298417161
1 -0.701999027
1 -0.535769896
1 -0.508360674
1 -0.005595776
1 -0.750484560
1 -0.354829978
1  0.131375156
1 -0.843663149
1  0.421494663
1 -0.420142406
1 -0.851159266
1 -0.158692766
1  0.042973017
1 -0.543667000
1 -0.772560625
1  0.200224414
1 -1.397268040
1 -0.389106984
1 -0.209620122
1 -0.552541996
1 -0.383867542
1 -1.429613902
1 -1.713756387
1 -0.479271857
1  0.502732454
1 -0.448564284
1 -0.692315549
1 -0.183885751
1 -0.186333824
1 -0.544189699
1 -0.495206180
1  0.221929019
1 -0.156274383
1 -0.034184364
1 -0.493381070
1  0.151192428
```

1 -0.468278486
1 -0.556160879
1 -0.396559617
1 -0.901800401
1 -0.427545015
1 0.240685383
1 -0.220741245
1 -0.577221050
1 -0.722727998
1 -1.007459642
1 -1.159542398
1 -1.248566902
1 -0.968003438
1 -0.597001365
1 -0.329236058
1 -0.556761037
1 -0.597558233
1 0.220571539
1 -0.775489030
1 -0.884414429
1 -0.061262761
1 -0.002979200
1 -0.510280452
1 -0.309778947
1 -0.483023768
1 -0.088096732
1 -0.355736164
1 -0.602745527
1 -1.688515416
1 -0.980530340
1 -1.117942845
1 -0.742080937
1 -0.491842049
1 -0.510131927
1 -1.397089615
1 -1.147414047
1 -0.803034441
1 -0.248388309
1 -0.345207312
1 -1.250701859
1 -0.227330940
1 -0.732155207
1 -1.203985465
1 -1.090607486
1 -0.613327079
1 -1.613684071
1 -0.555214033
1 -0.462444555
1 0.206029987
1 -0.919398103
1 -1.043938402
1 -0.756236889
1 -0.197777052
1 -0.262209084
1 -1.325952750
1 -0.861582863
1 -0.899985783
1 -1.539458225
2 -0.202828716

2 1.026295492
2 0.490196372
2 1.075459584
2 -0.340102851
2 1.513892974
2 0.868364573
2 1.030099156
2 0.577715163
2 0.857332023
2 1.069925402
2 1.469007119
2 0.899944711
2 0.410217280
2 0.734481858
2 1.560319147
2 0.557039204
2 0.730361239
2 0.417786957
2 1.032402610
2 1.004329677
2 0.434968886
2 0.138620532
2 0.728289498
2 1.300247546
2 0.389834256
2 1.121758834
2 1.277057733
2 -0.476809438
2 0.191295878
2 0.150799991
2 0.018480178
2 0.971015391
2 0.438576787
2 -0.254204609
2 0.896160457
2 0.886237377
2 0.058082056
2 0.152208394
2 0.503418272
2 0.074349863
2 0.444532664
2 1.098207061
2 0.957857977
2 -0.248934770
2 0.810873554
2 0.307585201
2 1.068327866
2 0.047232498
2 -0.090960194
2 0.813553270
2 0.620248160
2 0.697988876
2 1.106604917
2 1.103185411
2 0.811286378
2 -0.172669696
2 0.890645542
2 0.906732199
2 0.440715846

```
2  0.846898388
2  0.240053535
2 -0.293058088
2  0.228906555
2 -0.987482407
2  0.762486115
2  0.081153321
2  0.022766257
2  0.480971337
2  1.509409482
2  0.220409331
2 -0.655609917
2  0.001703930
2 -0.039851229
2  1.350584174
2  0.624713120
2 -0.030082394
2  1.273310889
2  0.749202695
2  1.007474400
2  0.115533249
2  0.912124445
2  1.155007328
2  0.565808851
2  0.644194559
2  0.794392040
2  0.499380506
2  0.269123637
2  0.010051061
2  0.555722280
2  1.172587536
2 -0.159639153
2  0.334597286
2  0.796994358
2  0.643529886
2  0.365780820
2  0.750162772
2  0.507183424
2  1.184512839
2  0.561463888
2  0.441596032

$coefficients
                [,1]
Intercept  9.993456419
TPB       -0.070404096
TCN       -0.002616215
TDB       -0.084004746

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 4

attr(,"class")
```

```
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(TPB,TCN,TDB)~sex,data =
+                                                                    lan
dmark_data,FUN=mean)
>
> centroids<-fda_model$means
> print(centroids)
        v1
1 -1.160838
2  1.137851
attr(,"scaled:scale")
[1] 0.8701044
```

3. FDA output for Coloured South Africans

i. Humerus, femur and tibia

```
> library(foreign)
> library(caret)
> library(ROSE)
> library(haven)
> landmark_data<-read_sav ("C:/Users/Puseletso Maboea/Downloads/cOLOURED
POPULATION.sav")
> colnames(landmark_data) <-
+         c("HHD","HEB","FHD","FMC","FDB","TPB","TCN","TDB","sex")
>
> landmark_data$HHD <- as.numeric(landmark_data$HHD)
> landmark_data$HEB <- as.numeric(landmark_data$HEB)
> landmark_data$FHD <- as.numeric(landmark_data$FHD)
> landmark_data$FMC <- as.numeric(landmark_data$FMC)
> landmark_data$FDB <- as.numeric(landmark_data$FDB)
> landmark_data$TCN <- as.numeric(landmark_data$TCN)
> landmark_data$TPB <- as.numeric(landmark_data$TPB)
> landmark_data$TDB <- as.numeric(landmark_data$TDB)
> library(dplyr)
> library(earth)
> library(mda)
> fda_model <- fda(sex ~ HHD + HEB + FHD + FMC + FDB + TPB + TCN + TDB,
data =
+ landmark_data)
>
> print(fda_model)
Call:
fda(formula = sex ~ HHD + HEB + FHD + FMC + FDB + TPB + TCN +
    TDB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 9

Training Misclassification Error: 0.09211 ( N = 76 )
> predictions<-predict(fda_model,landmark_data)
```

```
> predictions <- as.factor(predictions)
> landmark_data$sex <- as.factor(landmark_data$sex)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 53  4
         2  3 16

               Accuracy : 0.9079
                 95% CI : (0.8194, 0.9622)
    No Information Rate : 0.7368
    P-Value [Acc > NIR] : 0.0001837

                  Kappa : 0.7586

 Mcnemar's Test P-Value : 1.0000000

            Sensitivity : 0.9464
            Specificity : 0.8000
         Pos Pred Value : 0.9298
         Neg Pred Value : 0.8421
             Prevalence : 0.7368
         Detection Rate : 0.6974
   Detection Prevalence : 0.7500
      Balanced Accuracy : 0.8732

