

https://dspace.org/

A comparison of multifactorial statistical models for age-at-death estimation from the adult skeleton, tailored to a South African forensic context

Jooste, Nicolene

2021
https://hdl.handle.net/10539/33560

Downloaded from a DSpace repository. https://dspace.org/

A COMPARISON OF MULTIFACTORIAL STATISTICAL MODELS FOR AGE-AT-DEATH ESTIMATION FROM THE ADULT SKELETON, TAILORED TO A SOUTH AFRICAN FORENSIC CONTEXT

Nicolene Jooste

A Thesis submitted to the Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, in fulfilment of the requirements for the degree of Doctor of Philosophy in Anatomical Sciences

Johannesburg, 2021

I dedicate this thesis to my grandparents:

They gave me the moon,

They shaped me,

They will always be in my heart,

They are dearly missed.

Stella Dawn van Vuuren

(my cheerleader, my sounding board, my best friend)

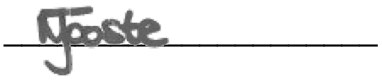
30/04/1940 - 25/06/2020

Faan Janse van Vuuren

01/07/1938 - 03/06/2020

DECLARATION

I, Nicolene Jooste, declare that this Thesis is my own, unaided work. It is being submitted for the Degree of Doctor of Philosophy in Anatomical Sciences at the University of the Witwatersrand, Johannesburg. It has not been submitted before for any degree or examination at any other University.



15th day of October 2021 in Johannesburg

Nicolene Jooste

ABSTRACT

Age-at-death estimation from the skeleton is routinely completed as part of a forensic anthropological investigation. The changes in the appearance of the skeleton that are associated with age, are also influenced by various biological and lifestyle factors. The imperfect relationship between skeletal appearance (i.e., biological age) and chronological age makes age estimation difficult. Research to improve the results of age-at-death estimation includes more complex statistical analyses, combining multiple indicators from the skeleton into a single technique and reducing or accounting for confounding factors (e.g., population and sex). The aim of this study was to assess the accuracy and usability of various statistical models commonly used in age estimation, in a South African population. Approximately 330 skeletons of known individuals from the Raymond A Dart and Pretoria Bone Collections (South Africa) were used to gather population specific data related to age changes in the skeleton from 51 age-related components identified from literature. Components that contained the most age-related information (vertebral bodies, pubic symphysis and acetabulum) were combined into five multifactorial models (2 non-specific for sex, 1 for females, 2 for males). The first non-specific model combined information from the acetabular fossa, posterior median palatine suture, S1/S2, superior rim of L5. The second non-specific model combined information from the pubic symphysis, acetabular fossa, posterior iliac exostoses, zygomaticomaxillary suture and the superior rim of L5. The male model duplicated the second non-specific model but contained either information from the phase-based pubic symphysis or only the superior apex respectively. The female model duplicated the first non-specific model but substituted the pubic symphysis for the posterior median palatine suture. Three separate statistical methods - basic descriptive statistics, multiple linear regression and transition analysis - were used to combine the selected components. The accuracy and precision of the age estimates produced by each statistical method were tested using a hold-out sample (N = 30). Most of the age indicators used expressed low coefficients of determination (r^2-values = 30 - 50%). The coefficient of determination could be strengthened by a maximum of 10% by combining traits, but multicollinearity and sample size are concerns when creating multifactorial models. Age estimation results from the validation study indicate that statistical complexity does not necessarily improve accuracy. Also, precision for intervals produced by the transition analysis method was particularly large. More advanced statistical methods alone are not the solution to improve age-at-death estimation from the skeleton.

ACKNOWLEDGEMENTS

I would like to acknowledge the body donors from the Raymond A Dart Skeletal Collection and the Pretoria Bone Collection, as well as the University of the Witwatersrand and the University of Pretoria who provided access to these collections.

I would also like to acknowledge the National Research Foundation and the JJJ Smieszek Award for the funding they provided.

Finally, I would like to acknowledge the valuable guidance of my supervisor, Professor Maryna Steyn, and the assistance of Ms Samantha Pretorius, Dr Deona Botha and Dr Tobias Houlton.

CONTENTS

DECLARATION iii
ABSTRACT iv
ACKNOWLEDGEMENTS v
CONTENTS vi
LIST OF FIGURES ix
LIST OF TABLES xiv
TERMINOLOGY xvi
CHAPTER 1: INTRODUCTION ..... - 1 -
1.1. Introduction ..... - 1 -
1.2. Aims and objectives ..... - 5 -
CHAPTER 2: LITERATURE REVIEW ..... - 7 -
2.1. Skeletal changes with age ..... - 7 -
2.1.1. Adult developmental changes ..... - 8 -
2.1.2. Pubic symphysis ..... - 9 -
2.1.3. Auricular surface ..... - 10 -
2.1.4. Ribs ..... - 10 -
2.1.5. Cranial sutures ..... - 11 -
2.1.6. Arthritic changes ..... - 12 -
2.1.7. Microscopic and biochemical analyses ..... - 13 -
2.1.8. Biological versus chronological age ..... - 13 -
2.1.9. Skeletal variation/Confounder effect ..... - 14 -
2.2. Creating age-at-death estimation methods ..... - 17 -
2.2.1. Effect of reference sample size and composition ..... - 18 -
2.2.2. Component- versus phase-method ..... - 21 -
2.3. Recognising error and evaluating success ..... - 22 -
2.3.1. Validation studies ..... - 24 -
2.4. Potential solutions ..... - 26 -

2.4.1. Reliability/Observer agreement ..... - 26 -
2.4.2. Combining indicators ..... - 27 -
2.4.3. Statistics ..... - 31 -
2.5. Figures ..... - 40 -
CHAPTER 3: MATERIALS AND METHODS ..... - 42 -
3.1. Materials ..... - 42 -
3.2. Methods ..... - 44 -
3.3. Data analysis ..... - 46 -
3.4. Validation Study ..... - 48 -
3.5. Ethics ..... - 50 -
3.6. Figures ..... - 51 -
CHAPTER 4: RESULTS ..... - 61 -
4.1. Sample distribution ..... - 61 -
4.2. Differences between bilateral paired features ..... - 62 -
4.3. Differences between vertebral body margins ..... - 62 -
4.4. Descriptive statistics ..... - 63 -
4.5. Difference between sexes ..... - 65 -
4.6. Regression analysis ..... - 67 -
4.7. Transition analysis/Generalized linear models ..... - 71 -
4.8. Validating results ..... - 75 -
4.9. Observer agreement ..... - 80 -
4.10. Figures ..... - 83 -
4.11. Tables ..... - 129 -
CHAPTER 5: DISCUSSION ..... - 149 -
5.1. Statistical methods ..... - 151 -
5.2. Age indicators and confounders ..... - 153 -
5.3. Multicollinearity ..... - 158 -
5.4. Sample size ..... - 161 -

5.5. Observer agreement ..... - 161 -
5.6. Bilateral asymmetry ..... - 164 -
5.7. Using the results from this study ..... - 164 -
5.8. Conclusions and future directions ..... - 165 -
CHAPTER 6: CONCLUSION ..... - 168 -
REFERENCES ..... - 170 -
APPENDIX A ..... - 187 -
APPENDIX B ..... - 363 -
APPENDIX C ..... - 364 -
APPENDIX D ..... - 365 -
APPENDIX E ..... - 366 -

LIST OF FIGURES

Figure 2.1: Trajectory effect increases error around the mean with increasing age. [Graph produced by N Jooste]..... - 40 -
Figure 2.2: Combining the 95% age intervals of multiple indicators can be approached in two ways. Maximum overlap incorporates the full intervals of each indicator. Minimum overlap includes the interval between the average of all minimum values and the average of all maximum values. [Graph produced by N Jooste] .. - 40 -
Figure 2.3: The 95% age intervals of multiple indicators within a single individual does not always overlap. In this case it would be impossible to create an interval from minimum overlap. [Graph produced by N Jooste] ..... - 41 -
Figure 3.1: Sample size per feature with all components present (Total N = 332)- 51 -
Figure 3.2: Sample distribution for each decade and sex..... - 52 -
Figure 3.3: Skeletal features selected: cranial sutures (Nawrocki, 1998; Boldsen *et al.*, 2002), medial epiphysis of clavicle (Scheuer and Black, 2000), iliac crest (Scheuer and Black, 2000), auricular surface (Boldsen *et al.*, 2002; Osborne *et al.*, 2004), acetabulum (Rissech *et al.*, 2006), pubic symphysis (Katz and Suchey, 1986; Boldsen *et al.*, 2002), sacrum (McKern and Stewart, 1957; Passalacqua, 2009), vertebral bodies (Stewart, 1958; van der Merwe *et al.*, 2006). [Artwork provided by TMR Houlton] ..... - 53 -
Figure 3.4: Cranial sutures considered from the skull vault and facial region: (1) midlambdoid, (2) lambda, (3) obelion, (4) sagittal vertex, (5) bregma, (6) midcoronal, (7) sphenofrontal, (8) pterion, (9) superior sphenotemporal, (10) zygomaxillary (Nawrocki, 1998). [Artwork provided by TMR Houlton]..... - 54 -
Figure 3.5: Cranial sutures considered from the inferior skull and palate region: (1) incisive, (2) anterior median palatine, (3) transverse palatine, (4) posterior median palatine, (5) inferior sphenotemporal (Mann *et al.*, 1991; Nawrocki, 1998). [Artwork provided by TMR Houlton]..... - 55 -
Figure 3.6: Descriptive categories 1. ..... - 56 -
Figure 3.7: Descriptive categories 2. ..... - 57 -
Figure 3.8: Descriptive categories 3. ..... - 58 -
Figure 3.9: Descriptive categories 4. ..... - 59 -
Figure 3.10: Descriptive categories 5. ..... - 60 -
Figure 4.1: Histogram of sample distribution per stage of left and right acetabular groove, rim, apex and fossa. ..... - 83 -

Figure 4.2: Histogram of sample distribution per stage of left and right auricular surface topography, morphology, texture and posterior iliac exostoses. ..... - 84 -
Figure 4.3: Histogram of sample distribution per stage of left and right medial epiphysis of the clavicle. ..... - 84 -
Figure 4.4: Histogram of sample distribution per stage of left and right midlambdoid, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary sutures, as well as, lambda, obelion, vertex, bregma, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures. ..... - 85 -
Figure 4.5: Histogram of sample distribution per stage of left and right iliac crest. - 86 -
Figure 4.6: Histogram of sample distribution per stage of left and right pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin. ..... - 87 -
Figure 4.7: Histogram of sample distribution per stage of S1/S2 fusion. ..... - 88 -
Figure 4.8: Histogram of sample distribution per stage of left and right pubic symphysis (Suchey-Brooks stage-based method). ..... - 88 -
Figure 4.9: Histogram of sample distribution per stage of superior and inferior cervical vertebral bodies (C3 - C7). ..... - 89 -
Figure 4.10: Histogram of sample distribution per stage of superior and inferior lumbar vertebral bodies (L1 - L5). ..... - 90 -
Figure 4.11: Boxplots of age distribution per stage of acetabular groove, rim, apex and fossa. ..... - 91 -
Figure 4.12: Boxplots of age distribution per stage of auricular surface topography, morphology, texture and posterior iliac exostoses. ..... - 91 -
Figure 4.13: Boxplots of age distribution per stage of fusion of medial epiphysis of the clavicle. ..... - 92 -
Figure 4.14: Boxplots of age distribution per stage of midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures. ..... - 93 -
Figure 4.15: Boxplots of age distribution per stage of iliac crest fusion. ..... - 94 -
Figure 4.16: Boxplots of age distribution per stage of pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin. ..... - 94 -
Figure 4.17: Boxplots of age distribution per stage of S1/S2 fusion. ..... - 95 -
Figure 4.18: Boxplots of age distribution per stage of pubic symphysis (Suchey-Brooks stage-based method). ..... - 95 -

Figure 4.19: Boxplots of age distribution per stage of cervical vertebral bodies (C3 - C7). ..... - 96 -
Figure 4.20: Boxplots of age distribution per stage of lumbar vertebral bodies (L1 - L5). ..... - 97 -
Figure 4.21: Comparison of age distributions per stage of acetabular groove, rim, apex and fossa between females and males..... - 98 -
Figure 4.22: Comparison of age distributions per stage of auricular surface topography, morphology, texture and posterior iliac exostoses between females and males..... - 98 -
Figure 4.23: Comparison of age distributions per stage of medial epiphysis of the clavicle between females and males. ..... - 99 -
Figure 4.24: Comparison of age distributions per stage of midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures between females and males. ..... - 100 -
Figure 4.25: Comparison of age distributions per stage of iliac crest fusion..... - 101 -
Figure 4.26: Comparison of age distributions per stage of pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin between females and males..... - 101 -
Figure 4.27: Comparison of age distributions per stage of S1/S2 fusion between females and males. ..... - 102 -
Figure 4.28: Comparison of age distributions per stage of pubic symphysis (Suchey-Brooks stage-based method). ..... - 102 -
Figure 4.29: Comparison of age distributions per stage of cervical vertebral bodies (C3 - C7) between females and males. ..... - 103 -
Figure 4.30: Comparison of age distributions per stage of lumbar vertebral bodies (L1 - L5) between females and males. ..... - 104 -
Figure 4.31: Transition curves for stages of the acetabular groove, rim, apex and fossa..... - 105 -
Figure 4.32: Transition curves for stages of auricular surface topography, morphology, texture and posterior iliac exostoses..... - 105 -
Figure 4.33: Transition curves for stages of the medial epiphysis of the clavicle- 106 -
Figure 4.34: Transition curves for stages of midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior

sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median, palatine and transverse palatine sutures. ..... - 107 -
Figure 4.35: Transition curves for stages of iliac crest fusion. ..... - 108 -
Figure 4.36: Transition curves for stages of pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin. ..... - 108 -
Figure 4.37: Transition curves for stage of S1/S2 fusion. ..... - 109 -
Figure 4.38: Transition curves for stages of the pubic symphysis (Suchey-Brooks stage-based method). ..... - 109 -
Figure 4.39: Transition curves for stages of the superior and inferior cervical vertebral bodies (C3 - C7). ..... - 110 -
Figure 4.40: Transition curves for stages of the superior and inferior lumbar vertebral bodies (L1 - L5). ..... - 111 -
Figure 4.41: Transition curves comparing female and male stages of the acetabular groove, rim, apex and fossa. ..... - 112 -
Figure 4.42: Transition curves comparing female and male stages of the auricular surface topography, morphology, texture and posterior iliac exostoses. ..... - 113 -
Figure 4.43: Transition curves comparing female and male stages of medial clavicle epiphysis. ..... - 114 -
Figure 4.44: Transition curves for stages of female midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures. ..... - 115 -
Figure 4.45: Transition curves for stages of male midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures. ..... - 116 -
Figure 4.46: Transition curves comparing female and male stages of iliac crest fusion. ..... - 117 -
Figure 4.47: Transition curves comparing female and male stages of pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin. .... - 118 -
Figure 4.48: Transition curves comparing female and male stages of S1/S2 fusion. .. - 119 -
Figure 4.49: Transition curves comparing female and male stages of the pubic symphysis (Suchey-Brooks stage-based method). ..... - 119 -

Figure 4.50: Transition curves for stages of female superior and inferior cervical vertebral bodies (C3 - C7). ..... - 120 -
Figure 4.51: Transition curves for stages of female superior and inferior lumbar vertebral bodies (L1 - L5). ..... - 121 -
Figure 4.52: Transition curves for stages of male superior and inferior cervical vertebral bodies (C3 - C7). ..... - 122 -
Figure 4.53: Transition curves for stages of male superior and inferior lumbar vertebral bodies (L1 - L5). ..... - 123 -
Figure 4.54: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 1. - 124 -
Figure 4.55: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 2. - 125 -
Figure 4.56: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 3. - 126 -
Figure 4.57: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 4. - 127 -
Figure 4.58: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 5. - 128 -

LIST OF TABLES

Table 4.1: Numerical assessment of sample distribution shape using Shapiro-Wilks test for normality, skewness and kurtosis values. - 129 -
Table 4.2: Wilcoxon signed-rank test for significant differences between right and left indicators. - 132 -
Table 4.3: Wilcoxon signed-rank test for significant difference between superior and inferior vertebral bodies. - 132 -
Table 4.4: Wilcoxon signed-rank test for significant difference between adjacent vertebral bodies. - 133 -
Table 4.5: Descriptive statistics for left and median indicators. - 133 -
Table 4.6: Mann-Whitney U test for significant difference between female and male subgroups. - 137 -
Table 4.7: Comparison of goodness-of-fit (r^2-value) for linear and non-linear regression. - 139 -
Table 4.8: Linear regression models for individual skeletal indicators to evaluate strength of association, goodness-of-fit, statistical significance and significance of contribution of the coefficients. - 141 -
Table 4.9: Linear regression models for combining multiple skeletal indicators to evaluate strength of association, goodness-of-fit, statistical significance and significance of contribution of the coefficients. - 144 -
Table 4.10: Final multifactorial linear regression models. - 145 -
Table 4.11: Comparing bias, accuracy and precision for estimates obtained using basic statistics, regression analysis and transition analysis models. - 146 -
Table 4.12: Observer agreement for single and multiple observers. - 147 -
E 1: Descriptive statistics of right-side indicators. - 366 -
E 2: Descriptive statistics for left side and median female indicators. - 368 -
E 3: Descriptive statistics for left side and median male indicators. - 372 -
E 4: Correlations between indicators and age for females and males combined - 376 -
E 5: Transition analysis model 1 age estimation table. - 377 -
E 6: Transition analysis model 2 age estimation table. - 379 -
E 7: Transition analysis model 3 age estimation table. - 396 -
E 8: Transition analysis model 4 age estimation table. - 399 -
E 9: Transition analysis model 5 age estimation table. - 413 -
E 10: Validation results using multifactorial model 1 (not sex specific). - 431 -
E 11: Validation results using multifactorial model 2 (not sex specific). - 432 -

E 12: Validation results using multifactorial model 3 (female specific). ..... - 433 -
E 13: Validation results using multifactorial model 4 (male specific). ..... - 434 -
E 14: Validation results using multifactorial model 5 (male specific). ..... - 435 -

TERMINOLOGY

Accuracy: corresponds to the correct point estimate or includes the correct age within an interval.

Biological age: the growth, size and maturity represented by the anatomy and physiology of an individual.

Chronological/Calendar age: the passage of time calculated from birth.

Confidence interval: the likely range of values (e.g., 95%) associated with the population.

Confounders: factors other than the age-at-death that influence the skeletal indicator.

Highest posterior density distribution/Posterior probability: the probability after prior information has been accounted for in Bayesian analysis.

Maximum overlap: a collective interval that integrates the full intervals from all individual indicators.

Minimum overlap: a collective interval that integrates intersecting intervals from all individual indicators.

Multifactorial methods: statistical combination of several age estimates.

$\mathbf{n_{stage1}}$**:** sample size of stage 1 etc.

Prediction interval: an estimated range (e.g., 95%) predicted for an individual observation.

Precision: considers the width of an interval; a wide interval is imprecise, whereas a narrow interval is precise.

Preservation bias: bias introduced by selectively available skeletal material due to poor preservation associated with certain indicators.

Prior distribution: a distribution used in Bayesian analysis using prior experience/documentation to modify the likelihood of an outcome.

Validity: considers the accuracy and precision of a method.

CHAPTER 1: INTRODUCTION

1.1. Introduction

One goal of forensic anthropology is to assist in identifying unknown skeletal remains, which includes establishing a probable age-at-death estimate for the deceased. This is possible as a number of skeletal features have been shown to undergo structural changes with age, in a predictable manner (Todd, 1920; İşcan *et al.*, 1984b; Lovejoy, Meindl, Pryzbeck *et al.*, 1985; Boldsen *et al.*, 2002; DiGangi *et al.*, 2009; Langley-Shirley and Jantz, 2010; Passalacqua, 2010). The juvenile skeleton experiences a set of growth and developmental changes such as long-bone lengthening, epiphyseal fusion and dental eruption (Scheuer and Black, 2000; Smith and Buschang, 2004, 2005). Skeletal features that indicate the onset of adulthood include complete fusion of all long bone epiphyses, eruption of the third molar and fusion of the spheno-occipital synchondrosis (Scheuer and Black, 2000; Falys and Lewis, 2011; Ubelaker and Khosrowshahi, 2019). Age changes present in the adult skeleton are related to skeletal maintenance and degeneration, with a few exceptions such as fusion of the medial clavicle. The four main regions that are traditionally used as adult age indicators include the pubic symphysis, auricular surface, sternal rib ends and cranial sutures (White and Folkens, 2005; Garvin and Passalacqua, 2012; Garvin *et al.*, 2012; İşcan and Steyn, 2013; Uhl, 2013). An array of additional skeletal indicators are constantly researched, including arthritic changes in the joints (Rissech *et al.*, 2006; van der Merwe *et al.*, 2006; Calce and Rogers, 2011; Zukowski *et al.*, 2012; Brennaman *et al.*, 2017; Alves-Cardoso and Assis, 2018) and bone mineral density (Navega, d'Oliveira Coelho *et al.*, 2018; Botha *et al.*, 2019).

The age-related changes observed in the skeleton can be used to estimate a biological age. This biological age is imperfectly aligned with chronological/calendar age, which is defined as the number of years passed since birth. The imperfect relationship between biological and chronological age can be attributed to extrinsic and intrinsic factors such as health, nutrition and biomechanical stress that influence the appearance of the skeleton (i.e., biological age) (Cunha *et al.*, 2009; Nawrocki, 2010; Garvin *et al.*, 2012; Merrit, 2015). Sex and population are specifically well documented factors that introduce variation in the biological aging pattern (Gilbert and McKern, 1973; Katz and Suchey, 1989; Hoppa, 2000; Berg, 2008; Zukowski *et al.*, 2012; Michopoulou *et al.*, 2017; Oikonomopoulou *et al.*, 2017).

As each individual, of the same chronological age, will have various unique extrinsic and intrinsic influences, each individual will display a unique biological age (İşcan, 1989; Garvin *et al.*, 2012). The skeletal appearance and associated biological age may even vary between individual skeletal features and the left and right sides within an individual due to the impact of environmental factors on skeletal structure (Albert and Greene, 1999). Additionally, the factors that influence skeletal appearance accumulate with progressing age, resulting in greater variation and broader age estimates in older individuals (Cunha *et al.*, 2009; Garvin *et al.*, 2012).

One solution to the influence of extrinsic and intrinsic factors on age is to control for these factors where possible (e.g., introduce sex- and population-specific data) (Gilbert and McKern, 1973; Katz and Suchey, 1989; Nawrocki, 1998; Suchey and Katz, 1998; Jackes, 2000; Mays, 2015; Xanthopoulou *et al.*, 2018). An alternative solution is to shift focus from minor variations introduced by sex and population, in favour of larger overall reference samples that better document age-related changes in a multitude of individuals (Katz and Suchey, 1986; Boldsen *et al.*, 2002; Konigsberg *et al.*, 2008).

Reference samples contain a series of skeletal individuals with known biological profiles. Skeletal information from the reference sample can be used to develop age estimation methods that can estimate the age of unknown skeletons (i.e., target sample). Developing skeletal age estimation methods usually entail recording observed skeletal characteristics that are categorized into age-related stages and accompanied by various statistical age descriptors (e.g., age intervals, mean ages, standard errors or standard deviations) (Hoppa, 2000; White and Folkens, 2005; DiGangi *et al.*, 2009).

The ideal age estimation method should be quantifiable and produce accurate, precise and reliable age estimates (Ousley and Hollinger, 2012). Precision (i.e., a narrow age interval) is helpful when eliminating possible identities. However, an interval which is too narrow may reduce accuracy by erroneously eliminating the true age of the individual. By comparison, a broad age interval (i.e., less precise) may include the true age but become impractical when attempting to identify an individual (Garvin *et al.*, 2012). A high reliability is achieved if a method is consistently repeatable (Ousley and Hollinger, 2012).

Some skeletal indicators are more accurate and precise when applied to certain age groups. As an example, the pubic symphysis, regardless of specific method, produces more accurate and precise estimates for individuals under 40 years (Todd, 1920; Gilbert and McKern, 1973; Katz and Suchey, 1986; Berg, 2008; Xanthopoulou *et al.*, 2018) and the sternal ends of the rib produces more accurate and precise estimates after 60 years (İşcan *et al.*, 1984b, 1985; Ritz-Timme *et al.*, 2000; Cunha *et al.*, 2009).

As different skeletal features produce better results for different age groups, this could indicate that different traits may be under different influences. Thus, many researchers suggest using multiple features to estimate age (Brooks, 1955; Saunders *et al.*, 1992; Suchey and Katz, 1998; Matrille *et al.*, 2007; Uhl and Nawrocki, 2010). Some researchers first consider one indicator and then follow up with a second indicator depending on the previous indicator's results (e.g., if Suchey-Brooks phase falls into 4, 5 or 6 progress to Lamendin technique) (Matrille *et al.*, 2007; Cunha *et al.*, 2009). Other researchers make use of features combined into a formal multifactorial method (Acsádi and Nemeskéri, 1970; Lovejoy, Meindl, Mensforth *et al.*, 1985; Boldsen *et al.*, 2002). Unfortunately, not many multifactorial methods exist and simply combining various single indicators is not suggested, as single indicators' methods will each produce different expressions of error. In the absence of a dedicated multifactorial method, combining indicators using interpolation performed by Principal Component Analysis, has been suggested (Matrille *et al.*, 2007). Although combined methods have been reported to outperform individual indicators (Baccino *et al.*, 1999; Matrille *et al.*, 2007), the level of success achieved from combined methods may be partially attributable to differences in sample size and distribution, as well as the affinity of the method to a particular age range (Matrille *et al.*, 2007).

The effect of the reference sample is notable when comparing different methods, for example various methods using the pubic symphysis produced different age estimates when tested on the same target sample (Brooks and Suchey, 1990; Klepinger *et al.*, 1992; Jackes, 2000; Brown, 2010). Similar trends were observed for cranial suture methods (Acsádi and Nemeskéri, 1970; Meindl and Lovejoy, 1985; Masset, 1989), where certain methods produced better accuracies when used with specific, non-overlapping age categories (Galera *et al.*, 1998). These trends were also noticed for the auricular surface methods when comparing the Buckberry and

Chamberlain (2002) method with the Osborne *et al.* (2004) method (Gocha *et al.*, 2015; Xanthopoulou *et al.*, 2018). The differences reported in age estimates from different methods could be attributed to the age distribution of the reference sample. Bocquet-Appel and Masset (1982) first noticed the undesirable effect that the age structure of the reference sample had on the age estimates of the target sample; this effect is referred to as age mimicry.

Statistical solutions were proposed to minimise the effect of the reference sample and increase the level of accuracy and precision. Improving the quality of age estimation, in this way, is suggested for both forensic (Grivas and Komar, 2008; National Research Council, 2009; Ousley and Hollinger, 2012) and archaeological contexts (Hoppa and Vaupel, 2002).

Bayesian analysis is specifically promoted as suitable for the type of data representative of biological age. Bayesian analysis does not require linear or continuous distribution of age-related indicator stages. The data distribution, associated with age-related indicator stages, has been highlighted as a limitation when estimating age using regression analysis or phase-based methods that attribute a central tendency and interval to each indicator stage (Konigsberg and Frankenberg, 1992; Lucy *et al.*, 1996; Boldsen *et al.*, 2002; Konigsberg *et al.*, 2008). The prior distribution, incorporated into Bayesian analysis, is another reported advantage as it modifies information from the reference sample with document-based survivorship models and in so doing minimises age mimicry from the reference sample (Konigsberg and Frankenberg, 1992; Boldsen *et al.*, 2002; Konigsberg *et al.*, 2008). Due to these claimed advantages, many existing age indicators have been revised, using Bayesian analysis to potentially improve the age estimates (Boldsen *et al.*, 2002; DiGangi *et al.*, 2009; Langley-Shirley and Jantz, 2010; Godde and Hens, 2012; Hens and Godde, 2016).

Transition analysis, a Bayesian approach, is considered particularly promising as it incorporates numerous age indicators (Boldsen *et al.*, 2002; Bullock *et al.*, 2013) However, various tests of the transition analysis method found accuracy and correlation values comparable to other methods and age intervals were unpractically large (Bethard, 2005; Milner and Boldsen, 2012b; Jooste *et al.*, 2016). Additionally, Hurst (2010) concluded that the Suchey-Brooks phase-based method outperformed the accuracy of transition analysis when only the pubic symphysis was considered. Other research similarly reports that less statistically complex methods such as

regression analysis outperforms Bayesian approaches (Uhl and Nawrocki, 2010; Nikita and Nikitas, 2019) or other similarly more advanced analyses (Passalacqua, 2010; Kotěrová *et al.*, 2018).

Bayesian analysis is still recognised as the more appropriate method of estimating age, even though it is also subject to a number of assumptions that need to be met (DiGangi *et al.*, 2009; Nikita *et al.*, 2018; Nikita and Nikitas, 2019).Even though there is currently no evidence that Bayesian analysis outperforms previously established methods (e.g., Katz and Suchey (1986), Lovejoy *et al.* (Lovejoy, Meindl, Pryzbeck *et al.*, 1985)), its value is recognised in the statistically appropriate combination of multiple age indicators (Hurst, 2010; Jooste *et al.*, 2016). Overall, some research indicates that more complex multifactorial methods, even though more statistically appropriate, do not necessarily improve results (Uhl and Nawrocki, 2010; Kotěrová *et al.*, 2018).

The aim of this study is thus to test whether a multifactorial method, using the same reference sample, can be improved when using Bayesian analysis compared to less complex methods such as regression analysis and combining basic statistics for phase-based methods. We will consider whether a method can be more appropriate if the results do not improve by using the method, and also whether the additional statistical complexity and computational intricacy justifies the results obtained.

1.2. Aims and objectives

This study aims to compare the accuracy, precision and ease-of-use of multifactorial statistical models for adult age-at-death estimation from the skeleton that are appropriate in a forensic context, using a South African sample. From this the best methods will be identified for use in future multifactorial age-at-death estimation.

The objectives of this study are to:

- Document and assess the relationship between various skeletal features and age in a forensically appropriate research sample (i.e., geographically and temporally relevant sample from the Raymond A Dart Collection of Human Skeletons and the Pretoria Bone Collection).
- Assess the contribution of each single feature to estimate age within multifactorial techniques.

- Combine relevant features into multifactorial methods using established techniques (i.e., reference sample ranges, multiple linear regression and transition analysis).
- Compare the accuracy, precision and repeatability of these methods in a validation study to evaluate the success of each.
- Establish whether any method holds a clear advantage over another and advise what methods we should use in future research.

CHAPTER 2: LITERATURE REVIEW

2.1. Skeletal changes with age

Publications as early as 1878 recognised basic changes in skeletal appearance with age progression (Dwight, 1878; Ubelaker, 2010). The subadult skeleton experiences age-related changes associated with growth and development, such as long-bone lengthening, epiphyseal fusion and dental eruption (Scheuer and Black, 2000; Smith and Buschang, 2004, 2005). Developmental changes are largely influenced by genetic control and experiences less of an environmental influence compared to older individuals (Uhl, 2013; Buckberry, 2015). Thus, changes in the subadult skeleton are frequently considered relatively easy to identify and closely associated with age (Ritz-Timme *et al.*, 2000; İşcan and Steyn, 2013). However, once one considers the rate of the changes that occur in childhood (i.e., body size, social development and intellectual ability), age intervals of 3 to 5 years become impractical (Nawrocki, 2010).

The distinction between what is subadult and adult is not always clear and can vary within social constructs. Falys and Lewis (2011) propose that adulthood begins at 20 years and suggest that skeletal indicators that denote its onset include the eruption of the third molar, closure of the epiphyseal plates and fusion of the spheno-occipital synchondrosis (Scheuer and Black, 2000; Falys and Lewis, 2011; Ubelaker and Khosrowshahi, 2019). Some developmental processes that are ongoing into early adulthood include the fusion of the medial epiphysis of the clavicle, S1/S2 segment of the sacrum and the iliac crests (McKern and Stewart, 1957; Scheuer and Black, 2000; İşcan and Steyn, 2013). The remaining age-related changes in the adult skeleton are related to skeletal maintenance and degeneration. Four main regions are traditionally considered as adult age indicators - the pubic symphysis, auricular surface, sternal rib ends and cranial sutures (White and Folkens, 2005; Garvin and Passalacqua, 2012; Garvin *et al.*, 2012; İşcan and Steyn, 2013; Uhl, 2013).

Age indicators do not need to be restricted to these four regions but can be any skeletal feature that displays progressive, unidirectional changes with advancing age. Age changes can be either typologically categorised or measured and should produce repeatable results. The changes in appearance of age indicators should be relatively consistent if not in the population as a whole, then in smaller groups split by population and/or sex (Milner and Boldsen, 2012a; Algee-Hewitt, 2017). The skeletal

features and their potential as age indicators discussed here include only adult indicators (pubic symphysis, auricular surface, ribs, cranial sutures) and also a number of arthritic changes to joint surfaces (i.e., acetabulum, vertebral bodies and the glenoid cavity).

2.1.1. Adult developmental changes

Although most epiphyses are united in the adult after 20 years, there are a few for which fusion is finalised in the early 20s. For example, the iliac crest has been noted to complete the fusion process between 18 and 22 years (McKern and Stewart, 1957; Webb and Suchey, 1985; Scheuer and Black, 2000; Coqueugniot and Weaver, 2007; Cardoso, 2008). However, Lottering *et al.* (2017) found it necessary to update fusion ages for the iliac crest due to secular trends in growth and development. Their findings using MSCT and Bayesian analysis for an Australian sample placed complete fusion between 17 and 20 years.

McKern and Stewart (1957) found the lateral epiphysis of the clavicle highly variable and difficult to judge, but the medial epiphysis contains slow progressing age-related information. The medial epiphysis is considered a thin flake of bone that fuses to the medial end of the clavicle between 18 and 29 years (McKern and Stewart, 1957; Webb and Suchey, 1985; Scheuer and Black, 2000; Schultz *et al.*, 2005). McKern and Stewart (1957) observed some minor differences between fusion of the right and left sides of the medial clavicle. The bilateral asymmetry was predominantly reported in the younger individuals and could potentially be attributed to the loss of epiphyseal end plates when processing the remains. A modern Bayesian approach for estimating age from the medial clavicle, reported secular trends in a modern American sample with fusion times on average four years earlier (Langley-Shirley and Jantz, 2010).

The sacrum is still incompletely united in early adulthood. Fusion of the sacral segments begin from inferior and progress superiorly, with complete fusion occurring by 24 years for S2/S3 and 33 years for S1/S2 (McKern and Stewart, 1957). A slight gap in the anterior segment between S1 and S2 may persist. This gap could possibly be related to the distance between the two adjacent vertebral bodies (McKern and Stewart, 1957). Passalacqua (2009) combined the developmental indicators of the sacrum (fusion of S1/S2 and S2/S3) with degenerative traits observed for the articular surface of the ilium. The addition of degenerative traits appeared to increase the calculated age intervals (Passalacqua, 2009).

2.1.2. Pubic symphysis

The pubic symphysis currently remains a popular age indicator and has been revisited extensively since Todd's (1920) initial interest (Brooks, 1955; McKern and Stewart, 1957; Acsádi and Nemeskéri, 1970; Meindl *et al.*, 1985; Brooks and Suchey, 1990; Suchey and Katz, 1998; Slice and Algee-Hewitt, 2015; Stoyanova *et al.*, 2017; Joubert *et al.*, 2020). Later methods introduced more natural variation of the pubic symphysis, as the Todd (1920) method described only model phases representative of central tendencies. Methods developed by Katz and Suchey (1986), Meindl *et al.* (1985) and Acsádi and Nemeskéri (1970) describe changes in appearance similar to those from the method developed by Todd (1920, 1921b), but with some adjustment to the number and length of the phases. McKern and Stewart (1957) chose a different approach and adapted the Todd (1920) method by splitting the pubic symphysis into three individual components, which are investigated independently. However, McKern and Stewart (1957) refer to a developmental sequence between the three components, which may imply that the development of the components are not independent of one another. Further development of the pubic symphysis as an age indicator resulted in a series of equations that produce an age estimate when used along with the categorical classification system of the pubic symphysis (Hanihara and Suzuki, 1978; Snow, 1983; Chen *et al.*, 2008, 2011).

The results from different methods of age-at-death estimation from the pubic symphysis are surprisingly different from one another (Jackes, 2000). However, the majority of methods using the pubic symphysis to estimate age-at-death produces better age estimates in younger individuals - under 50 years (Todd, 1920; Gilbert and McKern, 1973; Katz and Suchey, 1986; Klepinger *et al.*, 1992; Berg, 2008; Xanthopoulou *et al.*, 2018). Research found the pubic symphysis to be bilaterally asymmetrical and to vary according to population and sex (Todd, 1920, 1921b; Suchey, 1979; Suchey and Katz, 1998; Schmitt, 2004; Berg, 2008; Chen *et al.*, 2008, 2011). Not only were different structural appearances noticed between males and females, but the pubic symphysis was also modified by pregnancy, parturition, body mass and postmenopausal osteoporosis in females (Stewart, 1957; Kelley, 1979; Suchey *et al.*, 1979; Tague, 1988; Anderson, 1990; Budinoff and Tague, 1990; Snodgrass and Galloway, 2003; Berg, 2008). Some difficulty was noted when differentiating between the build-up and break-down phases of the ventral rampart,

which could potentially result in difficulties with accuracy and repeatability (Brooks and Suchey, 1990; Kimmerle, Prince *et al.*, 2008).

2.1.3. Auricular surface

Lovejoy *et al.* (1985) developed the first method using the auricular surface as an age indicator. Testing of the auricular surface method revealed notable differences between the age distribution of the validation samples (i.e. true ages) and the estimated ages (Murray and Murray, 1991; Jackes, 2000). Many authors attempted to improve the method by introducing adaptations such as adjusting the number of categories (Osborne *et al.*, 2004), dividing the surface into separate components (Buckberry and Chamberlain, 2002; Schmitt, 2005), excluding the retroauricular area (Buckberry and Chamberlain, 2002) or adding information from the acetabulum (Rougé-Maillart *et al.*, 2004). A series of multiple regression analysis equations were also developed in an attempt to improve results (Igarashi *et al.*, 2005). The Buckberry and Chamberlain (2002) method was noted to produce better results in older individuals (82% accurate over 50 years compared to <30% accurate under 50 years) (Xanthopoulou *et al.*, 2018). Although the auricular surface is an area frequently well preserved, high error rates and broad intervals have been noted with poor accuracy and correlations between structural changes and age, as well as bilateral asymmetry (Buckberry and Chamberlain, 2002; Schmitt, 2004, 2005; Michopoulou *et al.*, 2017). The poor accuracy is likely not attributed to description clarity, as good inter- and intra-observer agreement has been reported using specimens and photographs (Michopoulou *et al.*, 2017).

2.1.4. Ribs

The sternal end of the ribs and costal cartilages' relationship with age was described by a number of researchers between 1970 and 1980 (Kerley, 1970; Ubelaker, 1978; McCormick, 1980). İşcan *et al.* (1984b, 1984a, 1985) thereafter converted the age relationship of the fourth rib into a formal age estimation method. İşcan *et al.* 's method (1984a, 1985) was also applied successfully using two- and three-dimensional imaging (Dedouit *et al.*, 2008). Poor preservation and sex differences were notable concerns for this method (Jackes, 2000; Nikita, 2013), as was the narrow age intervals provided (Nawrocki, 2010; İşcan and Steyn, 2013) and the small sample sizes used to construct sex- and population-specific methods (Garvin *et al.*, 2012). The rate of rib changes with age differs between distinct populations and population-specific adjustments were made to the method (Oettlé and Steyn, 2000;

Gocha *et al.*, 2015). In a study using 3D morphometrics to assess structure differences and age at the fourth rib, researchers did not recommend the method due to much individual variability. This notable variability raises concerns about the original fourth rib method. Additionally, the structure of the sternal end differed significantly between the fourth rib and all other ribs, except for rib three (Nikita, 2013). This contradicts previous research that indicated the İşcan method (1984b) could be extended to other ribs as similar changes with age were observed (Dudar, 1993).

A separate method was also developed for age estimation from the first rib. Similar to the fourth rib, the aging pattern of the sternal end is considered along with the rib head and tubercle facet (Kunos *et al.*, 1999). A Bayesian approach was also used to further expand on this method (DiGangi *et al.*, 2009)

2.1.5. Cranial sutures

Cranial sutures as age indicators were one of the first skeletal structures to be investigated and remains an indicator that is frequently researched and used to estimate age-at-death. The popularity of the cranial sutures can likely be attributed to the successful preservation and recovery of the skull, even though the reliability and usefulness of the cranial sutures as age indicators are hotly debated (Brooks, 1955; Powers, 1962; Perizonius, 1984; Key *et al.*, 1994; İşcan and Steyn, 2013). One joint of the skull - the spheno-occipital synchondrosis or basilar suture - seems to perform relatively well when estimating subadult age-at-death (Scheuer and Black, 2000; Bassed *et al.*, 2010; Shirley and Jantz, 2011). However, considerable concerns are raised about the remaining 24 sutures of the skull including their low age correlation and observer agreement, bilateral asymmetry and influencing factors such as muscle attachments and sex (Meindl and Lovejoy, 1985; Key *et al.*, 1994). Additionally, even though sutures are normally categorised into four or five groups of progressive union, Key *et al.* (1994) found only the first and last score to provide significant data for age-at-death estimation. Efforts to improve results from the cranial sutures include substituting endocranial sutures (Todd and Lyon, 1924; Acsádi and Nemeskéri, 1970), modifying the classification of closure (Acsádi and Nemeskéri, 1970), and adding sutures from the facial region (Meindl and Lovejoy, 1985) and the palate (Mann *et al.*, 1991).

Besides cranial sutures, Albert *et al.* (2017) documented other general shape and size changes in the cranium with progressing age. Nikita (2014a) found these types

of changes to be small and not statistically significant. However, as with cranial suture closure, these changes were found to differ between sexes (Nikita, 2014a; Albert *et al.*, 2017).

2.1.6. Arthritic changes

Osteoarthritic and entheseal changes have traditionally been associated with physical activity, but are increasingly being researched for their contribution to age estimation (Milella *et al.*, 2020). Milella *et al.* (2020) found that entheseal changes were highly correlated to age-at-death (r = 0.70 and 0.71), which is comparable to or better than many other age estimation methods including correlations achieved with multifactorial “gold-standards” such as the ADBOU transition analysis method (Bethard, 2005; Jooste *et al.*, 2016; Xanthopoulou *et al.*, 2018; Milella *et al.*, 2020). Sex differences were noted in the performance of entheseal robusticity as an age estimation method (Milella *et al.*, 2020).

Degenerative, osteoarthritic changes of the acetabulum were introduced by Rougé-Maillart *et al.* (2004). The trait and its relationship with age has been thoroughly researched thereafter (Rissech *et al.*, 2006, 2007; Rougé-Maillart *et al.*, 2007, 2009; Calce, 2012; San-Millán *et al.*, 2017). Varied success has been reported for the acetabulum with between 45% and 81% of individuals assigned to the correct age, depending on the method used (Calce and Rogers, 2011; Mays, 2014; Navega, Godinho *et al.*, 2018).

Osteophyte formation on the vertebral bodies occur with age progression (McKern and Stewart, 1957; Watanabe and Terazawa, 2006) and as vertebrae are often well-preserved, they are ideal for age estimation in conjunction with other age indicators (Watanabe and Terazawa, 2006). The vertebral osteophytes likely form due to the degeneration of the intervertebral discs and load bearing activities. The presence and degree of osteophyte formation is likely also modified by posture, motion and metabolic diseases (Watanabe and Terazawa, 2006). The occurrence of vertebral lipping in some instances has been attributed to potential injury, but lipping due to injury is difficult to separate from changes due to mechanical stress without access to medical records (McKern and Stewart, 1957). Osteophyte formation was especially correlated with age in the lumbar vertebrae for males and the thoracic vertebrae for females. Some individuals, regardless of their age, did not present with any cervical osteophyte formation (Watanabe and Terazawa, 2006). Overall, vertebral osteophyte formation is variably correlated with age (between r = 0.34 and r = 0.73) (Jackes,

2000; Watanabe and Terazawa, 2006). Snodgrass (2004) found intermediate phases difficult to assign, which suggests that this indicator could benefit from a reduction of stages.

2.1.7. Microscopic and biochemical analyses

In addition to the macroscopic methods of age-at-death estimation, microscopic and biochemical analysis provide additional insights. Some researchers consider microscopic and biochemical techniques to produce more accurate results (Ritz-Timme et al., 2000; Ubelaker and Khosrowshahi, 2019).

Bone histology, which focuses on the remodelling of the microstructure of bone has been available since 1965 (Kerley, 1965). Recently advances in histological methods include research into additional bones and areas within bones (Streeter, 2012). Bone mineral density has also been found to be strongly correlated to age-at-death (Navega et al., 2018; Botha et al., 2019).

Biochemical analyses focus mainly on modifications to molecules or DNA and chromosomes within the cells and tissues of the bone. Biochemical methods include aspartic acid racemization, lead accumulation, collagen cross-links, Ramon microspectrometry, advanced glycation end products (AGEs), telomere shortening and mitochondrial mutations (Zapico and Ubelaker, 2013, 2016; Freire-Aradas et al., 2016).

As this study only focuses on macroscopic methods of age-at-death estimation, microscopic and biochemical analysis will not be investigated further here.

2.1.8. Biological versus chronological age

The difficulties noted with the age indicators, discussed above, can be related to their relationship with age. An indirect relationship exists between skeletal appearance (sometimes referred to as biological age) and age-at-death (also referred to as calendar/chronological age) (Nawrocki, 2010; Garvin *et al.*, 2012; Uhl, 2013; Sironi *et al.*, 2020). The true relationship exists between skeletal appearance and the effects of biomechanical stress as well as physiological processes, which accumulate with time (i.e., chronological age). Biomechanical stress is influenced by body size, muscularity and activity levels and physiological processes include various and continuous stressors (e.g., oxygen metabolism, nutrient absorption, waste elimination, tissue repair, endocrine activity, immune activity, growth and

reproduction) (Rissech *et al.*, 2006; Nawrocki, 2010; Zukowski *et al.*, 2012; Mays, 2015; Merrit, 2015).

As biomechanical and physiological forces accumulate with increasing age, age estimation becomes less precise. Nawrocki (2010) labelled this the trajectory effect (Figure 2.1). These biomechanical and physiological forces are unique to each individual and magnification with time can cause small cumulative changes to result in different individual appearance in skeletons who share chronological ages. The trajectory effect can obscure the relationship between age and the indicator, especially in more advanced ages. This is reflected, for example, by the minimal correlation between suture closure and ages over 50 years (Nawrocki, 2010).

The consequences of this effect are often noted in archaeological populations, where individuals over 50 years receive an open-ended interval (i.e., 50+ years). This is not due to low incidences of older adults in the assemblage, but rather the inability to estimate age precisely and reliably (Konigsberg and Frankenberg, 1992). However, Milner and Boldsen (2012b) noted that this uncertainty plateaued at around 60 or 70 years of age, after which it decreased slightly. The researchers proposed that this slight decrease in interval length in advanced ages could be due to the effect of selective mortality (Milner and Boldsen, 2012b).

The trajectory effect is not limited to traditional age estimation methods, but is also observed in more modern shape-based quantification methods (Soto *et al.*, 2018). The trajectory effect is also present in linear regression, but the effect could be masked by the error line of best fit, which does not consider areas that are more variable (e.g., advanced ages). Thus, confidence intervals for regression lines can be artificially symmetrical and true error will only be visible if calculated separately for each decade (Nawrocki, 2010).

2.1.9. Skeletal variation/Confounder effect

Only 30% to 70% (r^2-value) of changes observed in the skeleton throughout life can be explained by age, depending on the specific age indicator. This supports the idea of accumulated biomechanical and physiological effects that are indirectly associated with the passage of time (İşcan *et al.*, 1984b, 1985; Jackes, 2000; Igarashi *et al.*, 2005; Nawrocki, 2010; Mays, 2015). Information about possible confounding factors is not always available when creating age-at-death estimation methods. Unless previous studies or experience identified a confounding variable that can be

controlled when developing a method, there is no way of knowing whether an observation has any confounding variables. Confounder effect can be controlled within the study design or statistical modelling (e.g., multiple regression analysis) (Obertová and Stewart, 2020b).

As factors that influence skeletal appearance will differ between individuals and across an individual's lifespan, each individual will have a unique biological age (Rissech *et al.*, 2006; Nawrocki, 2010; Zukowski *et al.*, 2012; Mays, 2015; Merrit, 2015). The variation expressed at individual level can occur as a general anomaly throughout a single skeleton or as one or more anomalous indicators that appears contradictory to the rest of the skeleton (Todd, 1921a; Boldsen *et al.*, 2002; Overbury *et al.*, 2009). Indicators from the left and the right side can also have contradicting appearances (Overbury *et al.*, 2009). For example, asymmetrical aging patterns are documented for the cranial sutures from the facial region (Jackes, 2000) and the pubic symphysis (Overbury *et al.*, 2009; Baccino *et al.*, 2014). Variation should be accounted for by the reference sample, used to develop the method, by incorporating as much individual variation as possible. Additionally, any variation exhibited by the reference sample should be comparable to the variation exhibited in the target population or sample.

The vast variation identified in most age indicators is likely responsible for many observed outliers, which should not be considered abnormal or atypical (Nawrocki, 1998). Eliminating individuals or outliers, for whatever reason, from the reference sample creates an artificial reduction in variability and bias any results obtained from the method (Meindl and Lovejoy, 1985; Katz and Suchey, 1986). Dwight (1878) suggested addressing indicator variability by investigating larger sample sizes, a tactic that remains popular into the 20th and 21st century (Katz and Suchey, 1986; Klepinger and Giles, 1998; Nawrocki, 1998, 2010; Boldsen *et al.*, 2002; Konigsberg *et al.*, 2008). Jackes (2000) elaborates by stating that larger sample sizes minimises the bias that can be introduced when making generalisations from small sample sizes (Jackes, 2000).

Well-known confounders that are responsible for some of the observed variation are sex and population differences. Differences in skeletal appearance between males and females are specifically noted for the pubic symphysis. The ventral rampart is found between the symphyseal face and ventral arc for females, but on the symphyseal face for males (Suchey and Katz, 1998). The pelvis is likely more

sensitive to sex differences as it is structured for habitual bipedalism and additionally facilitates birth in females (Meindl *et al.*, 1985; Tague, 1988; Klepinger *et al.*, 1992). Once sex-specific appearances are accounted for by using distinct methods, the accuracy obtained for both sexes are approximately equal (Nawrocki, 1998; Suchey and Katz, 1998; Igarashi *et al.*, 2005).

Traits have similar appearances in different populations, but differences in rate of progression may occur due to geographic location or time period (Katz and Suchey, 1989; Suchey and Katz, 1998; Hoppa, 2000; Franklin and Flavel, 2019; Franklin and Blau, 2020). Differences in the rate of progression observed between populations could be due to different genetic or environmental factors, such as nutrition, physical activity and disease (Sinha and Gupta, 1995; Suchey and Katz, 1998; Hoppa, 2000; Schmitt, 2004; Uhl, 2013). Some pathologies that can potentially influence the age-related appearance of the skeleton include rheumatoid arthritis, ankylosing spondylitis, Reiter's syndrome and tuberculosis (Kotěrová, 2019). Lifestyle factors, such as body weight or physical activity, could also complicate the age-related information contained within skeletal indicators. Additional biomechanical stress introduced at joints due to excess body weight could result in an older appearance (Merrit, 2015). Similarly, high levels of physical activity can increase the amount of joint degeneration and result in an older appearance (Campanacho *et al.*, 2012; Mays, 2015). Defining populations according to their shared genetic and environmental influences is an oversimplification as people can be transient and populations are dynamic (Franklin and Blau, 2020).

An opinion gaining popularity considers that population variation merely accounts for broader individual level variation and the effects of sample distribution; larger sample sizes instead of population-specific samples are suggested to resolve this (Boldsen *et al.*, 2002; Konigsberg *et al.*, 2008; Soto *et al.*, 2018). This perspective also maintains that even if the rate of change differs between populations, most ages will likely remain accounted for by the broad range of the age interval (Kimmerle, Konigsberg *et al.*, 2008). However, combining multiple populations into a single large reference sample is a relatively new idea and requires additional research (Kotěrová, 2019).

In some cases (Lovejoy, Meindl, Pryzbeck *et al.*, 1985; Kunos *et al.*, 1999; Buckberry and Chamberlain, 2002; Osborne *et al.*, 2004) no explicit differences between populations are observed. However, some populations have more pronounced sex

differences for specific indicators (Nawrocki, 1998; Kimmerle, Konigsberg *et al.*, 2008; Oikonomopoulou *et al.*, 2017; Ubelaker and DeGaglia, 2017). Thus, population specific estimation methods are encouraged by many researchers (Todd, 1921b; Nawrocki, 1998; Suchey and Katz, 1998; Mays, 2015; Xanthopoulou *et al.*, 2018; Franklin and Blau, 2020), as are sex specific estimation methods (Gilbert and McKern, 1973; Jackes, 2000; Ubelaker and DeGaglia, 2017; Franklin and Flavel, 2019). Nevertheless, Falys and Lewis (2011) discovered that not many anthropologists make use of population-specific data, likely as the data are unavailable. Even when these confounders are concluded to have an effect (Acsádi and Nemeskéri, 1970; Gilbert and McKern, 1973; İşcan *et al.*, 1985; Nawrocki, 1998; Suchey and Katz, 1998; Oettlé and Steyn, 2000), the variance they contribute is small (i.e. a few years) compared to the error margin attributed to biological age (i.e., upwards of 20 years in most cases).

2.2. Creating age-at-death estimation methods

Initially, chronological ages associated with skeletal changes were reported as unsubstantiated and oversimplified central tendencies and absolute values in anatomical textbooks (McKern and Stewart, 1957). Formalised age estimation techniques, which emerged during the 1920s, used reference samples to relate grouped skeletal features of similar appearance to age progression (McKern and Stewart, 1957; White and Folkens, 2005; Nawrocki, 2010; Uhl, 2013). When grouping skeletal features into categories (compared to using a continuous scale), some information may be lost, as all individuals grouped into the same category are treated the same regardless of small variations that may occur (Obertová and Stewart, 2020b).

A reference sample is a standard series of skeletal individuals with known age, sex and population affinity (White and Folkens, 2005; Franklin and Blau, 2020). The reference sample can consist of skeletal material, radiographic images from living individuals or coroner based samples (White and Folkens, 2005). Data from the reference sample can clarify relationships between the skeletal feature and age using measures of strength such as correlation, odds or risk ratio. When measuring strength of association, correlation between two variables does not necessarily equal causation as both variables may be associated by an unknown third variable. Furthermore, maximum likelihood point values can be obtained. A maximum likelihood is the maximum probability value calculated from the dataset (Obertová

and Stewart, 2020a). Maximum likelihood values and associated confidence intervals are used to estimate ages for unknown individuals.

In order to produce the best results, the reference sample should be representative of the current modern population. A contemporary population should accurately represent the present living population of the area (Franklin and Blau, 2020). The reference sample and the unknown/target sample should have similar distributions and appearances to obtain the best results (Hoppa, 2000; White and Folkens, 2005; DiGangi *et al.*, 2009; Franklin and Blau, 2020).

2.2.1. Effect of reference sample size and composition

The size and composition of the reference sample is an important consideration as the representation and distribution of each age/age group, as well as confounders (i.e., sex and population), can influence the success of the developed method. Every individual - and by association age group - in a population does not have an equal representation in a reference collection. Reference collection composition may be biased according to social stigma, socioeconomic and education background, age and sex (Franklin and Blau, 2020). Depending on the composition of the selected reference sample, errors from the trajectory effect, confounder effect and age mimicry may be intensified. Error may also be introduced due to possible transcription errors and mistaken or fabricated birth dates in the documentation of early skeletal collections (Scheuer and Black, 2000; White and Folkens, 2005). If deviations from normal distribution are suspected, non-parametric tests, that are robust to outliers, should be used (Sifakis *et al.*, 2020).

The overall sample size used in a research study has direct consequences regarding whether a meaningful effect can be detected, the level of significance possible, the power of the results and the estimates' precision. Small and medium sized samples may erroneously lead to accepting the null hypothesis (i.e. Type II errors) (Sifakis *et al.*, 2020). Larger samples are needed to account for additional variance, as is often observed in the skeleton. Larger samples are also beneficial when categorical variables' distributions favour one category, when categories are unassigned or where multicollinearity is observed (Obertová and Stewart, 2020b). Unfortunately, even large samples produce very few individuals when split by decade, sex and population (Jackes, 2000; Nawrocki, 2010; Buckberry, 2015; Obertová and Stewart, 2020b). Additionally, more extreme values are noted with larger sample sizes as

lower minimum and higher maximum ages frequently accompany larger samples (Konigsberg *et al.*, 2019).

Most collections contain only adults, frequently weighted towards advanced age. A sample with an increased number of older individuals artificially decreases accuracy by intensifying the trajectory effect. An increased number of younger individuals has the opposite effect. For this reason, samples with age distributions weighted towards advanced age will produce unsatisfactory results when tested in the general population.

Furthermore, due to the imperfect relationship between skeletal appearance and chronological age, each age-related stage of a skeletal indicator is not equally strongly associated with chronological age. This results in age intervals that are unequally sized for each stage and consequently different error rates associated with each stage. Practically, these different error rates cause samples with high numbers of young or advanced aged adults to have inflated error rates, whereas more middle-aged adults have decreased error rates – this effect of the reference sample's age distribution on the results is also referred to as age mimicry (Boldsen *et al.*, 2002; Nawrocki, 2010; Franklin and Blau, 2020). Reference sample mimicry often leads to overestimation of young adults and underestimation of old adults (Milner and Boldsen, 2012b). Mimicry of the reference sample is noted when validation samples with similar age distributions are analysed by various methods, with each providing different results. In contrast, validation samples with different distributions, analysed using the same methods, provide similar results (Jackes, 2000). Ideally, reference samples should have a uniform distribution that contains approximately equal numbers of specimens from each decade (Jackes, 2000; Nawrocki, 2010; Buckberry, 2015; Obertová and Stewart, 2020b). The end-points of a uniform distribution (i.e., the minimum and maximum age within the sample) should be carefully considered as they will influence the average age-within-stage for the first and last indicator category when making use of Bayesian analysis. During analysis the end-points should rather reflect the ages represented in each category instead of arbitrary points based on the sample distribution (Konigsberg *et al.*, 2019).

Sampling strategy could also artificially intensify the confounder effect (i.e., sex and population), as larger error margins observed in males compared to females could equally be due to physiological causes or to samples containing more advanced aged males compared to females (Nawrocki, 2010). The sample may also artificially

create population differences that can be attributed to generational and socio-economic status (Uhl and Nawrocki, 2010). A good example of potentially introducing confounder effect through the reference sample is demonstrated by the young male sample used by McKern and Stewart (1957). This all male, young adult sample may include effects from short- and long term prisoner of war conditions (Jackes, 2000).

The fragmentary and damaged nature of the remains frequently investigated (especially the pubic symphysis and sternal ribs), makes preservation bias an important consideration in both the reference sample and the target sample (Saunders *et al.*, 1992; Jackes, 2000; Ritz-Timme *et al.*, 2000; Uhl and Nawrocki, 2010; Baccino *et al.*, 2014). Preservation of the remains may influence the number of indicators available for use on a case-by-case basis. If weakly correlated indicators are the only ones available, due to poor preservation, the final results may be less successful compared to using all indicators from the skeleton. When testing combination methods, the influence of preservation bias on the final results should be considered (Acsádi and Nemeskéri, 1970; Katz and Suchey, 1989; Suchey and Katz, 1998; Jackes, 2000). The recurrence of the cranial sutures as an age indicator in literature, can likely be attributed to the skull's superior preservation (20% and more compared to traits such as pubic symphysis, ribs and auricular surface) and not its accuracy in estimating age-at-death (Jackes, 2000; İşcan and Steyn, 2013).

Although large, representative samples are ideal, the nature of the skeletal reference collections used in forensic anthropology often predefines the available sample size and composition (Obertová and Stewart, 2020b). Sample size is sometimes further constrained by the number of variables needed for each individual, the age range of the sample and the sex distribution (Adalian, 2020). Additional complications also include inaccuracy of the data accompanying the reference sample. This along with the size and distribution of the reference sample can influence the success of the age-at-death estimation method (Klepinger *et al.*, 1992). Annulling methods developed using these collections is impractical, especially considering the small amount of potential error introduced, by the collection, compared to the already tenuous link between chronological age and skeletal indicators (Saunders *et al.*, 1992). Also, including details about sample size and composition (i.e., age, sex and population structure) and standardised statistical procedures could benefit comparability, reproducibility and verification (Ritz-Timme *et al.*, 2000). Likewise, results may be flawed if the sample age distribution is not aligned between the

reference sample and the test sample (i.e., the test sample should have the same age-at-death distribution and mean age as the reference sample). Additionally, although a test sample's size and distribution is an important statistical consideration, any test of a method generates valuable data as the demographic profile cannot be controlled in forensic investigations (Saunders *et al.*, 1992).

2.2.2. Component- versus phase-method

Some methods consider the skeletal indicator in its entirety (Todd, 1920; Katz and Suchey, 1986; Osborne *et al.*, 2004), while others divide the indicator area into distinct components (McKern and Stewart, 1957; İşcan *et al.*, 1984b; Buckberry and Chamberlain, 2002). Component methods are presumed to capture small changes better and prevent indecision when all components do not progress with the same rate in an indicator (McKern and Stewart, 1957; Boldsen *et al.*, 2002).

Component-based methods, for example transition analysis (Boldsen *et al.*, 2002) and those used by McKern and Stewart (1957), have been considered time consuming (Meindl *et al.*, 1985; Brooks and Suchey, 1990; Hurst, 2010). However, Buckberry and Chamberlain (2002) considered using a component-based method easier to apply. This may be supported by the fact that the component-based method is considered more objective and less dependent on observer experience (Shirley and Ramirez Montes, 2015). Additionally, Brown (2010) concluded that the McKern and Stewart method improved precision. A major concern when considering multiple components of an indicator (whether components of the McKern and Stewart pubic symphysis method or combining multiple suture segments) is the resulting loss of information in the combination process; some components are likely better indicators than others, but all are equally weighted when producing a summed score (Lucy *et al.*, 1996; Nawrocki, 1998). Additionally, component-based methods work on the assumption that the individual components are only associated with one another through age (i.e., no intercorrelation exists). However, relationships between the components may be more complex (McKern and Stewart, 1957).

Conversely, phase-based methods (i.e., Todd (1920) and Suchey-Brooks (1986)) have been considered more user-friendly and efficient, especially with the addition of casts (Meindl *et al.*, 1985; Brooks and Suchey, 1990; Hurst, 2010). Additionally, Brooks and Suchey (1990) maintain that the individual components do not contain independent variation and Brown (2010) concluded that the Suchey-Brooks phase-based method improved accuracy.

Existing literature provides no firm conclusions as to whether the component- or phase-based method is more appropriate or easier to use.

2.3. Recognising error and evaluating success

Following the Daubert court case ('Daubert versus Merrel Dow Pharmaceuticals Inc', 1993), scientific queries such as method testability, peer review, potential error rates and method acceptability gained more strength in forensic testimony compared to expert qualifications (Ousley and Hollinger, 2012; Sifakis *et al.*, 2020). Thus, success became synonymous with accuracy, precision and reliability. Reliability considerations include the intra- and interobserver differences for a method. Accuracy expresses how close the estimated results are to the true value and precision refers to the width of dispersion around an estimated result. Accuracy and precision, sometimes collectively referred to as validity, should consider the performance of the method in distinct samples, the confidence in the relationship between the skeletal feature and age and also the amount that confidence is influenced by other factors (i.e., confounders) (Tabachnick and Fidell, 2001; Adalian, 2020; Obertová and Stewart, 2020b). Unfortunately, a reliable method is not always a valid method. A method that can be reproduced well does not necessarily generate high accuracy and precision (Obertová and Stewart, 2020b). Similarly, a high accuracy and precision are seldom both achievable as one is usually at the expense of the other (Buckberry, 2015).

Accepted error from the mathematical perspective considers the differences between the calculated and true value. Error in the context discussed here is closely associated with accuracy and precision (i.e., expected bias and imprecision) and should not be confused with practitioner error or mistakes (Christensen *et al.*, 2014; Sifakis *et al.*, 2020). In adult age-at-death estimation, a degree of imprecision is expected as discrete categories partition the entire lifespan into a small number of wide segments (e.g., six phases of the Suchey-Brooks method). Additionally, each category contains a degree of variation that is unrelated to age. This variation within each category may eclipse the age-related information in age increments smaller than a decade (Nawrocki, 2010).

The inevitable error that accompanies age estimation methods should be recognised, quantified and minimised (where possible). Estimates may be biased if confounders are not accounted for, misclassification occurs or if selection bias was present in the

reference sample. Even when bias is present, unbiased results can be obtained by mitigating the effects using statistical modelling. Additionally, some differences will naturally occur between the estimates produced for a target sample compared to the overall population (represented by the reference sample). These errors (i.e., the differences between the sample estimates and the population) should not be represented by a point estimate only. A 95% confidence interval, which expresses the precision of the estimate and the variation within the population, can be calculated using the standard error. A 95% confidence interval would include 95% of the population related to the assigned score. Confidence intervals only account for sampling variability in the population, not for systemic bias (Obertová and Stewart, 2020b).

Once the inherent error associated with estimating chronological age from the skeleton was recognised, it was expressed as much larger age intervals. Age intervals expanded from approximately five years (Todd, 1920, 1921b; McKern and Stewart, 1957; İşcan *et al.*, 1984b; Lovejoy, Meindl, Pryzbeck *et al.*, 1985) to up to 20 years (Suchey and Katz, 1998). An appropriate interval, for a forensic setting, is calculated from a 95% prediction interval. A prediction interval corresponds to the likelihood of an unknown individual, from the same population as the sample, to be included in a category. The 95% prediction interval should be published for each typological category of the aging method and not only for the series as a whole (Nawrocki, 2010) and should not merely consist of two standard deviations (Klepinger *et al.*, 1992). Nawrocki (2010) states that calculating an appropriate error interval may render previously dismissed indicators, such as the cranial sutures (Brooks (1955) and Powers (1962)), comparable with other indicators. Many researchers consider these large interval estimates too imprecise for a forensic setting (Saunders *et al.*, 1992; Ritz-Timme *et al.*, 2000; Brown, 2010; Stull and James, 2010; Uhl, 2013).

Dispersion error from regression analysis is often quantified as the standard error of the estimate (SEE), which indicates dispersion for the entire regression line and a 95% prediction interval for individual estimates (Nawrocki, 2010). A 95% prediction interval can only be calculated as ± 2 SEE if the sample is large and normally distributed (Klepinger and Giles, 1998; Nawrocki, 1998). Constructing an interval that truly represents 95% of the population requires not only the SEE of the regression, but also the category number assigned to the individual (x), the mean category for

the sample ($\bar{x}$), the sample variance for the category (s^2), the sample size (n) and the t-distribution with n – 2 degrees of freedom (t) to be substituted in the formula $\pm t \cdot SEE \sqrt{1 + \frac{1}{n} + \frac{(x - \overline{x})^2}{(n-1)s^2}}$ (Klepinger and Giles, 1998). Measures of covariance (r and r^2) and dispersion (SEE) can provide some accuracy and interval information respectively, but are inadequate to inform about individual calculated estimates (Ritz-Timme *et al.*, 2000; Nawrocki, 2010).

Although reporting error provides valuable information about a method, comparing multiple methods' results can prove even more informative. Multiple measures of error provide more comparison points with other studies (Saunders *et al.*, 1992; Jackes, 2000; Ritz-Timme *et al.*, 2000; Nawrocki, 2010). Jackes (2000) alternatively suggests providing the raw data in matrix form for comparison purposes and subdividing it by sex, population and laterality to understand confounders.

2.3.1. Validation studies

Assessing and reporting a method's ability to make predictions and generalisations using an independent sample is a necessity in a forensic context (Grivas and Komar, 2008; Adalian, 2020; Obertová and Stewart, 2020a; Sifakis *et al.*, 2020). Validation studies test and improve existing methods and novel age indicators as a crucial component of ensuring forensic integrity (Russel *et al.*, 1993; Ritz-Timme *et al.*, 2000; Schmitt, 2004; Schmitt and Murail, 2004; Kurki, 2005; National Research Council, 2009; Ousley and Hollinger, 2012; Buckberry, 2015; Slice and Algee-Hewitt, 2015; Jooste *et al.*, 2016). The most rigorous of these tests use entirely independent samples (i.e., different from the reference sample) (Nawrocki, 1998; Suchey and Katz, 1998; Milner and Boldsen, 2012b). The tests consider among other things subjectivity in classification, reducing inaccuracies and imprecision and fostering standard methods and scientific rigor (Ritz-Timme *et al.*, 2000; Grivas and Komar, 2008; Holden, 2009; Buckberry, 2015). A large amount of research also considers the suitability of the methods to distinct (in either time or location) population groups as discussed in section 2.1.8 (Oettlé and Steyn, 2000; Schmitt, 2004; Gocha *et al.*, 2015; Jooste *et al.*, 2016; Xanthopoulou *et al.*, 2018).

Some validation studies confirm that certain age indicators outperform others (Jackes, 2000; Gocha *et al.*, 2015; Jooste *et al.*, 2016; Xanthopoulou *et al.*, 2018). It is generally accepted that the pubic symphysis outperforms results from most other indicators and that cranial sutures are the least reliable age estimator (Jackes, 2000;

Scheuer, 2002; Cunha *et al.*, 2009; Garvin and Passalacqua, 2012; İşcan and Steyn, 2013; Gocha *et al.*, 2015). Additionally, some researchers conclude that some age indicators have a greater affinity for a specific age interval. This can be attributed to the variation in precision achieved throughout the adult lifespan (Acsádi and Nemeskéri, 1970; Meindl *et al.*, 1985; Galera *et al.*, 1998; İşcan and Steyn, 2013; Baccino *et al.*, 2014). Other researchers take this even further and specify that certain skeletal indicators only contribute information about a specific stage of the aging process (Galera *et al.*, 1998; Xanthopoulou *et al.*, 2018). The pubic symphysis optimally informs about ages 20 to 40/50 years (Todd, 1920; Xanthopoulou *et al.*, 2018). Distinct methods developed for the same indicator could also be preferentially suited to a specific stage of the adult lifespan – for example, the Buckberry and Chamberlain (2002) auricular surface method is more suited to adults older than 50 years, while the Osborne *et al.* method (2004) is more suited to adults younger than 50 years (Gocha *et al.*, 2015; Xanthopoulou *et al.*, 2018). This is also true for various cranial suture methods, which each exhibits varying success for non-overlapping age intervals; where Masset's (1989) endocranial method is more suited to individuals younger than 20 years and then again for individuals between 60 and 65 years, while the Acsádi and Nemeskéri (1970) method is more suited to individuals between 21 and 25, as well as older than 66 years (Galera *et al.*, 1998). Although some literature attributes this to the suitability of the indicator and/or specific method to a specific age interval, other literature ascribes this to the influence of the sample distribution (i.e., age mimicry as discussed in section 2.2.1). For this reason, the target and reference samples' age distribution should be similar.

Some researchers (Ritz-Timme *et al.*, 2000; Rősing *et al.*, 2007) suggest that methods achieving intervals larger than ± 14 years are unsuitable. They conclude that skeletal indicators (i.e., pubic symphysis and cranial sutures) only supply a rough assessment and recommend aspartic acid racemization and histology to improve assessments. The results of many validation studies confirm that adult age-at-death estimation methods produce broad and overlapping age intervals and a number of researchers have indicated that only three very broad categories may be possible (Falys and Lewis, 2011; Buk *et al.*, 2012).

Additionally, researchers sometimes choose preferred methods subjectively (e.g., for familiarity instead of statistical substantiation). Thus, even methods that are

commonly considered inaccurate (i.e., cranial sutures) remain recommended in literature (Ritz-Timme *et al.*, 2000; Garvin and Passalacqua, 2012).

2.4. Potential solutions

2.4.1. Reliability/Observer agreement

The probability of introducing error during classification of categorical variables is high, as classification contains a notable amount of subjectivity (Zeman and Beňuš, 2020). Observer consistency is influenced by the experience of the observer and their amount of practice with the method (Baccino *et al.*, 1999; Kimmerle, Prince *et al.*, 2008). Additionally, categories associated with younger ages are considered more repeatable due to their more consistent changes with age progression. Overall, the appearance of each skeletal indicator can vary quite substantially within each category compared to the available description. Thus, the skeletal appearance as described for each category is not rigidly attributed to the specific category, but is in a constant state of transition as expected for a continuous biological process such as aging (Kimmerle, Prince *et al.*, 2008).

Some researchers suggest that precision can be improved through improved classification success and observer agreement. Standardising methods and classification systems could improve observer agreement (Baccino *et al.*, 1999). Attempts to improve the classification system often lead to reducing the number of categories (Katz and Suchey, 1986; Osborne *et al.*, 2004; Rissech *et al.*, 2006; DiGangi *et al.*, 2009). Drastic reduction to binary (i.e., present or absent) categories is sometimes employed (Igarashi *et al.*, 2005; Passalacqua, 2009; Stull and James, 2010). Passalacqua (2009) found that scoring indicators as binary present-absent traits increased correlation with age, potentially due to increased observer agreement. Other researchers add categories, frequently representing the most advanced age groups in the hope of improving the uncertainty that is affiliated with this group (Berg, 2008; Hartnett, 2010).

Slice and Algee-Hewitt (2015) and Stoyanova *et al.* (2017) consider the subjective nature of the categories the biggest obstacle in age estimation. Difficulty recognising the appearance of consecutive categories is supported by the disappointing observer agreement obtained for indicators as varied as the pubic symphysis, ribs and cranial sutures (Saunders *et al.*, 1992; Kimmerle, Prince *et al.*, 2008). Classification systems that are inadequately represented by descriptions and images alone, could benefit

from a three-dimensional model system that reduces observer error (Suchey and Katz, 1998). Alternatively, contemporary research investigates quantifying the shape changes that occur on the indicator surfaces (i.e., pubic symphysis) (Slice and Algee-Hewitt, 2015; Stoyanova *et al.*, 2017) or to bone mineral density (Navega, d'Oliveira Coelho *et al.*, 2018; Botha *et al.*, 2019) as an age estimation model.

Although a continuous scale could improve accuracy and estimation error, aside from the abovementioned quantitative methods, difficulties exist when attempting to convert degenerative descriptive categories into a continuous scale (Nawrocki, 2010). Furthermore, results from categorical and continuous indicators may be equally imprecise (Soto *et al.*, 2018), as age often accounts for less than half of the changes to the skeletal appearance as discussed in 2.1.7 (Nawrocki, 1998; Jackes, 2000; Osborne *et al.*, 2004; Igarashi *et al.*, 2005; Mays, 2015). Even with some category disagreement between observers, age intervals remain wide enough that not much accuracy difference is noted (Kimmerle, Prince *et al.*, 2008).

2.4.2. Combining indicators

Literature regularly recommends combining multiple skeletal indicators due to the limitations of single skeletal indicators as age estimators (Brooks, 1955; Saunders *et al.*, 1992; Suchey and Katz, 1998; Matrille *et al.*, 2007; Uhl and Nawrocki, 2010; Baccino *et al.*, 2014). When combining multiple indicators into one method, it is important to understand the relationship between each indicator and age and also the relationship between indicators, as the unique effects of individual indicators may be more difficult to analyse once they are combined (Jackes, 2000). Conditional independence between skeletal indicators (i.e., only age effects the relationships between indicators) is often assumed. This is not biologically realistic as body parts are rarely independent from each other. Perpetuating this assumption could lead to overly narrow age estimates, which may exclude the true age of the deceased (Sironi *et al.*, 2020). The correlation between single indicators could be studied appropriately using a correlation matrix. Unfortunately, a correlation matrix requires an enormous reference sample (Boldsen *et al.*, 2002). Multiple indicators should also be studied jointly, especially if the indicator's appearance is influenced by multiple factors (i.e., age, activity level, sex, population etc.), as the combined results may exhibit more complex interactions such as information sharing (Henderson and Nikita, 2016; Sifakis *et al.*, 2020).

Multiple regression analysis can be a useful statistical tool when confounders are present. However, multicollinearity within a multiple regression model causes large changes to the model's indicator coefficients and proportion of variance in response to small changes in the reference data. In cases where multicollinearity is not complete - such as between age indicators - the reliability of the model is not reduced but predictions are effected (Obertová and Stewart, 2020a)

Most researchers consider that combination methods can only perform as well as the single indicator methods used to compile them (Osborne *et al.*, 2004; Milner and Boldsen, 2012b; İşcan and Steyn, 2013). However, some researchers consider that combining a more accurate indicator with a less accurate indicator could reduce the quality of the estimation (Saunders *et al.*, 1992; Matrille *et al.*, 2007; Jooste *et al.*, 2016), while others conclude that each skeletal indicator may contribute information about a specific aspect of the aging process and even a poor indicator could notably contribute (Brooks, 1955; Johnson, 1976; Meindl and Lovejoy, 1985; Brooks and Suchey, 1990; Baccino *et al.*, 1999; Uhl and Nawrocki, 2010). Thus, combining skeletal indicators has the potential to include low information indicators, which contain very little information individually (e.g., under or over 20 years), but contribute to the combined age estimate (Milner and Boldsen, 2012b; İşcan and Steyn, 2013; Boldsen and Milner, 2018). Although it is possible to include all age indicators in a multifactorial model, mathematically and practically a model should contain only informative indicators (Sifakis *et al.*, 2020).

The most basic method of combining indicators considers the averages of the age estimates produced by individual indicators (further referred to as the averaging method). This method is often selected by researchers when combining individual indicators (Garvin and Passalacqua, 2012), possibly as it is more simplistic but also less statistically founded. The averaging method may conceal the effects of atypical indicators in the individual and could lead to broader intervals and less effective estimates. Unfortunately, averaging does not produce statistically substantiated prediction intervals, as individual error margins (i.e. standard deviations) are not additive (Uhl and Nawrocki, 2010).

Prediction intervals for multiple indicators could potentially be generated by using the overlapping error intervals for individual indicators or using more complex statistical methods such as regression analysis (Nawrocki, 1998, 2010; Garvin and Passalacqua, 2012). Although using the overlapping error intervals (Figure 2.2) is not

a statistical construct, the simplicity of the method is appealing to many researchers (Garvin and Passalacqua, 2012). It is important to note, if only using the minimum overlap, imperfect overlap may exist that could exclude one or more indicators (Figure 2.3). Suchey and Katz (1998) maintain that total overlap should be used, especially for methods developed using small sample sizes.

Linear regression and principal components analysis weigh each skeletal indicator according to individual contribution (i.e., regression coefficient) and produces error intervals, while remaining easy to apply. The disadvantages of regression analysis include the dependence of having all indicators available, considering age-related skeletal changes on a continuous scale instead of the more appropriate ordinal (categorical) scale and enforcing the obligatory linear model even though the pattern of skeletal age progression is likely not linear (Jackes, 2000; Uhl and Nawrocki, 2010). One proposed solution is creating multiple equations with fewer and differently combined indicators to compensate for the unique conditions of each case (Saunders *et al.*, 1992; Ritz-Timme *et al.*, 2000; Uhl and Nawrocki, 2010); this is unfortunately counterproductive to introducing standardised estimation methods (Jackes, 2000).

Similarly, Lovejoy, Meindl, Mensforth *et al.*'s (1985) multifactorial method investigates the relationships between multiple variables of the skeleton and provide weightings depending on the proportion of overall information represented by each indicator using principal component analysis. This method provides a cumulative percentage of variation using the indicators with the highest variability (i.e., eigen-values), and at the same time accounts for variation present in the remaining variables. True age, confounder influence and direct correlation between indicators do not seem to be accounted for in this statistical method. The effect of adding weakly associated indicators (i.e., cranial sutures) to the multifactorial method is unclear, especially since preservation bias may have contributed to the regularity with which certain indicators were used. A central tendency for each calculated age-at-death estimation is used in the principal component analysis and the variance explained by each indicator is calculated. Lovejoy, Meindl, Mensforth *et al.* (1985) use the percentage variance explained by each indicator as a weighting to calculate a final combined age-at-death estimate. In a separate study, weighing age indicators according to principal component analysis correlation with chronological age noted that accuracy only improved by a maximum of 0.8 years compared to simple averaging of the individual indicator results (Saunders *et al.*, 1992).

The likelihood ratios used in Bayesian analysis makes this method particularly suitable to combining multiple skeletal indicators into a single model. In order to combine multiple skeletal indicators, each indicator needs to relate to the same research question (e.g., this pubic symphysis belongs to a 20-year-old; this skull belongs to a 20-year-old etc.). If multiple indicators are used, each indicator could be used to update the prior probability distribution of the subsequent indicator (i.e., a pubic symphysis estimated to be between 20 and 40 years old becomes the prior probability of 20 to 40 years when assessing the data from the auricular surface, etc.) In order to combine indicators in such a way, using Bayesian analysis, indicators should be either independent or conditionally independent of one another (Berger *et al.*, 2020). The benefits and limitations are discussed in more detail in section 2.4.3 as Bayesian analysis is not exclusively used in combination methods but has also received much attention for its role in improving age estimation using individual indicators.

A method called the two-step procedure uses a completely different approach to combining multiple indicators. The method's premise considers that although information from multiple indicators should be combined, combining methods developed using various distinct reference samples and mathematical approaches is not sound. The two-step procedure combines two separate individual methods - the Suchey-Brooks pubic symphysis method (1990) and the Lamendin dental method (1992). During the first step the Suchey-Brooks method is used to decide whether the remains belong to a young adult (phases I - III) or a mature adult (phases IV - VI). An individual that is classified as Suchey-Brooks phase I to III, is allocated the age estimate attributed to the Suchey-Brooks phase without employing any further methods. An individual classified as Suchey-Brooks phase IV to VI is reassessed using the Lamendin method in what is known as the second step. The two-step method produced better results than either of the individual methods alone (i.e., Suchey-Brooks or Lamendin alone) and showed similar accuracies when compared to a principal component analysis (Baccino *et al.*, 1999, 2014; Matrille *et al.*, 2007). The complex method developed by Acsádi and Nemeskéri (1970) follows similar principles, where the pubic symphysis stage is established initially and then used as a weighting factor for the age estimates produced by the cranial sutures, humerus and femur in the second step of the method.

In a method comparison study by Uhl and Nawrocki (2010), the averaging method slightly improved the accuracy and bias compared to standalone skeletal indicators and had the added benefit of being relatively easy to use. In the method using the minimum overlap of the intervals, 62% of ages were correctly predicted with some age intervals as small as two years. Contrastingly, intervals produced by the maximum overlap often included the entire range of ages, but allowed for 100% correct prediction. Inaccuracy of the regression point estimate resembles the averaging method and the intervals included the correct age in 66% and 95% of cases (depending on the level of confidence used) (Uhl and Nawrocki, 2010).

Although a combination of multiple skeletal indicators for estimating age-at-death is ideal, a scientific, quantitative and easily applied method to do so remains elusive. Additionally, the quality of the individual indicator methods determine the effectiveness of a combination method, requiring continued refinement of the methods as well as the statistics involved (Uhl and Nawrocki, 2010; Baccino *et al.*, 2014). Sample sizes also need to be adjusted when combining multiple indicators as small samples cannot account for multiple predictors and may fail to identify statistically significant effects (Henderson and Nikita, 2016).

2.4.3. Statistics

As validation studies (e.g., Russel *et al.* (1993), Schmitt and Murail (2004), Kurki (2005) and Jooste *et al.* (2016)) frequently find low accuracies when assessing existing methods, research has turned to ever more sophisticated statistical techniques to minimise and account for error (Boldsen *et al.*, 2002). A statistical model should be informative regarding the uncertainty in the relationship between biological and chronological age (Nawrocki, 1998; Boldsen *et al.*, 2002; Passalacqua, 2010; Sironi *et al.*, 2020). However, scientific validity depends on appropriate method selection, analytical rigor and correct interpretation of results in addition to statistical methods (Klepinger and Giles, 1998; Adalian, 2020). Some researchers remain unconvinced that sophisticated statistics can improve method accuracy without considering sample similarities and population specific information about the human aging process (Jackes, 2000).

Methods using phase-based classifications that report a central tendency (i.e., mean) and interval (i.e., standard deviation) remain popular. Many of these phase-based methods are based on linear regression principles and thus assume a linear relationship between the skeletal indicator and age (Kotěrová, 2019; Sifakis *et al.*,

2020). Regression analysis is widely used and requires variables that are independent, and with normality and homogeneity of the residuals (Sifakis *et al.*, 2020). As mentioned above, oversimplifying the relationship between the skeletal indicator and age could lead to overestimating younger ages and underestimating older ages and also age mimicry of the reference sample (Konigsberg and Frankenberg, 1992; Lucy *et al.*, 1996; Boldsen *et al.*, 2002).

Phase-based methods, discussed above, rely on frequentist statistics to describe the potential frequency of an outcome within the wider population (Adalian, 2020; Obertová and Stewart, 2020a). The frequentist approach assumes that with an infinite sample, predictions can be made without any doubt. A Bayesian approach incorporates randomness into the analysis. Thus, regardless of sample size, probabilistic statements can be made (Sifakis *et al.*, 2020). Consequently, Bayesian methods have been increasingly investigated for their potential to improve age estimates from already existing phase-based methods (Langley-Shirley and Jantz, 2010; Godde and Hens, 2012; Bullock *et al.*, 2013; Uhl, 2013; Hens and Godde, 2016). Bayesian analysis combines prior information about age distributions within the population with likelihood functions calculated from the reference data (Obertová and Stewart, 2020a). A likelihood function makes use of observed data to model the relationship between skeletal appearance and age (i.e., biological and chronological age). The prior information, or prior probability, together with observational data produce a posterior probability (Sironi *et al.*, 2020).

Lucy *et al.* (1996) claim that Bayesian analysis are better suited to ordinal data, predominantly used in adult age estimation, compared to other statistical methods such as multiple regression analysis, as it negates assumptions such as linear and continuous representation of age and parametric distribution of residuals (difference between expected and observed values). Bayesian analysis improves average accuracy and decreases 95% confidence intervals according to Lucy *et al.* (1996). The use of the 95% confidence interval has the additional benefit of eliminating open ended age estimates (i.e., 50+ years), albeit replacing them with often-times large intervals (Bethard, 2005; Milner and Boldsen, 2012b; Jooste *et al.*, 2016). The Bayesian method is also reported to minimise age estimates mimicking the age structure of the reference sample (as discussed in 2.2.1) (Konigsberg and Frankenberg, 1992; Boldsen *et al.*, 2002; Konigsberg *et al.*, 2008).

Age estimation that requires outcomes expressed as continuous age or a number of age groups is considered more complicated when applying a Bayesian approach compared to binary elements (Berger *et al.*, 2020). Bayesian analysis also contains a host of assumptions that require fulfilment. Bayesian analyses are sensitive to assumption violation and may produce poor results if all the following assumptions are not met. Firstly, the informative prior and target sample (i.e., validation sample or unknown deceased) should contain a similar distribution. If a similar distribution is not possible a uniform distribution may be a possible solution (Nikita *et al.*, 2018). The use of a uniform prior distribution ensures that the reference sample's distribution is not imposed (as seen in age mimicry cases mentioned in section 2.2.1), but a uniform prior distribution could yield potentially poor age estimation results as it places disproportional weight on the extremely old ages (Milner and Boldsen, 2012b; Nikita *et al.*, 2018). A uniform prior distribution is still considered preferential to an informative prior that uses the information from the test sample to both calculate the prior distribution and estimate age (Boldsen *et al.*, 2002). Secondly, Bayesian models make use of probit or logit regression models; there is little practical difference between these models but they should describe the reference data well (Sironi *et al.*, 2020). A good fit between the reference data and the probit or logit regression model is more easily achieved if the reference sample is relatively large and all descriptive categories (i.e., transition stages) are sufficiently represented (Nikita *et al.*, 2018; Nikita and Nikitas, 2019). Lastly, the log age distribution of the reference sample should follow a normal distribution. Only if all the above assumptions are fulfilled will age mimicry be reduced and age estimations improve compared to traditionally used methods (Nikita *et al.*, 2018).

Introducing a prior probability requires information in addition to the skeletal appearance or arbitrary assumptions. Without a prior probability, only a likelihood ratio based on observational data is possible and not posterior probabilities, as a posterior probability includes all available background information, observations about the skeletal appearance and expert knowledge. Alternatively, the likelihood ratio can be reworked to refer to specific discrete age intervals. This method foregoes making posterior probability predictions in a continuous random variable format and allows quantification of uncertainty in situations where additional (i.e., prior probability) information is scarce (Sironi *et al.*, 2020).

A Bayesian method for estimating age-at-death was first developed by Konigsberg and Frankenberg (1992). Thereafter a Bayesian approach was implemented by many researchers (DiGangi *et al.*, 2009; Langley-Shirley and Jantz, 2010; Godde and Hens, 2012; Bullock *et al.*, 2013; Tangmose *et al.*, 2015; Hens and Godde, 2016; Nikita *et al.*, 2018). Transition analysis – a well-known and heavily researched method of the 21st century – is also considered Bayesian in nature as prior information (i.e., a prior distribution) is used to calculate the highest posterior density probability distribution (i.e., age-at-transition modified with prior information), which can be used as a point age estimate. A percentage of the distribution can also be calculated to provide an interval (similar to a confidence interval) (Boldsen *et al.*, 2002; Milner and Boldsen, 2012b).

Prior distributions modify information from the reference sample (preferably similar to the demographic profile of the unknown population or validation sample) with document-based information. Documentary information about the age distribution of the general population is available for a number of countries. Information modelling age-at-death is not necessarily more suitable to a forensic context as this information often refers to natural causes. Thus, experience and logical thinking are crucial when choosing a prior probability (Berger *et al.*, 2020). If the prior distribution is derived from the distribution of the validation sample or a sample with a similar demographic profile, the reference sample bias (i.e., age mimicry) can be reduced but not completely eliminated (Uhl, 2013; Nikita and Nikitas, 2019). In cases where prior information is unavailable, a noninformative prior probability can be introduced. A noninformative prior could take the form of a uniform distribution. In a uniform distribution all possible age values in a range are considered equally likely and age values outside of the range are not possible. While uniform priors have been shown to be reasonable in some scenarios, posterior conclusions should be minimally dependent on these prior probabilities (Sironi *et al.*, 2020). Incorrect predictions result if mismatched distributions are introduced or if a uniform distribution is used as an informative prior distribution (Uhl, 2013; Nikita and Nikitas, 2019). The effect of the prior distribution is influenced by the strength of the observational data (Berger *et al.*, 2020). It was also noted that, when the Bayesian method's performance is acceptable the informative prior distribution has a small impact on the overall performance. However, when the Bayesian method's performance is poor the

informative prior has a large, significant impact on the prediction, but fails to improve the age estimation (Nikita *et al.*, 2018).

Alternatively, the prior distribution could be used to introduce information based on personal experience of the scientist. This is particularly useful if seemingly no background data is available to choose more specific prior distributions. This data can take the form of unpublished data or data from reference studies (Klepinger and Giles, 1998; Sironi *et al.*, 2020).