       'Positive' Class : 1

> fda_model$fit
$fitted.values
          [,1]
1 -0.434284469
1  0.178258167
1 -0.274970877
1  0.675909251
1 -0.577047947
1 -1.029377376
1 -0.007570067
1  0.622129073
1 -0.409713964
1 -0.030914868
1 -0.197914683
1 -0.654950210
1 -0.638541084
1 -0.394982607
1 -0.969049668
1 -0.702689369
1 -0.158932339
1 -0.039093444
1 -1.271504409
1  0.419652702
1  0.341877949
1 -0.184991129
1  0.255121736
1 -0.564555538
1 -0.250024833
1 -0.990198046
```

1 -0.892559696
1 -0.028829724
1 -0.023991693
1 0.109108886
1 -0.605531333
1 -1.270068683
1 -0.439042586
1 -0.242264039
1 -0.468556929
1 -1.106938315
1 -0.394332179
1 -0.175261263
1 -0.310964175
1 -0.637656511
1 -0.610856121
1 -0.635766862
1 -0.247682230
1 0.426976545
1 0.319691681
1 -0.304858994
1 -0.211645708
1 1.039686564
1 -0.206345304
1 -0.808171607
1 -0.062841399
1 -0.795863048
1 -0.584578310
1 -0.428409616
1 0.121079304
1 -0.130769642
2 1.330907490
2 0.262719072
2 1.420746586
2 1.425019144
2 0.872546032
2 0.740290947
2 0.417462078
2 0.926836486
2 0.840670660
2 1.165452066
2 1.029852562
2 -1.015368858
2 0.835924142
2 0.575151037
2 1.271191771
2 1.604324156
2 0.463731863
2 0.900336793
2 0.697750211
2 1.130056797

$coefficients
[,1]
Intercept 9.204653809
HHD   0.039376541
HEB   -0.025079813
FHD   -0.049997209
FMC   -0.002180596
FDB   0.063862894

```
TPB      -0.130092314
TCN      -0.018828679
TDB      -0.014657377

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 9

attr(,"class")
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(HHD,HEB,FHD,FMC,FDB,TPB,TCN,TDB)~sex,data
=
+                                                    landmark_data,FUN=mean)
>
> centroids<-fda_model$means
> print(centroids)
        v1
1 -0.6034427
2  1.6896397
attr(,"scaled:scale")
[1] 0.9903414
```

ii. Humerus

```
fda_model <- fda(sex ~ HHD + HEB, data =
+                                              landmark_data)
>
> print(fda_model)
Call:
fda(formula = sex ~ HHD + HEB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 3

Training Misclassification Error: 0.11842 ( N = 76 )
> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 52  5
         2  4 15

               Accuracy : 0.8816
                 95% CI : (0.7871, 0.9444)
    No Information Rate : 0.7368
```

```
   P-Value [Acc > NIR] : 0.001721

                 Kappa : 0.6897

 Mcnemar's Test P-Value : 1.000000

            Sensitivity : 0.9286
            Specificity : 0.7500
         Pos Pred Value : 0.9123
         Neg Pred Value : 0.7895
             Prevalence : 0.7368
         Detection Rate : 0.6842
   Detection Prevalence : 0.7500
      Balanced Accuracy : 0.8393

       'Positive' Class : 1

> fda_model$fit
$fitted.values
         [,1]
1  0.19299838
1  0.25807365
1  0.22122760
1  0.59713961
1 -0.35358600
1 -1.00720761
1 -0.20508387
1  0.73858289
1 -0.18289070
1 -0.15863503
1 -0.25854753
1 -0.92426914
1 -0.23937394
1 -0.45710370
1 -0.50439049
1 -0.30359116
1  0.04299789
1 -0.46508414
1 -0.97092243
1  0.40798447
1  0.01439599
1 -0.23804758
1  0.57439217
1 -0.54098139
1  0.18682493
1 -0.91994737
1 -1.08961022
1  0.16098006
1 -0.14489417
1 -0.04068580
1 -0.27113428
1 -0.09039487
1 -0.73999984
1 -0.76929618
1 -0.20018497
1 -0.20960306
1 -0.20172745
1 -0.15556953
1 -0.86405839
```

```
1 -1.11474287
1 -0.63976037
1 -0.24457167
1  0.11413641
1 -0.24852794
1 -0.92208809
1  1.13178222
1  0.01295465
1 -0.02189948
1 -0.06925033
1 -0.53895022
1 -0.12043150
1  0.05000102
1  0.13213585
1 -0.24367779
2  0.76022229
2  0.52957547
2  0.88008480
2  0.47747785
2  0.94152425
2  0.63761778
2  0.44925488
2  0.64621967
2  0.94204247
2  0.92914971
2  0.73866096
2 -1.18182638
2  1.04089320
2  0.15891095
2  1.10396661
2  1.25029182
2  0.68880853
2  1.02671283
2 -0.32053617
2  1.10557743

$coefficients
               [,1]
Intercept  7.26187285
HHD       -0.05343267
HEB       -0.08529639

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 3

attr(,"class")
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(HHD,HEB)~sex,data =
+                                                    landmark_data,FU
N=mean)
>
> centroids<-fda_model$means
```

```
> print(centroids)
        v1
1 -0.4704578
2  1.3172819
attr(,"scaled:scale")
[1] 1.270282
```

iii. Femur

```
> fda_model <- fda(sex ~ FHD + FMC + FDB, data =
+ landmark_data)
>
> print(fda_model)
Call:
fda(formula = sex ~ FHD + FMC + FDB, data = landmark_data)

Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 4

Training Misclassification Error: 0.11842 ( N = 76 )
> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 51  4
         2  5 16

               Accuracy : 0.8816
                 95% CI : (0.7871, 0.9444)
    No Information Rate : 0.7368
    P-Value [Acc > NIR] : 0.001721

                  Kappa : 0.6995

 Mcnemar's Test P-Value : 1.000000

            Sensitivity : 0.9107
            Specificity : 0.8000
         Pos Pred Value : 0.9273
         Neg Pred Value : 0.7619
             Prevalence : 0.7368
         Detection Rate : 0.6711
   Detection Prevalence : 0.7237
      Balanced Accuracy : 0.8554

       'Positive' Class : 1

> fda_model$fit
$fitted.values
         [,1]
```

1 -0.270366259
1 0.150137982
1 0.016907837
1 0.630286346
1 -0.547016223
1 -1.067112537
1 -0.075181859
1 0.616819725
1 -0.152424559
1 -0.037411029
1 -0.195080533
1 -0.957451277
1 -0.635864602
1 -0.053342359
1 -0.745276935
1 -0.683103076
1 -0.370754201
1 -0.295161769
1 -1.028586618
1 0.316578954
1 -0.195550972
1 -0.056672625
1 0.539620440
1 -0.685580578
1 0.065726924
1 -0.816003865
1 -0.710822713
1 -0.361786040
1 -0.348618864
1 -0.092873862
1 -0.803101463
1 -1.317412879
1 -0.233232527
1 -0.314060149
1 -0.393075233
1 -0.766954553
1 -0.230839251
1 -0.476561420
1 -0.345156713
1 -0.003725953
1 -0.348060501
1 -0.971018448
1 -0.420689084
1 0.174534224
1 0.547827571
1 0.278936005
1 -0.414784446
1 1.090286049
1 -0.203736128
1 -0.186689333
1 -0.004671073
1 -0.606072899
1 -0.519891643
1 0.015423551
1 0.147518983
1 -0.217643243
2 1.000292027
2 1.007897644
2 1.291371381

```
2  0.774325304
2  0.976656020
2  0.396413858
2  0.163397772
2  0.538134752
2  0.657628484
2  1.133825971
2  0.781947899
2 -1.221910729
2  0.863736388
2  0.357581391
2  1.182417782
2  1.786982239
2  0.566648233
2  0.714210591
2  0.514044759
2  1.083213936

$coefficients
              [,1]
Intercept  8.42847048
FHD       -0.09610574
FMC       -0.03423705
FDB       -0.01774498

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 4

attr(,"class")
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(FHD,FMC,FDB)~sex,data =
+                                                    landmark_data,FU
N=mean)
>
> centroids<-fda_model$means
> print(centroids)
         v1
1 -0.5247228
2  1.4692239
attr(,"scaled:scale")
[1] 1.138914
```

iv. Tibia

```
> fda_model <- fda(sex ~ TPB + TCN + TDB, data =
+                                                landmark_data)
>
> print(fda_model)
Call:
fda(formula = sex ~ TPB + TCN + TDB, data = landmark_data)
```

```
Dimension: 1

Percent Between-Group Variance Explained:
 v1
100

Degrees of Freedom (per dimension): 4

Training Misclassification Error: 0.10526 ( N = 76 )
> predictions<-predict(fda_model,landmark_data)
> confusionMatrix(predictions,landmark_data$sex)
Confusion Matrix and Statistics

          Reference
Prediction  1  2
         1 54  6
         2  2 14

               Accuracy : 0.8947
                 95% CI : (0.8031, 0.9534)
    No Information Rate : 0.7368
    P-Value [Acc > NIR] : 0.0005992

                  Kappa : 0.7099

 Mcnemar's Test P-Value : 0.2888444

            Sensitivity : 0.9643
            Specificity : 0.7000
         Pos Pred Value : 0.9000
         Neg Pred Value : 0.8750
             Prevalence : 0.7368
         Detection Rate : 0.7105
   Detection Prevalence : 0.7895
      Balanced Accuracy : 0.8321

       'Positive' Class : 1

> fda_model$fit
$fitted.values
          [,1]
1 -0.18762838
1  0.26341436
1 -0.10989342
1  0.84087995
1 -0.55033811
1 -1.00659188
1 -0.10760106
1  0.49422252
1 -0.31182237
1 -0.05200325
1 -0.13264288
1 -0.47363857
1 -0.40786120
1 -0.37125468
1 -0.93246844
1 -0.85218560
1 -0.23251849
1 -0.13019199
```

1 -1.39430291
1 0.27004181
1 0.36522915
1 -0.04097258
1 0.11370551
1 -0.63939604
1 -0.23581893
1 -0.75719995
1 -1.03914499
1 -0.35027636
1 -0.22794885
1 0.11030661
1 -0.39959600
1 -1.13962304
1 -0.41365468
1 -0.06346728
1 -0.43822832
1 -1.16906521
1 -0.36103948
1 -0.34767007
1 -0.38873100
1 -0.57357800
1 -0.67989821
1 -0.78941049
1 -0.15741972
1 0.27508985
1 0.33164523
1 -0.19035385
1 -0.25172032
1 1.02488594
1 -0.09185729
1 -0.51949435
1 0.04367128
1 -0.85939927
1 -0.75096769
1 -0.08871093
1 0.05262175
1 -0.15065224
2 1.01382412
2 0.43918641
2 1.50554468
2 1.08898038
2 0.98571588
2 0.81234591
2 0.40428237
2 0.48385150
2 0.79262509
2 1.16555730
2 1.01979861
2 -1.11161991
2 0.79689366
2 0.46321144
2 1.26766465
2 1.71515735
2 0.47461913
2 0.95701582
2 0.59221962
2 1.31565038

```
$coefficients
              [,1]
Intercept  9.19556209
TPB       -0.06850882
TCN       -0.02310555
TDB       -0.04107422