Thus, the crucial experience component should not be discarded. Experience is an often-used aid (whether consciously or not) to assist with age-at-death estimation (Garvin and Passalacqua, 2012; Milner and Boldsen, 2012b). Experience assists with decisions about single skeletal indicators that deviates from the majority pattern (due to normal variation, trauma, physical activity etc.), adding information from low information traits and refining age intervals (Saunders *et al.*, 1992; Suchey and Katz, 1998; Nawrocki, 2010; Milner and Boldsen, 2012b).

The transition analysis method, developed by Boldsen and Milner (2002), makes use of numerical categories from the pubic symphysis, auricular surface and cranial sutures individually or in combination. However, the transition analysis method is continuously updated with additional reference information and broader skeletal indicator information such as vertebral lipping, sternal rib ends, the medial clavicle and changes associated with the humerus and the femur are included in version 3 of the scoring manual and software program available from https://www.statsmachine.net/software/TA3/. A category description can be selected for both the left and the right side, as well as multiple adjacent categories if the distinguishing features are ambiguous. It is unclear whether these multiple data points (from the left/right side and adjacent categories) are averaged or both included. Including numerous data points that represent a single indicator could artificially weigh the results towards those indicators.

Likelihood functions are calculated using generalized linear models with a probit/logit link (Boldsen *et al.*, 2002). Generalized linear models extend the capabilities of ordinary linear regression to include non-normal distributions. Generalized linear models include three elements: 1) a probability distribution for the response variable (the variable being calculated), 2) a linear predictor and 3) a link function that provides the relationship between the linear predictor and the mean of the distribution

function. Generalized linear models are satisfactory for ordinal or scale responses, but generalized estimating equations are suggested for paired samples. Generalized estimating equations and generalized linear mixed models are extensions of generalized linear models that allows for correlated observations and individual variable contributions to the outcome respectively (Nikita, 2014b; Obertová and Stewart, 2020a). Henderson and Nikita (2016) found that generalized linear models did not fare well if reference samples were small, but could potentially be improved by increasing the width of the age intervals considered. This is similar to the solution that considers the vast intrinsic variability observed when using traditional methods, as discussed in section 2.3.

Transition analysis accounts for information from skeletal indicators as well as the mortality characteristics of the population, by using a prior age distribution (i.e., a modification of the estimate based on documentary information that provides the likelihood of death at each age in a specific context). Milner and Boldsen (2012b) noted that the choice of prior distribution (their method allows for archaeological or forensic contexts) influenced the final result, but was overshadowed by the inaccuracy and imprecision of the age estimates. Jackes (2000) reports that age distributions created using Bayesian methods – and by extension transition analysis – are more heavily influenced by the prior probabilities and are ineffective at replicating the true age-at-death distribution of the population under study. The effect of the prior probability on the estimated age-at-death distribution is intensified if the iterative proportional fitting technique is used in the statistical method as suggested by Bocquet-Appel and Masset (1996) and Konigsberg and Frankenberg (1992) (Jackes, 2000).

Continuous refinement between the reference sample and the prior distribution is required to improve age estimation results through optimal alignment with the validation/unknown sample (Nikita *et al.*, 2018; Xanthopoulou *et al.*, 2018). Accuracy and precision may be increased when the reference sample is the same as the validation/test sample or if data from the validation sample is used to modify the model. In cases where this was not implemented, Nikita and Nikitas (2019) found results from simple regression models to outperform the Bayesian statistical approach. Nikita and Nikitas (2019) demonstrated that regression analysis was also capable of reducing reference sample distribution bias (i.e., age mimicry) by either including weighted factors from the demographic profile of the target sample or

constructing a reference sample with a similar demographic profile to the validation sample. These two regression analysis approaches outperformed the Bayesian method in 90% of the scenarios studied. Similarly, when using a reference sample with a uniform distribution (which is widely recommended in the literature), or the reference sample and validation sample demographic profiles match, simple regression analysis was found to outperform Bayesian approaches (Nikita and Nikitas, 2019).

The verdict is still out regarding the best statistical methods to estimate age, as less complex methods frequently outshine methods such as transition analysis. In a study that compared various statistical approaches, linear regression produced the smallest amount of error, using the sacrum, compared to approaches including decision tree regression, a component-based method and principal component analysis (Passalacqua, 2010). Multiple indicators provide similar results, with multiple linear regression outperforming an interval-based model, K nearest neighbours, artificial neural network, decision tree and probabilistic models (Kotěrová *et al.*, 2018). However, the results produced by using regression models have been questioned due to the potential bias introduced (see the masking of the trajectory effect and also bias introduced by the reference sample collection in section 2.2.1) (Bocquet-Appel and Masset, 1982; Nikita and Nikitas, 2019).

As transition analysis is reported to minimise this bias associated with other methods (including regression analysis as mentioned above), some authors claim that transition analysis is currently the best method for age estimation (Konigsberg and Frankenberg, 1992; Boldsen and Milner, 2018). However, various tests of the transition analysis method has produced relatively low accuracies and correlation values (Bethard, 2005; Bullock *et al.*, 2013; Jooste *et al.*, 2016). A comparison of the transition analysis (Boldsen *et al.*, 2002), McKern and Stewart (1957) and Suchey-Brooks (1986) methods of pubic symphysis age estimation, revealed that the Suchey-Brooks method (i.e., a phase-based method) achieved the highest percentage accuracy (Hurst, 2010). The addition of the cranial sutures and auricular surface to the pubic symphysis slightly improved the results achieved using the transition analysis method (Hurst, 2010). This contrasts with observations by Jooste *et al.* (2016) that indicated adding cranial sutures to the combined method decreased interval accuracies in some instances. Unfortunately, Hurst's (2010) sample composition (more males, many subadults and young adults) may have affected the

accuracies. The young ages in the sample could be especially problematic, as the methods tested can only estimate ages above 15 and 18 years respectively. Additionally, the researchers noted that the transition analysis method was encumbered by the uncertainty of ancestry as well as the narrow context applied to the forensic prior distribution (i.e., only applicable to homicide) (Hurst, 2010).

Nikita *et al.* (2018) agree that Bayesian analysis does not necessarily lead to significant improvement compared to traditional methods (the auricular surface methods by Lovejoy, Meindl, Pryzbeck *et al.* (1985) and Buckberry and Chamberlain (2002) in this instance). Using a transition analysis approach yielded little to no improvement in either of the two Greek samples tested despite, testing the method by using one sample as both the target sample and the reference sample and also including a suited informative prior (from documented ages of the target assemblages). The authors observed sex differences impacted their results, as well as the demographic information of the reference sample impacted the age-at-transition parameters constructed in their method. Thus, the reference sample should be aligned to the target sample or unknown deceased according to time period, geographic location and population group. The authors do go on to clarify that some variation with these parameters were observed, but that the actual impact on age estimation should be small as the transition analysis calculations are not particularly sensitive to demographic considerations of the reference sample (Nikita *et al.*, 2018).

In a separate study on Greek assemblages, Xanthopoulou *et al.* (2018) concluded similarly that the well-known transition analysis method (Boldsen *et al.*, 2002) in general produced less accurate results than traditional methods of the cranial sutures (i.e., Meindl and Lovejoy (1985)) and pelvic joints (i.e., Lovejoy, Meindl, Pryzbeck *et al.* (1985), Katz and Suchey (1986) and Buckberry and Chamberlain (2002)) even though the accuracy improved with younger adults. The transition analysis results improved when the three features were combined, as reported by Hurst (2010), but it was also noted that although the pubic symphysis and auricular surface also provided accurate estimations, the cranial sutures alone provided the least accurate estimations (Xanthopoulou *et al.*, 2018). Xanthopoulou *et al.* (2018) also noted inter- and intra-population variation as well as sex differences related to the accuracies obtained with methods from the pelvic joints and cranial sutures (regardless of the nature of the statistics). High observer agreements lead the authors to conclude that

the inadequate accuracy and reliability of the tested methods were not related to recording errors (Xanthopoulou *et al.*, 2018).

An unfortunate side effect of the powerful statistical potential of both transition analysis and other Bayesian methods is the necessity of the original reference data as well as large computational power and specialized software, which makes these methods less accessible (İşcan and Steyn, 2013; Buckberry, 2015; Nikita *et al.*, 2018; Obertová and Stewart, 2020a; Sironi *et al.*, 2020). Bayesian Networks (probabilistic graphical models) may simplify the analytical handling of Bayesian models, especially in models where multicollinearity exists (Sironi *et al.*, 2020). Despite its limitations, Bayesian methods (including transition analysis) have useful aspects that are not available in many other methods. The method allows for combination of different skeletal indicators and can accommodate missing or deliberately omitted category values (Nikita *et al.*, 2018). The models also enable consecutive categories to be collapsed or removed without effecting the transition curves of the remaining categories (Konigsberg *et al.*, 2019; Sironi *et al.*, 2020). This could be beneficial as many skeletal indicators contain a number of age-related category steps that may overlap with each other and lead to inconsistencies associated with generic developmental categories. Although a number of studies conclude improved accuracy and precision using frequentist statistics compared to Bayesian analysis, researchers are increasingly considering Bayesian analysis as the most appropriate approach to forensic casework (Obertová and Stewart, 2020a; Sironi *et al.*, 2020). This may change again as more research is conducted into alternative measures of frequentist inference success over the p-value approach, which has long been considered inadequate. Alternatives include using confidence intervals, effect size and degree of compatibility (Sifakis *et al.*, 2020).

It can thus be concluded that the complexity of the statistics alone may not improve accuracy without combining effective skeletal traits (Hurst, 2010; Jooste *et al.*, 2016) and much needed changes that replace visual classification methods with methods such as 3D bone models, mathematical quantification of surface changes and machine learning methods (Kotěrová *et al.*, 2018). Some researchers even conclude that, regardless of the statistical tools used, without a novel skeletal indicator that is more strongly correlated to age, age estimations are certain to remain broad (Lucy, 2010). Other researchers remind us that although statistically impressive results may

be academically applauded, a forensically applicable method also needs to consider how user-friendly, cost-effective and time efficient a method is (Baccino *et al.*, 2014).

2.5. Figures

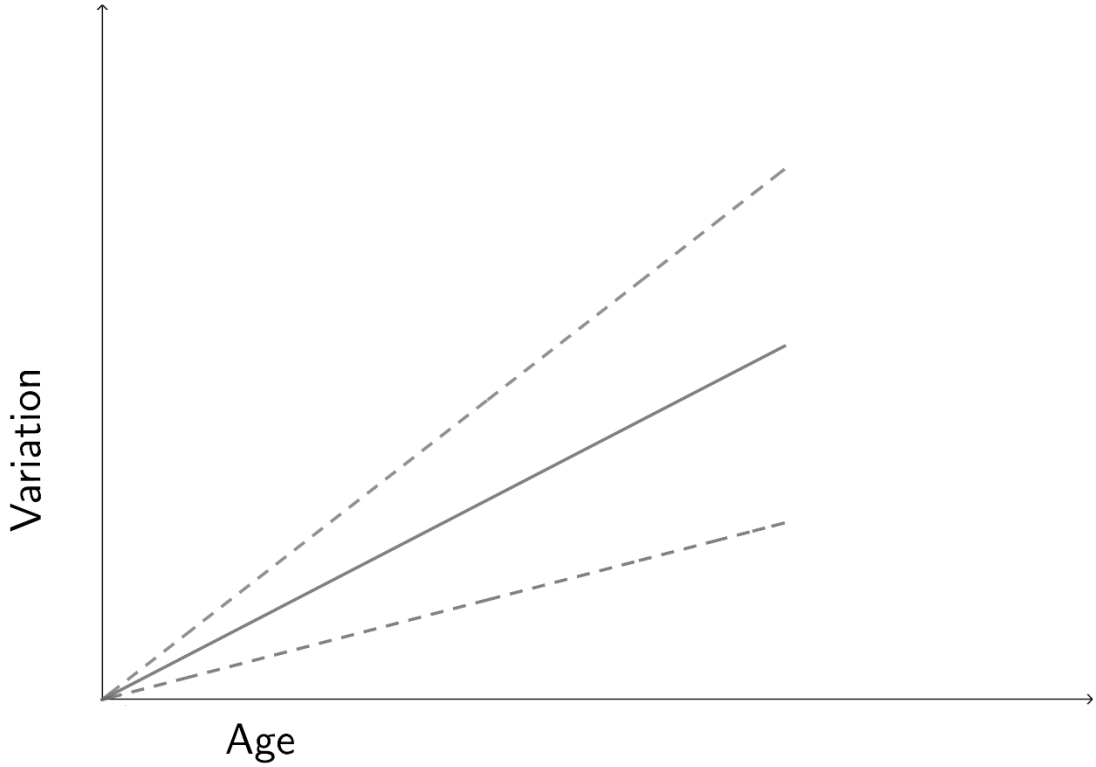


Figure 2.1: Trajectory effect increases error around the mean with increasing age. [Graph produced by N Jooste]

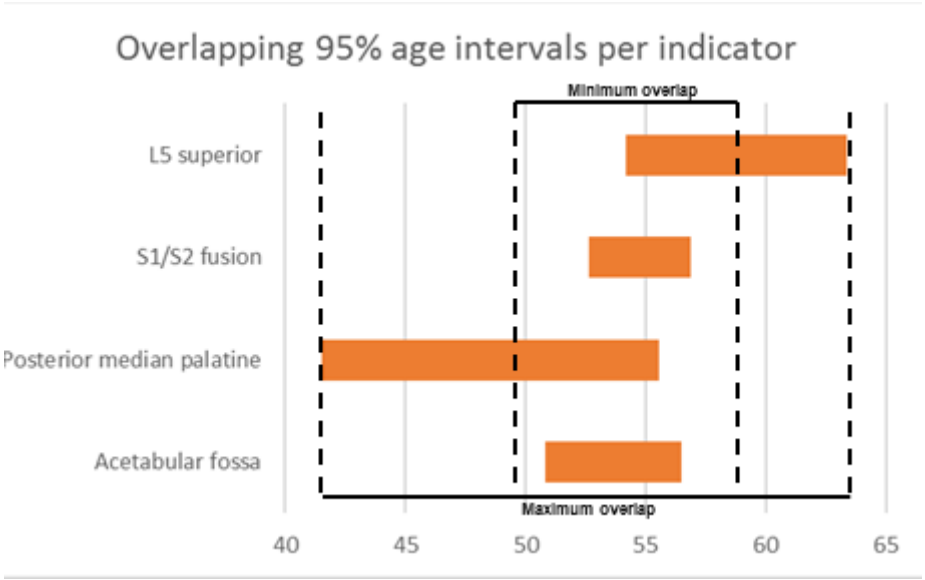


Figure 2.2: Combining the 95% age intervals of multiple indicators can be approached in two ways. Maximum overlap incorporates the full intervals of each indicator. Minimum overlap includes the interval between the average of all minimum values and the average of all maximum values. [Graph produced by N Jooste]

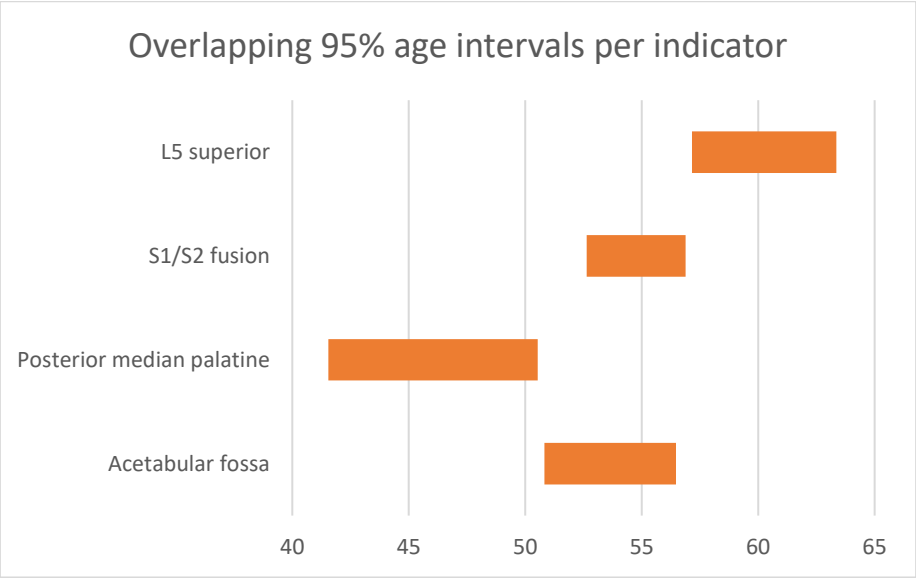


Figure 2.3: The 95% age intervals of multiple indicators within a single individual does not always overlap. In this case it would be impossible to create an interval from minimum overlap. [Graph produced by N Jooste]

CHAPTER 3: MATERIALS AND METHODS

3.1. Materials

The Raymond A Dart Collection of Human Skeletons (Dayal *et al.*, 2009) was used to construct a skeletal reference sample. The collection is housed in the School of Anatomical Sciences at the University of the Witwatersrand and comprises over 2500 human skeletons with documented demographic profiles (i.e., age, sex and population affinity), collected from the early 1920s to the present. The skeletal material originates from cadavers previously dissected within the School and are sourced from both unclaimed bodies from the Gauteng Provincial hospitals and bodies bequeathed to science (collected according to the Human Tissues Act 65 of 1983 (Republic of South Africa, 1983) and the National Health Act 61 of 2003 (Republic of South Africa, 2004)). Information about the availability and completeness of the cranium and mandible is available, but none exists for the postcranial remains. Unfortunately, in 1959, the locale of the collection was flooded and many of the remains became commingled (Dayal *et al.*, 2009). As the provenance of remains before the flood remains uncertain, only remains accessioned after 1960 were used in this study.

Any shortfall in the skeletal sample was supplemented with material from the Pretoria Bone Collection (L'Abbé *et al.*, 2005). This research collection, housed in the Department of Anatomy at the University of Pretoria, has been growing since 1943 and includes information about the age, sex and population affinity of the sample, as well as whether the skull and postcranial skeleton are complete. Remains are acquired in a similar manner as those in the Raymond A Dart Collection of Human Skeletons (in accordance with the Human Tissues Act 65 of 1983 (Republic of South Africa, 1983) and the National Health Act 61 of 2003 (Republic of South Africa, 2004)).

The nature of both skeletal reference collections introduced some limitations to the study. The source and composition of these skeletal collections contribute potential bias to the sample concerning the age, sex, health and socioeconomic representation, but this bias was minimised by appropriate sample selection as explained below.

Remains were not excluded from the sample due to absent or damaged skeletal features as this would severely limit the sample size. Figure 3.1 shows the sample

size, reflecting the fact that each skeletal indicator was not equally represented. The sample size ranged from 178 for total complete vertebral bodies, to 322 for iliac crests. Data represented in Figure 3.1. are conservative as only indicators containing all components were included in the sample counts depicted, even though partially complete indicators were also documented (i.e., individually available vertebrae were documented, but only included in the count if all vertebrae (C3 – C7 and L1 – L5) were available). The sample sizes of the cranium, pubic symphysis and vertebral bodies may limit the power of statistics conducted. However, this was considered when building the predictive models and often only single components from these features were included. The sternal end of the fourth rib was documented, but due to very low sample numbers (N < 20) was excluded from the study.

The selection of a sample that equally represents each decade and sex is crucial. A method developed from a sample dominated by older individuals contains a much larger error (associated with older ages) that artificially decreases the accuracy of the method. A method developed from a sample dominated by younger individuals artificially inflates the accuracy of the method, but the method is ultimately less accurate in a population with a wider age construct (Nawrocki, 2010). A total of ±330 skeletons were selected from a South African Black population to equally represent each decade and sex (Figure 3.2). The most recent additions (after 1960) to the collections were preferentially selected to represent the current population that would be encountered in forensic investigations. These are also groups that may potentially benefit from improved demographic documentation methods and exclude remains affected by the flooding of 1959 (Dayal *et al.*, 2009). Although the possibility exists for some erroneous information within the collections, this occurrence was minimised by using more recent additions to the collections.

The sample was confined to include only South African Black individuals as they represent the majority (approximately 80%) of the South African population according to the 2011 census statistics (Statistics South Africa., 2012). As a result, a large, uniformly distributed sample size was obtained as South African Black individuals are well-represented in each decade in the collections. Ancestry categories in the collections were self-reported, in the majority of cases, or from medical records (L'Abbé *et al.*, 2005; Dayal *et al.*, 2009).

The sample's age construct starts at 20 years as suggested by Falys and Lewis (2011) for onset of adulthood. The final selected decade remained open-ended to

include individuals over the age of 80 years; this allowed for much needed information about variation during the final decade(s) of life, but also ensured adequate numbers for the underrepresented final categories. Although each category contained a small number of individuals, all age groups were combined into a single age-at-death category for analysis.

3.2. Methods

To ensure ease-of-use and repeatability of methods and results, a set of established age-related changes associated with bilateral and median skeletal indicators were selected from the literature. Stage-based methods (which use the feature in its entirety) are considered less complicated, more repeatable and less influenced by surrounding components (Meindl *et al.*, 1985). Component-based methods (which separate a feature into individual parts) allow assessment of more individual variation (Suchey *et al.*, 1986; Dudzik and Langley, 2015). Although both methods have their merits, methods that are frequently used by South African scientists or were developed on South African samples received preference (Jooste and Steyn, 2016). The performance of component- versus stage-based methods was evaluated and thus both types of classification methods were included for the pubic symphysis.

The following age-related structural changes were considered: epiphyseal closure of the medial clavicle and iliac crest from Scheuer and Black (2000), cranial suture closure from Nawrocki (1998), Mann *et al.* (1991) and Boldsen *et al.* (2002), vertebral osteophyte formation from Stewart (1958) and van der Merwe *et al.* (2006), sacral segment fusion from McKern and Stewart (1957) and Passalacqua (2009), auricular surface transformation from Boldsen *et al.* (2002), acetabulum transformation from Rissech *et al.* (2006) and pubic symphysis transformation from Katz and Suchey (1986), Brooks and Suchey (1990) and Boldsen *et al.* (2002) as indicated in Figures 3.3 to 3.5.

The subjectivity of the age-related changes was minimised as much as possible by using detailed category descriptions and illustrations/photographs that accompanied the original publications. Binary features such as the iliac crest, the medial clavicle (identified as unfused (1) or fused (2)) and vertebral bodies (identified as osteophytes absent (1) or osteophytes present (2)) were less subjective and less complex to classify. Regions with more age-related variation optimally contain a maximum of six categories (the approximate number of decades in the adult lifespan) to obtain

prediction intervals of at least ten years. If the prediction interval within a category becomes less than ten years, the large variation result in overlapping categories (Nawrocki, 2010). This study combined any minimally represented stages (i.e., n ≤ 5 or < 2% of sample) with adjacent stages. Minimally represented stages identified were associated with the end stages (i.e., stages 1, 4 or 5) and were combined with adjacent stages to incorporate maximum variation, whilst maintaining optimal predictive value. As the stages were from the end categories, the overall result was the reduction of the number of stages for the acetabular fossa, auricular surface morphology, pubic symphyseal relief, pubic dorsal margin, pubic ventral margin, pubic symphysis (Suchey-Brooks stage-based method) and some cranial sutures including the incisive, superior, and inferior sphenotemporal, zygomaticomaxillary and anterior median palatine sutures. The data and the stages that were collapsed to obtain population-specific stages for each feature are further discussed in Chapter 4, section 4.4. The modified category descriptions and accompanying photographs, as used in this study, can be found in Figures 3.6 – 3.10.

Each skeletal feature was classified according to appearance, using descriptions in Figures 3.6 – 3.10, to document data about the relationship of age with each stage. A hold-out sample (n = 30) was reclassified by the primary observer (intra-observer agreement) as well as by a second observer (interobserver agreement). Both observers are equally experienced with osteology theory and practice, but the primary observer had more experience with the methods developed for this specific study at the time of data collection. The primary investigator only provided the classification descriptions to the second observer and no further guidance was provided. Observers collected data completely independent of one another with approximately a month in between interobserver data collection and approximately two days in between intra-observer data collection.

The features were considered on a skeleton-by-skeleton basis, however, each feature was considered separately and conflicting information was documented as observed (i.e., without adjustments based on observations from other regions). Only the age-related appearance of the skeleton was observed and classified into stages during data collection; the actual age of the skeletons was only revealed later, during statistical analyses (i.e., blind collection). Skeletal material was made available in a random fashion by an individual other than the primary investigator and any age-at-death information associated with the skeletons were hidden or removed during data

collection. Unfortunately, due to logistical restrictions within the collection and the size of the sample, age indicators could not be considered individually. However, all attempts were made to record separate scores for each indicator or component.

3.3. Data analysis

Firstly, IBM SPSS Statistics version 25 was used to calculate descriptive statistics (sample size, mean, median, minimum, maximum and 95% confidence interval) per stage of each skeletal feature. Categories represented by less than five individuals (<2% of the sample population) were considered incapable of contributing sufficient data to draw definitive predictive conclusions. This minimally representative data were combined with that from adjacent categories to incorporate information about these minor population variations as described in section 3.2 above. Descriptive statistics were recalculated for the modified stages.

From the descriptive statistics, boxplots representing the sample within each category were constructed to consider any outliers. Outliers were investigated for any documented pathologies or clear evidence of erroneous ages. The raw data recording sheet was also examined as difficult or problematic skeletons and indicators were documented during the data collection process. In general, outliers were concluded to be representative of normal biological variation and all were retained to include information about minor population variations.

General assumptions were tested before proceeding with any predictive statistical computations. Shapiro-Wilk normality tests were conducted for all features to determine whether parametric or nonparametric tests were more suitable for further statistical consideration. All features were non-normally distributed; thus, all statistical calculations were conducted using strictly non-parametric tests.

Intra- and interobserver agreement (n = 30) were analysed using a Cohen's kappa test. Cohen's kappa compares the agreement between two classification attempts (i.e., either two scoring attempts by the same observer or a scoring attempt from two observers each) with that of pure chance (i.e., were repeat classifications worse than, equal to or better than chance guessing). Cohen's kappa values were further analysed according to the scale proposed by Landis and Koch (1977), with observer agreement achieving Cohen's kappa values > 0.6 considered good.

Additionally, Cohen's kappa test values were compared to weighted Cohen's kappa test values. The weighted Cohen's kappa test takes the number of categories of

disagreement into account (i.e., did agreement differ by one or more categories) (Zeman and Beňuš, 2020). If the kappa value improves from the Cohen's kappa test to the weighted Cohen's kappa test, this indicates a disagreement over fewer categories (e.g., one stage differences versus four stages differences).

As data were collected from right and left bilateral features, a Wilcoxon signed-rank significance test was conducted to determine if significant differences exist between the two sides. Differences between the median values from the right and left features of the skeleton were not significant, and all further statistical calculations were conducted using only features from the left to prevent introducing bias by "double weighting" bilateral features as would be the case if both left and right sides were included.

A Wilcoxon signed-rank significance test was also conducted to consider the differences between median values from the superior and inferior rim of each vertebral body and the adjoining rims of adjacent vertebral bodies. Median values of vertebral rims from both tests were significantly different and all regions were retained for further statistical calculations.

Possible differences between median values for male and female groups were assessed using the Mann-Whitney U significance test. Categories of the auricular surface of the ilium, the pubic symphysis, vertebral bodies and cranial sutures were significantly different between male and female groups. Thus, all further calculations were conducted using both the pooled and separate groups for males and females.

Linear and non-linear regression calculations were conducted for each of the selected features. The r-values and r^2-values from non-linear regression calculations were never more than 0.1 larger than those for the linear regressions; linear regression was thus preferred for its simplistic approach and interpretation. Features were also combined using sequential/hierarchical multiple linear regression. Sequential addition of each independent variable/group of variables considers the added variation they explain within the dependent variable (i.e., age). Sequential multiple linear regression allowed construction of an equation with a useful level of prediction, while selecting only independent variables that contributed significantly to the proportion of variance in age. Multiple linear regressions were conducted on combined and separate male and female groups.

The R statistical package (version 3.4.3), with additional VGAM and xlsx packages were used to calculate generalized linear models with a logit link function (also known as transition analysis) for each of the selected regions for pooled and separate male and female groups. The proportions of the sample population represented in each category at a specific age were then predicted using the intercept and the slope of the logistic regression model and graphic representations were generated using Microsoft Excel 365.

Data from the validation sample were entered (i.e., the scores attributed to each individual in the validation sample) to obtain a maximum likelihood estimate of the logit regression function (i.e., the likelihood function) that represents the average age-at-transition for each specific individual. The likelihood function was then combined with a prior probability function using Bayesian analysis to obtain a posterior probability (also known as a probability density function), which can be considered a probability estimate of the most likely age-at-death. In this study, a uniform distribution was selected to represent the prior probability. The uniform distribution attributes equal likelihood to all ages between 20 and 100 years. The uniform distribution is suited to the chosen distribution for both the reference and validation samples. Each skeletal indicator was handled as conditionally independent (i.e., only related by age) and the likelihood functions from multiple indicators could therefore be multiplied. This statistical model was constructed by modifying code written for the software program R by L Konigsberg, which was available at http://konig.la.utk.edu (the website unfortunately no longer exists). Data were adapted from the original code was reconfigured for programming in GNU Octave; this code is available in Appendix A.

3.4. Validation Study

Age-related data were gathered from a hold-out test sample (n = 30) from the Pretoria Bone Collection, in an identical manner to the reference sample. The hold-out sample contained a similar uniform distribution to the original reference sample, with as close to equal numbers of skeletons from each decade and sex as possible. However, obtaining adequate numbers of very young and very advanced ages was difficult (the sample distribution is illustrated in Figure 3.2). The full complement of skeletal features was classified twice on each skeleton in the validation sample by the primary investigator and once by a second researcher to assess observer

agreement. The researchers collected the data independently from one another and on separate occasions.

The validation data (hold-out sample) were analysed and the results compared using the three calculation methods created with the initial reference data. The first method applied basic statistics produced using the reference sample (i.e., mean ages and 95% confidence interval ranges per stage of each skeletal feature). The mean ages from each selected skeletal feature were averaged to obtain a point estimate. Both a narrow and wide age interval was constructed using the first method. The narrow age interval averaged both the lower and upper interval values obtained from the reference sample, while the wide age interval used the outer bounds of the interval values (i.e., included all values between the minimum and the maximum interval value), as previously illustrated in Figure 2.2.

The second calculation method produced point estimates and age intervals using multiple linear regression equations selected for statistical significance over the mean model (F-statistic) and the most variance explained (r^2-values). As with the first method, a narrow and wide age interval were constructed. The narrow interval made use of a 95% confidence interval (a narrower interval is obtained as the values only refer to the generalised population), while the wide age interval made use of a 95% prediction interval (a wider interval is necessary when inferences are made at the individual level).

The third calculation method produced point estimates (maximum likelihood values) and age intervals (95% confidence interval) using the transition analysis model constructed in R (version 3.4.3) and explained in 3.3 above.

The same skeletal age indicators were used for all three methods for comparative purposes. The decision about which indicators to combine arose from results interpreted for the linear regression equations. Regression analysis was chosen as the starting point for indicator selection as method one (i.e., basic descriptive statistics) does not contain information about indicator interactions and method three (i.e., transition analysis) requires substantial increases in computational data for each indicator added into the combination method.

The first criterium considered for including an age indicator in the combination method was intercorrelation, as it is undesirable for indicators in a multifactorial method to influence one another. A correlation matrix was calculated to identify

coefficients above 0.7, which are considered undesirable. In general, indicators were selected with the lowest between indicator correlation and the highest correlation with age.

The second criterium considered for including an age indicator in the combination method was statistical contribution to the multiple regression equation ($p < 0.05$; see Chapter 4: Results, section 4.6). This was analysed in a sequential manner by adding or eliminating potential indicators on merit of their statistical contribution until a final complement of indicators was reached.

Using the hold-out validation data (n = 30), point estimates and confidence intervals were calculated using the three calculation methods explained in section 3.2 (i.e., reference sample basic statistics, multiple linear regression and transition analysis). Point estimates were evaluated for bias (difference between the calculated and true age) as well as inaccuracy (absolute difference between the calculated and true age). Mean bias provides information about consistent under- or overestimation using a specific method, whereas mean inaccuracy provided information about the average distance between the calculated and true age. As a method can only be considered as good as its most inaccurate estimate, information about the maximum inaccuracy for each calculation method was also provided.

Age intervals were calculated, for each of the 30 individuals, using the three calculation methods. Age intervals were evaluated using the mean and maximum width of each method's range (i.e., precision) and also the percentage of true ages contained within the calculated age intervals (i.e., accuracy). As an age interval is more desired during forensic investigation, particular attention was given to the interval width and accuracy of each methods' age interval.

The merit of each method was considered based on the accuracy of the point estimate and interval generated for the hold-out validation sample and also for the precision (i.e., widths) of the intervals achieved. Accuracy and precision values were also compared for combined versus separate male and female models to assess whether sex-specific models improve outcomes.

3.5. Ethics

An ethics waiver (number W-CJ-140604-1), shown in Appendix B, was granted for this study. This waiver applies to studies conducted on material in collections housed

in the School of Anatomical Sciences that were donated for the purposes of training and research.

Permission for access to the Raymond A Dart Collection of Human Skeletons and the Pretoria Bone Collection was granted by the relevant curators (Appendices C and D).

3.6. Figures

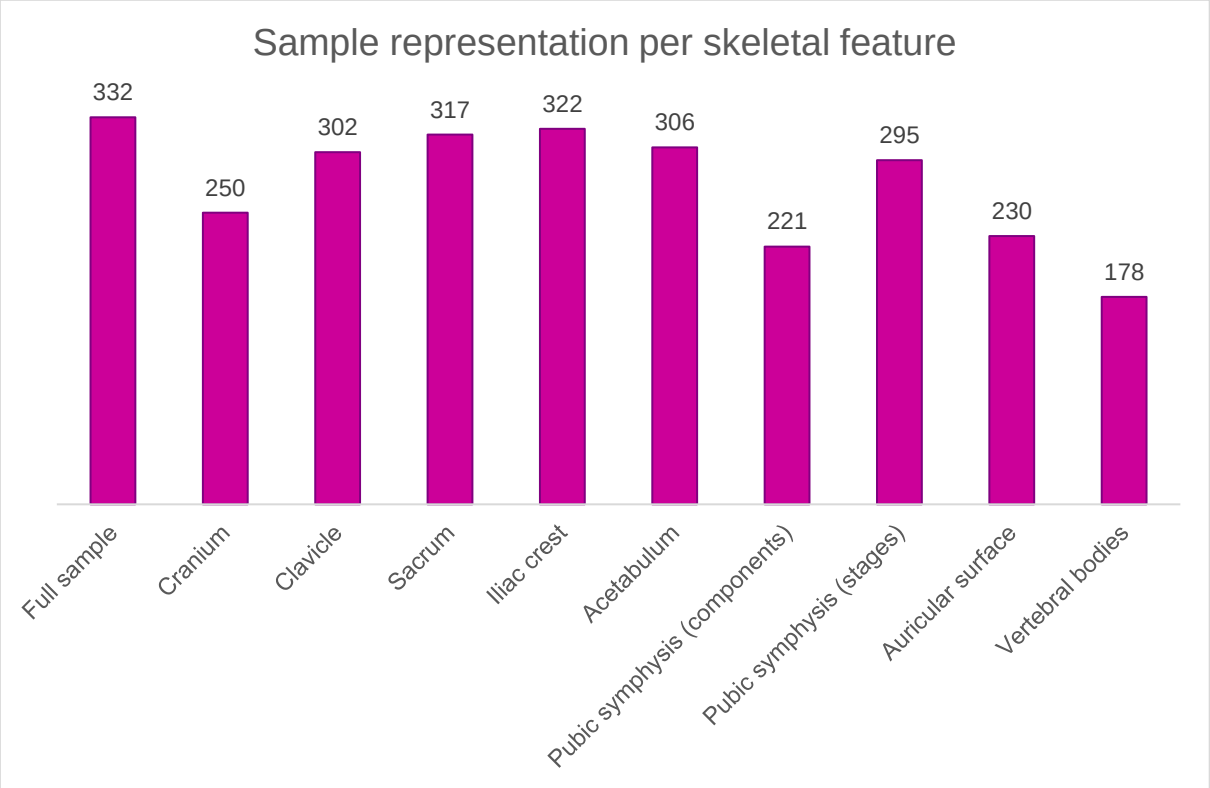


Figure 3.1: Sample size per feature with all components present (Total N = 332).

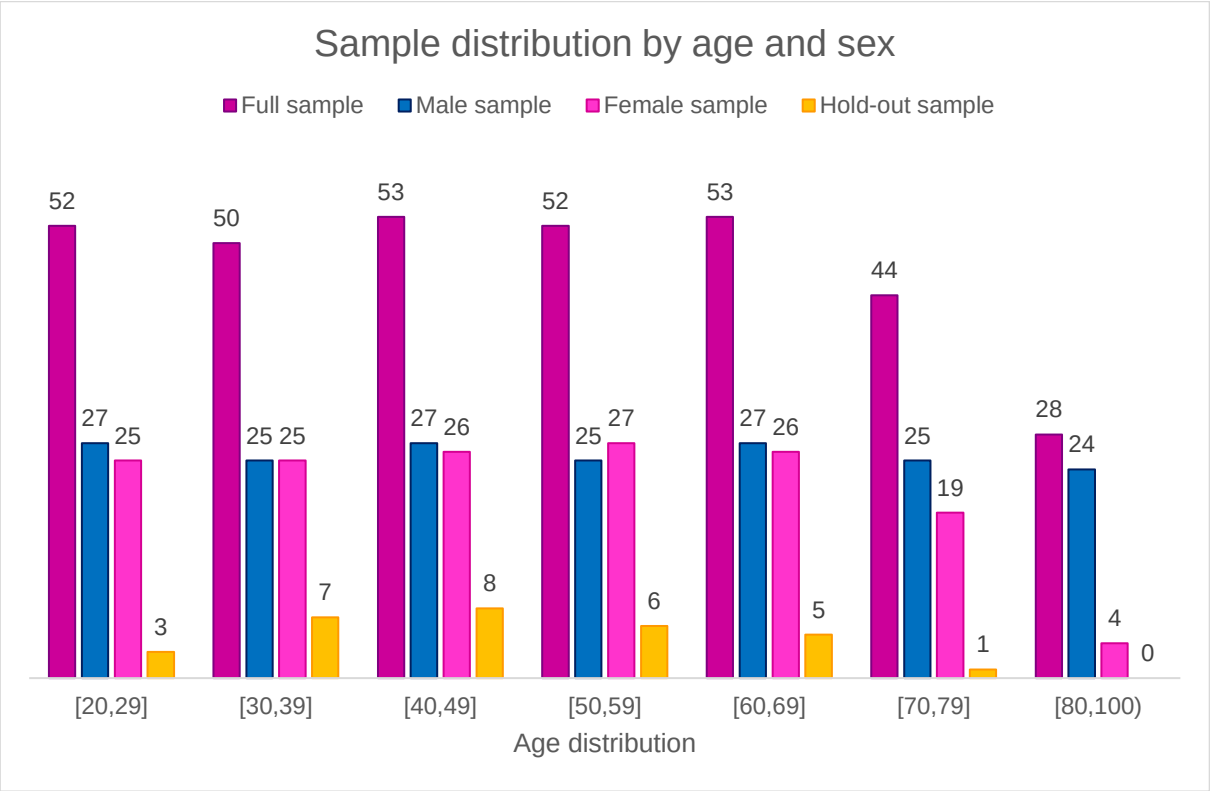


Figure 3.2: Sample distribution for each decade and sex.

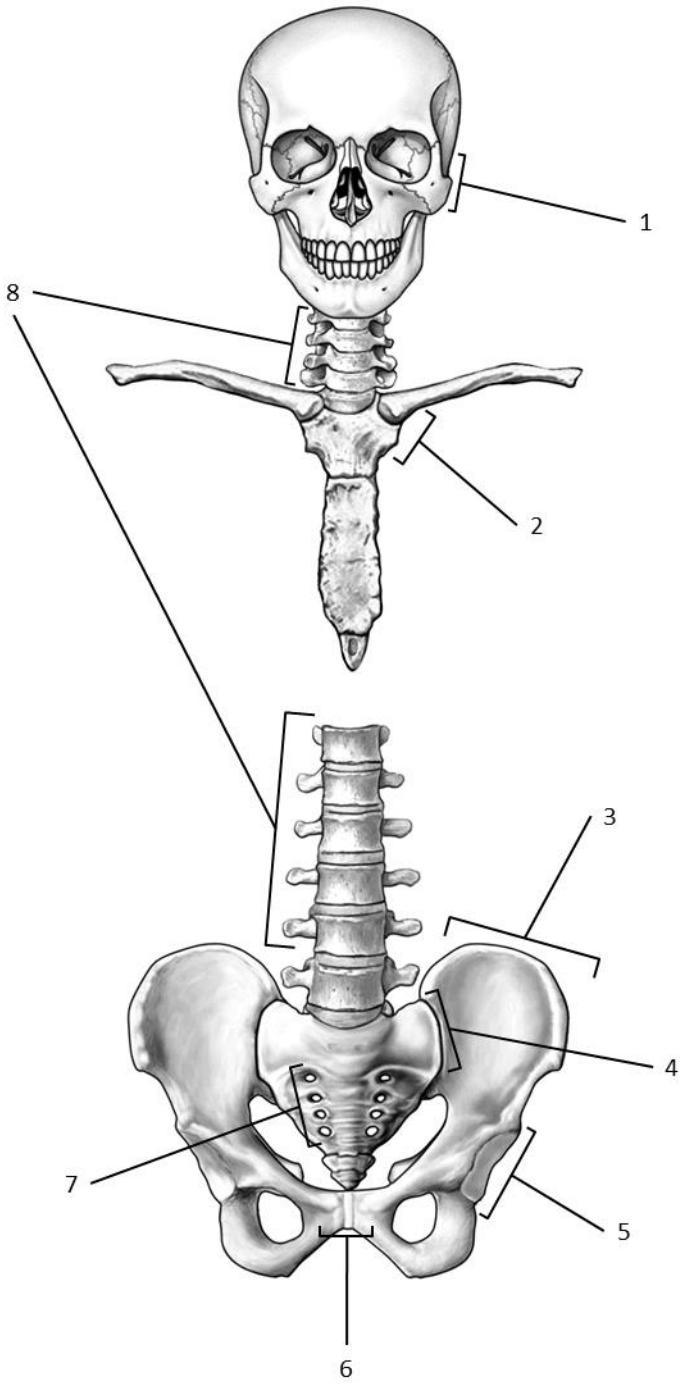


Figure 3.3: Skeletal features selected: cranial sutures (Nawrocki, 1998; Boldsen *et al.*, 2002)*, medial epiphysis of clavicle* (Scheuer and Black, 2000)*, iliac crest* (Scheuer and Black, 2000)*, auricular surface* (Boldsen *et al.*, 2002; Osborne *et al.*, 2004)*, acetabulum* (Rissech *et al.*, 2006)*, pubic symphysis* (Katz and Suchey, 1986; Boldsen *et al.*, 2002)*, sacrum* (McKern and Stewart, 1957; Passalacqua, 2009)*, vertebral bodies* (Stewart, 1958; van der Merwe *et al.*, 2006)*. [Artwork provided by TMR Houlton]*

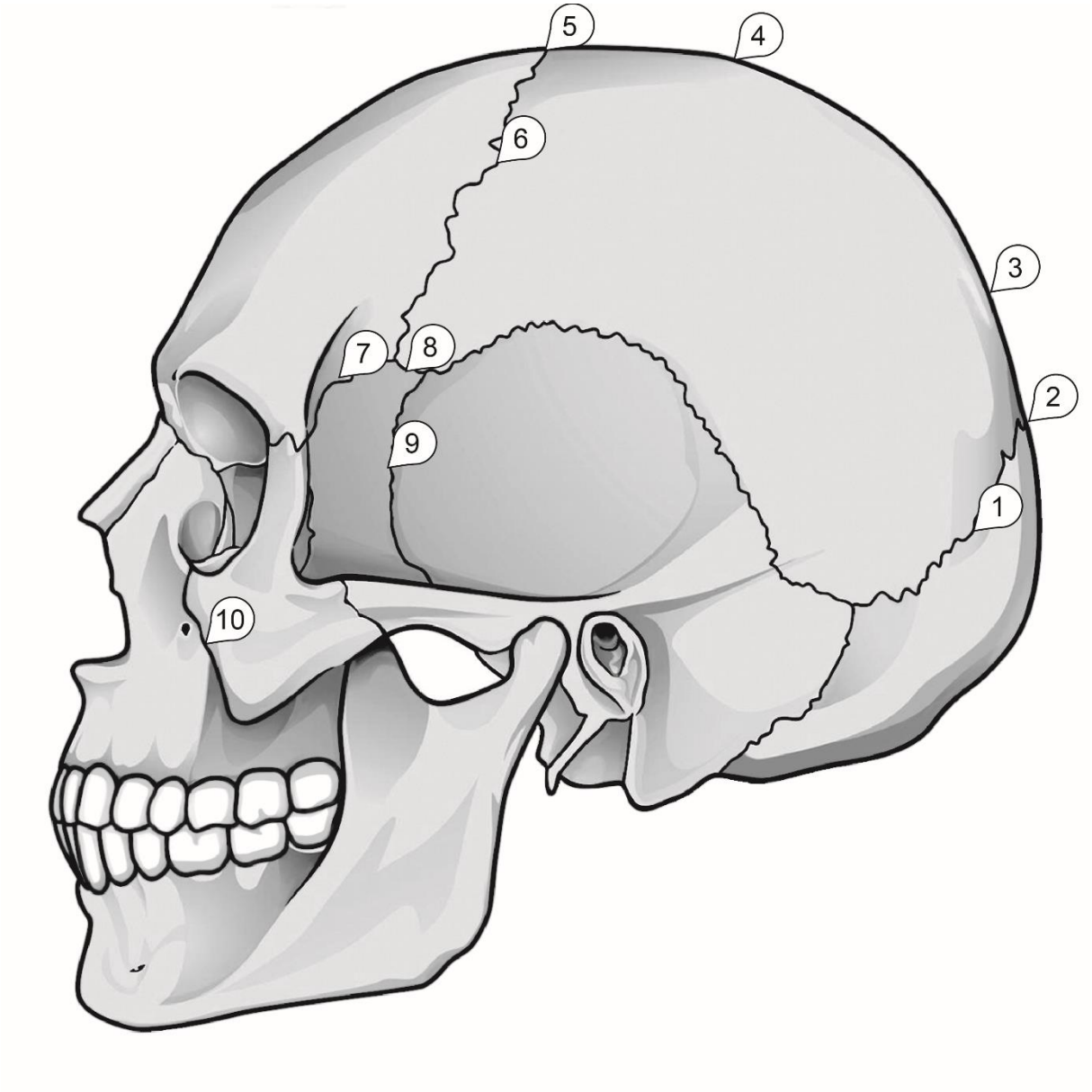


Figure 3.4: Cranial sutures considered from the skull vault and facial region: (1) midlambdoid, (2) lambda, (3) obelion, (4) sagittal vertex, (5) bregma, (6) midcoronal, (7) sphenofrontal, (8) pterion, (9) superior sphenotemporal, (10) zygomaxillary (Nawrocki, 1998). [Artwork provided by TMR Houlton]

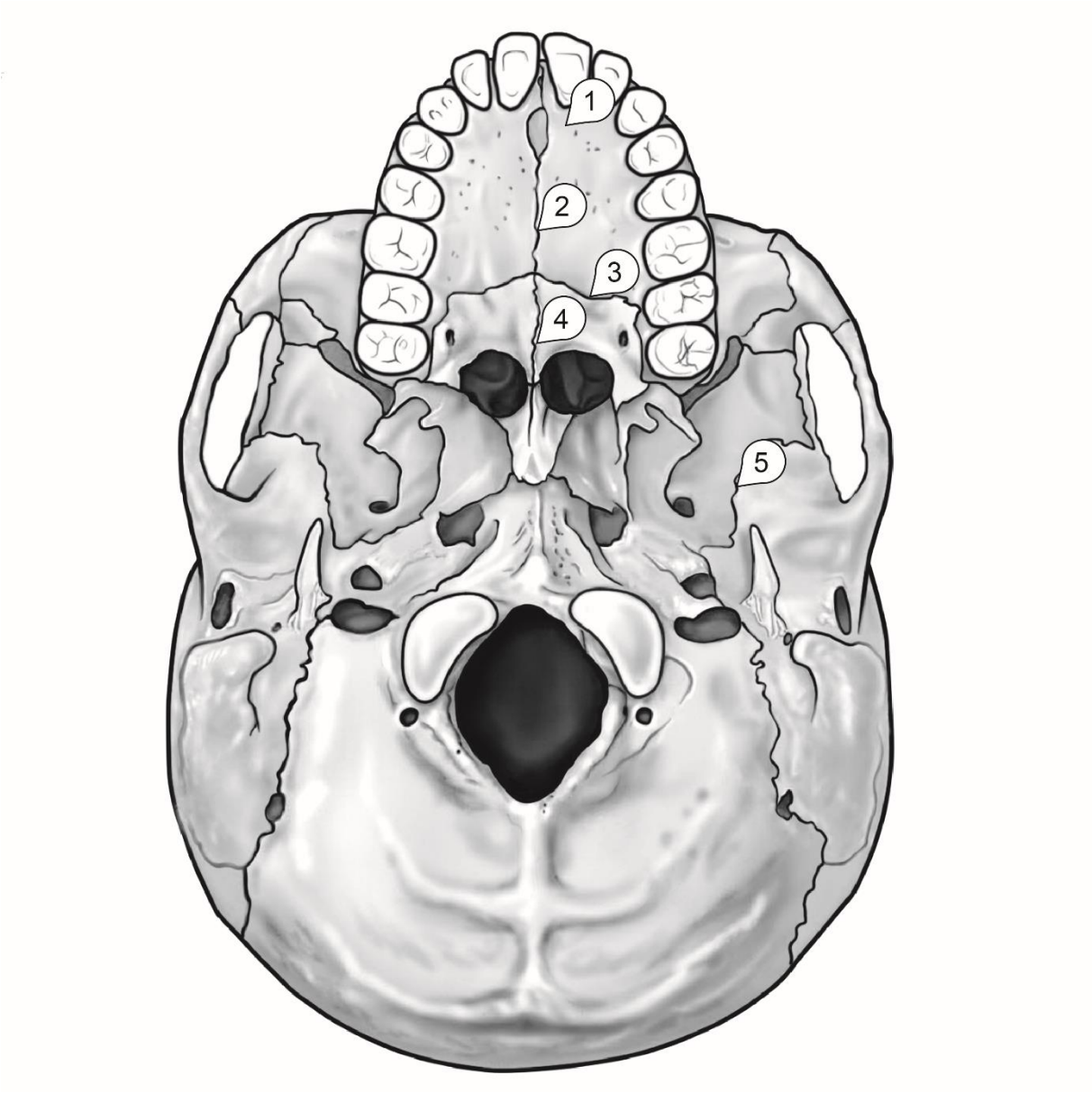


Figure 3.5: Cranial sutures considered from the inferior skull and palate region: (1) incisive, (2) anterior median palatine, (3) transverse palatine, (4) posterior median palatine, (5) inferior sphenotemporal (Mann *et al.*, 1991; Nawrocki, 1998)*. [Artwork provided by TMR Houlton]*



Figure 3.6: Descriptive categories 1.

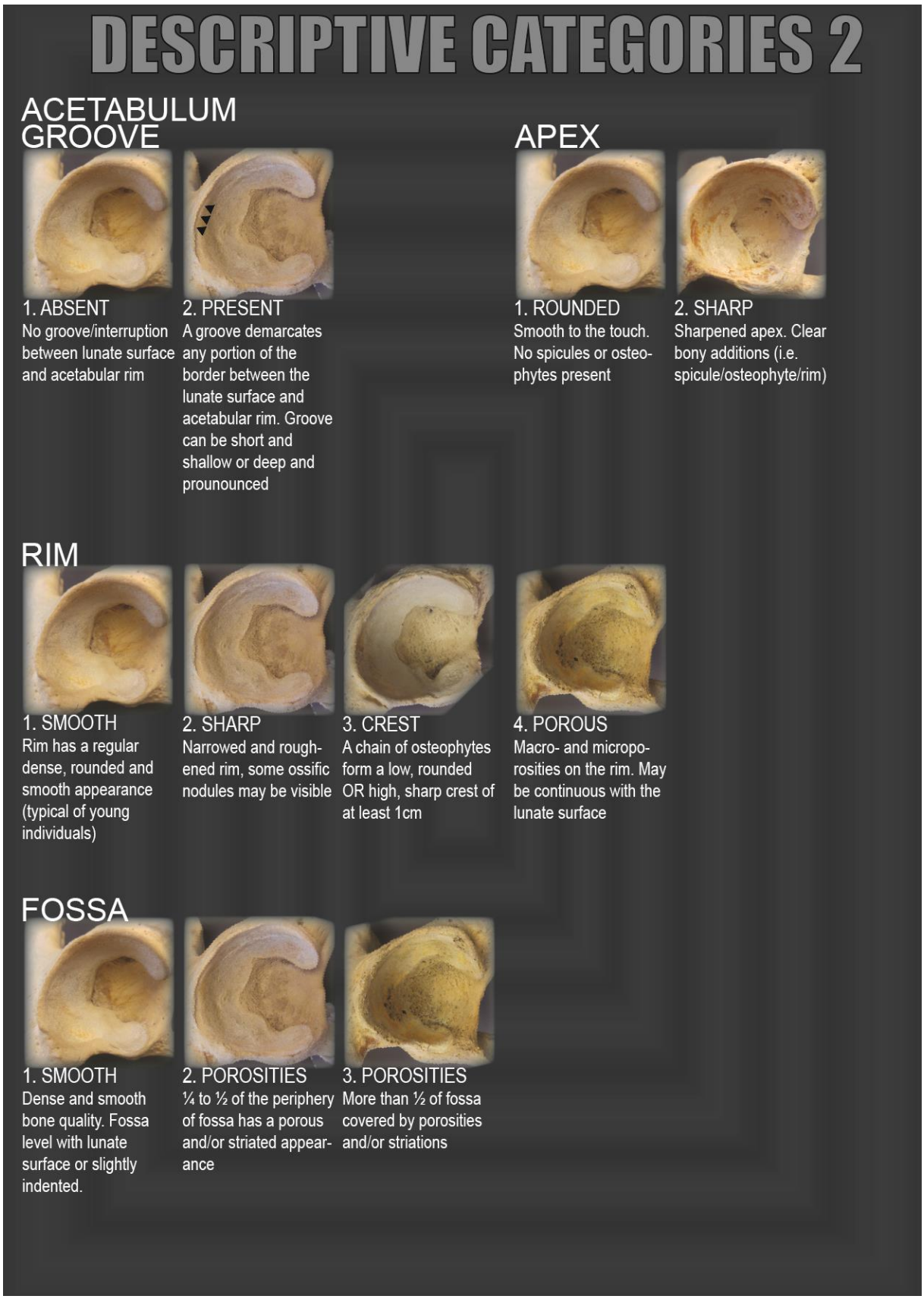


Figure 3.7: Descriptive categories 2.

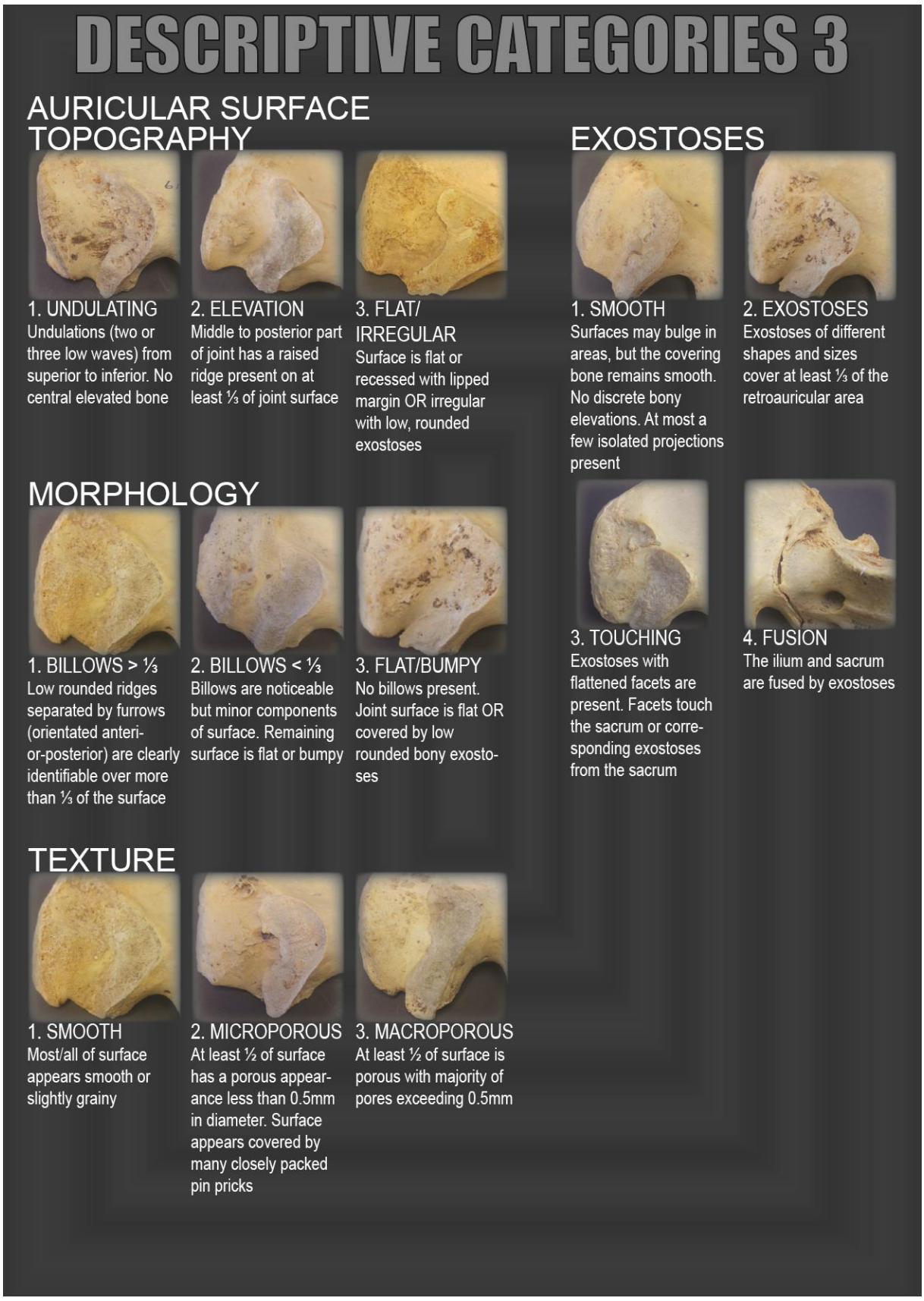


Figure 3.8: Descriptive categories 3.



Figure 3.9: Descriptive categories 4.



Figure 3.10: Descriptive categories 5.

CHAPTER 4: RESULTS

Firstly, data were considered for sample distribution and general relationships (i.e., between right and left indicators, anatomically adjacent indicators and females and males). Descriptive statistics were then calculated for all indicator stages before progressing to inferential statistics. Both regression and transition analysis models were constructed. Inferences were tested using hold-out validation data, with a similar distribution to the reference data. Lastly, observer agreement was considered for single and multiple observers.

4.1. Sample distribution

Visual inspection of histograms (Figures 4.1 – 4.10) and various statistical analyses (i.e., Shapiro-Wilks test, skewness z-scores and kurtosis z-scores in Table 4.1) confirmed non-normal distribution of all skeletal features. Non-normal distribution was logically expected for all binary categorised features but was observed for all bilateral and median skeletal features using a Shapiro-Wilks test for normality that yielded p-values smaller than 0.001 (Table 4.1).

Skeletal features that display negative skewness (skewness z-scores in Table 4.1) and contain a tail to the left of the mean, include the acetabular groove and apex (Figure 4.1), auricular surface topography and morphology (Figure 4.2), medial epiphysis of the clavicle (Figure 4.3), superior sphenotemporal and incisive sutures (Figure 4.4), iliac crest (Figure 4.5), pubic symphyseal relief and superior apex (Figure 4.6), S1/S2 fusion (Figure 4.7) and the superior vertebral bodies of L4 and L5 (Figure 4.10). Skeletal features that display positive skewness (skewness z-scores in Table 4.1) and contain a tail to the right of the mean include auricular surface texture (Figure 4.2), midcoronal, pterion, sphenofrontal, anterior median palatine, posterior median palatine and transverse palatine sutures (Figure 4.4), pubic symphyseal texture (Figure 4.6) and the superior vertebral body of C3 (Figure 4.9). Distributions of features that are negatively skewed result in a mean age that is lower than the median age, while distributions with features that are positively skewed result in a mean age that is higher than the median age.

Skeletal features that display negative kurtosis (kurtosis z-scores in Table 4.1) have either a uniform distribution or increased representation in the outer stages and include the vertebral bodies (Figures 4.9 and 4.10) and incisive suture (Figure 4.4) respectively. Skeletal features that display positive kurtosis (kurtosis z-scores in

Table 4.1) have increased representation in one or two central stages and include the acetabular groove (Figure 4.1), auricular surface topography (Figure 4.2), medial epiphysis of the clavicle (Figure 4.3), superior sphenotemporal and transverse palatine sutures (Figure 4.4), iliac crest fusion (Figure 4.5), pubic symphyseal relief and superior apex (Figure 4.6).

Thus, as all bilateral and median skeletal features are non-normally distributed, further statistical analyses were conducted using nonparametric tests.

4.2. Differences between bilateral paired features

A Wilcoxon signed-rank test determined that there are no statistically significant differences between the median values of the right and left observations for bilateral features (Table 4.2). Where differences occurred, they were random and did not show a consistent trend for a specific side. As most of the right and left features were allocated to the same stage (right = left in Table 4.2), methods developed from either side should have a comparable predictive value and substituting one side with another should be possible if incomplete remains are encountered. However, developing a predictive method that includes both bilateral features will create bias towards the age construct of these features that essentially will be duplicated in the model. Thus, as the right and left features are not statistically different, further statistical analyses were only conducted on the median and left features.

4.3. Differences between vertebral body margins

A Wilcoxon signed-rank test determined that there is a statistically significant difference between the median values representing the superior and inferior appearance of the vertebral body margins in the same vertebra (Table 4.3). Most of the superior and inferior vertebral body margins were allocated to the same stage (inferior = superior in Table 4.3). However, where vertebral body margins differed higher stages were more frequent for the inferior margins of cervical vertebrae (inferior>superior in Table 4.3) and the superior margins of lumbar vertebrae (superior>inferior in Table 4.3). The differences between the superior and inferior vertebral body margins are considered statistically significant except for vertebral bodies of L1 and L2. Thus, as most of the superior and inferior vertebral bodies are considered significantly different, all further statistical analyses were conducted using both features for each vertebral body.

A Wilcoxon signed-rank test determined that there is a statistically significant difference between the median values representing adjacent vertebral bodies (e.g., inferior vertebral body margin L1 and superior vertebral body margin L2) (Table 4.4). Most adjacent vertebral bodies were allocated to the same stage (inferior = superior in Table 4.4). However, where vertebral body margins differed, higher stages were more frequent for the inferior margins of cervical vertebrae (inferior>superior in Table 4.4) and the superior margins of lumbar vertebrae (superior>inferior in Table 4.4). The differences between adjacent vertebral body margins are considered statistically significant except for the margins between C4 and C5. Thus, as most of the adjacent vertebral bodies are considered significantly different, all further statistical analyses were conducted using all vertebral body margins.

4.4. Descriptive statistics

Initial descriptive statistics, describing age ranges representing each skeletal feature per stage, indicate certain stages are minimally represented within this population (i.e., $n \leq 5$ or $< 2\%$ of sample). These minimally represented stages are either associated with the younger adult form (stage 1) or cranial sutures (stages 1, 4 or 5) that are known from literature to deviate notably from successive ossification patterns. These stages were combined with adjacent stages to incorporate maximum variation, whilst maintaining optimal predictive value. As these minimally represented stages were either the upper or lower end categories, stages could only be combined in one direction (i.e., with the next highest category for stage 1 and the next lowest category for stage 4 or 5). Features where stages 1 and 2 were combined, include the acetabular fossa ($n_{stage1} = 3$), auricular surface morphology ($n_{stage1} = 0$), pterion ($n_{stage1} = 5$), pubic symphyseal relief ($n_{stage1} = 1$), pubic dorsal margin ($n_{stage1} = 5$), pubic ventral margin ($n_{stage1} = 3$), S2/S3 ($n_{stage1} = 4$), pubic symphysis (Suchey-Brooks method) ($n_{stage1} = 5$). Features where stages 1 and 2 were combined with stage 3, include the incisive suture ($n_{stage1} = 1$ and $n_{stage2} = 0$). Features where stages 4 and 5 were combined with stage 3, include superior sphenotemporal ($n_{stage4} = 1$ and $n_{stage5} = 0$) and inferior sphenotemporal sutures ($n_{stage4} = 1$ and $n_{stage5} = 3$). Features where stage 5 was incorporated into stage 4, include auricular surface morphology ($n_{stage5} = 4$), bregma ($n_{stage5} = 4$), zygomaticomaxillary ($n_{stage5} = 3$) and anterior median palatine sutures ($n_{stage5} = 5$).

Recalculated descriptive statistics for median and left-sided skeletal features using the modified staging system highlighted several mean and median ages that do not

increase with increasing stage number (indicated in bold in Table 4.5). Similar patterns were also observed for the right-sided skeletal features and can be viewed as Table E1 in Appendix E (as expected from the Wilcoxon sign rank test comparing data from the left and right side of the skeleton). The central tendencies that diverge from the expected pattern are mainly observed in a few cranial suture stages and in some stages that rely on texture of the bone (i.e., acetabular rim and auricular surface texture). As this phenomenon could potentially be linked to the smaller sample sizes representing these specific stages, all features were retained and further evaluated for potential contribution to the statistical models.

Summary statistics that analyse binary age indicators, such as the medial clavicle, iliac crest and S1/S2 fusion, are likely to misrepresent the true aging patterns as these low information indicators contain limited data individually (usually only one stage contains useful data). For example, a clavicle in stage 1 includes individuals in a small, but useful range (e.g., 20 - 26 years), but a clavicle in stage 2 can include ages from 20 to 100 years (i.e., stage 2 is not exclusionary). In turn, this indicates that the mean ages produced for stage 2 of the clavicle, iliac crest and S1/S2 fusion are an artificial product of including the entire sample distribution (i.e., the mean of an age interval containing ages 20 - 100 will be 50 years, regardless of the distribution within the interval).

The reference sample contains only individuals between ages 20 and 100, however, the lower bound of the 95% confidence interval was calculated as 19.82 and 19.10 for stage 1 of the medial epiphysis of the clavicle and the pubic symphyseal relief respectively (Table 4.5). These young ages indicate that these stages are probably more representative of younger individuals and could include individuals below 20 years; due to the age construct of the reference sample the calculated lower 95% confidence interval is likely artificially extended and the true bounds of the stage could potentially be identified by including younger individuals in future studies.

Many of the stages presented in Table 4.5 have wide age intervals including ages between 20 and 80+ years (as seen from the minimum and maximum ages). This demonstrates the variable relationship between age and these skeletal features. However, stages with smaller age intervals are observed in the acetabular rim, medial epiphysis of the clavicle, lambda, midcoronal, sphenofrontal, superior sphenotemporal, zygomaticomaxillary, anterior median palatine, posterior median palatine, transverse palatine, iliac crest, pubic ventral margin, pubic superior apex,

pubic symphysis (Suchey-Brooks method) and superior vertebral body of L4. These smaller age intervals indicate the possibility of more precise predictions from these features.

Boxplots were produced from the descriptive statistics to visualise the age distributions per stage of each skeletal feature (Figures 4.11 – 4.20). All outliers were investigated and concluded to be due to normal individual variation within the stage. These outliers were thus retained for all further statistical analyses.

The majority of the median ages observed in the boxplots increase with successive stages. Stages with medians that decrease or remain constant were either associated with textural changes such as the acetabular rim (stage 4 in Figure 4.11) and auricular surface texture (stage 3 in Figure 4.12) or cranial suture closure (i.e., midlambdoid stages 2 and 5, lambda stage 3, obelion stages 2 and 5, vertex stages 2 and 5, bregma stage 2, midcoronal stage 5, pterion stage 4, sphenofrontal stage 5, superior sphenotemporal stage 2, inferior sphenotemporal stage 2, incisive stage 5, anterior median palatine stage 2, posterior median palatine stage 2 and transverse palatine stage 5 in Figure 4.14).

Many stages include individuals from the sample's full age range (20 – 80+ years), for example pubic symphysis (Suchey-Brooks method) stage 4 (Figure 4.18), that contains individuals from 22 to 98 years. These large age intervals indicate much variation associated with the timing of some of the age-related skeletal changes and suggest that they have minimal predictive value (i.e., an individual assigned a pubic symphysis stage 4 could be as young as 22 or as old as 98 years). In contrast, smaller age intervals observed for pubic symphysis (Suchey-Brooks method) stages 2 or 6 contain more precise predictive information.

4.5. Difference between sexes

Boxplots of the sample divided by sex (Figures 4.21 – 4.30) produce a similar pattern to the combined sample (i.e., median ages generally progressing unidirectionally per stage, and generally large age intervals). However, when comparing the male and female groups per stage, the male group exhibits a higher median value for certain stages of the acetabular groove, rim and fossa (Figure 4.21), auricular surface topography and morphology (Figure 4.22), various cranial sutures (Figure 4.24), pubic symphyseal texture and ventral margin (Figure 4.26) and pubic symphysis (Suchey-Brooks method) (Figure 4.28), while the female group exhibits a higher

median value for certain stages of auricular surface texture (Figure 4.22) and various cranial sutures (Figure 4.24). The higher median ages suggest that structures within the abovementioned sex-specific stages appear younger (biologically) compared to the other sex; whereas lower median ages suggest an older appearance that was assigned to a higher stage. Differences in ageing patterns between sexes are particularly apparent for the cranial sutures, where many of the boxplots represent an older age distribution for the male compared to the female group (Figure 4.24).

The male group exhibits larger age intervals for specific stages of the acetabular rim and fossa (Figure 4.21), posterior iliac exostoses (Figure 4.22), cranial sutures (Figure 4.24), pubic symphyseal texture, superior apex, ventral margin and dorsal margin (Figure 4.26) and S1/S2 fusion (Figure 4.27), while the female group exhibits larger age ranges for specific stages of posterior iliac exostoses (Figure 4.22), cranial sutures (Figure 4.24) and pubic symphysis (Suchey-Brooks method) (Figure 4.28). Larger age intervals suggest more age-related variation associated with specific structural appearances and ultimately will result in less precise predictions (i.e., wider intervals).

Although smaller age intervals could result in more precise predictions, very narrow age intervals may indicate that the stage and associated appearance is underrepresented because this appearance is uncommon within the population sample or group. For example, the small ranges for the female medial epiphysis of the clavicle stage 1 (Figure 4.23) and the female iliac crest stage 1 (Figure 4.25) possibly indicate that these stages are associated with ages younger than 20 years; as no ages below 20 years were included in this sample, these stages are not well-represented in this sample. Small age intervals could also indicate the affinity of a specific structural appearance with a specific sex group; for example, the small range for the male group of pubic symphysis (Suchey-Brooks method) stage 6 (Figure 4.28) suggests that this structural appearance is more commonly found in females. Descriptive statistics (i.e., means, 95% confidence intervals, medians, minimums, maximums and ranges) separated by sex that support observations from the boxplots are included as Tables E2 and E3 in Appendix E.

A Mann-Whitney U test confirmed that the visual differences observed in median values between males and females were statistically significant (Table 4.6) for the auricular surface topography (Figure 4.22), midlambdoid, lambda, obelion, vertex, bregma, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary,

anterior median palatine, posterior median palatine and transverse palatine sutures (Figure 4.24), pubic symphyseal texture, ventral and dorsal margin (Figure 4.26) and specific vertebral bodies – most notably those of the cervical region (Figures 4.29 and 4.30).

The mean ranks indicate that the male group was allocated statistically significantly higher stages for the abovementioned features compared to the female group, except for the pubic symphyseal texture where the female group was allocated statistically significantly higher stages (Table 4.6). Although the female group is also allocated a slightly higher median and mean rank compared to the male group for auricular surface texture and sphenofrontal suture (Table 4.6), these values were not statistically significantly different.

As there is a statistically significant difference between various median stages of male and female groups, all further statistical analyses were calculated for the male and female groups separately. Statistical analyses were also calculated for the combined sex groups as the sex may not be known when estimating age-at-death; combining data from both sexes are expected to yield a lower accuracy.

4.6. Regression analysis

Visual inspection of the relationship (i.e., linear or nonlinear) between age (dependent variable) and skeletal indicators (independent variables) using a scatter plot proved problematic due to the categorical nature of the skeletal indicators. Alternatively, goodness-of-fit (r^2-value) was compared for six types of relationships: linear, logarithmic, quadratic, cubic, exponential and logistic (Table 4.7). Although a number of relationships indicated improved goodness-of-fit (higher r^2-values) using logarithmic, quadratic, cubic, exponential and logistic models compared to the linear model, the majority only indicated a slight improvement (r^2-change ≤ 0.02) and the maximum improvement was only 0.05 for the cubic model of the acetabular rim. As more complex models only produced slight improvement to the goodness-of-fit and no general relationship pattern was observed for all features, the linear model was selected for all further regression calculations for easy usability and interpretation.

The regression models constructed included equations that were produced from the combined sample and separate female and male groups due to the previously highlighted differences between the sexes in section 4.5. Although using only single skeletal indicators to predict unknown age-at-death is not suggested, regression

analyses using single skeletal indicators were calculated to generate data to inform decisions about combining indicators (Table 4.8). For this study, an equation using a single indicator included all contributing components of the indicator, similar to traditional methods that use information from all components to estimate age-at-death.

The acetabulum (Equations 1 to 3) therefore contains independent variables representing the acetabular groove, acetabular rim, acetabular apex and acetabular fossa. The auricular surface (Equations 4 to 6) contains independent variables representing the surface topography, surface morphology, inferior surface texture and posterior iliac exostoses. The clavicle (Equations 7 to 9), iliac crest (Equations 13 to 15), sacrum (Equations 19 to 21) and pubic symphysis stage-based method (Equations 22 to 24) all contain only one independent variable. Cranial sutures were combined in Equations 10 to 12. The pubic symphysis component method (Equations 16 to 18) contains independent variables representing symphyseal relief, symphyseal texture, superior apex, ventral and dorsal margin. Different combinations of the vertebral bodies were included in separate equations, with all superior and inferior rims for the cervical and lumbar regions included in Equations 25 to 27, only superior rims included in Equations 28 to 30 or only inferior rims included in Equations 31 to 33.

These single skeletal indicators were evaluated for the strength of association (r-value) between the skeletal feature(s) and age, the variance in age explained by the skeletal feature(s) (r^2-value) and the statistical significance (F-value) of the predicting capability of the model; this data as well as data about the significant contribution of each feature (p-values of coefficients) to the regression models were considered when choosing the final features. Standard error of estimation (SEE) for each equation is included in Tables 4.8 – 4.10 for the sake of completeness. However, as SEE provides general information based on the reference sample, the predictive precision is discussed as part of the validation results in section 4.8 below.

When considering the models using single skeletal indicators, the most variance in age (r^2-value ranging from 0.387 to 0.638) is accounted for by different combinations of the vertebral bodies (Equations 25 to 33 in Table 4.8). However, only some of the vertebral bodies contributed statistically significantly to the equations (e.g., C6 superior and inferior and L5 superior and inferior). Additionally, many of the vertebral bodies were quite highly correlated with one another, which violates an important

assumption of multiple linear regression analysis (see the correlation matrix E4 in Appendix E). Thus, final multiple linear regression equations only include a single vertebral feature (L5 superior).

Other skeletal indicators that accounted for considerable amounts of variance in age were the pubic symphysis and acetabulum (Equations 1 to 3, 16 to 18 and 22 to 24 in Table 4.8). The pubic symphysis stage-based method improved both the coefficient of determination (r^2-values ranging from 0.257 to 0.377) and combined correlation (r-values ranging from 0.507 to 0.614) compared to the pubic symphysis component-based method (r^2-values ranging from 0.272 to 0.287; r-values ranging from 0.521 to 0.536) and also outperformed the acetabulum for the combined (r^2-value = 0.302) and male groups (r^2-value = 0.268), as well as the superior vertebral bodies for the male group (r^2-value = 0.387). All components for the component-based methods of the pubic symphysis and the acetabulum did not contribute statistically significantly to the model. Additionally, the symphyseal relief component was highly correlated with other symphyseal components in the equation potentially violating a multiple linear regression assumption (see correlation matrix E4 in Appendix E) as expected.

Even though it was concluded that some individual indicators contributed only small amounts to the variance in age, an equation was generated that contained all available indicators for the combined female and male sample to evaluate each indicator's contributions and significance in a combined scenario (Equations 34 and 35 in Table 4.9, using the pubic symphysis component compared to stage method respectively). The coefficient of determination (r^2-value = 0.974 and 0.771 respectively) and combined correlation (r-value = 0.987 and 0.878 respectively) appear very high, but may be artificially increased due to the limited sample size (n = 59 and n = 77 respectively) and the large number of skeletal indicators (50 and 46 variables respectively) included in the equations. The sample size is severely limited for Equations 34 and 35 as all indicators are required to construct the equations (i.e., only skeletons containing data from all skeletal indicators are used). Additionally, Equations 34 and 35 produced tolerance values greater than 0.1, indicating strong multicollinearity (correlations between indicators) when combining all indicators into a single equation.

In order to achieve more realistic goodness-of-fit and correlation values, only features that contributed statistically significantly to previous equations were selected. Models were constructed separately using either a component-based or stage-based method

for the pubic symphysis; both were never included in the same equation as this would introduce bias by increasing the weighting of information contributed by the pubic symphysis disproportionately compared to other indicators. Indicators were excluded on a model-by-model basis (i.e., sequentially) until only statistically significantly contributing features were included in the regression model. No single components for the pubic symphysis were included in the final model as they were not considered statistically significant. However, the pubic symphysis stage-based method was considered statistically significant and this variable statistically significantly improved the regression model (Equation 39 in Table 4.10) by r^2-change = 0.050.

As the pubic symphysis components from the component-based method did not contribute statistically significantly to the multifactorial equation, an equation excluding the pubic symphysis was constructed. The statistically significantly contributing indicators that remained, included the acetabular fossa, posterior median palatine suture, bodies of S1/S2 and the superior rim of vertebral body L5 (Equation 38 in Table 4.10). When including the pubic symphysis, the stage-based method (Suchey-Brooks) should be used along with the following statistically significantly contributing indicators: the acetabular fossa, posterior iliac exostoses, zygomaticomaxillary suture and the superior rim of vertebral body L5 (Equation 39 in Table 4.10).

When dividing the sample by sex, the inclusion of the full number of skeletal indicators overwhelmed the divided sample sizes (i.e., sample size varied between 39 and 48 depending on sex and included indicators) completely. Thus, a reduced number of promising indicators were included that did not limit the sample size as drastically (Equations 36 and 37 in Table 4.9 for females and males respectively). Indicators that did not statistically significantly contribute to the regression models were eliminated on a model-by-model basis (i.e., sequentially). The statistically significantly contributing features in the final multifactorial model for the female group include the acetabular fossa, bodies of S1/S2, pubic symphysis (Suchey-Brooks stage-based method) and superior rim of vertebral body L5 (Equation 40 in Table 4.10). Two final multifactorial equations were produced for the male sample; one containing a single statistically significant component (superior apex) from the pubic symphysis (Equation 41 in Table 4.10) and one including the Suchey-Brooks stage-based method (Equation 42 in Table 4.10). Both equations include the following

statistically significantly contributing features: the acetabular fossa, posterior iliac exostoses, zygomaticomaxillary sutures and the superior rim of vertebral body L5. The final multifactorial female model (Equation 40 in Table 4.10) achieves a similar goodness of fit ($r^2 = 0.567$) compared to the multifactorial male model ($r^2 = 0.566$) that contains the pubic symphysis stage-based method (Equation 42 in Table 4.10). The sex-specific equations slightly outperform the final multifactorial combined sample model ($r^2 = 0.521$) (Equation 15 in Table 4.8).

Assumptions were tested for all regression models and were considered satisfactory unless explicitly stated otherwise in section 4.6 (i.e., reported tolerance values and intercorrelation/multicollinearity values).

4.7. Transition analysis/Generalized linear models

Generalized linear models, which were constructed for each skeletal indicator, are graphically represented in Figures 4.42 – 4.53. The curves depict the proportion of the population that is associated with each available stage for the ages of 20 to 100 years. These transition curves reflect females and males combined (Figures 4.31 – 4.41) and separated (Figures 4.42 – 4.53).

A skeletal indicator that contains structural information related to age progression produces a pattern of curves where lower stages decrease with age progression as higher stages increase. This pattern relates to both dichotomous indicators (i.e., 2 stages) and also polychotomous indicators (i.e., 3 – 6 stages).

In some instances, the researched population is dominated by one stage; for example, stage 2 of the acetabular groove (Figure 4.31) represents over 70% of the population between 20 and 100 years. A clear transition from stage 1 to 2 is present, however, the transition of stages occurs before or at 20 years. This early transition pattern is also observed for dichotomous stages of the acetabular apex (Figure 4.31), medial epiphysis of the clavicle (Figure 4.33) and iliac crest (Figure 4.35), as expected. Although these features certainly contain age-related information, they mainly inform about ages 20 years and younger. Once the transition to stage 2 has occurred the individual's age could be anywhere between 20 and 100 years, which corresponds to trends known from literature.

In other dichotomous indicators the transition from one stage to another (i.e., stage 1 to stage 2) occurs at an older age. Indicators such as the fusion of S1/S2 (Figure 4.37) contain a higher proportion of the population up to the late 20s, in stage 1 and

thereafter transitions to higher proportions of the population in stage 2. Indicators such as the cervical vertebral bodies transition from stage 1 to 2 between 40 and 70 years (Figure 4.39) while the lumbar vertebral bodies transition from stages 1 to 2 between 30 and 55 years (Figure 4.40). Both stages of these indicators contain proportional information about adult age within the researched population.

Similar interactions, albeit more complex, between stages can be seen for the polychotomous indicators. Each stage within the sequence should account for the majority of the population in a specific and sequential age range such as observed with the stages representing the acetabular fossa (Figure 4.31), pubic symphyseal texture, ventral margin and dorsal margin (Figure 4.36) and pubic symphysis stage-based method (Suchey-Brooks) (Figure 4.38).

Some stages closely overlap the age ranges of an adjacent stage, for example stages 3 and 4 of the acetabular rim (Figure 4.31), stages 1 and 2 of midlambdoid and obelion and also stages 4 and 5 of midlambdoid, lambda, obelion, midcoronal, pterion, sphenofrontal and posterior median palatine sutures (Figure 4.34) and stages 2 and 3 of pubic symphyseal relief and stages 1 and 2 of the superior apex (Figure 4.36).

Some stages appear to contribute little or no age information with the curve remaining approximately constant for the entire age distribution. These stages include stage 2 of the auricular surface topography and morphology as well as stage 3 of inferior surface texture and posterior iliac exostoses (Figure 4.32) and stage 5 of the vertex and the transverse palatine suture (Figures 4.34).

Overlapping stages and stages remaining constant (i.e., maintain equal population proportions throughout the entire age distribution) suggest insufficient age-related information. Indicators with categories containing insufficient age-related information may benefit from reducing the number of categories. This is confirmed by the improved transition curves obtained by cranial sutures that naturally contain less stages (as observed in the collected data) including, superior sphenotemporal, inferior sphenotemporal and especially zygomaticomaxillary sutures (Figure 4.34).

Data obtained from the transition curves corroborate conclusions from the descriptive statistics in section 4.4, displaying means and medians of sequential stages for some indicators that did not increase. Indicators where all stages present age-related data, as seen with transition curves that sequentially account for the majority of the

researched population, accounted for the most variance (r^2-value) and significantly contributed to the multiple regression models produced in section 4.6.

Similar curve patterns, with similar ages-of-transition (i.e., where the proportion of the higher stage exceeds that of the lower stage), are observed for the separated sexes for the acetabulum (Figure 4.41), medial epiphysis of the clavicle (Figure 4.43) and iliac crest (Figure 4.46). Some indicators contain similar curve patterns, with female transitions occurring at an earlier age, such as the posterior iliac exostoses (Figure 4.42) or at a later age, such as the fusion of S1/S2 (Figure 4.48) and the vertebral bodies relative to males (Figures 4.50 – 4.53).

Occasionally, aging patterns represented by the transition curves differ completely between females and males. For example, the curve representing stage 3 of auricular surface texture (Figure 4.42) increases (i.e., proportion of population increases) with increasing age for the female sample while the curve decreases (i.e., proportion of population decreases) with increasing age for the male sample. The described pattern is also observed for stages 2 and 3 of the auricular surface topography (Figure 4.42) as well as stage 3 of lambda and stage 5 of the incisive suture (Figure 4.44 and 4.45).

Overall aging patterns can also differ between sexes with regard to the proportion of the population that is represented by the peak of each curve. For example, the curve representing stage 2 of the posterior iliac exostoses (Figure 4.42) represents approximately 70% of the female population but only 60% of the male population. The described pattern is also observed for stages 3 and 4 of pubic symphyseal relief, stage 3 of pubic symphyseal texture, stages 2 to 5 of the ventral margin and stages 2 to 4 of the dorsal margin (Figure 4.47) as well as stages 2 to 6 of pubic symphysis Suchey-Brooks stage-based method (Figure 4.49).

Lastly, once sexes were separated, some curves become approximately constant, representing the same proportion of the population for the entire age distribution. This indicates that not all stages are equally appropriate for each sex as the stage only provides information for either the male or female group. For the female sample, these curves include stage 4 of the posterior iliac exostoses (Figure 4.41) and also stages 1 to 3 of the superior sphenotemporal, stage 2 of the inferior sphenotemporal, stages 1 to 3 of the anterior median palatine, stages 1 and 5 of the transverse palatine sutures (Figure 4.44). For the male sample these curves include stages 3

and 4 of obelion, stages 3 and 5 of vertex, stage 5 of midcoronal, stage 1 of sphenofrontal and stages 4 and 5 of transverse palatine sutures (Figure 4.45) and also stage 3 of symphyseal texture (Figure 4.47).

There are thus notable age differences between sex groups for the auricular surface, cranial sutures, pubic symphysis component-based and stage-based method, sacrum and the vertebral bodies. Combinations using any of these indicators should ideally make use of sex-specific models.

Multifactorial generalized linear models with a logit link (transition models) were constructed using a uniform age distribution for the skeletal indicators used in regression Equations 38 to 42 in Table 4.10 for optimal comparison between the results obtained. Indicators included from Equation 38 were the acetabular fossa, posterior median palatine suture, S1/S2 fusion and L5 superior vertebral body. Indicators included from Equation 39 were the acetabular fossa, posterior iliac exostoses, zygomaticomaxillary suture, pubic symphysis (Suchey-Brooks stage-based method) and L5 superior vertebral body. Indicators included from Equation 40 were the acetabular fossa, S1/S2 fusion, pubic symphysis (Suchey-Brooks stage-based method) and L5 superior vertebral body. Indicators included from Equation 41 were the acetabular fossa, posterior iliac exostoses, zygomaticomaxillary suture, pubic symphysis superior apex and L5 superior vertebral body. Indicators included from Equation 42 were the acetabular fossa, posterior iliac exostoses, zygomaticomaxillary suture, pubic symphysis (Suchey-Brooks stage-based method) and L5 superior vertebral body. Transition analysis models using variables from regression Equations 40 to 42 were constructed using sex-specific data. These skeletal indicators were included in the transition analysis models, as they were found to provide the best age-related information and enabled comparison with results from the regression analysis models.

All possible indicator combinations and the resulting point estimates and intervals are recorded in Tables E5 to E9 in Appendix E. These tables represent the reference data used to construct the transition analysis models and the age estimates (point and interval estimates) calculated from these data. These data represent the information contained in programs such as ADBOU, from which age estimates can be calculated for unknown remains. Although the goal of this study was not to produce a program such as ADBOU, but rather to test the performance of the different models constructed, the tables can be used to obtain an age estimate from

a set of scores. The tables can be used in the following way to obtain an age point estimate and 95% confidence interval: from Table D5's first row of scores, a skeleton with S1/S2 = 1; L5 superior = 1; acetabular fossa = 2; posterior median palatine suture = 1, will have a point estimate of 20 years and an interval of 20 to 21 years. In another example from Table D5, a skeleton with S1/S2 = 2; L5 superior = 2; acetabular fossa = 3; posterior median palatine suture = 4, will have a point estimate of 79 years and an interval of 20 to 80 years. From Tables D5 to D9 it can be seen that ages predicted from lower scores often only encompass a single year, whereas ages predicted from higher scores often encompass the entire adult age distribution (i.e., 20 – 100 years).

4.8. Validating results

Three methods were used to calculate age-at-death estimates for the validation sample (n = 30). The first method used the basic descriptive statistics generated from the reference sample. A point estimate was calculated by averaging the mean age for each of the age indicators selected. Two intervals were calculated for this method. A narrow interval was constructed by averaging upper limit values as well as lower limit values (from the 95% confidence interval calculated from the reference sample) for the selected indicators. A wide interval was constructed by using the smallest lower limit value and the largest upper limit value (from the 95% confidence intervals calculated from the reference sample), which created a comprehensive interval that included full intervals from all indicators selected. The basic statistics method used here is not suggested as a statistically appropriate method as statistically no confidence interval or mean error can be calculated for this method for forensic purposes, however, it serves as a comparison point (similar to a mean model) for the two statistical methods (regression and transition analysis).

The second method used Equations 38 - 42 (Table 4.10) to generate a point estimate. Two intervals were also calculated for each test subject using the equations along with the calculation capabilities of the IBM SPSS statistical package (version 25) and the reference sample data. A narrow interval was constructed by generating a 95% confidence interval; a confidence interval consists of a range that contains 95% of the population. A wide interval was constructed by generating a 95% prediction interval; a prediction interval indicates the range in which an unknown individual will fall with 95% confidence. The prediction interval, which is associated

with a specific individual prediction, produces a much wider range compared to the confidence interval that is associated with the general population.

The third method used the multifactorial transition analysis models generated in R to produce a point estimate and an age interval. A uniform prior distribution was used with the calculations as this is suited to the reference and validation data used.

Each of the three statistical methods described above was used with five multifactorial models, each with a different set of age indicators and suitable to a different sex-specific scenario. Model 1 includes the acetabular fossa, posterior median palatine suture, S1/S2 sacral segment, and vertebral body L5 superior margin. Model 2 includes the acetabular fossa, auricular surface posterior exostoses, zygomaticomaxillary suture, pubic symphysis stage-based method (Suchey-Brooks) and the vertebral body L5 superior margin. Model 3 includes the acetabular fossa, S1/S2 sacral segment, pubic symphysis stage-based method (Suchey-Brooks) and the vertebral body L5 superior margin. Model 4 includes the acetabular fossa, auricular surface posterior exostoses, zygomaticomaxillary suture, pubic symphysis superior apex component and the vertebral body L5 superior margin. Model 5 includes the acetabular fossa, auricular surface posterior exostoses, zygomaticomaxillary suture, pubic symphysis stage-based method (Suchey-Brooks) and the vertebral body L5 superior margin.