$degree
[1] 1

$monomial
[1] FALSE

$df
[1] 4

attr(,"class")
[1] "polyreg"
> b<-coefficients[,1]
> centroids<-aggregate(cbind(TPB,TCN,TDB)~sex,data =
+                                                                    la
ndmark_data,FUN=mean)
>
> centroids<-fda_model$means
> print(centroids)
         v1
1 -0.5782605
2  1.6191294
attr(,"scaled:scale")
[1] 1.033469
```

Appendix 6: DFA output

1. DFA output for White South Africans
    i. Humerus, femur and tibia

Analysis Case Processing Summary

Unweighted Cases		N	Percent
Valid		200	98,0
Excluded	Missing or out-of-range group codes	0	,0
	At least one missing discriminating variable	0	,0
	Both missing or out-of-range group codes and at least one missing discriminating variable	4	2,0
	Total	4	2,0
Total		204	100,0

Group Statistics

sex		Valid N (listwise) Unweighted	Weighted
Male	HHD	99	99,000
	HEB	99	99,000
	FHD	99	99,000
	FMC	99	99,000
	FDB	99	99,000
	TPB	99	99,000
	TCN	99	99,000
	TDB	99	99,000
Female	HHD	101	101,000
	HEB	101	101,000
	FHD	101	101,000
	FMC	101	101,000
	FDB	101	101,000
	TPB	101	101,000
	TCN	101	101,000
	TDB	101	101,000
Total	HHD	200	200,000
	HEB	200	200,000
	FHD	200	200,000
	FMC	200	200,000
	FDB	200	200,000
	TPB	200	200,000
	TCN	200	200,000
	TDB	200	200,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

Step	Entered	Wilks' Lambda Statistic	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	HHD	,438	1	1	198,000	254,500	1	198,000	,000
2	TDB	,399	2	1	198,000	148,380	2	197,000	,000
3	HEB	,386	3	1	198,000	103,757	3	196,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 16.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove	Wilks' Lambda
1	HHD	1,000	254,500	
2	HHD	,637	35,832	,472
	TDB	,637	19,054	,438
3	HHD	,554	18,844	,424
	TDB	,525	7,430	,401
	HEB	,525	6,391	,399

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	HHD	1,000	1,000	254,500	,438
	HEB	1,000	1,000	217,277	,477
	FHD	1,000	1,000	222,978	,470
	FMC	1,000	1,000	135,927	,593
	FDB	1,000	1,000	216,997	,477
	TPB	1,000	1,000	231,029	,462
	TCN	1,000	1,000	102,535	,659
	TDB	1,000	1,000	221,892	,472
1	HEB	,637	,637	17,950	,401
	FHD	,445	,445	9,076	,418
	FMC	,760	,760	8,476	,420
	FDB	,468	,468	8,891	,419
	TPB	,558	,558	16,471	,404
	TCN	,849	,849	7,925	,421
	TDB	,637	,637	19,054	,399
2	HEB	,525	,525	6,391	,386
	FHD	,373	,373	1,708	,396
	FMC	,674	,564	2,120	,395
	FDB	,295	,295	,159	,399
	TPB	,383	,383	3,437	,392
	TCN	,733	,550	1,520	,396
3	FHD	,369	,369	1,099	,384
	FMC	,604	,471	,446	,385
	FDB	,277	,277	,059	,386
	TPB	,370	,370	1,933	,383
	TCN	,674	,483	,277	,386

Wilks' Lambda

Step	Number of Variables	Lambda	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	1	,438	1	1	198	254,500	1	198,000	<,001
2	2	,399	2	1	198	148,380	2	197,000	<,001
3	3	,386	3	1	198	103,757	3	196,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	1,588[a]	100,0	100,0	,783

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,386	186,857	3	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
HHD	,508
HEB	,313
TDB	,337

Structure Matrix

	Function 1
HHD	,900
FDB[a]	,842
TDB	,840
HEB	,831

FHD[a]	,784
TPB[a]	,780
FMC[a]	,610
TCN[a]	,532

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions
Variables ordered by absolute size of correlation within function.
a. This variable not used in the analysis.

Canonical Discriminant Function Coefficients

	Function 1
HHD	,198
HEB	,080
TDB	,115
(Constant)	-20,140

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	1,266
Female	-1,241

Unstandardized canonical discriminant functions evaluated at group means

Classification Processing Summary

Processed		204
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	4
Used in Output		200

Prior Probabilities for Groups

		Cases Used in Analysis	
sex	Prior	Unweighted	Weighted
Male	,500	99	99,000
Female	,500	101	101,000
Total	1,000	200	200,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	90	9	99
		Female	10	91	101
	%	Male	90,9	9,1	100,0
		Female	9,9	90,1	100,0

a. 90,5% of original grouped cases correctly classified.

ii. Humerus

Group Statistics

sex		Mean	Std. Deviation	Valid N (listwise) Unweighted	Weighted
Male	HHD	49,1942	2,59139	99	99,000
	HEB	64,7678	3,83823	99	99,000
Female	HHD	43,4147	2,53207	101	101,000
	HEB	56,5934	4,00076	101	101,000
Total	HHD	46,2756	3,86273	200	200,000
	HEB	60,6398	5,66444	200	200,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

Step	Entered	Wilks' Lambda Statistic	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	HHD	,438	1	1	198,000	254,500	1	198,000	,000
2	HEB	,401	2	1	198,000	147,118	2	197,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 4.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove	Wilks' Lambda
1	HHD	1,000	254,500	
2	HHD	,637	37,217	,477
	HEB	,637	17,950	,438

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	HHD	1,000	1,000	254,500	,438
	HEB	1,000	1,000	217,277	,477

1	HEB	,637	,637	17,950	,401

Wilks' Lambda

Step	Number of Variables	Lambda	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	1	,438	1	1	198	254,500	1	198,000	<,001
2	2	,401	2	1	198	147,118	2	197,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	1,494[a]	100,0	100,0	,774

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,401	180,003	2	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
HHD	,646
HEB	,468

Structure Matrix

	Function 1
HHD	,928
HEB	,857

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions
Variables ordered by absolute size of correlation within function.

Canonical Discriminant Function Coefficients

	Function 1
HHD	,252
HEB	,119
(Constant)	-18,899

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	1,228
Female	-1,204

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed		200
Excluded	Missing or out-of-range group codes	0

At least one missing discriminating variable	0
Used in Output	200

Prior Probabilities for Groups

sex	Prior	Cases Used in Analysis	
		Unweighted	Weighted
Male	,500	99	99,000
Female	,500	101	101,000
Total	1,000	200	200,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	88	11	99
		Female	10	91	101
	%	Male	88,9	11,1	100,0
		Female	9,9	90,1	100,0

a. 89,5% of original grouped cases correctly classified.

iii. Femur

Group Statistics

sex		Mean	Std. Deviation	Valid N (listwise) Unweighted	Weighted
Male	FHD	48,9468	2,56095	99	99,000
	FMC	94,6936	6,08457	99	99,000
	FDB	84,3359	4,32309	99	99,000
Female	FHD	43,4090	2,68093	101	101,000
	FMC	85,1980	5,42057	101	101,000
	FDB	75,5080	4,15154	101	101,000
Total	FHD	46,1502	3,81395	200	200,000
	FMC	89,8983	7,45986	200	200,000
	FDB	79,8778	6,11909	200	200,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

Step	Entered	Wilks' Lambda Statistic	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	FHD	,470	1	1	198,000	222,978	1	198,000	,000
2	FDB	,446	2	1	198,000	122,510	2	197,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 6.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	FHD	1,000	1,000	222,978	,470

	FMC	1,000	1,000	135,927	,593
	FDB	1,000	1,000	216,997	,477
1	FMC	,704	,704	8,280	,451
	FDB	,380	,380	10,897	,446
2	FMC	,561	,303	2,286	,441

Wilks' Lambda

Step	Number of Variables	Lambda	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	1	,470	1	1	198	222,978	1	198,000	<,001
2	2	,446	2	1	198	122,510	2	197,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	1,244[a]	100,0	100,0	,745

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,446	159,206	2	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
FHD	,559
FDB	,499

Structure Matrix

	Function 1
FHD	,952
FDB	,939
FMC[a]	,634

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions

Variables ordered by absolute size of correlation within function.

a. This variable not used in the analysis.

Canonical Discriminant Function Coefficients

	Function 1
FHD	,213
FDB	,118
(Constant)	-19,238

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	1,121
Female	-1,099

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed	200

Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	0
Used in Output		200

Prior Probabilities for Groups

		Cases Used in Analysis	
sex	Prior	Unweighted	Weighted
Male	,500	99	99,000
Female	,500	101	101,000
Total	1,000	200	200,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	85	14	99
		Female	14	87	101
	%	Male	85,9	14,1	100,0
		Female	13,9	86,1	100,0

a. 86,0% of original grouped cases correctly classified.

iv. Tibia

Group Statistics

				Valid N (listwise)	
sex		Mean	Std. Deviation	Unweighted	Weighted
Male	TPB	78,9907	3,85094	99	99,000
	TCN	100,5719	9,11683	99	99,000
	TDB	56,4720	2,81837	99	99,000
Female	TPB	70,6358	3,92126	101	101,000
	TCN	88,7641	7,29043	101	101,000
	TDB	50,2914	3,04255	101	101,000
Total	TPB	74,7715	5,70674	200	200,000
	TCN	94,6090	10,13255	200	200,000
	TDB	53,3508	4,26150	200	200,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

		Wilks' Lambda				Exact F			
Step	Entered	Statistic	df1	df2	df3	Statistic	df1	df2	Sig.
1	TPB	,462	1	1	198,000	231,029	1	198,000	,000
2	TDB	,431	2	1	198,000	129,952	2	197,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 6.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove	Wilks' Lambda
1	TPB	1,000	231,029	
2	TPB	,460	18,453	,472
	TDB	,460	13,864	,462

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	TPB	1,000	1,000	231,029	,462
	TCN	1,000	1,000	102,535	,659
	TDB	1,000	1,000	221,892	,472
1	TCN	,634	,634	,635	,460
	TDB	,460	,460	13,864	,431
2	TCN	,626	,387	,131	,431

Wilks' Lambda

	Number of					Exact F			
Step	Variables	Lambda	df1	df2	df3	Statistic	df1	df2	Sig.
1	1	,462	1	1	198	231,029	1	198,000	<,001
2	2	,431	2	1	198	129,952	2	197,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	1,319[a]	100,0	100,0	,754

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,431	165,730	2	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
TPB	,572
TDB	,501

Structure Matrix

	Function 1
TPB	,940
TDB	,922
TCN[a]	,599

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions

Variables ordered by absolute size of correlation within function.

a. This variable not used in the analysis.

Canonical Discriminant Function Coefficients

	Function 1
TPB	,147
TDB	,171
(Constant)	-20,122

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	1,154
Female	-1,131

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed		200
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	0
Used in Output		200

Prior Probabilities for Groups

		Cases Used in Analysis	
sex	Prior	Unweighted	Weighted
Male	,500	99	99,000

Female	,500	101	101,000
Total	1,000	200	200,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	87	12	99
		Female	13	88	101
	%	Male	87,9	12,1	100,0
		Female	12,9	87,1	100,0

a. 87,5% of original grouped cases correctly classified.

2. DFA output for Black South Africans

i. Humerus, femur, tibia

Discriminant

Analysis Case Processing Summary

Unweighted Cases		N	Percent
Valid		200	99,0
Excluded	Missing or out-of-range group codes	0	,0
	At least one missing discriminating variable	0	,0
	Both missing or out-of-range group codes and at least one missing discriminating variable	2	1,0
	Total	2	1,0
Total		202	100,0

Group Statistics

			Valid N (listwise)	
sex			Unweighted	Weighted
Male	HHD		100	100,000
	HEB		100	100,000
	FHD		100	100,000
	FMC		100	100,000

	FDB	100	100,000
	TPB	100	100,000
	TCN	100	100,000
	TDB	100	100,000
Female	HHD	100	100,000
	HED	100	100,000
	FHD	100	100,000
	FMC	100	100,000
	FDB	100	100,000
	TPD	100	100,000
	TCN	100	100,000
	TDB	100	100,000
Total	HHD	200	200,000
	HED	200	200,000
	FHD	200	200,000
	FMC	200	200,000
	FDB	200	200,000
	TPB	200	200,000
	TCN	200	200,000
	TDB	200	200,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

			Wilks' Lambda				Exact F			
Step	Entered	Removed	Statistic	df1	df2	df3	Statistic	df1	df2	Sig.
1	FHD		,405	1	1	198,000	290,952	1	198,000	,000
2	FMC		,351	2	1	198,000	181,907	2	197,000	,000
3	HHD		,331	3	1	198,000	131,893	3	196,000	,000
4	HEB		,319	4	1	198,000	103,964	4	195,000	,000
5		FHD	,323	3	1	198,000	136,650	3	196,000	,000
6	TPB		,316	4	1	198,000	105,633	4	195,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 16.
b. Minimum partial F to enter is 3.84.
c. Maximum partial F to remove is 2.71.
d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove	Wilks' Lambda
1	FHD	1,000	290,952	
2	FHD	,813	62,438	,463
	FMC	,813	30,101	,405
3	FHD	,430	6,737	,343
	FMC	,813	28,957	,380
	HHD	,482	11,842	,351
4	FHD	,392	2,587	,323
	FMC	,796	22,459	,356
	HHD	,469	8,168	,333
	HEB	,644	7,353	,331
5	FMC	,858	30,710	,374
	HHD	,732	25,368	,365
	HEB	,706	11,626	,343
6	FMC	,811	21,843	,351
	HHD	,568	10,043	,332
	HEB	,642	6,284	,326
	TPB	,498	4,747	,323

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	HHD	1,000	1,000	262,257	,430