Models 1 and 2 use reference sample data from males and females combined and are suited to both male and female remains. Model 3 uses reference sample data from females only and is best suited to female remains. Models 4 and 5 use reference sample data from males only and are best suited to male remains.

The validation results obtained, using the three methods in combination with each of the five multifactorial models, are available in Tables E10 - E14 in Appendix E. Results are provided in point estimate and interval format as described above. It is worth noting that the lower margin for the wide interval of the regression analysis occasionally includes a value below 20 years. These subadult lower margins are an artefact from the statistics, even though the reference sample only contains ages between 20 and 100. As subadult skeletal appearance differs markedly from the indicators investigated in this study, the lower margin can be practically set at 20 years minimum. This narrows the age range, without excluding any adult individuals to which this study is specific. All other methods' intervals automatically fall within the

practical margins (20 - 100 years) dictated by the reference sample. If the lower margins are restricted to 20 years minimum age, the mean range for the wide interval of the regression analysis method decreases by three to four years per model while maintaining the same interval accuracy.

This validation data, per individual skeleton, are represented visually in Figures 4.54 to 4.58. When observing the known ages (blue line), it is apparent that the known ages are well represented by the point estimates (purple diamond) of the basic statistics and regression analysis methods for most of the validation sample. Some point estimates from the transition analysis method are closely associated with the known ages, however, many point estimates calculated by this method indicate a large inaccuracy margin, apparent by the large spaces between the known ages and the point estimates. A similar pattern is observed for all multifactorial models (Models 1 to 5).

When considering interval width, the narrow intervals (orange bar) for both the basic statistics and regression analysis methods can be considered quite precise, spanning approximately 10 years or less. The calculated wide intervals (pink bar) are considerably less precise than the calculated narrow intervals (orange bar), with intervals for some individuals spanning over 40 years for the basic statistics and over 50 years for regression analysis. The age intervals provided by the transition analysis method, either spanned large ranges (30 to 80 year intervals), or provided small, inadequate intervals of only one or two years. Many intervals calculated by the basic statistics and regression analysis methods captured the known ages of the individuals. However, many of the intervals calculated for the transition analysis method underestimated the known age (i.e., the calculated age interval fell below the line representing the known ages).

Although the basic statistics method included the known ages in many cases, the method does not accurately represent information from very young or very advanced aged adults as many of the estimates (point estimates and narrow intervals) are located around 40 to 60 years. The point estimates and narrow intervals produced by the regression analysis method appear to more closely approximate the known ages from each decade of the lifespan. Transition analysis does not match the pattern of ages represented by the validation sample.

Summary data comparing the bias, accuracy and precision of the validation data reflects the value of each statistical method as both the reference and validation data remain the same and only the analyses differ (Table 4.11). Mean inaccuracies (i.e., the average difference between the point estimate and true age) calculated for the point estimates obtained by the basic statistics and regression analysis methods were very similar with regression analysis being slightly more accurate. The transition analysis method contained larger inaccuracies in all instances. The maximum inaccuracy documented (i.e., largest difference between the point estimate and the true age) was equal to or smaller than 21 and 25 years for the basic statistics and regression analysis respectively (Table 4.11). However, large, concerning maximum inaccuracies for the transition analysis method included 37 and 44 years for Models 1 and 3 respectively.

The pattern of bias for each method differs notably. The basic descriptive statistics method is predominantly negatively biased with point estimated ages being overestimated. The transition analysis method is predominantly positively biased with the point estimate ages being underestimated. The regression analysis method contains both negative bias in point estimates from the female equation (Model 3) and combined sex equation without the pubic symphysis (Model 1) and positive bias for Models 2, 4 and 5. The tendency for transition analysis to underestimate the point estimate ages is also clearly visualised in Figures 4.54 to 4.58 for each of the five models. All calculated bias was considered minimal, however, the largest biases were observed from the transition analysis method.

Although the interval accuracy for the regression analysis wide interval method outperformed all other models, the age ranges were impractically wide and included most of the adult lifespan (e.g., 20 – 70 years). The second-best range accuracies were obtained using the basic statistics wide interval method (i.e. all encompassing). The age intervals using basic statistics, were more realistic with mean intervals between 28 and 34 years.

When comparing interval accuracy between the regression analysis and transition analysis methods, the regression analysis narrow interval method’s accuracy equalled or outperformed the transition analysis method for Models 1, 2, 3 and 5 (using the Suchey-Brooks stage-based feature). Additionally, the mean and maximum age intervals for each of the models using the regression analysis method were narrower than the transition analysis method, with the exception of the

maximum age range for Model 1. However, the interval accuracies for Model 4 (not using the Suchey-Brooks stage-based feature) was markedly higher for transition analysis compared to regression analysis. Although the mean intervals produced practical ranges, the maximum age intervals remain impractically large for both regression and transition analysis.

Overall, it seems that reasonable accuracy with age estimation can be obtained especially using the regression analysis method. Unfortunately, the obtained intervals remain large specifically for the regression analysis wide interval method and transition analysis. Surprisingly, using averaged ages and all-inclusive age intervals from the reference sample basic statistics notably outperformed the statistically refined methods.

When considering the success of sex-specific models (Table 4.11), it is clear that Model 3, for females only, shows a very slight improvement in accuracy compared to Models 1 and 2 for males and females combined. Models 4 and 5 (for males only) achieve either a similar or decreased accuracy compared to Models 1 and 2 for males and females combined. The small or absent improvement with sex-specific data could be explained by the smaller reference sample sizes once the group is split by sex (sample sizes for separate sexes are between n = 123 and n = 145, whereas sample sizes for the combined group are between n = 258 and n = 264, depending on the included variables). It could also suggest that the majority of features selected for these models, were not influenced by sex. This is supported by the fact that only the zygomaticomaxillary suture from the selected indicators, was considered statistically significantly different between the sexes.

The accuracy of the sex-specific age intervals, calculated using Models 3 and 5, equals or outperforms the pooled sample (Models 1 and 2), but Model 4 (the male model that includes the acetabular fossa, posterior iliac exostoses, zygomaticomaxillary, pubic symphysis superior apex and L5 superior vertebral rim) was less accurate, especially for the narrow interval basic statistics and regression analysis methods. The accuracy obtained for females (Model 3) are especially noteworthy due to the narrow intervals obtained compared to the pooled sample (Models 1 and 2).

Using sex-specific models could thus only slightly improve results. Improved results using sex-specific models are subject to specific age indicators included in the model

This is supported by the fact that sex-specific models for males improved results when using the Suchey-Brooks pubic symphysis method, but not when using the superior apex component from the pubic symphysis (Model 4 versus 5). Improvement using the sex-specific models also varied depending on the statistical method used, with basic statistics and regression analysis generally showing better results than transition analysis.

4.9. Observer agreement

Skeletal indicators from the hold-out validation sample (n = 30) achieved high percentage single (intra) observer agreement (average agreement = 85%), but lower agreement between multiple observers (average agreement = 58%) (Table 4.13). Indicators that achieved lower than average percentage agreement between multiple observers included the acetabular rim (50% agreement), auricular surface topography (47% agreement), morphology (33% agreement), texture (42% agreement) and posterior iliac exostoses (52% agreement), the cranial sutures (between 3 - 36% agreement; excluding obelion and zygomaticomaxillary) and pubic symphyseal texture (40% agreement), superior apex (38% agreement), ventral margin (53% agreement) and pubic symphysis stage-based method (53% agreement). Even problematic indicators achieved at least 30% agreement, except for cranial sutures that achieved particularly poor agreement. The zygomaticomaxillary suture does achieve higher than average agreement. Unfortunately, this is not the case for the posterior median palatine suture.

Table 4.13 reports Cohen's kappa values, weighted Cohen's kappa values and their associated p-values for single and multiple observer agreement. Indicators that fared particularly well for single observer agreement (> 0.6 according to Landis and Koch (1977)) include the acetabular groove, apex and fossa, auricular surface topography, morphology and texture, the cranial sutures (excluding midlambdoid and palatine sutures), pubic symphyseal ventral margin, S1/S2 fusion and the vertebral bodies (excluding L1 superior).

The p-value for the posterior iliac exostoses (p = 0.054) indicates category agreement statistically significantly equal to or lower than chance for single observer agreement (i.e., a p-value that indicates chance agreement). However, the p-value is very close to significant.

Additional information is gained by comparing Cohen's kappa values with weighted Cohen's kappa values. Weighted Cohen's kappa values consider the magnitude of the disagreement (i.e., is the difference in agreement across one or more categories). If the weighted Cohen's kappa value is higher than the Cohen's kappa value, it indicates a smaller category disagreement (disagreement over fewer categories). If the weighted Cohen's kappa value is lower than the Cohen's kappa value, it indicates a larger category disagreement (disagreement over multiple categories). Indicators with higher weighted Cohen's kappa values include the acetabular rim and fossa, auricular surface morphology and texture, the cranial sutures and pubic symphyseal relief, texture, apex and dorsal margin as well as pubic symphysis stage-based method. Indicators with lower weighted Cohen's kappa values include the auricular surface topography and pubic symphyseal ventral margin. When considering magnitude, all single observer agreement becomes statistically significantly better than chance. Thus, some single observer disagreement is observed, but the overall disagreement is small (i.e., only one stage different).

Indicators that fared particularly well for multiple observer agreement (> 0.6 according to Landis and Koch (1977)) include acetabular fossa and vertebral bodies of C4, C6 and C7 superior, as well as L3 – L5. Indicators with less than chance agreement for multiple observers (negative Cohen's kappa values) include the bregma, midcoronal, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, anterior median palatine, posterior median palatine and transverse palatine sutures. Cohen's kappa values that indicate category agreement statistically significantly equal to or lower than chance for multiple observer agreement (a p-value that indicates chance agreement) include the acetabular rim and apex, auricular surface topography, morphology, texture and posterior iliac exostoses, midlambdoid, lambda, bregma, midcoronal, sphenofrontal, superior sphenotemporal, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures and pubic symphyseal texture and superior apex.

As with single observer agreement, weighted Cohen's kappa values were compared to Cohen's kappa values. Indicators with higher weighted Cohen's kappa values include the acetabular rim, auricular surface features, cranial sutures (except incisive which displayed less agreement) and the pubic symphyseal features including the

stage-based method. Indicators that did not improve statistical significance (i.e., p-value indicates chance agreement) using weighted Cohen's kappa include the auricular surface topography, morphology and posterior iliac exostoses, sphenofrontal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine and posterior median palatine sutures and the pubic symphyseal texture (Table 4.13).

The medial clavicle and iliac crest were both categorised into only one category by single and multiple observers and could not produce a Cohen's kappa value.

Three of the indicators that were selected for one or more of the final mathematical models namely the posterior median palatine and zygomaticomaxillary suture as well as the auricular surface exostoses, achieved poor agreement values that were equal to or lower than chance agreement (Table 4.13). The two cranial sutures were problematic between multiple observers, whereas the auricular surface exostoses were problematic between single and multiple observers. These indicators were retained within the multifactorial models as observer agreement could possibly be improved whereas the age-related data that an indicator contributes is a valuable attribute. The observer agreement of these indicators could potentially be improved through observer training and improved category descriptions and photos.

4.10. Figures

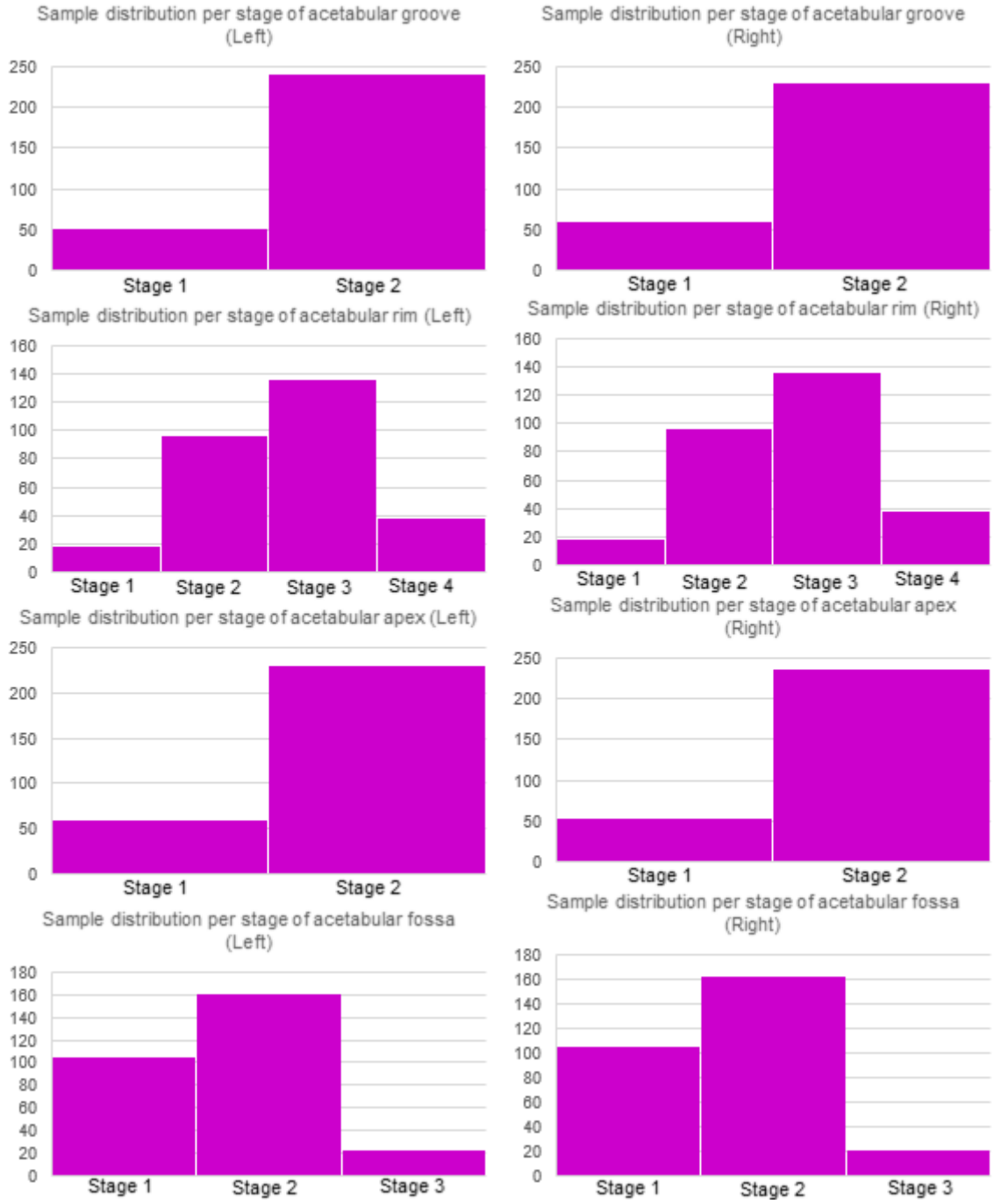


Figure 4.1: Histogram of sample distribution per stage of left and right acetabular groove, rim, apex and fossa.

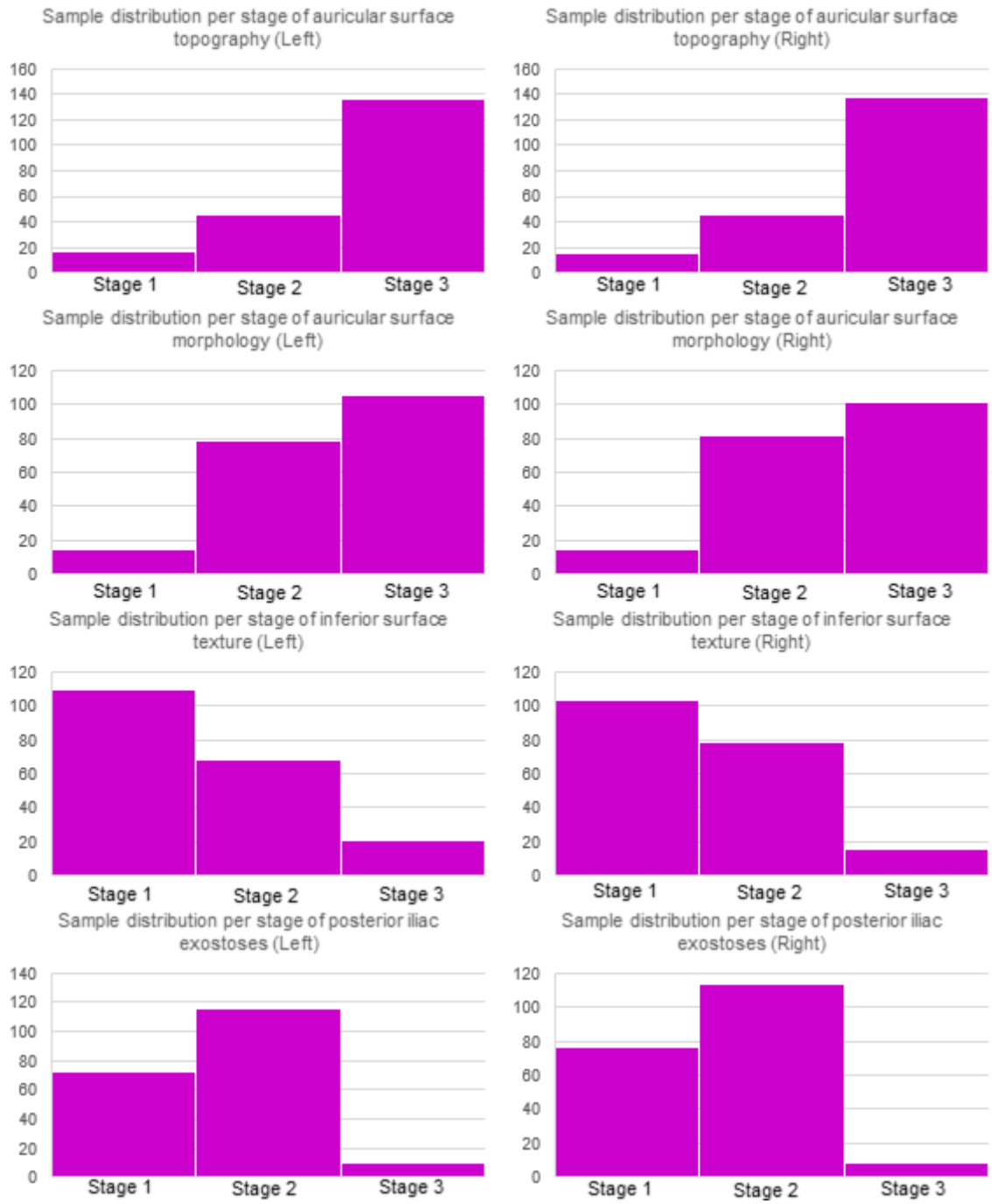


Figure 4.2: Histogram of sample distribution per stage of left and right auricular surface topography, morphology, texture and posterior iliac exostoses.

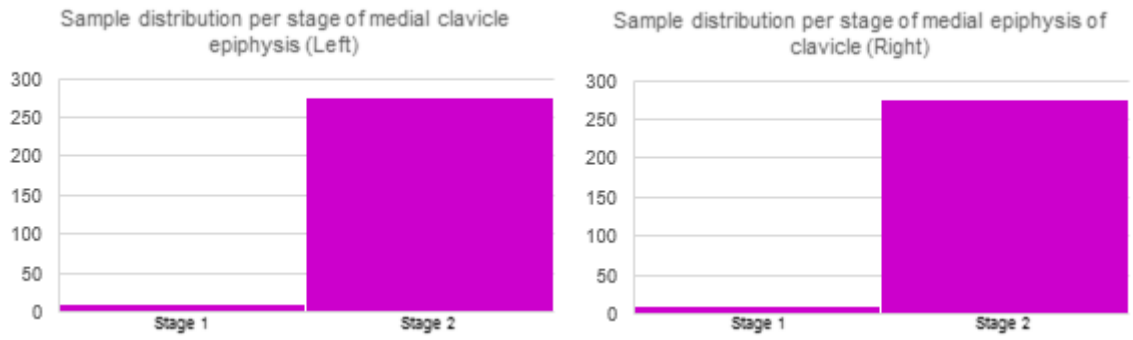


Figure 4.3: Histogram of sample distribution per stage of left and right medial epiphysis of the clavicle.



Figure 4.4: Histogram of sample distribution per stage of left and right midlambdoid, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary sutures, as well as, lambda, obelion, vertex, bregma, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures.

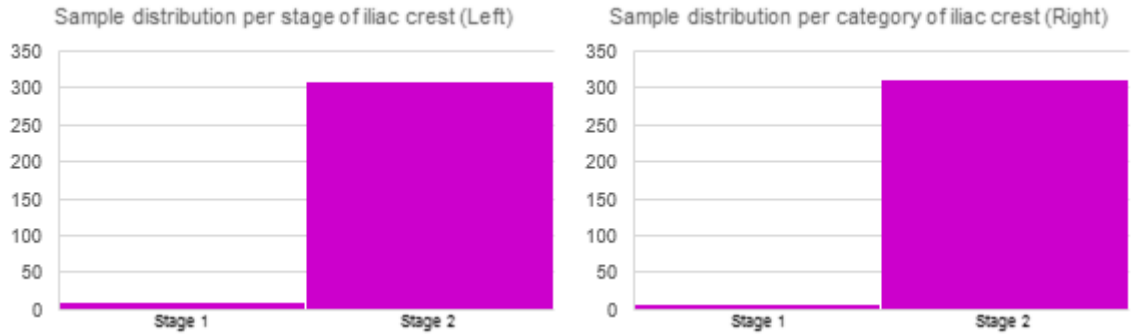


Figure 4.5: Histogram of sample distribution per stage of left and right iliac crest.

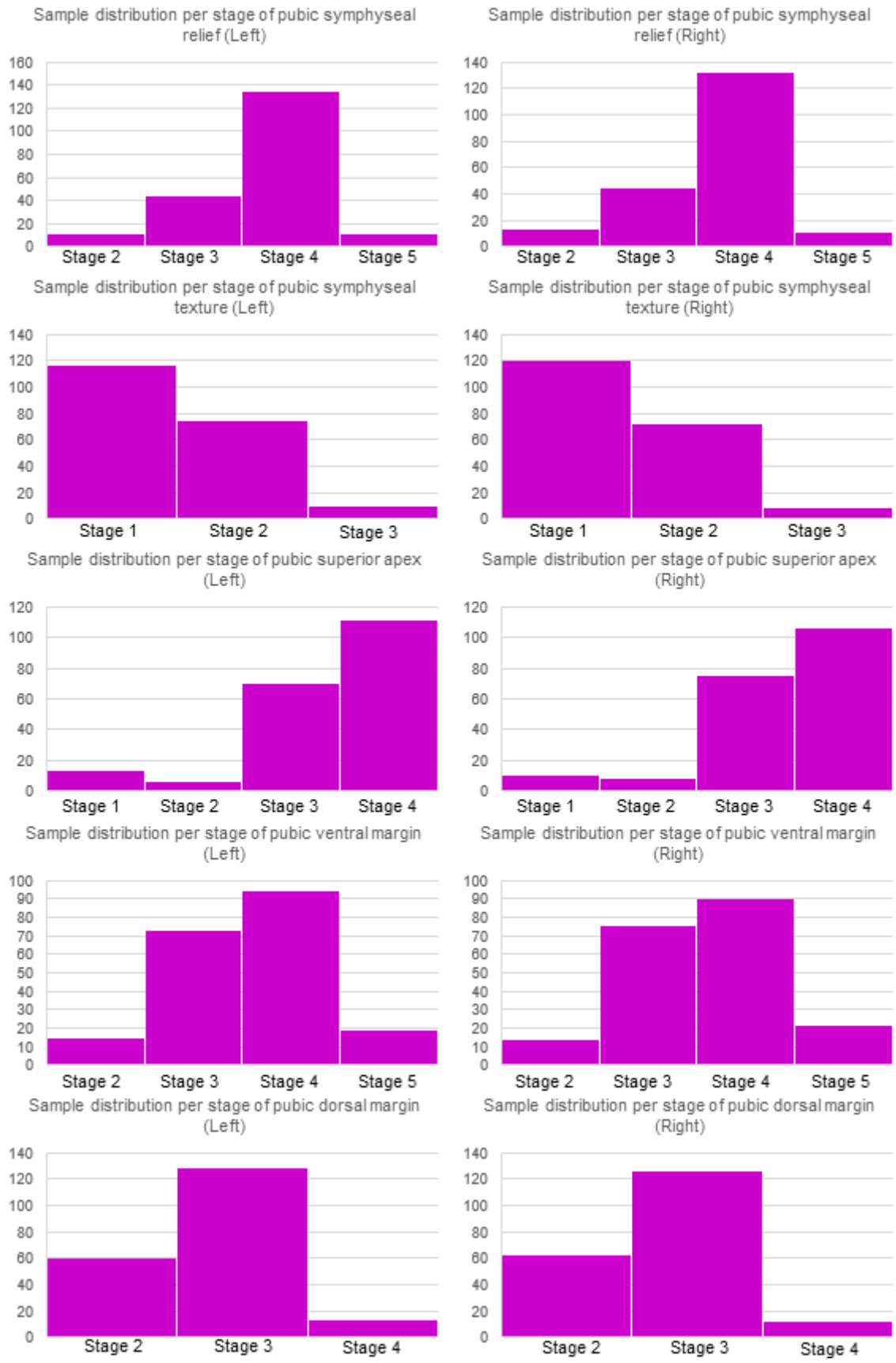


Figure 4.6: Histogram of sample distribution per stage of left and right pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin.

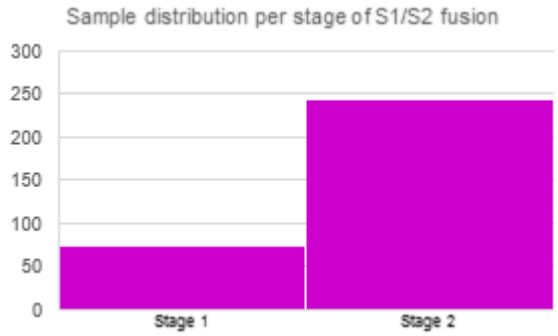


Figure 4.7: Histogram of sample distribution per stage of S1/S2 fusion.

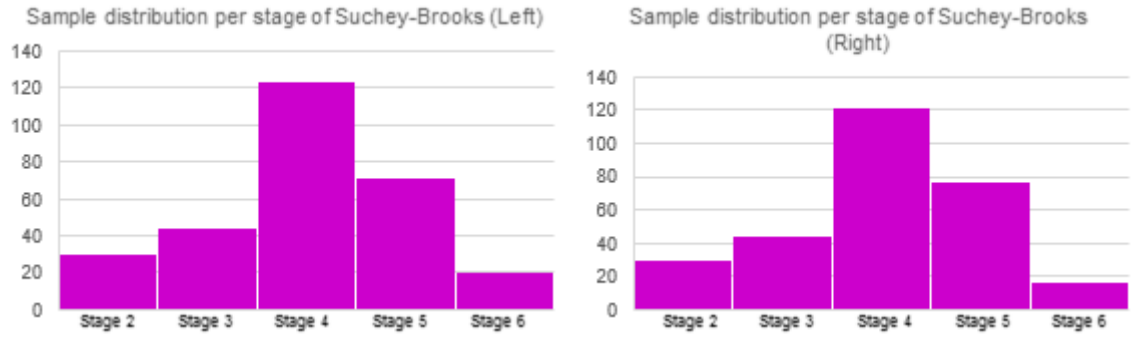


Figure 4.8: Histogram of sample distribution per stage of left and right pubic symphysis (Suchey-Brooks stage-based method).

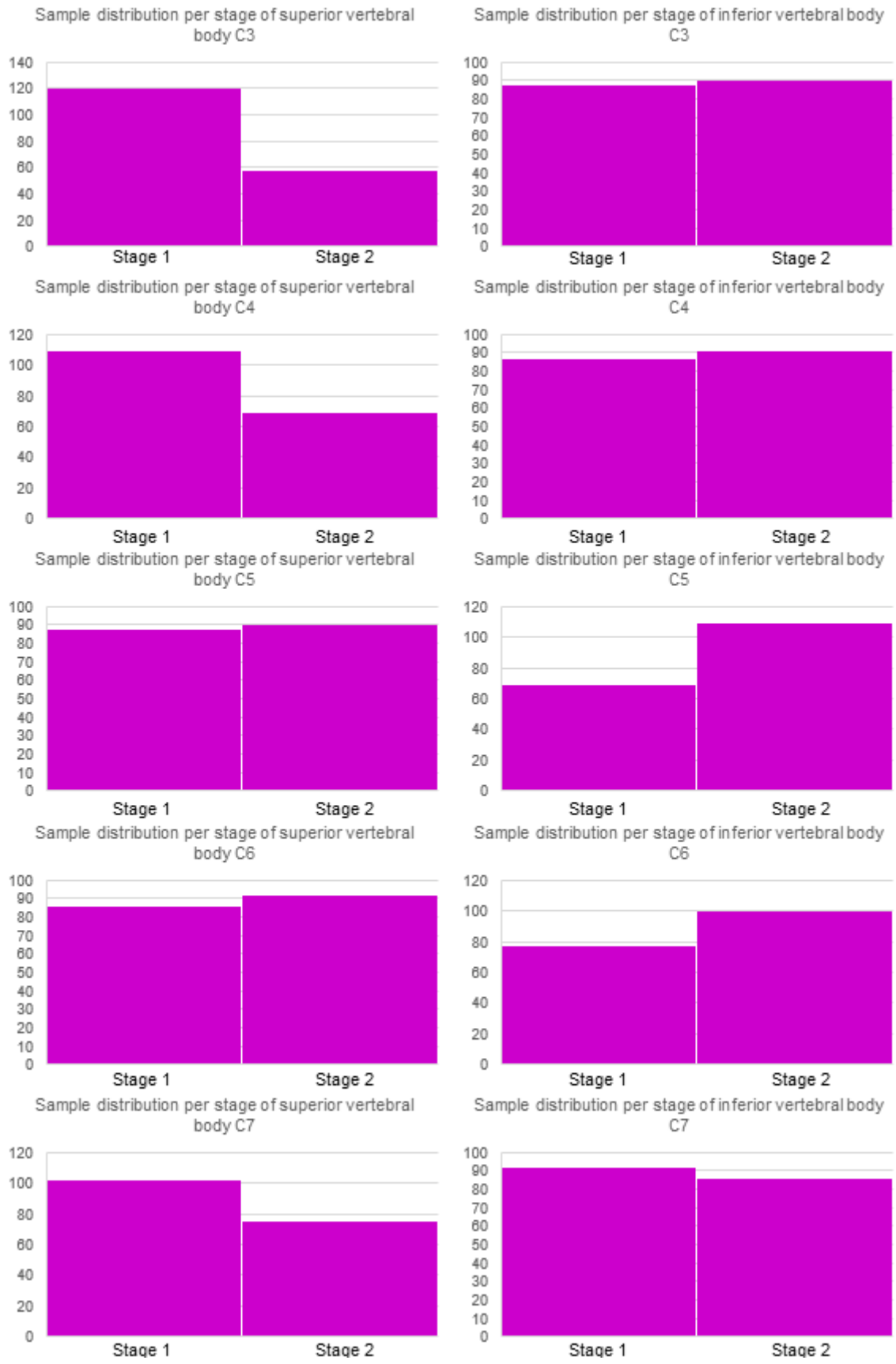


Figure 4.9: Histogram of sample distribution per stage of superior and inferior cervical vertebral bodies (C3 - C7).

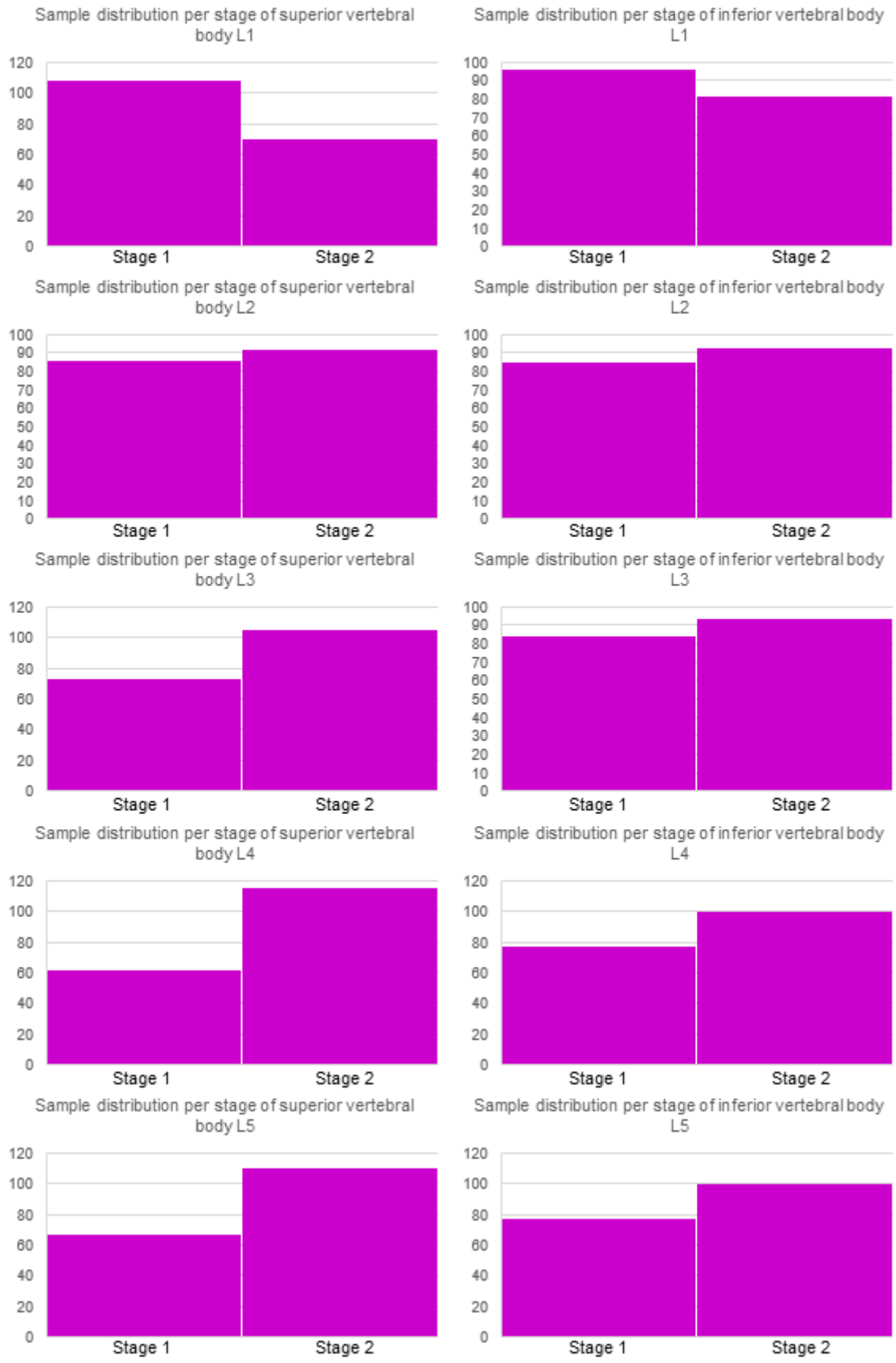


Figure 4.10: Histogram of sample distribution per stage of superior and inferior lumbar vertebral bodies (L1 - L5).

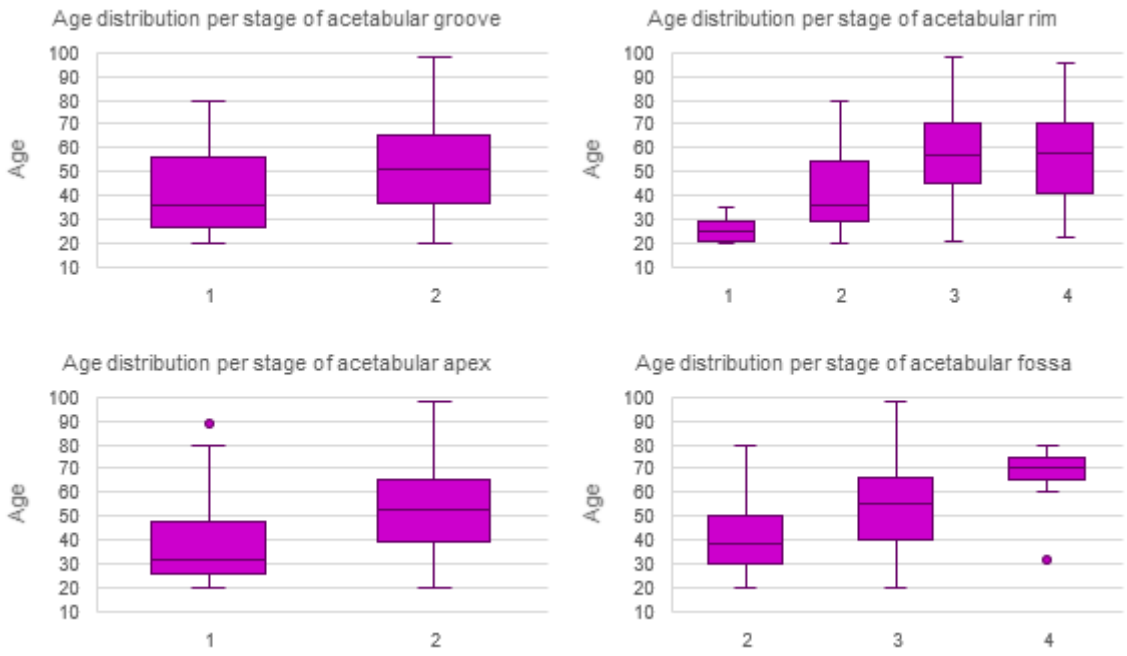


Figure 4.11: Boxplots of age distribution per stage of acetabular groove, rim, apex and fossa.

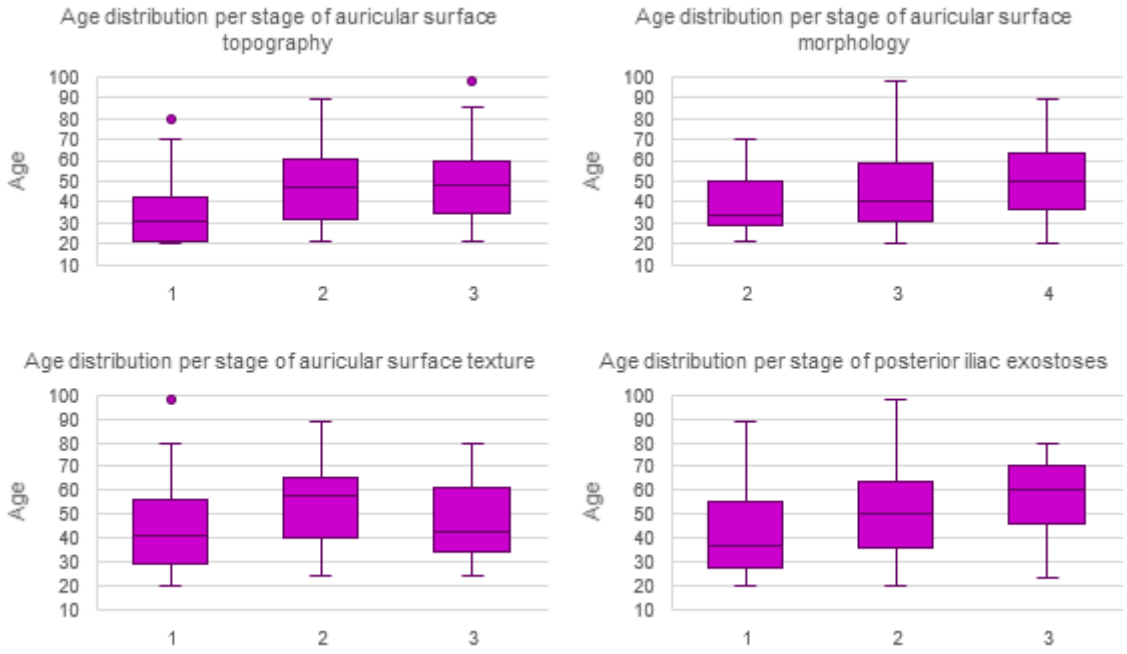


Figure 4.12: Boxplots of age distribution per stage of auricular surface topography, morphology, texture and posterior iliac exostoses.

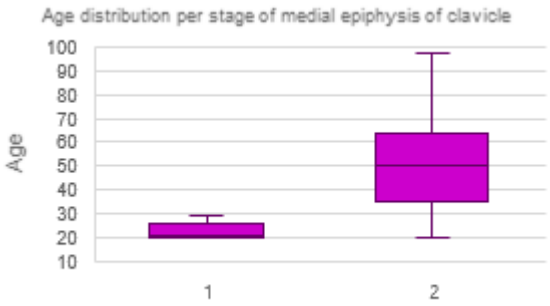


Figure 4.13: Boxplots of age distribution per stage of fusion of medial epiphysis of the clavicle.

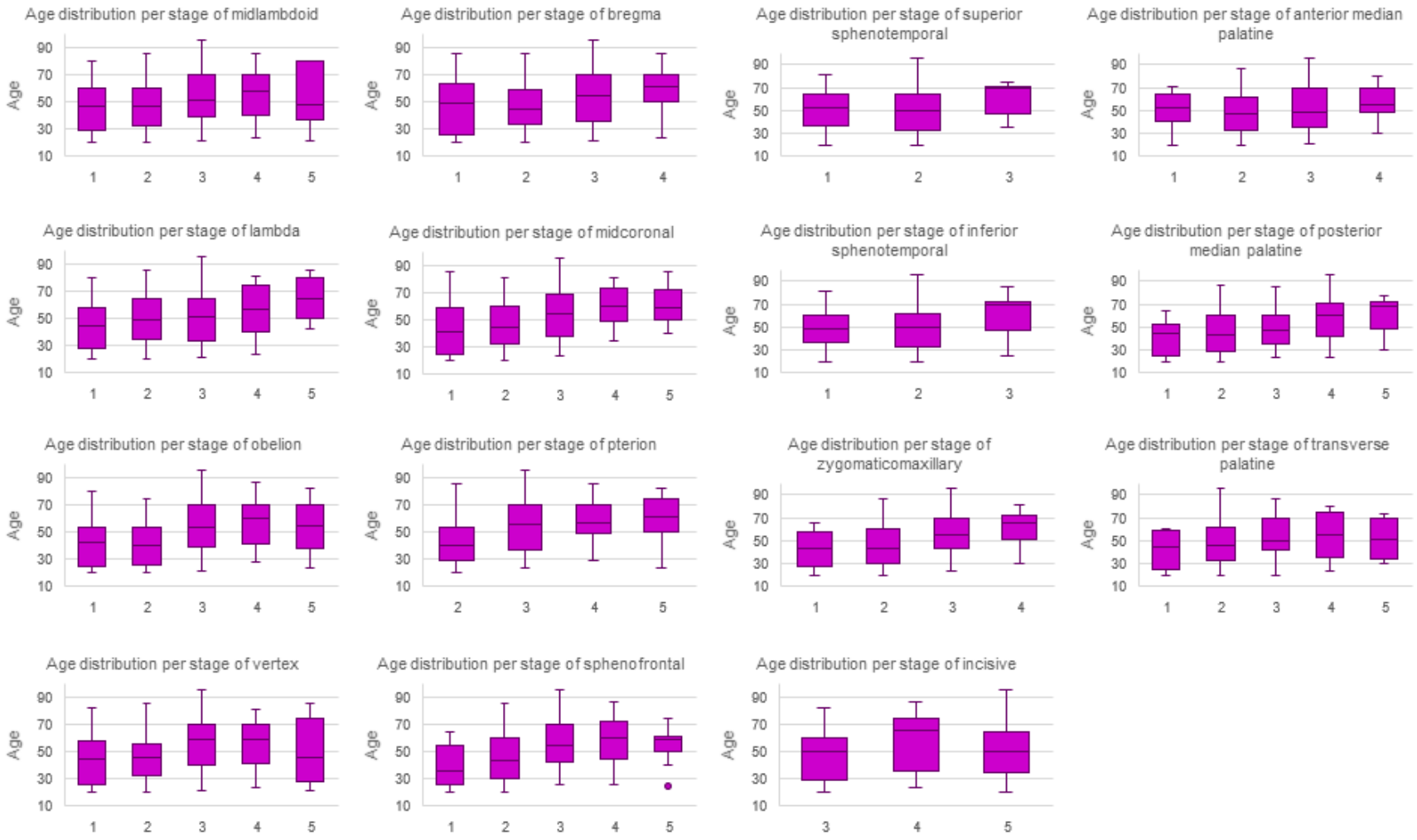


Figure 4.14: Boxplots of age distribution per stage of midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures.

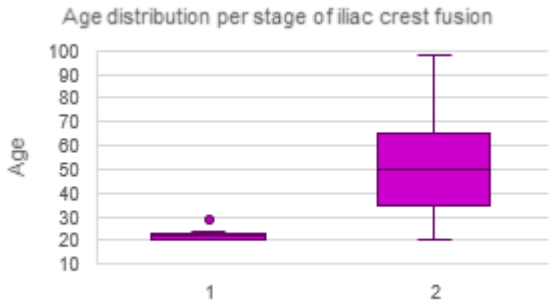


Figure 4.15: Boxplots of age distribution per stage of iliac crest fusion.

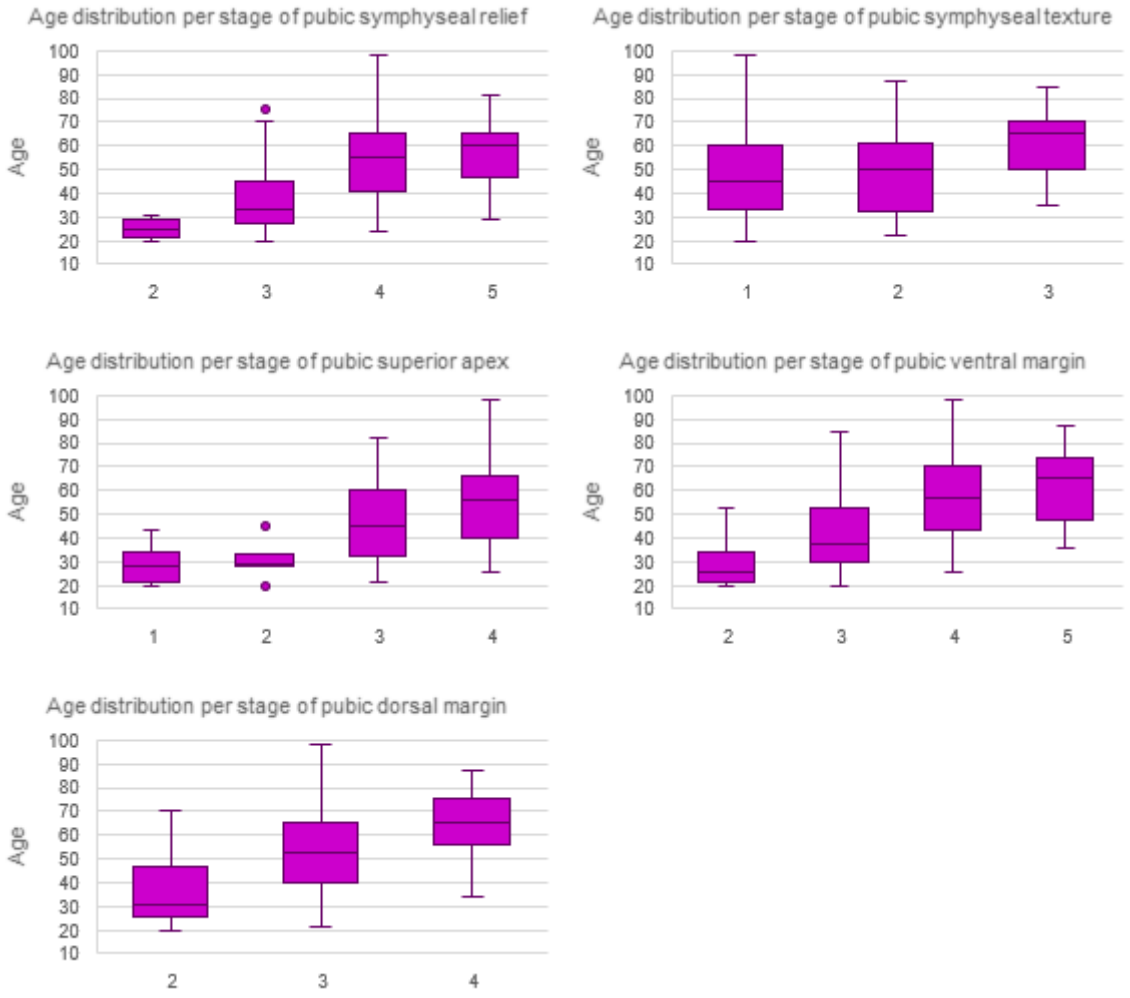


Figure 4.16: Boxplots of age distribution per stage of pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin.

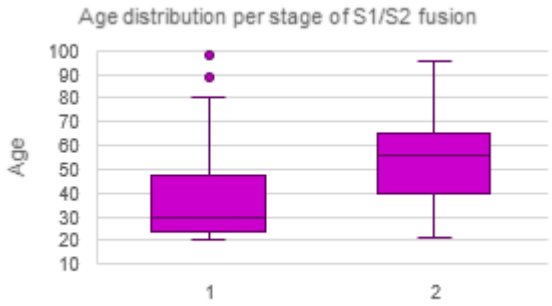


Figure 4.17: Boxplots of age distribution per stage of S1/S2 fusion.

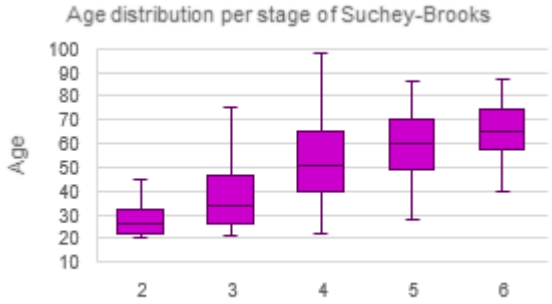


Figure 4.18: Boxplots of age distribution per stage of pubic symphysis (Suchey-Brooks stage-based method).

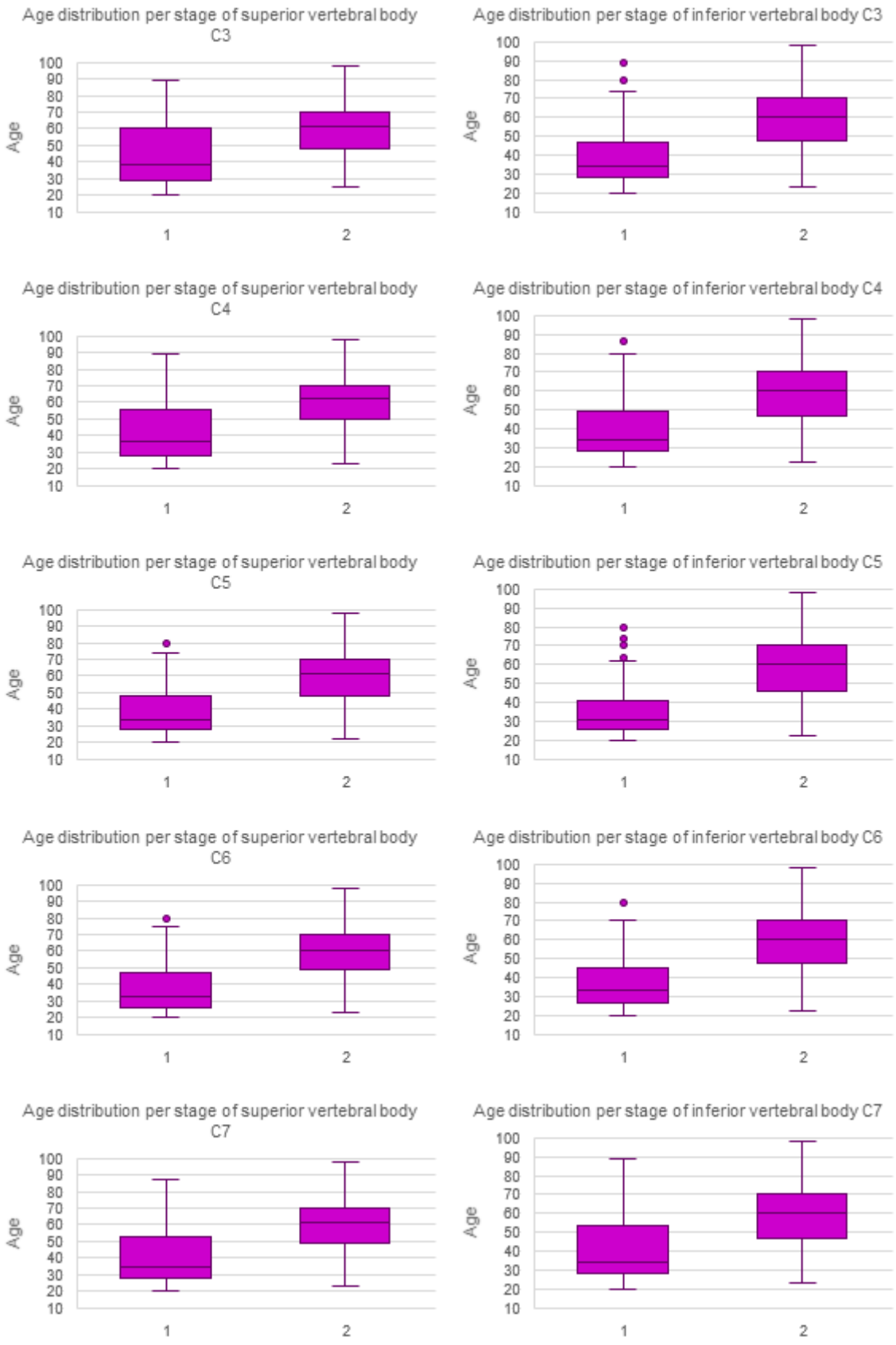


Figure 4.19: Boxplots of age distribution per stage of cervical vertebral bodies (C3 - C7).

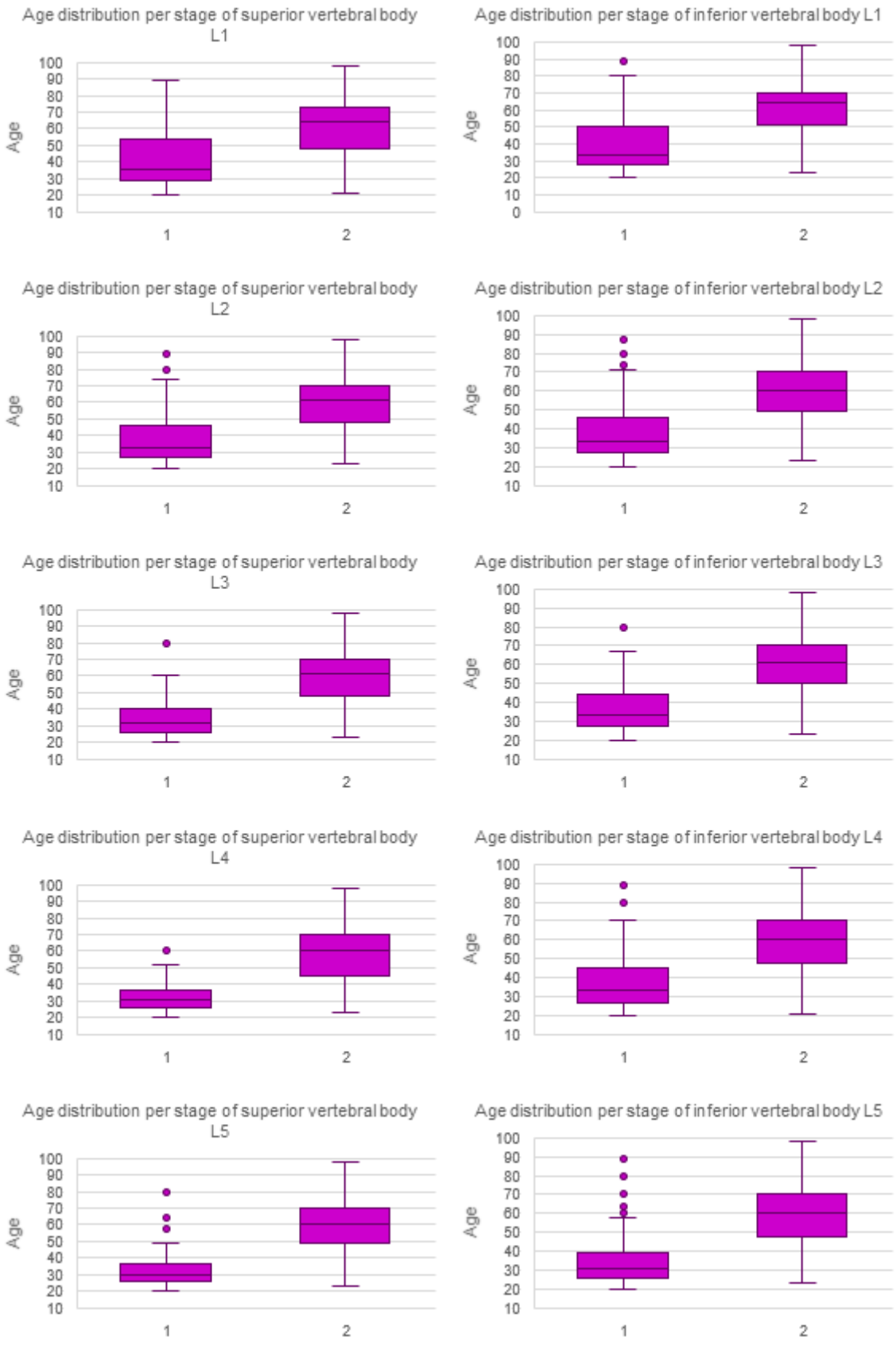


Figure 4.20: Boxplots of age distribution per stage of lumbar vertebral bodies (L1 - L5).

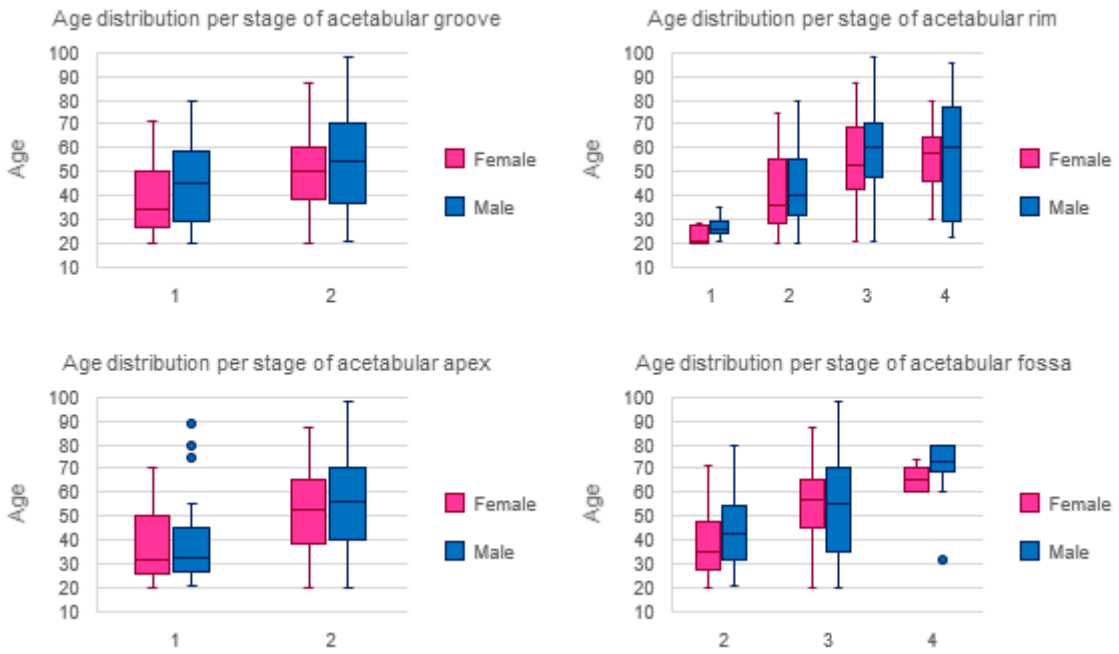


Figure 4.21: Comparison of age distributions per stage of acetabular groove, rim, apex and fossa between females and males.

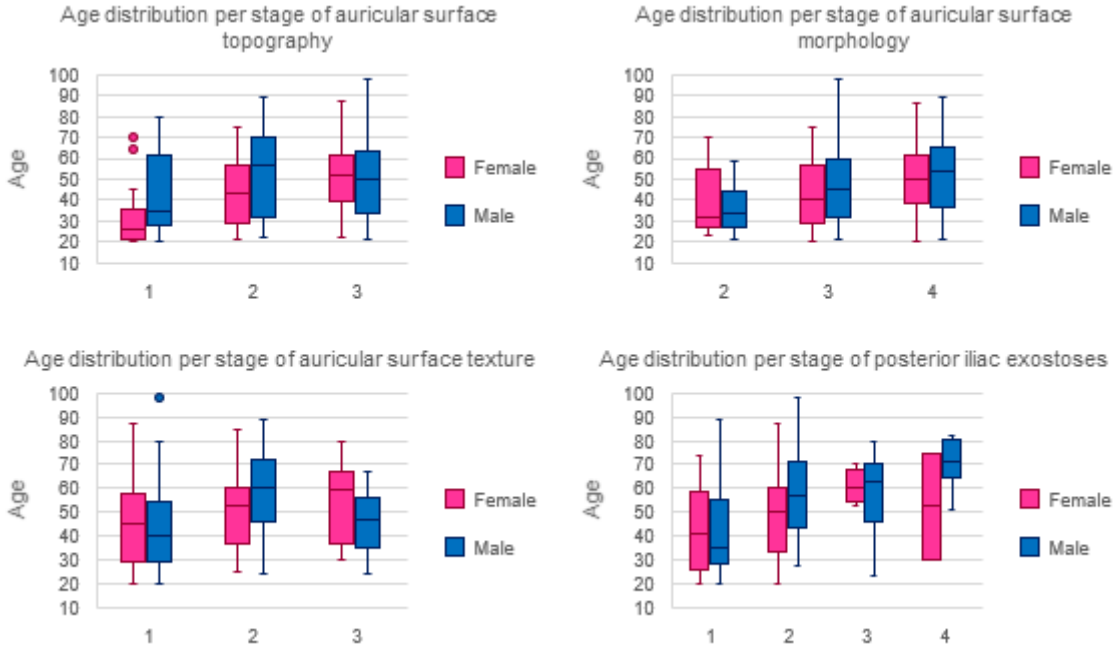


Figure 4.22: Comparison of age distributions per stage of auricular surface topography, morphology, texture and posterior iliac exostoses between females and males.

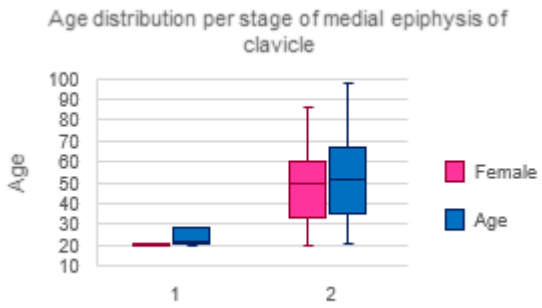


Figure 4.23: Comparison of age distributions per stage of medial epiphysis of the clavicle between females and males.

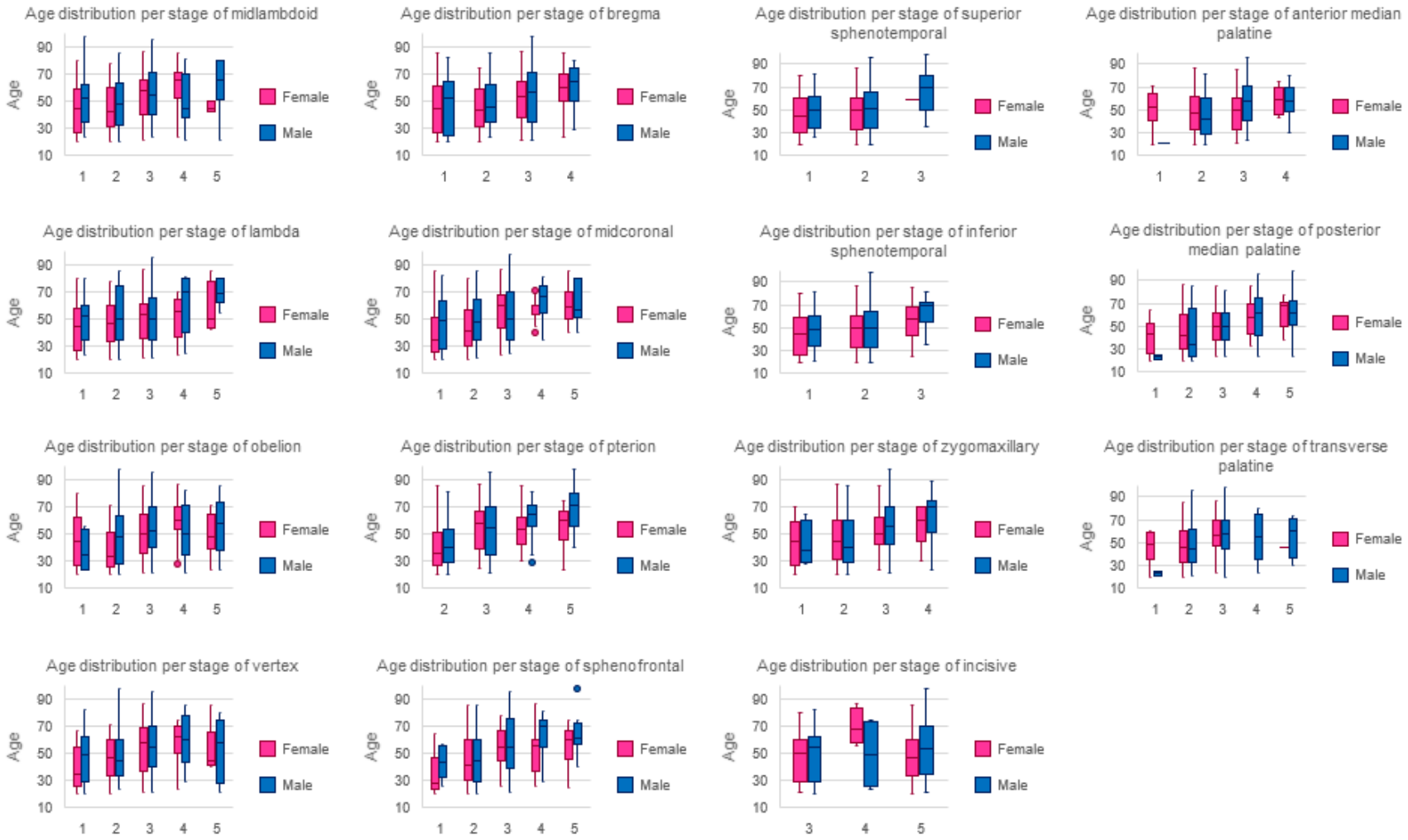


Figure 4.24: Comparison of age distributions per stage of midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures between females and males.

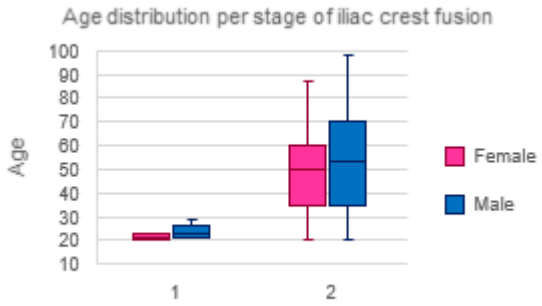


Figure 4.25: Comparison of age distributions per stage of iliac crest fusion.

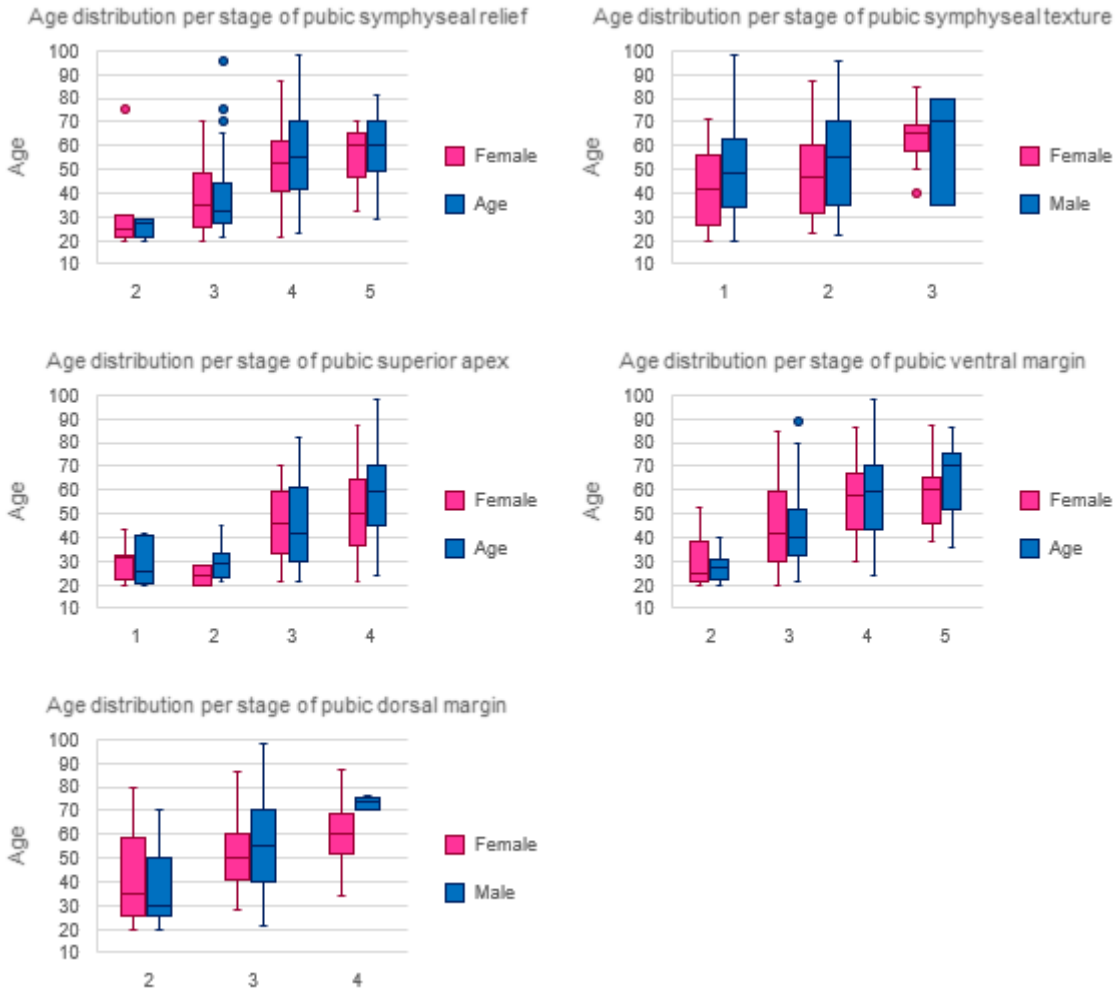


Figure 4.26: Comparison of age distributions per stage of pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin between females and males.

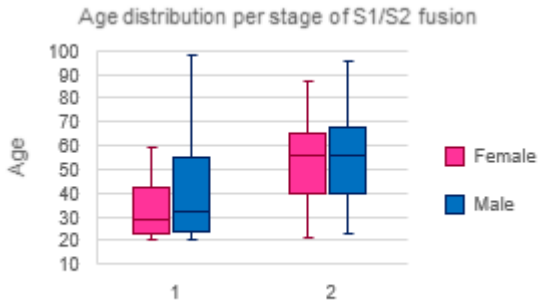


Figure 4.27: Comparison of age distributions per stage of S1/S2 fusion between females and males.

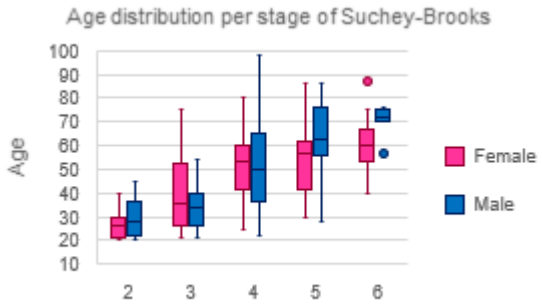


Figure 4.28: Comparison of age distributions per stage of pubic symphysis (Suchey-Brooks stage-based method).

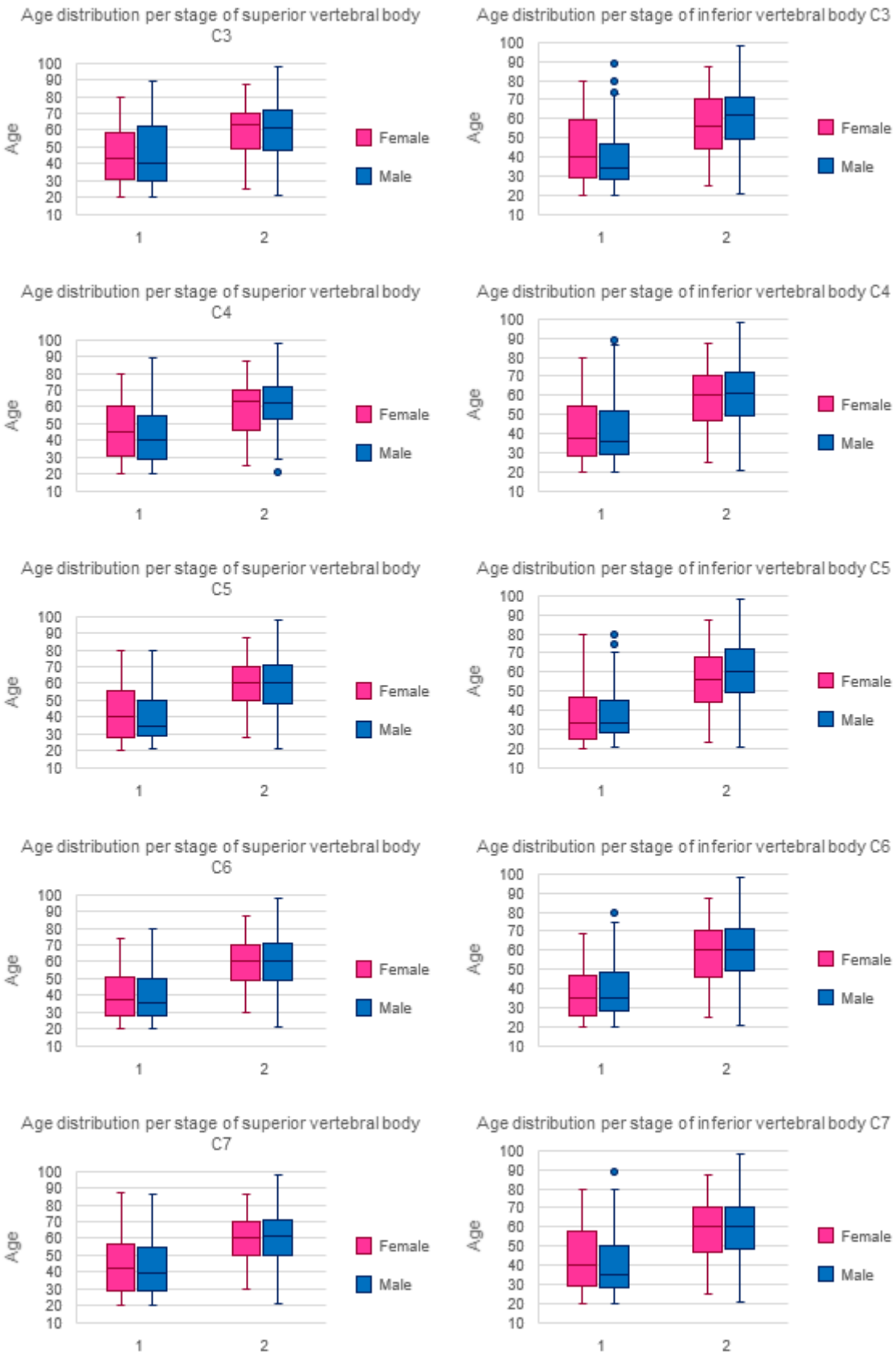


Figure 4.29: Comparison of age distributions per stage of cervical vertebral bodies (C3 - C7) between females and males.

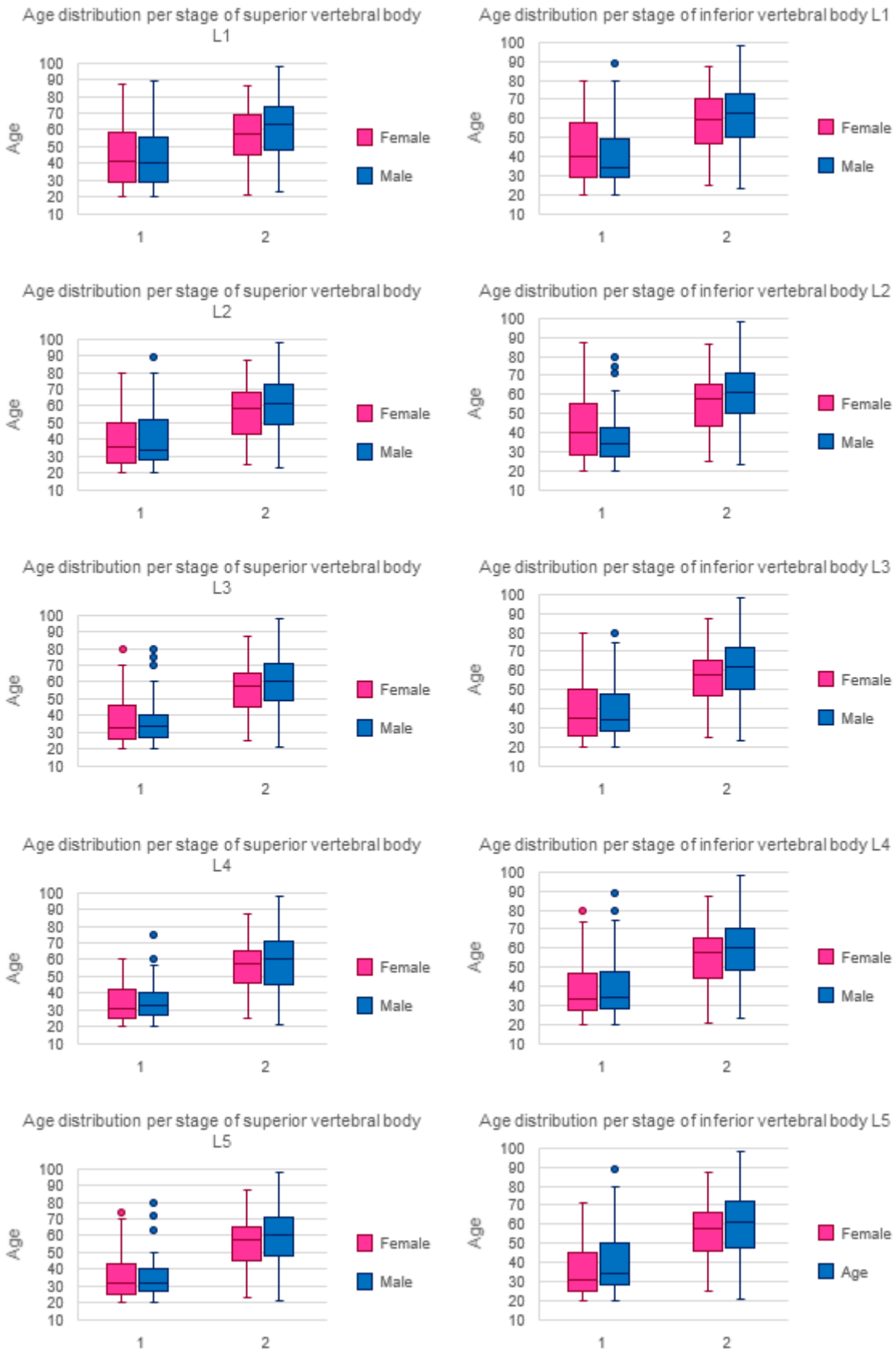


Figure 4.30: Comparison of age distributions per stage of lumbar vertebral bodies (L1 - L5) between females and males.

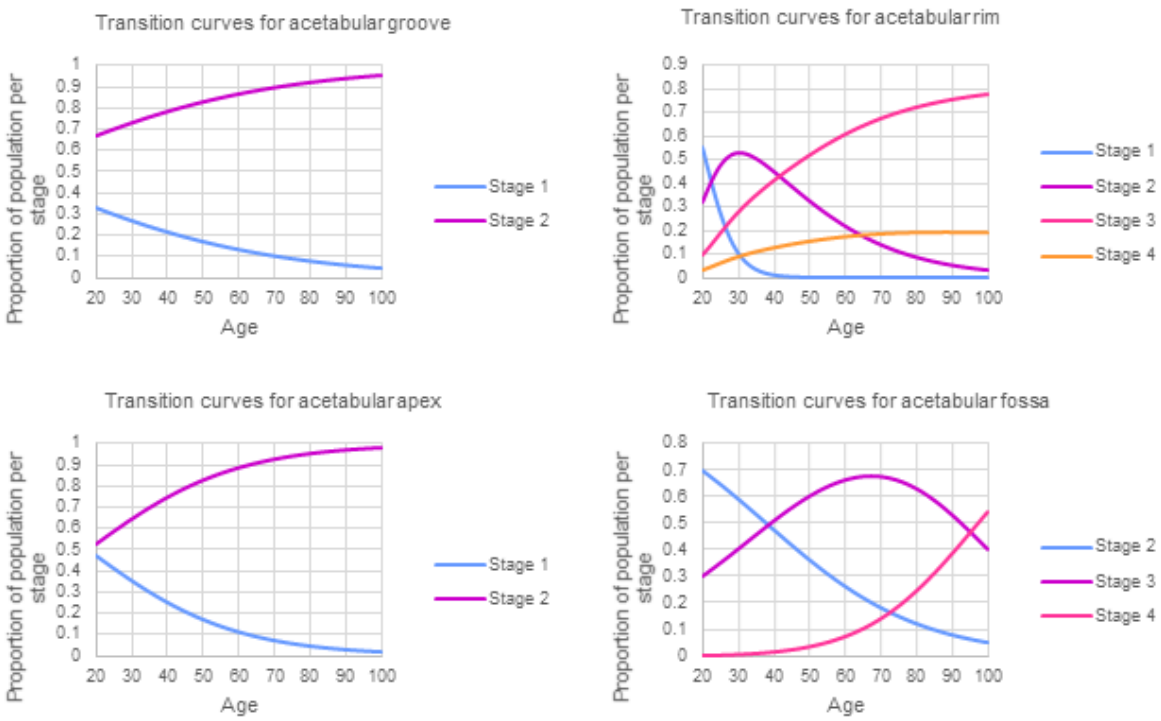


Figure 4.31: Transition curves for stages of the acetabular groove, rim, apex and fossa.

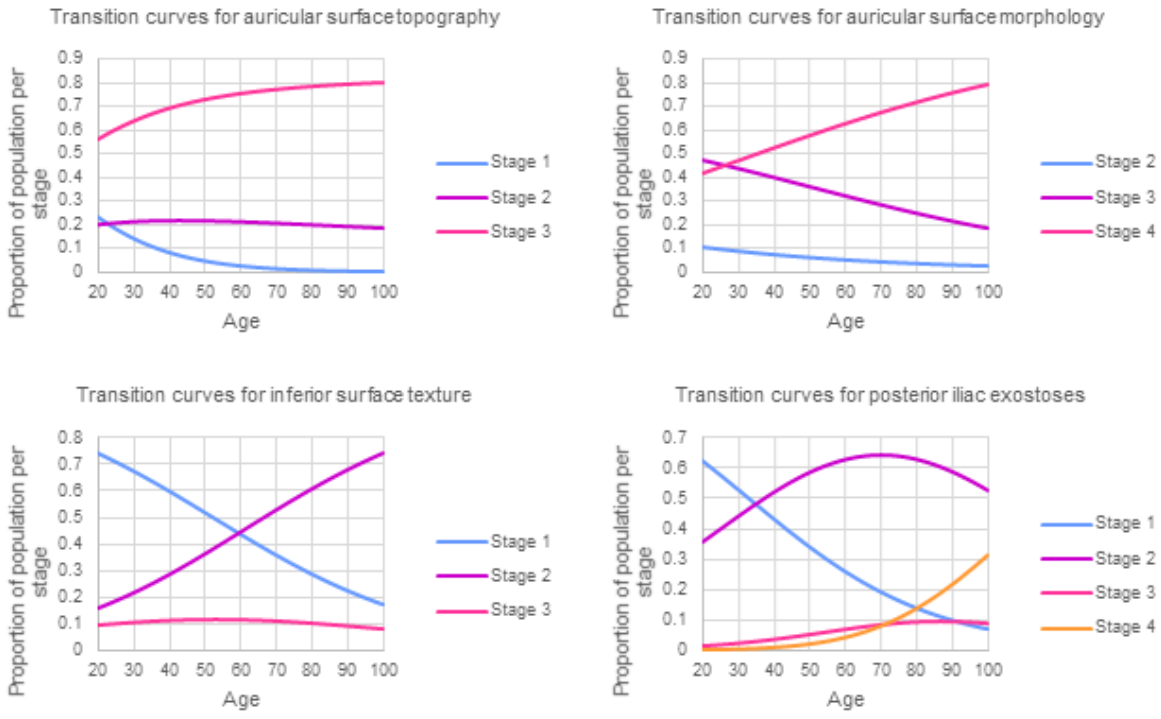


Figure 4.32: Transition curves for stages of auricular surface topography, morphology, texture and posterior iliac exostoses.

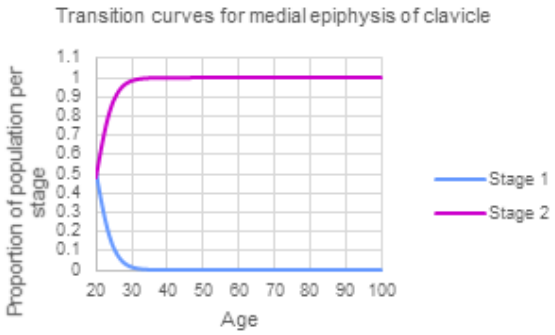


Figure 4.33: Transition curves for stages of the medial epiphysis of the clavicle.

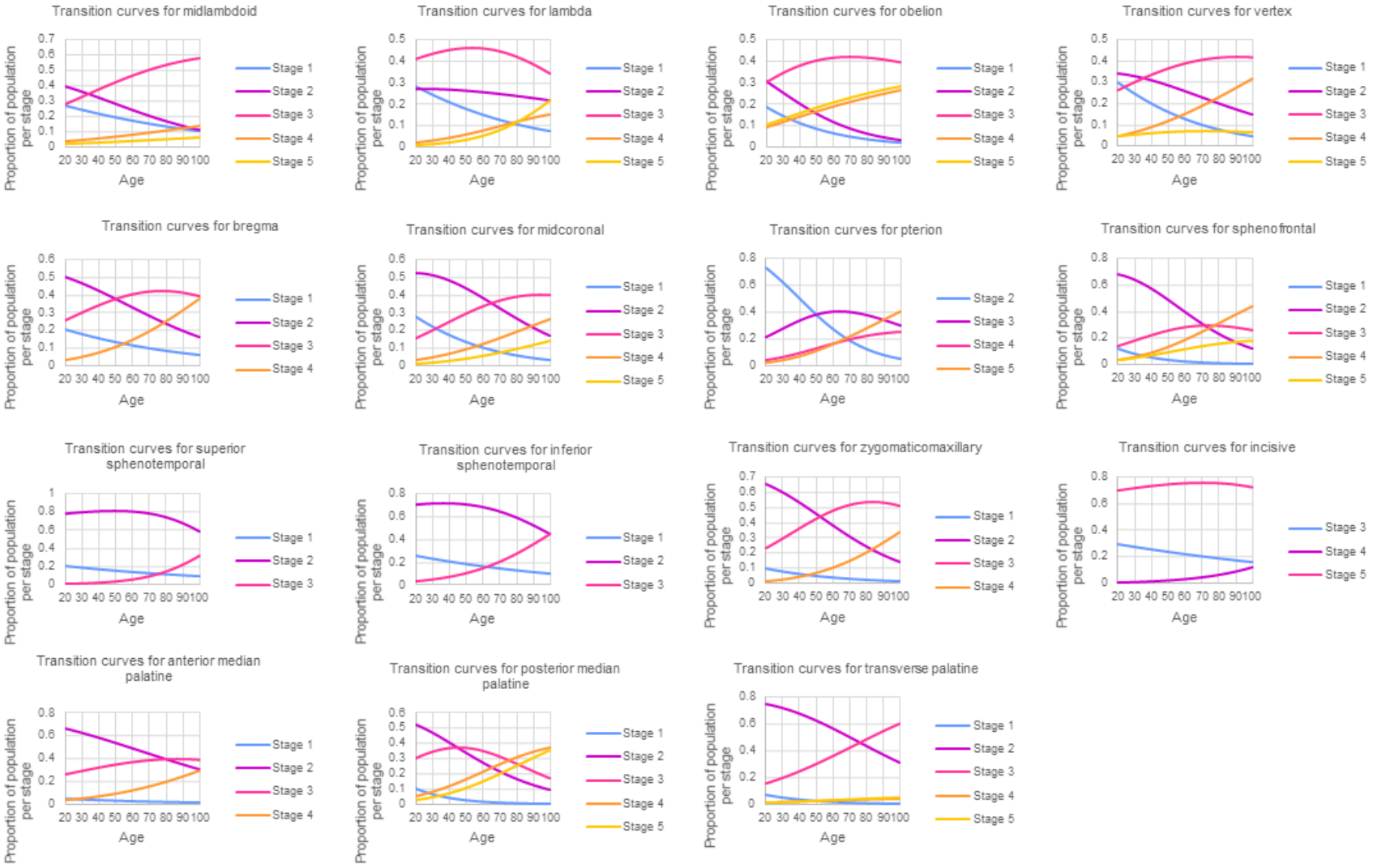


Figure 4.34: Transition curves for stages of midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median, palatine and transverse palatine sutures.

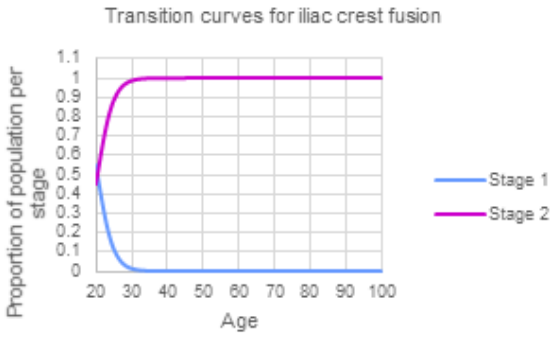


Figure 4.35: Transition curves for stages of iliac crest fusion.