	HEB	1,000	1,000	233,902	,458
	FHD	1,000	1,000	290,952	,405
	FMC	1,000	1,000	230,006	,463
	FDB	1,000	1,000	257,976	,434
	TPB	1,000	1,000	280,841	,413
	TCN	1,000	1,000	182,949	,520
	TDB	1,000	1,000	206,185	,490
1	HHD	,482	,482	12,822	,380
	HEB	,674	,674	18,420	,370
	FMC	,813	,813	30,101	,351

	FDB	,415	,415	8,807	,388
	TPB	,449	,449	15,061	,376
	TCN	,744	,744	12,961	,380
	TDB	,464	,464	3,036	,399
2	HHD	,482	,430	11,842	,331
	HEB	,661	,612	11,008	,333
	FDB	,409	,395	4,832	,343
	TPB	,440	,429	8,406	,337
	TCN	,399	,399	,030	,351
	TDB	,450	,446	,543	,350
3	HEB	,644	,392	7,353	,319
	FDB	,392	,310	2,177	,328
	TPB	,419	,329	4,592	,324
	TCN	,396	,396	,178	,331
	TDB	,437	,329	,028	,331
4	FDB	,363	,305	,563	,318
	TPB	,405	,318	2,652	,315
	TCN	,396	,381	,237	,319
	TDB	,411	,321	,253	,319
5	FHD	,392	,392	2,587	,319
	FDB	,466	,466	2,027	,320
	TPB	,498	,498	4,747	,316
	TCN	,407	,407	,049	,323
	TDB	,502	,502	,051	,323
6	FHD	,318	,318	,526	,315
	FDB	,192	,192	,142	,316
	TCN	,390	,390	,456	,315
	TDB	,337	,334	1,517	,313

Wilks' Lambda

Step	Number of Variables	Lambda	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	1	,405	1	1	198	290,952	1	198,000	<,001
2	2	,351	2	1	198	181,907	2	197,000	<,001
3	3	,331	3	1	198	131,893	3	196,000	<,001
4	4	,319	4	1	198	103,964	4	195,000	<,001
5	3	,323	3	1	198	136,650	3	196,000	<,001

6	4	,316	4	1	198	105,633	4	195,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	2,167[a]	100,0	100,0	,827

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,316	225,935	4	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
HHD	,355
HEB	,267
FMC	,426
TPD	,264

Structure Matrix

	Function 1
TPD	,809
FDB[a]	,790
FHD[a]	,788
HHD	,782
TDB[a]	,755
HEB	,738
FMC	,732

TCN[a]	,690

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions
Variables ordered by absolute size of correlation within function.
a. This variable not used in the analysis.

Canonical Discriminant Function Coefficients

	Function 1
HHD	,166
HEB	,085
FMC	,070
TPD	,076
(Constant)	-23,475

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	1,465
Female	-1,465

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed	202

Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	2
Used in Output		200

Prior Probabilities for Groups

sex	Prior	Cases Used in Analysis Unweighted	Weighted
Male	,500	100	100,000
Female	,500	100	100,000
Total	1,000	200	200,000

Classification Results[a]

			Predicted Group Membership 1,00	2,00	Total
Original	Count	Male	94	6	100
		Female	6	94	100
	%	Male	94,0	6,0	100,0
		Female	6,0	94,0	100,0

a. 94,0% of original grouped cases correctly classified.

ii. Humerus

Discriminant

Analysis Case Processing Summary

Unweighted Cases		N	Percent
Valid		200	99,0
Excluded	Missing or out-of-range group codes	0	,0
	At least one missing discriminating variable	0	,0
	Both missing or out-of-range group codes and at least one missing discriminating variable	2	1,0
	Total	2	1,0

Total	202	100,0

Group Statistics

sex		Mean	Std. Deviation	Valid N (listwise) Unweighted	Weighted
Male	HHD	43,7100	2,21219	100	100,000
	HEB	61,9071	3,13171	100	100,000
Female	HHD	38,8178	2,05727	100	100,000
	HEB	55,1087	3,15476	100	100,000
Total	HHD	41,2639	3,24864	200	200,000
	HEB	58,5079	4,63069	200	200,000

Variables Entered/Removed[a,b,c,d]

Step	Entered	Wilks' Lambda Statistic	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	HHD	,430	1	1	198,000	262,257	1	198,000	,000
2	HEB	,374	2	1	198,000	164,770	2	197,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 4.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove	Wilks' Lambda
1	HHD	1,000	262,257	
2	HHD	,750	44,386	,458
	HEB	,750	29,515	,430

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	HHD	1,000	1,000	262,257	,430
	HEB	1,000	1,000	233,902	,458
1	HEB	,750	,750	29,515	,374

Wilks' Lambda

Step	Number of Variables	Lambda	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	1	,430	1	1	198	262,257	1	198,000	<,001
2	2	,374	2	1	198	164,770	2	197,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	1,673[a]	100,0	100,0	,791

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,374	193,676	2	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
HHD	,626
HEB	,527

Structure Matrix

	Function 1
HHD	,890
HEB	,840

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions
Variables ordered by absolute size of correlation within function.

Canonical Discriminant Function Coefficients

	Function 1
HHD	,293
HEB	,168
(Constant)	-21,904

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	1,287
Female	-1,287

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed		202
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	2

Used in Output	200

Prior Probabilities for Groups

sex	Prior	Cases Used in Analysis	
		Unweighted	Weighted
Male	,500	100	100,000
Female	,500	100	100,000
Total	1,000	200	200,000

Classification Results[a]

			Predicted Group Membership		
		sex	1,00	2,00	Total
Original	Count	Male	92	8	100
		Female	9	91	100
	%	Male	92,0	8,0	100,0
		Female	9,0	91,0	100,0

a. 91,5% of original grouped cases correctly classified.

iii. Femur

Group Statistics

sex		Mean	Std. Deviation	Valid N (listwise)	
				Unweighted	Weighted
Male	FHD	45,5964	2,23038	100	100,000
	FMC	94,1067	6,93207	100	100,000
	FDB	79,0602	3,74320	100	100,000
Female	FHD	40,3069	2,15450	100	100,000
	FMC	81,1067	5,04211	100	100,000
	FDB	70,6727	3,64116	100	100,000
Total	FHD	42,9516	3,43715	200	200,000
	FMC	87,6067	8,88909	200	200,000
	FDB	74,8665	5,58945	200	200,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

		Wilks' Lambda				Exact F			
Step	Entered	Statistic	df1	df2	df3	Statistic	df1	df2	Sig.
1	FHD	,405	1	1	198,000	290,952	1	198,000	,000
2	FMC	,351	2	1	198,000	181,907	2	197,000	,000
3	FDB	,343	3	1	198,000	125,241	3	196,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 6.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove	Wilks' Lambda
1	FHD	1,000	290,952	
2	FHD	,813	62,438	,463
	FMC	,813	30,101	,405
3	FHD	,395	10,586	,361
	FMC	,803	25,612	,388
	FDB	,409	4,832	,351

Wilks' Lambda

	Number of					Exact F			
Step	Variables	Lambda	df1	df2	df3	Statistic	df1	df2	Sig.
1	1	,405	1	1	198	290,952	1	198,000	<,001
2	2	,351	2	1	198	181,907	2	197,000	<,001
3	3	,343	3	1	198	125,241	3	196,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	1,917[a]	100,0	100,0	,811

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,343	210,361	3	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
FHD	,444
FMC	,468
FDB	,299

Structure Matrix

	Function 1
FHD	,876
FDB	,824
FMC	,778

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions

Variables ordered by absolute size of correlation within function.

Canonical Discriminant Function Coefficients

	Function 1
FHD	,203
FMC	,077
FDB	,081
(Constant)	-21,534

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	1,378
Female	-1,378

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed		202
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	2
Used in Output		200

Prior Probabilities for Groups

sex	Prior	Cases Used in Analysis	
		Unweighted	Weighted
Male	,500	100	100,000
Female	,500	100	100,000
Total	1,000	200	200,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	91	9	100
		Female	9	91	100
	%	Male	91,0	9,0	100,0
		Female	9,0	91,0	100,0

a. 91,0% of original grouped cases correctly classified.

iv. Tibia

Group Statistics

sex		Mean	Std. Deviation	Valid N (listwise) Unweighted	Weighted
Male	TPB	76,0345	3,51235	100	100,000
	TCN	102,2700	7,84655	100	100,000
	TDB	53,9764	2,90947	100	100,000
Female	TPB	67,8445	3,39809	100	100,000
	TCN	87,7933	7,27907	100	100,000
	TDB	48,2726	2,70432	100	100,000
Total	TPB	71,9395	5,36049	200	200,000
	TCN	95,0317	10,47118	200	200,000
	TDB	51,1245	4,00295	200	200,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

Step	Entered	Wilks' Lambda Statistic	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	TPB	,413	1	1	198,000	280,841	1	198,000	,000
2	TCN	,385	2	1	198,000	157,075	2	197,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 6.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove	Wilks' Lambda
1	TPB	1,000	280,841	
2	TPB	,748	68,673	,520
	TCN	,748	14,360	,413

Variables Not in the Analysis

Step	Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda

0	TPB	1,000	1,000	280,841	,413
	TCN	1,000	1,000	182,949	,520
	TDB	1,000	1,000	206,185	,490
1	TCN	,748	,748	14,360	,385
	TDB	,384	,384	1,554	,410
2	TDB	,355	,355	,041	,385

Wilks' Lambda

Step	Number of Variables	Lambda	df1	df2	df3	Exact F Statistic	df1	df2	Sig.
1	1	,413	1	1	198	280,841	1	198,000	<,001
2	2	,385	2	1	198	157,075	2	197,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	1,595[a]	100,0	100,0	,784

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,385	187,832	2	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
TPB	,750
TCN	,385

Structure Matrix

	Function 1
TPB	,943
TDB[a]	,797
TCN	,761

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions

Variables ordered by absolute size of correlation within function.

a. This variable not used in the analysis.

Canonical Discriminant Function Coefficients

	Function 1
TPB	,217
TCN	,051
(Constant)	-20,441

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	1,256
Female	-1,256

Unstandardized
canonical
discriminant
functions evaluated
at group means

Classification Statistics

Classification Processing Summary

Processed		202
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	2
Used in Output		200

Prior Probabilities for Groups

sex	Prior	Cases Used in Analysis	
		Unweighted	Weighted
Male	,500	100	100,000
Female	,500	100	100,000
Total	1,000	200	200,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	89	11	100
		Female	12	88	100
	%	Male	89,0	11,0	100,0
		Female	12,0	88,0	100,0

a. 88,5% of original grouped cases correctly classified.

3. DFA output for Coloured South Africans

i. Humerus, Tibia and femur

Discriminant

Analysis Case Processing Summary

Unweighted Cases		N	Percent
Valid		76	100,0
Excluded	Missing or out-of-range group codes	0	,0
	At least one missing discriminating variable	0	,0
	Both missing or out-of-range group codes and at least one missing discriminating variable	0	,0
	Total	0	,0
Total		76	100,0

Group Statistics

sex		Mean	Std. Deviation	Valid N (listwise) Unweighted	Weighted
Male	HHD	43,8523	3,09162	56	56,000
	HEB	60,3470	3,94608	56	56,000
	FHD	44,8136	2,60573	56	56,000
	FMC	87,6488	6,22326	56	56,000
	FDB	77,8220	4,34845	56	56,000
	TPD	74,3466	3,75515	56	56,000
	TCN	96,2798	7,67438	56	56,000
	TDB	52,7470	2,71547	56	56,000
Female	HHD	38,7752	3,79393	20	20,000
	HEB	53,3408	4,49506	20	20,000
	FHD	39,6172	3,33617	20	20,000
	FMC	77,5000	5,59292	20	20,000
	FDB	69,8350	6,00029	20	20,000
	TPD	66,0836	4,84622	20	20,000
	TCN	83,6167	6,97554	20	20,000
	TDB	46,9180	3,84269	20	20,000
Total	HHD	42,5162	3,96493	76	76,000
	HEB	58,5033	5,11693	76	76,000
	FHD	43,4461	3,62003	76	76,000
	FMC	84,9781	7,52090	76	76,000
	FDB	75,7201	5,96003	76	76,000
	TPD	72,1721	5,45038	76	76,000
	TCN	92,9474	9,32874	76	76,000
	TDB	51,2130	3,97799	76	76,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

Step	Entered	Wilks' Lambda				Exact F			
		Statistic	df1	df2	df3	Statistic	df1	df2	Sig.
1	TPD	,548	1	1	74,000	60,942	1	74,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 16.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove
1	TPD	1,000	60,942

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	HHD	1,000	1,000	35,174	,678
	HEB	1,000	1,000	43,158	,632
	FHD	1,000	1,000	50,344	,595
	FMC	1,000	1,000	41,228	,642
	FDB	1,000	1,000	40,350	,647
	TPD	1,000	1,000	60,942	,548
	TCN	1,000	1,000	41,998	,638
	TDB	1,000	1,000	54,003	,578
1	HHD	,332	,332	,333	,546
	HEB	,458	,458	,800	,542
	FHD	,275	,275	,394	,545
	FMC	,587	,587	1,812	,535
	FDB	,147	,147	2,730	,529
	TCN	,701	,701	3,779	,521
	TDB	,337	,337	1,578	,537

Wilks' Lambda

Step	Number of Variables	Lambda	df1	df2	df3	Exact F Statistic	Exact F df1	Exact F df2	Exact F Sig.
1	1	,548	1	1	74	60,942	1	74,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	,824[a]	100,0	100,0	,672

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,548	44,157	1	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
TPB	1,000

Structure Matrix

	Function 1
TPB	1,000
FDB[a]	,924
FHD[a]	,852
HHD[a]	,818
TDB[a]	,814
HEB[a]	,736
FMC[a]	,643

TCN[a]	,547

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions
Variables ordered by absolute size of correlation within function.
a. This variable not used in the analysis.

Canonical Discriminant Function Coefficients

	Function 1
TPB	,246
(Constant)	-17,762

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	,535