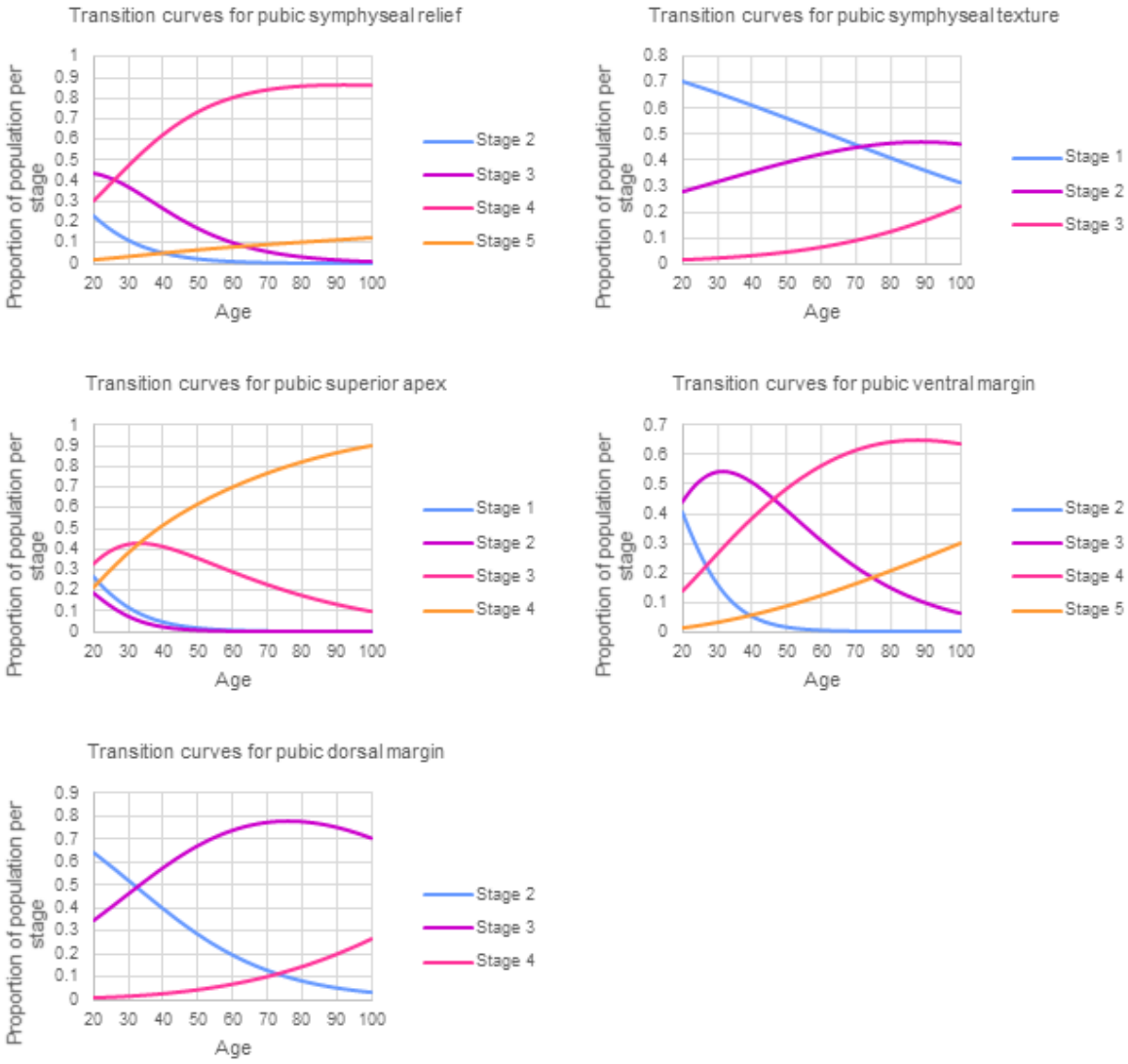


Figure 4.36: Transition curves for stages of pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin.

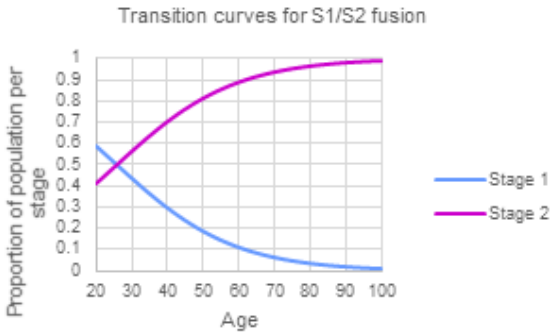


Figure 4.37: Transition curves for stage of S1/S2 fusion.

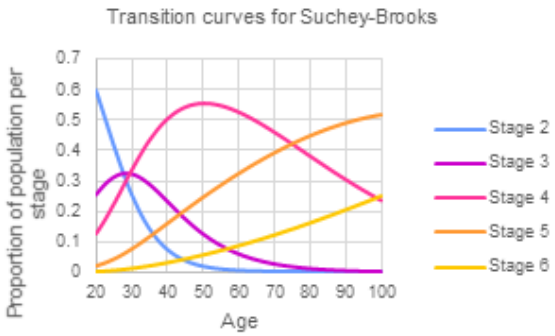


Figure 4.38: Transition curves for stages of the pubic symphysis (Suchey-Brooks stage-based method).

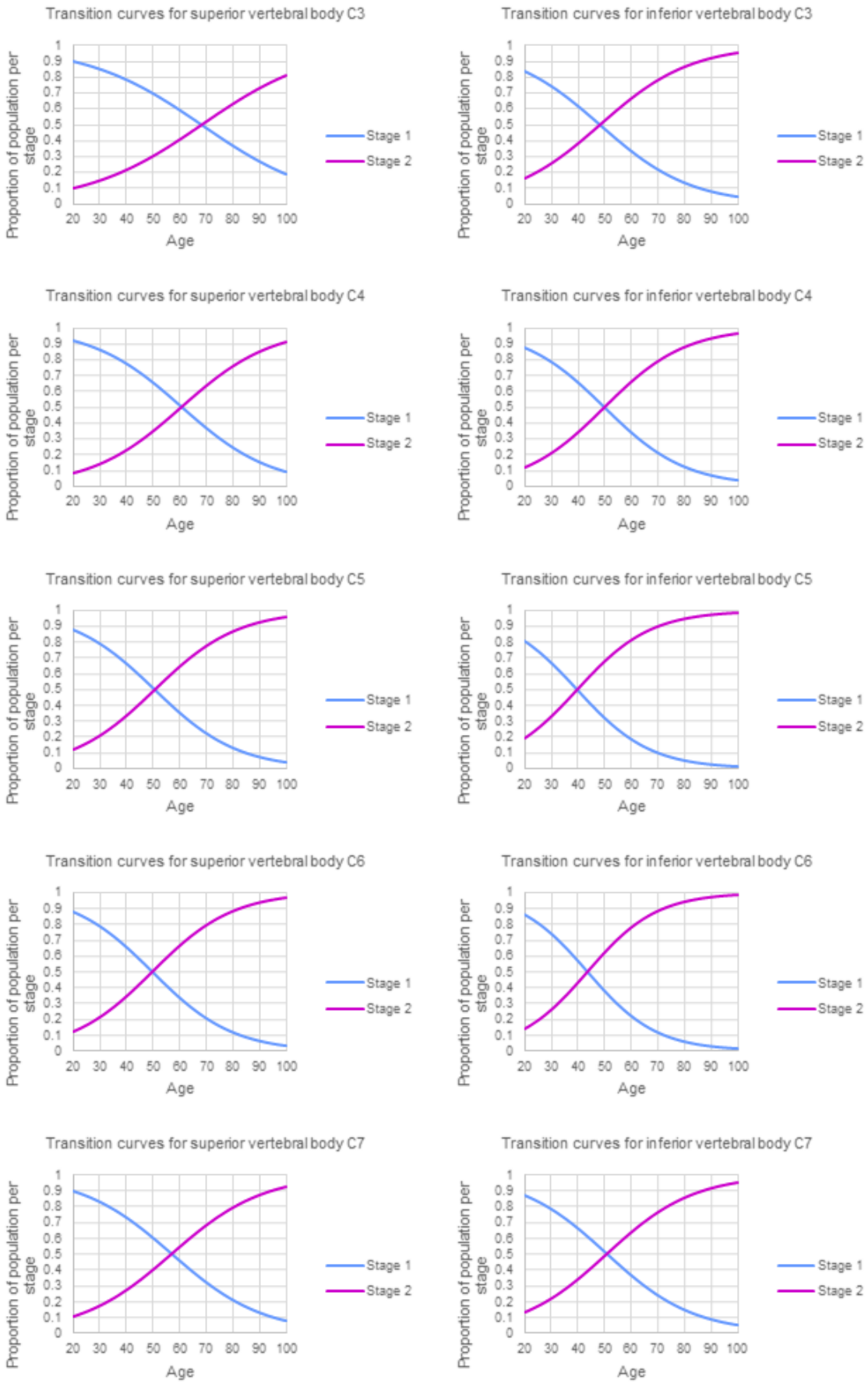


Figure 4.39: Transition curves for stages of the superior and inferior cervical vertebral bodies (C3 - C7).

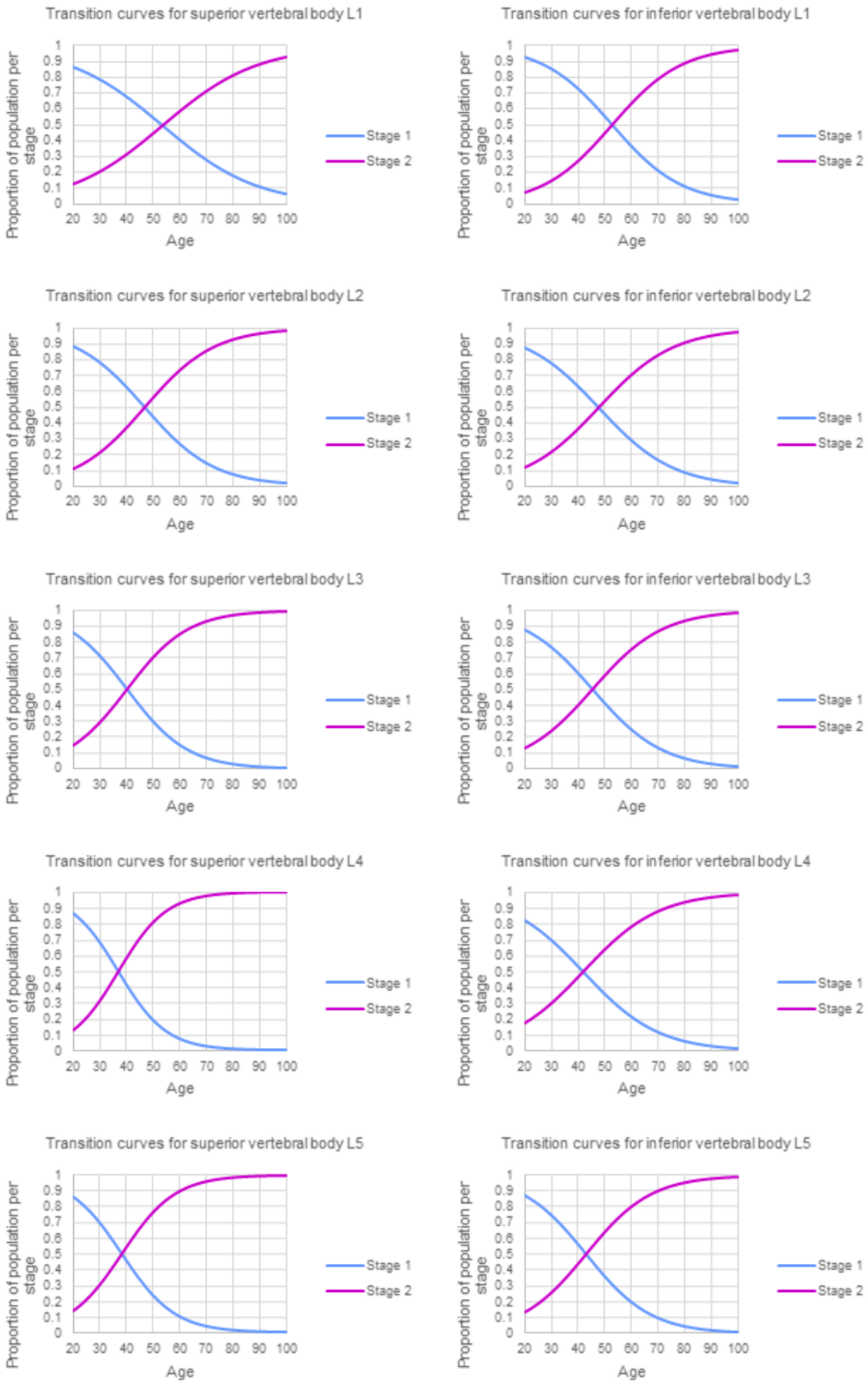


Figure 4.40: Transition curves for stages of the superior and inferior lumbar vertebral bodies (L1 - L5).

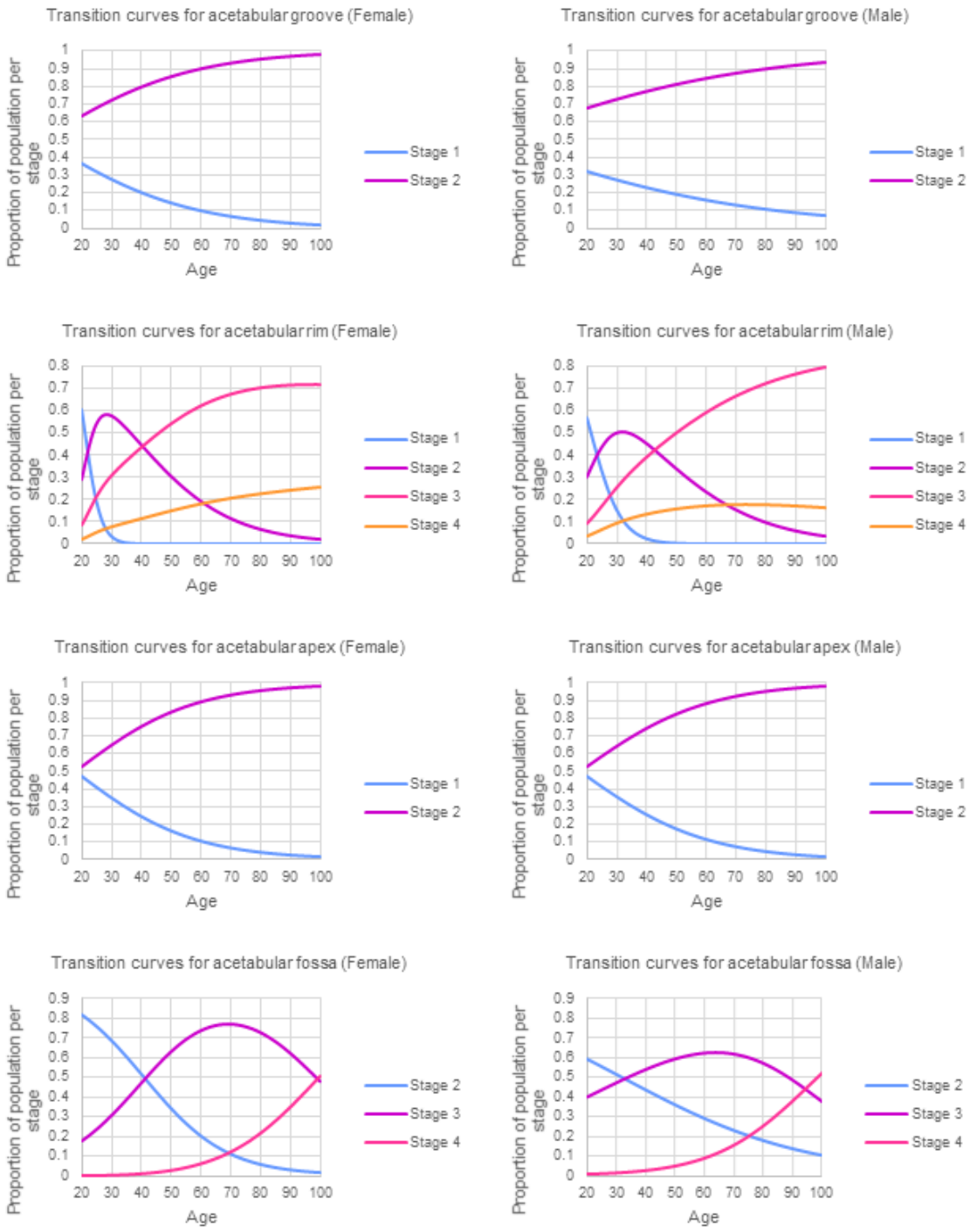


Figure 4.41: Transition curves comparing female and male stages of the acetabular groove, rim, apex and fossa.

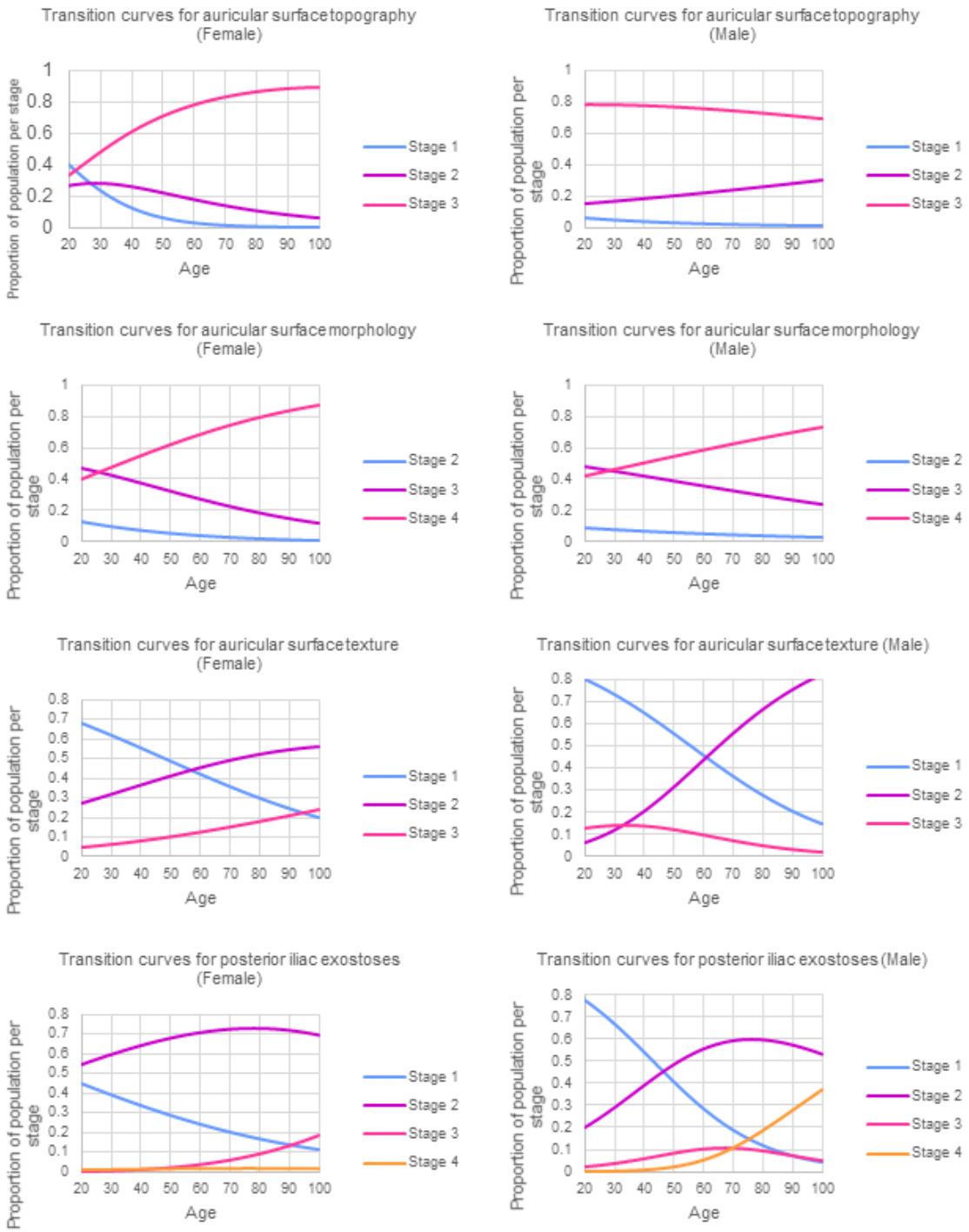


Figure 4.42: Transition curves comparing female and male stages of the auricular surface topography, morphology, texture and posterior iliac exostoses.

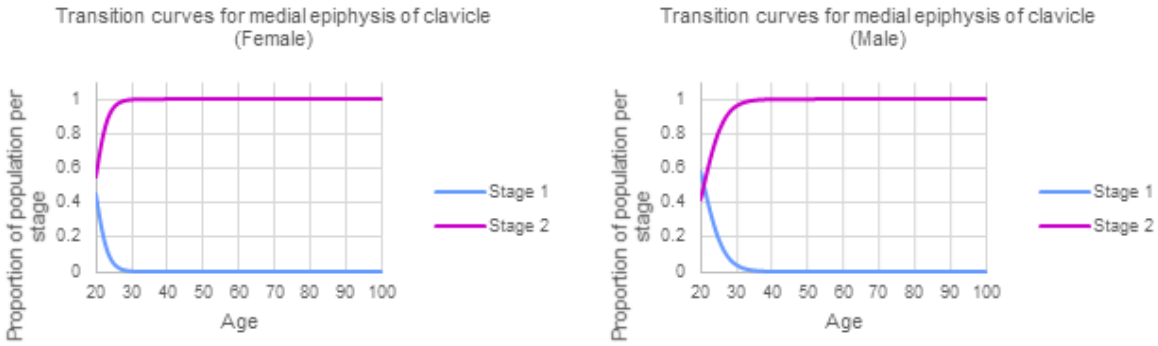


Figure 4.43: Transition curves comparing female and male stages of medial clavicle epiphysis.

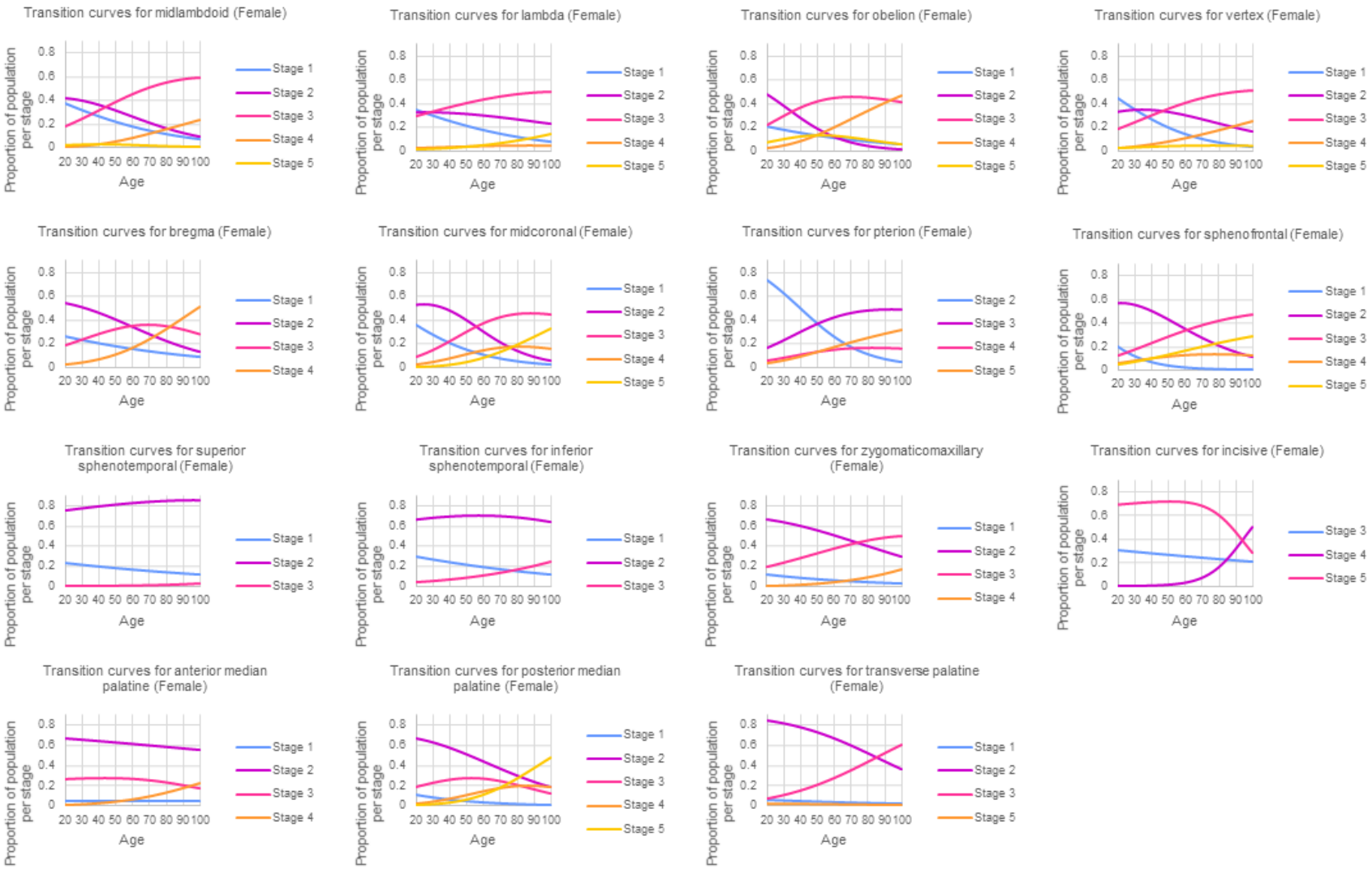


Figure 4.44: Transition curves for stages of female midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures.

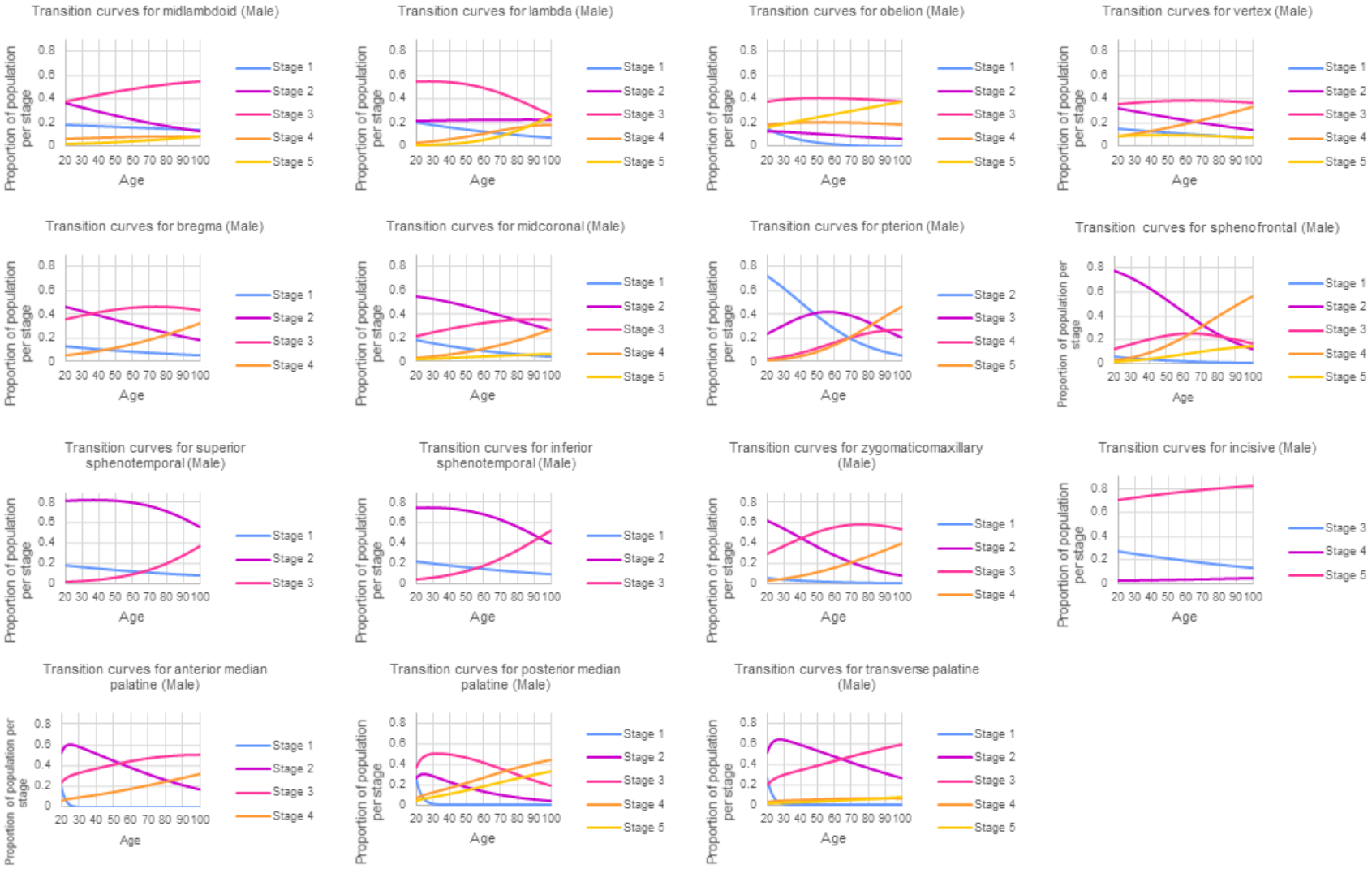


Figure 4.45: Transition curves for stages of male midlambdoid, lambda, obelion, vertex, bregma, midcoronal, pterion, sphenofrontal, superior sphenotemporal, inferior sphenotemporal, zygomaticomaxillary, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures.

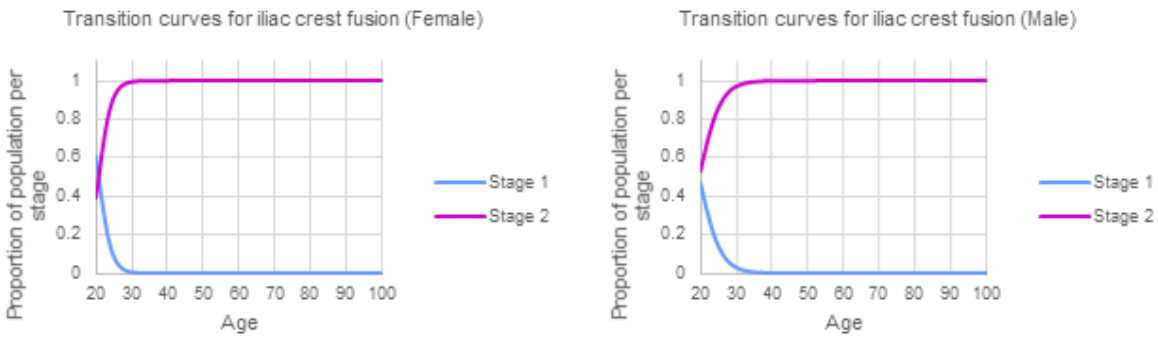


Figure 4.46: Transition curves comparing female and male stages of iliac crest fusion.

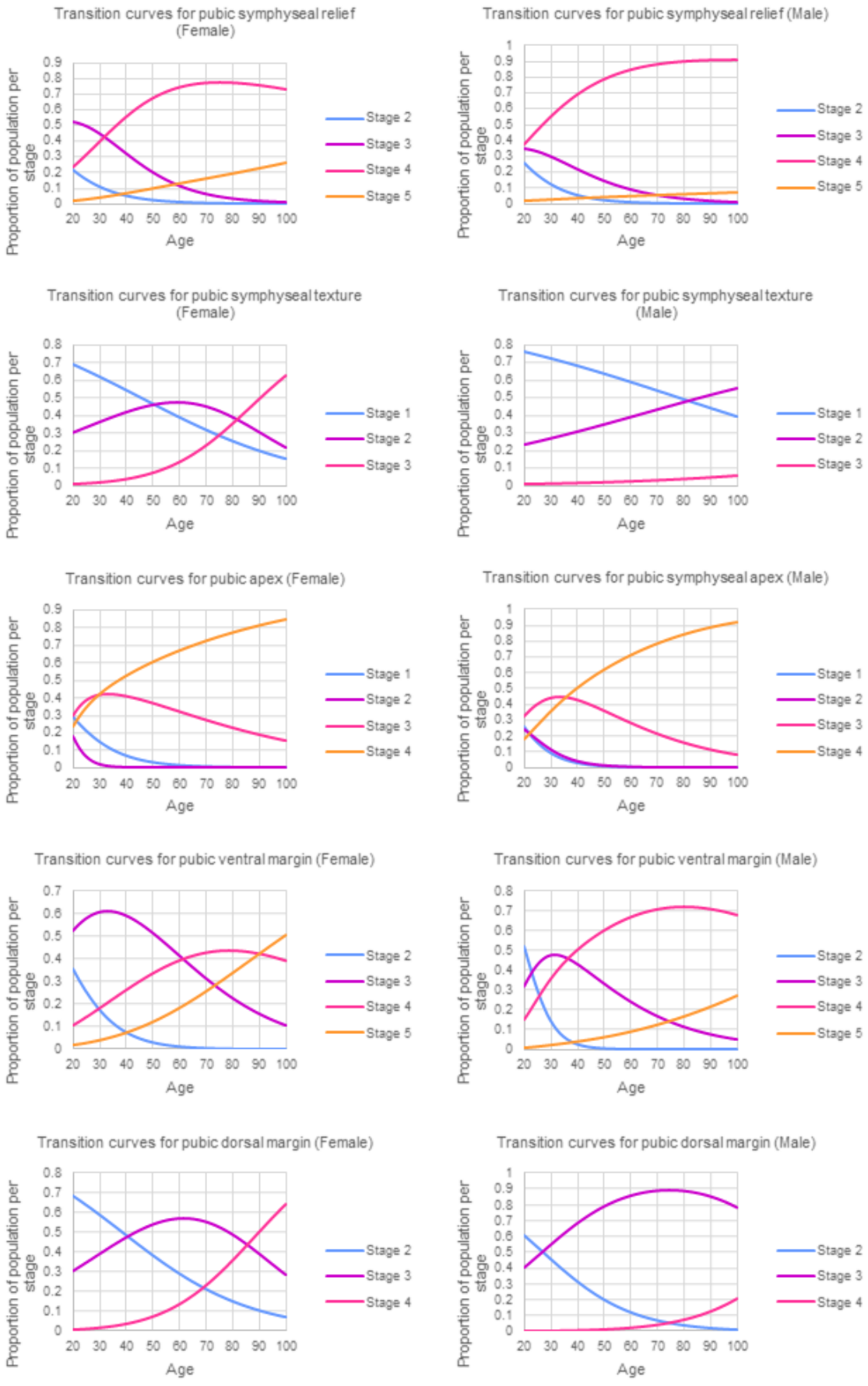


Figure 4.47: Transition curves comparing female and male stages of pubic symphyseal relief, texture, superior apex, ventral margin and dorsal margin.

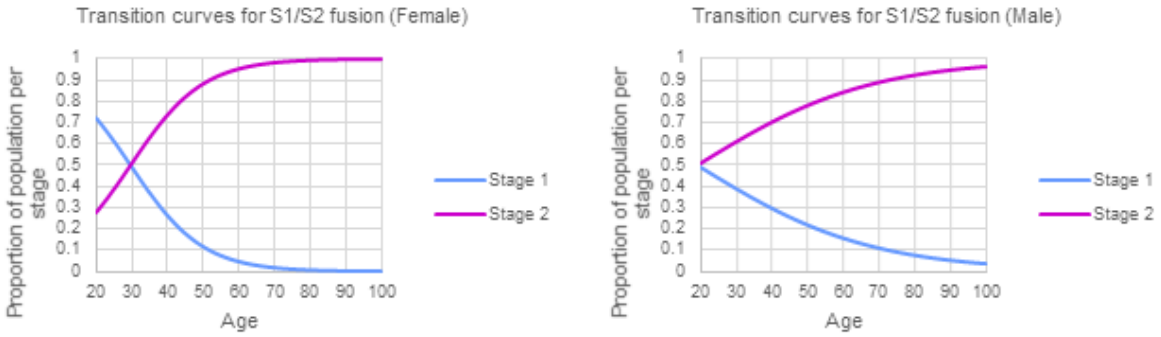


Figure 4.48: Transition curves comparing female and male stages of S1/S2 fusion.

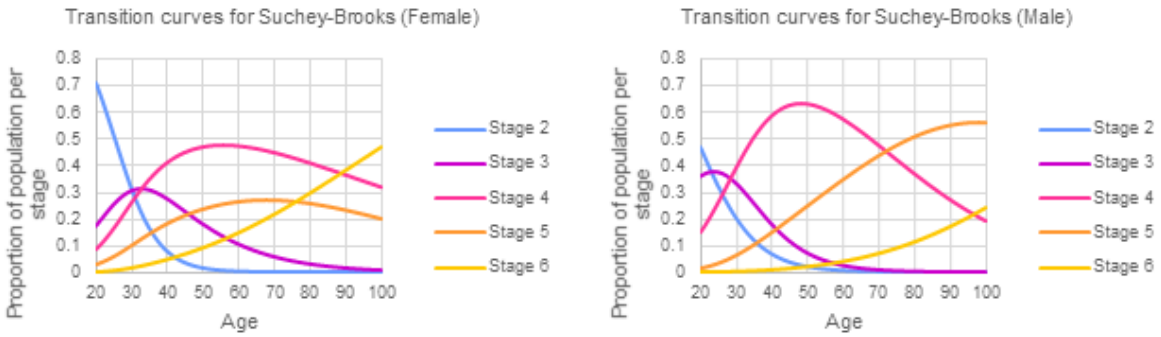


Figure 4.49: Transition curves comparing female and male stages of the pubic symphysis (Suchey-Brooks stage-based method).

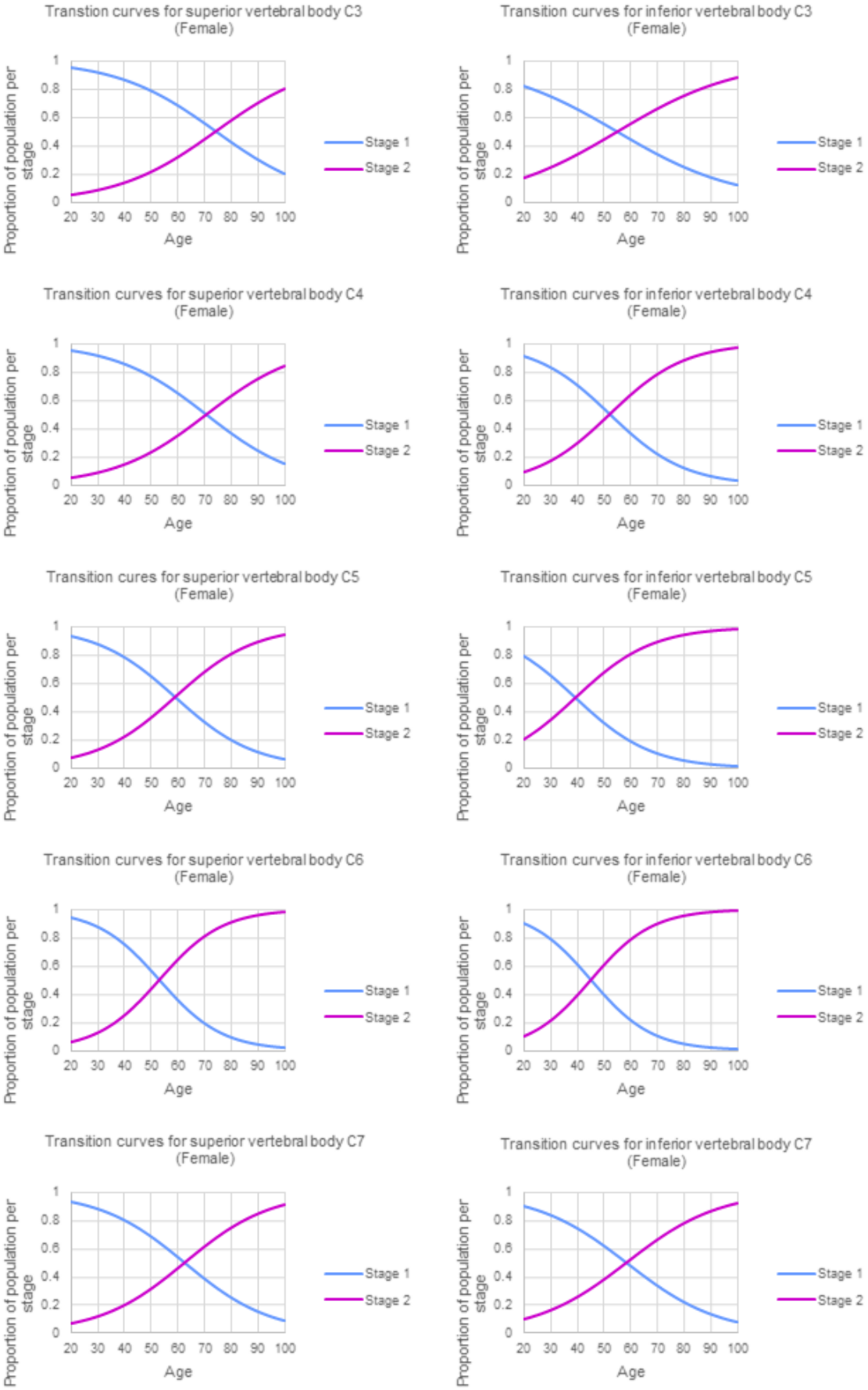


Figure 4.50: Transition curves for stages of female superior and inferior cervical vertebral bodies (C3 - C7).

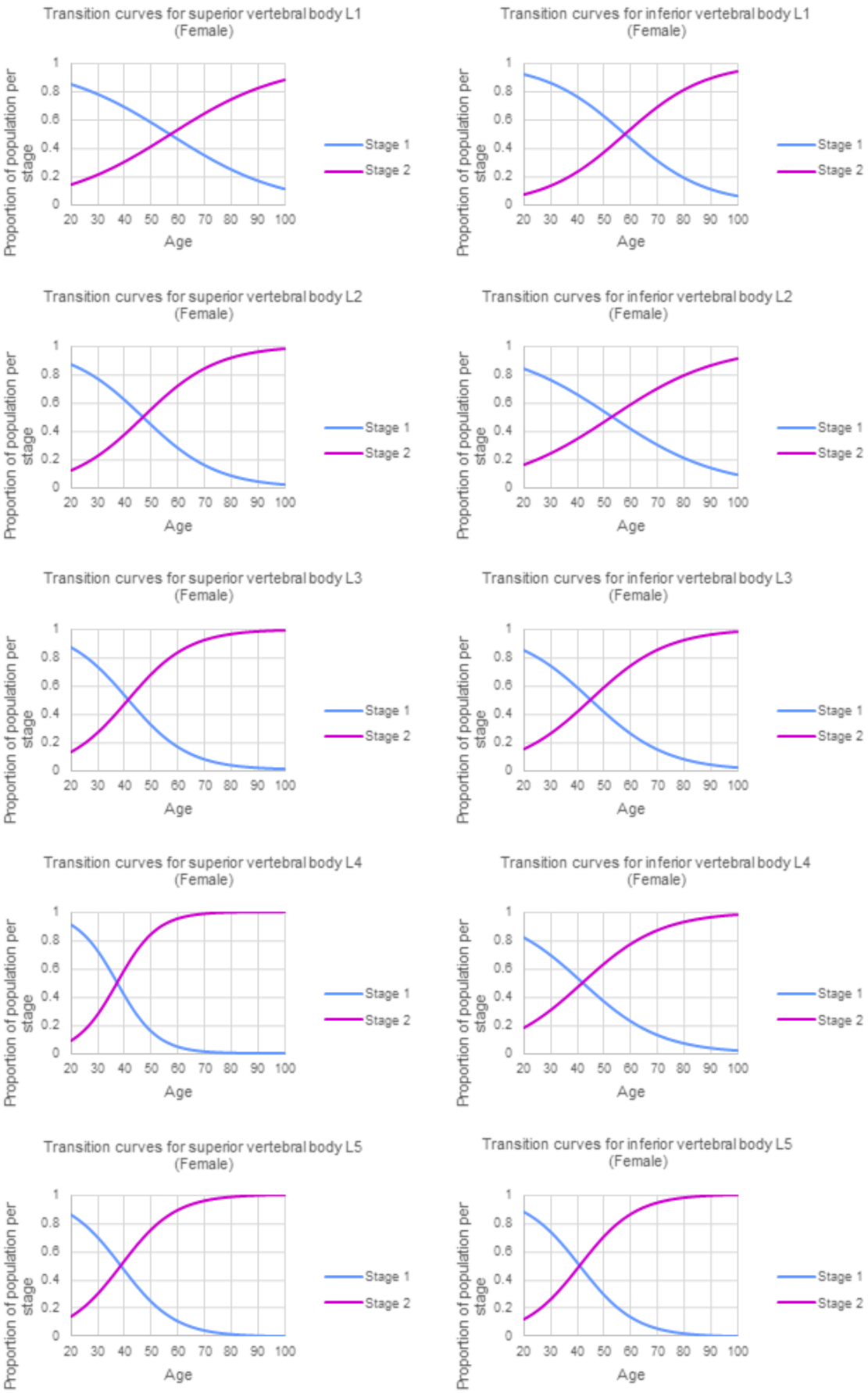


Figure 4.51: Transition curves for stages of female superior and inferior lumbar vertebral bodies (L1 - L5).

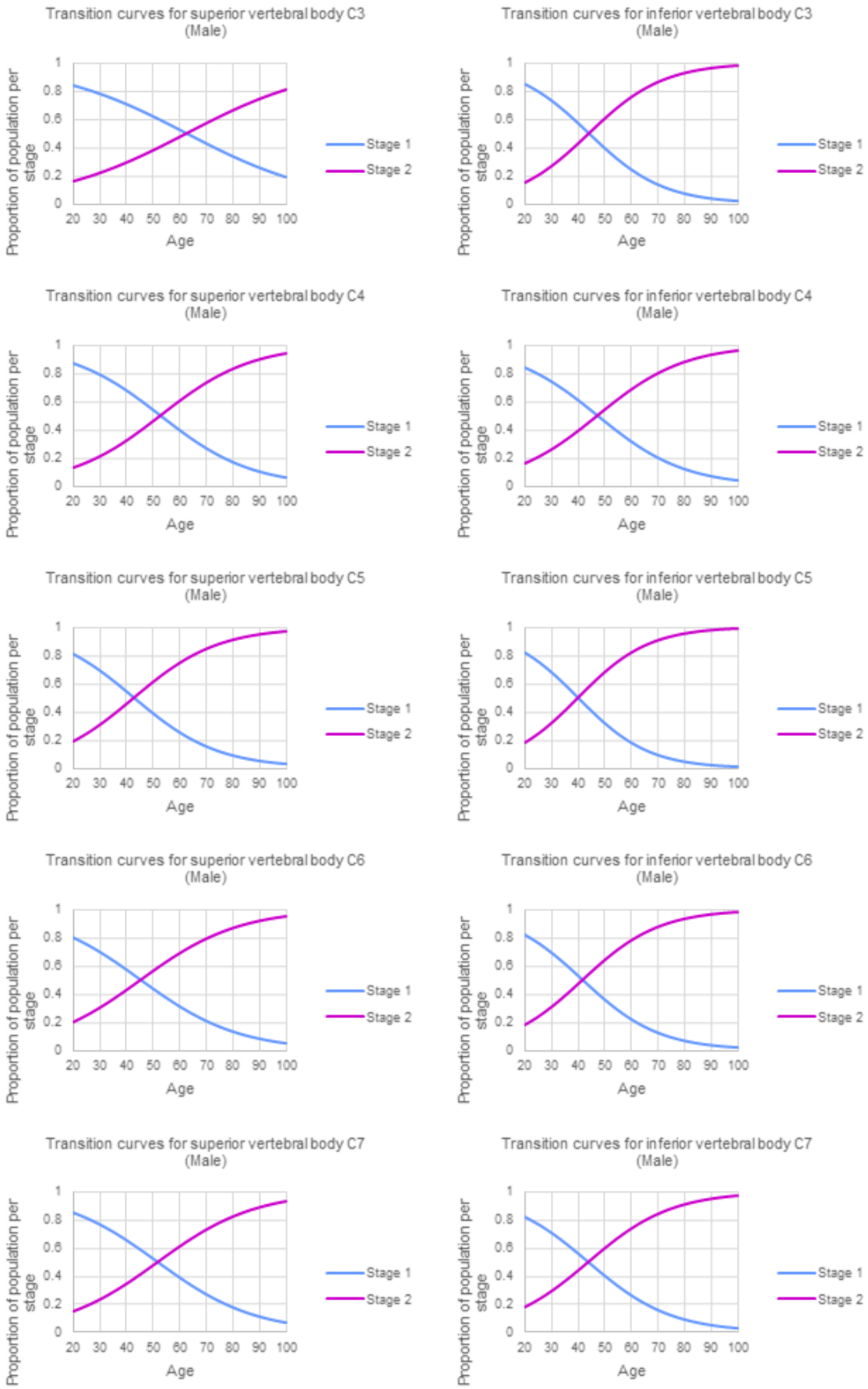


Figure 4.52: Transition curves for stages of male superior and inferior cervical vertebral bodies (C3 - C7).

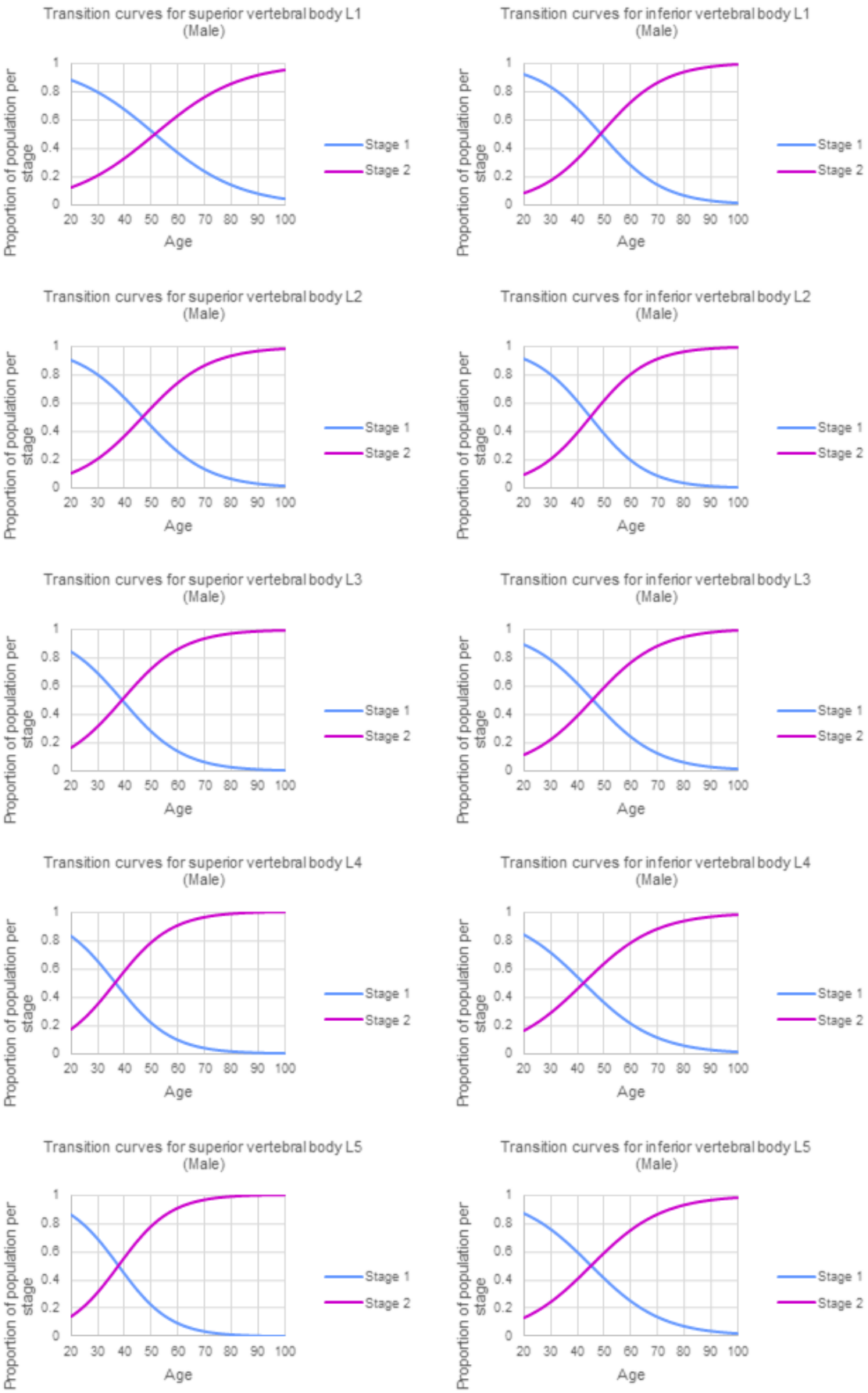


Figure 4.53: Transition curves for stages of male superior and inferior lumbar vertebral bodies (L1 - L5).

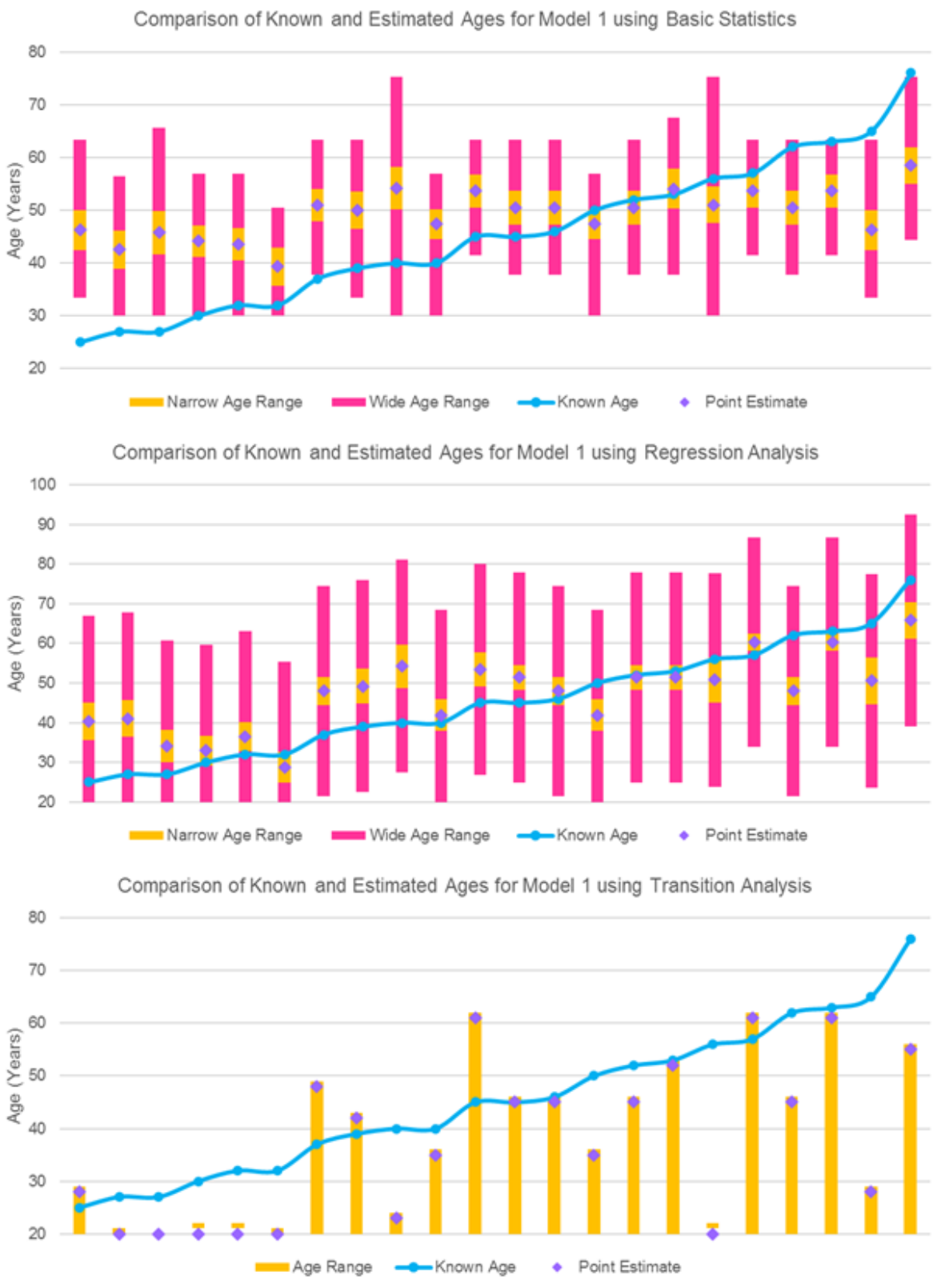


Figure 4.54: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 1.

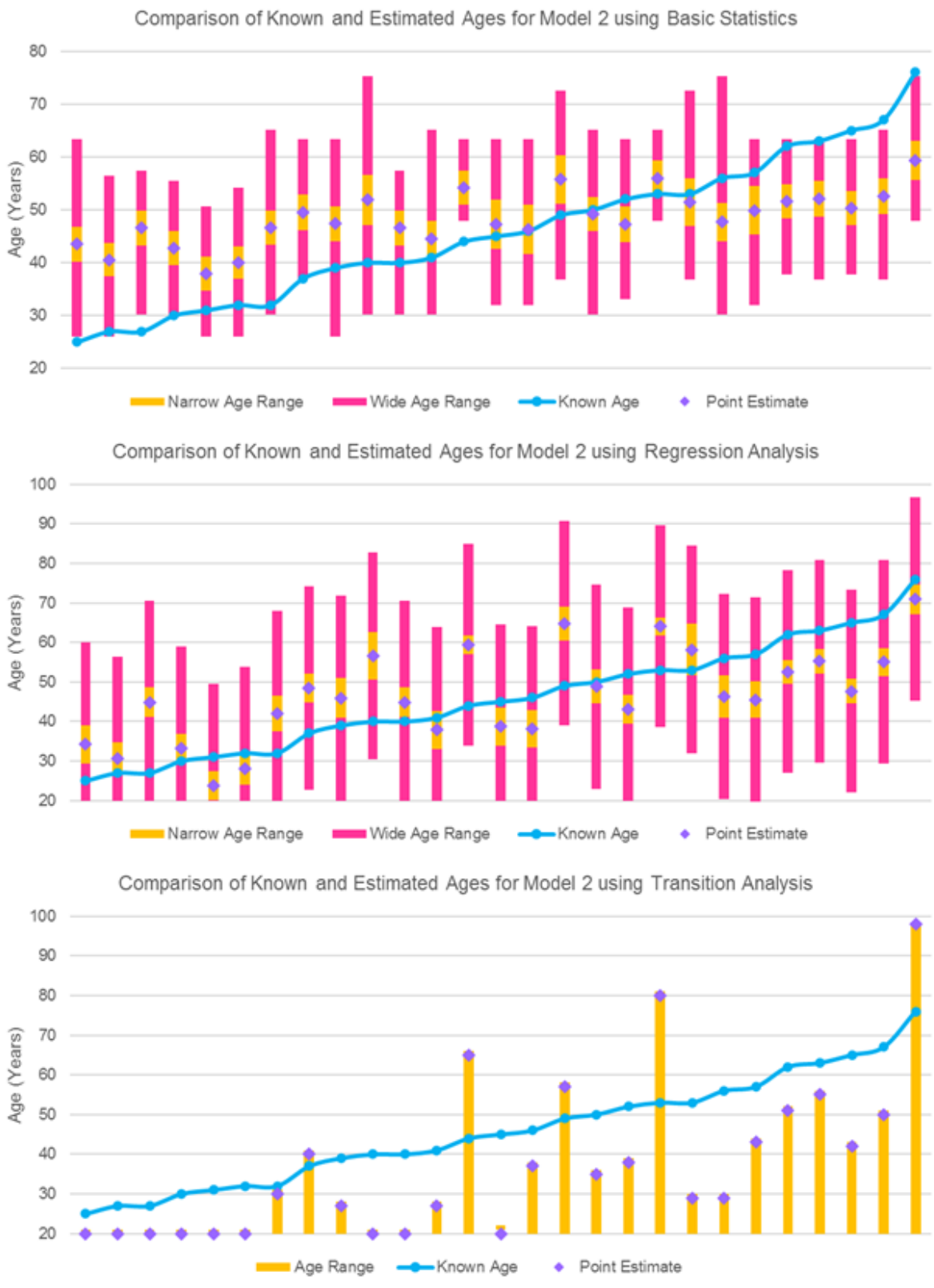


Figure 4.55: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 2.



Figure 4.56: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 3.



Figure 4.57: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 4.



Figure 4.58: A comparison between the known ages and the ages estimated using basic statistics, regression analysis and transition analysis for multifactorial model 5.

4.11. Tables

Table 4.1: Numerical assessment of sample distribution shape using Shapiro-Wilks test for normality, skewness and kurtosis values.

	Shapiro-Wilks value*	***Skewness***	***SE***	***z-score***	***Kurtosis***	***SE***	***z-score***
Acetabulum							
Acetabular groove: Right	0.496	-1.460	0.143	**-10.210**	0.133	0.285	0.467
Acetabular groove: Left	0.460	-1.717	0.143	**-12.007**	0.955	0.285	**3.351**
Acetabular rim: Right	0.858	-0.149	0.143	-1.042	-0.382	0.285	-1.340
Acetabular rim: Left	0.855	-0.220	0.143	-1.538	-0.321	0.285	-1.126
Apex: Right	0.477	-1.597	0.143	**-11.168**	0.554	0.285	1.944
Apex: Left	0.496	-1.460	0.143	**-10.210**	0.133	0.285	0.467
Acetabular fossa: Right	0.780	0.208	0.143	1.455	-0.585	0.285	-2.053
Acetabular fossa: Left	0.791	0.231	0.143	1.615	-0.596	0.285	-2.091
Auricular surface							
Surface topography: Right	0.653	-1.394	0.173	**-8.058**	0.763	0.046	**16.587**
Surface topography: Left	0.658	-1.367	0.173	**-7.902**	0.656	0.344	1.907
Surface morphology: Right	0.772	-0.665	0.173	**-3.844**	-0.526	0.344	-1.529
Surface morphology: Left	0.787	-0.735	0.173	**-4.248**	-0.456	0.344	-1.325
Inferior surface texture: Right	0.737	0.708	0.173	**4.092**	-0.500	0.344	-1.453
Inferior surface texture: Left	0.730	0.827	0.173	**4.780**	-0.478	0.344	-1.390
Posterior iliac exostoses: Right	0.718	0.075	0.173	0.434	-0.740	0.344	-2.151
Posterior iliac exostoses: Left	0.727	0.082	0.173	0.474	-0.616	0.344	-1.791
Clavicle							
Medial epiphysis: Right	0.165	-5.375	0.145	**-37.069**	27.084	0.288	**94.042**
Medial epiphysis: Left	0.165	-5.375	0.145	**-37.069**	27.084	0.288	**94.042**
Cranial sutures							
Midlambdoid: Right	0.885	0.236	0.172	1.372	-0.274	0.343	-0.799
Midlambdoid: Left	0.884	0.214	0.172	1.244	-0.236	0.343	-0.688
Lambda	0.878	0.202	0.172	1.174	-0.076	0.343	-0.222
Obelion	0.901	-0.240	0.172	-1.395	-0.852	0.343	-2.484
Vertex	0.901	0.327	0.172	1.901	-0.411	0.343	-1.198
Bregma	0.895	0.072	0.172	0.419	-0.790	0.343	-2.303
Midcoronal: Right	0.886	0.571	0.172	**3.320**	0.029	0.343	0.085
Midcoronal: Left	0.884	0.582	0.172	**3.384**	0.047	0.343	0.137
Pterion: Right	0.836	0.881	0.172	**5.122**	-0.231	0.343	-0.673
Pterion: Left	0.844	0.821	0.172	**4.773**	-0.399	0.343	-1.163
Sphenofrontal: Right	0.835	0.767	0.172	**4.459**	-0.142	0.343	-0.414

	*Shapiro-Wilks value**	*Skewness*	*SE*	*z-score*	*Kurtosis*	*SE*	*z-score*
Sphenofrontal: Left	0.838	0.758	0.172	**4.407**	-0.271	0.343	-0.790
Superior sphenotemporal: Right	0.605	-0.604	0.172	**-3.512**	1.293	0.343	**3.770**
Superior sphenotemporal: Left	0.545	-0.704	0.172	**-4.093**	1.445	0.343	**4.213**
Inferior sphenotemporal: Right	0.685	-0.155	0.172	-0.901	0.450	0.343	1.312
Inferior sphenotemporal: Left	0.720	-0.027	0.172	-0.157	0.133	0.343	0.388
Zygomaticomaxillary: Right	0.816	0.234	0.172	1.360	-0.186	0.343	-0.542
Zygomaticomaxillary: Left	0.830	0.247	0.172	1.436	0.207	0.343	0.603
Incisive	0.590	-0.979	0.172	**-5.691**	-0.987	0.343	**-2.878**
Anterior median palatine	0.779	0.681	0.172	**3.959**	-0.132	0.343	-0.385
Posterior median palatine	0.879	0.476	0.172	**2.767**	-0.541	0.343	-0.577
Transverse palatine	0.737	1.380	0.172	**8.023**	2.656	0.343	**7.743**
Iliac crest							
Iliac crest: Right	0.140	-6.114	0.136	**-44.956**	35.598	0.272	**130.875**
Iliac crest: Left	0.164	-5.414	0.136	**-39.809**	27.478	0.272	**101.022**
Pubic symphysis							
Symphyseal relief: Right	0.747	-0.875	0.171	**-5.117**	0.838	0.341	2.457
Symphyseal relief: Left	0.739	-0.899	0.171	**-5.257**	0.978	0.341	**2.868**
Symphyseal texture: Right	0.687	0.905	0.171	**5.292**	-0.165	0.341	-0.484
Symphyseal texture: Left	0.699	0.844	0.171	**4.936**	-0.265	0.341	-0.777
Superior apex: Right	0.718	-1.405	0.171	**-8.216**	1.742	0.341	**5.109**
Superior apex: Left	0.693	-1.529	0.171	**-8.942**	1.891	0.341	**5.545**
Ventral margin: Right	0.859	-0.059	0.171	-0.345	-0.370	0.341	-1.085
Ventral margin: Left	0.853	-0.152	0.171	-0.889	-0.293	0.341	-0.859
Dorsal margin: Right	0.764	-0.020	0.171	-0.117	-0.378	0.341	-1.109
Dorsal margin: Left	0.760	-0.033	0.171	-0.193	-0.293	0.341	-0.859
Sacrum							
S1/S2 fusion	0.521	-1.287	0.137	**-9.394**	-0.345	0.273	-1.264
Suchey-Brooks							
Suchey-Brooks: Right	0.904	-0.294	0.143	-2.056	-0.315	0.286	-1.101
Suchey-Brooks: Left	0.907	-0.232	0.143	-1.622	-0.298	0.286	-1.042
Vertebral bodies							
C3 superior	0.610	0.749	0.182	**4.115**	-1.455	0.362	**-4.019**
C3 inferior	0.687	-0.023	0.182	-0.126	-2.022	0.362	**-5.586**
C4 superior	0.651	0.465	0.182	2.554	-1.804	0.362	**-4.983**
C4 inferior	0.697	-0.045	0.182	-0.247	-2.021	0.362	**-5.583**
C5 superior	0.705	-0.023	0.182	-0.126	-2.022	0.362	**-5.586**

	Shapiro-Wilks value*	***Skewness***	***SE***	***z-score***	***Kurtosis***	***SE***	***z-score***
C5 inferior	0.724	-0.465	0.182	-2.555	-1.804	0.362	**-4.983**
C6 superior	0.687	-0.068	0.182	-0.374	-2.018	0.362	**-5.575**
C6 inferior	0.715	-0.251	0.182	-1.379	-1.959	0.362	**-5.412**
C7 superior	0.677	0.298	0.182	1.637	-1.933	0.362	**-5.340**
C7 inferior	0.684	0.068	0.182	0.374	-2.018	0.362	**-5.575**
L1 superior	0.685	0.441	0.182	2.423	-1.826	0.362	**-5.044**
L1 inferior	0.687	0.159	0.182	0.874	-1.997	0.362	**-5.517**
L2 superior	0.737	-0.068	0.182	-0.374	-2.018	0.362	**-5.575**
L2 inferior	0.721	-0.091	0.182	-0.500	-2.015	0.362	**-5.566**
L3 superior	0.745	-0.369	0.182	-2.027	-1.885	0.362	**-5.207**
L3 inferior	0.721	-0.113	0.182	-0.621	-2.010	0.362	**-5.552**
L4 superior	0.754	-0.642	0.182	**-3.527**	-1.606	0.362	**-4.436**
L4 inferior	0.733	-0.251	0.182	-1.379	-1.959	0.362	**-3.809**
L5 superior	0.752	-0.515	0.182	**-2.830**	-1.755	0.362	**-4.848**
L5 inferior	0.754	-0.251	0.182	-1.379	-1.959	0.362	**-5.412**

**p < 0.001*
z-scores in bold indicate skewness and kurtosis respectively

Table 4.2: Wilcoxon signed-rank test for significant differences between right and left indicators.

	Z statistic	***p-value***	***right<left***	***right>left***	***right=left***
Acetabulum					
Acetabular groove	-1.347	0.178	17	10	286
Acetabular rim	-1.559	0.119	30	21	261
Apex	-1.091	0.275	8	13	278
Acetabular fossa	-0.316	0.752	21	19	274
Auricular surface					
Surface topography	-0.182	0.856	20	18	250
Surface morphology	-0.492	0.622	35	31	192
Inferior surface texture	-0.180	0.857	13	15	183
Posterior iliac exostoses	-0.728	0.467	32	24	255
Clavicle					
Medial epiphysis	0.000	1.000	0	0	284
Cranial sutures					
Midlambdoid	-0.962	0.336	14	10	264
Midcoronal	-0.680	0.497	20	27	246
Pterion	-0.283	0.777	25	24	253
Sphenofrontal	-1.057	0.290	22	17	278
Superior sphenotemporal	-0.775	0.439	7	5	310
Inferior sphenotemporal	-1.414	0.157	18	11	291
Zygomaticomaxillary	-1.026	0.305	18	23	275
Iliac crest					
Iliac crest	-1.414	0.157	0	2	318
Pubic symphysis					
Symphyseal relief	-0.870	0.384	19	14	251
Symphyseal texture	-1.800	0.072	15	7	216
Superior apex	-0.457	0.647	22	18	222
Ventral margin	-0.378	0.705	14	11	247
Dorsal margin	-0.973	0.330	22	16	235
Suchey-Brooks					
Suchey-Brooks	0.000	1.000	7	7	275

Table 4.3: Wilcoxon signed-rank test for significant difference between superior and inferior vertebral bodies.

	Z statistic	***p-value***	***inferior<superior***	***inferior>superior***	***inferior=superior***
C3	-6.037	**<0.001**	7	58	206
C4	-4.500	**<0.001**	15	54	225
C5	-4.327	**<0.001**	17	58	215
C6	-3.802	**<0.001**	21	53	236
C7	-2.474	**0.013**	20	39	249
L1	-0.818	0.414	43	36	223
L2	-0.801	0.423	36	29	244
L3	-2.860	**0.004**	45	18	240
L4	-4.426	**<0.001**	63	22	221
L5	-2.257	**0.024**	52	30	228

Table 4.4: Wilcoxon signed-rank test for significant difference between adjacent vertebral bodies.

	Z statistic	***p-value***	***inferior<superior***	***inferior>superior***	***inferior=superior***
C3/C4	-4.627	**<0.001**	10	44	212
C4/C5	-0.263	0.793	26	29	234
C5/C6	-5.498	**<0.001**	11	56	228
C6/C7	-6.567	**<0.001**	10	68	230
L1/L2	-3.799	**<0.001**	54	20	227
L2/L3	-4.154	**<0.001**	51	17	237
L3/L4	-6.268	**<0.001**	64	10	221
L4/L5	-3.397	**0.001**	54	24	228

Table 4.5: Descriptive statistics for left and median indicators.

	Mean age	***95% Lower CI***	***95% Upper CI***	***Median***	***Minimum***	***Maximum***	***Range***
Acetabulum							
Acetabular groove 1 (N=51)	42.25	36.92	47.59	35.00	20	86	66
Acetabular groove 2 (N=240)	52.11	49.78	54.45	50.00	20	98	78
Acetabular rim 1 (N=18)	25.17	23.06	27.28	24.50	20	35	15
Acetabular rim 2 (N=89)	41.51	38.25	44.76	36.00	20	80	60
Acetabular rim 3 (N=142)	57.32	54.58	60.06	57.50	21	98	77
Acetabular rim 4 (N=42)	**56.55**	50.40	62.69	59.00	22	96	74
Apex activity 1 (N=60)	38.63	34.17	43.10	32.00	20	89	69
Apex activity 2 (N=231)	53.44	51.10	55.77	53.00	20	98	78
Acetabular fossa 2 (N=106)	40.84	37.81	43.87	37.50	20	90	70
Acetabular fossa 3 (N=161)	53.65	50.83	56.47	55.00	20	98	78
Acetabular fossa 4 (N=24)	70.63	65.95	75.30	71.50	32	86	54
Auricular surface							
Surface topography 1 (N=17)	34.59	26.09	43.08	31.00	20	80	60
Surface topography 2 (N=45)	46.60	40.72	52.48	40.00	21	89	68
Surface topography 3 (N=136)	49.26	46.44	52.09	48.00	21	98	77
Surface morphology 2 (N=15)	42.20	32.10	52.30	34.00	21	82	61
Surface morphology 3 (N=78)	43.85	39.91	47.78	39.50	20	98	78
Surface morphology 4 (N=105)	50.78	47.42	54.14	50.00	20	89	69
Inferior surface texture 1 (N=109)	43.10	39.80	46.41	40.00	20	98	78
Inferior surface texture 2 (N=68)	54.32	50.25	58.40	58.00	26	89	63
Inferior surface texture 3 (N=21)	**47.29**	40.09	54.49	**43.00**	24	80	56
Posterior iliac exostoses 1 (N=72)	40.56	36.74	44.37	36.00	20	89	69
Posterior iliac exostoses 2 (N=116)	51.03	47.82	54.23	50.00	20	98	78
Posterior iliac exostoses 3 (N=10)	54.60	41.77	67.43	56.50	23	80	63
Clavicle							

	Mean age	***95% Lower CI***	***95% Upper CI***	***Median***	***Minimum***	***Maximum***	***Range***
Medial epiphysis 1 (N=9)	22.67	19.82	25.52	21.00	20	29	9
Medial epiphysis 2 (N=275)	51.40	49.26	53.54	51.00	20	98	78
Cranial sutures							
Midlambdoid 1 (N=39)	46.13	40.36	51.90	48.00	20	86	66
Midlambdoid 2 (N=57)	**46.82**	42.12	51.53	**46.00**	20	86	66
Midlambdoid 3 (N=81)	53.46	49.38	57.53	53.00	21	96	75
Midlambdoid 4 (N=16)	55.81	45.52	66.11	57.50	24	86	62
Midlambdoid 5 (N=6)	**53.00**	28.72	77.28	**47.50**	21	80	59
Lambda 1 (N=36)	43.47	37.87	49.08	44.50	20	80	60
Lambda 2 (N=55)	50.69	45.62	55.76	50.00	20	86	66
Lambda 3 (N=87)	**50.64**	46.78	54.51	**50.00**	21	96	75
Lambda 4 (N=14)	56.93	45.55	68.31	56.50	24	86	62
Lambda 5 (N=7)	64.71	47.66	81.77	71.00	42	85	43
Obelion 1 (N=21)	41.62	33.75	49.48	42.00	20	80	60
Obelion 2 (N=35)	**41.86**	36.06	47.65	**41.00**	20	75	55
Obelion 3 (N=72)	52.15	47.87	56.43	50.00	21	96	75
Obelion 4 (N=31)	54.87	48.47	61.27	58.00	29	87	58
Obelion 5 (N=40)	55.35	49.41	61.29	**56.00**	24	86	62
Vertex 1 (N=36)	44.56	38.01	51.10	45.00	20	86	66
Vertex 2 (N=55)	**44.71**	40.43	48.99	**44.00**	20	86	66
Vertex 3 (N=72)	54.64	50.47	58.81	58.00	21	96	75
Vertex 4 (N=22)	58.86	51.32	66.41	60.00	24	86	62
Vertex 5 (N=14)	**51.21**	38.01	64.42	**45.50**	21	86	65
Bregma 1 (N=30)	48.30	40.40	56.20	52.50	20	86	66
Bregma 2 (N=75)	**44.57**	40.85	48.30	**42.00**	20	86	66
Bregma 3 (N=66)	53.64	49.11	58.17	54.50	21	96	75
Bregma 4 (N=28)	59.89	53.45	66.34	60.50	24	86	62
Midcoronal 1 (N=27)	41.74	34.17	49.31	36.00	20	85	65
Midcoronal 2 (N=82)	45.62	41.79	49.45	44.50	20	81	61
Midcoronal 3 (N=60)	55.65	50.90	60.40	58.00	24	96	72
Midcoronal 4 (N=20)	59.20	52.95	65.45	60.00	35	80	45
Midcoronal 5 (N=10)	61.80	51.49	72.11	**59.00**	40	86	46
Pterion 2 (N=79)	42.18	38.43	45.93	40.00	20	85	65
Pterion 3 (N=73)	53.64	49.37	57.92	55.00	24	96	72
Pterion 4 (N=22)	55.82	48.26	63.37	**52.50**	29	86	57
Pterion 5 (N=25)	61.32	54.83	67.81	60.00	24	86	62
Sphenofrontal 1 (N=9)	41.11	28.58	53.64	43.00	20	64	44
Sphenofrontal 2 (N=95)	45.04	41.39	48.70	45.00	20	86	66
Sphenofrontal 3 (N=50)	53.98	48.94	59.02	52.50	26	96	70
Sphenofrontal 4 (N=27)	62.41	54.86	69.95	70.00	29	87	58
Sphenofrontal 5 (N=18)	**54.22**	48.56	59.88	**56.50**	25	75	50
Superior sphenotemporal 1 (N=34)	48.15	42.44	53.85	51.00	20	80	60
Superior sphenotemporal 2 (N=158)	50.34	47.36	53.31	**50.00**	20	96	76
Superior sphenotemporal 3 (N=7)	59.86	43.68	76.03	70.00	35	78	43
Inferior sphenotemporal 1 (N=41)	47.27	41.91	52.62	48.00	20	86	66
Inferior sphenotemporal 2 (N=135)	49.07	45.93	52.20	**48.00**	20	96	76
Inferior spenotemporal 3 (N=23)	62.91	55.42	70.41	70.00	25	86	61
Zygomaticomaxillary 1 (N=11)	42.18	32.01	52.36	43.00	20	64	44
Zygomaticomaxillary 2 (N=97)	46.85	43.14	50.55	45.00	20	87	67

	Mean age	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Zygomaticomaxillary 3 (N=76)	53.38	49.30	57.46	52.00	23	96	73
Zygomaticomaxillary 4 (N=15)	62.93	53.37	72.49	70.00	30	86	56
Incisive 3 (N=52)	47.19	42.11	52.27	50.00	20	80	60
Incisive 4 (N=8)	59.63	40.86	78.39	66.00	24	87	63
Incisive 5 (N=139)	**50.92**	47.86	53.98	**50.00**	20	96	76
Anterior median palatine 1 (N=6)	45.67	29.95	61.38	48.50	20	64	44
Anterior median palatine 2 (N=113)	49.01	45.51	52.51	**48.00**	20	87	67
Anterior median palatine 3 (N=60)	50.88	45.97	55.80	50.00	21	96	75
Anterior median palatine 4 (N=20)	57.20	50.03	64.37	56.00	30	86	56
Posterior median palatine 1 (N=7)	42.71	28.15	57.28	45.00	20	64	44
Posterior median palatine 2 (N=73)	46.04	41.55	50.53	**42.00**	20	87	67
Posterior median palatine 3 (N=65)	48.28	44.32	52.23	47.00	23	85	62
Posterior median palatine 4 (N=35)	58.91	52.21	65.62	60.00	24	96	72
Posterior median palatine 5 (N=19)	60.47	53.48	67.47	68.00	30	78	48
Transverse palatine 1 (N=7)	43.14	28.47	57.82	45.00	20	60	40
Transverse palatine 2 (N=122)	48.13	44.81	51.46	46.00	20	96	76
Transverse palatine 3 (N=57)	54.67	49.92	59.41	53.00	20	87	67
Transverse palatine 4 (N=7)	55.29	35.81	74.76	55.00	24	80	56
Transverse palatine 5 (N=6)	**55.33**	36.19	74.47	**52.00**	30	78	48
Iliac crest							
Iliac crest 1 (N=10)	22.50	20.58	24.42	22.00	20	29	9
Iliac crest 2 (N=320)	51.83	49.79	53.87	50.50	20	98	78
Pubic symphysis							
Symphyseal relief 2 (N=12)	29.50	19.10	39.90	26.00	20	80	60
Symphyseal relief 3 (N=44)	38.32	33.85	42.79	33.00	21	75	54
Symphyseal relief 4 (N=135)	54.97	52.05	57.89	56.00	24	98	74
Symphyseal relief 5 (N=11)	56.36	46.18	66.55	60.00	29	81	52
Dorsal margin 2 (N=60)	37.62	33.54	41.69	31.00	20	85	65
Dorsal margin 3 (N=129)	54.19	51.23	57.15	54.00	21	98	77
Dorsal margin 4 (N=13)	64.08	54.41	73.74	65.00	34	87	53
Ventral margin 2 (N=15)	28.93	23.61	34.26	26.00	20	53	33
Ventral margin 3 (N=73)	41.79	38.10	45.49	37.00	21	85	64
Ventral margin 4 (N=95)	57.09	53.69	60.50	58.00	26	98	72
Ventral margin 5 (N=19)	61.68	54.41	68.96	65.00	36	87	51
Superior apex 1 (N=14)	29.21	24.54	33.89	28.50	20	43	23
Superior apex 2 (N=6)	32.67	26.01	39.33	30.50	28	45	17
Superior apex 3 (N=70)	46.29	42.03	50.54	45.50	21	82	61
Superior apex 4 (N=112)	55.68	52.44	58.92	58.00	26	98	72

	Mean age	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Symphyseal texture 1 (N=117)	47.59	44.32	50.86	46.00	20	98	78
Symphyseal texture 2 (N=75)	52.04	47.62	56.46	55.00	22	87	65
Symphyseal texture 3 (N=10)	61.00	49.59	72.41	62.50	35	85	50
Sacrum							
S1/S2 fusion 1 (N=73)	37.79	33.42	42.17	30.00	20	98	78
S1/S2 fusion 2 (N=244)	54.76	52.64	56.88	56.50	21	96	75
Suchey-Brooks							
Suchey-Brooks 2 (N=30)	28.80	25.93	31.67	27.50	20	47	27
Suchey-Brooks 3 (N=44)	37.16	33.02	41.30	34.00	21	75	54
Suchey-Brooks 4 (N=124)	52.50	49.47	55.53	51.50	22	98	76
Suchey-Brooks 5 (N=71)	61.42	57.72	65.12	60.00	28	90	62
Suchey-Brooks 6 (N=20)	64.50	59.12	69.88	65.00	40	87	47
Vertebral bodies							
C3 superior 1 (N=120)	44.06	40.80	47.31	38.50	20	89	69
C3 superior 2 (N=58)	61.93	57.26	66.60	63.50	25	98	73
C3 inferior 1 (N=88)	39.78	36.25	43.32	34.00	20	89	69
C3 inferior 2 (N=90)	59.76	56.10	63.41	60.50	23	98	75
C4 superior 1 (N=109)	42.50	39.21	45.78	37.00	20	89	69
C4 superior 2 (N=69)	61.55	57.29	65.81	64.00	23	98	75
C4 inferior 1 (N=87)	39.48	36.09	42.88	34.00	20	89	69
C4 inferior 2 (N=91)	59.82	56.10	63.55	61.00	22	98	76
C5 superior 1 (N=88)	38.93	35.85	42.02	34.00	20	80	60
C5 superior 2 (N=90)	60.59	56.76	64.42	62.00	22	98	76
C5 inferior 1 (N=69)	35.91	32.51	39.32	31.00	20	80	60
C5 inferior 2 (N=109)	58.72	55.39	62.06	60.00	22	98	76
C6 superior 1 (N=86)	38.14	34.92	41.36	33.00	20	80	60
C6 superior 2 (N=92)	60.86	57.30	64.42	60.50	23	98	75
C6 inferior 1 (N=78)	36.88	33.83	39.94	33.00	20	80	60
C6 inferior 2 (N=100)	60.02	56.48	63.56	61.00	22	98	76
C7 superior 1 (N=102)	41.20	37.90	44.49	35.00	20	87	67
C7 superior 2 (N=76)	61.54	57.57	65.51	63.50	23	98	75
C7 inferior 1 (N=92)	40.21	36.82	43.60	34.50	20	89	69
C7 inferior 2 (N=86)	60.23	56.42	64.04	61.00	23	98	75
L1 superior 1 (N=108)	41.55	38.44	44.65	35.50	20	89	69
L1 superior 2 (N=70)	62.74	58.52	66.96	65.00	21	98	77
L1 inferior 1 (N=96)	38.48	35.47	41.49	33.50	20	89	69
L1 inferior 2 (N=82)	63.23	59.70	66.77	65.00	23	98	75
L2 superior 1 (N=86)	37.76	34.50	41.01	33.00	20	89	69
L2 superior 2 (N=92)	61.22	57.79	64.65	62.50	23	98	75
L2 inferior 1 (N=85)	37.80	34.55	41.05	33.00	20	87	67
L2 inferior 2 (N=93)	60.92	57.45	64.40	61.00	23	98	75
L3 superior 1 (N=73)	34.64	31.82	37.46	32.00	20	80	60
L3 superior 2 (N=105)	60.48	57.20	63.75	61.00	23	98	75
L3 inferior 1 (N=84)	36.80	33.83	39.77	33.00	20	80	60
L3 inferior 2 (N=94)	61.57	58.13	65.02	62.00	23	98	75
L4 superior 1 (N=62)	33.11	30.54	35.68	31.00	20	60	40
L4 superior 2 (N=116)	58.84	55.59	62.10	60.00	23	98	75
L4 inferior 1 (N=78)	37.15	33.89	40.41	33.00	20	89	69
L4 inferior 2 (N=100)	59.81	56.33	63.29	60.50	21	98	77
L5 superior 1 (N=67)	32.69	30.11	35.27	30.00	20	80	60
L5 superior 2 (N=111)	60.26	57.16	63.36	60.00	23	98	75
L5 inferior 1 (N=78)	35.71	32.49	38.92	30.50	20	89	69
L5 inferior 2 (N=100)	60.94	57.76	64.12	60.50	23	98	75

Bold values indicate ages that do not show unidirectional progress from one stage to the next

Table 4.6: Mann-Whitney U test for significant difference between female and male subgroups.

	Mean rank for		***Median for***		***Mann-Whitney U statistic***	***Z statistic***	***p-value***
	Female	***Male***	***Female***	***Male***			
Acetabulum							
Acetabular groove	159.76	157.43	2.0	2.0	12215.000	-0.339	0.735
Acetabular rim	157.81	158.16	3.0	3.0	12298.000	-0.036	0.971
Apex	155.02	156.81	2.0	2.0	11846.500	-0.254	0.800
Acetabular fossa	151.87	164.13	3.0	3.0	11435.500	-1.341	0.180
Auricular surface							
Surface topography	139.95	156.75	3.0	3.0	9719.500	-2.107	**0.035**
Surface morphology	139.29	133.91	4.0	4.0	8870.000	-0.634	0.526
Inferior surface texture	125.05	119.12	**1.5**	**1.0**	7015.500	-0.733	0.463
Posterior iliac exostoses	159.87	156.45	2.0	2.0	12031.000	-0.374	0.709
Clavicle							
Medial epiphysis	152.76	150.41	2.0	2.0	11163.000	-0.427	0.427
Cranial sutures							
Midlambdoid	136.40	157.73	**2.0**	**3.0**	9222.000	-2.272	**0.023**
Lambda	130.47	160.40	**2.0**	**3.0**	8396.000	-3.219	**0.001**
Obelion	125.21	170.27	3.0	3.0	7608.500	-4.710	**<0.001**
Vertex	127.18	163.81	**2.0**	**3.0**	7959.500	-3.849	**<0.001**
Bregma	135.62	160.37	**2.0**	**3.0**	9105.500	-2.625	**0.009**
Midcoronal	145.73	149.13	2.0	2.0	10537.000	-0.361	0.718
Pterion	151.13	157.54	3.0	3.0	11334.000	-0.663	0.507
Sphenofrontal	161.92	159.26	**3.0**	**2.0**	12527.500	-0.274	0.784
Superior sphenotemporal	151.48	172.76	2.0	2.0	11395.000	-2.888	**0.004**
Inferior sphenotemporal	151.76	170.56	2.0	2.0	11430.000	-2.199	**0.028**
Zygomaticomaxillary	132.69	182.84	**2.0**	**3.0**	8612.500	-5.292	**<0.001**
Incisive	145.36	155.24	5.0	5.0	10492.500	-1.279	0.201
Anterior median palatine	115.59	152.86	**2.0**	**3.0**	6479.500	-4.365	**<0.001**
Posterior median palatine	114.90	172.89	**2.0**	**3.0**	6241.500	-6.153	**<0.001**
Transverse palatine	123.24	161.04	2.0	2.0	7444.000	-4.490	**<0.001**
Iliac crest							
Iliac crest	161.02	161.90	2.0	2.0	12792.500	-0.280	0.779
Pubic symphysis							
Symphyseal relief	141.73	150.27	4.0	4.0	9898.500	-1.048	0.295
Symphyseal texture	134.64	116.28	**2.0**	**1.0**	6477.500	-2.294	**0.022**
Superior apex	134.02	140.90	4.0	4.0	8760.500	-0.808	0.419
Ventral margin	127.40	151.94	**3.0**	**4.0**	8028.500	-2.709	**0.007**
Dorsal margin	131.67	151.38	3.0	3.0	8598.000	-2.363	**0.018**
Sacrum							
S1/S2 fusion	158.33	159.56	2.0	2.0	12373.500	-0.163	0.871
S2/S3 fusion	162.40	160.74	2.0	2.0	12729.500	-0.833	0.405
Suchey-Brooks							
Suchey-Brooks	141.04	153.41	4.0	4.0	9809.000	-1.303	0.193
Vertebral bodies							
C3 superior	126.32	152.79	1.0	1.0	7906.000	-3.337	**0.001**
C3 inferior	128.61	152.29	**1.0**	**2.0**	8189.000	-2.800	**0.005**
C4 superior	130.69	167.60	**1.0**	**2.0**	8436.500	-4.325	**<0.001**

	Mean rank for		*Median for*		*Mann-Whitney U statistic*	*Z statistic*	*p-value*
	Female	***Male***	***Female***	***Male***			
C4 inferior	141.86	160.48	**1.0**	**2.0**	9985.000	-2.108	**0.035**
C5 superior	129.80	170.81	**1.0**	**2.0**	8312.500	-4.637	**<0.001**
C5 inferior	146.89	153.70	2.0	2.0	10700.500	-0.796	0.426
C6 superior	143.72	170.03	**1.0**	**2.0**	10255.500	-2.926	**0.003**
C6 inferior	149.43	165.50	2.0	2.0	11087.500	-1.798	**0.072**
C7 superior	142.50	171.05	**1.0**	**2.0**	10080.500	-3.215	**0.001**
C7 inferior	137.28	170.46	**1.0**	**2.0**	9328.500	-3.738	**<0.001**
L1 superior	140.40	162.09	**1.0**	**2.0**	9786.000	-2.429	**0.015**
L1 inferior	139.18	167.61	**1.0**	**2.0**	9610.000	-3.186	**0.001**
L2 superior	148.89	162.21	2.0	2.0	11004.000	-1.464	0.143
L2 inferior	143.23	169.59	**1.0**	**2.0**	10184.500	-2.904	**0.004**
L3 superior	147.54	163.11	2.0	2.0	10797.500	-1.756	**0.079**
L3 inferior	148.38	160.41	2.0	2.0	10894.500	-1.342	0.180
L4 superior	147.77	158.46	2.0	2.0	10830.000	-1.209	0.227
L4 inferior	154.35	161.11	2.0	2.0	11795.500	-0.748	0.454
L5 superior	148.46	162.42	2.0	2.0	10934.000	-1.574	0.116
L5 inferior	159.28	153.21	2.0	2.0	11543.500	-0.667	0.505

Bold median values indicate differences between males and females; whereas bold p-values indicate that these differences are considered significant

Table 4.7: Comparison of goodness-of-fit (r^2-value) for linear and non-linear regression.

	Linear	***Logarithmic***	***Quadratic***	***Cubic***	***Exponential***	***Logistic***
Acetabulum						
Acetabular groove	0.029	0.029	0.029	0.029	0.036	0.036
Acetabular rim	0.186	0.214	0.233	0.238	0.208	0.208
Apex	0.076	0.076	-	-	0.092	0.092
Acetabular fossa	0.168	0.163	0.170	0.170	0.156	0.156
Auricular surface						
Surface topography	0.039	0.041	0.041	0.042	0.052	0.052
Surface morphology	0.031	0.030	0.032	0.032	0.032	0.032
Inferior surface texture	0.043	0.055	0.083	0.083	0.051	0.051
Posterior iliac exostoses	0.113	0.109	0.114	0.114	0.113	0.113
Clavicle						
Medial epiphysis	0.072	0.072	0.072	0.072	0.110	0.110
Cranial sutures						
Midlambdoid	0.038	0.033	0.038	0.049	0.039	0.039
Lambda	0.046	0.037	0.051	0.053	0.044	0.044
Obelion	0.059	0.062	0.065	0.072	0.064	0.064
Vertex	0.048	0.052	0.055	0.063	0.048	0.048
Bregma	0.060	0.048	0.067	0.068	0.065	0.065
Midcoronal	0.091	0.089	0.093	0.098	0.106	0.106
Pterion	0.164	0.175	0.179	0.179	0.166	0.166
Sphenofrontal	0.123	0.130	0.136	0.143	0.131	0.131
Superior sphenotemporal	0.029	0.021	0.046	0.046	0.024	0.024
Inferior sphenotemporal	0.044	0.033	0.059	0.059	0.042	0.042
Zygomaticomaxillary	0.102	0.089	0.104	0.107	0.099	0.099
Incisive	0.003	0.003	0.016	0.016	0.005	0.005
Anterior median palatine	0.044	0.040	0.046	0.046	0.049	0.049
Posterior median palatine	0.128	0.124	0.128	0.129	0.131	0.131
Transverse palatine	0.049	0.055	0.060	0.062	0.051	0.051
Iliac crest						
Iliac crest	0.075	0.075	0.075	-	0.113	0.113
Pubic symphysis						
Symphyseal relief	0.157	0.161	0.163	0.169	0.199	0.199

	Linear	*Logarithmic*	*Quadratic*	*Cubic*	*Exponential*	*Logistic*
Symphyseal texture	0.032	0.028	0.040	0.040	0.031	0.031
Superior apex	0.168	0.151	0.170	0.171	0.192	0.192
Ventral margin	0.155	0.160	0.160	0.161	0.182	0.182
Dorsal margin	0.117	0.115	0.117	0.117	0.140	0.140
Sacrum						
S1/S2 fusion	0.147	0.147	0.147	-	0.189	0.189
Suchey-Brooks						
Suchey-Brooks	0.312	0.314	0.318	0.323	0.348	0.348
Vertebral bodies						
C3 superior	0.096	0.096	0.096	-	0.092	0.092
C3 inferior	0.146	0.146	-	-	0.154	0.154
C4 superior	0.147	0.147	0.147	0.147	0.141	0.141
C4 inferior	0.213	0.213	0.213	0.213	0.205	0.205
C5 superior	0.199	0.199	-	-	0.196	0.196
C5 inferior	0.194	0.194	0.194	-	0.213	0.213
C6 superior	0.210	0.210	-	-	0.215	0.215
C6 inferior	0.238	0.238	0.238	-	0.237	0.237
C7 superior	0.160	0.160	-	-	0.163	0.163
C7 inferior	0.193	0.193	0.193	-	0.194	0.194
L1 superior	0.147	0.147	-	-	0.146	0.146
L1 inferior	0.248	0.248	-	-	0.250	0.250
L2 superior	0.248	0.248	0.248	0.248	0.260	0.260
L2 inferior	0.235	0.235	0.235	0.235	0.249	0.249
L3 superior	0.260	0.260	0.260	0.260	0.282	0.282
L3 inferior	0.240	0.240	-	-	0.260	0.260
L4 superior	0.293	0.293	0.293	0.293	0.320	0.320
L4 inferior	0.202	0.202	0.202	-	0.224	0.224
L5 superior	0.290	0.290	0.290	0.290	0.324	0.324
L5 inferior	0.251	0.251	-	-	0.278	0.278

Table 4.8: Linear regression models for individual skeletal indicators to evaluate strength of association, goodness-of-fit, statistical significance and significance of contribution of the coefficients.

Acetabulum				
Equation 1 (sexes combined; n = 305): Age = -7.745 + (0.892 x acetabular groove) + (6.734* x acetabular rim) + (7.059* x acetabular apex) + (9.503* x acetabular fossa)				
R = 0.550	R^2 = 0.302	Adj R^2 = 0.293	SEE = 15.507	F(4,300) = 32.495, p < 0.001
Equation 2 (female; n = 142) Age = -14.664 + (4.170 x acetabular groove) + (5.018* x acetabular rim) + (6.120* x acetabular apex) + (11.610* x acetabular fossa)				
R = 0.613	R^2 = 0.375	Adj R^2 = 0.357	SEE = 13.555	F(4,137) = 20.590, p < 0.001
Equation 3 (male; n = 163) Age = -2.890 + (-1.050 x acetabular groove) + (8.194* x acetabular rim) + (7.734* x acetabular apex) + (7.648* x acetabular fossa)				
R = 0.517	R^2 = 0.268	Adj R^2 = 0.249	SEE = 16.969	F(4,158) = 14.425, p < 0.001
Auricular surface				
Equation 4 (sexes combined; n = 228): Age = 10.516 + (3.016 x surface topography) + (3.328 x surface morphology) + (3.568* x inferior surface texture) + (7.601* x posterior iliac exostoses)				
R = 0.360	R^2 = 0.130	Adj R^2 = 0.114	SEE = 16.757	F(4,223) = 8.306, p < 0.001
Equation 5 (female; n = 109) Age = 4.445 + (7.619* x auricular surface topography) + (3.548 x auricular surface morphology) + (3.296 x inferior surface texture) + (3.369 x posterior iliac exostoses)				
R = 0.444	R^2 = 0.197	Adj R^2 = 0.167	SEE = 15.138	F(4, 104) = 6.397, p < 0.001
Equation 6 (male; n = 119): Age = 22.841 + (-3.852 x auricular surface topography) + (4.514 x auricular surface morphology) + (3.479 x inferior surface texture) + (9.688* x posterior iliac exostoses)				
R = 0.402	R^2 = 0.162	Adj R^2 = 0.132	SEE = 17.553	F(4, 114) = 5.500, p < 0.001
Clavicle				
Equation 7 (sexes combined; n = 302): Age = -6.346 + (29.013* x clavicle medial epiphysis)				
R = 0.268	R^2 = 0.072	Adj R^2 = 0.069	SEE = 17.772	F(1,300) = 23.271, p < 0.001
Equation 8 (female; n = 138): Age = -8.163 + (28.496* x clavicle medial epiphysis)				
R = 0.253	R^2 = 0.064	Adj R^2 = 0.057	SEE = 16.031	F(1,136) = 9.273, p < 0.001
Equation 9 (male; n = 164): Age = -6.447 + (30.281* x clavicle medial epiphysis)				
R = 0.290	R^2 = 0.084	Adj R^2 = 0.078	SEE = 18.880	F(1,162) = 14.870, p < 0.001
Cranial sutures				
Equation 10 (sexes combined; n = 205): Age = 27.383 + (-1.902 x midlambdoid) + (-0.200 x lambda) + 2.505 x obelion) + (-0.035 x vertex) + (-2.330 x bregma) + (4.352* x midcoronal) + (2.057 x pterion) + (0.421 x sphenofrontal) + (-7.286 x superior sphenotemporal) + (6.930 x inferior sphenotemporal) + (1.747 x zygomaticomaxillary) + (-0.351 x incisive) + (-2.287 x anterior median palatine) + (3.737* x posterior median palatine) + (0.057 x transverse palatine)				
R = 0.464	R^2 = 0.216	Adj R^2 = 0.153	SEE = 16.947	F(15,189) = 3.464, p < 0.001

Equation 11 (female; n = 106)				
Age = 45.833 + (-2.031 x midlambdoid) + (-0.963 x lambda) + (2.567 x obelion) + (4.014 x vertex) + (-5.533 x bregma) + (7.055* x midcoronal) + (-1.507 x pterion) + (-1.156 x sphenofrontal) + (-7.619 x superior sphenotemporal) + (3.957 x inferior sphenotemporal) + (-0.243 x zygomaticomaxillary) + (-1.195 x incisive) + (-6.081 x anterior median palatine) + (5.547* x posterior median palatine) + (3.401 x transverse palatine)				
R = 0.511	R^2 = 0.261	Adj R^2 = 0.138	SEE = 15.936	F(15,90) = 2.122, p < 0.001
Equation 12 (male; n = 99)				
Age = 17.361 + (-2.717 x midlambdoid) + (-0.513 x lambda) + (2.994 x obelion) + (-2.073 x vertex) + (-0.848 x bregma) + (4.600 x midcoronal) + (3.330 x sphenofrontal) + (-8.791 x superior sphenotemporal) + (9.634 x inferior sphenotemporal) + (3.520 x zygomaticomaxillary) + (-0.687 x incisive) + (0.482 x anterior median palatine) + (1.549 x posterior median palatine) + (-2.132 x transverse palatine)				
R = 0.552	R^2 = 0.305	Adj R^2 = 0.179	SEE = 17.803	F(15,83) = 2.423, p < 0.001
Iliac crest				
Equation 13 (sexes combined; n = 322):				
Age = -6.740 + (29.240 x iliac crest)				
R = 0.273	R^2 = 0.075	Adj R^2 = 0.072	SEE = 17.916	F(1,320) = 25.809, p < 0.001
Equation 14 (female; n = 148)				
Age = -6.340 + (27.740* x iliac crest)				
R = 0.298	R^2 = 0.089	Adj R^2 = 0.082	SEE = 16.186	F(1,146) = 14.189, p < 0.001
Equation 15 (male; n = 174)				
Age = -6.741 + (30.341* x iliac crest)				
R = 0.258	R^2 = 0.067	Adj R^2 = 0.061	SEE = 19.088	F(1,172) = 12.270, p < 0.001
Pubic symphysis (component method)				
Equation 16 (sexes combined; n = 221):				
Age = -5.071 + (2.339 x symphyseal relief) + (0.323 x symphyseal texture) + (4.781* x superior apex) + (4.393* x ventral margin) + (4.925* x dorsal margin)				
R = 0.521	R^2 = 0.272	Adj R^2 = 0.255	SEE = 15.604	F(5,215) = 16.052, p < 0.001
Equation 17 (female; n = 98)				
Age = 1.592 + (0.097 x pubic symphyseal relief) + (-0.483 x pubic symphyseal texture) + (4.014* x superior apex) + (4.175* x ventral margin) + (6.638* x dorsal margin)				
R = 0.536	R^2 = 0.287	Adj R^2 = 0.248	SEE = 14.588	F(5,92) = 7.403, p < 0.001
Equation 18 (male; n = 123)				
Age = -14.571 + (5.074 x pubic symphyseal relief) + (2.755 x pubic symphyseal texture) + (5.258* x superior apex) + (3.752 x ventral margin) + (4.101 x dorsal margin)				
R = 0.522	R^2 = 0.272	Adj R^2 = 0.241	SEE = 16.409	F(1,117) = 8.755, p < 0.001
Sacrum				
Equation 19 (sexes combined; n = 317):				
Age = 20.795 + (16.945* x S1/S2 fusion)				
R = 0.384	R^2 = 0.147	Adj R^2 = 0.144	SEE = 17.232	F(1,315) = 54.330, p < 0.001
Equation 20 (female; n = 145)				
Age = 17.900 + (17.100* x S1/S2 fusion)				
R = 0.435	R^2 = 0.189	Adj R^2 = 0.184	SEE = 15.241	F(1,143) = 33.425, p < 0.001
Equation 21 (male; n = 172)				
Age = 23.720 + (16.543* x S1/S2 fusion)				
R = 0.349	R^2 = 0.122	Adj R^2 = 0.117	SEE = 18.547	F(1,170) = 23.551, p < 0.001
Pubic symphysis (stage method)				
Equation 22 (sexes combined; n = 295):				

Age = 11.011 + (9.851* x Suchey-Brooks stage)

R = 0.558	R^2 = 0.312	Adj R^2 = 0.310	SEE = 15.292	F(1,293) = 132.782, p < 0.001

Equation 23 (female; n = 131)

Age = 19.106 + (7.340* x Suchey-Brooks stage)

R = 0.507	R^2 = 0.257	Adj R^2 = 0.251	SEE = 14.600	F(1,129) = 44.581, p < 0.001

Equation 24 (male; n = 164)

Age = 0.695 + (12.728* x Suchey-Brooks stage)

R = 0.614	R^2 = 0.377	Adj R^2 = 0.373	SEE = 15.312	F(1,162) = 98.094, p < 0.001

Vertebral bodies

Equation 25 (sexes combined; n = 178):

Age = -3.042 + (0.041 x C3 superior) + (-1.070 x C3 inferior) + (-4.685 x C4 superior) + (0.083 x C4 inferior) + (4.738 x C5 superior) + (-4.468 x C5 inferior) + (6.683 x C6 superior) + (6.265 x C6 inferior) + (-1.783 x C7 superior) + (0.088 x C7 inferior) + (-1.019 x L1 superior) + (7.621 x L1 inferior) + (1.696 x L2 superior) + (-0.319 x L2 inferior) + (1.952 x L3 superior) + (-0.747 x L3 inferior) + (3.539 x L4 superior) + (1.048 x L4 inferior) + (9.816* x L5 superior) + (4.261 x L5 inferior)

R = 0.720	R^2 = 0.518	Adj R^2 = 0.456	SEE = 14.436	F(20,157) = 8.432, p < 0.001

Equation 26 (female; n = 84)

Age = -3.963 + (-3.358 x C3 superior) + (-5.893 x C3 inferior) + (-5.364 x C4 superior) + (4.681 x C4 inferior) + (9.962 x C5 superior) + (-1.400 x C5 inferior) + (6.706 x C6 superior) + (1.325 x C6 inferior) + (-4.633 x C7 superior) + (3.561 x C7 inferior) + (-0.638 x L1 superior) + (6.099 x L1 inferior) + (7.343 x L2 superior) + (-0.636 x L2 inferior) + (-0.027 x L3 superior) + (-4.272 x L3 inferior) + (4.726 x L4 superior) + (-0.865 x L4 inferior) + (11.327 x L5 superior) + (4.735 x L5 inferior)

R = 0.799	R^2 = 0.638	Adj R^2 = 0.523	SEE = 12.582	F(20,63) = 5.549

Equation 27 (male; n = 94)

Age = -3.291 + (-0.236 x C3 superior) + (0.139 x C3 inferior) + (-2.772 x C4 superior) + (-2.898 x C4 inferior) + (2.320 x C5 superior) + (-5.686 x C5 inferior) + (6.046 x C6 superior) + (10.938 x C6 inferior) + (-1.070 x C7 superior) + (-2.964 x C7 inferior) + (-1.589 x L1 superior) + (8.973 x L1 inferior) + (-4.929 x L2 superior) + (7.408 x L2 inferior) + (-1.142 x L3 superior) + (-0.104 x L3 inferior) + (4.053 x L4 superior) + (3.742 x L4 inferior) + (8.792 x L5 superior) + (5.189 x L5 inferior)

R = 0.686	R^2 = 0.471	Adj R^2 = 0.326	SEE = 16.910	F(20,73) = 3.246, p < 0.001

Equation 28 (sexes combined; n = 196):

Age = -1.286 + (1.048 x C3 superior) + (-2.508 x C4 superior) + (5.129 x C5 superior) + (8.416* x C6 superior) + (-2.134 x C7 superior) + (2.808 x L1 superior) + (3.347 x L2 superior) + (2.578 x L3 superior) + (3.210 x L4 superior) + (12.170* x L5 superior)

R = 680	R^2 = 0.462	Adj R^2 = 0.430	SEE = 14.582	F(11,184) = 14.372, p < 0.001

Equation 29 (female; n = 95)

Age = -4.294 + (4.420 x C3 superior) + (-9.371* x C4 superior) + (-9371 x C5 superior) + (8.8862* x C6 superior) + (-0.840 x C7 superior) + (3.033 x L1 superior) + (0.747 x L2 superior) + (4.054 x L3 superior) + (7.494 x L4 superior) + (9.172* x L5 superior)

R = 0.766	R^2 = 0.586	Adj R^2 = 0.537	SEE = 12.142	F(10,84) = 11.911, p < 0.001

Equation 30 (male; n = 108)

Age = 2.224 + (-1.005 x C3 superior) + (2.287 x C4 superior) + (2.259 x C5 superior) + (5.740 x C6 superior) + (-1.627 x C7 superior) + (5.611 x L1 superior) + (3.241 x L2 superior) + (-0.109 x L3 superior) + (0.635 x L4 superior) + (14.149* x L5 superior)

R = 0.622	R^2 = 0.387	Adj R^2 = 0.323	SEE = 16.425	F(10,97) = 6.112, p < 0.001

Equation 31 (sexes combined; n = 209):

Age = 1.775 + (1.893 x C3 inferior) + (2.287 x C4 inferior) + (-0.931 x C5 inferior) + (6.944* x C6 inferior) + (-0.863 x C7 inferior) + (5.019 x L1 inferior) + (3.047 x L2 inferior) + (3.056 x L3 inferior) + (1.696 x L4 inferior) + (9.985* x L5 inferior)

R = 0.661	R^2 = 0.437	Adj R^2 = 0.408	SEE = 14.816	F(10,198) = 15.342, p < 0.001

Equation 32 (female; n = 100)
Age = 1.197 + (0.122 x C3 inferior) + (5.536 x C4 inferior) + (-0.942 x C5 inferior) + (4.104 x C6 inferior) + (0.653 x C7 inferior) + (2.918 x L1 inferior) + (1.336 x L2 inferior) + (0.862 x L3 inferior) + (2.852 x L4 inferior) + (13.891* x L5 inferior)

R = 0.696	R^2 = 0.485	Adj R^2 = 0.427	SEE = 13.457	F(10,89) = 8.367, p < 0.001

Equation 33 (male; n = 109)
Age = 1.834 + (3.104 x C3 inferior) + (-0.963 x C4 inferior) + (0.924 x C5 inferior) + (7.796 x C6 inferior) + (-3.740 x C7 inferior) + (8.082 x L1 inferior) + (6.315 x L2 inferior) + (4.494 x L3 inferior) + (1.551 x L4 inferior) + (4.985 x L5 inferior)

R = 0.657	R^2 = 0.431	Adj R^2 = 0.373	SEE = 16.175	F(10,98) = 7.431, p < 0.001

*coefficient significantly contributes to equation, p < 0.05

Table 4.9: Linear regression models for combining multiple skeletal indicators to evaluate strength of association, goodness-of-fit, statistical significance and significance of contribution of the coefficients.

Equation 34 (sexes combined; n = 59):
Age = -38.614 + (7.815 x acetabular groove) + (0.218 x acetabular rim) + (0.303 x acetabular apex) + (12.347* x acetabular fossa) + (0.506 x surface topography) + (-3.692 x surface morphology) + (3.584 x inferior surface texture) + (-7.372 x posterior iliac exostoses) + (2.235 x midlambdoid) + (-3.061 x lambda) + (-1.933 x obelion) + (0.726 x vertex) + (6.026 x bregma) + (-11.519 x midcoronal) + (9.158 x pterion) + (-4.725 x sphenofrontal) + (-6.991 x superior sphenotemporal) + (15.074 x inferior sphenotemporal) + (-9.891* x zygomaticomaxillary) + (3.272 x incisive) + (5.097 x anterior median palatine) + (-2.641 x posterior median palatine) + (5.883 x transverse palatine) + (-17.105 x iliac crest) + (-10.468 x symphyseal relief) + (-2.4547 x symphyseal texture) + (4.187 x superior apex) + (6.544 x ventral margin) + (9.967 x dorsal margin) + (12.575* x S1/S2 fusion) + (-1.572 x C3 superior) + (16.626 x C3 inferior) + (-21.186* x C4 superior) + (-11.502 x C4 inferior) + (6.912 x C5 superior) + (-10.745 x C5 inferior) + (9.036 x C6 superior) + (11.470 x C6 inferior) + (-24.146* x C7 superior) + (11.379 x C7 inferior) + (6.255 x L1 superior) + (-23.654 x L1 inferior) + (6.620 x L2 superior) + (6.172 x L2 inferior) + (2.022 x L3 superior) + (15.718 x L3 inferior) + (1.467 x L4 superior) + (-5.224 x L4 inferior) + (0.547 x L5 superior) + (16.775 x L5 inferior)

R = 0.987	R^2 = 0.974	Adj R^2 = 0.809	SEE = 6.994	F(50,8) = 5.909, p = 0.006

Equation 35 (sexes combined; n = 77):
Age = -18.665 + (1.865 x acetabular groove) + (-0.184 x acetabular rim) + (0.632 x acetabular apex) + (6.960 x acetabular fossa) + (0.033 x surface topography) + (-0.363 x surface morphology) + (-2.736 x inferior surface texture) + (3.252 x posterior iliac exostoses) + (-12.257* x midlambdoid) + (9.607 x lambda) + (-0.062 x obelion) + (-2.153 x vertex) + (0.517 x bregma) + (3.504 x midcoronal) + (4.023 x pterion) + (-2.807 x sphenofrontal) + (-0.550 x superior sphenotemporal) + (3.328 x inferior sphenotemporal) + (-2.617 x zygomaticomaxillary) + (0.601 x incisive) + (-1.040 x anterior median palatine) + (-0.843 x posterior median palatine) + (0.146 x transverse palatine) + (-0.920 x iliac crest) + (0.838 x S1/S2 fusion) + (2.250 x Suchey-Brooks stage) + (0.643 x C3 superior) + (-1.936 x C3 inferior) + (3.813 x C4 superior) + (-5.478 x C4 inferior) + (2.380 x C5 superior) + (-5.229 x C5 inferior) + (4.382 x C6 superior) + (15.066 x C6 inferior) + (-12.299 x C7 superior) + (-4.062 x C7 inferior) + (-1.469 x L1 superior) + (1.156 x L1 inferior) + (10.636 x L2 superior) + (-0.552 x L2 inferior) + (2.684 x L3 superior) + (0.424 x L3 inferior) + (0.213 x L4 superior) + (-4.348 x L4 inferior) + (6.189 x L5 superior) + (10.267 x L5 inferior)

R = 0.878	R^2 = 0.771	Adj R^2 = 0.420	SEE = 12.940	F(46,30) = 2.198, p = 0.012

Equation 36 (female; n = 104)				
Age = -40.359 + (2.967 x acetabular groove) + (-0.610 x acetabular rim) + (6.425* x acetabular fossa) + (1.737 x posterior iliac exostoses) + (-3.316 x midlambdoid) + (1.162 x obelion) + (3.554 x vertex) + (-2.779 x sphenofrontal) + (3.060 x zygomaticomaxillary) + (8.985 x iliac crest) + (8.092* x S1/S2 fusion) + (1.813 x Suchey-Brooks stage) + (12.088* x L5 superior)				
R = 0.776	R^2 = 0.602	Adj R^2 = 0.539	SEE = 11.508	F(14,89) = 9.6004, p < 0.001
Equation 37 (male; n = 113)				
Age = -19.548 + (-3.051 x acetabular groove) + (4.026* x acetabular rim) + (4.352* x acetabular fossa) + (4.204* x posterior iliac exostoses) + (-2.835 x midlambdoid) + (0.889 x obelion) + (-2.248 x vertex) + (1.038 x midcoronal) + (2.234 x sphenofrontal) + (3.955* x zygomaticomaxillary) + (-1.710 x iliac crest) + (0.433 x S1/S2 fusion) + (6.561* x Suchey-Brooks stage) + (8.374* x L5 superior)				
R = 0.767	R^2 = 588	Adj R^2 = 529	SEE = 12.815	F(14,98) = 9.989, p < 0.001
*coefficient significantly contributes to equation, p < 0.05				

Table 4.10: Final multifactorial linear regression models.

Equation 38 (combined sexes; n = 258)				
Age = -18.547 + (8.961* x acetabular fossa) + (1.420* x posterior median palatine) + (7.746* x S1/S2 fusion) + (14.928* x L5 superior)				
R = 0.701	R^2 = 0.491	Adj R^2 = 0.483	SEE = 13.342	F(4,253) = 61.072, p < 0.001
Equation 39 (combined sexes; n = 264)				
Age = -23.377 + (6.822* x acetabular fossa) + (4.138* x posterior iliac exostoses) + (4.862* x zygomaticomaxillary) + (4.677* x Suchey-Brooks stage) + (10.359* x L5 superior)				
R = 0.722	R^2 = 0.521	Adj R^2 = 0.512	SEE = 12.931	F(5,258) = 56.085, p < 0.001
Equation 40 (female; n = 123)				
Age = -21.629 + (9.612* x acetabular fossa) + (7.753* x S1/S2 fusion) + (2.605* x Suchey-Brooks stage) + (11.933* x L5 superior)				
R = 0.753	R^2 = 0.567	Adj R^2 = 0.553	SEE = 11.234	F(4,118) = 38.707, p < 0.001
Equation 41 (male; n = 136)				
Age = -29.187 + (7.363* x acetabular fossa) + (6.258* x posterior iliac exostoses) + (5.554* x zygomaticomaxillary) + (3.420* x pubic symphyseal superior apex) + (13.676* x L5 superior)				
R = 0.748	R^2 = 0.559	Adj R^2 = 0.542	SEE = 13.058	F(5,130) = 32.933, p < 0.001
Equation 42 (male; n = 145)				
Age = -29.679 + (4.870* x acetabular fossa) + (4.648* x posterior iliac exostoses) + (5.762* x zygomaticomaxillary) + (6.357* x Suchey-Brooks stage) + (11.323* x L5 superior)				
R = 0.753	R^2 = 0.566	Adj R^2 = 0.551	SEE = 13.044	F(5,139) = 36.301, p < 0.001
*coefficient significantly contributes to equation, p < 0.05				

Table 4.11: Comparing bias, accuracy and precision for estimates obtained using basic statistics, regression analysis and transition analysis models.

	Basic statistics									Regression analysis									Transition analysis					
		Inaccuracy		Mean range		Max range		Range accuracy			Inaccuracy		Mean range		Max range		Range accuracy			Inaccuracy				
n	Bias	Mean	Max	Narrow*	Wide**	Narrow*	Wide**	Narrow*	Wide**	Bias	Mean	Max	Narrow#	Wide##	Narrow#	Wide##	Narrow#	Wide##	Bias	Mean	Max	Mean range	Max range	Range accuracy
Model 1: (acetabular fossa; posterior median palatine; S1/S2 fusion; L5 superior)																								
22	-4	10	21	7	28	8	45	14%	68%	-2	7	15	8	53	12	54	32%	100%	8	11	37	18	42	27%
Model 2: (acetabular fossa; auricular surfaces exostoses; zygomaticomaxillary; Suchey-Brooks; L5 superior)																								
27	-3	9	20	7	30	9	45	19%	74%	1	9	18	8	52	13	53	19%	100%	8	14	27	18	78	19%
Model 3 (female only): (acetabular fossa; S1/S2 fusion; Suchey-Brooks; L5 superior)																								
14	0	8	20	8	28	9	42	21%	79%	-2	8	25	10	46	15	47	43%	93%	8	11	44	21	55	29%
Model 4 (male only): (acetabular fossa; auricular surface exostoses; zygomaticomaxillary; pubic symphysis superior apex; L5 superior)																								
13	-6	12	21	10	32	14	51	15%	69%	4	11	19	11	53	16	54	15%	100%	2	13	24	24	54	38%
Model 5 (male only): (acetabular fossa; auricular surface exostoses; zygomaticomaxillary; Suchey-Brooks; L5 superior)																								
13	-6	11	20	10	34	15	51	8%	85%	4	9	17	11	53	17	54	38%	100%	6	17	28	20	78	31%

* range constructed using mean values for 95% confidence interval; ** range constructed using min value for 95% lower confidence interval and max value for upper confidence interval

range constructed using the mean confidence interval produced by IBM SPSS statistics package (version 25); ## range constructed using the individual confidence interval (prediction interval) produced by IBM SPSS statistics package (version 25)

Table 4.12: Observer agreement for single and multiple observers.

	Intra-observer				**Inter-observer**			
	Number	%	Cohen's kappa	Weighted Cohen's kappa	Number	%	Cohen's kappa	Weighted Cohen's kappa
Acetabulum								
Acetabular groove	28/30	93	**0.792***	**0.792***	24/30	80	0.444**	0.444**
Acetabular rim	20/30	67	0.513*	**0.581***	15/30	50	0.229***	0.245**
Apex	27/29	93	**0.861***	**0.861***	18/29	62	0.280***	0.280**
Acetabular fossa	24/30	80	**0.641***	**0.684***	24/30	80	**0.648***	**0.647***
Auricular surface								
Surface topography	25/30	83	**0.749***	**0.648***	14/30	47	0.171***	0.181***
Surface morphology	23/30	77	**0.634***	**0.656***	10/30	33	0.000***	0.070***
Inferior surface texture	22/25	88	**0.747***	**0.772***	11/26	42	0.177***	0.216**
Posterior iliac exostoses	20/29	69	0.300***	0.300**	15/29	52	0.145***	0.175***
Clavicle								
Medial epiphysis	27/27	100	a	a	27/27	100	a	a
Cranial sutures								
Midlambdoid	22/30	73	0.588*	**0.714***	8/30	27	0.049***	0.338*
Lambda	23/28	82	**0.753***	**0.822***	7/28	25	0.058***	0.396*
Obelion	20/28	71	**0.626***	**0.786***	19/28	68	0.486*	**0.677***
Vertex	22/28	79	**0.719***	**0.813***	10/28	36	0.211**	0.485*
Bregma	23/28	82	**0.732***	**0.824***	5/28	18	-0.099***	0.306*
Midcoronal	23/28	82	**0.751***	**0.853***	4/28	14	-0.091***	0.345*
Pterion	26/30	87	**0.799***	**0.882***	9/30	30	0.153**	0.361*
Sphenofrontal	25/30	83	**0.755***	**0.851***	6/30	20	-0.034***	0.035***
Superior sphenotemporal	26/30	87	**0.730***	**0.730***	1/30	3	-0.007***	a
Inferior sphenotemporal	24/30	80	**0.623***	**0.675***	1/30	3	-0.075**	0.009***
Zygomaticomaxillary	24/30	80	**0.689***	**0.722***	19/30	63	-0.181**	0.059***
Incisive	22/28	79	0.483**	0.530*	1/28	4	0.004***	-0.019***
Anterior median palatine	21/29	72	0.542*	**0.610***	3/29	10	-0.80***	0.009***
Posterior median palatine	19/27	70	0.575*	**0.668***	5/27	19	-0.092***	0.033***
Transverse palatine	21/26	81	0.527*	**0.604***	1/26	4	-0.059***	0.075**
Iliac crest								

Iliac crest	30/30	100	a	a	27/28	100	a	a
Pubic symphysis								
Symphyseal relief	26/30	87	**0.732***	**0.783***	18/30	60	0.392*	0.494*
Symphyseal texture	23/30	77	0.583*	**0.624***	12/30	40	0.036***	0.105***
Superior apex	21/29	72	0.497*	**0.609***	11/29	38	0.078***	0.321*
Ventral margin	25/30	83	**0.734***	**0.714***	16/30	53	0.302**	0.418*
Dorsal margin	21/29	72	0.470**	0.509*	18/29	62	0.333**	0.410*
Sacrum								
S1/S2 fusion	27/27	100	**1.0***	**1.0***	23/27	85	0.514**	0.514**
Suchey-Brooks								
Suchey-Brooks	19/30	63	0.478*	**0.619***	16/30	53	0.389*	0.589*
Vertebral bodies								
C3 superior	26/27	96	**0.922***	**0.922***	20/26	77	0.490**	0.490**
C3 inferior	21/26	81	**0.606***	**0.606***	20/26	77	0.538**	0.539*
C4 superior	27/27	100	**1.000***	**1.000***	26/27	96	**0.908***	**0.908***
C4 inferior	24/28	86	**0.710***	**0.710***	24/27	89	**0.767***	**0.767***
C5 superior	25/28	89	**0.772***	**0.772***	22/27	81	0.577**	0.577**
C5 inferior	24/28	86	**0.659***	**0.659***	20/27	74	0.496**	0.496**
C6 superior	26/28	93	**0.857***	**0.857***	23/28	82	**0.624***	**0.624***
C6 inferior	24/27	89	**0.743***	**0.743***	18/27	67	0.397**	0.397**
C7 superior	24/28	86	**0.680***	**0.680***	28/28	100	**1.000***	**1.000***
C7 inferior	24/28	86	**0.719***	**0.719***	23/28	82	0.593*	0.593*
L1 superior	23/28	82	0.562*	**0.563***	17/28	61	0.313**	0.313**
L1 inferior	23/26	88	**0.769***	**0.769***	19/26	73	0.462**	0.462**
L2 superior	27/27	100	**1.000***	**1.000***	21/28	75	0.529**	0.529*
L2 inferior	25/27	93	**0.841***	**0.841***	17/27	63	0.318**	0.318**
L3 superior	26/28	93	**0.845***	**0.845***	25/29	86	**0.722***	**0.723***
L3 inferior	26/29	90	**0.789***	**0.789***	24/29	83	**0.659***	**0.659***
L4 superior	26/27	96	**0.919***	**0.919***	25/26	96	**0.920**	**0.920***
L4 inferior	26/28	93	**0.854***	**0.854***	24/27	89	**0.780***	**0.781***
L5 superior	25/28	89	**0.772***	**0.772***	24/28	86	**0.701***	**0.701***
L5 inferior	25/27	93	**0.841***	**0.841***	23/28	82	**0.650***	**0.650***

*p < 0.001, statistically significantly better than chance agreement
**p < 0.05, statistically significantly better than chance agreement
***p > 0.05, not statistically significantly better than chance agreement
a – full sample allocated to one category (i.e. iliac crest fusion scored as 2), Cohen's kappa value cannot be calculated

CHAPTER 5: DISCUSSION

This study aimed to compare the accuracy, precision and ease-of-use of multifactorial statistical models for adult age-at-death estimation from the skeleton that are appropriate for a forensic context.

These aims were achieved by collecting age-related data, specific to a South African population, from 332 skeletons. Age-related indicators that were examined included 15 cranial suture segments (seven which were bilaterally collected), the medial clavicles, the S1/S2 sacral segments, the iliac crests, four components from the acetabula, four components from the auricular surfaces of the ilia, five components as well as a stage-based method for the pubic symphyses and lastly the typical cervical and lumbar vertebral bodies.

The data were analysed for sample distribution, statistical differences between the left and right sided features, sexes and also the vertebral body margins. Descriptive statistics for each indicator/ individual component were calculated and assessed for their representation within the study population and progression with age. Category stages that were minimally represented in the population were combined with adjacent stages.

Regression analysis equations were constructed for each indicator to analyse the strength of association (r-values) and variance in age explained by each indicator (r^2-values), as well as the significant contribution of each indicator/individual component. This information was used to construct five multifactorial regression equations (three which were sex-specific; one for females and two for males).

Generalized linear models with a logit link were calculated for each indicator and transition curves constructed. The transition curves were analysed for age-related information and unidirectional progression with age. A Bayesian approach, with uniform prior distribution, was used to combine multiple indicators into a multifactorial transition analysis method. The same indicators were used as those in the five multifactorial regression analysis equations to optimise comparison.

Validation data, from a hold-out sample (n = 30), were used to test the accuracy and precision of the statistical methods. Accuracy and bias were analysed for the calculated point estimates, for the chosen combination of indicators. Point estimates

were obtained by 1) averaging the mean age per stage as calculated from the descriptive statistics, 2) from the regression analysis equations and 3) from the transition analysis method. Accuracy and precision were analysed for age intervals, which were calculated by 1) including the entire combined interval from the descriptive statistics, 2) including an interval between the average of the lower limit and the average of the upper limit from descriptive statistics, 3) a 95% confidence interval from the regression analysis method, 4) a 95% prediction interval from the regression analysis method and 5) a 95% confidence interval from the transition analysis method. Lastly, observer agreement was considered for each of the indicators/individual components for single and multiple observers.

Good forensic practice requires statistically calculated error margins (National Research Council, 2009). Simultaneously, both accuracy and precision are crucial as inaccurate intervals will provide incorrect information, whereas imprecise intervals (even if accurate) will include too much information. Good accuracy is pointless if the interval is impractically large to the extent of including the full age range (i.e., 20 to 100 years). Obtaining a balance between accuracy and precision for age-at-death estimation has a reputation in literature of being particularly challenging due to numerous additional factors that influence the appearance of the skeleton with time (Jackes, 2000; Nawrocki, 2010; Mays, 2015; Merrit, 2015; Henderson and Nikita, 2016).

The current study calls attention to many of the same problems. Sophisticated statistical methods did not necessarily produce improved accuracy and precision even though meeting the required forensic guidelines. The following discussion considers the benefits and limitations introduced by each of the three statistical methods tested, the indicators that contained the most age-related information, the best combinations of these indicators and their potential contribution in future methods for age-at-death estimation. Multicollinearity and its importance when deciding on component- or stage-based methods is addressed and the effectiveness of the sample size and results of multifactorial methods are discussed. The differences between the appearance of bilateral features are also discussed and interpreted in practical terms. The observer agreement for each feature and its potential effect on the results of age-at-death are considered. Finally, some suggestions are made for future research in age-at-death estimation.

5.1. Statistical methods

From the validation results of this study, it is clear that reasonable interval accuracy is often only achieved at the expense of precision. High accuracy due to particularly large intervals were observed for the wide interval regression analysis method; 100% accuracy was achieved but approximately 50 year ranges were obtained. More desirable mean intervals were obtained using the narrow interval regression analysis method and transition analysis. Although mean intervals of 8 to 11 and 18 to 24 years respectively are more realistic, interval accuracy for these methods decreases to 19% - 43% and 19% - 38% respectively. Maximum age intervals of up to 54 and 78 years for regression analysis and transition analysis respectively are still not ideal.

Contrastingly, consistently narrow intervals were achieved from the basic descriptive statistics method (7 to 10 years using the narrow interval method and 28 to 34 years using the wide interval method). Surprisingly, the narrower intervals observed using basic descriptive statistics frequently achieved relatively accurate results (especially for the wide intervals calculated achieving between 68% and 85% accuracy). When considering interval size and accuracy only (i.e., not considering whether a method is statistically defensible), the intervals provided by the basic statistics wide interval method are more accurate and precise and would be the preferred method. This method could potentially be used as a starting point before calculating age estimations using methods that employ more advanced statistics for evidentiary purposes.

When weighing the two more complex statistical methods according to interval precision and accuracy, the intervals calculated using the narrow interval regression analysis method (i.e., using 95% confidence intervals) outperform transition analysis in each model except for Model 4 (for males). Thus, the regression analysis, which also has the benefit of being relatively easy to use and does not require massive computational power, appears to be the better statistical choice based on interval results. However, one should remember that neither of these statistical methods achieved more than 43% and 38% interval accuracy for regression and transition analysis respectively.

Accuracy at the expense of precision is seen time-and-again in the literature (Katz and Suchey, 1986; Milner and Boldsen, 2012b; Jooste *et al.*, 2016) and while 95% confidence intervals may be legally and scientifically verifiable, wide intervals do not assist much in actual forensic cases where one needs to narrow down a list of potential matching individuals. This problem has led to a number of authors stating that sophisticated statistics alone may not be the answer to improving the performance of age-at-death estimation (Jackes, 2000; Hurst, 2010; Slice and Algee-Hewitt, 2015; Jooste *et al.*, 2016; Stoyanova *et al.*, 2017).

Although point estimates are not necessarily encouraged for use in forensic investigation, the results obtained provide a useful measure of the accuracy of each statistical method. Once again, the point estimates achieve better accuracy using basic descriptive statistics and regression analysis, as compared to transition analysis (Table 4.11 and Figures 4.54 - 4.58). This ability for statistically less sophisticated methods to potentially outperform statistically advanced methods has previously been noted in the literature (Passalacqua, 2009; Hurst, 2010; Uhl and Nawrocki, 2010; Nikita and Nikitas, 2019).

Even though relatively simple statistics, including regression analysis, seems to outperform the complex Bayesian analysis, there is a larger consideration. Many researchers believe that Bayesian analysis are better suited to the type of data characteristic of age estimation (Konigsberg and Frankenberg, 1992; Lucy *et al.*, 1996; Boldsen *et al.*, 2002). Bayesian analysis is specifically recommended as it does not require the linear and continuous representation of age or a parametric distribution of residuals as is required by linear regression (Lucy *et al.*, 1996). However, the literature does not frequently elaborate on the assumptions required by Bayesian analysis to produce valid results. Nikita *et al.* (2018) explain a host of assumptions that require fulfilment for Bayesian analysis including an appropriate prior distribution that is aligned with the target sample distribution (which is likely unknown in forensic investigations), a reference data set that is a good fit for a probit or logit regression model and a normal distribution for log age of the reference sample. DiGangi *et al.* (2009) also highlights a potential problem with transition analysis as transition curve distributions are calculated from observed ages-of-death and not direct observation of ages-of-transition.

Results for assumptions required for Bayesian analysis are infrequently reported and not necessarily satisfactory. In a rare discussion of assumptions, DiGangi *et al.* (2009) report that four of their 11 age indicators did not fit a normal or log-normal ages-to-transition distribution. These researchers go on to highlight that intercorrelation between age indicators remains an important aspect and should be reduced; they accomplish this by choosing only two indicators from the initial 11 for their age estimation method. This is in direct opposition of one of the benefits of using a Bayesian method - to combine multiple skeletal indicators in a statistically sound way to include more age information from the skeleton.

The results from the current study emphasize that transition analysis does not outperform regression analysis when considering interval precision and accuracy. A straightforward, user-friendly regression analysis equation may achieve better results in a forensic investigation. The basic statistics method far outperforms both regression and transition analysis and may achieve much more satisfactory results in forensic investigations. Although this method is also more user-friendly and less time consuming, it unfortunately does not produce statistically calculated confidence intervals or mean error margins. The basic statistics method and the requirements to make this a forensically acceptable method may warrant future investigation.

5.2. Age indicators and confounders

A more appropriate question than which statistical method best captures the age-at-death data, may be whether any statistical model captures the complexities of changes in skeletal appearance with progressing age. Literature seems to acknowledge that no amount of statistical complexity in analysis can improve or account for information that does not exist in the skeleton (Jackes, 2000; Hurst, 2010; Lucy, 2010; Nawrocki, 2010; Milner and Boldsen, 2012b; Jooste *et al.*, 2016). The results of this study, as well as a large body of evidence from literature (Brooks and Suchey, 1990; Nawrocki, 1998; Baccino *et al.*, 1999; Osborne *et al.*, 2004; White and Folkens, 2005; Konigsberg *et al.*, 2008), unequivocally indicates that the skeleton contains some age-related information associated with structural changes observed in certain skeletal indicators. However, this observed relationship between age and the skeleton is not only imperfect, but likely influenced by a myriad of biological and lifestyle influences (i.e., confounders) (Nawrocki, 2010; Milner and Boldsen, 2012a; Zukowski *et al.*, 2012; Mays, 2015; Merrit, 2015).

This study confirms that limitations in the information available from the skeleton are a major problem in age-at-death estimation. The first indication that the relationship between age and skeletal appearance is imperfect is indicated by the mean and median values of the indicator categories that do not always increase sequentially (Table 4.5). This deviation from the expected pattern occurred in some cranial sutures from the vault and palate, as well as textural changes to the auricular surface and acetabular rim. The cranial sutures have previously been criticised for their limited age-related information and their tendency to provide very broad age categorisation (Brooks, 1955; Meindl and Lovejoy, 1985; Key *et al.*, 1994). Additionally, Key *et al.* (1994) found that only the first and last category of the cranial sutures (i.e., open and obliterated) provided significant age-related data. Changes in porosity and texture that occur on the skull and hip bones (i.e., auricular surface and acetabular rim) have also been associated with pathology, lifestyle factors or child bearing in the literature (Boldsen *et al.*, 2002; Campanacho *et al.*, 2012; İşcan and Steyn, 2013; Mays, 2015; Merrit, 2015). These lifestyle factors could influence, or even obscure, age-related changes associated with these specific skeletal indicators and render data obtained from them unreliable.

This study also found very low (i.e., representative of < 2% of the reference sample) representation in certain skeletal indicator categories. These minimally represented categories, that were selected from literature for their relationship with age included the lowest/youngest stages in some cases and the highest/oldest stages in others. The young stages (i.e., stage 1) that were minimally represented include skeletal indicator categories from the acetabular fossa, auricular surface morphology, pterion, pubic symphyseal relief, pubic dorsal margin, pubic ventral margin, fusion of S2/S3, pubic symphyseal stage-based method (Suchey-Brooks) and the incisive suture. The advanced stages (i.e., stage 4 or 5) that were minimally represented include categories from the superior and inferior sphenotemporal, bregma, zygomaticomaxillary and anterior median palatine sutures and the auricular surface morphology. The fact that very few individuals could be classified into these categories indicates that these category variants are not well represented in this specific population. In some instances, it may be that individuals from this population progress from stage 1 to 2 before age 20 (the minimum age chosen for this study). These young stages are associated with the late teens and early twenties in

literature (McKern and Stewart, 1957; Katz and Suchey, 1986; Mann *et al.*, 1991; Rissech *et al.*, 2006) and suggest that progress from stage 1 to 2 occurs at an earlier age in this population. Similarly, individuals from this population likely progress to the final stage at a later age, or sometimes not at all for the abovementioned old stages. As the majority of the identified stages that do not progress with advancing age include cranial sutures, it is possible that these sutures never fully obliterate in this population, which is a phenomenon known from literature (Todd and Lyon, 1925b, 1925a; Meindl and Lovejoy, 1985; Key *et al.*, 1994).

The transition curves generated from generalized linear models, also confirms the imperfect relationship between age and the skeletal indicators. Two or more stages with similar transition curves (i.e., similar shapes and areas under the curve) suggest that multiple stages of the age indicator represent similar proportions of the population for the same ages and are thus equally likely to occur at those ages. These closely overlapping curves included stages 3 and 4 of the acetabular rim (Figure 4.31), stages 1 and 2 of the midlambdoid and obelion and also stages 4 and 5 of the midlamboid, lambda, obelion, midcoronal, pterion, sphenofrontal and posterior median palatine sutures (Figure 4.34) and stages 2 and 3 of pubic symphyseal relief and stages 1 and 2 of superior apex (Figure 4.36). These overlapping stages do not provide unique age information in this population. The stages can potentially be combined into a single stage without sacrificing any age-related information. Two stages that differ by description of skeletal appearance, but provide the same age information, could be indicative of the individual-level variation reported in the literature (Todd, 1921a; Konigsberg and Frankenberg, 1992; Boldsen *et al.*, 2002; Nawrocki, 2010; Soto *et al.*, 2018). Thus, instead of being two distinct stages the above stages could rather be considered as pattern variations of a single stage.

Some transition curves emphasize stages of indicators that contain very little or no age-related information. Some transition curves remain approximately constant throughout the entire age distribution and contain equal proportions of individuals throughout the entire age construct. This would suggest that the skeletal appearance associated with this stage is not related to age and can potentially be removed. Stages that remain approximately constant throughout the age distribution include stage 2 of the auricular surface topography and morphology; stage 3 of inferior

surface texture and posterior iliac exostoses (Figure 4.32); and stage 5 of the vertex and transverse palatine suture (Figure 4.34). It is important to note that one stage of dichotomous variables (i.e., indicators with only two stages) can be approximately constant for the majority of the age distribution as illustrated in the medial epiphysis of the clavicle (Figure 4.33), iliac crest (Figure 4.35) and the acetabular apex (Figure 4.31). These constant stages should not be removed as the indicators contribute low-level age information by the presence of one stage. Thus, the presence of stage 1 will provide information about early adulthood (i.e., early twenties), but once the transition to stage 2 has occurred the individual's age can be anywhere between 20 and 100 years. These low-level contributions of dichotomous variables are best utilised in combination methods or in a method using multiple steps, such as the two-step procedure of Baccino *et al.* (2014).

It is promising to note that data from the transition curves corroborate conclusions from the descriptive statistics (i.e., means and medians that do/do not progress with age). These curves are very helpful in visualising trends that occur with age. Transition curves that display a consecutive rise in proportions with age for each consecutive stage corresponds to indicators with high coefficients of determination (r^2-values), which significantly contribute to the multiple regression models. This strengthens the conclusion that not all skeletal indicators strongly contribute age information and that other mechanisms may be contributing to changes in skeletal appearance.

Another clear indication from this study that the relationship between age and skeletal appearance is imperfect and influenced by other factors is the coefficient of determination (r^2-values) generated for the individual indicators during regression analysis (Table 4.8). The r^2-value represents the total variation in age that can be explained by the appearance of the skeletal indicator and is very low for all individual indicators. The most variance in the appearance of the skeleton that can be attributed to age in this study is 50% for some instances of the vertebral bodies. Other r^2-values are even lower than 50% with the pubic symphysis stage-based method (Suchey-Brooks) and the acetabulum achieving between 20 and 40%, pubic symphysis component-based method between 20 and 30%, the auricular surface, cranial sutures and S1/S2 fusion of the sacrum between 10 and 20% and the clavicle and iliac crest below 10%. Even when combining multiple indicators into

multifactorial equations (Table 4.10), the r^2-value only increases to a maximum of 60%. This means that 40% of the changes in appearance of skeletal indicators are related to factors other than age. This imperfect relationship is supported by r^2-values in the literature that never rise above 70%, and are realistically closer to between 30% and 50% (İşcan *et al.*, 1985; Jackes, 2000; Igarashi *et al.*, 2005; Nawrocki, 2010; Mays, 2015).

A small percentage of the unexplained variation is likely attributed to differences in appearance of the skeletal indicator that occurs at sex and population level. However, these factors in no way account for the entire remainder of the r^2-value. Sex-specific regression equations improved the r^2-values by a maximum of 10% (Table 4.8). Similarly, population differences should already be accounted for in the equations of Tables 4.8 to 4.10 as this study was conducted using only one population. Thus, the assumption can be made that the remaining 40% of variance in appearance of the skeletal indicators can be attributed to individual lifestyle and physiological influences. Although this is widely accepted, it is very difficult to account for these factors during age-at-death estimation from the skeleton.

One possible method to account for lifestyle factors in future studies, would be to use a living reference sample. Imaging modalities, such as MRI (magnetic resonance imaging) and CT (computed tomography) scans, could be used to record skeletal information from living individuals. Living individuals could provide documentary information regarding confounders such as physical activity, health and other lifestyle factors, but as this could never be known about an unidentified body, the usefulness of such an approach remains limited.

Even though the relationship between skeletal appearance and chronological age is clearly imperfect, some age indicators contain more useful information than others. From this study, the indicators that contributed the most age-related data included the acetabulum, the pubic symphysis (specifically the Suchey-Brooks stage method) and the vertebral bodies. These indicators obtained the largest coefficient of determination values (r^2-values above 0.3; Table 4.8). These indicators also presented with transition curves that indicated clear transitions between each successive stage (Figures 4.31, 4.38 to 4.40).

Interestingly, the two methods from the pubic symphysis did not perform equally well. The stage-based (Suchey-Brooks) method obtained higher r^2-values compared to the component-based method (an r^2-value of 0.312 for the stage method compared to 0.272 for the component method, for males and females combined). The strength of association is similarly higher for the stage-based method compared to the component-method (r-value of 0.558 versus 0.521 for the stage- and component-method respectively, for males and females combined). Additionally, all components did not contribute significantly to the regression equations for the component-based method. For the sexes combined and the female sample, only the symphyseal relief and symphyseal texture contributed significant information to the equation. The ventral and dorsal margins contributed additional significant information to the male sample. However, the stage-based method still outperformed the component-based method for the male sample. Furthermore, multicollinearity becomes a consideration when using component methods, as further discussed in 5.3 below. From this study, a more holistic approach to skeletal indicator regions seems to contribute more overall information.

Although indicators that contain small amounts of age information could contribute to multifactorial methods, a few high quality indicators such as the acetabulum, pubic symphysis and vertebrae are best to prevent multicollinearity and optimise the power of the sample size.

5.3. Multicollinearity

Combining multiple indicators from the skeleton has always been considered best practice (Brooks, 1955; Suchey and Katz, 1998; Uhl and Nawrocki, 2010). There is a general impression that additional indicators will provide additional age-related information and compensate for the variation attributed to biology and lifestyle (Brooks, 1955; Johnson, 1976; Lovejoy, Meindl, Mensforth *et al.*, 1985; Brooks and Suchey, 1990; Baccino *et al.*, 1999; Uhl and Nawrocki, 2010). This study indicates that care must be taken when combining multiple skeletal indicators as the potential improvement in results may have statistical pitfalls.

Although combining skeletal indicators into a multifactorial method may have the ability to improve age-at-death estimation, the relationship between the single indicators and its influence on the results needs to be well understood.

Multicollinearity occurs when two or more of the skeletal indicators are highly correlated (i.e., above 0.7) with each other (Akoglu, 2018). Ideally, the only correlation between skeletal indicators should be their mutual relationship with age. Highly correlated age indicators (Table E4 in Appendix E) include lambda and the midlambdoid suture, bregma and the vertex, bregma and the midcoronal suture, pterion and the spenofrontal suture and the superior and inferior sphenotemporal sutures. The multicollinearity of these cranial suture areas is understandable as these sutures are spatially very closely related to one another and have similar functions. Similarly, certain vertebral bodies are highly correlated with one another (Table E4 in Appendix E) including L4 superior vertebral margin and L5 superior vertebral margin, L3 superior vertebral margin and L4 superior vertebral margin and L2 inferior vertebral margin and L3 inferior vertebral margin. As with the cranial sutures, multicollinearity of the vertebral bodies is understandable as they are closely related and also perform the same broad function in movement and stabilisation of the trunk. Highly correlated age indicators were not used in combination in this study as this would violate one of the assumptions of multiple regression analysis.

Although the remainder of the age indicators are not as highly correlated with each other and are considered acceptable in combination, many of the indicators still show statistically significant correlation even though they are correlated to a lesser degree (i.e., $p \leq 0.01$, but correlation value below 0.7). Age indicators that have small, but statistically significant relationships include correlations of various pelvic age indicators with each other; this includes components of the acetabulum, auricular surface, pubic symphysis (both the component and stage-based method) and the iliac crest. The various pelvic age indicators also displayed correlation to a number of cranial sutures. Additionally, the dichotomous age indicators (i.e., medial clavicle, iliac crest, S1/S2 and the vertebral bodies) displayed low, but significant correlation with most of the other indicators.

The various degrees of multicollinearity observed between age indicators suggest a complex relationship between several age indicators that cannot only be attributed to a mutual relationship with age. Correlation between indicators, in this case, does not indicate causation (e.g., changes in the pubic symphysis are not responsible for changes in the acetabulum). The intercorrelation more likely indicates multiple common interactions, including but not limited to age changes. Common factors that

can influence appearance that are acknowledged by the literature include muscle attachments (Key *et al.*, 1994), activity levels (Rissech *et al.*, 2006; Nawrocki, 2010; Mays, 2015; Merrit, 2015), degenerative diseases (Berg, 2008; Zukowski *et al.*, 2012; Botha *et al.*, 2019) as well as pregnancy and parturition (Kelley, 1979).

Multicollinearity, observed to varying degrees between the indicators of this study, is one of the statistical considerations that may have a variety of consequences for the results obtainable from the multifactorial method. The impact of one indicator on age is less precise when indicators are correlated with one another. This affects the coefficient of the indicator in the regression equation. As multicollinearity results in imprecise coefficients, predictions using out-of-sample indicators (i.e., from an unknown sample) will also be imprecise. Additionally, correlated indicators contain the same age-related information and one or more indicators become redundant to the multifactorial method. This could also result in small changes to reference data causing large changes in the multifactorial model results.

Multicollinearity also produces the same effects in single indicator age estimation methods that consist of multiple components. Component methods contain multiple variables that may interact with one another in a similar manner to multiple indicators. Components centred around a single region will be even more likely to present with intercorrelation as seen in Table E4 in Appendix E. An example of intercorrelation within a region is the pubic symphysis relief component that obtained high correlations with other pubic symphysis components.

A potential solution to keep the influence of multicollinearity as low as possible, would be to include as few as possible interacting variables in a multifactorial method. At the same time, the variables should include as much information about the skeleton as possible. Substituting component-based methods with stage-based methods has the potential of including a similar amount of information about a skeletal indicator without effecting calculations by using multiple intercorrelated components. Additionally, there will be no information loss from individual components during the combination process, which has been a concern in the literature (Lucy *et al.*, 1996; Nawrocki, 1998).

5.4. Sample size

An additional consideration for multifactorial models is the power analysis or the minimum sample size that allows for a reasonable ability to obtain statistically significant results. Sample size for multifactorial models is a function of effect size and the number of indicators in the model (Green, 1991). Most multifactorial methods require an enormous sample size to effectively incorporate large numbers of indicators. The sample size becomes even larger if a multifactorial method is used for estimation and not just for testing statistical significance (i.e., hypothesis testing) (Maxwell, 2000; Tabachnick and Fidell, 2001; Knofczynski and Mundfrom, 2008).

Tabachnik and Fidell (2001) suggest a very conservative estimation of sample size for multivariate predictors of five times the number of indicators. This study contains the potential of 51 indicators, which would need a minimum sample size of 255. This doubles when dividing the sample by sex. This is also heavily influenced by preservation bias as all indicators need to be present to be counted towards the sample size.

Less conservative sample size calculations include $N \geq 20 \times m$ or $N \geq 50 + 8m$ or $N \geq 104 + m$ (m refers to the number of indicators) (Green, 1991). The sample size, especially for samples divided by sex becomes unpractical, especially considering that each age group should contain equal numbers (Nawrocki, 2010). With limited skeletal material in reference samples it becomes impractical to create large multifactorial models with unlimited numbers of age indicators. A more selective approach to multifactorial models has been considered in this study, with only indicators with the strongest association with age included in the final models in order to maximise the power of the sample size.

In this study the sample size for the final age estimation methods varied between 123 (for the female model) and 264 for Model 2 with sexes combined. As a maximum of five indicators were included in each model, even less conservative methods estimate the required sample size at around 100. Thus, the sample size would be considered sufficient for the number of indicators used.

5.5. Observer agreement

It is widely accepted that improved observer agreement will improve precision and accuracy of a method by improved classification success (Kimmerle, Prince *et al.*,

2008; Slice and Algee-Hewitt, 2015; Stoyanova *et al.*, 2017). Although attempts to strengthen agreement with improved classification descriptions, images and three-dimensional casts and models (McKern and Stewart, 1957; Suchey and Katz, 1998), quantification of shape changes (Slice and Algee-Hewitt, 2015; Stoyanova *et al.*, 2017) and reduction of category numbers (Katz and Suchey, 1986; Osborne *et al.*, 2004; Igarashi *et al.*, 2005; Rissech *et al.*, 2006; DiGangi *et al.*, 2009; Stull and James, 2010) achieved various levels of success, the consistently problematic observer agreement may be yet another indication of the vast amount of variation that cannot be attributed to age and is difficult to quantify and describe. Reliable observer classification could be influenced by many factors including a predictable and well-recorded change in skeletal appearance associated with age. A multimodal cause in change of the skeletal appearance as observed by the variation in pattern introduced by physiological and lifestyle factors can result in low classification agreement.

Intra-observer results for this study indicated very good reliability (> 0.6 Cohen's kappa values in Table 4.12). Further improving observer agreement for the indicators that obtained moderate agreement (using the Landis and Koch (1977) categories of agreement) could improve overall results. These indicators include the acetabular rim, midlamboid, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures, symphyseal texture, superior apex, dorsal margin and the stage-based method (Suchey-Brooks) as well as vertebral body L1 superior margin. However, agreement values increased when conducting a weighted Cohen's kappa test, which indicates that although some category disagreement is present, the disagreement is relatively small (i.e., one category disagreement). The reliability of only one indicator proved problematic for the intra-observer agreement; the posterior iliac exostoses was not considered statistically significantly better than chance agreement ($p > 0.05$). Thus, the posterior iliac exostoses cannot be reliably classified according to the current classification system and amendments may improve not only the agreement obtained from this indicator but also the precision and accuracy achieved using this indicator.

Interobserver results for this study were less reliable compared to the intra-observer results (Table 4.12), as expected. Indicators with particularly problematic reliability for interobserver agreement ($p > 0.05$) included the acetabular rim and apex,

auricular surface topography, morphology, inferior surface texture and posterior iliac exostoses, the midlambdoid, lambda, bregma, midcoronal, sphenofrontal, superior sphenotemporal, incisive, anterior median palatine, posterior median palatine and transverse palatine sutures, symphyseal texture and apex. Indicators with agreement values that increased with the weighted Cohen's kappa test and indicate only small category differences (i.e., one stage different) include the acetabular rim and apex, auricular surface topography, morphology, inferior surface texture and posterior iliac exostoses, the midlamboid, lambda, bregma, midcoronal, incisive and transverse palatine sutures and also the pubic symphyseal texture and apex. Indicators with agreement values that decreased with the weighted Cohen's kappa test and indicate disagreement by more than one category include the inferior sphenotemporal, zygomaticomaxillary, anterior median palatine and posterior median palatine sutures. These cranial sutures could potentially benefit from decreasing the categories to be either open or obliterated.

Indicators that were considered particularly reliable for both intra- and interobserver agreement included the acetabular fossa, obelion and the vertebral bodies (especially the lumbar vertebral bodies). Other indicators that were moderately reliable and can yield relatively good agreement include the acetabular groove, pubic symphyseal relief, ventral and dorsal margin and the stage-based method (Suchey-Brooks), as well as S1/S2 fusion. Although the clavicle and iliac crest did not produce a Cohen's kappa value, they can also be considered reliable as they were all sorted into a single category by all observers.

Reliability of category descriptions has a reputation of being problematic due to the subjective nature of the method (Slice and Algee-Hewitt, 2015; Stoyanova et al., 2017; Zeman and Beňuš, 2020). The continuous biological processes associated with the age indicators change constantly and can be influenced by many factors other than age (Kimmerle et al., 2008). This study agrees with other research that binary present-absent traits provide higher observer agreement (Passalacqua, 2009). Indicators that achieved poor reliability in this study have performed similarly in other studies from a South African context. These indicators, which achieved kappa values of less than 0.6, include the acetabulum (Botha et al., 2016), auricular surface and pubic symphysis (Jones et al., 2018). In a previous test of transition analysis in a south African population the palatine sutures and zygomaticomaxillary

suture also achieved low reliability, especially between multiple observers (Jooste et al., 2016). However, in a study developed for a South African population, using category descriptions from the Acsádi and Nemeskéri Complex Method, cranial suture reliability achieved above 0.7 and the pubic symphysis achieved above 0.7 for intra-observer agreement, but as low as 0.5 for interobserver agreement (Meyer et al., 2021). These higher observer agreement values reported by Meyer et al. (2021) and also values for the acetabular fossa and intra-observer values for the cranial sutures and pubic symphysis from this study indicates that reliability can potentially improve with training and familiarity with the method and also adjustment of category descriptions for clarity.

Indicators, in this study, that could benefit most from improved reliability include the zygomaticomaxillary and posterior median palatine sutures, posterior iliac exostoses and pubic symphyseal apex. These indicators indicated particular affinity for change with age progression and were included in the multifactorial models. Thus, improving classification agreement for these specific indicators may improve accuracy and precision further.

5.6. Bilateral asymmetry

In this study, a Wilcoxon signed-rank test determined that there were no significant differences between scores from the right and left side. This contrasts with some observations from the literature that document differences between cranial sutures (Jackes, 2000) and the pubic symphysis (Overbury *et al.*, 2009; Baccino *et al.*, 2014) from the right and left side. As no significant differences were observed from our reference sample, information from any available side could be substituted into the constructed age estimation models. This would be beneficial in cases where preservation of the remains is problematic as it may increase the number of indicators available from the remains.

5.7. Using the results from this study

This study confirms that adult age-at-death estimation is far from ideal, regardless of the statistical methods employed. However, as age-at-death estimation remains a requirement, considering what is possible with the methods currently at our disposal would be beneficial.

As the basic statistics method performed exceedingly well, this method could have merit when drawing preliminary conclusions. Mean ages and 95% confidence intervals are available for the left and median indicators of all 51 indicators studied in Table 4.5. Similarly, mean ages and 95% confidence intervals are available for the right-side indicators in Table E1 (Appendix E). The method of combining this information successfully in this studied consisted of averaging the mean ages for the observed stage of each indicator used to obtain a point estimate. The entire 95% confidence interval range, including all indicators, should be used (i.e., the wide interval method). Although the information from Table 4.5 and D1 would enable any combination of skeletal indicators, the only combinations with known accuracies and precision are included in Table 4.11.

When choosing between regression and transition analysis, regression analysis seems to be the more accurate and precise method from this study's results. Regression equations 38 to 42 in Table 4.10 can be used to obtain age estimates with known accuracies and precision. Similarly, age estimates using transition analysis can be obtained from Tables E5 to E9 (Appendix E) by locating the observed score for each indicator.

All indicators need to be present to use both the regression analysis and transition analysis as available in this document. The reference sample data would need to be reanalysed for any other combinations of indicators. If all indicators needed for the combination methods are not available, age estimations can be calculated using the single indicators in regression equations 1 to 33 in Table 4.8. Although it is possible to use single indicator regression equations to obtain age estimates, these equations do not contain known accuracies and precision from the validation study.

5.8. Conclusions and future directions

This study aimed to evaluate the performance of various statistical methods commonly used in multifactorial age estimation. The more complex statistical method - transition analysis - did not seem to improve the age estimation results and in many cases produced impractically large age intervals. Additionally, the added mathematical complexity, necessity for large reference samples and computational power makes this method less user-friendly. An increase in statistical complexity and

power seems ineffectual when skeletal indicators can only provide 30 to 50% information that is related to age.

This would indicate that improving the ability to recognise age-related information obtained from skeletal indicators may improve estimation results. Some technology-based methods may have the potential to obtain more refined information from the indicators and reduce observer disagreement. Pattern recognition software along with machine learning has been investigated for other biological research such as neuroanatomy (Chen *et al.*, 2018) and cell biology (Shamir *et al.*, 2010; Sommer and Gerlich, 2013). Recently, pattern recognition and machine learning have been applied to sex and ancestry estimation in forensic anthropology (Cavalli *et al.*, 2017; Nikita and Nikitas, 2020). This technology could similarly benefit age-at-death estimation by training computer software systems to recognise small scale differences easily misclassified by the human eye.

These computerised categorisation tools might also improve results by reducing observer disagreement. However, confounder influence on the skeletal appearance remains an obstacle. An age indicator free from confounder influence such as biological and lifestyle changes is needed. After decades of research about the relationship between skeletal appearance and age, finding this perfect, confounder free indicator, seems unlikely. Alternatively, a method that can account for biological and lifestyle changes could improve age estimation. Developing a method that accounts for confounders, would require a reference sample for which confounders are documented. A living reference collection would be the most thorough method of obtaining information about confounder influence.

A cautious approach should be taken when combining indicators into multifactorial models as multicollinearity and sample size influence the success of the models. Combining indicators can increase the age information contained in the skeletal indicators, but only increases the coefficient of determination by approximately 10%.

An alternative approach to combining multiple indicators into a single multifactorial approach could be a multiple step method, similar to the two-step procedure of Baccino *et al.* (2014). A multiple step method would still incorporate information from multiple indicators, but as the method would only consider one indicator at a time, the effect of multicollinearity and sample size on the results would be reduced. The

results from the current study would suggest starting with the vertebral bodies, which transitions between stages around 40 to 70 years (depending on the chosen vertebra). Results from the vertebrae would indicate whether the remains are those of a young adult (e.g., below 40 years) or advanced age (e.g., above 70 years). If the vertebrae indicate an age below 40 years, an indicator such as the pubic symphysis could be used to refine the age estimate. If the vertebrae indicate an age above 70 years, an indicator such as the acetabular fossa could be used to refine the age estimate.

Although some age-related information was observed for the chosen skeletal indicators, approximately 50% to 70% of skeletal changes are not explained by age alone. Sophisticated statistical techniques, such as transition analysis, did not improve results compared to basic statistics and regression analysis. Thus, future research should look to other methods such as computerised classification systems and accounting for confounders to improve age estimation results.

CHAPTER 6: CONCLUSION

The aim of this study was to compare the accuracy, precision and ease-of-use of multifactorial statistical models for adult age-at-death estimation from the skeleton that are appropriate in a forensic context, using a South African sample. It was concluded that:

1. The basic statistics method produced the best interval accuracy and precision from the three methods tested. This method also produced the most accurate point estimates. However, this method does not provide forensically acceptable error margins, but could potentially be used to obtain preliminary results.
2. Regression analysis outperformed transition analysis in most cases and obtained more precise and accurate results. Without improving the accuracy and precision, transition analysis cannot be considered the better statistical technique no matter the statistical sophistication and suitability.
3. Both the regression and transition analysis methods can be utilised for age estimation in single cases, as presented in this document. However, if specific indicators need to be removed or switched due to poor preservation, the reference sample will be required to rework the statistical models. This calls attention to the fact that these methods may require more computational power compared to the basic statistics method.
4. Skeletal indicators that contained the most age-related information and will produce the best results include the acetabulum, pubic symphysis and vertebral bodies. Even though these indicators attributed the most variance to age and clearly transitioned between stages with progressing age, confounding factors still contributed up to 70% of variation observed at the indicator. Some of the confounder effect can be minimised by using sex specific data.
5. Combining multiple indicators slightly increases the information available about age, from the skeletal appearance. However, multicollinearity and sample size can become problematic when combining indicators. A multiple-step procedure may combine information from multiple skeletal indicators, while minimising the effects of multicollinearity and sample size. This should be investigated further.

6. Future research should include maximising age-related information obtained from the skeletal indicators by investigating the potential of pattern recognition software and machine learning. Automated classification systems would improve observer agreement. Lastly, accounting for the confounders' influence on skeletal indicators by using living reference collections may further improve the age estimation results.

REFERENCES

Acsádi, G. and Nemeskéri, J. (1970) *History of the Human Life Span and Mortality*. Budapest, HU: Akadémiai Kiadó.

Adalian, P. (2020) 'General considerations about data and selection of statistical approaches', in Obertová, Z., Stewart, A., and Cattaneo, C. (eds) *Statistics and Probability in Forensic Anthropology*. London, UK: Elsevier Academic Press, pp. 59–72. doi: 10.1016/C2017-0-03461-4.

Akoglu, H. (2018) 'User's guide to correlation coefficients', *Turkish Journal of Emergency Medicine*, 18, pp. 91–93. doi: 10.1016/j.tjem.2018.08.001.

Albert, A. M. and Greene, D. L. (1999) 'Bilateral asymmetry in skeletal growth and maturation as an indicator of environmental stress', *American Journal of Physical Anthropology*, 110, pp. 341–349. doi: 10.1002/(SICI)1096-8644(199911)110:3<341::AID-AJPA6>3.0.CO;2-8.

Albert, A. M., Ricanek, K. J. and Patterson, E. (2017) 'A review of the literature on the aging adult skull and face: implications for forensic science research and applications', *Forensic Science International*, 172, pp. 1–9. doi: 10.1016/j.forsciint.2007.03.015.

Algee-Hewitt, B. F. B. (2017) 'Age estimation in modern forensic anthropology', in Langley, N. and Tersigni-Tarrant, M. A. (eds) *Forensic Anthropology: A Comprehensive Introduction*. 2nd Ed. Boca Raton,FL: CRC Press, pp. 381–419. doi: 10.4324/9781315300030.

Alves-Cardoso, F. and Assis, S. (2018) 'Can osteophytes be used as age at death estimators? Testing correlations in skeletonized human remains with known age-at-death', *Forensic Science International*, 288, pp. 59–66. doi: 10.1016/j.forsciint.2018.04.034.

Anderson, B. E. (1990) 'Ventral arc of the os pubis: anatomical and developmental considerations', *American Journal of Physical Anthropology*, 83, pp. 449–458. doi: 10.1002/ajpa.1330830406.

Baccino, E., Sinfield, L., Colomb, S., Baum, T. P. and Matrille, L. (2014) 'Technical note: the two step procedure (TSP) for the determination of age at death of adult human remains in forensic cases', *Forensic Science International*, 244, pp. 247–251. doi: 10.1016/j.forsciint.2014.09.005.

Baccino, E., Ubelaker, D. H., Hayek, L. A. and Zerilli, A. (1999) 'Evaluation of seven methods of estimating age at death from mature human skeletal remains', *Journal of Forensic Sciences*, 44, pp. 931–936. doi: 10.1520/JFS12019J.

Bassed, R. B., Briggs, C. and Drummer, O. H. (2010) 'Analysis of time of closure of the spheno-occipital synchondrosis using computed tomography', *Forensic Science International*, 200, pp. 161–164. doi: 10.1016/j.forsciint.2010.04.009.

Berg, G. E. (2008) 'Pubic bone age estimation in adult women', *Journal of Forensic Sciences*, 53(3), pp. 569–577. doi: 10.1111/j.1556-4029.2008.00712.x.

Berger, C. E. H., van Wijk, M. and de Boer, H. H. (2020) 'Bayesian inference in personal identification', in Obertová, Z., Stewart, A., and Cattaneo, C. (eds) *Statistics*

and Probability in Forensic Anthropology. London, UK: Elsevier Academic Press, pp. 301–312. doi: 10.1016/C2017-0-03461-4.

Bethard, J. D. (2005) *A Test of the Transition Analysis Method for Estimation of Age-at-death in Adult Human Skeletal Remains. MA Thesis*. University of Knoxville, TN.

Bocquet-Appel, J. P. and Masset, C. (1982) 'Farewell to paleodemography', *Journal of Human Evolution*, 11, pp. 321–333. doi: 10.1016/S0047-2484(82)80023-7.

Bocquet-Appel, J. P. and Masset, C. (1996) 'Paleodemography: expectancy and false hope', *American Journal of Physical Anthropology*, 99, pp. 571–583. doi: 10.1002/(SICI)1096-8644(199604)99:4<571::AID-AJPA4>3.0.CO;2-X.

Boldsen, J. L. and Milner, G. R. (2018) 'Estimating adult age: transition analysis', in López Varela, S. L. (ed.) *The Encyclopedia of Archaeological Sciences*. John Wiley & Sons, Inc, pp. 1–2. doi: 10.1002/9781119188230.saseas0224.

Boldsen, J. L., Milner, G. R., Konigsberg, L. W. and Wood, J. W. (2002) 'Transition analysis: a new method for estimating age from skeletons', in Hoppa, R. D. and Vaupel, J. W. (eds) *Paleodemography: Age Distributions from Skeletal Samples*. Cambridge, UK: Cambridge University Press, pp. 73–106. doi: 10.1017/CBO9780511542428.

Botha, D., Lynnerup, N. and Steyn, M. (2019) 'Age estimation using bone mineral density in South Africans', *Forensic Science International*, 297, pp. 307–314. doi: 10.1016/j.forsciint.2019.02.020.

Botha, D., Pretorius, S., Myburgh, J. and Steyn, M. (2016) 'Age estimation from the acetabulum in South African black males', International Journal of Legal Medicine, 130, pp. 809–817. doi: 10.1007/s00414-015-1299-7.

Brennaman, A. L., Love, K. R. and Bethard, J. D. (2017) 'A Bayesian approach to age-at-death estimation from osteoarthritis of the shoulder in modern North Americans', *Journal of Forensic Sciences*, 62, pp. 573–584. doi: 10.1111/1556-4029.13327.

Brooks, S. T. (1955) 'Skeletal age at death: the reliability of cranial and pubic age indicators', *American Journal of Physical Anthropology*, 13(4), pp. 567–597. doi: 10.1002/ajpa.1330130403.

Brooks, S. T. and Suchey, J. M. (1990) 'Skeletal age determination based on the os pubis: a comparison of the Acsádi-Nemeskéri and Suchey-Brooks methods', *Human Evolution*, 5(3), pp. 227–238. doi: 10.1007/BF02437238.

Brown, C. A. (2010) 'Revisiting McKern and Stewart (1957): a comparison of pubic symphysis methods at the JPAC-CIL', in Latham, K. E. and Finnegan, M. (eds) *Age Estimation of the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. 161–176.

Buckberry, J. (2015) 'The (mis)use of adult age estimates in osteology', *Annals of Human Biology*, 42(4), pp. 323–331. doi: 10.3109/03014460.2015.1046926.

Buckberry, J. L. and Chamberlain, A. T. (2002) 'Age estimation from the auricular surface of the ilium: a revised method', *American Journal of Physical Anthropology*, 119, pp. 231–239. doi: 10.1002/ajpa.10130.

Budinoff, L. C. and Tague, R. G. (1990) 'Anatomical and developmental bases for

the ventral arc of the human pubis', *American Journal of Physical Anthropology*, 82, pp. 73–79. doi: 10.1002/ajpa.1330820109.

Buk, Z., Kordik, P., Bružek, J., Schmitt, A. and Snorek, M. (2012) 'The age at death assessment in a multi-ethnic sample of pelvic bones using nature-inspired data mining methods', *Forensic Science International*, 220, pp. 294.e1-294.e9. doi: 10.1016/j.forsciint.2012.02.019.

Bullock, M., Márquez, L., Hernández, P. and Ruíz, F. (2013) 'Paleodemographic age-at-death distributions of two Mexican skeletal collections: comparison of transition analysis and traditional aging methods', *American Journal of Physical Anthropology*, 152, pp. 67–78. doi: 10.1002/ajpa.22329.

Calce, S. E. (2012) 'A new method to estimate adult age-at-death using the acetabulum', *American Journal of Physical Anthropology*, 148, pp. 11–23. doi: 10.1002/ajpa.22026.

Calce, S. E. and Rogers, T. (2011) 'Evaluation of age estimation technique: testing traits of the acetabulum to estimate age at death in adult males', *Journal of Forensic Sciences*, 56, pp. 302–311. doi: 10.1111/j.1556-4029.2011.01700.x.

Campanacho, V., Santos, A. L. and Cardoso, H. F. V (2012) 'Assessing the influence of occupational and physical activity on the rate of degenerative change of the pubic symphysis in Portuguese males from the 19th and 20th century', *American Journal of Physical Anthropology*, 148, pp. 371–378. doi: 10.1002/ajpa.22059.

Cardoso, H. (2008) 'Epiphyseal union at the innominate and lower limb in modern Portuguese skeletal sample, and age estimation in adolescent and young adult male and female skeletons', *American Journal of Physical Anthropology*, 135(2), pp. 161–170. doi: 10.1002/ajpa.20717.

Cavalli, F., Lusnig, L. and Trentin, E. (2017) 'Use of pattern recognition and neural networks for non-metric sex diagnosis from lateral shape of calvarium: an innovative model for computer-aided diagnosis in forensic and physical anthropology', *International Journal of Legal Medicine*, 131, pp. 823–833. doi: 10.1007/s00414-016-1439-8.

Chen, C., Juan, H., Tsai, M. and Lu, H. H. (2018) 'Unsupervised learning and pattern recognition of biological data structures with density functional theory and machine learning', *Scientific Reports*, 8, p. 557. doi: 10.1038/s41598-017-18931-5.

Chen, X., Zhang, Z. and Tao, L. (2008) 'Determination of male age at death in Chinese Han population: using quantitative variables and statistical analysis from pubic bones', *Forensic Science International*, 175, pp. 36–43. doi: 10.1016/j.forsciint.2007.04.231.

Chen, X., Zhang, Z., Zhu, G. and Tao, L. (2011) 'Determining the age at death of females in the Chinese Han population: using quantitative variables and statistical analysis from pubic bones', *Forensic Science International*, 210, pp. 278.e1-278.e8. doi: 10.1016/j.forsciint.2011.04.024.

Christensen, A. M., Crowder, C. M., Ousley, S. D. and Houck, M. M. (2014) 'Error and its meaning in forensic sciences', *Journal of Forensic Sciences*, 59, pp. 123–

126. doi: 10.1111/1556-4029.12275.

Coqueugniot, H. and Weaver, T. (2007) ‘Infracranial maturation in the skeletal collection from Coimbra, Portugal: new aging standards for epiphyseal union’, *American Journal of Physical Anthropology*, 134(3), pp. 424–437. doi: 10.1002/ajpa.20683.

Cunha, E., Baccino, E., Matrille, L., Ramsthaler, F., Prieto, J., Schuliar, Y., Lynnerup, N. and Cattaneo, C. (2009) ‘The problem of aging human remains and living individuals: a review’, *Forensic Science International*, 193, pp. 1–13. doi: 10.1016/j.forsciint.2009.09.008.

‘Daubert versus Merrel Dow Pharmaceuticals Inc.’, Law Report 509 U.S. 579 (1993).

Dayal, M. R., Kegley, A. D. T., Štrkalj, G., Bidmos, M. A. and Kuykendall, K. L. (2009) ‘The history and composition of the Raymond A. Dart collection of human skeletons at the University of the Witwatersrand, Johannesburg, South Africa’, *American Journal of Physical Anthropology*, 140(2), pp. 324–335. doi: 10.1002/ajpa.21072.

Dedouit, F., Bindel, S., Gainza, D., Blanc, A., Joffre, F., Rouge, D. and Telmon, N. (2008) ‘Application of the İşcan method to two- and three-dimensional imaging of the sternal end of the right fourth rib’, *Journal of Forensic Sciences*, 53, pp. 288–295. doi: 10.1111/j.1556-4029.2007.00642.x.

DiGangi, E. A., Bethard, J. D., Kimmerle, E. H. and Konigsberg, L. W. (2009) ‘A new method for estimating age-at-death from the first rib’, *American Journal of Physical Anthropology*, 138, pp. 164–176. doi: 10.1002/ajpa.20916.

Dudar, J. (1993) ‘Identification of rib number and assessment of intercostal variation at the sternal rib end’, *Journal of Forensic Sciences*, 38(4), pp. 788–797. doi: 10.1520/JFS13474J.

Dudzik, B. and Langley, N. R. (2015) ‘Estimating age from the pubic symphysis: a new component-based system’, *Forensic Science International*, 257, pp. 98–105. doi: 10.1016/j.forsciint.2015.07.047.

Dwight, T. (1878) *The Identification of the Human Skeleton: A Medico-legal Study*. Boston: David Clapp & Son.

Falys, C. G. and Lewis, M. E. (2011) ‘Proposing a way forward: a review of standardisation in the use of age categories and ageing techniques in osteological analysis’, *International Journal of Osteoarchaeology*, 21(6), pp. 704–716. doi: 10.1002/oa.1179.

Franklin, D. and Blau, S. (2020) ‘Physical and virtual sources of biological data in forensic anthropology: considerations relative to practicioner and/or judicial requirements’, in Obertová, Z., Stewart, A., and Cattaneo, C. (eds) *Statistics and Probability in Forensic Anthropology*. London, UK: Elsevier Academic Press, pp. 17–45. doi: 10.1016/C2017-0-03461-4.

Franklin, D. and Flavel, A. (2019) ‘Population specificity in the estimation of skeletal age and sex: case studies using a Western Australian population’, *Australian Journal of Forensic Sciences*, 51, pp. S188–S192. doi: 10.1080/00450618.2019.1569722.

Freire-Aradas, A., Phillips, C., Mosquera-Miguel, A., Girón-Santamaría, L., Gómez-

Tato, A., Casares de Cal, M., Álvarez-Dios, J., Ansede-Bermejo, J., Torres-Español, M., Schneider, P. M., Pośpiech, E., Branicki, W., Carracedo, Á. and Lareu, M. V (2016) 'Development of a methylation marker set for forensic age estimation using analysis of public methylation data and the Agena Bioscience EpiTYPER system', Forensic Science International, 24, pp. 65–74.

Galera, V., Ubelaker, D. H. and Hayek, L. C. (1998) 'Comparison of macroscopic cranial methods of age estimation applied to skeletons from the Terry Collection', *Journal of Forensic Sciences*, 43, pp. 933–939. doi: 10.1520/JFS14337J.

Garvin, H. M. and Passalacqua, N. V (2012) 'Current practices by forensic anthropologists in adult skeletal age estimation', *Journal of Forensic Sciences*, 57(2), pp. 427–433. doi: 10.1111/j.1556-4029.2011.01979.x.

Garvin, H. M., Passalacqua, N. V, Uhl, N. M., Gipson, D. R., Overbury, R. S. and Cabo, L. L. (2012) 'Developments in forensic anthropology: age-at-death estimation', in Dirkmaat, D. C. (ed.) *A Companion to Forensic Anthropology*. Oxford, UK: Blackwell Publishing Ltd, pp. 202–223. doi: 10.1002/9781118255377.

Gilbert, B. M. and McKern, T. W. (1973) 'A method for aging the female Os pubis', *American Journal of Physical Anthropology*, 38(1), pp. 31–38. doi: 10.1002/ajpa.1330380109.

Gocha, T. P., Ingvoldstad, M. E., Kolatorowicz, A., Cossgriff-Hernandez, M. J. and Sciulli, P. W. (2015) 'Testing the applicability of six macroscopic skeletal aging techniques on a modern Southeast Asian sample', *Forensic Science International*, 249, pp. 318.e1-318.e7. doi: 10.1016/j.forsciint.2014.12.015.

Godde, K. and Hens, S. (2012) 'Age-at-death estimation in an Italian historic sample: a test of the Suchey-Brooks and transition analysis methods', *American Journal of Physical Anthropology*, 149, pp. 259–265. doi: 10.1002/ajpa.22126.

Green, S. B. (1991) 'How many subjects does it take to do a regression analysis', *Multivariate Behavioral Research*, 26(3), pp. 499–510. doi: 10.1207/s15327906mbr2603_7.

Grivas, C. R. and Komar, D. A. (2008) 'Kumho, Daubert and the nature of scientific inquiry: implications for forensic anthropology', *Journal of Forensic Sciences*, 53, pp. 771–776. doi: 10.1111/j.1556-4029.2008.00771.x.

Hanihara, K. and Suzuki, T. (1978) 'Estimation of age from the pubic symphysis by means of multiple regression analysis', *American Journal of Physical Anthropology*, 48, pp. 233–240. doi: 10.1002/ajpa.1330480218.

Hartnett, K. M. (2010) 'Analysis of age-at-death estimation using data from a new, modern autopsy sample - Part I: Pubic bone', *Journal of Forensic Sciences*, 55(5), pp. 1145–1151. doi: 10.1111/j.1556-4029.2010.01399.x.

Henderson, C. Y. and Nikita, E. (2016) 'Accounting for multiple effects and the problem of small sample sizes in osteology: a case study focussing on entheseal changes', *Archaeological and Anthropological Sciences*, 8(4), pp. 805–817. doi: 10.1007/s12520-015-0256-1.

Hens, S. and Godde, K. (2016) 'Auricular surface aging: comparing two methods that assess morphological change in the ilium with Bayesian analyses', *Journal of*

Forensic Sciences, 61 Suppl 1, pp. S30-38. doi: 10.1111/1556-4029.12982.

Holden, C. (2009) 'Forensic science needs a major overhaul, panel says', *Science*, 323, p. 1155. doi: 10.1126/science.323.5918.1155.

Hoppa, R. D. (2000) 'Population variation in osteological aging criteria: an example from the pubic symphysis', *American Journal of Physical Anthropology*, 111, pp. 185–191. doi: 10.1002/(SICI)1096-8644(200002)111:2<185::AID-AJPA5>3.0.CO;2-4.

Hoppa, R. D. and Vaupel, J. W. (2002) 'The Rostock manifesto for paleodemography: the way from stage to age', in Hoppa, R. D. and Vaupel, J. W. (eds) *Paleodemography: Age Distributions from Skeletal Samples*. Cambridge, UK: Cambridge University Press, pp. 1–8. doi: 10.1017/CBO9780511542428.

Hurst, C. V (2010) 'A test of the forensic application of transition analysis with the pubic symphysis', in Latham, K. E. and Finnegan, M. (eds) *Age Estimation of the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. 262–272.

Igarashi, Y., Uesu, K., Wakebe, T. and Kanazawa, E. (2005) 'New method for estimation of adult skeletal age at death from the morphology of the auricular surface of the ilium', *American Journal of Physical Anthropology*, 128, pp. 324–339. doi: 10.1002/ajpa.20081.

İşcan, M. Y. (1989) 'Research strategies in age estimation: the multiregional approach', in İşcan, M. Y. (ed.) *Age Markers in the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. 325–339.

İşcan, M. Y., Loth, S. R. and Wright, R. K. (1984a) 'Age estimation from the rib by phase analysis: White males', *American Journal of Physical Anthropology*, 65, pp. 147–156. doi: 10.1520/JFS11776J.

İşcan, M. Y., Loth, S. R. and Wright, R. K. (1984b) 'Metamorphosis at the sternal rib end: a new method to estimate age at death in White males', *American Journal of Physical Anthropology*, 65(2), pp. 147–156. doi: 10.1002/ajpa.1330650206.

İşcan, M. Y., Loth, S. R. and Wright, R. K. (1985) 'Age estimation from the rib by phase analysis: White females', *Journal of Forensic Sciences*, 30, pp. 853–863. doi: 10.1520/JFS11018J.

İşcan, M. Y. and Steyn, M. (2013) 'Skeletal age', in *The Human Skeleton in Forensic Medicine*. Springfield, IL: Charles C Thomas, pp. 59–142.

Jackes, M. (2000) 'Building the bases for paleodemographic analysis: adult age determination', in Katzenberg, M. A. and Saunders, S. R. (eds) *Biological Anthropology of the Human Skeleton*. Wiley-Liss Inc., pp. 417–466. doi: 10.1002/9780470245842.

Johnson, J. S. (1976) 'A comparison of age estimation using discriminant function analysis with some other age estimations of unknown skulls', *Journal of Anatomy*, 121(3), pp. 475–484.

Jones, M., Gordon, G. and Brits, D. (2018) 'Age estimation accuracies from black South African os coxae', HOMO - Journal of Comparative Human Biology, 69, pp. 248–258. doi: 10.1016/j.jchb.2018.08.004.