Female	-1,498

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed		76
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	0

Used in Output	76

Prior Probabilities for Groups

sex	Prior	Cases Used in Analysis	
		Unweighted	Weighted
Male	,500	56	56,000
Female	,500	20	20,000
Total	1,000	76	76,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	48	8	56
		Female	1	19	20
	%	Male	85,7	14,3	100,0
		Female	5,0	95,0	100,0

a. 88,2% of original grouped cases correctly classified.

ii. Humerus

Group Statistics

sex		Valid N (listwise)	
		Unweighted	Weighted
Male	HHD	56	56,000
	HEB	56	56,000
Female	HHD	20	20,000
	HEB	20	20,000
Total	HHD	76	76,000
	HEB	76	76,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

Step	Entered	Wilks' Lambda

						Exact F			
		Statistic	df1	df2	df3	Statistic	df1	df2	Sig.
1	HEB	,632	1	1	74,000	43,158	1	74,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 4.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove
1	HEB	1,000	43,158

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	HHD	1,000	1,000	35,174	,678
	HEB	1,000	1,000	43,158	,632
1	HHD	,464	,464	1,683	,617

Wilks' Lambda

						Exact F			
Step	Number of Variables	Lambda	df1	df2	df3	Statistic	df1	df2	Sig.
1	1	,632	1	1	74	43,158	1	74,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	,583[a]	100,0	100,0	,607

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,632	33,770	1	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
HEB	1,000

Structure Matrix

	Function 1
HEB	1,000
HHD[a]	,732

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions

Variables ordered by absolute size of correlation within function.

a. This variable not used in the analysis.

Functions at Group Centroids

sex	Function 1
Male	,450
Female	-1,261

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed		76
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	0
Used in Output		76

Prior Probabilities for Groups

		Cases Used in Analysis	
sex	Prior	Unweighted	Weighted
Male	,500	56	56,000
Female	,500	20	20,000
Total	1,000	76	76,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	47	9	56
		Female	3	17	20
	%	Male	83,9	16,1	100,0
		Female	15,0	85,0	100,0

a. 84,2% of original grouped cases correctly classified.

iii. Femur

Group Statistics

				Valid N (listwise)	
sex		Mean	Std. Deviation	Unweighted	Weighted
Male	FHD	44,8136	2,60573	56	56,000
	FMC	87,6488	6,22326	56	56,000
	FDB	77,8220	4,34845	56	56,000

Female	FHD	39,6172	3,33617	20	20,000
	FMC	77,5000	5,59292	20	20,000
	FDB	69,8350	6,00029	20	20,000
Total	FHD	43,4461	3,62003	76	76,000
	FMC	84,9781	7,52090	76	76,000
	FDB	75,7201	5,96003	76	76,000

Analysis 1

Stepwise Statistics

Variables Entered/Removed[a,b,c,d]

		Wilks' Lambda				Exact F			
Step	Entered	Statistic	df1	df2	df3	Statistic	df1	df2	Sig.
1	FHD	,595	1	1	74,000	50,344	1	74,000	,000

At each step, the variable that minimizes the overall Wilks' Lambda is entered.

a. Maximum number of steps is 6.

b. Minimum partial F to enter is 3.84.

c. Maximum partial F to remove is 2.71.

d. F level, tolerance, or VIN insufficient for further computation.

Variables in the Analysis

Step		Tolerance	F to Remove
1	FHD	1,000	50,344

Variables Not in the Analysis

Step		Tolerance	Min. Tolerance	F to Enter	Wilks' Lambda
0	FHD	1,000	1,000	50,344	,595
	FMC	1,000	1,000	41,228	,642
	FDB	1,000	1,000	40,350	,647
1	FMC	,597	,597	3,615	,567
	FDB	,333	,333	,546	,591

Wilks' Lambda

Step	Number of Variables	Lambda	df1	df2	df3	Exact F Statistic	df1	df2	Sig.

1	1	,595	1	1	74	50,344	1	74,000	<,001

Summary of Canonical Discriminant Functions

Eigenvalues

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	,680[a]	100,0	100,0	,636

a. First 1 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1	,595	38,146	1	<,001

Standardized Canonical Discriminant Function Coefficients

	Function 1
FHD	1,000

Structure Matrix

	Function 1
FHD	1,000
FDB[a]	,817
FMC[a]	,635

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions
Variables ordered by absolute size of correlation within function.
a. This variable not used in the analysis.

Canonical Discriminant Function Coefficients

	Function 1
FHD	,356
(Constant)	-15,453

Unstandardized coefficients

Functions at Group Centroids

sex	Function 1
Male	,486
Female	-1,362

Unstandardized canonical discriminant functions evaluated at group means

Classification Statistics

Classification Processing Summary

Processed		76
Excluded	Missing or out-of-range group codes	0
	At least one missing discriminating variable	0
Used in Output		76

Prior Probabilities for Groups

sex	Prior	Cases Used in Analysis	
		Unweighted	Weighted

Male	,500	56	56,000
Female	,500	20	20,000
Total	1,000	76	76,000

Classification Results[a]

			Predicted Group Membership		
		sex	Male	Female	Total
Original	Count	Male	49	7	56
		Female	2	18	20
	%	Male	87,5	12,5	100,0
		Female	10,0	90,0	100,0

a. 88,2% of original grouped cases correctly classified.

UNIVERSITY OF THE WITWATERSRAND, JOHANNESBURG | FACULTY OF HEALTH SCIENCES | Anatomical Sciences

SCHOOL OF ANATOMICAL SCIENCES ETHICS WAIVER CLEARANCE LETTER

Faculty of Health Sciences
School of Anatomical Sciences
University of the Witwatersrand
Johannesburg

Re: In terms of Chapter 8, sections 62-64 of the National Health Act No 61 of 2003 donated bodies and their tissues may be used for, among other purposes, health, and research. Use of such Material is subject only to permission from the responsible person in the School of Anatomical Sciences – the Head or person designated by the Head of School.

Human Research Ethics Committee (Medical) Clearance Certificate:

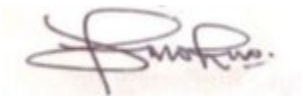
W-CBP-220504-01

This letter serves to confirm that the Head of School, based in the School of Anatomical Sciences, Faculty of Health Sciences, has reviewed the research proposal entitled:

A reassessment of single long bone dimensions to estimate sex in adult South African skeletal remains.

by principal investigator: **Selloane Kgadi Maboea**

and supervisor/collaborators: **Dr Anja Meyer and Mr. Okuhle Sapo**
and has granted approval for the ethics waiver to conduct the above-mentioned research study.



13.12.2023

Professor Amadi O. Ihunwo
Head of School: Anatomical Sciences
[B.Med.Sci (Hons), M.Sc., Ph.D]
Email: Amadi.Ihunwo@wits.ac.za

Dated