Jooste, N., L'Abbé, E. N., Pretorius, S. and Steyn, M. (2016) 'Validation of transition analysis as a method of adult age estimation in a modern South African sample', *Forensic Science International*, 266, pp. 580.e1-580.e7. doi: 10.1016/j.forsciint.2016.05.020.

Jooste, N. and Steyn, M. (2016) 'Current practices and future direction of adult age-at-death estimation from the skeleton in Southern Africa.', in *44th Annual Conference of the Anatomical Society of Southern Africa*. Bloemfontein.

Joubert, L. C., Briers, N. and Meyer, A. (2020) 'Evaluation of the enhanced computational methods of estimating age-at-death using the pubic symphyses of a White South African population', *Journal of Forensic Sciences*, 65(1), pp. 37–45. doi: 10.1111/1556-4029.14180.

Katz, D. and Suchey, J. M. (1986) 'Age determination of the male os pubis', *American Journal of Physical Anthropology*, 69(4), pp. 427–435. doi: 10.1002/ajpa.1330690402.

Katz, D. and Suchey, J. M. (1989) 'Race differences in pubic symphyseal aging patterns in the male', *American Journal of Physical Anthropology*, 80, pp. 167–172. doi: 10.1002/ajpa.1330800204.

Kelley, M. A. (1979) 'Parturition and pelvic changes', *American Journal of Physical Anthropology*, 51, pp. 541–546. doi: 10.1002/ajpa.1330510405.

Kerley, E. R. (1965) 'The microscopic determination of age in human bone', American Journal of Physical Anthropology, 23, pp. 149–163. doi: 10.1002/ajpa.1330230215.

Kerley, E. R. (1970) 'Estimation of skeletal age: after about age 30 years', in Steward, T. D. (ed.) *Personal Identification in Mass Disasters*. Washington, DC: National Museum of Natural History, pp. 57–70. doi: 10.5479/sil.30678.39088001440254.

Key, C. A., Aiello, L. C. and Molleson, T. (1994) 'Cranial suture closure and its implications for age estimation', *International Journal of Osteoarchaeology*, 4, pp. 193–207. doi: 10.1002/oa.1390040304.

Kimmerle, E. H., Konigsberg, L. W., Jantz, R. L. and Baraybar, J. P. (2008) 'Analysis of age-at-death estimation through the use of pubic symphyseal data', *Journal of Forensic Sciences*, 53(3), pp. 558–568. doi: 10.1111/j.1556-4029.2008.00711.x.

Kimmerle, E. H., Prince, D. A. and Berg, G. E. (2008) 'Inter-observer variation in methodologies involving the pubic symphysis, sternal ribs and teeth', *Journal of Forensic Sciences*, 53(3), pp. 594–600. doi: 10.1111/j.1556-4029.2008.00715.x.

Klepinger, L. and Giles, E. (1998) 'Clarification or confusion: statistical interpretation in forensic anthropology', in Reichs, K. J. (ed.) *Forensic Osteology: Advances in the Identification of Human Remains*. 2nd Ed. Springfield, IL: Charles C Thomas, pp. 427–440.

Klepinger, L., Katz, D., Micozzi, M. S. and Carroll, L. (1992) 'Evaluation of cast methods for estimating age from the os pubis', *Journal of Forensic Sciences*, 37, pp. 763–770. doi: 10.1520/JFS11988J.

Knofczynski, G. T. and Mundfrom, D. (2008) 'Sample sizes when using multiple

linear regression for prediction', *Educational and Psychological Measurement*, 68(3), pp. 431–442. doi: 10.1177/0013164407310131.

Konigsberg, L. W. and Frankenberg, S. R. (1992) 'Estimation of age structure in anthropological demography', *American Journal of Physical Anthropology*, 89(2), pp. 235–256. doi: 10.1002/ajpa.1330890208.

Konigsberg, L. W., Frankenberg, S. R. and Liversidge, H. M. (2019) 'Status of mandibular third molar development as evidence in legal age threshold cases', *Journal of Forensic Sciences*, 64, pp. 680–697. doi: 10.1111/1556-4029.13926.

Konigsberg, L. W., Herrmann, N. P. and Kimmerle, E. H. (2008) 'Estimation and evidence in forensic anthropology: age-at-death', *Journal of Forensic Sciences*, 53(3), pp. 541–557. doi: 10.1111/j.1556-4029.2008.00710.x.

Kotěrová, A. (2019) *Age-at-death Estimation of the Adult Skeleton: New Approaches to the Evaluation of Senescence Indicators. PhD Thesis*. Charles University, Prague.

Kotěrová, A., Navega, D., Štepanovsky, M., Buk, Z., Bružek, J. and Cunha, E. (2018) 'Age estimation of adult human remains from hip bones using advanced methods', *Forensic Science International*, 287, pp. 163–175. doi: 10.1016/j.forsciint.2018.03.047.

Kunos, C. A., Simpson, S. W., Russel, K. F. and Hershkovitz, I. (1999) 'First rib metamorphosis: its possible utility for human age-at-death estimation', *American Journal of Physical Anthropology*, 110, pp. 303–323. doi: 10.1002/(SICI)1096-8644(199911)110:3<303::AID-AJPA4>3.0.CO;2-O.

Kurki, H. (2005) 'Use of the first rib for adult age estimation: a test of one method', *International Journal of Osteoarchaeology*, 15, pp. 342–350. doi: 10.1002/oa.788.

L'Abbé, E. N., Loots, M. and Meiring, J. H. (2005) 'The Pretoria Bone Collection: a modern South African skeletal sample', *HOMO - Journal of Comparative Human Biology*, 56(2), pp. 197–205. doi: 10.1016/j.jchb.2004.10.004.

Lamendin, H., Baccino, E., Humbert, J. F., Tavernier, J. C., Nossintchouk, R. M. and Zerilli, A. (1992) 'A simple technique for age estimation in adult corpses: the two criteria dental method', *Journal of Forensic Sciences*, 37(5), pp. 1373–1379. doi: 10.1520/JFS13327J.

Landis, J. R. and Koch, G. G. (1977) 'The measurement of observer agreement for categorical data', *Biometrics*, 33(1), pp. 159–174. doi: 10.2307/2529310.

Langley-Shirley, N. and Jantz, R. L. (2010) 'A Bayesian approach to age estimation in modern Americans from the clavicle', *Journal of Forensic Sciences*, 55(3), pp. 571–583. doi: 10.1111/j.1556-4029.2010.01089.x.

Lottering, N., Alston, C., MacGregor, D., Izatt, M., Grant, C., Adam, C. and Gregory, L. (2017) 'Apophyseal ossification of the iliac crest in forensic age estimation: computed tomography standards for modern Australian subadults', *Journal of Forensic Sciences*, 62(2), pp. 292–307. doi: 10.1111/1556-4029.13285.

Lovejoy, C. O., Meindl, R. S., Mensforth, R. P. and Barton, T. J. (1985) 'Multifactorial determination of skeletal age at death: a method and blind tests of its accuracy', *American Journal of Physical Anthropology*, 68, pp. 1–14. doi: 10.1002/ajpa.1330680102.

Lovejoy, C. O., Meindl, R. S., Pryzbeck, T. R. and Mensforth, R. P. (1985) 'Chronological metamorphosis of the auricular surface of the ilium: a new method for the determination of adult skeletal age at death.', *American Journal of Physical Anthropology*, 68(1), pp. 15–28. doi: 10.1002/ajpa.1330680103.

Lucy, D. (2010) 'The presentation of results and statistics for legal purposes', in Black, S., Aggrawal, A., and Payne-James, J. (eds) *Age Estimation in the Living: The Practitioners Guide*. New York: John Wiley & Sons, Inc, pp. 267–283.

Lucy, D., Aykroyd, R. G., Pollard, A. M. and Solheim, T. (1996) 'A Bayesian approach to adult human age estimation from dental observations by Johanson's age changes', *Journal of Forensic Sciences*, 41(2), pp. 189–194. doi: 10.1520/JFS15411J.

Mann, R. W., Jantz, R. L., Bass, W. M. and Willey, P. S. (1991) 'Maxillary suture obliteration: a visual method for estimating skeletal age.', *Journal of Forensic Sciences*, 36(3), pp. 781–91. doi: 10.1520/JFS13088J.

Masset, C. (1989) 'Age estimation on the basis of cranial sutures', in İşcan, M. Y. (ed.) *Age Markers in the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. 71–103.

Matrille, L., Ubelaker, D. H., Cattaneo, C., Seguret, F., Tremblay, M. and Baccino, E. (2007) 'Comparison of four skeletal methods for the estimation of age at death on White and Black adults', *Journal of Forensic Sciences*, 52(2), pp. 302–307. doi: 10.1111/j.1556-4029.2006.00367.x.

Maxwell, S. E. (2000) 'Sample size and multiple regression analysis', *Psychological Methods*, 5, pp. 434–458. doi: 10.1037/1082-989x.5.4.434.

Mays, S. (2014) 'A test of a recently devised method of estimating skeletal age at death using features of the adult acetabulum', *Journal of Forensic Sciences*, 59, pp. 184–187. doi: 10.1111/1556-4029.12293.

Mays, S. (2015) 'The effect of factors other than age upon skeletal age indicators in the adult', *Annals of Human Biology*, 42(4), p. 330 339. doi: 10.3109/03014460.2015.1044470.

McCormick, W. F. (1980) 'Mineralization of the costal cartilages as an indicator of age: preliminary observations', *Journal of Forensic Sciences*, 25, pp. 736–741. doi: 10.1520/JFS11287J.

McKern, T. W. and Stewart, T. D. (1957) *Skeletal Age Changes in Young American Males. Technical Report EP-45*. Natick: Quatermaster Research and Development Command.

Meindl, R. S. and Lovejoy, C. O. (1985) 'Ectocranial suture closure: a revised method for the determination of skeletal age at death based on the lateral-anterior sutures', *American Journal of Physical Anthropology*, 68, pp. 57–66. doi: 10.1002/ajpa.1330680106.

Meindl, R. S., Lovejoy, C. O., Mensforth, R. P. and Walker, R. A. (1985) 'A revised method of age determination using the os pubis, with a review and tests of accuracy of other current methods of pubic symphyseal aging', *American Journal of Physical Anthropology*, 68, pp. 29–45. doi: 10.1002/ajpa.1330680104.

Merrit, C. E. (2015) ‘The influence of body size on adult skeletal age estimation methods’, *American Journal of Physical Anthropology*, 156, pp. 35–57. doi: 10.1002/ajpa.22626.

van der Merwe, A. E., İşcan, M. Y. and L’Abbé, E. N. (2006) ‘The pattern of vertebral osteophyte development in a South African population’, *International Journal of Osteoarchaeology*, 16, pp. 459–464. doi: 10.1002/oa.841.

Meyer, A., van der Merwe, A. E. and Steyn, M. (2021) ‘An evaluation of the Acsádi and Nemeskéri Complex Method of adult age estimation in a modern South African skeletal sample’, Forensic Science International, 321, p. 110740. doi: 10.1016/j.forsciint.2021.110740.

Michopoulou, E., Negre, P., Nikita, E. and Kranioti, E. (2017) ‘The auricular surface as age indicator in a modern Greek sample: a test of two qualitative methods’, *Forensic Science International*, 280, pp. 246.e1-246.e7. doi: 10.1016/j.forsciint.2017.08.004.

Milella, M., Belcastro, M. G., Mariotti, V. and Nikita, E. (2020) ‘Estimation of adult age-at-death from entheseal robusticity: a test using an identified Italian skeletal collection’, *American Journal of Physical Anthropology*, 173, pp. 190–199. doi: 10.1002/ajpa.24083.

Milner, G. R. and Boldsen, J. L. (2012a) ‘Skeletal age estimation: Where we are and where we should go’, in Dirkmaat, D. C. (ed.) *A Companion to Forensic Anthropology*. Burlington: Elsevier Academic Press. doi: 10.1002/9781118255377.

Milner, G. R. and Boldsen, J. L. (2012b) ‘Transition analysis: a validation study with known-age modern American skeletons’, *American Journal of Physical Anthropology*, 148, pp. 98–110. doi: 10.1002/ajpa.22047.

Murray, K. A. and Murray, T. M. (1991) ‘A test of the auricular surface aging technique’, *Journal of Forensic Sciences*, 36, pp. 1162–1169. doi: 10.1520/JFS13131J.

National Research Council (2009) *Strengthening Forensic Science in the United States: A Path Forward*. Washington, DC: The National Academies Press. doi: 10.17226/12589

Navega, D., d’Oliveira Coelho, J., Cunha, E. and Curate, F. (2018) ‘DXAGE: a new method for age at death estimation based on femoral bone mineral density and artificial neural networks’, *Journal of Forensic Sciences*, 63(2), pp. 497–503. doi: 10.1111/1556-4029.13582.

Navega, D., Godinho, M., Cunha, E. and Ferreira, M. T. (2018) ‘A test and analysis of Calce (2012) method for skeletal age-at-death estimation using the acetabulum in a modern skeletal sample’, *International Journal of Legal Medicine*, 132, pp. 1447–1455. doi: 10.1007/s00414-018-1902-9.

Nawrocki, S. P. (1998) ‘Regression formulae for estimating age at death from cranial suture closure’, in Reichs, K. J. (ed.) *Forensic Osteology: Advances in the Identification of Human Remains*. 2nd Ed. Springfield, IL: Charles C Thomas, pp. 276–292.

Nawrocki, S. P. (2010) ‘The nature and sources of error in the estimation of age at

death from the skeleton', in Latham, K. E. and Finnegan, M. (eds) *Age Estimation of the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. 79–101.

Nikita, E. (2013) 'Quantitative assessment of the sternal rib end morphology and implications for its application in aging human remains', *Journal of Forensic Sciences*, 58(2), pp. 324–329. doi: 10.1111/1556-4029.12047.

Nikita, E. (2014a) 'Age-associated variation and sexual dimorphism in adult cranial morphology: Implications in anthropological studies', *International Journal of Osteoarchaeology*, 24, pp. 557–569. doi: 10.1002/oa.2241.

Nikita, E. (2014b) 'The use of generalized linear models and generalized estimating equations in bioarchaeological studies', *American Journal of Physical Anthropology*, 153, pp. 473–483. doi: 10.1002/ajpa.22448.

Nikita, E. and Nikitas, P. (2019) 'Skeletal age-at-death estimation: Bayesian versus regression methods', *Forensic Science International*, 297, pp. 56–64. doi: 10.1016/j.forsciint.2019.01.033.

Nikita, E. and Nikitas, P. (2020) 'On the use of machine learning algorithms in forensic anthropology', *Legal Medicine*, 47, p. 101771. doi: 10.1016/j.legalmed.2020.101771.

Nikita, E., Xanthopoulou, P. and Kranioti, E. (2018) 'An evaluation of Bayesian age estimation using the auricular surface in modern Greek material', *Forensic Science International: Genetics*, 291, pp. 1–11. doi: 10.1016/j.forsciint.2018.07.029.

Obertová, Z. and Stewart, A. (2020a) 'Probability distributions, hypothesis testing, and analysis', in Obertová, Z., Stewart, A., and Cattaneo, C. (eds) *Statistics and Probability in Forensic Anthropology*. London, UK: Elsevier Academic Press, pp. 73–86. doi: 10.1016/C2017-0-03461-4.

Obertová, Z. and Stewart, A. (2020b) 'Study desing and sampling', in Obertová, Z., Stewart, A., and Cattaneo, C. (eds) *Statistics and Probability in Forensic Anthropology*. London, UK: Elsevier Academic Press, pp. 7–16. doi: 10.1016/C2017-0-03461-4.

Oettlé, A. C. and Steyn, M. (2000) 'Age estimation from sternal ends of ribs by phase analysis in South African Blacks', *Journal of Forensic Sciences*, 45, pp. 1071–1079. doi: 10.1520/JFS14831J.

Oikonomopoulou, E., Valakos, E. and Nikita, E. (2017) 'Population-specificity of sexual dimorphism in cranial and pelvic traits: evaluation of existing and proposal of new functions for sex assessment in a Greek assemblage', *International Journal of Legal Medicine*, 131, pp. 1731–1738. doi: 10.1007/s00414-017-1655-x.

Osborne, D. L., Simmons, T. L. and Nawrocki, S. P. (2004) 'Reconsidering the auricular surface as an indicator of age at death', *Journal of Forensic Sciences*, 49(5), pp. 1–7. doi: 10.1520/JFS2003348.

Ousley, S. D. and Hollinger, R. E. (2012) 'The pervasiveness of Daubert', in Dirkmaat, D. C. (ed.) *A Companion to Forensic Anthropology*. Blackwell Publishing Ltd. doi: 10.1002/9781118255377.

Overbury, R. S., Cabo, L. L., Dirkmaat, D. C. and Symes, S. A. (2009) 'Asymmetry of the os pubis: implications for the Suchey-Brooks method', *American Journal of*

Physical Anthropology, 139(2), pp. 261–268. doi: 10.1002/ajpa.20999.

Passalacqua, N. V. (2009) 'Forensic age-at-death estimation from the human sacrum', *Journal of Forensic Sciences*, 54(2), pp. 255–262. doi: 10.1111/j.1556-4029.2008.00977.x.

Passalacqua, N. V (2010) 'Applications of the human sacrum in the age at death estimation', in Latham, K. E. and Finnegan, M. (eds) *Age Estimation of the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. 102–117.

Perizonius, W. R. K. (1984) 'Closing and non-closing sutures in 256 crania of known age and sex from Amsterdam (A.D. 1883-1909)', *Journal of Human Evolution*, 13, pp. 201–216. doi: 10.1016/S0047-2484(84)80065-2.

Powers, R. (1962) 'The disparity between known age and age as estimated by cranial suture closure', *Man*, 62, pp. 52–54. doi: 10.2307/2796987.

Republic of South Africa (1983) 'Human Tissue Act 65 of 1983', *Government Gazette*.

Republic of South Africa (2004) 'National Health Act 61 of 2003', *Government Gazette*, 469(26595), pp. 1–94.

Rissech, C., Estabrook, G. F. and Cunha, E. (2007) 'Estimation of age-at-death for adult males using the acetabulum, applied to four Western European populations', *Journal of Forensic Sciences*, 52(4), pp. 774–778. doi: 10.1111/j.1556-4029.2007.00486.x.

Rissech, C., Estabrook, G. F., Cunha, E. and Malgosa, A. (2006) 'Using the acetabulum to estimate age at death of adult males', *Journal of Forensic Sciences*, 51(2), pp. 213–229. doi: 10.1111/j.1556-4029.2006.00060.x.

Ritz-Timme, S., Cattaneo, C., Collins, M. J., Waite, E. R., Schűtz, H. W., Kaatsch, H. J. and Borrman, H. I. M. (2000) 'Age estimation: the state of the art in relation to the specific demands of forensic practice', *International Journal of Legal Medicine*, 113, pp. 129–136. doi: 10.1007/s004140050283.

Rősing, F. W., Graw, M., Marré, B., Ritz-Timme, S., Rothschild, M. A., Rőtzscher, K., Schmeling, A., Schrőder, I. and Geserick, G. (2007) 'Recommendations for the forensic diagnosis of sex and age from skeletons', *HOMO - Journal of Comparative Human Biology*, 58, pp. 75–89. doi: 10.1016/j.jchb.2005.07.002.

Rougé-Maillart, C., Jousset, N., Vielle, B., Gaudin, A. and Telmon, N. (2007) 'Contribution of the study of acetabulum for the estimation of adult subjects', *Forensic Science International*, 171, pp. 103–110. doi: 10.1016/j.forsciint.2006.10.007.

Rougé-Maillart, C., Telmon, N., Rissech, C., Malgosa, A. and Rougé, D. (2004) 'The determination of male adult age at death by central and posterior coxal analysis - a preliminary study', *Journal of Anatomy*, 49, pp. 208–214. doi: 10.1520/JFS2002056.

Rougé-Maillart, C., Vielle, B., Jousset, N., Chappard, D., Telmon, N. and Cunha, E. (2009) 'Development of a method to estimate skeletal age at death in adults using the acetabulum and the auricular surface on a Portuguese population', *Forensic Science International*, 188, pp. 91–95. doi: 10.1016/j.forsciint.2009.03.019.

Russel, K. F., Simpson, S. W., Genovese, J., Kinkel, M. D., Meindl, R. S. and Lovejoy, C. O. (1993) 'Independent test of the fourth rib aging technique', *American Journal of Physical Anthropology*, 92, pp. 53–62. doi: 10.1002/ajpa.1330920105.

San-Millán, M., Rissech, C. and Turbón, D. (2017) 'Shape variability of the adult human acetabulum and acetabular fossa related to sex and age by geometric morphometrics. Implications for adult age estimation', *Forensic Science International*, 272, pp. 50–63. doi: Shape variability of the adult human acetabulum and acetabular fossa related to sex and age by geometric morphometrics. Implications for adult age estimation.

Saunders, S. R., Fitzgerald, C., Rogers, T., Dudar, C. and McKillop, H. (1992) 'A test of several methods of skeletal age estimation using a documented archaeological sample', *Canadian Society of Forensic Science Journal*, 25(2), pp. 97–118. doi: 10.1080/00085030.1992.10757005.

Scheuer, L. (2002) 'Application of osteology to forensic medicine', *Clinical Anatomy*, 15, pp. 297–312. doi: 10.1002/ca.10028.

Scheuer, L. and Black, S. (2000) *Developmental Juvenile Osteology*. Bath: Elsevier Academic Press. doi: 10.1016/B978-0-12-624000-9.X5000-X.

Schmitt, A. (2004) 'Age-at-death assessment using the os pubis and the auricular surface of the ilium: a test on an identified Asian sample', *International Journal of Osteoarchaeology*, 14, pp. 1–6. doi: 10.1002/oa.693.

Schmitt, A. (2005) 'Une nouvelle méthode pour estimer l'âge au décès des adultes à partir de la surface sacro-pelvienne iliaque', *Bulletins et Memoires de la Societe d'Anthropologie de Paris*, 17, pp. 89–101.

Schmitt, A. and Murail, P. (2004) 'Is the first rib a reliable indicator of age at death assessment? Test of the method developed by Kunos et al (1999)', *HOMO - Journal of Comparative Human Biology*, 54, pp. 207–214. doi: 10.1078/0018-442x-00070.

Schultz, R., Mühler, M., Mutze, S., Schmidt, S., Reisinger, W. and Schmeling, A. (2005) 'Studies on the time frame for ossification of the medial epiphysis of the clavicle as revealed by CT scans', *International Journal of Legal Medicine*, 119, pp. 142–145. doi: 10.1007/s00414-005-0529-9.

Shamir, L., Delaney, J. D., Orlov, N., Eckley, D. M. and Goldberg, I. G. (2010) 'Pattern recognition software and techniques for biological image analysis', *PLoS Computational Biology*, 6(11), p. e1000974. doi: doi.org/10.1371/journal.pcbi.1000974.

Shirley, N. R. and Jantz, R. L. (2011) 'Spheno-occipital synchondrosis fusion in modern Americans', *Journal of Forensic Sciences*, 56, pp. 580–585. doi: 10.1111/j.1556-4029.2011.01705.x.

Shirley, N. R. and Ramirez Montes, P. A. (2015) 'Age estimation in forensic anthropology: quantification of observer error in phase versus component-based methods', *Journal of Forensic Sciences*, 60, pp. 107–111. doi: 10.1111/1556-4029.12617.

Sifakis, M., Kalochristianakis, M. N., García-Donas, J. G., Ekizoglu, O. and Krianoti, E. F. (2020) 'Frequentist approach to data analysis and interpretation in forensic

anthropology', in Obertová, Z., Stewart, A., and Cattaneo, C. (eds) *Statistics and Probability in Forensic Anthropology*. London, UK: Elsevier Academic Press, pp. 109–124. doi: 10.1016/C2017-0-03461-4.

Sinha, A. and Gupta, V. (1995) 'A study on estimation of age from pubic symphysis', *Forensic Science International*, 75, pp. 73–78. doi: 10.1016/0379-0738(95)01772-b.

Sironi, E., Bozza, S. and Taroni, F. (2020) 'Age estimation of living persons: a coherent approach to inference and decision', in Obertová, Z., Stewart, A., and Cattaneo, C. (eds) *Statistics and Probability in Forensic Anthropology*. London, UK: Elsevier Academic Press, pp. 183–208. doi: 10.1016/C2017-0-03461-4.

Slice, D. E. and Algee-Hewitt, B. F. B. (2015) 'Modeling bone surface morphology: a fully quantitative method of age-at-death estimation using the pubic symphysis', *Journal of Forensic Sciences*, 60(4), pp. 835–843. doi: 10.1111/1556-4029.12778.

Smith, S. L. and Buschang, P. H. (2004) 'Variation in longitudinal diaphyseal long bone growth in children three to ten years of age', *American Journal of Human Biology*, 16, pp. 648–657. doi: 10.1002/ajhb.20077.

Smith, S. L. and Buschang, P. H. (2005) 'Longitudinal models of long bone growth during adolescence', *American Journal of Human Biology*, 17, pp. 731–745. doi: 10.1002/ajhb.20441.

Snodgrass, J. J. (2004) 'Sex differences and aging of the vertebral column', *Journal of Forensic Sciences*, 49, pp. 1–6. doi: 10.1520/JFS2003198.

Snodgrass, J. J. and Galloway, A. (2003) 'Technical Note: utility of dorsal pits and pubic tubercle height in parity assessment', *Journal of Forensic Sciences*, 48, pp. 1226–1230. doi: 10.1520/JFS2003027.

Snow, C. C. (1983) 'Equations for estimating age at death from the pubic symphysis: a modification of the McKern-Stewart method', *Journal of Forensic Sciences*, 28, pp. 864–870. doi: 10.1520/JFS11593J.

Sommer, C. and Gerlich, D. W. (2013) 'Machine learning in cell biology - teaching computers to recongize phenotypes', *Journal of Cell Science*, 126, pp. 5529–5539. doi: 10.1242/jcs.123604.

Soto, C. F., Algee-Hewitt, B. F. B., Morante, G. B., Slice, D. E. and Steadman, D. W. (2018) 'Age-at-death estimation for modern populations in Mexico and Puerto Rico through the use of 3D laser scans of the pubic symphysis', *Human Biology*, 90(3), pp. 213–229. doi: 10.13110/humanbiology.90.3.02.

Statistics South Africa. (2012) 'Census 2011 Statistical release – P0301.4 / Statistics South Africa', *Statistics South Africa*. Available at: www.statssa.gov.za.

Stewart, T. D. (1957) 'Distortion of the pubic symphyseal surface in females and its effect on age determination', *American Journal of Physical Anthropology*, 15, pp. 9–18. doi: 10.1002/ajpa.1330150109.

Stewart, T. D. (1958) 'The rate of development of vertebral osteoarthritis in American whites and its significance in skeletal age identification', *Leech*, 28, pp. 144–151.

Stoyanova, D. K., Algee-Hewitt, B. F. B., Kim, J. and Slice, D. E. (2017) 'A computational framework for age-at-death estimation from the skeleton: surface and outline analysis of 3D laser scans of the adult pubic symphysis', *Journal of Forensic Sciences*, 62(6), pp. 1434–1444. doi: 10.1111/1556-4029.13439.

Streeter, M. (2012) 'Histological age-at-death estimation', in Crowder, C. M. and Stout, S. (eds) Bone Histology - An Anthropological Perspective. Boca Raton,FL: CRC Press, pp. 135–152.

Stull, K. E. and James, D. M. (2010) 'Determination of age at death using the acetabulum of the Os Coxa', in Latham, K. E. and Finnegan, M. (eds) *Age Estimation of the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. 134–146.

Suchey, J. M. (1979) 'Problems in the aging of females using the Os pubis', *American Journal of Physical Anthropology*, 51, pp. 467–470. doi: 10.1002/ajpa.1330510319.

Suchey, J. M. and Katz, D. (1998) 'Applications of pubic age determination in a forensic setting', in Reichs, K. J. (ed.) *Forensic Osteology: Advances in the Identification of Human Remains*. 2nd Ed. Springfield, IL: Charles C Thomas, pp. 204–236.

Suchey, J. M., Wiseley, D. V, Green, R. F. and Noguchi, T. T. (1979) 'Analysis of dorsal pitting in the os pubis in an extensive sample of modern American females', *American Journal of Physical Anthropology*, 51, pp. 517–540. doi: 10.1002/ajpa.1330510404.

Suchey, J. M., Wiseley, D. V and Katz, D. (1986) 'Evaluation of the Todd and McKern-Stewart methods for aging the male os pubis.', in Reichs, K. J. (ed.) *Forensic Osteology: Advances in the Identification of Human Remains.* Springfield, IL: Charles C Thomas, pp. 33–67.

Tabachnick, B. G. and Fidell, L. S. (2001) *Using multivariate statistics*. 4th Ed. Needham Heights, MA: Allyn & Bacon.

Tague, R. G. (1988) 'Bone resorption of the pubis and preauricular area in humans and nonhuman mammals', *American Journal of Physical Anthropology*, 76, pp. 251–267. doi: 10.1002/ajpa.1330760214.

Tangmose, S., Thevissen, P., Lynnerup, N., Willems, G. and Boldsen, J. L. (2015) 'Age estimation in the living: transition analysis on developing third molars', *Forensic Science International*, 257, pp. 512.e1-512.e7. doi: 10.1016/j.forsciint.2015.07.049.

Todd, T. W. (1920) 'Age changes in the pubic bone. I. The male White pubis', *American Journal of Physical Anthropology*, 3(3), pp. 285–334. doi: 10.1002/ajpa.1330030301.

Todd, T. W. (1921a) 'Age changes in the pubic bone. VI. The interpretation of variation in the symphyseal area', *American Journal of Physical Anthropology*, 4(4), pp. 407–424. doi: 10.1002/ajpa.1330040403.

Todd, T. W. (1921b) 'Age changes in the pubic bone', *American Journal of Physical Anthropology*, 4(1), pp. 1–77. doi: 10.1002/ajpa.1330040102.

Todd, T. W. and Lyon, D. W. (1924) 'Endocranial suture closure. Its progress and age relationship. Part I - Adult males of White stock', *American Journal of Physical*

Anthropology, 7(3), pp. 325–384. doi: 10.1002/ajpa.1330070320.

Todd, T. W. and Lyon, D. W. (1925a) 'Cranial suture closure. Its progress and age relationship. Part III - Endocranial closure in adult males of Negro stock', *American Journal of Physical Anthropology*, 8, pp. 47–71. doi: 10.1002/ajpa.1330080104.

Todd, T. W. and Lyon, D. W. (1925b) 'Cranial sutures closure. Its progress and age relationship. Part II - Ectocranial closure in adult males of White stock', *American Journal of Physical Anthropology*, 8(1), pp. 23–45. doi: 10.1002/ajpa.1330080103.

Ubelaker, D. H. (1978) *Human Skeletal Remains: Excavation, Analysis, Interpretation*. Chicago, IL: Aldine Publishing Company.

Ubelaker, D. H. (2010) 'A history of methodology in the estimation of age at death from the skeleton', in Latham, K. E. and Finnegan, M. (eds) *Age Estimation of the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. xvii–xxv.

Ubelaker, D. H. and DeGaglia, C. M. (2017) 'Population variation in skeletal sexual dimorphism', *Forensic Science International*, 278, pp. 407.e1-407.e7. doi: 10.1016/j.forsciint.2017.06.012.

Ubelaker, D. H. and Khosrowshahi, H. (2019) 'Estimation of age in forensic anthropology: historical perspective and recent methodological advances', *Forensic Sciences Research*, 4(1), pp. 1–9. doi: 10.1080/20961790.2018.1549711.

Uhl, N. M. (2013) 'Age-at-death estimation', in DiGangi, E. A. and Moore, M. K. (eds) *Research Methods in Human Skeletal Biology*. Oxford, UK: Elsevier Academic Press, pp. 63–90. doi: 10.1016/C2010-0-65850-0.

Uhl, N. M. and Nawrocki, S. P. (2010) 'Multifactorial estimation of age at death from the human skeleton', in Latham, K. E. and Finnegan, M. (eds) *Age Estimation of the Human Skeleton*. Springfield, IL: Charles C Thomas, pp. 243–261.

Watanabe, S. and Terazawa, K. (2006) 'Age estimation from the degree of osteophyte formation of vertebral columns in Japanese', *Legal Medicine*, 8, pp. 156–160. doi: 10.1016/j.legalmed.2006.01.001.

Webb, P. A. O. and Suchey, J. M. (1985) 'Epiphyseal union of the anterior iliac crest and medial clavicle in a modern sample of American males and females', *American Journal of Physical Anthropology*, 68, pp. 457–466. doi: 10.1002/ajpa.1330680402.

White, T. D. and Folkens, P. A. (2005) *The Human Bone Manual*. Burlington: Elsevier Academic Press. doi: 10.1016/C2009-0-00102-0.

Xanthopoulou, P., Valakos, E., Youlatos, D. and Nikita, E. (2018) 'Assessing the accuracy of cranial and pelvic ageing methods on human skeletal remains from a modern Greek assemblage', *Forensic Science International*, 286, pp. 266.e1-266.e8. doi: 10.1016/j.forsciint.2018.03.005.

Zapico, S. C. and Ubelaker, D. H. (2013) 'Applications of physiological bases of ageing to forensic sciences. Estimation of age-at-death', Ageing Research Reviews, 12, pp. 605–617.

Zapico, S. C. and Ubelaker, D. H. (2016) 'Relationship between mitochondrial DNA

mutations and aging. Estimation of age-at-death', The Journals of Gerontology Series A Biological Sciences and Medical Sciences, 71, pp. 445–450.

Zeman, T. and Beňuš, R. (2020) 'Initial assessment: measurement errors and interrater reliability', in Obertová, Z., Stewart, A., and Cattaneo, C. (eds) *Statistics and Probability in Forensic Anthropology*. London, UK: Elsevier Academic Press, pp. 47–56. doi: 10.1016/C2017-0-03461-4.

Zukowski, L. A., Falsetti, A. B. and Tillman, M. D. (2012) 'The influence of sex, age and BMI on the degeneration of the lumbar spine', *Journal of Anatomy*, 220, pp. 57–66. doi: 10.1111/j.1469-7580.2011.01444.x.

```
%% Program Transition_Analysis_Eq38

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq14 Fit Data - All.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
```

```
Age = data(:,1);

V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);


%%xx = linspace(0,100)';

%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';

[cnt1,~] = size(xx);

%%display(yy);



%% V1 CR Model

[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C1 = zeros(cnt1,2);


%% Calculate probabilities for V1
```

```
PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A1 = PROB1;


for i = 1:cnt1

C1(i,1) = A1(i,1);

C1(i,2) = 1-A1(i,1);

end;


%% V2 CR Model

[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C2 = zeros(cnt1,2);


%% Calculate probabilities for V2



PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A2 = PROB2;


for i = 1:cnt1

C2(i,1) = A2(i,1);

C2(i,2) = A2(i,2)-A2(i,1);
```

```
C2(i,3) = 1-A2(i,2);

end;


%% V3 CR Model

[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C3 = zeros(cnt1,2);


%% Calculate probabilities for V3



PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;


for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = 1-A3(i,1);

end;


%% V4 CR Model

[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);
```

```
C4 = zeros(cnt1,2);

%% Calculate probabilities for V4

PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A4 = PROB4;

for i = 1:cnt1
C4(i,1) = A4(i,1);
C4(i,2) = A4(i,2)-A4(i,1);
C4(i,3) = A4(i,3)-A4(i,2);
C4(i,4) = A4(i,4)-A4(i,3);
C4(i,5) = 1-A4(i,4);

end;

%% Calculate general probability expressions
syms a;
```

```
pi1(1,1) = (exp(fitV1(1,1)+fitV1(2,1)*a))/(1+exp(fitV1(1,1)+fitV1(2,1)*a));
pi1(2,1) = 1 - pi1(1,1);



pi2(1,1) = (exp(fitV2(1,1)+fitV2(2,1)*a))/(1+exp(fitV2(1,1)+fitV2(2,1)*a));
pi2(2,1) = (exp(fitV2(1,2)+fitV2(2,2)*a))/(1+exp(fitV2(1,2)+fitV2(2,2)*a))-pi2(2-1,1);
pi2(3,1) = 1 - pi2(2,1);

pi3(1,1) = (exp(fitV3(1,1)+fitV3(2,1)*a))/(1+exp(fitV3(1,1)+fitV3(2,1)*a));
pi3(2,1) = 1 - pi3(1,1);

pi4(1,1) = (exp(fitV4(1,1)+fitV4(2,1)*a))/(1+exp(fitV4(1,1)+fitV4(2,1)*a));
for i = 2:4
    pi4(i,1) = (exp(fitV4(1,i)+fitV4(2,i)*a))/(1+exp(fitV4(1,i)+fitV4(2,i)*a))-pi4(i-1,1);
end;
pi4(5,1) = 1 - pi4(4,1);



%% Import prediction data yourself

%% Prediction
```

```
%G = [1,2,3,4];

%Predict = [0 2 2 3];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq14 Ref Data - All.csv');

%%Predict = PredictAll;

[rnum,cnum] = size(Predict);

fpred = sym('fpred',[rnum,1]);


display('Predictions')

for j = 1:rnum

    display(j);

    k = Predict(j,1);

    if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;

    l = Predict(j,2);

    if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;

    m = Predict(j,3);

    if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;

    n = Predict(j,4);

    if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;

end;



zz = agerange';
```

```
display('Predplot');
predplot = vpa(zeros(cnt1,rnum),10);
predplot = double(predplot);
   for j = 1:rnum
       display(j);
       FUN = matlabFunction(fpred(j,1));
       predplot(:,j) = feval(FUN,zz);
    end;

    pplot = double(predplot);

%% Determine max likelihood point estimate for all combinations:

ahat = zeros(rnum,1);
ahatl = ahat;
results = zeros(rnum,3);


display('Point estimates')
for j = 1:rnum
    display(j);
 likelihood = predplot(:,j);
 likelihood = double(likelihood);
 maxprob = max(likelihood);
```

```
 [row,col] = find(likelihood==maxprob);
 ahat(j,1) = yy(row,1); % these are the point estimates
 ahatl(j,1) = maxprob;
 results(j,1) = ahat(j,1);
end;

% %% Confidence Intervals
% % We assume conditional independence, i.e. there are no correlations
% % between traits except for age ** expand this later on.
display('Confidence Intervals')
alphalow = chi2inv(0.05,1);
alphahi = chi2inv(0.95,1);
varZ = zeros(rnum,1);
LCI = zeros(cnt1,rnum);
CI = zeros(cnt1,rnum);
UCI = zeros(cnt1,rnum);

Zscoreneg = CI;
Zscorepos = CI;


UCII = zeros(rnum,1);
LCII = UCII;
calcvarZ = zeros(rnum,1);
```

```
counter = calcvarZ;

delta = zeros(rnum,2);
alpha = 0.05;

for j = 1:rnum
    delta(j,1) = -2*log(ahatl(j,1));
    probdelta = chi2cdf(delta(j,1),3);
    if probdelta < alpha
        delta(j,2) = 1;
    else
        if probdelta > 1-alpha
            delta(j,2) = 1;
        end;
    end;
end;

for j = 1:rnum
    display(j);
    likelihood = predplot(:,j);
    likelihood = double(likelihood);
    for i = 1:cnt1
        interm=likelihood(i,1)/ahatl(j,1);
        CI(i,j) = (-2*log(interm));
```

```
    Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
    Zscorepos(i,j) = sqrt(abs(CI(i,j)));
    calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
 end;
 counter(j,1)= (2*cnt1);
varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
for i = 1:cnt1
   interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
   CI(i,j) = real(-2*log(interm));
end;
 [lrow,~] = find(CI(:,j)>=alphalow);
 [lm,~] = size(lrow);
 for t = 1:lm
   lrownums = lrow(t,1);
   if lrownums==1
    LCI(t,j) = yy(lrownums,1);
   else
       LCI(t,j) = yy(lrownums-1,1);
   end;
 end;
 pe=results(j,1);
 if min(LCI(:,j)) > pe
    LCII(j,1)=min(Age);
 else
```

```
        [rows,cols] = find(0<LCI(:,j)<pe,1);
        LCII(j,1) = LCI(rows,j);
    end;
    results(j,2) = LCII(j,1);
    [urow,col] = find(CI(:,j)<= alphahi);
    [m,~] = size(urow);
%     for t = 1:m
%         rownums = urow(t,1);
%         if rownums==cnt1
%          UCI(t,j) = yy(rownums,1);
%         else
%             UCI(t,j) = yy(rownums+1,1);
%         end;
%     end;
    for t = 1:m
        rownums = urow(t,1);
        if rownums==cnt1
         UCI(t,j) = yy(rownums,1);
        else
            UCI(t,j) = yy(rownums,1);
        end;
    end;
%     for t = 1:m
%         rownums = urow(t,1);
```

```
%        UCI(t,j) = yy(rownums,1);
%     end;
    if max(UCI(:,j)) <= pe
        UCII(j,1)=max(yy);
    else
        [rows,cols] = find(UCI(:,j)>pe,1);
        UCII(j,1) = UCI(rows,j);
        %If rows == 0
          %UCII(j,1) = max(zz);
    end;
    results(j,3) = UCII(j,1);
end;

%% End of Program Transition_Analysis_eq38
```

```
%% Program Transition_Analysis_eq39

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq15 Fit Data - All.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
Age = data(:,1);
```

```
V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);

V5 = data(:,6);


%%xx = linspace(0,100)';

%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';

[cnt1,~] = size(xx);

%%display(yy);



%% V1 CR Model

[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C1 = zeros(cnt1,2);


%% Calculate probabilities for V1
```

```
PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A1 = PROB1;


for i = 1:cnt1

C1(i,1) = A1(i,1);

C1(i,2) = A1(i,2)-A1(i,1);

C1(i,3) = 1-A1(i,2);

end;


%% V2 CR Model

[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C2 = zeros(cnt1,2);


%% Calculate probabilities for V2



PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A2 = PROB2;


for i = 1:cnt1

C2(i,1) = A2(i,1);
```

```
C2(i,2) = A2(i,2)-A2(i,1);

C2(i,3) = A2(i,3)-A2(i,2);

C2(i,4) = A2(i,4)-A2(i,3);

C2(i,5) = 1-A2(i,4);

end;


%% V3 CR Model

[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C3 = zeros(cnt1,2);


%% Calculate probabilities for V3



PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;


for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = A3(i,2)-A3(i,1);

C3(i,3) = A3(i,3)-A3(i,2);

C3(i,4) = 1-A3(i,3);

end;
```

```
%% V4 CR Model

[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);


%% Calculate probabilities for V4



PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A4 = PROB4;


for i = 1:cnt1

C4(i,1) = A4(i,1);

C4(i,2) = 1-A4(i,1);


end;


[fitV5,~,~] = mnrfit(Age,V5,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);
```

```
%% Calculate probabilities for V5

PROB5 = mnrval(fitV5,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A5 = PROB5;

for i = 1:cnt1
C5(i,1) = A5(i,1);
C5(i,2) = A5(i,2)-A5(i,1);
C5(i,3) = A5(i,3)-A5(i,2);
%C5(i,4) = A5(i,4)-A5(i,3);
C5(i,4) = 1-A5(i,3);
end;



%% Calculate general probability expressions
syms a;

pi1(1,1) = (exp(fitV1(1,1)+fitV1(2,1)*a))/(1+exp(fitV1(1,1)+fitV1(2,1)*a));
pi1(2,1) = (exp(fitV1(1,2)+fitV1(2,2)*a))/(1+exp(fitV1(1,2)+fitV1(2,2)*a))-pi1(2-1,1);
pi1(3,1) = 1 - pi1(2,1);

pi2(1,1) = (exp(fitV2(1,1)+fitV2(2,1)*a))/(1+exp(fitV2(1,1)+fitV2(2,1)*a));
for i = 2:4
```

```
    pi2(i,1) = (exp(fitV2(1,i)+fitV2(2,i)*a))/(1+exp(fitV2(1,i)+fitV2(2,i)*a))-pi2(i-1,1);
end;
pi2(5,1) = 1 - pi2(4,1);


pi3(1,1) = (exp(fitV3(1,1)+fitV3(2,1)*a))/(1+exp(fitV3(1,1)+fitV3(2,1)*a));
for i = 2:3
    pi3(i,1) = (exp(fitV3(1,i)+fitV3(2,i)*a))/(1+exp(fitV3(1,i)+fitV3(2,i)*a))-pi3(i-1,1);
end;
pi3(4,1) = 1 - pi3(3,1);

pi4(1,1) = (exp(fitV4(1,1)+fitV4(2,1)*a))/(1+exp(fitV4(1,1)+fitV4(2,1)*a));
pi4(2,1) = 1 - pi4(1,1);

pi5(1,1) = (exp(fitV5(1,1)+fitV5(2,1)*a))/(1+exp(fitV5(1,1)+fitV5(2,1)*a));
for i = 2:3
    pi5(i,1) = (exp(fitV5(1,i)+fitV5(2,i)*a))/(1+exp(fitV5(1,i)+fitV5(2,i)*a))-pi5(i-1,1);
end;
pi5(4,1) = 1 - pi5(3,1);
```

```
%% Import prediction data yourself


%% Prediction


%G = [1,2,3,4];
%Predict = [0 2 2 3];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq15 Ref Data - All 8.csv');
%%Predict = PredictAll;
[rnum,cnum] = size(Predict);
fpred = sym('fpred',[rnum,1]);


display('Predictions')
for j = 1:rnum
   display(j);
   k = Predict(j,1);
   if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;
   l = Predict(j,2);
   if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;
   m = Predict(j,3);
   if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;
   n = Predict(j,4);
   if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;
   o = Predict(j,5);
```

```
    if (o == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi5(o,1); endif;
end;



zz = agerange';
display('Predplot');
predplot = vpa(zeros(cnt1,rnum),10);
predplot = double(predplot);
   for j = 1:rnum
        display(j);
        FUN = matlabFunction(fpred(j,1));
        predplot(:,j) = feval(FUN,zz);
    end;

    pplot = double(predplot);

%% Determine max likelihood point estimate for all combinations:

ahat = zeros(rnum,1);
ahatl = ahat;
results = zeros(rnum,3);



display('Point estimates')
```

```
for j = 1:rnum
    display(j);
 likelihood = predplot(:,j);
 likelihood = double(likelihood);
 maxprob = max(likelihood);
 [row,col] = find(likelihood==maxprob);
 ahat(j,1) = yy(row,1); % these are the point estimates
 ahatl(j,1) = maxprob;
 results(j,1) = ahat(j,1);
end;

% %% Confidence Intervals
% % We assume conditional independence, i.e. there are no correlations
% % between traits except for age ** expand this later on.
display('Confidence Intervals')
alphalow = chi2inv(0.05,1);
alphahi = chi2inv(0.95,1);
varZ = zeros(rnum,1);
LCI = zeros(cnt1,rnum);
CI = zeros(cnt1,rnum);
UCI = zeros(cnt1,rnum);

Zscoreneg = CI;
Zscorepos = CI;
```

```
UCII = zeros(rnum,1);
LCII = UCII;
calcvarZ = zeros(rnum,1);
counter = calcvarZ;

delta = zeros(rnum,2);
alpha = 0.05;

for j = 1:rnum
    delta(j,1) = -2*log(ahatl(j,1));
    probdelta = chi2cdf(delta(j,1),3);
    if probdelta < alpha
        delta(j,2) = 1;
    else
        if probdelta > 1-alpha
            delta(j,2) = 1;
        end;
    end;
end;

for j = 1:rnum
    display(j);
```

```
 likelihood = predplot(:,j);
 likelihood = double(likelihood);
 for i = 1:cnt1
     interm=likelihood(i,1)/ahatl(j,1);
     CI(i,j) = (-2*log(interm));
     Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
     Zscorepos(i,j) = sqrt(abs(CI(i,j)));
     calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
 end;
 counter(j,1)= (2*cnt1);
varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
for i = 1:cnt1
    interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
    CI(i,j) = real(-2*log(interm));
end;
 [lrow,~] = find(CI(:,j)>=alphalow);
 [lm,~] = size(lrow);
 for t = 1:lm
    lrownums = lrow(t,1);
    if lrownums==1
     LCI(t,j) = yy(lrownums,1);
    else
        LCI(t,j) = yy(lrownums-1,1);
    end;
```

```
    end;
    pe=results(j,1);
    if min(LCI(:,j)) > pe
        LCII(j,1)=min(Age);
    else
        [rows,cols] = find(0<LCI(:,j)<pe,1);
        LCII(j,1) = LCI(rows,j);
    end;
    results(j,2) = LCII(j,1);
    [urow,col] = find(CI(:,j)<= alphahi);
    [m,~] = size(urow);
%     for t = 1:m
%         rownums = urow(t,1);
%         if rownums==cnt1
%          UCI(t,j) = yy(rownums,1);
%         else
%             UCI(t,j) = yy(rownums+1,1);
%         end;
%     end;
    for t = 1:m
       rownums = urow(t,1);
       if rownums==cnt1
        UCI(t,j) = yy(rownums,1);
       else
```

```
            UCI(t,j) = yy(rownums,1);
        end;
    end;
%     for t = 1:m
%         rownums = urow(t,1);
%         UCI(t,j) = yy(rownums,1);
%     end;
    if max(UCI(:,j)) <= pe
        UCII(j,1)=max(yy);
    else
        [rows,cols] = find(UCI(:,j)>pe,1);
        UCII(j,1) = UCI(rows,j);
        %If rows == 0
          %UCII(j,1) = max(zz);
    end;
    results(j,3) = UCII(j,1);
end;


%% End of Program Transition_Analysis_eq39
```

```
%% Program Transition_Analysis_eq40

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq28 Fit Data - Female.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
Age = data(:,1);
```

```
V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);


%%xx = linspace(0,100)';

%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';

[cnt1,~] = size(xx);

%%display(yy);



%% V1 CR Model

[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C1 = zeros(cnt1,2);


%% Calculate probabilities for V1



PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
```

```
A1 = PROB1;

for i = 1:cnt1
C1(i,1) = A1(i,1);
C1(i,2) = 1-A1(i,1);
end;

%% V2 CR Model
[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');

%A1 = zeros(r,3);
C2 = zeros(cnt1,2);

%% Calculate probabilities for V2


PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A2 = PROB2;

for i = 1:cnt1
C2(i,1) = A2(i,1);
C2(i,2) = A2(i,2)-A2(i,1);
C2(i,3) = 1-A2(i,2);
end;
```

```
%% V3 CR Model
[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');

%A1 = zeros(r,3);
C4 = zeros(cnt1,2);

%% Calculate probabilities for V3


PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A4 = PROB4;

for i = 1:cnt1
C4(i,1) = A4(i,1);
C4(i,2) = 1-A4(i,1);
end;

%% V4 CR Model
[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');

%A1 = zeros(r,3);
C3 = zeros(cnt1,2);
```

```
%% Calculate probabilities for V4


PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;


for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = A3(i,2)-A3(i,1);

C3(i,3) = A3(i,3)-A3(i,2);

C3(i,4) = A3(i,4)-A3(i,3);

C3(i,5) = 1-A3(i,4);


end;




%% Calculate general probability expressions

syms a real;


pi1(1,1) = (exp(fitV1(1,1)+fitV1(2,1)*a))/(1+exp(fitV1(1,1)+fitV1(2,1)*a));

pi1(2,1) = 1 - pi1(1,1);
```

```
pi2(1,1) = (exp(fitV2(1,1)+fitV2(2,1)*a))/(1+exp(fitV2(1,1)+fitV2(2,1)*a));
pi2(2,1) = (exp(fitV2(1,2)+fitV2(2,2)*a))/(1+exp(fitV2(1,2)+fitV2(2,2)*a))-pi2(2-1,1);
pi2(3,1) = 1 - pi2(2,1);

pi4(1,1) = (exp(fitV4(1,1)+fitV4(2,1)*a))/(1+exp(fitV4(1,1)+fitV4(2,1)*a));
pi4(2,1) = 1 - pi4(1,1);

pi3(1,1) = (exp(fitV3(1,1)+fitV3(2,1)*a))/(1+exp(fitV3(1,1)+fitV3(2,1)*a));
for i = 2:4
    pi3(i,1) = (exp(fitV3(1,i)+fitV3(2,i)*a))/(1+exp(fitV3(1,i)+fitV3(2,i)*a))-pi3(i-1,1);
end;
pi3(5,1) = 1 - pi3(4,1);

%% Import prediction data yourself

%% Prediction

%G = [1,2,3,4];
```

```
%Predict = [0 2 2 3];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq28 Ref Data - Female.csv');
%%Predict = PredictAll;
[rnum,cnum] = size(Predict);
fpred = sym('fpred',[rnum,1]);


display('Predictions')
for j = 1:rnum
    display(j);
    k = Predict(j,1);
    if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;
    l = Predict(j,2);
    if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;
    m = Predict(j,3);
    if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;
    n = Predict(j,4);
    if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;
end;



zz = agerange';
display('Predplot');
%%predplot = vpa(zeros(cnt1,rnum),10);
```

```
predplot = zeros(cnt1,rnum);
predplot = double(predplot);
   for j = 1:rnum
       display(j);
       FUN = matlabFunction(fpred(j,1));
       predplot(:,j) = feval(FUN,zz);
    end;

    pplot = double(predplot);

%% Determine max likelihood point estimate for all combinations:

ahat = zeros(rnum,1);
ahatl = ahat;
results = zeros(rnum,3);



display('Point estimates')
for j = 1:rnum
    display(j);
 likelihood = predplot(:,j);
 likelihood = double(likelihood);
 maxprob = max(likelihood);
 [row,col] = find(likelihood==maxprob);
```

```
 ahat(j,1) = yy(row,1); % these are the point estimates
 ahatl(j,1) = maxprob;
 results(j,1) = ahat(j,1);
end;

% %% Confidence Intervals
% % We assume conditional independence, i.e. there are no correlations
% % between traits except for age ** expand this later on.
display('Confidence Intervals')
alphalow = chi2inv(0.05,1);
alphahi = chi2inv(0.95,1);
varZ = zeros(rnum,1);
LCI = zeros(cnt1,rnum);
CI = zeros(cnt1,rnum);
UCI = zeros(cnt1,rnum);

Zscoreneg = CI;
Zscorepos = CI;



UCII = zeros(rnum,1);
LCII = UCII;
calcvarZ = zeros(rnum,1);
counter = calcvarZ;
```

```
delta = zeros(rnum,2);
alpha = 0.05;

for j = 1:rnum
    delta(j,1) = -2*log(ahatl(j,1));
    probdelta = chi2cdf(delta(j,1),3);
    if probdelta < alpha
        delta(j,2) = 1;
    else
        if probdelta > 1-alpha
            delta(j,2) = 1;
        end;
    end;
end;

for j = 1:rnum
    display(j);
    likelihood = predplot(:,j);
    likelihood = double(likelihood);
    for i = 1:cnt1
        interm=likelihood(i,1)/ahatl(j,1);
        CI(i,j) = (-2*log(interm));
        Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
```

```
    Zscorepos(i,j) = sqrt(abs(CI(i,j)));
    calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
 end;
 counter(j,1)= (2*cnt1);
varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
for i = 1:cnt1
   interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
   CI(i,j) = real(-2*log(interm));
end;
 [lrow,~] = find(CI(:,j)>=alphalow);
 [lm,~] = size(lrow);
 for t = 1:lm
   lrownums = lrow(t,1);
   if lrownums==1
    LCI(t,j) = yy(lrownums,1);
   else
       LCI(t,j) = yy(lrownums-1,1);
   end;
 end;
 pe=results(j,1);
 if min(LCI(:,j)) > pe
    LCII(j,1)=min(Age);
 else
    [rows,cols] = find(0<LCI(:,j)<pe,1);
```

```
        LCII(j,1) = LCI(rows,j);
    end;
    results(j,2) = LCII(j,1);
    [urow,col] = find(CI(:,j)<= alphahi);
    [m,~] = size(urow);
%     for t = 1:m
%         rownums = urow(t,1);
%         if rownums==cnt1
%          UCI(t,j) = yy(rownums,1);
%         else
%             UCI(t,j) = yy(rownums+1,1);
%         end;
%     end;
    for t = 1:m
        rownums = urow(t,1);
        if rownums==cnt1
         UCI(t,j) = yy(rownums,1);
        else
            UCI(t,j) = yy(rownums,1);
        end;
    end;
%     for t = 1:m
%         rownums = urow(t,1);
%         UCI(t,j) = yy(rownums,1);
```

```
%     end;
    if max(UCI(:,j)) <= pe
        UCII(j,1)=max(yy);
    else
        [rows,cols] = find(UCI(:,j)>pe,1);
        UCII(j,1) = UCI(rows,j);
        %If rows == 0
          %UCII(j,1) = max(zz);
    end;
    results(j,3) = UCII(j,1);
end;

%% End of Program Transition_Analysis_eq40
```

```
%% Program Transition_Analysis_eq40_vpa

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq28 Fit Data - Female.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
Age = data(:,1);
```

```
V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);


%%xx = linspace(0,100)';

%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';

[cnt1,~] = size(xx);

%%display(yy);



%% V1 CR Model

[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C1 = zeros(cnt1,2);


%% Calculate probabilities for V1



PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
```

```
A1 = PROB1;

for i = 1:cnt1
C1(i,1) = A1(i,1);
C1(i,2) = 1-A1(i,1);
end;

%% V2 CR Model
[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');

%A1 = zeros(r,3);
C2 = zeros(cnt1,2);

%% Calculate probabilities for V2


PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A2 = PROB2;

for i = 1:cnt1
C2(i,1) = A2(i,1);
C2(i,2) = A2(i,2)-A2(i,1);
C2(i,3) = 1-A2(i,2);
end;
```

```
%% V3 CR Model
[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');

%A1 = zeros(r,3);
C4 = zeros(cnt1,2);

%% Calculate probabilities for V3


PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A4 = PROB4;

for i = 1:cnt1
C4(i,1) = A4(i,1);
C4(i,2) = 1-A4(i,1);
end;

%% V4 CR Model
[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');

%A1 = zeros(r,3);
C3 = zeros(cnt1,2);
```

```
%% Calculate probabilities for V4


PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;


for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = A3(i,2)-A3(i,1);

C3(i,3) = A3(i,3)-A3(i,2);

C3(i,4) = A3(i,4)-A3(i,3);

C3(i,5) = 1-A3(i,4);


end;




%% Calculate general probability expressions

syms a real;


pi1(1,1) = (vpa(exp(fitV1(1,1)+fitV1(2,1)*a)))/(1+vpa(exp(fitV1(1,1)+fitV1(2,1)*a)));

pi1(2,1) = 1 - pi1(1,1);
```

```
pi2(1,1) = (vpa(exp(fitV2(1,1)+fitV2(2,1)*a)))/(1+vpa(exp(fitV2(1,1)+fitV2(2,1)*a)));

pi2(2,1) = (vpa(exp(fitV2(1,2)+fitV2(2,2)*a)))/(1+vpa(exp(fitV2(1,2)+fitV2(2,2)*a)))-
pi2(2-1,1);

pi2(3,1) = 1 - pi2(2,1);


pi4(1,1) = vpa((exp(fitV4(1,1)+fitV4(2,1)*a)))/(1+vpa(exp(fitV4(1,1)+fitV4(2,1)*a)));

pi4(2,1) = 1 - pi4(1,1);


pi3(1,1) = vpa((exp(fitV3(1,1)+fitV3(2,1)*a)))/(1+vpa(exp(fitV3(1,1)+fitV3(2,1)*a)));

for i = 2:4

   pi3(i,1) = vpa((exp(fitV3(1,i)+fitV3(2,i)*a)))/(1+vpa(exp(fitV3(1,i)+fitV3(2,i)*a)))-
pi3(i-1,1);

end;

pi3(5,1) = 1 - pi3(4,1);




%% Import prediction data yourself


%% Prediction
```

```
%G = [1,2,3,4];

%Predict = [0 2 2 3];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq28 Ref Data - Female.csv');

%%Predict = PredictAll;

[rnum,cnum] = size(Predict);

fpred = sym('fpred',[rnum,1]);


display('Predictions')

for j = 1:rnum

    display(j);

    k = Predict(j,1);

    if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;

    l = Predict(j,2);

    if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;

    m = Predict(j,3);

    if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;

    n = Predict(j,4);

    if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;

end;



zz = agerange';

display('Predplot');
```

```
%%predplot = vpa(zeros(cnt1,rnum),10);
predplot = zeros(cnt1,rnum);
predplot = double(predplot);
   for j = 1:rnum
       display(j);
       FUN = matlabFunction(fpred(j,1));
       predplot(:,j) = feval(FUN,zz);
    end;

    pplot = double(predplot);

%% Determine max likelihood point estimate for all combinations:

ahat = zeros(rnum,1);
ahatl = ahat;
results = zeros(rnum,3);



display('Point estimates')
for j = 1:rnum
    display(j);
 likelihood = predplot(:,j);
 likelihood = double(likelihood);
 maxprob = max(likelihood);
```

```
 [row,col] = find(likelihood==maxprob);
 ahat(j,1) = yy(row,1); % these are the point estimates
 ahatl(j,1) = maxprob;
 results(j,1) = ahat(j,1);
end;

% %% Confidence Intervals
% % We assume conditional independence, i.e. there are no correlations
% % between traits except for age ** expand this later on.
display('Confidence Intervals')
alphalow = chi2inv(0.05,1);
alphahi = chi2inv(0.95,1);
varZ = zeros(rnum,1);
LCI = zeros(cnt1,rnum);
CI = zeros(cnt1,rnum);
UCI = zeros(cnt1,rnum);

Zscoreneg = CI;
Zscorepos = CI;


UCII = zeros(rnum,1);
LCII = UCII;
calcvarZ = zeros(rnum,1);
```

```
counter = calcvarZ;

delta = zeros(rnum,2);
alpha = 0.05;

for j = 1:rnum
    delta(j,1) = -2*log(ahatl(j,1));
    probdelta = chi2cdf(delta(j,1),3);
    if probdelta < alpha
        delta(j,2) = 1;
    else
        if probdelta > 1-alpha
            delta(j,2) = 1;
        end;
    end;
end;

for j = 1:rnum
    display(j);
    likelihood = predplot(:,j);
    likelihood = double(likelihood);
    for i = 1:cnt1
        interm=likelihood(i,1)/ahatl(j,1);
        CI(i,j) = (-2*log(interm));
```

```
    Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
    Zscorepos(i,j) = sqrt(abs(CI(i,j)));
    calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
 end;
 counter(j,1)= (2*cnt1);
varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
for i = 1:cnt1
   interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
   CI(i,j) = real(-2*log(interm));
end;
 [lrow,~] = find(CI(:,j)>=alphalow);
 [lm,~] = size(lrow);
 for t = 1:lm
   lrownums = lrow(t,1);
   if lrownums==1
    LCI(t,j) = yy(lrownums,1);
   else
       LCI(t,j) = yy(lrownums-1,1);
   end;
 end;
 pe=results(j,1);
 if min(LCI(:,j)) > pe
    LCII(j,1)=min(Age);
 else
```

```
        [rows,cols] = find(0<LCI(:,j)<pe,1);
        LCII(j,1) = LCI(rows,j);
    end;
    results(j,2) = LCII(j,1);
    [urow,col] = find(CI(:,j)<= alphahi);
    [m,~] = size(urow);
%     for t = 1:m
%         rownums = urow(t,1);
%         if rownums==cnt1
%          UCI(t,j) = yy(rownums,1);
%         else
%             UCI(t,j) = yy(rownums+1,1);
%         end;
%     end;
    for t = 1:m
        rownums = urow(t,1);
        if rownums==cnt1
         UCI(t,j) = yy(rownums,1);
        else
            UCI(t,j) = yy(rownums,1);
        end;
    end;
%     for t = 1:m
%         rownums = urow(t,1);
```

```
%        UCI(t,j) = yy(rownums,1);
%     end;
    if max(UCI(:,j)) <= pe
        UCII(j,1)=max(yy);
    else
        [rows,cols] = find(UCI(:,j)>pe,1);
        UCII(j,1) = UCI(rows,j);
        %If rows == 0
          %UCII(j,1) = max(zz);
    end;
    results(j,3) = UCII(j,1);
end;

%% End of Program Transition_Analysis_eq40_vpa
```

```
%% Program Transition_Analysis_eq41

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq41 Fit Data - Males.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
Age = data(:,1);
```

```
V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);

V5 = data(:,6);


%%xx = linspace(0,100)';

%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';

[cnt1,~] = size(xx);

%%display(yy);



%% V1 CR Model

[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C1 = zeros(cnt1,2);


%% Calculate probabilities for V1
```

```
PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A1 = PROB1;


for i = 1:cnt1

C1(i,1) = A1(i,1);

C1(i,2) = A1(i,2)-A1(i,1);

C1(i,3) = 1-A1(i,2);

end;


%% V2 CR Model

[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C2 = zeros(cnt1,2);


%% Calculate probabilities for V2



PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A2 = PROB2;


for i = 1:cnt1

C2(i,1) = A2(i,1);
```

```
C2(i,2) = A2(i,2)-A2(i,1);

C2(i,3) = A2(i,3)-A2(i,2);

C2(i,4) = 1-A2(i,3);

end;


%% V3 CR Model

[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C3 = zeros(cnt1,2);


%% Calculate probabilities for V3



PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;


for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = A3(i,2)-A3(i,1);

C3(i,3) = A3(i,3)-A3(i,2);

C3(i,4) = 1-A3(i,3);

end;
```

```
%% V4 CR Model

[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);


%% Calculate probabilities for V4



PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A4 = PROB4;


for i = 1:cnt1

C4(i,1) = A4(i,1);

C4(i,2) = 1-A4(i,1);


end;


[fitV5,~,~] = mnrfit(Age,V5,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);


%% Calculate probabilities for V5
```

```
PROB5 = mnrval(fitV5,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A5 = PROB5;


for i = 1:cnt1

C5(i,1) = A5(i,1);

C5(i,2) = A5(i,2)-A5(i,1);

C5(i,3) = A5(i,3)-A5(i,2);

%C5(i,4) = A5(i,4)-A5(i,3);

C5(i,4) = 1-A5(i,3);

end;




%% Calculate general probability expressions

syms a;


pi1(1,1) = (exp(fitV1(1,1)+fitV1(2,1)*a))/(1+exp(fitV1(1,1)+fitV1(2,1)*a));

pi1(2,1) = (exp(fitV1(1,2)+fitV1(2,2)*a))/(1+exp(fitV1(1,2)+fitV1(2,2)*a))-pi1(2-1,1);

pi1(3,1) = 1 - pi1(2,1);


pi2(1,1) = (exp(fitV2(1,1)+fitV2(2,1)*a))/(1+exp(fitV2(1,1)+fitV2(2,1)*a));

for i = 2:3

    pi2(i,1) = (exp(fitV2(1,i)+fitV2(2,i)*a))/(1+exp(fitV2(1,i)+fitV2(2,i)*a))-pi2(i-1,1);
```

```
end;
pi2(4,1) = 1 - pi2(3,1);



pi3(1,1) = (exp(fitV3(1,1)+fitV3(2,1)*a))/(1+exp(fitV3(1,1)+fitV3(2,1)*a));
for i = 2:3
    pi3(i,1) = (exp(fitV3(1,i)+fitV3(2,i)*a))/(1+exp(fitV3(1,i)+fitV3(2,i)*a))-pi3(i-1,1);
end;
pi3(4,1) = 1 - pi3(3,1);

pi4(1,1) = (exp(fitV4(1,1)+fitV4(2,1)*a))/(1+exp(fitV4(1,1)+fitV4(2,1)*a));
pi4(2,1) = 1 - pi4(1,1);

pi5(1,1) = (exp(fitV5(1,1)+fitV5(2,1)*a))/(1+exp(fitV5(1,1)+fitV5(2,1)*a));
for i = 2:3
    pi5(i,1) = (exp(fitV5(1,i)+fitV5(2,i)*a))/(1+exp(fitV5(1,i)+fitV5(2,i)*a))-pi5(i-1,1);
end;
pi5(4,1) = 1 - pi5(3,1);



%% Import prediction data yourself
```

```
%% Prediction


%G = [1,2,3,4];

%Predict = [0 2 2 3];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq41 Ref Data - Male - Copy (4).csv');

%%Predict = PredictAll;

[rnum,cnum] = size(Predict);

fpred = sym('fpred',[rnum,1]);


display('Predictions')

for j = 1:rnum

   display(j);

   k = Predict(j,1);

   if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;

   l = Predict(j,2);

   if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;

   m = Predict(j,3);

   if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;

   n = Predict(j,4);

   if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;

   o = Predict(j,5);

   if (o == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi5(o,1); endif;
```

```
end;



zz = agerange';
display('Predplot');
predplot = sym(zeros(cnt1,rnum));
predplot = double(predplot);
   for j = 1:rnum
        display(j);
        FUN = matlabFunction(fpred(j,1));
        predplot(:,j) = feval(FUN,zz);
    end;


    pplot = double(predplot);


%% Determine max likelihood point estimate for all combinations:


ahat = zeros(rnum,1);
ahatl = ahat;
results = zeros(rnum,3);



display('Point estimates')
for j = 1:rnum
```

```
   display(j);
 likelihood = predplot(:,j);
 likelihood = double(likelihood);
 maxprob = max(likelihood);
 [row,col] = find(likelihood==maxprob);
 ahat(j,1) = yy(row,1); % these are the point estimates
 ahatl(j,1) = maxprob;
 results(j,1) = ahat(j,1);
end;

% %% Confidence Intervals
% % We assume conditional independence, i.e. there are no correlations
% % between traits except for age ** expand this later on.
display('Confidence Intervals')
alphalow = chi2inv(0.05,1);
alphahi = chi2inv(0.95,1);
varZ = zeros(rnum,1);
LCI = zeros(cnt1,rnum);
CI = zeros(cnt1,rnum);
UCI = zeros(cnt1,rnum);

Zscoreneg = CI;
Zscorepos = CI;
```

```
UCII = zeros(rnum,1);
LCII = UCII;
calcvarZ = zeros(rnum,1);
counter = calcvarZ;

delta = zeros(rnum,2);
alpha = 0.05;

for j = 1:rnum
    delta(j,1) = -2*log(ahatl(j,1));
    probdelta = chi2cdf(delta(j,1),3);
    if probdelta < alpha
        delta(j,2) = 1;
    else
        if probdelta > 1-alpha
            delta(j,2) = 1;
        end;
    end;
end;

for j = 1:rnum
    display(j);
    likelihood = predplot(:,j);
```

```
 likelihood = double(likelihood);
 for i = 1:cnt1
     interm=likelihood(i,1)/ahatl(j,1);
     CI(i,j) = (-2*log(interm));
     Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
     Zscorepos(i,j) = sqrt(abs(CI(i,j)));
     calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
 end;
 counter(j,1)= (2*cnt1);
varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
for i = 1:cnt1
    interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
    CI(i,j) = real(-2*log(interm));
end;
 [lrow,~] = find(CI(:,j)>=alphalow);
 [lm,~] = size(lrow);
 for t = 1:lm
    lrownums = lrow(t,1);
    if lrownums==1
     LCI(t,j) = yy(lrownums,1);
    else
        LCI(t,j) = yy(lrownums-1,1);
    end;
 end;
```

```
    pe=results(j,1);
    if min(LCI(:,j)) > pe
        LCII(j,1)=min(Age);
    else
        [rows,cols] = find(0<LCI(:,j)<pe,1);
        LCII(j,1) = LCI(rows,j);
    end;
    results(j,2) = LCII(j,1);
    [urow,col] = find(CI(:,j)<= alphahi);
    [m,~] = size(urow);
%     for t = 1:m
%         rownums = urow(t,1);
%         if rownums==cnt1
%          UCI(t,j) = yy(rownums,1);
%         else
%             UCI(t,j) = yy(rownums+1,1);
%         end;
%     end;
    for t = 1:m
       rownums = urow(t,1);
       if rownums==cnt1
        UCI(t,j) = yy(rownums,1);
       else
           UCI(t,j) = yy(rownums,1);
```

```
      end;
   end;
%    for t = 1:m
%       rownums = urow(t,1);
%       UCI(t,j) = yy(rownums,1);
%    end;
   if max(UCI(:,j)) <= pe
      UCII(j,1)=max(yy);
   else
      [rows,cols] = find(UCI(:,j)>pe,1);
      UCII(j,1) = UCI(rows,j);
      %If rows == 0
        %UCII(j,1) = max(zz);
   end;
   results(j,3) = UCII(j,1);
end;

%% End of Program Transition_Analysis_eq41
```

```
%% Program Transition_Analysis_eq42

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq42 Fit Data - Male.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
Age = data(:,1);
```

```
V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);

V5 = data(:,6);


%%xx = linspace(0,100)';

%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';

[cnt1,~] = size(xx);

%%display(yy);



%% V1 CR Model

[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C1 = zeros(cnt1,2);


%% Calculate probabilities for V1
```

```
PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A1 = PROB1;


for i = 1:cnt1

C1(i,1) = A1(i,1);

C1(i,2) = A1(i,2)-A1(i,1);

C1(i,3) = 1-A1(i,2);

end;


%% V2 CR Model

[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C2 = zeros(cnt1,2);


%% Calculate probabilities for V2



PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A2 = PROB2;


for i = 1:cnt1

C2(i,1) = A2(i,1);

C2(i,2) = A2(i,2)-A2(i,1);
```

```
C2(i,3) = A2(i,3)-A2(i,2);

C2(i,4) = A2(i,4)-A2(i,3);

C2(i,5) = 1-A2(i,4);

end;


%% V3 CR Model

[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C3 = zeros(cnt1,2);


%% Calculate probabilities for V3



PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;


for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = A3(i,2)-A3(i,1);

C3(i,3) = A3(i,3)-A3(i,2);

C3(i,4) = 1-A3(i,3);

end;
```

```
%% V4 CR Model

[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);


%% Calculate probabilities for V4



PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A4 = PROB4;


for i = 1:cnt1

C4(i,1) = A4(i,1);

C4(i,2) = 1-A4(i,1);


end;


[fitV5,~,~] = mnrfit(Age,V5,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);


%% Calculate probabilities for V5
```

```
PROB5 = mnrval(fitV5,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A5 = PROB5;


for i = 1:cnt1

C5(i,1) = A5(i,1);

C5(i,2) = A5(i,2)-A5(i,1);

C5(i,3) = A5(i,3)-A5(i,2);

%C5(i,4) = A5(i,4)-A5(i,3);

C5(i,4) = 1-A5(i,3);

end;




%% Calculate general probability expressions

syms a;


pi1(1,1) = (exp(fitV1(1,1)+fitV1(2,1)*a))/(1+exp(fitV1(1,1)+fitV1(2,1)*a));

pi1(2,1) = (exp(fitV1(1,2)+fitV1(2,2)*a))/(1+exp(fitV1(1,2)+fitV1(2,2)*a))-pi1(2-1,1);

pi1(3,1) = 1 - pi1(2,1);


pi2(1,1) = (exp(fitV2(1,1)+fitV2(2,1)*a))/(1+exp(fitV2(1,1)+fitV2(2,1)*a));

for i = 2:4

   pi2(i,1) = (exp(fitV2(1,i)+fitV2(2,i)*a))/(1+exp(fitV2(1,i)+fitV2(2,i)*a))-pi2(i-1,1);
```

```
end;
pi2(5,1) = 1 - pi2(4,1);



pi3(1,1) = (exp(fitV3(1,1)+fitV3(2,1)*a))/(1+exp(fitV3(1,1)+fitV3(2,1)*a));
for i = 2:3
    pi3(i,1) = (exp(fitV3(1,i)+fitV3(2,i)*a))/(1+exp(fitV3(1,i)+fitV3(2,i)*a))-pi3(i-1,1);
end;
pi3(4,1) = 1 - pi3(3,1);

pi4(1,1) = (exp(fitV4(1,1)+fitV4(2,1)*a))/(1+exp(fitV4(1,1)+fitV4(2,1)*a));
pi4(2,1) = 1 - pi4(1,1);

pi5(1,1) = (exp(fitV5(1,1)+fitV5(2,1)*a))/(1+exp(fitV5(1,1)+fitV5(2,1)*a));
for i = 2:3
    pi5(i,1) = (exp(fitV5(1,i)+fitV5(2,i)*a))/(1+exp(fitV5(1,i)+fitV5(2,i)*a))-pi5(i-1,1);
end;
pi5(4,1) = 1 - pi5(3,1);



%% Import prediction data yourself
```

```
%% Prediction


%G = [1,2,3,4];
%Predict = [0 2 2 3];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\Eq42 Ref Data - Males - Copy (7).csv');
%%Predict = PredictAll;
[rnum,cnum] = size(Predict);
fpred = sym('fpred',[rnum,1]);


display('Predictions')
for j = 1:rnum
   display(j);
   k = Predict(j,1);
   if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;
   l = Predict(j,2);
   if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;
   m = Predict(j,3);
   if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;
   n = Predict(j,4);
   if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;
   o = Predict(j,5);
   if (o == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi5(o,1); endif;
end;
```

```
zz = agerange';
display('Predplot');
predplot = vpa(zeros(cnt1,rnum),10);
predplot = double(predplot);
  for j = 1:rnum
      display(j);
      FUN = matlabFunction(fpred(j,1));
      predplot(:,j) = feval(FUN,zz);
   end;

   pplot = double(predplot);

%% Determine max likelihood point estimate for all combinations:

ahat = zeros(rnum,1);
ahatl = ahat;
results = zeros(rnum,3);


display('Point estimates')
for j = 1:rnum
   display(j);
 likelihood = predplot(:,j);
```

```
 likelihood = double(likelihood);
 maxprob = max(likelihood);
 [row,col] = find(likelihood==maxprob);
 ahat(j,1) = yy(row,1); % these are the point estimates
 ahatl(j,1) = maxprob;
 results(j,1) = ahat(j,1);
end;

% %% Confidence Intervals
% % We assume conditional independence, i.e. there are no correlations
% % between traits except for age ** expand this later on.
display('Confidence Intervals')
alphalow = chi2inv(0.05,1);
alphahi = chi2inv(0.95,1);
varZ = zeros(rnum,1);
LCI = zeros(cnt1,rnum);
CI = zeros(cnt1,rnum);
UCI = zeros(cnt1,rnum);

Zscoreneg = CI;
Zscorepos = CI;



UCII = zeros(rnum,1);
LCII = UCII;
```

```
calcvarZ = zeros(rnum,1);
counter = calcvarZ;

delta = zeros(rnum,2);
alpha = 0.05;

for j = 1:rnum
   delta(j,1) = -2*log(ahatl(j,1));
   probdelta = chi2cdf(delta(j,1),3);
   if probdelta < alpha
      delta(j,2) = 1;
   else
      if probdelta > 1-alpha
         delta(j,2) = 1;
      end;
   end;
end;

for j = 1:rnum
   display(j);
   likelihood = predplot(:,j);
   likelihood = double(likelihood);
   for i = 1:cnt1
      interm=likelihood(i,1)/ahatl(j,1);
      CI(i,j) = (-2*log(interm));
```

```
    Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
    Zscorepos(i,j) = sqrt(abs(CI(i,j)));
    calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
 end;
 counter(j,1)= (2*cnt1);
varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
for i = 1:cnt1
   interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
   CI(i,j) = real(-2*log(interm));
end;
 [lrow,~] = find(CI(:,j)>=alphalow);
 [lm,~] = size(lrow);
 for t = 1:lm
   lrownums = lrow(t,1);
   if lrownums==1
    LCI(t,j) = yy(lrownums,1);
   else
      LCI(t,j) = yy(lrownums-1,1);
   end;
 end;
 pe=results(j,1);
 if min(LCI(:,j)) > pe
    LCII(j,1)=min(Age);
 else
    [rows,cols] = find(0<LCI(:,j)<pe,1);
```

```
        LCII(j,1) = LCI(rows,j);
    end;
    results(j,2) = LCII(j,1);
    [urow,col] = find(CI(:,j)<= alphahi);
    [m,~] = size(urow);
%     for t = 1:m
%         rownums = urow(t,1);
%         if rownums==cnt1
%          UCI(t,j) = yy(rownums,1);
%         else
%             UCI(t,j) = yy(rownums+1,1);
%         end;
%     end;
    for t = 1:m
        rownums = urow(t,1);
        if rownums==cnt1
         UCI(t,j) = yy(rownums,1);
        else
            UCI(t,j) = yy(rownums,1);
        end;
    end;
%     for t = 1:m
%         rownums = urow(t,1);
%         UCI(t,j) = yy(rownums,1);
%     end;
```

```
    if max(UCI(:,j)) <= pe
        UCII(j,1)=max(yy);
    else
        [rows,cols] = find(UCI(:,j)>pe,1);
        UCII(j,1) = UCI(rows,j);
        %If rows == 0
          %UCII(j,1) = max(zz);
    end;
    results(j,3) = UCII(j,1);
end;

%% End of Program Transition_Analysis_eq42
```

```
%% Program Transition_Analysis_PS

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\PS Fit Data - Males.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
Age = data(:,1);
```

```
V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);

V5 = data(:,6);

V6 = data(:,7);

V7 = data(:,8);

V8 = data(:,9);

V9 = data(:,10);

V10 = data(:,11);

V11 = data(:,12);

V12 = data(:,13);

V13 = data(:,14);

V14 = data(:,15);

V15 = data(:,16);

V16 = data(:,17);

V17 = data(:,18);

V18 = data(:,19);

V19 = data(:,20);

V20 = data(:,21);

V21 = data(:,22);

V22 = data(:,23);

V23 = data(:,24);

V24 = data(:,25);

%%xx = linspace(0,100)';
```

```
%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';

[cnt1,~] = size(xx);

%%display(yy);



%% V1 CR Model

[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C1 = zeros(cnt1,2);


%% Calculate probabilities for V1



PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A1 = PROB1;


for i = 1:cnt1

C1(i,1) = A1(i,1);

C1(i,2) = 1-A1(i,1);

end;
```

```
%% V2 CR Model

[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C2 = zeros(cnt1,2);


%% Calculate probabilities for V2



PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A2 = PROB2;


for i = 1:cnt1

C2(i,1) = A2(i,1);

C2(i,2) = 1-A2(i,1);

end;


%% V3 CR Model

[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C3 = zeros(cnt1,2);
```

```
%% Calculate probabilities for V3


PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;


for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = 1-A3(i,1);

end;


%% V4 CR Model

[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);


%% Calculate probabilities for V4


PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A4 = PROB4;


for i = 1:cnt1
```

```
C4(i,1) = A4(i,1);

C4(i,2) = 1-A4(i,1);

end;



%% V5 CR Model

[fitV5,~,~] = mnrfit(Age,V5,'model','hierarchical','link','logit','interactions','on');


%A2 = zeros(r,3);

C5 = zeros(cnt1,4);


%% Calculate probabilities for V5



PROB5 = mnrval(fitV5,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A5 = PROB5;


for i = 1:cnt1

C5(i,1) = A5(i,1);

C5(i,2) = A5(i,2)-A5(i,1);

C5(i,3) = A5(i,3)-A5(i,2);

C5(i,4) = 1-A5(i,3);

end;
```

```
%% V6 CR Model

[fitV6,~,~] = mnrfit(Age,V6,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C6 = zeros(cnt1,2);


%% Calculate probabilities for V6



PROB6 = mnrval(fitV6,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A6 = PROB6;


for i = 1:cnt1

C6(i,1) = A6(i,1);

C6(i,2) = 1-A6(i,1);

end;


%% V7 CR Model

V7 = V7 -1;

[fitV7,~,~] = mnrfit(Age,V7,'model','hierarchical','link','logit','interactions','on');


%A3 = zeros(r,3);

C7 = zeros(cnt1,4);
```

```
%% Calculate probabilities for V7


PROB7 = mnrval(fitV7,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A7 = PROB7;


for i = 1:cnt1

C7(i,1) = A7(i,1);

C7(i,2) = A7(i,2)-A7(i,1);

%C7(i,3) = A7(i,3)-A7(i,2);

C7(i,3) = 1-A7(i,2);

end;


%% V8 CR Model

V8 = V8 -1;

[fitV8,~,~] = mnrfit(Age,V8,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C8 = zeros(cnt1,5);


%% Calculate probabilities for V8


PROB8 = mnrval(fitV8,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
```

```
A8 = PROB8;


for i = 1:cnt1
C8(i,1) = A8(i,1);
C8(i,2) = A8(i,2)-A8(i,1);
C8(i,3) = A8(i,3)-A8(i,2);
%C8(i,4) = A8(i,4)-A8(i,3);
C8(i,4) = 1-A8(i,3);


end;


%% V9 CR Model
[fitV9,~,~] = mnrfit(Age,V9,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);
C9 = zeros(cnt1,3);


%% Calculate probabilities for V9



PROB9 = mnrval(fitV9,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A9 = PROB9;


for i = 1:cnt1
```

```
C9(i,1) = A9(i,1);

C9(i,2) = A9(i,2)-A9(i,1);

C9(i,3) = 1-A9(i,2);

end;


%% V10 CR Model

[fitV10,~,~] = mnrfit(Age,V10,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C10 = zeros(cnt1,4);


%% Calculate probabilities for V10



PROB10 = mnrval(fitV10,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A10 = PROB10;


for i = 1:cnt1

C10(i,1) = A10(i,1);

C10(i,2) = A10(i,2)-A10(i,1);

C10(i,3) = A10(i,3)-A10(i,2);

C10(i,4) = 1-A10(i,3);

end;
```

```
%% V11 CR Model

V11 = V11-1;

[fitV11,~,~] = mnrfit(Age,V11,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C11 = zeros(cnt1,5);


%% Calculate probabilities for V11


PROB11 = mnrval(fitV11,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A11 = PROB11;


for i = 1:cnt1

C11(i,1) = A11(i,1);

C11(i,2) = A11(i,2)-A11(i,1);

C11(i,3) = A11(i,3)-A11(i,2);

%C11(i,4) = A11(i,4)-A11(i,3);

C11(i,4) = 1-A11(i,3);


end;


%% V12 CR Model
```

```
V12 = V12-1;

[fitV12,~,~] = mnrfit(Age,V12,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C12 = zeros(cnt1,4);


%% Calculate probabilities for V12



PROB12 = mnrval(fitV12,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A12 = PROB12;


for i = 1:cnt1

C12(i,1) = A12(i,1);

C12(i,2) = A12(i,2)-A12(i,1);

%C12(i,3) = A12(i,3)-A12(i,2);

C12(i,3) = 1-A12(i,2);

end;



%% V13 CR Model

[fitV13,~,~] = mnrfit(Age,V13,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);
```

```
C13 = zeros(cnt1,3);

%% Calculate probabilities for V13

PROB13 = mnrval(fitV13,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A13 = PROB13;

for i = 1:cnt1

C13(i,1) = A13(i,1);

C13(i,2) = A13(i,2)-A13(i,1);

C13(i,3) = 1-A13(i,2);

end;

%% V14 CR Model

V14 = V14-1;

[fitV14,~,~] = mnrfit(Age,V14,'model','hierarchical','link','logit','interactions','on');

%A6 = zeros(r,3);

C14 = zeros(cnt1,4);

%% Calculate probabilities for V14
```

```
PROB14 = mnrval(fitV14,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A14 = PROB14;


for i = 1:cnt1

C14(i,1) = A14(i,1);

C14(i,2) = A14(i,2)-A14(i,1);

%C14(i,3) = A14(i,3)-A14(i,2);

C14(i,3) = 1-A14(i,2);

end;



%% V15 CR Model

[fitV15,~,~] = mnrfit(Age,V15,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);

C15 = zeros(cnt1,3);


%% Calculate probabilities for V15



PROB15 = mnrval(fitV15,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A15 = PROB15;
```

```
for i = 1:cnt1

C15(i,1) = A15(i,1);

C15(i,2) = A15(i,2)-A15(i,1);

C15(i,3) = 1-A15(i,2);

end;


%% V16 CR Model

[fitV16,~,~] = mnrfit(Age,V16,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C16 = zeros(cnt1,4);


%% Calculate probabilities for V16



PROB16 = mnrval(fitV16,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A16 = PROB16;


for i = 1:cnt1

C16(i,1) = A16(i,1);

C16(i,2) = A16(i,2)-A16(i,1);

C16(i,3) = A16(i,3)-A16(i,2);

C16(i,4) = 1-A16(i,3);

end;
```

```
%% V17 CR Model

[fitV17,~,~] = mnrfit(Age,V17,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C17 = zeros(cnt1,2);


%% Calculate probabilities for V17



PROB17 = mnrval(fitV17,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A17 = PROB17;


for i = 1:cnt1

C17(i,1) = A17(i,1);

C17(i,2) = 1-A17(i,1);

end;



%% V18 CR Model

[fitV18,~,~] = mnrfit(Age,V18,'model','hierarchical','link','logit','interactions','on');
```

```
%A = zeros(r,3);

C18 = zeros(cnt1,2);


%% Calculate probabilities for V18



PROB18 = mnrval(fitV18,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A18 = PROB18;


for i = 1:cnt1

C18(i,1) = A18(i,1);

C18(i,2) = 1-A18(i,1);

end;



%% V19 CR Model

[fitV19,~,~] = mnrfit(Age,V19,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C19 = zeros(cnt1,2);


%% Calculate probabilities for V19
```

```
PROB19 = mnrval(fitV19,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A19 = PROB19;


for i = 1:cnt1

C19(i,1) = A19(i,1);

C19(i,2) = 1-A19(i,1);

end;



%% V20 CR Model

[fitV20,~,~] = mnrfit(Age,V20,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C20 = zeros(cnt1,5);


%% Calculate probabilities for V20



PROB20 = mnrval(fitV20,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A20 = PROB20;


for i = 1:cnt1

C20(i,1) = A20(i,1);

C20(i,2) = A20(i,2)-A20(i,1);
```

```
C20(i,3) = A20(i,3)-A20(i,2);

C20(i,4) = A20(i,4)-A20(i,3);

C20(i,5) = 1-A20(i,4);


end;



%% V21 CR Model

[fitV21,~,~] = mnrfit(Age,V21,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C21 = zeros(cnt1,5);


%% Calculate probabilities for V21



PROB21 = mnrval(fitV21,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A21 = PROB21;


for i = 1:cnt1

C21(i,1) = A21(i,1);

C21(i,2) = A21(i,2)-A21(i,1);

C21(i,3) = A21(i,3)-A21(i,2);

C21(i,4) = A21(i,4)-A21(i,3);
```

```
C21(i,5) = 1-A21(i,4);

end;


%% V22 CR Model
[fitV22,~,~] = mnrfit(Age,V22,'model','hierarchical','link','logit','interactions','on');

%A4 = zeros(r,3);
C22 = zeros(cnt1,4);

%% Calculate probabilities for V22


PROB22 = mnrval(fitV22,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A22 = PROB22;

for i = 1:cnt1
C22(i,1) = A22(i,1);
C22(i,2) = A22(i,2)-A22(i,1);
C22(i,3) = A22(i,3)-A22(i,2);
C22(i,4) = 1-A22(i,3);

end;
```

```
%% V23 CR Model

[fitV23,~,~] = mnrfit(Age,V23,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C23 = zeros(cnt1,4);


%% Calculate probabilities for V23



PROB23 = mnrval(fitV23,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A23 = PROB23;


for i = 1:cnt1

C22(i,1) = A23(i,1);

C22(i,2) = A23(i,2)-A23(i,1);

C22(i,3) = A23(i,3)-A23(i,2);

C22(i,4) = 1-A23(i,3);


end;



%% V24 CR Model
```

```
[fitV24,~,~] = mnrfit(Age,V24,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C24 = zeros(cnt1,4);


%% Calculate probabilities for V24



PROB24 = mnrval(fitV24,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A24 = PROB24;


for i = 1:cnt1

C24(i,1) = A24(i,1);

C24(i,2) = A24(i,2)-A24(i,1);

C24(i,3) = A24(i,3)-A24(i,2);

C24(i,4) = 1-A24(i,3);


end;



%% Calculate general probability expressions

syms a;


pi1(1,1) = (exp(fitV1(1,1)+fitV1(2,1)*a))/(1+exp(fitV1(1,1)+fitV1(2,1)*a));
```

```
pi1(2,1) = 1 - pi1(1,1);



pi2(1,1) = (exp(fitV2(1,1)+fitV2(2,1)*a))/(1+exp(fitV2(1,1)+fitV2(2,1)*a));
pi2(2,1) = 1 - pi2(1,1);

pi3(1,1) = (exp(fitV3(1,1)+fitV3(2,1)*a))/(1+exp(fitV3(1,1)+fitV3(2,1)*a));
pi3(2,1) = 1 - pi3(1,1);

pi4(1,1) = (exp(fitV4(1,1)+fitV4(2,1)*a))/(1+exp(fitV4(1,1)+fitV4(2,1)*a));
pi4(2,1) = 1 - pi4(1,1);

pi5(1,1) = (exp(fitV5(1,1)+fitV5(2,1)*a))/(1+exp(fitV5(1,1)+fitV5(2,1)*a));
for i = 2:3
    pi5(i,1) = (exp(fitV5(1,i)+fitV5(2,i)*a))/(1+exp(fitV5(1,i)+fitV5(2,i)*a))-pi5(i-1,1);
end;
pi5(4,1) = 1 - pi5(3,1);

pi6(1,1) = (exp(fitV6(1,1)+fitV6(2,1)*a))/(1+exp(fitV6(1,1)+fitV6(2,1)*a));
pi6(2,1) = 1 - pi6(1,1);

pi7(1,1) = (exp(fitV7(1,1)+fitV7(2,1)*a))/(1+exp(fitV7(1,1)+fitV7(2,1)*a));
pi7(2,1) = (exp(fitV7(1,2)+fitV7(2,2)*a))/(1+exp(fitV7(1,2)+fitV7(2,2)*a))-pi7(2-1,1);
pi7(3,1) = 1 - pi7(2,1);
```

```
pi8(1,1) = (exp(fitV8(1,1)+fitV8(2,1)*a))/(1+exp(fitV8(1,1)+fitV8(2,1)*a));
for i = 2:3
   pi8(i,1) = (exp(fitV8(1,i)+fitV8(2,i)*a))/(1+exp(fitV8(1,i)+fitV8(2,i)*a))-pi8(i-1,1);
end;
pi8(4,1) = 1 - pi8(3,1);

pi9(1,1) = (exp(fitV9(1,1)+fitV9(2,1)*a))/(1+exp(fitV9(1,1)+fitV9(2,1)*a));
pi9(2,1) = (exp(fitV9(1,2)+fitV9(2,2)*a))/(1+exp(fitV9(1,2)+fitV9(2,2)*a))-pi9(2-1,1);
pi9(3,1) = 1 - pi9(2,1);

pi10(1,1) = (exp(fitV10(1,1)+fitV10(2,1)*a))/(1+exp(fitV10(1,1)+fitV10(2,1)*a));
for i = 2:3
   pi10(i,1) = (exp(fitV10(1,i)+fitV10(2,i)*a))/(1+exp(fitV10(1,i)+fitV10(2,i)*a))-pi10(i-
1,1);
end;
pi10(4,1) = 1 - pi10(3,1);

pi11(1,1) = (exp(fitV11(1,1)+fitV11(2,1)*a))/(1+exp(fitV11(1,1)+fitV11(2,1)*a));
for i = 2:3
   pi11(i,1) = (exp(fitV11(1,i)+fitV11(2,i)*a))/(1+exp(fitV11(1,i)+fitV11(2,i)*a))-pi11(i-
1,1);
end;
pi11(4,1) = 1 - pi11(3,1);

pi12(1,1) = (exp(fitV12(1,1)+fitV12(2,1)*a))/(1+exp(fitV12(1,1)+fitV12(2,1)*a));
```

```
pi12(2,1) = (exp(fitV12(1,2)+fitV12(2,2)*a))/(1+exp(fitV12(1,2)+fitV12(2,2)*a))-pi12(2-1,1);

pi12(3,1) = 1 - pi12(2,1);


pi13(1,1) = (exp(fitV13(1,1)+fitV13(2,1)*a))/(1+exp(fitV13(1,1)+fitV13(2,1)*a));

pi13(2,1) = (exp(fitV13(1,2)+fitV13(2,2)*a))/(1+exp(fitV13(1,2)+fitV13(2,2)*a))-pi13(2-1,1);

pi13(3,1) = 1 - pi13(2,1);



pi14(1,1) = (exp(fitV14(1,1)+fitV14(2,1)*a))/(1+exp(fitV14(1,1)+fitV14(2,1)*a));

pi14(2,1) = (exp(fitV14(1,2)+fitV14(2,2)*a))/(1+exp(fitV14(1,2)+fitV14(2,2)*a))-pi14(2-1,1);

pi14(3,1) = 1 - pi14(2,1);


pi15(1,1) = (exp(fitV15(1,1)+fitV15(2,1)*a))/(1+exp(fitV15(1,1)+fitV15(2,1)*a));

pi15(2,1) = (exp(fitV15(1,2)+fitV15(2,2)*a))/(1+exp(fitV15(1,2)+fitV15(2,2)*a))-pi15(2-1,1);

pi15(3,1) = 1 - pi15(2,1);


pi16(1,1) = (exp(fitV16(1,1)+fitV16(2,1)*a))/(1+exp(fitV16(1,1)+fitV16(2,1)*a));

for i = 2:3

   pi16(i,1) = (exp(fitV16(1,i)+fitV16(2,i)*a))/(1+exp(fitV16(1,i)+fitV16(2,i)*a))-pi16(i-1,1);

end;

pi16(4,1) = 1 - pi16(3,1);
```

```
pi17(1,1) = (exp(fitV17(1,1)+fitV17(2,1)*a))/(1+exp(fitV17(1,1)+fitV17(2,1)*a));
pi17(2,1) = 1 - pi17(1,1);

pi18(1,1) = (exp(fitV18(1,1)+fitV18(2,1)*a))/(1+exp(fitV18(1,1)+fitV18(2,1)*a));
pi18(2,1) = 1 - pi18(1,1);

pi19(1,1) = (exp(fitV19(1,1)+fitV19(2,1)*a))/(1+exp(fitV19(1,1)+fitV19(2,1)*a));
pi19(2,1) = 1 - pi19(1,1);


pi20(1,1) = (exp(fitV20(1,1)+fitV20(2,1)*a))/(1+exp(fitV20(1,1)+fitV20(2,1)*a));
for i = 2:4
    pi20(i,1) = (exp(fitV20(1,i)+fitV20(2,i)*a))/(1+exp(fitV20(1,i)+fitV20(2,i)*a))-pi20(i-
1,1);
end;
pi20(5,1) = 1 - pi20(4,1);

pi21(1,1) = (exp(fitV21(1,1)+fitV21(2,1)*a))/(1+exp(fitV21(1,1)+fitV21(2,1)*a));
for i = 2:4
    pi21(i,1) = (exp(fitV21(1,i)+fitV21(2,i)*a))/(1+exp(fitV21(1,i)+fitV21(2,i)*a))-pi21(i-
1,1);
end;
pi21(5,1) = 1 - pi21(4,1);

pi22(1,1) = (exp(fitV22(1,1)+fitV22(2,1)*a))/(1+exp(fitV22(1,1)+fitV22(2,1)*a));
for i = 2:3
```

```
    pi22(i,1) = (exp(fitV22(1,i)+fitV22(2,i)*a))/(1+exp(fitV22(1,i)+fitV22(2,i)*a))-pi22(i-
1,1);

end;

pi22(4,1) = 1 - pi22(3,1);


pi23(1,1) = (exp(fitV23(1,1)+fitV23(2,1)*a))/(1+exp(fitV23(1,1)+fitV23(2,1)*a));

for i = 2:3

    pi23(i,1) = (exp(fitV23(1,i)+fitV23(2,i)*a))/(1+exp(fitV23(1,i)+fitV23(2,i)*a))-pi23(i-
1,1);

end;

pi23(4,1) = 1 - pi23(3,1);


pi24(1,1) = (exp(fitV24(1,1)+fitV24(2,1)*a))/(1+exp(fitV24(1,1)+fitV24(2,1)*a));

for i = 2:3

    pi24(i,1) = (exp(fitV24(1,i)+fitV24(2,i)*a))/(1+exp(fitV24(1,i)+fitV24(2,i)*a))-pi24(i-
1,1);

end;

pi24(4,1) = 1 - pi24(3,1);




%% Import prediction data yourself


%% Prediction


%G = [1,2,3,4];
```

```
%Predict = [2 4 3 2 3 4];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\PS Test Data - Males.csv');
%%Predict = PredictAll;
[rnum,cnum] = size(Predict);
fpred = sym('fpred',[rnum,1]);


display('Predictions')
for j = 1:rnum
   display(j);
   k = Predict(j,1);
   if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;
   l = Predict(j,2);
   if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;
   m = Predict(j,3);
   if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;
   n = Predict(j,4);
   if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;
   o = Predict(j,5);
   if (o == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi5(o,1); endif;
   p = Predict(j,6);
   if (p == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi6(p,1); endif;
   q = Predict(j,7);
   if (q == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi7(q,1); endif;
```

```
r = Predict(j,8);
if (r == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi8(r,1); endif;
s = Predict(j,9);
if (s == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi9(s,1); endif;
t = Predict(j,10);
if (t == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi10(t,1); endif;
u = Predict(j,11);
if (u == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi11(u,1); endif;
v = Predict(j,12);
if (v == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi12(v,1); endif;
w = Predict(j,13);
if (w == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi13(w,1); endif;
x = Predict(j,14);
if (x == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi14(x,1); endif;
y = Predict(j,15);
if (y == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi15(y,1); endif;
z = Predict(j,16);
if (z == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi16(z,1); endif;
a = Predict(j,17);
if (a == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi17(a,1); endif;
b = Predict(j,18);
if (b == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi18(b,1); endif;
c = Predict(j,19);
if (c == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi19(c,1); endif;
d = Predict(j,20);
```

```
    if (d == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi20(d,1); endif;
    e = Predict(j,21);
    if (e == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi21(e,1); endif;
    f = Predict(j,22);
    if (f == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi22(f,1); endif;
    g = Predict(j,23);
    if (g == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi23(g,1); endif;
    h = Predict(j,24);
    if (h == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi24(h,1); endif;
end;



zz = 20:98;
display('Predplot');
predplot = vpa(zeros(cnt1,rnum),10);
predplot = double(predplot);
  for j = 1:rnum
      display(j);
      FUN = matlabFunction(fpred(j,1));
      predplot(:,j) = feval(FUN,zz);
    end;

    pplot = double(predplot);

%% Determine max likelihood point estimate for all combinations:
```

```
ahat = zeros(rnum,1);
ahatl = ahat;
results = zeros(rnum,3);



display('Point estimates')
for j = 1:rnum
    display(j);
 likelihood = predplot(:,j);
 likelihood = double(likelihood);
 maxprob = max(likelihood);
 [row,col] = find(likelihood==maxprob);
 ahat(j,1) = yy(row,1); % these are the point estimates
 ahatl(j,1) = maxprob;
 results(j,1) = ahat(j,1);
end;

% %% Confidence Intervals
% % We assume conditional independence, i.e. there are no correlations
% % between traits except for age ** expand this later on.
display('Confidence Intervals')
alphalow = chi2inv(0.05,1);
alphahi = chi2inv(0.95,1);
varZ = zeros(rnum,1);
```

```
LCI = zeros(cnt1,rnum);

CI = zeros(cnt1,rnum);

UCI = zeros(cnt1,rnum);


Zscoreneg = CI;

Zscorepos = CI;



UCII = zeros(rnum,1);

LCII = UCII;

calcvarZ = zeros(rnum,1);

counter = calcvarZ;


delta = zeros(rnum,2);

alpha = 0.05;


for j = 1:rnum

   delta(j,1) = -2*log(ahatl(j,1));

   probdelta = chi2cdf(delta(j,1),3);

   if probdelta < alpha

      delta(j,2) = 1;

   else

      if probdelta > 1-alpha

         delta(j,2) = 1;

      end;
```

```
    end;
end;


for j = 1:rnum
    display(j);
    likelihood = predplot(:,j);
    likelihood = double(likelihood);
    for i = 1:cnt1
        interm=likelihood(i,1)/ahatl(j,1);
        CI(i,j) = (-2*log(interm));
        Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
        Zscorepos(i,j) = sqrt(abs(CI(i,j)));
        calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
    end;
    counter(j,1)= (2*cnt1);
   varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
   for i = 1:cnt1
       interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
       CI(i,j) = real(-2*log(interm));
   end;
    [lrow,~] = find(CI(:,j)>=alphalow);
    [lm,~] = size(lrow);
    for t = 1:lm
       lrownums = lrow(t,1);
       if lrownums==1
```

```
        LCI(t,j) = yy(lrownums,1);
      else
         LCI(t,j) = yy(lrownums-1,1);
      end;
   end;
   pe=results(j,1);
   if min(LCI(:,j)) > pe
      LCII(j,1)=min(Age);
   else
      [rows,cols] = find(0<LCI(:,j)<pe,1);
      LCII(j,1) = LCI(rows,j);
   end;
   results(j,2) = LCII(j,1);
   [urow,col] = find(CI(:,j)<= alphahi);
   [m,~] = size(urow);
%    for t = 1:m
%       rownums = urow(t,1);
%       if rownums==cnt1
%        UCI(t,j) = yy(rownums,1);
%       else
%          UCI(t,j) = yy(rownums+1,1);
%       end;
%    end;
   for t = 1:m
      rownums = urow(t,1);
```

```
      if rownums==cnt1
       UCI(t,j) = yy(rownums,1);
      else
         UCI(t,j) = yy(rownums,1);
      end;
   end;
%    for t = 1:m
%       rownums = urow(t,1);
%       UCI(t,j) = yy(rownums,1);
%    end;
   if max(UCI(:,j)) <= pe
      UCII(j,1)=max(yy);
   else
      [rows,cols] = find(UCI(:,j)>pe,1);
      UCII(j,1) = UCI(rows,j);
      If rows = 0
        UCII(j,1) = max(zz);
   end;
   results(j,3) = UCII(j,1);
end;

%% End of Program Transition_Analysis_PS
```

```
%% Program Transition_Analysis_SB

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\SB Fit Data - Males.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
Age = data(:,1);
```

```
V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);

V5 = data(:,6);

V6 = data(:,7);

V7 = data(:,8);

V8 = data(:,9);

V9 = data(:,10);

V10 = data(:,11);

V11 = data(:,12);

V12 = data(:,13);

V13 = data(:,14);

V14 = data(:,15);

V15 = data(:,16);

V16 = data(:,17);

V17 = data(:,18);

V18 = data(:,19);

V19 = data(:,20);

V20 = data(:,21);

%%xx = linspace(0,100)';

%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';
```

```
[cnt1,~] = size(xx);


%% V1 CR Model
[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');

%A1 = zeros(r,3);
C1 = zeros(cnt1,2);

%% Calculate probabilities for V1


PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A1 = PROB1;

for i = 1:cnt1
C1(i,1) = A1(i,1);
C1(i,2) = 1-A1(i,1);
end;

%% V2 CR Model
[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');

%A1 = zeros(r,3);
```

```
C2 = zeros(cnt1,2);

%% Calculate probabilities for V2


PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A2 = PROB2;


for i = 1:cnt1

C2(i,1) = A2(i,1);

C2(i,2) = 1-A2(i,1);

end;


%% V3 CR Model

[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C3 = zeros(cnt1,2);


%% Calculate probabilities for V3


PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;
```

```
for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = 1-A3(i,1);

end;


%% V4 CR Model

[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);


%% Calculate probabilities for V4



PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A4 = PROB4;


for i = 1:cnt1

C4(i,1) = A4(i,1);

C4(i,2) = 1-A4(i,1);

end;
```

```
%% V5 CR Model

[fitV5,~,~] = mnrfit(Age,V5,'model','hierarchical','link','logit','interactions','on');


%A2 = zeros(r,3);

C5 = zeros(cnt1,4);


%% Calculate probabilities for V5



PROB5 = mnrval(fitV5,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A5 = PROB5;


for i = 1:cnt1

C5(i,1) = A5(i,1);

C5(i,2) = A5(i,2)-A5(i,1);

C5(i,3) = A5(i,3)-A5(i,2);

C5(i,4) = 1-A5(i,3);

end;


%% V6 CR Model

[fitV6,~,~] = mnrfit(Age,V6,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C6 = zeros(cnt1,2);
```

```
%% Calculate probabilities for V6


PROB6 = mnrval(fitV6,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A6 = PROB6;


for i = 1:cnt1

C6(i,1) = A6(i,1);

C6(i,2) = 1-A6(i,1);

end;


%% V7 CR Model

V7 = V7 -1;

[fitV7,~,~] = mnrfit(Age,V7,'model','hierarchical','link','logit','interactions','on');


%A3 = zeros(r,3);

C7 = zeros(cnt1,3);


%% Calculate probabilities for V7


PROB7 = mnrval(fitV7,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A7 = PROB7;
```

```
for i = 1:cnt1

C7(i,1) = A7(i,1);

C7(i,2) = A7(i,2)-A7(i,1);

C7(i,3) = 1-A7(i,2);

end;


%% V8 CR Model

V8 = V8 -1;

[fitV8,~,~] = mnrfit(Age,V8,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C8 = zeros(cnt1,5);


%% Calculate probabilities for V8



PROB8 = mnrval(fitV8,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A8 = PROB8;


for i = 1:cnt1

C8(i,1) = A8(i,1);

C8(i,2) = A8(i,2)-A8(i,1);

C8(i,3) = A8(i,3)-A8(i,2);
```

```
C8(i,4) = A8(i,4)-A8(i,3);

C8(i,5) = 1-A8(i,4);


end;


%% V9 CR Model

[fitV9,~,~] = mnrfit(Age,V9,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);

C9 = zeros(cnt1,3);


%% Calculate probabilities for V9



PROB9 = mnrval(fitV9,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A9 = PROB9;


for i = 1:cnt1

C9(i,1) = A9(i,1);

C9(i,2) = A9(i,2)-A9(i,1);

C9(i,3) = 1-A9(i,2);

end;


%% V10 CR Model
```

```
V10 = V10 -1;

[fitV10,~,~] = mnrfit(Age,V10,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C10 = zeros(cnt1,3);


%% Calculate probabilities for V10



PROB10 = mnrval(fitV10,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A10 = PROB10;


for i = 1:cnt1

C10(i,1) = A10(i,1);

C10(i,2) = A10(i,2)-A10(i,1);

C10(i,3) = 1-A10(i,2);

end;



%% V11 CR Model

[fitV11,~,~] = mnrfit(Age,V11,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C11 = zeros(cnt1,3);
```

```
%% Calculate probabilities for V11


PROB11 = mnrval(fitV11,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A11 = PROB11;


for i = 1:cnt1

C11(i,1) = A11(i,1);

C11(i,2) = A11(i,2)-A11(i,1);

C11(i,3) = 1-A11(i,2);

end;


%% V12 CR Model

%V12 = V12-1;

[fitV12,~,~] = mnrfit(Age,V12,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C12 = zeros(cnt1,4);


%% Calculate probabilities for V12


PROB12 = mnrval(fitV12,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
```

```
A12 = PROB12;


for i = 1:cnt1
C12(i,1) = A12(i,1);
C12(i,2) = A12(i,2)-A12(i,1);
C12(i,3) = A12(i,3)-A12(i,2);
C12(i,4) = 1-A12(i,3);
end;



%% V13 CR Model
[fitV13,~,~] = mnrfit(Age,V13,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);
C13 = zeros(cnt1,2);


%% Calculate probabilities for V13



PROB13 = mnrval(fitV13,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A13 = PROB13;


for i = 1:cnt1
C13(i,1) = A13(i,1);
```

```
C13(i,2) = 1-A13(i,1);

end;



%% V14 CR Model

%V14 = V14-1;

[fitV14,~,~] = mnrfit(Age,V14,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C14 = zeros(cnt1,2);


%% Calculate probabilities for V14



PROB14 = mnrval(fitV14,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A14 = PROB14;


for i = 1:cnt1

C14(i,1) = A14(i,1);

C14(i,2) = 1-A14(i,1);

end;



%% V15 CR Model
```

```
[fitV15,~,~] = mnrfit(Age,V15,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);

C15 = zeros(cnt1,3);


%% Calculate probabilities for V15



PROB15 = mnrval(fitV15,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A15 = PROB15;


for i = 1:cnt1

C15(i,1) = A15(i,1);

C15(i,2) = 1-A15(i,1);

end;


%% V16 CR Model

[fitV16,~,~] = mnrfit(Age,V16,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C16 = zeros(cnt1,5);


%% Calculate probabilities for V16
```

```
PROB16 = mnrval(fitV16,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A16 = PROB16;


for i = 1:cnt1

C16(i,1) = A16(i,1);

C16(i,2) = A16(i,2)-A16(i,1);

C16(i,3) = A16(i,3)-A16(i,2);

C16(i,4) = A16(i,3)-A16(i,3);

C16(i,5) = 1-A16(i,4);

end;



%% V17 CR Model

[fitV17,~,~] = mnrfit(Age,V17,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C17 = zeros(cnt1,5);


%% Calculate probabilities for V17



PROB17 = mnrval(fitV17,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A17 = PROB17;
```

```
for i = 1:cnt1

C17(i,1) = A17(i,1);

C17(i,2) = A17(i,2)-A17(i,1);

C17(i,3) = A17(i,3)-A17(i,2);

C17(i,4) = A17(i,4)-A17(i,3);

C17(i,5) = 1-A17(i,4);

end;




%% V18 CR Model

[fitV18,~,~] = mnrfit(Age,V18,'model','hierarchical','link','logit','interactions','on');


%A = zeros(r,3);

C18 = zeros(cnt1,4);


%% Calculate probabilities for V18



PROB18 = mnrval(fitV18,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A18 = PROB18;


for i = 1:cnt1
```

```
C18(i,1) = A18(i,1);

C18(i,2) = A18(i,2)-A18(i,1);

C18(i,3) = A18(i,3)-A18(i,2);

C18(i,4) = 1-A18(i,3);

end;



%% V19 CR Model

[fitV19,~,~] = mnrfit(Age,V19,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C19 = zeros(cnt1,4);


%% Calculate probabilities for V19



PROB19 = mnrval(fitV19,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A19 = PROB19;


for i = 1:cnt1

C19(i,1) = A19(i,1);

C19(i,2) = A19(i,2)-A19(i,1);

C19(i,3) = A19(i,3)-A19(i,2);

C19(i,4) = 1-A19(i,3);
```

```
end;


%% V20 CR Model
[fitV20,~,~] = mnrfit(Age,V20,'model','hierarchical','link','logit','interactions','on');

%A4 = zeros(r,3);
C20 = zeros(cnt1,4);

%% Calculate probabilities for V20


PROB20 = mnrval(fitV20,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A20 = PROB20;

for i = 1:cnt1
C20(i,1) = A20(i,1);
C20(i,2) = A20(i,2)-A20(i,1);
C20(i,3) = A20(i,3)-A20(i,2);
%C20(i,4) = A20(i,4)-A20(i,3);
C20(i,4) = 1-A20(i,3);

end;
```

```
%% Calculate general probability expressions
syms a;

pi1(1,1) = (exp(fitV1(1,1)+fitV1(2,1)*a))/(1+exp(fitV1(1,1)+fitV1(2,1)*a));
pi1(2,1) = 1 - pi1(1,1);


pi2(1,1) = (exp(fitV2(1,1)+fitV2(2,1)*a))/(1+exp(fitV2(1,1)+fitV2(2,1)*a));
pi2(2,1) = 1 - pi2(1,1);

pi3(1,1) = (exp(fitV3(1,1)+fitV3(2,1)*a))/(1+exp(fitV3(1,1)+fitV3(2,1)*a));
pi3(2,1) = 1 - pi3(1,1);

pi4(1,1) = (exp(fitV4(1,1)+fitV4(2,1)*a))/(1+exp(fitV4(1,1)+fitV4(2,1)*a));
pi4(2,1) = 1 - pi4(1,1);

pi5(1,1) = (exp(fitV5(1,1)+fitV5(2,1)*a))/(1+exp(fitV5(1,1)+fitV5(2,1)*a));
for i = 2:3
    pi5(i,1) = (exp(fitV5(1,i)+fitV5(2,i)*a))/(1+exp(fitV5(1,i)+fitV5(2,i)*a))-pi5(i-1,1);
end;
pi5(4,1) = 1 - pi5(3,1);

pi6(1,1) = (exp(fitV6(1,1)+fitV6(2,1)*a))/(1+exp(fitV6(1,1)+fitV6(2,1)*a));
```

```
pi6(2,1) = 1 - pi6(1,1);

pi7(1,1) = (exp(fitV7(1,1)+fitV7(2,1)*a))/(1+exp(fitV7(1,1)+fitV7(2,1)*a));
pi7(2,1) = (exp(fitV7(1,2)+fitV7(2,2)*a))/(1+exp(fitV7(1,2)+fitV7(2,2)*a))-pi7(2-1,1);
pi7(3,1) = 1 - pi7(2,1);


pi8(1,1) = (exp(fitV8(1,1)+fitV8(2,1)*a))/(1+exp(fitV8(1,1)+fitV8(2,1)*a));
for i = 2:4
    pi8(i,1) = (exp(fitV8(1,i)+fitV8(2,i)*a))/(1+exp(fitV8(1,i)+fitV8(2,i)*a))-pi8(i-1,1);
end;
pi8(5,1) = 1 - pi8(4,1);

pi9(1,1) = (exp(fitV9(1,1)+fitV9(2,1)*a))/(1+exp(fitV9(1,1)+fitV9(2,1)*a));
pi9(2,1) = (exp(fitV9(1,2)+fitV9(2,2)*a))/(1+exp(fitV9(1,2)+fitV9(2,2)*a))-pi9(2-1,1);

pi9(3,1) = 1 - pi9(2,1);

pi10(1,1) = (exp(fitV10(1,1)+fitV10(2,1)*a))/(1+exp(fitV10(1,1)+fitV10(2,1)*a));
pi10(2,1) = (exp(fitV10(1,2)+fitV10(2,2)*a))/(1+exp(fitV10(1,2)+fitV10(2,2)*a))-pi10(2-
1,1);
pi10(3,1) = 1 - pi10(2,1);

pi11(1,1) = (exp(fitV11(1,1)+fitV11(2,1)*a))/(1+exp(fitV11(1,1)+fitV11(2,1)*a));
pi11(2,1) = (exp(fitV11(1,2)+fitV11(2,2)*a))/(1+exp(fitV11(1,2)+fitV11(2,2)*a))-pi11(2-
1,1);
```

```
pi11(3,1) = 1 - pi11(2,1);


pi12(1,1) = (exp(fitV12(1,1)+fitV12(2,1)*a))/(1+exp(fitV12(1,1)+fitV12(2,1)*a));
for i = 2:3
    pi12(i,1) = (exp(fitV12(1,i)+fitV12(2,i)*a))/(1+exp(fitV12(1,i)+fitV12(2,i)*a))-pi12(i-
1,1);
end;
pi12(4,1) = 1 - pi12(3,1);


pi13(1,1) = (exp(fitV13(1,1)+fitV13(2,1)*a))/(1+exp(fitV13(1,1)+fitV13(2,1)*a));
pi13(2,1) = 1 - pi13(1,1);



pi14(1,1) = (exp(fitV14(1,1)+fitV14(2,1)*a))/(1+exp(fitV14(1,1)+fitV14(2,1)*a));
pi14(2,1) = 1 - pi14(1,1);


pi15(1,1) = (exp(fitV15(1,1)+fitV15(2,1)*a))/(1+exp(fitV15(1,1)+fitV15(2,1)*a));
pi15(2,1) = 1 - pi15(1,1);


pi16(1,1) = (exp(fitV16(1,1)+fitV16(2,1)*a))/(1+exp(fitV16(1,1)+fitV16(2,1)*a));
for i = 2:4
    pi16(i,1) = (exp(fitV16(1,i)+fitV16(2,i)*a))/(1+exp(fitV16(1,i)+fitV16(2,i)*a))-pi16(i-
1,1);
end;
pi16(5,1) = 1 - pi16(4,1);
```

```
pi17(1,1) = (exp(fitV17(1,1)+fitV17(2,1)*a))/(1+exp(fitV17(1,1)+fitV17(2,1)*a));

for i = 2:4

   pi17(i,1) = (exp(fitV17(1,i)+fitV17(2,i)*a))/(1+exp(fitV17(1,i)+fitV17(2,i)*a))-pi17(i-
1,1);

end;

pi17(5,1) = 1 - pi17(4,1);


pi18(1,1) = (exp(fitV18(1,1)+fitV18(2,1)*a))/(1+exp(fitV18(1,1)+fitV18(2,1)*a));

for i = 2:3

   pi18(i,1) = (exp(fitV18(1,i)+fitV18(2,i)*a))/(1+exp(fitV18(1,i)+fitV18(2,i)*a))-pi18(i-
1,1);

end;

pi18(4,1) = 1 - pi18(3,1);


pi19(1,1) = (exp(fitV19(1,1)+fitV19(2,1)*a))/(1+exp(fitV19(1,1)+fitV19(2,1)*a));

for i = 2:3

   pi19(i,1) = (exp(fitV19(1,i)+fitV19(2,i)*a))/(1+exp(fitV19(1,i)+fitV19(2,i)*a))-pi19(i-
1,1);

end;

pi19(4,1) = 1 - pi19(3,1);



pi20(1,1) = (exp(fitV20(1,1)+fitV20(2,1)*a))/(1+exp(fitV20(1,1)+fitV20(2,1)*a));

for i = 2:4

   pi20(i,1) = (exp(fitV20(1,i)+fitV20(2,i)*a))/(1+exp(fitV20(1,i)+fitV20(2,i)*a))-pi20(i-
1,1);
```

```
end;
pi20(5,1) = 1 - pi20(4,1);




%% Import prediction data yourself


%% Prediction


%G = [1,2,3,4];
%Predict = [2 4 3 2 3 4];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\SB Test Data - Males.csv');
[rnum,cnum] = size(Predict);
fpred = sym('fpred',[rnum,1]);


display('Predictions')
for j = 1:rnum
   display(j);
   k = Predict(j,1);
   if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;
   l = Predict(j,2);
```

```
if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;
m = Predict(j,3);
if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;
n = Predict(j,4);
if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;
o = Predict(j,5);
if (o == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi5(o,1); endif;
p = Predict(j,6);
if (p == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi6(p,1); endif;
q = Predict(j,7);
if (q == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi7(q,1); endif;
r = Predict(j,8);
if (r == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi8(r,1); endif;
s = Predict(j,9);
if (s == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi9(s,1); endif;
t = Predict(j,10);
if (t == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi10(t,1); endif;
u = Predict(j,11);
if (u == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi11(u,1); endif;
v = Predict(j,12);
if (v == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi12(v,1); endif;
w = Predict(j,13);
if (w == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi13(w,1); endif;
x = Predict(j,14);
if (x == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi14(x,1); endif;
```

```
    y = Predict(j,15);
    if (y == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi15(y,1); endif;
    z = Predict(j,16);
    if (z == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi16(z,1); endif;
    a = Predict(j,17);
    if (a == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi17(a,1); endif;
    b = Predict(j,18);
    if (b == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi18(b,1); endif;
    c = Predict(j,19);
    if (c == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi19(c,1); endif;
    d = Predict(j,20);
    if (d == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi20(d,1); endif;
end;

display('Predplot');
predplot = vpa(zeros(cnt1,rnum),10);
%%predplot = double(predplot);
    for j = 1:rnum
        display(j);
        predplot(:,j) = subs(fpred(j,1),a,yy);
    end;

    pplot = double(predplot);

%% Determine max likelihood point estimate for all combinations:
```

```
ahat = zeros(rnum,1);

ahatl = ahat;

results = zeros(rnum,3);



display('Point estimates');

for j = 1:rnum

    display(j);

 likelihood = pplot(:,j);

 %likelihood = double(likelihood);

 maxprob = max(likelihood);

 [row,col] = find(likelihood==maxprob);

 ahat(j,1) = yy(row,1); % these are the point estimates

 ahatl(j,1) = maxprob;

 results(j,1) = ahat(j,1);

end;


% %% Confidence Intervals

% % We assume conditional independence, i.e. there are no correlations

% % between traits except for age ** expand this later on.

display('Confidence Intervals')

alphalow = chi2inv(0.05,1);

alphahi = chi2inv(0.95,1);

varZ = zeros(rnum,1);
```

```
LCI = zeros(cnt1,rnum);

CI = zeros(cnt1,rnum);

UCI = zeros(cnt1,rnum);


Zscoreneg = CI;

Zscorepos = CI;



UCII = zeros(rnum,1);

LCII = UCII;

calcvarZ = zeros(rnum,1);

counter = calcvarZ;


delta = zeros(rnum,2);

alpha = 0.05;


for j = 1:rnum
    delta(j,1) = -2*log(ahatl(j,1));
    probdelta = chi2cdf(delta(j,1),3);
    if probdelta < alpha
        delta(j,2) = 1;
    else
        if probdelta > 1-alpha
            delta(j,2) = 1;
        end;
```

```
    end;
end;


for j = 1:rnum
    display(j);
    likelihood = predplot(:,j);
    likelihood = double(likelihood);
    for i = 1:cnt1
        interm=likelihood(i,1)/ahatl(j,1);
        CI(i,j) = (-2*log(interm));
        Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
        Zscorepos(i,j) = sqrt(abs(CI(i,j)));
        calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
    end;
    counter(j,1)= (2*cnt1);
   varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
   for i = 1:cnt1
       interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
       CI(i,j) = real(-2*log(interm));
   end;
    [lrow,~] = find(CI(:,j)>=alphalow);
    [lm,~] = size(lrow);
    for t = 1:lm
       lrownums = lrow(t,1);
       if lrownums==1
```

```
        LCI(t,j) = yy(lrownums,1);
      else
         LCI(t,j) = yy(lrownums-1,1);
      end;
   end;
   pe=results(j,1);
   if min(LCI(:,j)) > pe
      LCII(j,1)=min(Age);
   else
      [rows,cols] = find(0<LCI(:,j)<pe,1);
      LCII(j,1) = LCI(rows,j);
   end;
   results(j,2) = LCII(j,1);
   [urow,col] = find(CI(:,j)<= alphahi);
   [m,~] = size(urow);
%    for t = 1:m
%       rownums = urow(t,1);
%       if rownums==cnt1
%        UCI(t,j) = yy(rownums,1);
%       else
%          UCI(t,j) = yy(rownums+1,1);
%       end;
%    end;
   for t = 1:m
      rownums = urow(t,1);
```

```
      if rownums==cnt1
       UCI(t,j) = yy(rownums,1);
      else
         UCI(t,j) = yy(rownums,1);
      end;
   end;
%    for t = 1:m
%       rownums = urow(t,1);
%       UCI(t,j) = yy(rownums,1);
%    end;
   if max(UCI(:,j)) < pe
      UCII(j,1)=max(yy);
   else
      [rows,cols] = find(UCI(:,j)>pe,1);
      UCII(j,1) = UCI(rows,j);
   end;
   results(j,3) = UCII(j,1);
end;

%% End of Program Transition_Analysis_SB
```

```
%% Program Transition_Analysis_SB_fun

% This program will calculate transition probabilities for ordinal data
% collected on skeletal traits connected to age and will generate both a
% plot of the transition probabilities [P(y<i|a)] and the likelihood
% functions [P(y=i|a)].
% This will be done by means of the continuation ratio or discrete time
% proportional hazards model. This is similar to the model described by
% Boldsen et al in the paper Transition Analysis.
% Additionally, the theoretical likelihoods are calculated and used to
% calculate likelihood functions for certain skeletons that are not part of
% the sample on which the data is based.

%% Import data

clear;

data = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\SB Fit Data - Males.csv');

%% Clean data

data(data == 0) = NaN;
[r,c] = size(data);
Age = data(:,1);
```

```
V1 = data(:,2);

V2 = data(:,3);

V3 = data(:,4);

V4 = data(:,5);

V5 = data(:,6);

V6 = data(:,7);

V7 = data(:,8);

V8 = data(:,9);

V9 = data(:,10);

V10 = data(:,11);

V11 = data(:,12);

V12 = data(:,13);

V13 = data(:,14);

V14 = data(:,15);

V15 = data(:,16);

V16 = data(:,17);

V17 = data(:,18);

V18 = data(:,19);

V19 = data(:,20);

V20 = data(:,21);

%%xx = linspace(0,100)';

%%yy = linspace(min(Age),max(Age))';

agerange = [min(Age):max(Age)];

xx = agerange';

yy = agerange';
```

```
[cnt1,~] = size(xx);



%% V1 CR Model

[fitV1,~,~] = mnrfit(Age,V1,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C1 = zeros(cnt1,2);


%% Calculate probabilities for V1



PROB1 = mnrval(fitV1,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A1 = PROB1;


for i = 1:cnt1

C1(i,1) = A1(i,1);

C1(i,2) = 1-A1(i,1);

end;


%% V2 CR Model

[fitV2,~,~] = mnrfit(Age,V2,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);
```

```
C2 = zeros(cnt1,2);

%% Calculate probabilities for V2


PROB2 = mnrval(fitV2,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A2 = PROB2;


for i = 1:cnt1

C2(i,1) = A2(i,1);

C2(i,2) = 1-A2(i,1);

end;


%% V3 CR Model

[fitV3,~,~] = mnrfit(Age,V3,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C3 = zeros(cnt1,2);


%% Calculate probabilities for V3


PROB3 = mnrval(fitV3,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A3 = PROB3;
```

```
for i = 1:cnt1

C3(i,1) = A3(i,1);

C3(i,2) = 1-A3(i,1);

end;


%% V4 CR Model

[fitV4,~,~] = mnrfit(Age,V4,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C4 = zeros(cnt1,2);


%% Calculate probabilities for V4



PROB4 = mnrval(fitV4,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A4 = PROB4;


for i = 1:cnt1

C4(i,1) = A4(i,1);

C4(i,2) = 1-A4(i,1);

end;
```

```
%% V5 CR Model

[fitV5,~,~] = mnrfit(Age,V5,'model','hierarchical','link','logit','interactions','on');


%A2 = zeros(r,3);

C5 = zeros(cnt1,4);


%% Calculate probabilities for V5



PROB5 = mnrval(fitV5,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A5 = PROB5;


for i = 1:cnt1

C5(i,1) = A5(i,1);

C5(i,2) = A5(i,2)-A5(i,1);

C5(i,3) = A5(i,3)-A5(i,2);

C5(i,4) = 1-A5(i,3);

end;


%% V6 CR Model

[fitV6,~,~] = mnrfit(Age,V6,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C6 = zeros(cnt1,2);
```

```
%% Calculate probabilities for V6


PROB6 = mnrval(fitV6,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A6 = PROB6;


for i = 1:cnt1

C6(i,1) = A6(i,1);

C6(i,2) = 1-A6(i,1);

end;


%% V7 CR Model

V7 = V7 -1;

[fitV7,~,~] = mnrfit(Age,V7,'model','hierarchical','link','logit','interactions','on');


%A3 = zeros(r,3);

C7 = zeros(cnt1,3);


%% Calculate probabilities for V7


PROB7 = mnrval(fitV7,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A7 = PROB7;
```

```
for i = 1:cnt1

C7(i,1) = A7(i,1);

C7(i,2) = A7(i,2)-A7(i,1);

C7(i,3) = 1-A7(i,2);

end;


%% V8 CR Model

V8 = V8 -1;

[fitV8,~,~] = mnrfit(Age,V8,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C8 = zeros(cnt1,5);


%% Calculate probabilities for V8



PROB8 = mnrval(fitV8,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A8 = PROB8;


for i = 1:cnt1

C8(i,1) = A8(i,1);

C8(i,2) = A8(i,2)-A8(i,1);

C8(i,3) = A8(i,3)-A8(i,2);
```

```
C8(i,4) = A8(i,4)-A8(i,3);

C8(i,5) = 1-A8(i,4);


end;


%% V9 CR Model

[fitV9,~,~] = mnrfit(Age,V9,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);

C9 = zeros(cnt1,3);


%% Calculate probabilities for V9



PROB9 = mnrval(fitV9,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A9 = PROB9;


for i = 1:cnt1

C9(i,1) = A9(i,1);

C9(i,2) = A9(i,2)-A9(i,1);

C9(i,3) = 1-A9(i,2);

end;


%% V10 CR Model
```

```
V10 = V10 -1;

[fitV10,~,~] = mnrfit(Age,V10,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C10 = zeros(cnt1,3);


%% Calculate probabilities for V10



PROB10 = mnrval(fitV10,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A10 = PROB10;


for i = 1:cnt1

C10(i,1) = A10(i,1);

C10(i,2) = A10(i,2)-A10(i,1);

C10(i,3) = 1-A10(i,2);

end;



%% V11 CR Model

[fitV11,~,~] = mnrfit(Age,V11,'model','hierarchical','link','logit','interactions','on');


%A4 = zeros(r,3);

C11 = zeros(cnt1,3);
```

```
%% Calculate probabilities for V11


PROB11 = mnrval(fitV11,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A11 = PROB11;


for i = 1:cnt1

C11(i,1) = A11(i,1);

C11(i,2) = A11(i,2)-A11(i,1);

C11(i,3) = 1-A11(i,2);

end;


%% V12 CR Model

%V12 = V12-1;

[fitV12,~,~] = mnrfit(Age,V12,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C12 = zeros(cnt1,4);


%% Calculate probabilities for V12


PROB12 = mnrval(fitV12,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
```

```
A12 = PROB12;


for i = 1:cnt1
C12(i,1) = A12(i,1);
C12(i,2) = A12(i,2)-A12(i,1);
C12(i,3) = A12(i,3)-A12(i,2);
C12(i,4) = 1-A12(i,3);
end;



%% V13 CR Model
[fitV13,~,~] = mnrfit(Age,V13,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);
C13 = zeros(cnt1,2);


%% Calculate probabilities for V13



PROB13 = mnrval(fitV13,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A13 = PROB13;


for i = 1:cnt1
C13(i,1) = A13(i,1);
```

```
C13(i,2) = 1-A13(i,1);

end;



%% V14 CR Model

%V14 = V14-1;

[fitV14,~,~] = mnrfit(Age,V14,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C14 = zeros(cnt1,2);


%% Calculate probabilities for V14



PROB14 = mnrval(fitV14,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A14 = PROB14;


for i = 1:cnt1

C14(i,1) = A14(i,1);

C14(i,2) = 1-A14(i,1);

end;



%% V15 CR Model
```

```
[fitV15,~,~] = mnrfit(Age,V15,'model','hierarchical','link','logit','interactions','on');


%A5 = zeros(r,3);

C15 = zeros(cnt1,3);


%% Calculate probabilities for V15



PROB15 = mnrval(fitV15,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A15 = PROB15;


for i = 1:cnt1

C15(i,1) = A15(i,1);

C15(i,2) = 1-A15(i,1);

end;


%% V16 CR Model

[fitV16,~,~] = mnrfit(Age,V16,'model','hierarchical','link','logit','interactions','on');


%A6 = zeros(r,3);

C16 = zeros(cnt1,5);


%% Calculate probabilities for V16
```

```
PROB16 = mnrval(fitV16,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A16 = PROB16;


for i = 1:cnt1

C16(i,1) = A16(i,1);

C16(i,2) = A16(i,2)-A16(i,1);

C16(i,3) = A16(i,3)-A16(i,2);

C16(i,4) = A16(i,3)-A16(i,3);

C16(i,5) = 1-A16(i,4);

end;



%% V17 CR Model

[fitV17,~,~] = mnrfit(Age,V17,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C17 = zeros(cnt1,5);


%% Calculate probabilities for V17



PROB17 = mnrval(fitV17,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A17 = PROB17;
```

```
for i = 1:cnt1

C17(i,1) = A17(i,1);

C17(i,2) = A17(i,2)-A17(i,1);

C17(i,3) = A17(i,3)-A17(i,2);

C17(i,4) = A17(i,4)-A17(i,3);

C17(i,5) = 1-A17(i,4);

end;




%% V18 CR Model

[fitV18,~,~] = mnrfit(Age,V18,'model','hierarchical','link','logit','interactions','on');


%A = zeros(r,3);

C18 = zeros(cnt1,4);


%% Calculate probabilities for V18



PROB18 = mnrval(fitV18,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A18 = PROB18;


for i = 1:cnt1
```

```
C18(i,1) = A18(i,1);

C18(i,2) = A18(i,2)-A18(i,1);

C18(i,3) = A18(i,3)-A18(i,2);

C18(i,4) = 1-A18(i,3);

end;



%% V19 CR Model

[fitV19,~,~] = mnrfit(Age,V19,'model','hierarchical','link','logit','interactions','on');


%A1 = zeros(r,3);

C19 = zeros(cnt1,4);


%% Calculate probabilities for V19



PROB19 = mnrval(fitV19,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');

A19 = PROB19;


for i = 1:cnt1

C19(i,1) = A19(i,1);

C19(i,2) = A19(i,2)-A19(i,1);

C19(i,3) = A19(i,3)-A19(i,2);

C19(i,4) = 1-A19(i,3);
```

```
end;


%% V20 CR Model
[fitV20,~,~] = mnrfit(Age,V20,'model','hierarchical','link','logit','interactions','on');

%A4 = zeros(r,3);
C20 = zeros(cnt1,4);

%% Calculate probabilities for V20


PROB20 = mnrval(fitV20,xx,'type','cumulative',
'model','hierarchical','interactions','on','link','logit');
A20 = PROB20;

for i = 1:cnt1
C20(i,1) = A20(i,1);
C20(i,2) = A20(i,2)-A20(i,1);
C20(i,3) = A20(i,3)-A20(i,2);
%C20(i,4) = A20(i,4)-A20(i,3);
C20(i,4) = 1-A20(i,3);

end;
```

```
%% Calculate general probability expressions
syms a;

pi1(1,1) = (exp(fitV1(1,1)+fitV1(2,1)*a))/(1+exp(fitV1(1,1)+fitV1(2,1)*a));
pi1(2,1) = 1 - pi1(1,1);



pi2(1,1) = (exp(fitV2(1,1)+fitV2(2,1)*a))/(1+exp(fitV2(1,1)+fitV2(2,1)*a));
pi2(2,1) = 1 - pi2(1,1);

pi3(1,1) = (exp(fitV3(1,1)+fitV3(2,1)*a))/(1+exp(fitV3(1,1)+fitV3(2,1)*a));
pi3(2,1) = 1 - pi3(1,1);

pi4(1,1) = (exp(fitV4(1,1)+fitV4(2,1)*a))/(1+exp(fitV4(1,1)+fitV4(2,1)*a));
pi4(2,1) = 1 - pi4(1,1);

pi5(1,1) = (exp(fitV5(1,1)+fitV5(2,1)*a))/(1+exp(fitV5(1,1)+fitV5(2,1)*a));
for i = 2:3
    pi5(i,1) = (exp(fitV5(1,i)+fitV5(2,i)*a))/(1+exp(fitV5(1,i)+fitV5(2,i)*a))-pi5(i-1,1);
end;
pi5(4,1) = 1 - pi5(3,1);

pi6(1,1) = (exp(fitV6(1,1)+fitV6(2,1)*a))/(1+exp(fitV6(1,1)+fitV6(2,1)*a));
```

```
pi6(2,1) = 1 - pi6(1,1);

pi7(1,1) = (exp(fitV7(1,1)+fitV7(2,1)*a))/(1+exp(fitV7(1,1)+fitV7(2,1)*a));
pi7(2,1) = (exp(fitV7(1,2)+fitV7(2,2)*a))/(1+exp(fitV7(1,2)+fitV7(2,2)*a))-pi7(2-1,1);
pi7(3,1) = 1 - pi7(2,1);


pi8(1,1) = (exp(fitV8(1,1)+fitV8(2,1)*a))/(1+exp(fitV8(1,1)+fitV8(2,1)*a));
for i = 2:4
    pi8(i,1) = (exp(fitV8(1,i)+fitV8(2,i)*a))/(1+exp(fitV8(1,i)+fitV8(2,i)*a))-pi8(i-1,1);
end;
pi8(5,1) = 1 - pi8(4,1);

pi9(1,1) = (exp(fitV9(1,1)+fitV9(2,1)*a))/(1+exp(fitV9(1,1)+fitV9(2,1)*a));
pi9(2,1) = (exp(fitV9(1,2)+fitV9(2,2)*a))/(1+exp(fitV9(1,2)+fitV9(2,2)*a))-pi9(2-1,1);

pi9(3,1) = 1 - pi9(2,1);

pi10(1,1) = (exp(fitV10(1,1)+fitV10(2,1)*a))/(1+exp(fitV10(1,1)+fitV10(2,1)*a));
pi10(2,1) = (exp(fitV10(1,2)+fitV10(2,2)*a))/(1+exp(fitV10(1,2)+fitV10(2,2)*a))-pi10(2-
1,1);
pi10(3,1) = 1 - pi10(2,1);

pi11(1,1) = (exp(fitV11(1,1)+fitV11(2,1)*a))/(1+exp(fitV11(1,1)+fitV11(2,1)*a));
pi11(2,1) = (exp(fitV11(1,2)+fitV11(2,2)*a))/(1+exp(fitV11(1,2)+fitV11(2,2)*a))-pi11(2-
1,1);
```

```
pi11(3,1) = 1 - pi11(2,1);


pi12(1,1) = (exp(fitV12(1,1)+fitV12(2,1)*a))/(1+exp(fitV12(1,1)+fitV12(2,1)*a));
for i = 2:3
    pi12(i,1) = (exp(fitV12(1,i)+fitV12(2,i)*a))/(1+exp(fitV12(1,i)+fitV12(2,i)*a))-pi12(i-
1,1);
end;
pi12(4,1) = 1 - pi12(3,1);


pi13(1,1) = (exp(fitV13(1,1)+fitV13(2,1)*a))/(1+exp(fitV13(1,1)+fitV13(2,1)*a));
pi13(2,1) = 1 - pi13(1,1);



pi14(1,1) = (exp(fitV14(1,1)+fitV14(2,1)*a))/(1+exp(fitV14(1,1)+fitV14(2,1)*a));
pi14(2,1) = 1 - pi14(1,1);


pi15(1,1) = (exp(fitV15(1,1)+fitV15(2,1)*a))/(1+exp(fitV15(1,1)+fitV15(2,1)*a));
pi15(2,1) = 1 - pi15(1,1);


pi16(1,1) = (exp(fitV16(1,1)+fitV16(2,1)*a))/(1+exp(fitV16(1,1)+fitV16(2,1)*a));
for i = 2:4
    pi16(i,1) = (exp(fitV16(1,i)+fitV16(2,i)*a))/(1+exp(fitV16(1,i)+fitV16(2,i)*a))-pi16(i-
1,1);
end;
pi16(5,1) = 1 - pi16(4,1);
```

```
pi17(1,1) = (exp(fitV17(1,1)+fitV17(2,1)*a))/(1+exp(fitV17(1,1)+fitV17(2,1)*a));

for i = 2:4

   pi17(i,1) = (exp(fitV17(1,i)+fitV17(2,i)*a))/(1+exp(fitV17(1,i)+fitV17(2,i)*a))-pi17(i-
1,1);

end;

pi17(5,1) = 1 - pi17(4,1);


pi18(1,1) = (exp(fitV18(1,1)+fitV18(2,1)*a))/(1+exp(fitV18(1,1)+fitV18(2,1)*a));

for i = 2:3

   pi18(i,1) = (exp(fitV18(1,i)+fitV18(2,i)*a))/(1+exp(fitV18(1,i)+fitV18(2,i)*a))-pi18(i-
1,1);

end;

pi18(4,1) = 1 - pi18(3,1);


pi19(1,1) = (exp(fitV19(1,1)+fitV19(2,1)*a))/(1+exp(fitV19(1,1)+fitV19(2,1)*a));

for i = 2:3

   pi19(i,1) = (exp(fitV19(1,i)+fitV19(2,i)*a))/(1+exp(fitV19(1,i)+fitV19(2,i)*a))-pi19(i-
1,1);

end;

pi19(4,1) = 1 - pi19(3,1);



pi20(1,1) = (exp(fitV20(1,1)+fitV20(2,1)*a))/(1+exp(fitV20(1,1)+fitV20(2,1)*a));

for i = 2:4

   pi20(i,1) = (exp(fitV20(1,i)+fitV20(2,i)*a))/(1+exp(fitV20(1,i)+fitV20(2,i)*a))-pi20(i-
1,1);
```

```
end;
pi20(5,1) = 1 - pi20(4,1);




%% Import prediction data yourself


%% Prediction


%G = [1,2,3,4];
%Predict = [2 4 3 2 3 4];  %%enter your test data here for a single observed skeleton


Predict = csvread('D:\Documents\002 Other Work\Research\Nicolene Jooste\GLMs - PHD\SB Test Data - Males.csv');
[rnum,cnum] = size(Predict);
fpred = sym('fpred',[rnum,1]);


display('Predictions')
for j = 1:rnum
   display(j);
   k = Predict(j,1);
   if (k == 0) fpred(j,1) = 1; else fpred(j,1) = pi1(k,1); endif;
   l = Predict(j,2);
```

```
if (l == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi2(l,1); endif;
m = Predict(j,3);
if (m == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi3(m,1); endif;
n = Predict(j,4);
if (n == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi4(n,1); endif;
o = Predict(j,5);
if (o == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi5(o,1); endif;
p = Predict(j,6);
if (p == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi6(p,1); endif;
q = Predict(j,7);
if (q == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi7(q,1); endif;
r = Predict(j,8);
if (r == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi8(r,1); endif;
s = Predict(j,9);
if (s == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi9(s,1); endif;
t = Predict(j,10);
if (t == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi10(t,1); endif;
u = Predict(j,11);
if (u == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi11(u,1); endif;
v = Predict(j,12);
if (v == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi12(v,1); endif;
w = Predict(j,13);
if (w == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi13(w,1); endif;
x = Predict(j,14);
if (x == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi14(x,1); endif;
```

```
    y = Predict(j,15);
    if (y == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi15(y,1); endif;
    z = Predict(j,16);
    if (z == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi16(z,1); endif;
    a = Predict(j,17);
    if (a == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi17(a,1); endif;
    b = Predict(j,18);
    if (b == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi18(b,1); endif;
    c = Predict(j,19);
    if (c == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi19(c,1); endif;
    d = Predict(j,20);
    if (d == 0) fpred(j,1) = fpred(j,1); else fpred(j,1) = fpred(j,1)*pi20(d,1); endif;
end;

zz = 20:98;
display('Predplot');
predplot = vpa(zeros(cnt1,rnum),10);
predplot = double(predplot);
  for j = 1:rnum
      display(j);
      FUN = matlabFunction(fpred(j,1));
      predplot(:,j) = feval(FUN,zz);
    end;

    pplot = double(predplot);
```

```
%% Determine max likelihood point estimate for all combinations:


ahat = zeros(rnum,1);

ahatl = ahat;

results = zeros(rnum,3);



display('Point estimates');

for j = 1:rnum

    display(j);

 likelihood = pplot(:,j);

 %likelihood = double(likelihood);

 maxprob = max(likelihood);

 [row,col] = find(likelihood==maxprob);

 ahat(j,1) = yy(row,1); % these are the point estimates

 ahatl(j,1) = maxprob;

 results(j,1) = ahat(j,1);

end;


% %% Confidence Intervals

% % We assume conditional independence, i.e. there are no correlations

% % between traits except for age ** expand this later on.

display('Confidence Intervals')

alphalow = chi2inv(0.05,1);
```

```
alphahi = chi2inv(0.95,1);
varZ = zeros(rnum,1);
LCI = zeros(cnt1,rnum);
CI = zeros(cnt1,rnum);
UCI = zeros(cnt1,rnum);

Zscoreneg = CI;
Zscorepos = CI;



UCII = zeros(rnum,1);
LCII = UCII;
calcvarZ = zeros(rnum,1);
counter = calcvarZ;

delta = zeros(rnum,2);
alpha = 0.05;

for j = 1:rnum
   delta(j,1) = -2*log(ahatl(j,1));
   probdelta = chi2cdf(delta(j,1),3);
   if probdelta < alpha
      delta(j,2) = 1;
   else
      if probdelta > 1-alpha
```

```
            delta(j,2) = 1;
        end;
    end;
end;

for j = 1:rnum
    display(j);
    likelihood = predplot(:,j);
    likelihood = double(likelihood);
    for i = 1:cnt1
        interm=likelihood(i,1)/ahatl(j,1);
        CI(i,j) = (-2*log(interm));
        Zscoreneg(i,j) = -sqrt(abs(CI(i,j)));
        Zscorepos(i,j) = sqrt(abs(CI(i,j)));
        calcvarZ(j,1) = Zscorepos(i,j)^2+Zscoreneg(i,j)^2+calcvarZ(j,1);
    end;
    counter(j,1)= (2*cnt1);
   varZ(j,1) = calcvarZ(j,1)/(counter(j,1));
   for i = 1:cnt1
       interm=(likelihood(i,1)/ahatl(j,1))^(1/varZ(j,1));
       CI(i,j) = real(-2*log(interm));
   end;
    [lrow,~] = find(CI(:,j)>=alphalow);
    [lm,~] = size(lrow);
    for t = 1:lm
```

```
    lrownums = lrow(t,1);
    if lrownums==1
     LCI(t,j) = yy(lrownums,1);
    else
       LCI(t,j) = yy(lrownums-1,1);
    end;
  end;
  pe=results(j,1);
  if min(LCI(:,j)) > pe
     LCII(j,1)=min(Age);
  else
     [rows,cols] = find(0<LCI(:,j)<pe,1);
     LCII(j,1) = LCI(rows,j);
  end;
  results(j,2) = LCII(j,1);
  [urow,col] = find(CI(:,j)<= alphahi);
  [m,~] = size(urow);
%    for t = 1:m
%       rownums = urow(t,1);
%       if rownums==cnt1
%        UCI(t,j) = yy(rownums,1);
%       else
%          UCI(t,j) = yy(rownums+1,1);
%       end;
%    end;
```

```
    for t = 1:m
       rownums = urow(t,1);
       if rownums==cnt1
        UCI(t,j) = yy(rownums,1);
       else
          UCI(t,j) = yy(rownums,1);
       end;
    end;
%     for t = 1:m
%        rownums = urow(t,1);
%        UCI(t,j) = yy(rownums,1);
%     end;
    if max(UCI(:,j)) < pe
       UCII(j,1)=max(yy);
    else
       [rows,cols] = find(UCI(:,j)>pe,1);
       UCII(j,1) = UCI(rows,j);
    end;
    results(j,3) = UCII(j,1);
end;

%% End of Program Transition_Analysis_SB_fun
```

Human Research Ethics Committee (Medical)

Research Office Secretariat: Senate House Room SH 10005, 10th floor. Tel +27 (0)11-717-1252
Medical School Secretariat: Medical School Room 10M07, 10th Floor. Tel +27 (0)11-717-2700
Private Bag 3, Wits 2050, www.wits.ac.za. Fax +27 (0)11-717-1265

Ref: W-CJ-140604-1

04/06/2014

TO WHOM IT MAY CONCERN:

Waiver: This certifies that the following research does not require clearance from the Human Research Ethics Committee (Medical).

Investigator: School of Anatomical Sciences (Head: Prof T J M Daly).

Project title: research on cadaveric material.

Reason: 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 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.

UNIVERSITY OF THE WITWATERSRAND
PROF PE CLEATON-JONES
HREC (MEDICAL)
2014 -06- 04
JOHANNESBURG

Professor Peter Cleaton-Jones

Chair: Human Research Ethics Committee (Medical)

Copy - HREC(Medical) Secretariat : Anisa Keshav, Zanele Ndlovu.

School of Anatomical Sciences

University of the Witwatersrand, Johannesburg

7 York Rd, Parktown, 2193, South Africa • Tel: (27 11) 717 2713 • Fax: (27 11) 717 2422 • www.wits.ac.za

15 February 2016

To whom this may concern

This letter confirms that Nicolene Jooste has been granted tentative permission to access the Raymond Dart Collection of Human skeletons for the assessment and analysis of her PhD degree. The title of her PhD project includes the following: **"A comparison of multifactorial statistical models for age-at-death estimation from the adult skeleton, tailored to a South African forensic context".** Full permission to access the Collection will be granted when her proposal has been accepted. Please don't hesitate to contact me if you require additional information.



Curator of the Raymond Dart Collection of Human skeletons

Chairman of the Collection's Committee

Anatomical Sciences

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

Faculty of Health Sciences

22 February 2015

To Whom it May Concern,

Ms Nicolene Jooste from the University of the Witwatersrand has been given permission to use the Pretoria Bone Collection which is housed in the Department of Anatomy, University of Pretoria for her PhD research entitled "*A comparison of multifactorial statistical models for age-at-death estimation from the adult skeleton, tailored to a South African forensic context*".

With kindest regards,

GC Krüger, MSc

Curator: Pretoria Bone Collection

Department of Anatomy
School of Medicine
Faculty of Health Sciences
University of Pretoria
Private Bag x323
ARCADIA 0007
Republic of South Africa

Tel +27 12 319 2539
Fax +27 12 319 2240

gabi.kruger@up.ac.za
http://www.up.ac.za

E 1: Descriptive statistics of right-side indicators.

	Mean	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Acetabulum							
Acetabular groove 1 (N=60)	44.72	39.88	49.56	39.50	20	86	66
Acetabular groove 2 (N=231)	51.86	49.45	54.27	50.00	20	98	78
Acetabular rim 1 (N=19)	24.89	22.53	27.26	24.00	20	40	20
Acetabular rim 2 (N=97)	42.66	39.37	45.95	36.00	20	80	60
Acetabular rim 3 (N=136)	56.74	53.93	59.54	56.00	21	98	77
Acetabular rim 4 (N=39)	59.87	54.01	65.73	64.00	23	86	63
Apex activity 1 (N=55)	34.89	30.85	38.93	30.00	20	80	60
Apex activity 2 (N=236)	54.00	51.72	56.28	54.00	20	98	78
Acetabular fossa 2 (N=106)	41.18	38.19	44.17	39.00	20	86	66
Acetabular fossa 3 (N=163)	53.77	50.90	56.63	55.00	20	98	78
Acetabular fossa 4 (N=22)	70.63	65.95	75.30	71.50	32	86	54
Auricular surface							
Surface topography 1 (N=16)	36.94	28.04	45.84	32.50	20	80	60
Surface topography 2 (N=45)	47.89	42.17	53.60	45.00	21	89	68
Surface topography 3 (N=137)	48.46	45.56	51.36	47.00	21	98	77
Surface morphology 2 (N=15)	44.87	32.14	57.59	34.00	20	98	78
Surface morphology 3 (N=82)	**42.87**	39.18	46.55	37.50	20	86	66
Surface morphology 4 (N=101)	51.46	48.13	54.78	50.00	21	89	68
Inferior surface texture 1 (N=103)	42.80	39.28	46.31	38.00	20	98	78
Inferior surface texture 2 (N=79)	52.54	48.93	56.16	53.00	23	89	66
Inferior surface texture 3 (N=16)	**51.63**	42.76	60.49	**53.50**	28	85	57
Posterior iliac exostoses 1 (N=76)	40.62	36.88	44.36	35.00	20	89	69
Posterior iliac exostoses 2 (N=114)	51.67	48.45	54.88	50.00	20	98	78
Posterior iliac exostoses 3 (N=8)	**51.00**	35.67	66.33	51.50	23	75	52
Clavicle							
Medial epiphysis 1 (N=9)	22.67	19.82	25.52	21.00	20	29	9
Medial epiphysis 2 (N=275)	51.40	49.26	53.54	51.00	20	98	78
Cranial sutures							
Midlambdoid 1 (N=41)	46.24	40.75	51.73	48.00	20	86	66
Midlambdoid 2 (N=57)	49.44	44.24	54.64	**48.00**	20	87	67
Midlambdoid 3 (N=79)	51.22	47.28	55.15	50.00	21	96	75
Midlambdoid 4 (N=16)	58.19	47.89	68.48	60.00	24	86	62
Midlambdoid 5 (N=6)	**53.00**	28.72	77.28	**47.50**	21	80	59
Midcoronal 1 (N=28)	44.21	36.14	52.29	44.00	20	87	67
Midcoronal 2 (N=79)	45.90	41.60	50.20	**41.00**	20	96	76
Midcoronal 3 (N=62)	53.31	49.39	57.22	53.00	24	86	62

	Mean	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Midcoronal 4 (N=19)	62.42	55.28	69.57	69.00	30	80	50
Midcoronal 5 (N=11)	**59.45**	49.85	69.06	**56.00**	40	86	46
Pterion 2 (N=78)	42.24	38.38	46.10	39.00	20	85	65
Pterion 3 (N=78)	52.79	48.92	56.67	51.50	24	96	72
Pterion 4 (N=18)	58.67	49.97	67.36	60.50	29	86	57
Pterion 5 (N=25)	61.60	54.41	68.79	**60.00**	24	86	62
Sphenofrontal 1 (N=8)	41.75	27.29	56.21	45.50	20	64	44
Sphenofrontal 2 (N=98)	45.80	42.09	49.50	**45.00**	20	86	66
Sphenofrontal 3 (N=51)	52.65	47.86	57.43	50.00	25	96	71
Sphenofrontal 4 (N=30)	60.60	53.54	67.66	65.50	27	87	60
Sphenofrontal 5 (N=12)	**57.00**	50.73	63.27	**58.00**	40	75	35
Superior sphenotemporal 1 (N=35)	48.20	42.79	53.61	52.00	20	75	55
Superior sphenotemporal 2 (N=156)	50.08	47.10	53.07	**49.00**	20	96	76
Superior sphenotemporal 3 (N=8)	63.63	47.82	79.43	72.00	35	86	51
Inferior sphenotemporal 1 (N=41)	46.95	41.78	52.12	48.00	20	86	66
Inferior sphenotemporal 2 (N=142)	49.84	46.72	52.96	50.00	20	96	76
Inferior sphenotemporal 3 (N=16)	62.94	54.20	71.67	70.00	35	86	51
Zygomaticomaxillary 1 (N=9)	44.00	31.67	56.33	45.00	20	64	44
Zygomaticomaxillary 2 (N=97)	47.60	43.88	51.31	46.00	20	87	67
Zygomaticomaxillary 3 (N=80)	52.98	48.84	57.11	50.50	23	96	73
Zygomaticomaxillary 4 (N=13)	58.31	48.16	68.46	60.00	30	80	50
Iliac crest							
Iliac crest 1 (N=8)	22.75	20.35	25.15	22.0	20	29	9
Iliac crest 2 (N=312)	51.63	49.59	53.68	50.00	20	98	78
Pubic symphysis							
Symphyseal relief 2 (N=13)	28.69	19.11	38.28	25.00	20	80	60
Symphyseal relief 3 (N=45)	39.07	34.74	43.39	34.00	22	75	53
Symphyseal relief 4 (N=133)	54.89	51.94	57.85	56.00	21	98	77
Symphyseal relief 5 (N=11)	59.00	49.12	68.88	60.00	29	81	52
Dorsal margin 2 (N=63)	38.37	34.34	42.39	32.00	20	85	65
Dorsal margin 3 (N=127)	54.18	51.17	57.19	56.00	21	98	77
Dorsal margin 4 (N=12)	65.25	55.83	74.67	65.50	40	87	47
Ventral margin 2 (N=14)	29.14	23.40	34.88	26.00	20	53	33
Ventral margin 3 (N=76)	41.74	38.08	45.39	36.50	21	85	64
Ventral margin 4 (N=90)	57.31	53.83	60.79	58.00	28	98	70
Ventral margin 5 (N=22)	61.05	54.27	67.82	62.50	36	87	51
Superior apex 1 (N=11)	29.18	23.91	34.45	32.00	20	43	23
Superior apex 2 (N=9)	37.78	25.94	49.62	**31.00**	21	70	49
Superior apex 3 (N=76)	44.63	40.69	48.58	40.00	21	82	61
Superior apex 4 (N=106)	56.87	53.58	60.16	58.50	27	98	71
Symphyseal texture 1 (N=121)	46.88	43.79	49.98	46.00	20	98	78
Symphyseal texture 2 (N=72)	54.18	49.45	58.91	56.00	22	87	65

	Mean	95% Lower CI	95% Upper CI	Median	Minimum	Maximum	Range
Symphyseal texture 3 (N=9)	56.33	45.13	67.53	60.00	35	80	45
Suchey-Brooks							
Suchey-Brooks 2 (N=30)	29.00	26.13	31.87	28.00	20	47	27
Suchey-Brooks 3 (N=44)	37.36	33.10	41.62	34.00	21	75	54
Suchey-Brooks 4 (N=121)	52.27	49.16	55.39	50.00	22	98	76
Suchey-Brooks 5 (N=77)	61.55	58.15	64.94	60.00	28	90	62
Suchey-Brooks 6 (N=17)	63.65	57.12	70.18	65.00	40	87	47

E 2: Descriptive statistics for left side and median female indicators.

	Mean	95% Lower CI	95% Upper CI	Median	Minimum	Maximum	Range
Acetabulum							
Acetabular groove 1 (N=24)	39.38	32.12	46.63	33.00	20	71	51
Acetabular groove 2 (N=117)	50.56	47.57	53.56	50.00	20	87	67
Acetabular rim 1 (**N=7**)	22.86	19.77	25.94	21.00	20	28	8
Acetabular rim 2 (N=45)	40.87	36.16	45.57	36.00	20	75	55
Acetabular rim 3 (N=69)	54.42	50.74	58.10	53.00	21	87	66
Acetabular rim 4 (N=20)	55.35	49.57	61.13	58.00	30	80	50
Apex activity 1 (N=29)	38.41	32.45	44.38	32.00	20	70	50
Apex activity 2 (N=112)	51.31	48.26	54.37	52.50	20	87	67
Acetabular fossa 2 (N=56)	38.21	34.38	42.05	34.50	20	71	51
Acetabular fossa 3 (N=78)	54.59	51.16	58.02	57.00	20	87	67
Acetabular fossa 4 (**N=7**)	66.14	61.32	70.96	65.00	60	74	14
Auricular surface							
Surface topography 1 (N=16)	33.00	24.59	41.41	26.00	20	70	50
Surface topography 2 (N=24)	44.71	37.77	51.65	43.50	21	75	54
Surface topography 3 (N=71)	50.93	47.31	54.55	50.00	23	85	62
Surface morphology 2 (N=8)	42.38	28.75	56.00	37.00	24	70	46
Surface morphology 3 (N=41)	**42.63**	37.39	47.88	**37.00**	20	75	55
Surface morphology 4 (N=62)	50.48	46.36	54.61	50.00	20	85	65
Inferior surface texture 1 (N=57)	43.47	39.08	47.87	45.00	20	75	55
Inferior surface texture 2 (N=45)	50.78	45.98	55.58	53.00	25	85	60
Inferior surface texture 3 (N=9)	**50.44**	36.41	64.48	**45.00**	30	80	50
Posterior iliac exostoses 1 (N=33)	43.48	37.48	49.49	40.00	20	74	54
Posterior iliac exostoses 2 (N=74)	47.81	43.96	51.66	47.00	20	85	65
Posterior iliac exostoses 3 (**N=4**)	61.00	49.90	72.10	60.50	53	70	17
Clavicle							
Medial epiphysis 1 (**N=3**)	20.33	18.90	21.77	20.00	20	21	1

	Mean	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Medial epiphysis 2 (N=137)	48.63	45.90	51.36	50.00	20	86	66
Cranial sutures							
Midlambdoid 1 (N=24)	45.04	37.61	52.47	47.50	20	80	60
Midlambdoid 2 (N=33)	**44.97**	39.07	50.87	**43.00**	20	78	58
Midlambdoid 3 (N=38)	52.42	47.03	57.81	53.00	21	87	66
Midlambdoid 4 (N=8)	61.38	45.94	76.81	66.00	24	86	62
Midlambdoid 5 (**N=3**)	**45.67**	35.63	55.71	**45.00**	42	50	8
Lambda 1 (N=24)	43.33	35.90	50.76	43.50	20	80	60
Lambda 2 (N=33)	48.45	42.65	54.26	50.00	20	78	58
Lambda 3 (N=40)	51.33	45.89	56.76	53.00	21	87	66
Lambda 4 (**N=4**)	50.00	19.36	80.64	**53.00**	24	70	46
Lambda 5 (**N=5**)	58.60	35.49	81.71	**50.00**	42	85	43
Obelion 1 (N=15)	44.00	33.53	54.47	45.00	20	80	60
Obelion 2 (N=24)	**40.00**	33.10	46.90	**36.50**	20	70	50
Obelion 3 (N=37)	51.35	45.85	56.85	50.00	21	86	65
Obelion 4 (N=16)	60.19	52.49	67.88	60.00	31	87	56
Obelion 5 (N=14)	**50.14**	42.44	57.84	**48.50**	24	71	47
Vertex 1 (N=24)	41.96	35.16	48.76	43.50	20	65	45
Vertex 2 (N=31)	44.68	39.14	50.22	47.00	20	70	50
Vertex 3 (N=37)	53.62	47.86	59.38	58.00	21	87	66
Vertex 4 (N=9)	61.11	49.00	73.22	69.00	24	74	50
Vertex 5 (**N=5**)	**51.80**	27.88	75.72	**45.00**	40	86	46
Bregma 1 (N=19)	48.05	38.51	57.59	52.00	20	85	65
Bregma 2 (N=44)	**43.45**	38.82	48.09	**41.50**	20	70	50
Bregma 3 (N=27)	52.15	45.62	58.68	**47.00**	21	87	66
Bregma 4 (N=16)	59.50	51.48	67.52	60.50	24	56	62
Midcoronal 1 (N=17)	41.82	32.45	51.19	40.00	20	85	65
Midcoronal 2 (N=41)	42.78	37.63	47.93	41.00	20	80	60
Midcoronal 3 (N=28)	55.75	49.50	62.00	59.50	24	87	63
Midcoronal 4 (N=12)	56.33	50.08	62.59	60.00	40	71	31
Midcoronal 5 (N=8)	60.38	48.24	72.51	**59.00**	40	86	46
Pterion 2 (N=43)	41.63	36.31	46.95	38.00	20	85	65
Pterion 3 (N=36)	54.50	48.84	60.16	58.50	25	87	62
Pterion 4 (N=13)	**52.31**	43.19	61.42	**50.00**	30	86	56
Pterion 5 (N=14)	**53.79**	46.66	60.91	**58.00**	24	70	46
Sphenofrontal 1 (**N=5**)	37.80	14.63	60.97	36.00	20	64	44
Sphenofrontal 2 (N=47)	44.79	39.52	50.05	42.00	20	85	65
Sphenofrontal 3 (N=28)	53.39	47.28	59.50	54.00	26	78	52
Sphenofrontal 4 (N=12)	55.08	43.36	66.80	**51.50**	30	87	57
Sphenofrontal 5 (N=14)	**52.50**	45.94	59.06	**53.00**	25	70	45
Superior sphenotemporal 1 (N=21)	48.38	40.67	56.09	52.00	20	80	60
Superior sphenotemporal 2 (N=85)	49.05	45.31	52.78	**50.00**	20	87	67
Superior sphenotemporal 3 (**N=0**)	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Inferior sphenotemporal 1 (N=24)	45.50	38.27	52.73	46.50	20	80	60
Inferior sphenotemporal 2 (N=75)	49.31	45.45	53.16	50.00	20	87	67
Inferior spenotemporal 3 (N=7)	56.43	36.73	76.13	**50.00**	25	86	61
Zygomaticomaxillary 1 (N=8)	45.00	31.07	58.93	49.00	20	64	44
Zygomaticomaxillary 2 (N=63)	47.75	43.25	52.24	**47.00**	20	87	67
Zygomaticomaxillary 3 (N=32)	51.78	46.05	57.52	51.50	23	86	63

	Mean	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Zygomaticomaxillary 4 (**N=3**)	53.33	1.62	105.04	60.00	30	70	40
Incisive 3 (N=31)	46.97	40.47	53.46	50.00	21	80	59
Incisive 4 (**N=4**)	69.75	47.92	91.58	68.00	56	87	31
Incisive 5 (N=71)	**48.59**	44.68	52.50	**47.00**	20	86	66
Anterior median palatine 1 (N=6)	45.67	29.95	61.38	48.50	20	64	44
Anterior median palatine 2 (N=68)	49.41	45.16	53.66	50.00	20	87	67
Anterior median palatine 3 (N=27)	**47.00**	40.05	53.95	**47.00**	21	85	64
Anterior median palatine 4 (**N=5**)	56.40	40.34	72.46	53.00	43	70	27
Posterior median palatine 1 (N=6)	45.67	29.95	61.38	48.50	20	64	44
Posterior median palatine 2 (N=55)	46.02	41.28	50.76	**45.00**	20	87	67
Posterior median palatine 3 (N=27)	47.22	40.83	53.61	**47.00**	23	85	62
Posterior median palatine 4 (N=11)	59.27	49.65	68.89	60.00	36	86	50
Posterior median palatine 5 (N=7)	64.71	53.71	75.72	70.00	46	78	32
Transverse palatine 1 (N=6)	46.17	30.41	61.92	49.00	20	60	40
Transverse palatine 2 (N=74)	**46.69**	42.76	50.62	**46.50**	20	85	65
Transverse palatine 3 (N=24)	56.67	49.34	63.99	54.50	24	87	63
Transverse palatine 4 (**N=0**)	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Transverse palatine 5 (**N=2**)	**46.50**	40.15	52.85	**46.50**	46	47	1
Iliac crest							
Iliac crest 1 (**N=5**)	21.40	19.52	23.28	21.00	20	23	3
Iliac crest 2 (N=142)	49.15	46.42	51.89	50.00	20	87	67
Pubic symphysis							
Symphyseal relief 2 (N=6)	24.67	20.23	29.10	24.00	20	31	11
Symphyseal relief 3 (N=27)	38.30	32.74	43.85	36.00	20	70	50
Symphyseal relief 4 (N=51)	52.51	48.05	56.97	56.00	25	87	62
Symphyseal relief 5 (N=9)	53.11	44.09	62.14	60.00	32	65	33
Dorsal margin 2 (N=36)	37.17	31.89	42.44	31.50	20	70	50
Dorsal margin 3 (N=47)	50.96	46.92	55.00	53.00	28	86	58
Dorsal margin 4 (N=10)	60.50	48.38	72.62	60.50	34	87	53
Ventral margin 2 (N=10)	31.20	22.63	39.77	25.50	20	53	33
Ventral margin 3 (N=44)	41.66	37.10	46.22	37.50	20	85	65
Ventral margin 4 (N=27)	54.41	48.57	60.24	58.00	31	86	55
Ventral margin 5 (N=12)	60.33	52.06	68.61	60.00	40	87	47
Superior apex 1 (N=9)	31.33	24.31	38.36	32.00	20	47	27
Superior apex 2 (**N=2**)	**24.00**	-26.82	74.82	**24.00**	20	28	8
Superior apex 3 (N=36)	45.22	40.28	50.17	47.00	21	70	49
Superior apex 4 (N=46)	51.74	46.65	56.83	54.00	26	87	61
Symphyseal texture 1 (N=47)	43.04	38.36	47.72	43.00	20	71	51

	Mean	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Symphyseal texture 2 (N=38)	48.03	42.48	53.58	47.00	23	87	64
Symphyseal texture 3 (N=8)	61.25	50.36	72.14	62.50	40	85	45
Sacrum							
S1/S2 fusion 1 (N=34)	32.82	28.80	36.85	28.50	20	59	39
S1/S2 fusion 2 (N=111)	52.82	49.89	55.75	56.00	21	87	66
Suchey-Brooks							
Suchey-Brooks 2 (N=18)	27.67	24.00	31.33	26.00	20	47	27
Suchey-Brooks 3 (N=24)	40.54	33.81	47.28	35.50	21	75	54
Suchey-Brooks 4 (N=49)	52.04	47.98	56.10	53.00	25	80	55
Suchey-Brooks 5 (N=25)	54.04	47.74	60.34	57.00	30	86	56
Suchey-Brooks 6 (N=13)	61.08	53.63	68.52	60.00	40	87	47
Vertebral bodies							
C3 superior 1 (N=63)	42.90	38.87	46.94	42.00	20	74	54
C3 superior 2 (N=20)	60.40	51.89	68.91	67.00	25	87	62
C3 inferior 1 (N=44)	39.52	34.78	44.27	35.50	20	74	54
C3 inferior 2 (N=39)	55.69	50.19	61.19	58.00	25	87	62
C4 superior 1 (N=60)	42.32	38.27	46.36	41.00	20	74	54
C4 superior 2 (N=23)	59.65	51.75	67.56	68.00	25	87	62
C4 inferior 1 (N=43)	36.93	32.81	41.05	33.00	20	64	44
C4 inferior 2 (N=40)	58.08	52.95	63.20	60.00	25	87	62
C5 superior 1 (N=51)	38.92	34.86	42.98	36.00	20	69	49
C5 superior 2 (N=32)	60.19	54.58	65.79	62.50	30	87	57
C5 inferior 1 (N=35)	35.00	30.02	39.98	30.00	20	74	54
C5 inferior 2 (N=48)	55.96	51.56	60.36	57.00	23	87	64
C6 superior 1 (N=48)	37.85	33.51	42.20	33.00	20	74	54
C6 superior 2 (N=35)	59.83	55.07	64.59	60.00	30	87	57
C6 inferior 1 (N=41)	35.59	31.36	39.81	31.00	20	69	49
C6 inferior 2 (N=42)	58.38	53.79	62.97	60.00	25	87	62
C7 superior 1 (N=56)	41.14	36.52	45.76	36.50	20	87	67
C7 superior 2 (N=27)	59.52	54.44	64.60	60.00	30	86	56
C7 inferior 1 (N=50)	39.46	35.07	43.85	34.00	20	70	50
C7 inferior 2 (N=33)	58.73	53.21	64.25	60.00	25	87	62
L1 superior 1 (N=57)	42.04	37.61	46.46	37.00	20	87	67
L1 superior 2 (N=26)	58.27	51.74	64.80	60.00	21	86	65
L1 inferior 1 (N=52)	39.56	35.36	43.76	36.00	20	74	54
L1 inferior 2 (N=31)	59.81	54.11	65.50	64.00	25	87	62
L2 superior 1 (N=44)	37.80	33.22	42.37	32.50	20	74	54
L2 superior 2 (N=39)	57.64	52.67	62.61	60.00	25	87	62
L2 inferior 1 (N=46)	39.59	34.66	44.51	34.50	20	87	67
L2 inferior 2 (N=37)	56.49	51.34	61.63	60.00	25	86	61
L3 superior 1 (N=38)	34.66	30.59	38.72	31.00	20	60	40
L3 superior 2 (N=45)	57.64	53.05	62.23	60.00	25	87	62
L3 inferior 1 (N=41)	35.63	31.49	39.77	32.00	20	65	45
L3 inferior 2 (N=42)	58.33	53.65	63.01	60.00	25	87	62
L4 superior 1 (N=32)	31.28	27.73	34.83	28.50	20	60	40
L4 superior 2 (N=51)	57.06	52.94	61.18	60.00	25	87	62
L4 inferior 1 (N=39)	35.82	31.45	40.19	32.00	20	70	50
L4 inferior 2 (N=44)	57.14	52.38	61.89	60.00	21	87	66
L5 superior 1 (N=36)	32.58	28.96	36.21	30.00	20	64	44
L5 superior 2 (N=47)	58.26	54.06	62.45	60.00	25	87	62
L5 inferior 1 (N=33)	31.33	27.58	35.09	29.00	20	64	44
L5 inferior 2 (N=50)	57.54	53.57	61.51	60.00	25	87	62

E 3: Descriptive statistics for left side and median male indicators.

	Mean	***95% Lower CI***	***95% Upper CI***	***Median***	***Minimum***	***Maximum***	***Range***
Acetabulum							
Acetabular groove 1 (N=31)	45.81	38.52	53.09	45.00	20	86	66
Acetabular groove 2 (N=133)	54.23	50.85	57.61	54.00	21	98	77
Acetabular rim 1 (N=11)	26.64	23.80	29.48	26.00	21	35	14
Acetabular rim 2 (N=49)	42.92	38.61	47.23	40.00	20	80	60
Acetabular rim 3 (N=81)	60.60	56.85	64.36	60.00	21	98	77
Acetabular rim 4 (N=23)	**57.74**	47.22	68.25	**60.00**	22	96	74
Apex activity 1 (N=33)	40.39	33.51	47.27	33.00	21	89	68
Apex activity 2 (N=131)	55.73	52.45	59.00	56.00	20	98	78
Acetabular fossa 2 (N=57)	44.65	40.28	49.02	42.00	21	90	69
Acetabular fossa 3 (N=90)	53.96	49.70	58.21	54.50	20	98	78
Acetabular fossa 4 (N=17)	72.47	66.09	78.85	75.00	32	86	54
Auricular surface							
Surface topography 1 (**N=4**)	48.00	13.65	82.35	38.50	35	80	45
Surface topography 2 (N=27)	50.30	42.12	58.47	49.00	22	89	67
Surface topography 3 (N=86)	**48.15**	44.40	51.90	**46.50**	21	98	77
Surface morphology 2 (N=8)	42.00	25.29	58.71	37.00	21	82	61
Surface morphology 3 (N=48)	46.71	41.41	52.00	43.50	21	98	77
Surface morphology 4 (N=61)	51.03	46.44	55.63	52.00	21	89	68
Inferior surface texture 1 (N=67)	43.76	39.43	48.10	40.00	21	98	77
Inferior surface texture 2 (N=38)	58.42	52.96	63.88	60.00	24	89	65
Inferior surface texture 3 (N=12)	**44.92**	35.97	53.86	**42.00**	24	67	43
Posterior iliac exostoses 1 (N=49)	39.47	34.94	44.00	34.00	21	89	68
Posterior iliac exostoses 2 (N=60)	55.40	51.05	59.75	54.00	27	98	71
Posterior iliac exostoses 3 (N=8)	**54.13**	37.22	71.03	**54.50**	23	80	57
Clavicle							
Medial epiphysis 1 (**N=6**)	23.83	19.51	28.16	22.00	20	29	9
Medial epiphysis 2 (N=156)	53.87	50.84	56.89	54.00	21	98	77
Cranial sutures							
Midlambdoid 1 (N=16)	47.56	37.96	57.17	49.00	24	86	62
Midlambdoid 2 (N=26)	**49.42**	41.90	56.95	**48.00**	20	86	66
Midlambdoid 3 (N=45)	53.80	47.80	59.80	50.00	24	96	72
Midlambdoid 4 (N=9)	**53.67**	37.45	69.88	**45.00**	25	86	61
Midlambdoid 5 (**N=3**)	60.33	-24.29	144.95	80.00	21	80	59
Lambda 1 (N=13)	44.08	35.37	52.79	45.00	24	63	39
Lambda 2 (N=24)	53.71	44.81	62.60	50.00	20	86	66
Lambda 3 (N=49)	**49.61**	44.16	55.06	**46.00**	21	96	75
Lambda 4 (N=11)	61.64	48.06	75.21	70.00	25	86	61
Lambda 5 (**N=2**)	80.00	80.00	80.00	80.00	80	80	0

	Mean	***95% Lower CI***	***95% Upper CI***	***Median***	***Minimum***	***Maximum***	***Range***
Obelion 1 (N=6)	35.67	23.54	47.79	34.00	24	53	29
Obelion 2 (N=12)	46.08	35.12	57.04	48.00	20	75	55
Obelion 3 (N=38)	52.58	46.19	58.97	**48.00**	21	96	75
Obelion 4 (N=16)	**51.19**	40.51	61.86	**47.50**	29	86	57
Obelion 5 (N=27)	57.30	49.13	65.46	57.00	24	86	62
Vertex 1 (N=13)	49.62	35.40	63.83	48.00	20	86	66
Vertex 2 (N=26)	**45.27**	38.55	51.99	**41.50**	23	86	63
Vertex 3 (N=36)	55.28	49.06	61.49	56.50	24	96	72
Vertex 4 (N=15)	57.40	46.86	67.94	57.00	29	86	57
Vertex 5 (N=9)	**50.89**	31.09	70.69	**57.00**	21	80	59
Bregma 1 (N=11)	48.73	32.38	65.08	53.00	20	86	66
Bregma 2 (N=35)	**46.34**	40.61	52.08	**44.00**	23	86	63
Bregma 3 (N=41)	54.83	48.53	61.13	57.00	21	96	75
Bregma 4 (N=12)	60.42	48.22	72.61	63.50	29	86	57
Midcoronal 1 (N=11)	41.73	27.94	55.52	33.00	20	82	62
Midcoronal 2 (N=44)	48.52	43.13	53.92	45.50	21	81	60
Midcoronal 3 (N=33)	54.94	47.70	62.18	50.00	25	96	71
Midcoronal 4 (N=9)	65.44	52.28	78.61	74.00	35	81	46
Midcoronal 5 (**N=2**)	67.50	-91.33	226.33	**67.50**	55	80	25
Pterion 2 (N=40)	43.33	38.31	48.34	43.00	20	81	61
Pterion 3 (N=38)	52.34	45.81	58.88	50.50	24	96	72
Pterion 4 (N=10)	62.90	49.12	76.68	70.00	29	86	57
Pterion 5 (N=11)	70.91	61.07	80.74	76.00	41	86	45
Sphenofrontal 1 (**N=4**)	45.25	22.58	67.92	49.00	26	57	31
Sphenofrontal 2 (N=52)	**45.48**	40.59	50.37	**45.00**	20	86	66
Sphenofrontal 3 (N=23)	53.87	45.10	62.64	50.00	27	96	69
Sphenofrontal 4 (N=16)	69.06	59.62	78.51	75.00	29	86	57
Sphenofrontal 5 (**N=4**)	**60.25**	43.44	77.06	**58.00**	50	75	25
Superior sphenotemporal 1 (N=14)	47.43	38.50	56.35	48.00	26	75	49
Superior sphenotemporal 2 (N=78)	51.90	47.29	56.51	49.00	20	96	76
Superior sphenotemporal 3 (N=7)	59.86	43.68	76.03	70.00	35	78	43
Inferior sphenotemporal 1 (N=18)	49.39	41.18	57.59	48.00	26	86	60
Inferior sphenotemporal 2 (N=65)	**49.08**	44.08	54.07	**45.00**	20	96	76
Inferior spenotemporal 3 (N=16)	65.75	57.65	73.85	70.00	35	86	51
Zygomaticomaxillary 1 (**N=3**)	34.67	15.69	53.64	33.00	28	43	15
Zygomaticomaxillary 2 (N=36)	45.53	39.08	51.98	41.50	20	86	66
Zygomaticomaxillary 3 (N=47)	54.55	48.90	60.21	51.00	24	96	72
Zygomaticomaxillary 4 (N=13)	63.38	52.99	73.78	70.00	30	86	56
Incisive 3 (N=22)	48.09	39.59	56.59	52.00	20	80	60
Incisive 4 (**N=4**)	49.50	6.99	92.01	**49.50**	24	75	51
Incisive 5 (N=73)	53.08	48.52	57.64	**50.00**	21	96	75
Anterior median palatine 1 (**N=0**)	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Anterior median palatine 2 (N=46)	48.11	42.01	54.21	45.00	20	86	66
Anterior median palatine 3 (N=37)	54.27	47.77	60.77	50.00	24	96	72
Anterior median palatine 4 (N=16)	56.88	48.32	65.43	56.00	30	86	56

	Mean	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Posterior median palatine 1 (**N=1**)	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Posterior median palatine 2 (N=19)	45.95	34.55	57.35	34.00	20	86	66
Posterior median palatine 3 (N=42)	49.21	44.17	54.26	45.50	24	82	58
Posterior median palatine 4 (N=25)	58.80	50.00	67.60	62.00	24	96	72
Posterior median palatine 5 (N=12)	**58.00**	47.97	68.03	**58.00**	30	75	45
Transverse palatine 1 (**N=1**)	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Transverse palatine 2 (N=51)	50.10	44.39	55.81	45.00	21	96	75
Transverse palatine 3 (N=36)	53.47	47.26	59.69	50.00	20	86	66
Transverse palatine 4 (N=7)	55.29	35.81	74.76	55.00	24	80	40
Transverse palatine 5 (**N=4**)	59.75	25.02	94.48	65.50	30	78	48
Iliac crest							
Iliac crest 1 (**N=5**)	23.60	19.52	27.68	23.00	21	29	8
Iliac crest 2 (N=170)	54.09	51.16	57.02	54.00	20	98	78
Pubic symphysis							
Symphyseal relief 2 (N=8)	32.50	16.18	48.82	28.00	20	80	60
Symphyseal relief 3 (N=20)	37.60	30.33	44.87	32.50	21	75	54
Symphyseal relief 4 (N=95)	55.81	52.29	59.33	55.00	24	98	74
Symphyseal relief 5 (**N=5**)	59.80	34.03	85.57	70.00	29	81	52
Dorsal margin 2 (N=30)	37.73	31.81	43.66	30.00	20	85	65
Dorsal margin 3 (N=94)	55.19	51.53	58.85	54.50	21	98	77
Dorsal margin 4 (**N=4**)	73.25	68.87	77.63	73.50	70	76	6
Ventral margin 2 (N=8)	27.88	22.54	33.21	28.00	20	40	20
Ventral margin 3 (N=37)	43.03	37.45	48.61	38.00	21	80	59
Ventral margin 4 (N=74)	57.09	53.02	61.17	56.50	26	98	72
Ventral margin 5 (N=9)	63.67	50.93	76.40	70.00	36	86	50
Superior apex 1 (**N=6**)	29.00	18.93	39.07	25.50	20	42	22
Superior apex 2 (**N=5**)	33.60	25.38	41.82	32.00	29	45	16
Superior apex 3 (N=44)	47.00	41.11	52.89	41.50	21	82	61
Superior apex 4 (N=73)	57.58	53.60	61.55	59.00	27	98	71
Symphyseal texture 1 (N=82)	49.77	45.82	53.71	48.00	20	98	78
Symphyseal texture 2 (N=43)	54.58	48.27	60.90	56.00	22	86	64
Symphyseal texture 3 (**N=3**)	61.67	2.97	120.36	70.00	35	80	45
Sacrum							
S1/S2 fusion 1 (N=39)	42.13	34.82	49.44	32.00	20	98	78
S1/S2 fusion 2 (N=133)	56.38	53.36	59.41	57.00	23	96	73
Suchey-Brooks							
Suchey-Brooks 2 (N=13)	29.69	24.66	34.72	28.00	20	45	25
Suchey-Brooks 3 (N=21)	33.67	29.52	37.81	34.00	21	54	33
Suchey-Brooks 4 (N=79)	53.16	49.01	57.32	51.00	22	98	76
Suchey-Brooks 5 (N=46)	65.43	61.15	69.72	64.50	28	90	62
Suchey-Brooks 6 (**N=7**)	70.86	64.83	76.88	72.00	57	76	19

	Mean	*95% Lower CI*	*95% Upper CI*	*Median*	*Minimum*	*Maximum*	*Range*
Vertebral bodies							
C3 superior 1 (N=57)	45.33	40.02	50.65	35.00	21	89	68
C3 superior 2 (N=38)	62.74	56.90	68.57	62.00	26	98	72
C3 inferior 1 (N=44)	40.05	34.61	45.48	34.00	21	89	68
C3 inferior 2 (N=51)	62.86	57.99	67.73	63.00	23	98	75
C4 superior 1 (N=49)	42.71	37.17	48.26	35.00	21	89	68
C4 superior 2 (N=46)	62.50	57.28	67.72	63.50	23	98	75
C4 inferior 1 (N=44)	41.98	36.54	47.42	34.50	21	89	68
C4 inferior 2 (N=51)	61.20	55.78	66.62	62.00	22	98	76
C5 superior 1 (N=37)	38.95	33.97	43.92	34.00	21	80	59
C5 superior 2 (N=58)	60.81	55.62	66.00	62.00	22	98	76
C5 inferior 1 (N=34)	36.85	31.96	41.74	32.50	21	80	59
C5 inferior 2 (N=61)	60.90	56.00	65.80	61.00	22	98	76
C6 superior 1 (N=38)	38.50	33.47	43.53	34.00	21	80	59
C6 superior 2 (N=57)	61.49	56.43	66.55	62.00	23	98	75
C6 inferior 1 (N=37)	38.32	33.72	42.93	34.00	21	80	59
C6 inferior 2 (N=58)	61.21	56.00	66.42	63.50	22	98	76
C7 superior 1 (N=46)	41.26	36.40	46.12	35.00	21	86	65
C7 superior 2 (N=49)	62.65	57.07	68.24	65.00	23	98	75
C7 inferior 1 (N=42)	41.10	35.63	46.56	34.50	21	89	68
C7 inferior 2 (N=53)	61.17	55.90	66.44	63.00	23	98	75
L1 superior 1 (N=51)	41.00	36.51	45.49	35.00	21	89	68
L1 superior 2 (N=44)	65.39	59.85	70.92	66.00	23	98	75
L1 inferior 1 (N=44)	37.20	32.74	41.67	33.00	21	89	68
L1 inferior 2 (N=51)	65.31	60.76	69.87	65.00	23	98	75
L2 superior 1 (N=42)	37.71	32.88	42.55	33.00	21	89	68
L2 superior 2 (N=53)	63.85	59.14	68.56	65.00	23	98	75
L2 inferior 1 (N=39)	35.69	31.49	39.89	33.00	21	80	59
L2 inferior 2 (N=56)	63.86	59.23	68.49	64.50	23	98	75
L3 superior 1 (N=35)	34.63	30.53	38.73	32.00	21	80	59
L3 superior 2 (N=60)	62.60	57.97	67.23	63.50	23	98	75
L3 inferior 1 (N=43)	37.91	33.51	42.31	34.00	21	80	59
L3 inferior 2 (N=52)	64.19	59.23	69.16	65.00	23	98	75
L4 superior 1 (N=30)	35.07	31.25	38.88	33.50	21	60	39
L4 superior 2 (N=65)	60.25	55.35	65.15	62.00	23	98	75
L4 inferior 1 (N=39)	38.49	33.49	43.48	34.00	21	89	68
L4 inferior 2 (N=56)	61.91	56.88	66.94	63.50	23	98	75
L5 superior 1 (N=31)	32.81	28.92	36.70	30.00	21	80	59
L5 superior 2 (N=64)	61.73	57.26	66.21	62.00	23	98	75
L5 inferior 1 (N=45)	38.91	34.16	43.66	33.00	21	89	68
L5 inferior 2 (N=50)	64.34	59.41	69.27	65.00	23	98	75

E 4: Correlations between indicators and age for females and males combined.

	Age	Groove	Rim	Apex	Fossa	Topography	Morphology	Inferior texture	Posterior iliac exostoses	Medial epiphysis	Midlambdoid	Lambda	Obelion	Vertex	Bregma	Midcoronal	Pterion	Sphenofrontal	Superior sphenotemporal	Inferior sphenotemporal	Zygomatico-maxillary	Incisive	Anterior median palatine	Posterior median palatine	Transverse palatine	Relief	Texture	Superior apex	Ventral margin	Dorsal margin	S1/S2 fusion	C3 superior	C3 inferior	C4 superior	C4 inferior	C5 superior	C5 inferior	C6 superior	C6 inferior	C7 superior	C7 inferior	L1 superior	L1 inferior	L2 superior	L2 inferior	L3 superior	L3 inferior	L4 superior	L4 inferior	L5 superior	L5 inferior
Age	1																																																	
Acetabulum																																																		
Groove	0.172**	1																																																
Rim	0.430**	0.306**	1																																														
Apex	0.282**	0.211**	0.274**	1																																													
Fossa	0.406**	0.132*	0.325**	0.108	1																																											
Auricular surface																																																	
Topography	0.182**	0.063	0.112	0.093	0.026	1																																										
Morphology	0.184**	0.104	0.178**	**0.204****	**0.193****	**0.262****	1																																									
Inferior texture	0.247**	0.026	0.153**	0.012	0.163*	0.089	0.176**	1																																								
Posterior iliac exostoses	0.333**	0.138*	0.220**	0.188**	0.125*	0.064	0.003	0.150*	1																																								
Clavicle																																																	
Medial epiphysis	0.275**	0.080	0.254**	0.231**	0.051	0.141*	0.091	0.180**	0.191**	1																																							
Cranial sutures																																																	
Midllambdoid	0.211**	0.143*	**0.264****	0.165**	0.120*	0.017	(-)0.006	(-)0.059	0.127*	0.110	1																																						
Lambda	0.191**	0.074	0.191**	0.089	0.173**	(-)0.022	0.043	(-)0.012	0.097	0.066	**0.771****	1																																						
Obelion	0.257**	0.077	0.217**	0.134*	0.203**	0.027	0.120	0.059	0.068	0.101	**0.520****	**0.675****	1																																					
Vertex	0.239**	0.101	0.234**	0.085	0.214**	0.124*	0.144*	(-)0.003	0.124*	0.044	**0.612****	**0.680****	**0.616****	1																																			
Bregma	0.252**	0.140*	0.197**	0.127*	0.174**	0.133*	0.168**	0.038	0.156**	0.113	**0.568****	**0.577****	**0.530****	**0.725****	1																																			
Midcoronal	0.318**	0.171**	0.262**	0.181**	0.172**	0.074	0.148*	0.069	0.177**	0.182**	**0.513****	**0.522****	**0.459****	**0.557****	**0.721****	1																																		
Pterion	0.424**	0.118*	0.313**	0.242**	0.258**	0.049	0.179**	0.105	0.211**	0.187**	0.406**	**0.427****	0.417**	**0.468****	**0.497****	**0.607****	1																																	
Sphenofrontal	0.373**	0.092	0.273**	0.251**	0.227**	0.035	0.223**	0.078	0.188**	0.163**	0.284**	0.362**	0.291**	**0.417****	**0.440****	**0.531****	**0.791****	1																																
Superior spheno-temporal	0.160**	0.009	0.038	0.023	0.151**	0.034	0.119	(-)0.042	0.071	<0.001	**0.237****	**0.211****	0.079	**0.229****	**0.274****	**0.205****	**0.230****	**0.336****	1																																
Inferior spheno-temporal	0.213**	0.022	0.120*	0.086	0.181**	0.051	0.136*	0.004	0.130*	0.046	**0.292****	**0.253****	0.095	**0.305****	**0.319****	**0.239****	**0.316****	**0.379****	**0.735****	1																															
Zygomatico-maxillary	0.324**	0.056	0.240**	0.122*	0.133*	0.121*	0.030	(-)0.040	0.097	0.171**	**0.337****	**0.328****	0.301**	0.322**	**0.351****	0.314**	**0.444****	**0.434****	**0.325****	**0.388****	1																													
Incisive	0.045	(-)0.051	(-)0.036	(-)0.039	(-)0.044	**0.048**	(-)0.035	(-)0.097	**0.105**	**0.111**	**0.120***	**0.135***	**0.052**	**0.074**	**0.106**	**0.113**	**0.100**	**0.086**	**0.078**	**0.064**	**0.126***	1																												
Anterior median palatine	0.210**	(-)0.019	0.109	0.060	0.041	0.066	0.002	0.004	0.104	0.140*	**0.296****	**0.228****	0.200**	**0.240****	**0.256****	**0.236****	**0.251****	0.195**	**0.250****	**0.259****	**0.444****	**0.269****	1																												
Posterior median palatine	0.357**	0.079	0.173**	0.167**	0.160**	0.164**	0.100	0.043	0.216**	0.214**	0.329**	0.280**	0.218**	0.310**	**0.359****	**0.385****	**0.388****	**0.369****	0.278**	0.282**	**0.459****	0.289**	**0.626****	1																										
Transverse palatine	0.249**	(-)0.024	0.151**	0.107	0.124*	0.092	0.032	(-)0.093	0.133*	0.111	**0.289****	0.217**	**0.258****	0.242**	**0.329****	0.228**	**0.264****	**0.285****	0.245**	**0.258****	**0.500****	0.167**	**0.464****	**0.519****	1																										
Iliac crest	0.283**	0.056	0.271**	0.250**	0.091	0.107	0.071	0.156*	0.165**	**0.699****	0.194**	0.161**	0.182**	0.135*	0.159**	0.200**	0.197**	0.167**	(-)0.004	0.074	0.145*	0.149*	0.134*	0.209**	0.180**	1																										
Pubic symphysis																																																		
Relief	0.404**	0.149*	0.270**	0.250**	0.146*	0.248**	0.298**	0.213**	0.253**	0.287**	0.164**	0.094	0.055	0.199**	0.227**	0.280**	0.289**	0.286**	0.115	0.201**	0.221**	0.136*	0.134*	0.266**	0.151*	0.265**	1																										
Texture	0.159**	0.111	**0.206****	0.043	**0.209****	(-)0.020	0.134*	**0.273****	0.054	0.106	0.051	0.021	0.114	0.018	(-)0.011	0.073	0.119	0.097	0.012	0.107	0.062	(-)0.031	(-)0.068	(-)0.039	0.011	0.101	**0.225****	1																										
Superior apex	0.401**	0.162**	0.328**	0.173**	0.173**	0.137*	0.282**	0.222**	0.177**	0.263**	0.214**	0.166**	0.192**	0.272**	0.265**	0.267**	0.311**	0.314**	0.160**	0.210**	0.258**	0.061	0.112	0.143*	0.116	0.257**	0.374**	0.237**	1																										
Ventral margin	0.393**	0.164**	0.289**	0.263**	0.166**	0.205**	0.279**	0.223**	0.217**	0.291**	0.235**	0.170**	0.203**	0.236**	0.241**	0.277**	0.228**	0.287**	0.103	0.226**	0.229**	0.087	0.178**	0.324**	0.243**	0.258**	**0.519****	0.219**	**0.454****	1																										
Dorsal margin	0.349**	0.109	0.262**	0.164**	0.150*	0.196**	0.133*	0.186**	0.182**	0.232**	0.281**	0.220**	0.236**	0.219**	0.251**	0.249**	0.228**	0.285**	0.060	0.183**	0.167**	0.157*	0.134*	0.220**	0.200**	0.239**	**0.510****	0.226**	0.293**	**0.523****	1																										
Sacrum																																																		
S1/S2 fusion	0.396**	0.158**	0.245**	0.284**	0.117*	0.266**	0.196**	0.229**	0.257**	0.327**	0.167**	0.065	0.172**	0.138*	0.197**	0.261**	0.205**	0.237**	0.038	0.092	0.153**	0.130*	0.133*	0.221**	0.205**	0.330**	0.388**	0.183**	0.286**	0.305**	0.274**	1																										
Suchey-Brooks	0.568**	0.201**	0.376**	0.291**	0.281**	0.221**	0.273**	0.190**	0.284**	0.256**	0.279**	0.197**	0.210**	0.285**	0.288**	0.329**	0.321**	0.333**	0.136*	0.252**	0.211**	0.033	0.188**	0.296**	0.247**	0.253**						0.382**	1																										
Vertebral bodies																																																	
C3 superior	0.304**	0.147*	**0.309****	0.260**	0.086	0.092	0.060	0.163*	0.182**	0.106	0.265**	0.213**	0.222**	0.166**	0.168**	0.063	0.130*	0.130*	0.070	0.171**	0.154*	0.037	0.202**	0.144*	0.252**	0.114	0.126*	0.114	0.185**	0.294**	0.141*	0.122*	0.269**	1																										
C3 inferior	0.385**	0.126*	0.341**	0.285**	0.121*	0.143*	0.068	0.159*	0.235**	0.170**	0.260**	0.222**	0.203**	0.183**	0.181**	0.156*	0.265**	0.267**	0.064	0.181**	0.342**	0.070	0.351**	0.339**	0.341**	0.180**	0.243**	0.087	0.223**	0.311**	0.259**	0.242**	0.337**	**0.599****	1																										
C4 superior	0.383**	0.030	0.297**	0.273**	0.110	0.162**	0.101	0.161*	0.190**	0.142*	0.301**	0.262**	0.276**	0.253**	0.294**	0.169**	0.281**	0.285**	0.132*	0.207**	0.317**	0.121*	0.357**	**0.400****	0.317**	0.133**	0.216**	0.030	0.273**	0.330**	0.299**	0.285**	0.370**	**0.513****	**0.634****	1																										
C4 inferior	0.465**	0.136*	0.427**	0.291**	0.308**	0.132*	0.168**	0.278**	0.256**	0.181**	0.264**	0.246**	0.238**	0.236**	0.272**	0.222**	0.299**	0.312**	0.155**	0.176**	0.233**	0.052	0.256**	0.306**	0.321**	0.180**	0.277**	0.170**	0.239**	0.370**	0.264**	0.300**	0.456**	**0.530****	**0.598****	**0.593****	1																										
C5 superior	0.448**	0.109	0.404**	0.272**	0.193**	0.142*	0.153*	0.230**	0.185**	0.158**	0.252**	0.272**	0.294**	0.218**	0.255**	0.158**	0.323**	0.250**	0.104	0.108	0.312**	(-)0.003	0.193**	0.308**	0.238**	0.185**	0.258**	0.115	0.243**	0.345**	0.259**	0.194**	0.390**	**0.462****	**0.559****	**0.617****	**0.661****	1																										
C5 inferior	0.438**	0.090	0.412**	0.270**	0.241**	0.025	0.195**	0.199**	0.192**	0.225**	0.254**	0.271**	0.300**	0.242**	0.302**	0.303**	0.369**	0.314**	0.163**	0.203**	0.248**	0.040	0.209**	0.209**	0.243**	0.196**	0.272**	0.068	0.293**	0.357**	0.311**	0.238**	0.398**	0.429**	**0.498****	**0.456****	**0.581****	**0.586****	1																										
C6 superior	0.461**	0.053	0.359**	0.352**	0.227**	0.127*	0.147*	0.176**	0.220**	0.178**	0.189**	0.192**	0.225**	0.215**	0.234**	0.223**	0.306**	0.251**	0.109	0.131**	0.226**	0.095	0.177**	0.316**	0.202**	0.186**	0.288**	0.068	0.253**	0.337**	0.273**	0.241**	0.392**	0.421**	**0.468****	**0.549****	**0.569****	**0.630****	**0.656****	1																										
C6 inferior	0.491**	0.112	0.412**	0.219**	0.273**	0.140*	0.155*	0.177**	0.247**	0.171**	0.241**	0.221**	0.232**	0.273**	0.283**	0.224**	0.289**	0.272**	0.121*	0.179**	0.325**	0.132*	0.242**	0.273**	0.220**	0.182**	0.226**	0.070	0.277**	0.303**	0.254**	0.262**	0.397**	0.384**	0.418**	0.491**	**0.587****	**0.545****	**0.674****	**0.609****	1																										
C7 superior	0.405**	0.087	0.311**	0.243**	0.198**	0.142*	0.112	0.177**	0.166**	0.151**	0.237**	0.190**	0.263**	0.182**	0.209**	0.206**	0.221**	0.151**	0.067	0.068	0.208**	0.007	0.178**	0.283**	0.212**	0.157**	0.165**	0.062	0.190**	0.287**	0.204**	0.255**	0.378**	0.401**	**0.466****	**0.548****	**0.547****	**0.603****	**0.569****	**0.653****	**0.613****	1																										
C7 inferior	0.440**	0.088	0.318**	0.172**	0.239**	0.096	0.057	0.131*	0.248**	0.176**	0.320**	0.251**	0.290**	0.192**	0.230**	0.209**	0.273**	0.238**	0.152**	0.178**	0.277**	0.102	0.279**	0.344**	0.320**	0.181**	0.208**	0.076	0.177**	0.205**	0.194**	0.271**	0.355**	**0.489****	**0.470****	**0.535****	**0.556****	**0.519****	**0.523****	**0.530****	**0.583****	**0.675****	1																										
L1 superior	0.379**	0.158**	**0.382****	0.257**	0.207**	0.075	0.092	0.066	0.281**	0.166**	0.291**	0.264**	0.227**	0.207**	0.237**	0.254**	0.296**	0.305**	0.064	0.115*	0.256**	0.113	0.206**	0.318**	0.300**	0.165**	0.175**	0.073	0.265**	0.310**	0.242**	0.260**	0.295**	**0.408****	0.365**	**0.416****	**0.395****	**0.380****	**0.460****	**0.465****	**0.454****	**0.430****	**0.470****	1																										
L1 inferior	0.495**	0.163**	0.382**	0.347**	0.195**	0.122*	0.117	0.097	0.339**	0.170**	0.273**	0.187**	0.208**	0.208**	0.208**	0.215**	0.286**	0.312**	0.126*	0.182**	0.296**	0.060	0.220**	0.348**	0.283**	0.173**	0.268**	0.060	0.249**	0.387**	0.309**	0.287**	0.414**	0.478**	**0.509****	**0.509****	**0.509****	**0.516****	0.490**	0.493**	0.484**	0.477**	**0.560****	**0.594****	1																										
L2 superior	0.501**	0.212**	0.468**	0.331**	0.273**	0.094	0.195**	0.212**	0.275**	0.192**	0.260**	0.225**	0.294**	0.250**	0.245**	0.294**	0.269**	0.250**	0.083	0.160**	0.226**	0.047	0.199**	0.269**	0.232**	0.198**	0.243**	0.140*	0.238**	0.347**	0.309**	0.382**	0.361**	0.467**	0.479**	0.423**	0.490**	0.459**	**0.535****	0.485**	0.492**	0.460**	**0.528****	**0.579****	**0.625****	1																										
L2 inferior	0.486**	0.122**	0.385**	0.315**	0.230**	0.062	0.177**	0.193**	0.378**	0.189**	0.242**	0.210**	0.246**	0.224**	0.219**	0.230**	0.293**	0.249**	0.119*	0.138*	0.256**	0.090	0.226**	0.289**	0.235**	0.192**	0.297**	0.065	0.267**	0.267**	0.270**	0.342**	0.385**	0.475**	**0.512****	0.485**	0.461**	**0.531****	**0.531****	**0.542****	**0.508****	**0.511****	**0.575****	**0.510****	**0.618****	**0.675****	1																										
L3 superior	0.515**	0.134**	0.431**	0.343**	0.222**	0.165**	0.167**	0.157*	0.314**	0.234**	0.283**	0.214**	0.237**	0.219**	0.278**	0.340**	0.368**	0.380**	0.129*	0.224**	0.307**	0.132*	0.261**	0.297**	0.258**	0.244**	0.328**	0.013	0.279**	0.360**	0.380**	0.381**	0.441**	0.385**	0.477**	0.507**	**0.536****	0.509**	**0.627****	0.515**	**0.587****	0.474**	**0.535****	**0.564****	**0.616****	**0.674****	**0.673****	1																										
L3 inferior	0.492**	0.187**	0.452**	0.316**	0.195**	0.129*	0.177**	0.150*	0.353**	0.205**	0.213**	0.132*	0.176**	0.140*	0.174**	0.210**	0.306**	0.342**	0.100	0.175**	0.280**	0.085	0.234**	0.283**	0.258**	0.198**	0.346**	0.170**	0.203**	0.327**	0.326**	0.348**	0.435**	0.399**	0.505**	0.479**	**0.517****	**0.540****	**0.568****	**0.545****	**0.547****	0.484**	**0.531****	0.487**	**0.672****	**0.659****	**0.730****	**0.697****	1																										
L4 superior	0.549**	0.198**	0.473**	0.335**	0.309**	0.157**	0.172**	0.208**	0.298**	0.256**	0.264**	0.213**	0.239**	0.250**	0.242**	0.279**	0.367**	0.358**	0.044	0.136*	0.281**	0.033	0.206**	0.242**	0.214**	0.249**	0.329**	0.100	0.337**	0.320**	0.295**	0.341**	0.446**	0.394**	0.450**	0.396**	0.471**	0.500	**0.554****	0.488**	0.479**	0.458**	0.435**	0.464**	0.493**	**0.577****	**0.584****	**0.715****	**0.658****	1																										
L4 inferior	0.456**	0.164**	0.434**	0.359**	0.217**	0.124*	0.117	0.129*	0.306**	0.204**	0.227**	0.161**	0.198**	0.201**	0.244**	0.255**	0.324**	0.311**	0.034	0.169**	0.219**	0.074	0.169**	0.299**	0.209**	0.177**	0.313**	0.104	0.237**	0.311**	0.290**	0.318**	0.406**	0.289**	0.406**	0.420**	0.449**	0.433**	0.440**	0.440**	0.424**	0.403**	0.438**	**0.475****	**0.521****	**0.602****	**0.584****	**0.596****	**0.662****	**0.592****	1																										
L5 superior	0.544**	0.167**	0.420**	0.389**	0.252**	0.174**	0.183**	0.197**	0.280**	0.254**	0.280**	0.175**	0.230**	0.180**	0.193**	0.259**	0.306**	0.300**	0.006	0.085	0.241**	0.008	0.217**	0.270**	0.197**	0.223**	0.374**	0.142*	0.330**	0.325**	0.348**	0.331**	0.463**	0.356**	0.452**	0.393**	0.486**	0.463**	0.502**	0.494**	0.477**	0.467**	0.485**	0.469**	0.515**	**0.575****	**0.613****	**0.654****	**0.659****	**0.737****	**0.644****	1														
L5 inferior	0.508**	0.192**	0.383**	0.347**	0.224**	0.142*	0.151*	0.133*	0.276**	0.219**	0.217**	0.146*	0.189**	0.246**	0.189**	0.233**	0.291**	0.286**	0.030	0.114*	0.196**	0.032	0.165**	0.269**	0.210**	0.224**	0.362**	0.100	0.215**	0.296**	0.343**	0.327**	0.466**	0.345**	0.416**	0.394**	0.461**	0.445**	**0.516****	0.496**	**0.515****	0.421**	0.450**	0.447**	0.508**	**0.564****	**0.564****	**0.599****	**0.631****	**0.632****	**0.558****	**0.655****	1

** p ≤ 0.05*
*** p ≤ 0.01*

E 5: Transition analysis model 1 age estimation table.

					95% confidence interval	
S1/S2 fusion	***L5 superior***	***Acetabular fossa***	***Posterior median palatine suture***	***Point estimate age***	***Lower margin***	***Upper margin***
1	1	2	1	20	20	21
1	1	2	2	20	20	21
1	1	2	3	20	20	21
1	1	2	4	20	20	21
1	1	2	5	20	20	21
1	1	3	1	20	20	21
1	1	3	2	20	20	21
1	1	3	3	20	20	21
1	1	3	4	20	21	21
1	1	3	5	20	20	21
1	1	4	1	20	20	21
1	1	4	2	20	20	21
1	1	4	3	20	20	21
1	1	4	4	20	20	21
1	1	4	5	20	20	21
1	2	2	1	20	20	21
1	2	2	2	28	20	29
1	2	2	3	29	20	30
1	2	2	4	31	20	32
1	2	2	5	31	20	32
1	2	3	1	30	20	31
1	2	3	2	40	20	41
1	2	3	3	42	20	43
1	2	3	4	45	20	46
1	2	3	5	44	20	45
1	2	4	1	20	20	21
1	2	4	2	28	20	29

S1/S2 fusion	*L5 superior*	*Acetabular fossa*	*Posterior median palatine suture*	*Point estimate age*	*95% confidence interval*	
					Lower margin	*Upper margin*
1	2	4	3	30	20	31
1	2	4	4	32	20	33
1	2	4	5	32	20	33
2	1	2	1	20	20	21
2	1	2	2	20	22	21
2	1	2	3	20	22	21
2	1	2	4	23	20	24
2	1	2	5	22	24	23
2	1	3	1	22	24	23
2	1	3	2	33	20	34
2	1	3	3	35	20	36
2	1	3	4	37	20	38
2	1	3	5	37	20	38
2	1	4	1	20	20	21
2	1	4	2	20	22	21
2	1	4	3	20	22	21
2	1	4	4	23	20	24
2	1	4	5	23	20	24
2	2	2	1	36	20	37
2	2	2	2	45	20	46
2	2	2	3	48	20	49
2	2	2	4	54	20	55
2	2	2	5	52	20	53
2	2	3	1	49	20	50
2	2	3	2	61	20	62
2	2	3	3	64	20	65
2	2	3	4	79	20	80
2	2	3	5	73	20	74

S1/S2 fusion	*L5 superior*	*Acetabular fossa*	*Posterior median palatine suture*	*Point estimate age*	*95% confidence interval* *Lower margin*	*Upper margin*
2	2	4	1	37	20	38
2	2	4	2	49	20	50
2	2	4	3	55	20	56
2	2	4	4	98	20	98
2	2	4	5	98	20	98

E 6: Transition analysis model 2 age estimation table.

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	1	2	1	20	20	21
1	2	1	2	2	20	20	21
1	2	1	2	3	20	20	21
1	2	1	2	4	20	20	21
1	2	1	3	1	25	20	26
1	2	1	3	2	26	20	27
1	2	1	3	3	28	20	29
1	2	1	3	4	27	20	28
1	2	1	4	1	20	20	21
1	2	1	4	2	20	20	21
1	2	1	4	3	20	20	21
1	2	1	4	4	20	20	21
1	2	1	5	1	26	20	27
1	2	1	5	2	27	20	28
1	2	1	5	3	29	20	30
1	2	1	5	4	27	20	28
1	2	1	6	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	1	6	2	20	20	21
1	2	1	6	3	20	20	21
1	2	1	6	4	20	20	21
1	2	2	2	1	20	20	21
1	2	2	2	2	20	20	21
1	2	2	2	3	20	20	21
1	2	2	2	4	20	20	21
1	2	2	3	1	28	20	29
1	2	2	3	2	29	20	30
1	2	2	3	3	31	20	32
1	2	2	3	4	29	20	30
1	2	2	4	1	20	20	21
1	2	2	4	2	20	20	21
1	2	2	4	3	20	20	21
1	2	2	4	4	20	20	21
1	2	2	5	1	29	20	30
1	2	2	5	2	30	20	31
1	2	2	5	3	33	20	34
1	2	2	5	4	30	20	31
1	2	2	6	1	20	20	21
1	2	2	6	2	20	20	21
1	2	2	6	3	20	20	21
1	2	2	6	4	20	20	21
1	2	3	2	1	20	20	21
1	2	3	2	2	20	20	21
1	2	3	2	3	20	20	21
1	2	3	2	4	20	20	21
1	2	3	3	1	25	20	26

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	3	3	2	25	20	26
1	2	3	3	3	27	20	28
1	2	3	3	4	26	20	27
1	2	3	4	1	20	20	21
1	2	3	4	2	20	20	21
1	2	3	4	3	20	20	21
1	2	3	4	4	20	20	21
1	2	3	5	1	25	20	26
1	2	3	5	2	26	20	27
1	2	3	5	3	28	20	29
1	2	3	5	4	26	20	27
1	2	3	6	1	20	20	21
1	2	3	6	2	20	20	21
1	2	3	6	3	20	20	21
1	2	3	6	4	20	20	21
1	2	4	2	1	20	20	21
1	2	4	2	2	20	20	21
1	2	4	2	3	20	20	21
1	2	4	2	4	20	20	21
1	2	4	3	1	28	20	29
1	2	4	3	2	29	20	30
1	2	4	3	3	31	20	32
1	2	4	3	4	29	20	30
1	2	4	4	1	20	20	21
1	2	4	4	2	20	20	21
1	2	4	4	3	20	20	21
1	2	4	4	4	20	20	21
1	2	4	5	1	29	20	30

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	4	5	2	30	20	31
1	2	4	5	3	33	20	34
1	2	4	5	4	31	20	32
1	2	4	6	1	20	20	21
1	2	4	6	2	20	20	21
1	2	4	6	3	20	20	21
1	2	4	6	4	20	20	21
1	3	1	2	1	20	20	21
1	3	1	2	2	20	20	21
1	3	1	2	3	20	20	21
1	3	1	2	4	20	20	21
1	3	1	3	1	29	20	30
1	3	1	3	2	30	20	31
1	3	1	3	3	32	20	33
1	3	1	3	4	30	20	31
1	3	1	4	1	20	20	21
1	3	1	4	2	20	20	21
1	3	1	4	3	20	20	21
1	3	1	4	4	20	20	21
1	3	1	5	1	30	20	31
1	3	1	5	2	31	20	32
1	3	1	5	3	34	20	35
1	3	1	5	4	32	20	33
1	3	1	6	1	20	20	21
1	3	1	6	2	20	20	21
1	3	1	6	3	20	21	21
1	3	1	6	4	20	20	21
1	3	2	2	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	3	2	2	2	20	20	21
1	3	2	2	3	20	21	21
1	3	2	2	4	20	20	21
1	3	2	3	1	32	20	33
1	3	2	3	2	33	20	34
1	3	2	3	3	36	20	37
1	3	2	3	4	33	20	34
1	3	2	4	1	20	20	21
1	3	2	4	2	21	23	22
1	3	2	4	3	33	20	34
1	3	2	4	4	23	20	24
1	3	2	5	1	34	20	35
1	3	2	5	2	35	20	36
1	3	2	5	3	40	20	41
1	3	2	5	4	36	20	37
1	3	2	6	1	20	21	21
1	3	2	6	2	23	20	24
1	3	2	6	3	36	20	37
1	3	2	6	4	25	20	26
1	3	3	2	1	20	20	21
1	3	3	2	2	20	20	21
1	3	3	2	3	20	20	21
1	3	3	2	4	20	20	21
1	3	3	3	1	28	20	29
1	3	3	3	2	29	20	30
1	3	3	3	3	30	20	31
1	3	3	3	4	29	20	30
1	3	3	4	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	3	3	4	2	20	20	21
1	3	3	4	3	20	20	21
1	3	3	4	4	20	20	21
1	3	3	5	1	28	20	29
1	3	3	5	2	30	20	31
1	3	3	5	3	32	20	33
1	3	3	5	4	30	20	31
1	3	3	6	1	20	20	21
1	3	3	6	2	20	20	21
1	3	3	6	3	20	20	21
1	3	3	6	4	20	20	21
1	3	4	2	1	20	20	21
1	3	4	2	2	20	20	21
1	3	4	2	3	20	21	21
1	3	4	2	4	20	20	21
1	3	4	3	1	32	20	33
1	3	4	3	2	33	20	34
1	3	4	3	3	36	20	37
1	3	4	3	4	34	20	35
1	3	4	4	1	20	20	21
1	3	4	4	2	22	25	23
1	3	4	4	3	36	20	37
1	3	4	4	4	24	20	25
1	3	4	5	1	34	20	35
1	3	4	5	2	36	20	37
1	3	4	5	3	41	20	42
1	3	4	5	4	37	20	38
1	3	4	6	1	20	21	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	3	4	6	2	25	20	26
1	3	4	6	3	38	20	39
1	3	4	6	4	27	20	28
1	4	1	2	1	20	20	21
1	4	1	2	2	20	20	21
1	4	1	2	3	20	20	21
1	4	1	2	4	20	20	21
1	4	1	3	1	25	20	26
1	4	1	3	2	26	20	27
1	4	1	3	3	28	20	29
1	4	1	3	4	27	20	28
1	4	1	4	1	20	20	21
1	4	1	4	2	20	20	21
1	4	1	4	3	20	20	21
1	4	1	4	4	20	20	21
1	4	1	5	1	26	20	27
1	4	1	5	2	27	20	28
1	4	1	5	3	29	20	30
1	4	1	5	4	27	20	28
1	4	1	6	1	20	20	21
1	4	1	6	2	20	20	21
1	4	1	6	3	20	20	21
1	4	1	6	4	20	20	21
1	4	2	2	1	20	20	21
1	4	2	2	2	20	20	21
1	4	2	2	3	20	20	21
1	4	2	2	4	20	20	21
1	4	2	3	1	28	20	29

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	4	2	3	2	29	20	30
1	4	2	3	3	31	20	32
1	4	2	3	4	29	20	30
1	4	2	4	1	20	20	21
1	4	2	4	2	20	20	21
1	4	2	4	3	20	20	21
1	4	2	4	4	20	20	21
1	4	2	5	1	29	20	30
1	4	2	5	2	30	20	31
1	4	2	5	3	33	20	34
1	4	2	5	4	31	20	32
1	4	2	6	1	20	20	21
1	4	2	6	2	20	20	21
1	4	2	6	3	20	20	21
1	4	2	6	4	20	20	21
1	4	3	2	1	20	20	21
1	4	3	2	2	20	20	21
1	4	3	2	3	20	20	21
1	4	3	2	4	20	20	21
1	4	3	3	1	25	20	26
1	4	3	3	2	26	20	27
1	4	3	3	3	27	20	28
1	4	3	3	4	26	20	27
1	4	3	4	1	20	20	21
1	4	3	4	2	20	20	21
1	4	3	4	3	20	20	21
1	4	3	4	4	20	20	21
1	4	3	5	1	25	20	26

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	4	3	5	2	26	20	27
1	4	3	5	3	28	20	29
1	4	3	5	4	26	20	27
1	4	3	6	1	20	20	21
1	4	3	6	2	20	20	21
1	4	3	6	3	20	20	21
1	4	3	6	4	20	20	21
1	4	4	2	1	20	20	21
1	4	4	2	2	20	20	21
1	4	4	2	3	20	20	21
1	4	4	2	4	20	20	21
1	4	4	3	1	28	20	29
1	4	4	3	2	29	20	30
1	4	4	3	3	32	20	33
1	4	4	3	4	30	20	31
1	4	4	4	1	20	20	21
1	4	4	4	2	20	20	21
1	4	4	4	3	20	20	21
1	4	4	4	4	20	20	21
1	4	4	5	1	29	20	30
1	4	4	5	2	31	20	32
1	4	4	5	3	34	20	35
1	4	4	5	4	31	20	32
1	4	4	6	1	20	20	21
1	4	4	6	2	20	20	21
1	4	4	6	3	20	20	21
1	4	4	6	4	20	20	21
1	2	1	2	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	1	2	2	20	20	21
1	2	1	2	3	20	21	21
1	2	1	2	4	20	20	21
1	2	1	3	1	33	20	34
1	2	1	3	2	34	20	35
1	2	1	3	3	37	20	38
1	2	1	3	4	35	20	36
1	2	1	4	1	20	22	21
1	2	1	4	2	26	20	27
1	2	1	4	3	40	20	41
1	2	1	4	4	29	20	30
1	2	1	5	1	36	20	37
1	2	1	5	2	37	20	38
1	2	1	5	3	44	20	45
1	2	1	5	4	39	20	40
1	2	1	6	1	22	24	23
1	2	1	6	2	29	20	30
1	2	1	6	3	42	20	43
1	2	1	6	4	33	20	34
1	2	2	2	1	20	21	21
1	2	2	2	2	22	24	23
1	2	2	2	3	25	20	26
1	2	2	2	4	22	20	23
1	2	2	3	1	37	20	38
1	2	2	3	2	38	20	39
1	2	2	3	3	42	20	43
1	2	2	3	4	39	20	40
1	2	2	4	1	38	20	39

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	2	4	2	42	20	43
1	2	2	4	3	51	20	52
1	2	2	4	4	45	20	46
1	2	2	5	1	43	20	44
1	2	2	5	2	45	20	46
1	2	2	5	3	60	20	61
1	2	2	5	4	49	20	50
1	2	2	6	1	40	20	41
1	2	2	6	2	44	20	45
1	2	2	6	3	53	20	54
1	2	2	6	4	47	20	48
1	2	3	2	1	20	20	21
1	2	3	2	2	20	20	21
1	2	3	2	3	20	21	21
1	2	3	2	4	20	20	21
1	2	3	3	1	31	20	32
1	2	3	3	2	32	20	33
1	2	3	3	3	35	20	36
1	2	3	3	4	33	20	34
1	2	3	4	1	20	21	21
1	2	3	4	2	21	24	22
1	2	3	4	3	31	20	32
1	2	3	4	4	23	20	24
1	2	3	5	1	33	20	34
1	2	3	5	2	34	20	35
1	2	3	5	3	38	20	39
1	2	3	5	4	35	20	36
1	2	3	6	1	20	21	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	3	6	2	23	20	24
1	2	3	6	3	33	20	34
1	2	3	6	4	25	20	26
2	2	4	2	1	20	22	21
2	2	4	2	2	22	24	23
2	2	4	2	3	26	20	27
2	2	4	2	4	23	20	24
2	2	4	3	1	37	20	38
2	2	4	3	2	39	20	40
2	2	4	3	3	43	20	44
2	2	4	3	4	40	20	41
2	2	4	4	1	40	20	41
2	2	4	4	2	44	20	45
2	2	4	4	3	54	20	55
2	2	4	4	4	47	20	48
2	2	4	5	1	44	20	45
2	2	4	5	2	47	20	48
2	2	4	5	3	66	20	67
2	2	4	5	4	54	20	55
2	2	4	6	1	42	20	43
2	2	4	6	2	45	20	46
2	2	4	6	3	56	20	57
2	2	4	6	4	49	20	50
2	3	1	2	1	21	23	22
2	3	1	2	2	24	20	25
2	3	1	2	3	27	20	28
2	3	1	2	4	24	20	25
2	3	1	3	1	38	20	39

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	3	1	3	2	40	20	41
2	3	1	3	3	44	20	45
2	3	1	3	4	41	20	42
2	3	1	4	1	43	20	44
2	3	1	4	2	46	20	47
2	3	1	4	3	55	20	56
2	3	1	4	4	49	20	50
2	3	1	5	1	47	20	48
2	3	1	5	2	50	20	51
2	3	1	5	3	67	20	68
2	3	1	5	4	57	20	58
2	3	1	6	1	45	20	46
2	3	1	6	2	47	20	48
2	3	1	6	3	58	20	59
2	3	1	6	4	51	20	52
2	3	2	2	1	27	20	28
2	3	2	2	2	29	20	30
2	3	2	2	3	33	20	34
2	3	2	2	4	30	20	31
2	3	2	3	1	43	20	44
2	3	2	3	2	45	20	46
2	3	2	3	3	50	20	51
2	3	2	3	4	46	20	47
2	3	2	4	1	54	20	55
2	3	2	4	2	55	20	56
2	3	2	4	3	65	20	66
2	3	2	4	4	60	20	61
2	3	2	5	1	65	20	66

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	3	2	5	2	66	20	67
2	3	2	5	3	80	20	81
2	3	2	5	4	79	20	80
2	3	2	6	1	56	20	57
2	3	2	6	2	58	20	59
2	3	2	6	3	69	20	70
2	3	2	6	4	64	20	65
2	3	3	2	1	20	22	21
2	3	3	2	2	22	24	23
2	3	3	2	3	25	20	26
2	3	3	2	4	23	20	24
2	3	3	3	1	36	20	37
2	3	3	3	2	37	20	38
2	3	3	3	3	40	20	41
2	3	3	3	4	37	20	38
2	3	3	4	1	34	20	35
2	3	3	4	2	37	20	38
2	3	3	4	3	43	20	44
2	3	3	4	4	39	20	40
2	3	3	5	1	39	20	40
2	3	3	5	2	41	20	42
2	3	3	5	3	45	20	46
2	3	3	5	4	42	20	43
2	3	3	6	1	36	20	37
2	3	3	6	2	39	20	40
2	3	3	6	3	44	20	45
2	3	3	6	4	40	20	41
2	3	4	2	1	27	20	28

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	3	4	2	2	30	20	31
2	3	4	2	3	34	20	35
2	3	4	2	4	31	20	32
2	3	4	3	1	44	20	45
2	3	4	3	2	46	20	47
2	3	4	3	3	52	20	53
2	3	4	3	4	48	20	49
2	3	4	4	1	56	20	57
2	3	4	4	2	58	20	59
2	3	4	4	3	68	20	69
2	3	4	4	4	64	20	65
2	3	4	5	1	70	20	71
2	3	4	5	2	70	20	71
2	3	4	5	3	85	20	86
2	3	4	5	4	87	20	88
2	3	4	6	1	59	20	60
2	3	4	6	2	60	20	61
2	3	4	6	3	74	20	75
2	3	4	6	4	70	20	71
2	4	1	2	1	20	20	21
2	4	1	2	2	20	20	21
2	4	1	2	3	20	21	21
2	4	1	2	4	20	20	21
2	4	1	3	1	33	20	34
2	4	1	3	2	35	20	36
2	4	1	3	3	38	20	39
2	4	1	3	4	35	20	36
2	4	1	4	1	20	22	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	4	1	4	2	27	20	28
2	4	1	4	3	43	20	44
2	4	1	4	4	31	20	32
2	4	1	5	1	36	20	37
2	4	1	5	2	39	20	40
2	4	1	5	3	49	20	50
2	4	1	5	4	40	20	41
2	4	1	6	1	22	20	23
2	4	1	6	2	31	20	32
2	4	1	6	3	45	20	46
2	4	1	6	4	35	20	36
2	4	2	2	1	20	21	21
2	4	2	2	2	22	24	23
2	4	2	2	3	26	20	27
2	4	2	2	4	23	20	24
2	4	2	3	1	37	20	38
2	4	2	3	2	39	20	40
2	4	2	3	3	43	20	44
2	4	2	3	4	40	20	41
2	4	2	4	1	41	20	42
2	4	2	4	2	45	20	46
2	4	2	4	3	60	20	61
2	4	2	4	4	50	20	51
2	4	2	5	1	46	20	47
2	4	2	5	2	50	20	51
2	4	2	5	3	98	20	98
2	4	2	5	4	98	20	98
2	4	2	6	1	43	20	44

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	4	2	6	2	47	20	48
2	4	2	6	3	91	20	92
2	4	2	6	4	98	20	98
2	4	3	2	1	20	20	21
2	4	3	2	2	20	20	21
2	4	3	2	3	20	21	21
2	4	3	2	4	20	20	21
2	4	3	3	1	31	20	32
2	4	3	3	2	33	20	34
2	4	3	3	3	35	20	36
2	4	3	3	4	33	20	34
2	4	3	4	1	20	20	21
2	4	3	4	2	22	24	23
2	4	3	4	3	32	20	33
2	4	3	4	4	23	20	24
2	4	3	5	1	33	20	34
2	4	3	5	2	35	20	36
2	4	3	5	3	39	20	40
2	4	3	5	4	36	20	37
2	4	3	6	1	20	21	21
2	4	3	6	2	24	20	25
2	4	3	6	3	34	20	35
2	4	3	6	4	26	20	27
2	4	4	2	1	20	22	21
2	4	4	2	2	22	20	23
2	4	4	2	3	26	20	27
2	4	4	2	4	23	20	24
2	4	4	3	1	38	20	39

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	4	4	3	2	40	20	41
2	4	4	3	3	45	20	46
2	4	4	3	4	41	20	42
2	4	4	4	1	44	20	45
2	4	4	4	2	47	20	48
2	4	4	4	3	78	20	79
2	4	4	4	4	54	20	55
2	4	4	5	1	98	20	98
2	4	4	5	2	95	20	96
2	4	4	5	3	98	20	98
2	4	4	5	4	98	20	98
2	4	4	6	1	46	20	47
2	4	4	6	2	50	20	51
2	4	4	6	3	98	20	98
2	4	4	6	4	98	20	98

E 7: Transition analysis model 3 age estimation table.

S1/S2 fusion	*L5 superior*	*Acetabular fossa*	*Suchey-Brooks*	*Point estimate age*	*95% confidence interval Lower margin*	*Upper margin*
1	1	2	2	20	20	21
1	1	2	3	31	20	32
1	1	2	4	20	20	21
1	1	2	5	23	20	24
1	1	2	6	20	20	21
1	1	3	2	20	20	21
1	1	3	3	35	20	36

S1/S2 fusion	*L5 superior*	*Acetabular fossa*	*Suchey-Brooks*	*Point estimate age*	*95% confidence interval*	
					Lower margin	*Upper margin*
1	1	3	4	20	21	21
1	1	3	5	31	20	32
1	1	3	6	20	22	21
1	1	4	2	20	20	21
1	1	4	3	31	20	32
1	1	4	4	20	20	21
1	1	4	5	23	20	24
1	1	4	6	20	20	21
1	2	2	2	20	21	21
1	2	2	3	36	20	37
1	2	2	4	21	23	22
1	2	2	5	33	20	34
1	2	2	6	23	20	24
1	2	3	2	28	20	29
1	2	3	3	43	20	44
1	2	3	4	44	20	45
1	2	3	5	42	20	43
1	2	3	6	48	20	49
1	2	4	2	20	20	21
1	2	4	3	37	20	38
1	2	4	4	22	23	23
1	2	4	5	33	20	34
1	2	4	6	24	20	25
2	1	2	2	20	20	21
2	1	2	3	36	20	37
2	1	2	4	20	21	21
2	1	2	5	32	20	33
2	1	2	6	21	23	22
2	1	3	2	27	20	28

S1/S2 fusion	*L5 superior*	*Acetabular fossa*	*Suchey-Brooks*	*Point estimate age*	*95% confidence interval*	
					Lower margin	*Upper margin*
2	1	3	3	42	20	43
2	1	3	4	41	20	42
2	1	3	5	41	20	42
2	1	3	6	45	20	46
2	1	4	2	20	20	21
2	1	4	3	36	20	37
2	1	4	4	20	21	21
2	1	4	5	32	20	33
2	1	4	6	22	20	23
2	2	2	2	28	20	29
2	2	2	3	44	20	45
2	2	2	4	46	20	47
2	2	2	5	43	20	44
2	2	2	6	50	20	51
2	2	3	2	39	20	40
2	2	3	3	56	20	57
2	2	3	4	74	20	75
2	2	3	5	54	20	55
2	2	3	6	83	20	84
2	2	4	2	29	20	30
2	2	4	3	45	20	46
2	2	4	4	87	20	87
2	2	4	5	44	20	45
2	2	4	6	87	20	87

E 8: Transition analysis model 4 age estimation table.

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
1	2	1	1	1	20	20	21
2	2	1	1	1	20	20	21
1	2	1	2	1	20	20	21
2	2	1	2	1	20	20	21
1	2	1	3	1	20	20	21
2	2	1	3	1	20	20	21
1	2	1	4	1	20	20	21
2	2	1	4	1	20	20	21
1	2	2	1	1	20	20	21
2	2	2	1	1	20	20	21
1	2	2	2	1	20	20	21
2	2	2	2	1	20	20	21
1	2	2	3	1	20	20	21
2	2	2	3	1	20	20	21
1	2	2	4	1	20	20	21
2	2	2	4	1	20	20	21
1	2	3	1	1	20	20	21
2	2	3	1	1	20	20	21
1	2	3	2	1	20	20	21
2	2	3	2	1	20	20	21
1	2	3	3	1	20	20	21
2	2	3	3	1	20	20	21
1	2	3	4	1	20	22	21
2	2	3	4	1	20	20	21
1	2	4	1	1	20	20	21

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
2	2	4	1	1	20	20	21
1	2	4	2	1	20	20	21
2	2	4	2	1	20	20	21
1	2	4	3	1	20	20	21
2	2	4	3	1	20	20	21
1	2	4	4	1	21	22	22
2	2	4	4	1	20	20	21
1	3	1	1	1	20	20	21
2	3	1	1	1	20	20	21
1	3	1	2	1	20	20	21
2	3	1	2	1	20	20	21
1	3	1	3	1	22	24	23
2	3	1	3	1	20	21	21
1	3	1	4	1	31	20	32
2	3	1	4	1	20	21	21
1	3	2	1	1	20	20	21
2	3	2	1	1	20	20	21
1	3	2	2	1	20	20	21
2	3	2	2	1	20	20	21
1	3	2	3	1	23	20	24
2	3	2	3	1	20	21	21
1	3	2	4	1	32	20	33
2	3	2	4	1	20	21	21
1	3	3	1	1	20	20	21
2	3	3	1	1	20	20	21
1	3	3	2	1	22	24	23
2	3	3	2	1	20	20	21

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
1	3	3	3	1	32	20	33
2	3	3	3	1	24	20	25
1	3	3	4	1	39	20	40
2	3	3	4	1	25	20	26
1	3	4	1	1	20	20	21
2	3	4	1	1	20	20	21
1	3	4	2	1	22	25	23
2	3	4	2	1	20	20	21
1	3	4	3	1	34	20	35
2	3	4	3	1	26	20	27
1	3	4	4	1	41	20	42
2	3	4	4	1	27	20	28
1	4	1	1	1	20	20	21
2	4	1	1	1	20	20	21
1	4	1	2	1	20	20	21
2	4	1	2	1	20	20	21
1	4	1	3	1	20	20	21
2	4	1	3	1	20	20	21
1	4	1	4	1	20	20	21
2	4	1	4	1	20	20	21
1	4	2	1	1	20	20	21
2	4	2	1	1	20	20	21
1	4	2	2	1	20	20	21
2	4	2	2	1	20	20	21
1	4	2	3	1	20	20	21
2	4	2	3	1	20	20	21
1	4	2	4	1	20	21	21

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
2	4	2	4	1	20	20	21
1	4	3	1	1	20	20	21
2	4	3	1	1	20	20	21
1	4	3	2	1	20	20	21
2	4	3	2	1	20	20	21
1	4	3	3	1	20	21	21
2	4	3	3	1	20	21	21
1	4	3	4	1	23	20	24
2	4	3	4	1	20	21	21
1	4	4	1	1	20	20	21
2	4	4	1	1	20	20	21
1	4	4	2	1	20	20	21
2	4	4	2	1	20	20	21
1	4	4	3	1	20	22	21
2	4	4	3	1	20	21	21
1	4	4	4	1	24	20	25
2	4	4	4	1	20	21	21
1	2	1	1	2	20	20	21
2	2	1	1	2	20	20	21
1	2	1	2	2	23	20	24
2	2	1	2	2	20	20	21
1	2	1	3	2	31	20	32
2	2	1	3	2	25	20	26
1	2	1	4	2	37	20	38
2	2	1	4	2	26	20	27
1	2	2	1	2	20	20	21
2	2	2	1	2	20	20	21

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
1	2	2	2	2	23	20	24
2	2	2	2	2	20	20	21
1	2	2	3	2	33	20	34
2	2	2	3	2	26	20	27
1	2	2	4	2	38	20	39
2	2	2	4	2	28	20	29
1	2	3	1	2	20	23	21
2	2	3	1	2	20	20	21
1	2	3	2	2	31	20	32
2	2	3	2	2	20	20	21
1	2	3	3	2	41	20	42
2	2	3	3	2	33	20	34
1	2	3	4	2	45	20	46
2	2	3	4	2	36	20	37
1	2	4	1	2	21	23	22
2	2	4	1	2	20	20	21
1	2	4	2	2	31	20	32
2	2	4	2	2	20	20	21
1	2	4	3	2	44	20	45
2	2	4	3	2	35	20	36
1	2	4	4	2	47	20	48
2	2	4	4	2	38	20	39
1	3	1	1	2	20	20	21
2	3	1	1	2	20	20	21
1	3	1	2	2	20	20	21
2	3	1	2	2	20	20	21
1	3	1	3	2	20	20	21

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
2	3	1	3	2	20	20	21
1	3	1	4	2	20	20	21
2	3	1	4	2	20	20	21
1	3	2	1	2	20	20	21
2	3	2	1	2	20	20	21
1	3	2	2	2	20	20	21
2	3	2	2	2	20	20	21
1	3	2	3	2	20	20	21
2	3	2	3	2	20	20	21
1	3	2	4	2	20	20	21
2	3	2	4	2	20	20	21
1	3	3	1	2	20	20	21
2	3	3	1	2	20	20	21
1	3	3	2	2	20	20	21
2	3	3	2	2	20	20	21
1	3	3	3	2	20	20	21
2	3	3	3	2	20	20	21
1	3	3	4	2	21	22	22
2	3	3	4	2	20	20	21
1	3	4	1	2	20	20	21
2	3	4	1	2	20	20	21
1	3	4	2	2	20	20	21
2	3	4	2	2	20	20	21
1	3	4	3	2	20	20	21
2	3	4	3	2	20	20	21
1	3	4	4	2	21	23	22
2	3	4	4	2	20	20	21

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
1	4	1	1	2	20	20	21
2	4	1	1	2	20	20	21
1	4	1	2	2	20	20	21
2	4	1	2	2	20	20	21
1	4	1	3	2	22	25	23
2	4	1	3	2	20	21	21
1	4	1	4	2	31	20	32
2	4	1	4	2	20	20	21
1	4	2	1	2	20	20	21
2	4	2	1	2	20	20	21
1	4	2	2	2	20	20	21
2	4	2	2	2	20	20	21
1	4	2	3	2	24	20	25
2	4	2	3	2	20	21	21
1	4	2	4	2	33	20	34
2	4	2	4	2	20	21	21
1	4	3	1	2	20	20	21
2	4	3	1	2	20	20	21
1	4	3	2	2	23	20	24
2	4	3	2	2	20	20	21
1	4	3	3	2	33	20	34
2	4	3	3	2	25	20	26
1	4	3	4	2	40	20	41
2	4	3	4	2	26	20	27
1	4	4	1	2	20	20	21
2	4	4	1	2	20	20	21
1	4	4	2	2	23	25	24

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
2	4	4	2	2	20	20	21
1	4	4	3	2	36	20	37
2	4	4	3	2	26	20	27
1	4	4	4	2	42	20	43
2	4	4	4	2	28	20	29
1	2	1	1	3	20	20	21
2	2	1	1	3	20	20	21
1	2	1	2	3	20	21	21
2	2	1	2	3	20	20	21
1	2	1	3	3	21	23	22
2	2	1	3	3	20	21	21
1	2	1	4	3	27	20	28
2	2	1	4	3	20	21	21
1	2	2	1	3	20	20	21
2	2	2	1	3	20	20	21
1	2	2	2	3	20	21	21
2	2	2	2	3	20	20	21
1	2	2	3	3	22	20	23
2	2	2	3	3	20	21	21
1	2	2	4	3	28	20	29
2	2	2	4	3	20	21	21
1	2	3	1	3	20	22	21
2	2	3	1	3	20	21	21
1	2	3	2	3	24	20	25
2	2	3	2	3	20	21	21
1	2	3	3	3	27	20	28
2	2	3	3	3	25	20	26

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
1	2	3	4	3	32	20	33
2	2	3	4	3	25	20	26
1	2	4	1	3	20	22	21
2	2	4	1	3	20	21	21
1	2	4	2	3	24	20	25
2	2	4	2	3	20	21	21
1	2	4	3	3	28	20	29
2	2	4	3	3	25	20	26
1	2	4	4	3	32	20	33
2	2	4	4	3	26	20	27
1	3	1	1	3	33	20	34
2	3	1	1	3	27	20	28
1	3	1	2	3	39	20	40
2	3	1	2	3	28	20	29
1	3	1	3	3	49	20	50
2	3	1	3	3	40	20	41
1	3	1	4	3	51	20	52
2	3	1	4	3	45	20	46
1	3	2	1	3	33	20	34
2	3	2	1	3	27	20	28
1	3	2	2	3	38	20	39
2	3	2	2	3	28	20	29
1	3	2	3	3	53	20	54
2	3	2	3	3	42	20	43
1	3	2	4	3	53	20	54
2	3	2	4	3	50	20	51
1	3	3	1	3	45	20	46

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
2	3	3	1	3	36	20	37
1	3	3	2	3	48	20	49
2	3	3	2	3	40	20	41
1	3	3	3	3	68	20	69
2	3	3	3	3	51	20	52
1	3	3	4	3	62	20	63
2	3	3	4	3	84	20	85
1	3	4	1	3	42	20	43
2	3	4	1	3	35	20	36
1	3	4	2	3	45	20	46
2	3	4	2	3	37	20	38
1	3	4	3	3	78	20	79
2	3	4	3	3	54	20	55
1	3	4	4	3	66	20	67
2	3	4	4	3	92	20	93
1	4	1	1	3	20	20	21
2	4	1	1	3	20	20	21
1	4	1	2	3	22	24	23
2	4	1	2	3	20	20	21
1	4	1	3	3	27	20	28
2	4	1	3	3	23	20	24
1	4	1	4	3	33	20	34
2	4	1	4	3	24	20	25
1	4	2	1	3	20	20	21
2	4	2	1	3	20	20	21
1	4	2	2	3	22	24	23
2	4	2	2	3	20	20	21

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
1	4	2	3	3	28	20	29
2	4	2	3	3	24	20	25
1	4	2	4	3	34	20	35
2	4	2	4	3	25	20	26
1	4	3	1	3	24	20	25
2	4	3	1	3	22	23	23
1	4	3	2	3	28	20	29
2	4	3	2	3	22	23	23
1	4	3	3	3	32	20	33
2	4	3	3	3	28	20	29
1	4	3	4	3	36	20	37
2	4	3	4	3	29	20	30
1	4	4	1	3	24	20	25
2	4	4	1	3	22	23	23
1	4	4	2	3	28	20	29
2	4	4	2	3	22	23	23
1	4	4	3	3	33	20	34
2	4	4	3	3	29	20	30
1	4	4	4	3	37	20	38
2	4	4	4	3	30	20	31
1	2	1	1	4	41	20	42
2	2	1	1	4	34	20	35
1	2	1	2	4	45	20	46
2	2	1	2	4	37	20	38
1	2	1	3	4	57	20	58
2	2	1	3	4	46	20	47
1	2	1	4	4	57	20	58

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
2	2	1	4	4	62	20	63
1	2	2	1	4	39	20	40
2	2	2	1	4	33	20	34
1	2	2	2	4	43	20	44
2	2	2	2	4	35	20	36
1	2	2	3	4	63	20	64
2	2	2	3	4	49	20	50
1	2	2	4	4	60	20	61
2	2	2	4	4	72	20	73
1	2	3	1	4	55	20	56
2	2	3	1	4	44	20	45
1	2	3	2	4	55	20	56
2	2	3	2	4	55	20	56
1	2	3	3	4	78	20	79
2	2	3	3	4	58	20	59
1	2	3	4	4	68	20	69
2	2	3	4	4	87	20	88
1	2	4	1	4	48	20	49
2	2	4	1	4	41	20	42
1	2	4	2	4	49	20	50
2	2	4	2	4	45	20	46
1	2	4	3	4	84	20	85
2	2	4	3	4	63	20	64
1	2	4	4	4	71	20	72
2	2	4	4	4	92	20	93
1	3	1	1	4	20	20	21
2	3	1	1	4	20	20	21

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
1	3	1	2	4	20	21	21
2	3	1	2	4	20	20	21
1	3	1	3	4	22	23	23
2	3	1	3	4	20	21	21
1	3	1	4	4	28	20	29
2	3	1	4	4	20	21	21
1	3	2	1	4	20	20	21
2	3	2	1	4	20	20	21
1	3	2	2	4	20	21	21
2	3	2	2	4	20	20	21
1	3	2	3	4	23	20	24
2	3	2	3	4	20	21	21
1	3	2	4	4	29	20	30
2	3	2	4	4	20	21	21
1	3	3	1	4	20	22	21
2	3	3	1	4	20	21	21
1	3	3	2	4	24	20	25
2	3	3	2	4	20	21	21
1	3	3	3	4	28	20	29
2	3	3	3	4	25	20	26
1	3	3	4	4	32	20	33
2	3	3	4	4	26	20	27
1	3	4	1	4	20	22	21
2	3	4	1	4	20	21	21
1	3	4	2	4	24	20	25
2	3	4	2	4	20	21	21
1	3	4	3	4	29	20	30

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval*	
						Lower margin	*Upper margin*
2	3	4	3	4	26	20	27
1	3	4	4	4	33	20	34
2	3	4	4	4	26	20	27
1	4	1	1	4	35	20	36
2	4	1	1	4	28	20	29
1	4	1	2	4	40	20	41
2	4	1	2	4	29	20	30
1	4	1	3	4	54	20	55
2	4	1	3	4	42	20	43
1	4	1	4	4	54	20	55
2	4	1	4	4	83	20	84
1	4	2	1	4	34	20	35
2	4	2	1	4	27	20	28
1	4	2	2	4	39	20	40
2	4	2	2	4	29	20	30
1	4	2	3	4	65	20	66
2	4	2	3	4	44	20	45
1	4	2	4	4	59	20	60
2	4	2	4	4	93	20	94
1	4	3	1	4	50	20	51
2	4	3	1	4	37	20	38
1	4	3	2	4	52	20	53
2	4	3	2	4	43	20	44
1	4	3	3	4	98	20	98
2	4	3	3	4	56	20	57
1	4	3	4	4	73	20	74
2	4	3	4	4	98	20	98

L5 superior	*Acetabular fossa*	*Pubic symphysis superior apex*	*Auricular surface exostoses*	*Zygomaticomaxillary suture*	*Point estimate age*	*95% confidence interval* *Lower margin*	*Upper margin*
1	4	4	1	4	44	20	45
2	4	4	1	4	36	20	37
1	4	4	2	4	47	20	48
2	4	4	2	4	39	20	40
1	4	4	3	4	98	20	98
2	4	4	3	4	65	20	66
1	4	4	4	4	79	20	80
2	4	4	4	4	98	20	98

E 9: Transition analysis model 5 age estimation table.

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	1	2	1	20	20	21
1	2	1	2	2	20	20	21
1	2	1	2	3	20	20	21
1	2	1	2	4	20	20	21
2	2	1	2	1	20	20	21
2	2	1	2	2	20	21	21
2	2	1	2	3	22	24	23
2	2	1	2	4	20	21	21
1	2	2	2	1	20	20	21
1	2	2	2	2	20	20	21
1	2	2	2	3	20	20	21
1	2	2	2	4	20	20	21
2	2	2	2	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	2	2	2	2	20	21	21
2	2	2	2	3	23	20	24
2	2	2	2	4	20	21	21
1	2	3	2	1	20	20	21
1	2	3	2	2	20	20	21
1	2	3	2	3	20	20	21
1	2	3	2	4	20	20	21
2	2	3	2	1	20	20	21
2	2	3	2	2	20	20	21
2	2	3	2	3	20	20	21
2	2	3	2	4	20	20	21
1	2	4	2	1	23	20	24
1	2	4	2	2	25	20	26
1	2	4	2	3	28	20	29
1	2	4	2	4	25	20	26
2	2	4	2	1	20	20	21
2	2	4	2	2	20	20	21
2	2	4	2	3	32	20	33
2	2	4	2	4	20	21	21
1	2	1	3	1	24	20	25
1	2	1	3	2	26	20	27
1	2	1	3	3	31	20	32
1	2	1	3	4	27	20	28
2	2	1	3	1	20	20	21
2	2	1	3	2	20	20	21
2	2	1	3	3	33	20	34
2	2	1	3	4	20	21	21
1	2	2	3	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	2	3	2	20	20	21
1	2	2	3	3	20	20	21
1	2	2	3	4	20	20	21
2	2	2	3	1	20	20	21
2	2	2	3	2	20	21	21
2	2	2	3	3	22	24	23
2	2	2	3	4	20	21	21
1	2	3	3	1	20	20	21
1	2	3	3	2	20	20	21
1	2	3	3	3	20	20	21
1	2	3	3	4	20	20	21
2	2	3	3	1	20	20	21
2	2	3	3	2	20	21	21
2	2	3	3	3	23	20	24
2	2	3	3	4	20	21	21
1	2	4	3	1	20	20	21
1	2	4	3	2	20	20	21
1	2	4	3	3	20	20	21
1	2	4	3	4	20	20	21
2	2	4	3	1	20	20	21
2	2	4	3	2	20	20	21
2	2	4	3	3	20	20	21
2	2	4	3	4	20	20	21
1	2	1	4	1	23	20	24
1	2	1	4	2	25	20	26
1	2	1	4	3	29	20	30
1	2	1	4	4	26	20	27
2	2	1	4	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	2	1	4	2	20	21	21
2	2	1	4	3	34	20	35
2	2	1	4	4	20	21	21
1	2	2	4	1	24	20	25
1	2	2	4	2	27	20	28
1	2	2	4	3	33	20	34
1	2	2	4	4	28	20	29
2	2	2	4	1	20	20	21
2	2	2	4	2	20	21	21
2	2	2	4	3	35	20	36
2	2	2	4	4	20	21	21
1	2	3	4	1	20	20	21
1	2	3	4	2	20	20	21
1	2	3	4	3	20	20	21
1	2	3	4	4	20	20	21
2	2	3	4	1	20	21	21
2	2	3	4	2	22	23	23
2	2	3	4	3	25	20	26
2	2	3	4	4	22	24	23
1	2	4	4	1	20	20	21
1	2	4	4	2	20	20	21
1	2	4	4	3	20	20	21
1	2	4	4	4	20	20	21
2	2	4	4	1	20	22	21
2	2	4	4	2	22	20	23
2	2	4	4	3	27	20	28
2	2	4	4	4	23	20	24
1	2	1	5	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	1	5	2	20	20	21
1	2	1	5	3	20	21	21
1	2	1	5	4	20	20	21
2	2	1	5	1	20	20	21
2	2	1	5	2	20	20	21
2	2	1	5	3	20	21	21
2	2	1	5	4	20	20	21
1	2	2	5	1	26	20	27
1	2	2	5	2	28	20	29
1	2	2	5	3	32	20	33
1	2	2	5	4	28	20	29
2	2	2	5	1	20	21	21
2	2	2	5	2	29	20	30
2	2	2	5	3	40	20	41
2	2	2	5	4	32	20	33
1	2	3	5	1	28	20	29
1	2	3	5	2	30	20	31
1	2	3	5	3	38	20	39
1	2	3	5	4	31	20	32
2	2	3	5	1	20	22	21
2	2	3	5	2	30	20	31
2	2	3	5	3	41	20	42
2	2	3	5	4	33	20	34
1	2	4	5	1	20	20	21
1	2	4	5	2	20	20	21
1	2	4	5	3	20	20	21
1	2	4	5	4	20	20	21
2	2	4	5	1	20	21	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	2	4	5	2	22	23	23
2	2	4	5	3	25	20	26
2	2	4	5	4	22	24	23
1	2	1	6	1	20	20	21
1	2	1	6	2	20	20	21
1	2	1	6	3	20	21	21
1	2	1	6	4	20	20	21
2	2	1	6	1	20	22	21
2	2	1	6	2	22	20	23
2	2	1	6	3	27	20	28
2	2	1	6	4	23	20	24
1	2	2	6	1	20	20	21
1	2	2	6	2	20	20	21
1	2	2	6	3	20	21	21
1	2	2	6	4	20	20	21
2	2	2	6	1	20	20	21
2	2	2	6	2	20	20	21
2	2	2	6	3	20	21	21
2	2	2	6	4	20	20	21
1	2	3	6	1	26	20	27
1	2	3	6	2	28	20	29
1	2	3	6	3	33	20	34
1	2	3	6	4	29	20	30
2	2	3	6	1	20	23	21
2	2	3	6	2	31	20	32
2	2	3	6	3	42	20	43
2	2	3	6	4	35	20	36
1	2	4	6	1	29	20	30

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	2	4	6	2	31	20	32
1	2	4	6	3	43	20	44
1	2	4	6	4	33	20	34
2	2	4	6	1	21	25	22
2	2	4	6	2	32	20	33
2	2	4	6	3	43	20	44
2	2	4	6	4	35	20	36
1	3	1	2	1	20	20	21
1	3	1	2	2	20	20	21
1	3	1	2	3	20	20	21
1	3	1	2	4	20	20	21
2	3	1	2	1	20	20	21
2	3	1	2	2	20	21	21
2	3	1	2	3	22	24	23
2	3	1	2	4	20	21	21
1	3	2	2	1	20	20	21
1	3	2	2	2	20	20	21
1	3	2	2	3	20	20	21
1	3	2	2	4	20	20	21
2	3	2	2	1	20	20	21
2	3	2	2	2	20	21	21
2	3	2	2	3	23	20	24
2	3	2	2	4	20	21	21
1	3	3	2	1	20	20	21
1	3	3	2	2	20	20	21
1	3	3	2	3	20	20	21
1	3	3	2	4	20	20	21
2	3	3	2	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	3	3	2	2	20	20	21
2	3	3	2	3	20	20	21
2	3	3	2	4	20	20	21
1	3	4	2	1	23	20	24
1	3	4	2	2	25	20	26
1	3	4	2	3	29	20	30
1	3	4	2	4	25	20	26
2	3	4	2	1	20	20	21
2	3	4	2	2	20	20	21
2	3	4	2	3	33	20	34
2	3	4	2	4	20	21	21
1	3	1	3	1	24	20	25
1	3	1	3	2	26	20	27
1	3	1	3	3	32	20	33
1	3	1	3	4	27	20	28
2	3	1	3	1	20	20	21
2	3	1	3	2	20	20	21
2	3	1	3	3	34	20	35
2	3	1	3	4	20	21	21
1	3	2	3	1	20	20	21
1	3	2	3	2	20	20	21
1	3	2	3	3	20	20	21
1	3	2	3	4	20	20	21
2	3	2	3	1	20	20	21
2	3	2	3	2	20	21	21
2	3	2	3	3	22	24	23
2	3	2	3	4	20	21	21
1	3	3	3	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	3	3	3	2	20	20	21
1	3	3	3	3	20	20	21
1	3	3	3	4	20	20	21
2	3	3	3	1	20	20	21
2	3	3	3	2	20	21	21
2	3	3	3	3	23	20	24
2	3	3	3	4	20	21	21
1	3	4	3	1	20	20	21
1	3	4	3	2	20	20	21
1	3	4	3	3	20	20	21
1	3	4	3	4	20	20	21
2	3	4	3	1	20	20	21
2	3	4	3	2	20	20	21
2	3	4	3	3	20	20	21
2	3	4	3	4	20	20	21
1	3	1	4	1	23	20	24
1	3	1	4	2	25	20	26
1	3	1	4	3	29	20	30
1	3	1	4	4	26	20	27
2	3	1	4	1	20	20	21
2	3	1	4	2	20	20	21
2	3	1	4	3	36	20	37
2	3	1	4	4	20	21	21
1	3	2	4	1	25	20	26
1	3	2	4	2	27	20	28
1	3	2	4	3	33	20	34
1	3	2	4	4	28	20	29
2	3	2	4	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	3	2	4	2	20	21	21
2	3	2	4	3	37	20	38
2	3	2	4	4	20	21	21
1	3	3	4	1	20	20	21
1	3	3	4	2	20	20	21
1	3	3	4	3	20	21	21
1	3	3	4	4	20	20	21
2	3	3	4	1	27	20	28
2	3	3	4	2	28	20	29
2	3	3	4	3	33	20	34
2	3	3	4	4	29	20	30
1	3	4	4	1	20	23	21
1	3	4	4	2	32	20	33
1	3	4	4	3	43	20	44
1	3	4	4	4	36	20	37
2	3	4	4	1	29	20	30
2	3	4	4	2	32	20	33
2	3	4	4	3	49	20	50
2	3	4	4	4	33	20	34
1	3	1	5	1	22	26	23
1	3	1	5	2	33	20	34
1	3	1	5	3	44	20	45
1	3	1	5	4	37	20	38
2	3	1	5	1	20	22	21
2	3	1	5	2	23	20	24
2	3	1	5	3	29	20	30
2	3	1	5	4	24	20	25
1	3	2	5	1	34	20	35

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	3	2	5	2	35	20	36
1	3	2	5	3	41	20	42
1	3	2	5	4	37	20	38
2	3	2	5	1	45	20	46
2	3	2	5	2	47	20	48
2	3	2	5	3	56	20	57
2	3	2	5	4	51	20	52
1	3	3	5	1	57	20	58
1	3	3	5	2	59	20	60
1	3	3	5	3	77	20	78
1	3	3	5	4	76	20	77
2	3	3	5	1	46	20	47
2	3	3	5	2	48	20	49
2	3	3	5	3	59	20	60
2	3	3	5	4	53	20	54
1	3	4	5	1	20	20	21
1	3	4	5	2	20	20	21
1	3	4	5	3	20	21	21
1	3	4	5	4	20	20	21
2	3	4	5	1	26	20	27
2	3	4	5	2	28	20	29
2	3	4	5	3	33	20	34
2	3	4	5	4	29	20	30
1	3	1	6	1	20	24	21
1	3	1	6	2	31	20	32
1	3	1	6	3	41	20	42
1	3	1	6	4	34	20	35
2	3	1	6	1	29	20	30

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	3	1	6	2	31	20	32
2	3	1	6	3	40	20	41
2	3	1	6	4	33	20	34
1	3	2	6	1	22	26	23
1	3	2	6	2	32	20	33
1	3	2	6	3	42	20	43
1	3	2	6	4	35	20	36
2	3	2	6	1	21	23	22
2	3	2	6	2	24	20	25
2	3	2	6	3	30	20	31
2	3	2	6	4	25	20	26
1	3	3	6	1	35	20	36
1	3	3	6	2	36	20	37
1	3	3	6	3	42	20	43
1	3	3	6	4	38	20	39
2	3	3	6	1	47	20	48
2	3	3	6	2	49	20	50
2	3	3	6	3	60	20	61
2	3	3	6	4	55	20	56
1	3	4	6	1	65	20	66
1	3	4	6	2	66	20	67
1	3	4	6	3	83	20	84
1	3	4	6	4	85	20	86
2	3	4	6	1	48	20	49
2	3	4	6	2	51	20	52
2	3	4	6	3	64	20	65
2	3	4	6	4	57	20	58
1	4	1	2	1	20	20	21

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	4	1	2	2	20	21	21
1	4	1	2	3	24	20	25
1	4	1	2	4	20	21	21
2	4	1	2	1	30	20	31
2	4	1	2	2	32	20	33
2	4	1	2	3	37	20	38
2	4	1	2	4	33	20	34
1	4	2	2	1	38	20	39
1	4	2	2	2	41	20	42
1	4	2	2	3	50	20	51
1	4	2	2	4	44	20	45
2	4	2	2	1	35	20	36
2	4	2	2	2	39	20	40
2	4	2	2	3	64	20	65
2	4	2	2	4	56	20	57
1	4	3	2	1	38	20	39
1	4	3	2	2	41	20	42
1	4	3	2	3	51	20	52
1	4	3	2	4	45	20	46
2	4	3	2	1	25	20	26
2	4	3	2	2	28	20	29
2	4	3	2	3	34	20	35
2	4	3	2	4	29	20	30
1	4	4	2	1	38	20	39
1	4	4	2	2	39	20	40
1	4	4	2	3	46	20	47
1	4	4	2	4	41	20	42
2	4	4	2	1	51	20	52

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	4	4	2	2	53	20	54
2	4	4	2	3	63	20	64
2	4	4	2	4	59	20	60
1	4	1	3	1	68	20	69
1	4	1	3	2	68	20	69
1	4	1	3	3	81	20	82
1	4	1	3	4	82	20	83
2	4	1	3	1	53	20	54
2	4	1	3	2	54	20	55
2	4	1	3	3	66	20	67
2	4	1	3	4	62	20	63
1	4	2	3	1	20	20	21
1	4	2	3	2	20	21	21
1	4	2	3	3	24	20	25
1	4	2	3	4	20	21	21
2	4	2	3	1	30	20	31
2	4	2	3	2	32	20	33
2	4	2	3	3	36	20	37
2	4	2	3	4	33	20	34
1	4	3	3	1	36	20	37
1	4	3	3	2	39	20	40
1	4	3	3	3	46	20	47
1	4	3	3	4	41	20	42
2	4	3	3	1	34	20	35
2	4	3	3	2	37	20	38
2	4	3	3	3	50	20	51
2	4	3	3	4	41	20	42
1	4	4	3	1	37	20	38

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	4	4	3	2	40	20	41
1	4	4	3	3	47	20	48
1	4	4	3	4	42	20	43
2	4	4	3	1	26	20	27
2	4	4	3	2	29	20	30
2	4	4	3	3	36	20	37
2	4	4	3	4	30	20	31
1	4	1	4	1	39	20	40
1	4	1	4	2	41	20	42
1	4	1	4	3	48	20	49
1	4	1	4	4	43	20	44
2	4	1	4	1	55	20	56
2	4	1	4	2	56	20	57
2	4	1	4	3	67	20	68
2	4	1	4	4	63	20	64
1	4	2	4	1	74	20	75
1	4	2	4	2	73	20	74
1	4	2	4	3	86	20	87
1	4	2	4	4	88	20	89
2	4	2	4	1	57	20	58
2	4	2	4	2	58	20	59
2	4	2	4	3	72	20	73
2	4	2	4	4	69	20	70
1	4	3	4	1	20	20	21
1	4	3	4	2	20	20	21
1	4	3	4	3	20	21	21
1	4	3	4	4	20	20	21
2	4	3	4	1	27	20	28

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	4	3	4	2	29	20	30
2	4	3	4	3	34	20	35
2	4	3	4	4	30	20	31
1	4	4	4	1	21	26	22
1	4	4	4	2	34	20	35
1	4	4	4	3	46	20	47
1	4	4	4	4	38	20	39
2	4	4	4	1	29	20	30
2	4	4	4	2	32	20	33
2	4	4	4	3	69	20	70
2	4	4	4	4	34	20	35
1	4	1	5	1	25	20	26
1	4	1	5	2	35	20	36
1	4	1	5	3	47	20	48
1	4	1	5	4	38	20	39
2	4	1	5	1	20	22	21
2	4	1	5	2	23	20	24
2	4	1	5	3	29	20	30
2	4	1	5	4	24	20	25
1	4	2	5	1	34	20	35
1	4	2	5	2	36	20	37
1	4	2	5	3	42	20	43
1	4	2	5	4	38	20	39
2	4	2	5	1	47	20	48
2	4	2	5	2	50	20	51
2	4	2	5	3	64	20	65
2	4	2	5	4	56	20	57
1	4	3	5	1	80	20	81

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
1	4	3	5	2	78	20	79
1	4	3	5	3	98	20	98
1	4	3	5	4	98	20	98
2	4	3	5	1	49	20	50
2	4	3	5	2	51	20	52
2	4	3	5	3	98	20	98
2	4	3	5	4	98	20	98
1	4	4	5	1	20	20	21
1	4	4	5	2	20	20	21
1	4	4	5	3	20	21	21
1	4	4	5	4	20	20	21
2	4	4	5	1	27	20	28
2	4	4	5	2	29	20	30
2	4	4	5	3	33	20	34
2	4	4	5	4	30	20	31
1	4	1	6	1	21	26	22
1	4	1	6	2	33	20	34
1	4	1	6	3	43	20	44
1	4	1	6	4	36	20	37
2	4	1	6	1	29	20	30
2	4	1	6	2	32	20	33
2	4	1	6	3	43	20	44
2	4	1	6	4	34	20	35
1	4	2	6	1	24	28	25
1	4	2	6	2	34	20	35
1	4	2	6	3	43	20	44
1	4	2	6	4	37	20	38
2	4	2	6	1	21	23	22

L5 superior	*Acetabular fossa*	*Auricular surface exostoses*	*Suchey-Brooks*	*Zygomaticomaxillary suture*	*Point estimate age*	95% confidence interval *Lower margin*	*Upper margin*
2	4	2	6	2	24	20	25
2	4	2	6	3	31	20	32
2	4	2	6	4	25	20	26
1	4	3	6	1	35	20	36
1	4	3	6	2	37	20	38
1	4	3	6	3	44	20	45
1	4	3	6	4	39	20	40
2	4	3	6	1	51	20	52
2	4	3	6	2	53	20	54
2	4	3	6	3	72	20	73
2	4	3	6	4	66	20	67
1	4	4	6	1	90	20	91
1	4	4	6	2	88	20	89
1	4	4	6	3	98	20	98
1	4	4	6	4	98	20	98
2	4	4	6	1	53	20	54
2	4	4	6	2	56	20	57
2	4	4	6	3	98	20	98
2	4	4	6	4	98	20	98

E 10: Validation results using multifactorial model 1 (not sex specific).

	Basic Statistics					**Regression Analysis**					**Transition analysis**		
Known Age	Point estimate	Narrow interval		Wide interval		Point estimate	Narrow interval		Wide interval		Point estimate	Interval	
63	54	51	57	42	63	60	58	62	34	87	61	20	62
76	58	55	62	44	75	66	61	70	39	93	55	20	56
45	54	51	57	42	63	53	49	58	27	80	61	20	62
40	54	50	58	30	75	54	49	60	27	81	23	20	24
32	44	41	47	30	57	36	33	40	10	63	20	22	21
30	44	41	47	30	57	33	29	37	6	60	20	22	21
32	39	36	43	30	51	29	25	33	2	55	20	20	21
37	51	48	54	38	63	48	44	52	21	75	48	20	49
62	50	47	54	38	63	48	44	52	21	75	45	20	46
45	50	47	54	38	63	51	48	55	25	78	45	20	46
50	47	44	50	30	57	42	38	46	15	69	35	20	36
46	50	47	54	38	63	48	44	52	21	75	45	20	46
65	46	42	50	33	63	51	45	56	24	78	28	20	29
53	54	50	58	38	67	51	48	55	25	78	52	20	53
39	50	46	54	33	63	49	45	54	22	76	42	20	43
27	43	39	46	30	56	41	36	46	14	68	20	20	21
27	46	42	50	30	66	34	30	38	8	61	20	21	21
25	46	42	50	33	63	40	36	45	14	67	28	20	29
56	51	48	54	30	75	51	45	56	24	78	20	22	21
57	54	51	57	42	63	60	58	62	34	87	61	20	62
40	47	44	50	30	57	42	38	46	15	69	35	20	36
52	50	47	54	38	63	51	48	55	25	78	45	20	46

E 11: Validation results using multifactorial model 2 (not sex specific).

	Basic Statistics					**Regression Analysis**					**Transition analysis**		
Known Age	Point estimate	Narrow interval		Wide interval		Point estimate	Narrow interval		Wide interval		Point estimate	Interval	
63	52	49	55	37	63	55	52	58	30	81	55	20	56
76	59	56	63	48	75	71	67	75	45	97	98	20	98
31	38	35	41	26	51	24	20	27	-2	50	20	20	21
40	52	47	57	30	75	57	50	63	30	83	20	20	21
49	56	51	60	37	72	65	60	69	39	91	57	20	58
53	56	53	59	48	65	64	62	66	38	90	80	20	81
32	40	37	43	26	54	28	24	32	2	54	20	20	21
30	43	39	46	30	56	33	30	37	7	59	20	20	21
32	47	43	50	30	65	42	37	47	16	68	30	20	31
37	50	46	53	37	63	48	45	52	23	74	40	20	41
62	52	48	55	38	63	53	50	56	27	78	51	20	52
45	47	43	52	32	63	39	34	44	13	65	20	22	21
50	49	46	52	30	65	49	45	53	23	75	35	20	36
46	46	42	51	32	63	38	33	43	12	64	37	20	38
65	50	47	54	38	63	48	45	51	22	73	42	20	43
53	51	47	56	37	72	58	52	65	32	84	29	20	30
39	47	44	51	26	63	46	41	51	20	72	27	20	28
27	41	37	44	26	56	31	27	35	5	56	20	20	21
27	47	43	50	30	57	45	41	49	19	71	20	20	21
25	43	40	47	26	63	34	29	39	8	60	20	20	21
56	48	44	51	30	75	46	41	52	20	72	29	20	30
57	50	45	54	32	63	46	41	50	20	71	43	20	44

40	47	43	50	30	57	45	41	49	19	71	20	20	21
52	47	44	51	33	63	43	39	47	17	69	38	20	39
67	53	49	56	37	65	55	51	59	29	81	50	20	51
41	44	41	48	30	65	38	33	43	12	64	27	20	28
44	54	51	57	48	63	59	57	62	34	85	65	20	66

E 12: Validation results using multifactorial model 3 (female specific).

	Basic Statistics					**Regression Analysis**					**Transition analysis**		
Known Age	Point estimate	Narrow interval		Wide interval		Point estimate	Narrow interval		Wide interval		Point estimate	Interval	
63	54	51	58	48	62	57	54	60	35	79	74	20	75
45	55	51	59	48	62	60	57	62	37	82	54	20	55
49	55	51	59	48	62	60	57	62	37	82	54	20	55
32	38	34	41	24	56	30	25	35	7	53	20	20	21
32	39	35	44	29	60	30	23	38	7	54	23	20	24
62	50	47	54	34	62	47	43	51	25	70	46	20	47
45	50	47	54	34	62	47	43	51	25	70	46	20	47
50	49	44	53	29	60	48	42	53	25	71	41	20	42
46	47	43	52	34	62	45	40	50	22	68	44	20	45
65	45	41	49	29	62	40	34	46	17	63	21	23	22
53	50	47	54	34	62	47	43	51	25	70	46	20	47
25	39	35	43	24	62	34	28	41	11	58	20	21	21
56	48	43	53	29	71	52	45	59	29	75	36	20	37
52	47	43	52	34	62	45	40	50	22	68	44	20	45

E 13: Validation results using multifactorial model 4 (male specific).

	Basic Statistics					**Regression Analysis**					**Transition analysis**		
Known Age	Point estimate	Narrow interval		Wide interval		Point estimate	Narrow interval		Wide interval		Point estimate	Interval	
76	60	55	65	49	79	70	65	75	44	97	73	20	74
40	53	47	59	29	79	56	48	64	29	83	20	20	21
53	57	52	61	49	66	63	60	66	37	89	68	20	69
30	44	39	49	29	62	30	24	37	4	57	20	20	21
37	52	47	56	35	66	49	44	55	23	76	48	20	49
39	53	49	58	35	66	57	53	61	31	83	55	20	56
27	44	39	49	29	58	34	29	39	8	60	20	20	21
27	48	43	52	29	62	43	38	49	17	70	31	20	32
57	49	42	57	16	66	46	38	53	19	73	55	20	56
40	48	43	52	29	62	43	38	49	17	70	31	20	32
67	52	47	56	35	66	51	46	57	25	78	44	20	45
41	42	37	47	29	53	27	22	32	1	53	20	20	21
44	57	52	61	49	66	63	60	66	37	89	68	20	69

E 14: Validation results using multifactorial model 5 (male specific).

	Basic Statistics					**Regression Analysis**					**Transition analysis**		
Known Age	Point estimate	Narrow interval		Wide interval		Point estimate	Narrow interval		Wide interval		Point estimate	Interval	
76	62	57	67	49	79	71	66	76	45	97	98	20	98
40	52	46	58	29	79	54	46	62	27	81	20	20	21
53	58	54	63	49	70	66	63	69	40	92	81	20	82
30	43	38	48	29	57	33	28	38	7	59	20	20	21
37	51	46	55	35	66	50	45	55	24	76	43	20	44
39	48	43	53	25	66	42	35	50	15	69	24	20	25
27	40	35	45	25	58	25	19	31	-1	52	20	20	21
27	47	42	51	29	60	44	39	48	17	70	20	20	21
57	49	41	56	16	66	43	37	50	17	70	38	20	39
40	47	42	51	29	60	44	39	48	17	70	20	20	21
67	53	48	58	35	70	56	50	61	29	82	39	20	40
41	46	41	50	29	70	39	32	46	13	66	20	21	21
44	56	51	60	49	66	60	57	63	34	86	63	20	64