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An Analysis of Bayesian Methods in Determining the Viability of Perinatal Remains

Tiffanie Sue Cave
University of Tennessee - Knoxville

To the Graduate Council:

I am submitting herewith a thesis written by Tiffanie Sue Cave entitled "An Analysis of Bayesian Methods in Determining the Viability of Perinatal Remains." I have examined the final electronic copy of this thesis for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Master of Arts, with a major in Anthropology.

Lyle Konigsberg, Major Professor

We have read this thesis and recommend its acceptance:

Richard Jantz, Lee Meadows Jantz

Accepted for the Council:
Carolyn R. Hodges

Vice Provost and Dean of the Graduate School

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AN ANALYSIS OF BAYESIAN METHODS IN DETERMINING THE VIABILITY OF PERINATAL REMAINS

A Thesis
Presented for the
Master of Arts
Degree
The University of Tennessee, Knoxville

Tiffanie Sue Cave
December 2006

DEDICATION

This thesis is dedicated to my loving husband, Dan Cave, whose constant support and faith in my abilities have helped me reach my highest goals.

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I would like to thank all those who helped me complete my Master of Arts degree in Anthropology. First, I would like to thank Dr. Oystein E. Olsen for his generosity in allowing me to use his data for this project. I also wish to thank Dr. Lyle Konigsberg for his extensive efforts in helping me to understand the concept of Bayes' Theorem. Without his assistance, this project would not have been possible. Finally, I would like to thank Dr. Richard Jantz and Dr. Lee Meadows Jantz for taking time out of their busy schedules to serve on my committee.

ABSTRACT

Bayes' theorem is a conditional probability formula with the potential for aiding in the development of more accurate age-at-death estimations in perinatal remains. This investigation tested the validity of a Bayesian method for aging by applying the formula to 495 sets of historical Native American remains from several Arikara sites in South Dakota. The dates for these sites range from the 1600's to the 1830's. Dr. Oystein E. Olsen generously provided the reference sample data of 348 sets of perinatal remains from Haukeland University Hospital in Bergen, Norway collected between January 1988 and December 1998. The goal of this analysis was to determine the probability that perinatal remains of an unknown age were at least 24 weeks gestation based on the length of the femur. Results of this study illustrated that Bayes' theorem can be useful in providing a probability of viability of unknown perinatal remains.

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CHAPTER 1: INTRODUCTION

Bayes' theorem is a conditional probability formula that may be used to provide a more accurate age estimation of perinatal skeletal remains in demographic and forensic settings. As a direct probability, Bayes' theorem is used to determine the probability of a particular outcome given a particular event. If used as an inverse probability, it can test the likelihood that a hypothesized outcome is true. This statistical method is currently being applied in many fields such as genetics, paleoanthropology and phylogeny, archeological investigations, and paleopathological diagnoses.

For instance, in the medical profession, Bayes' theorem is utilized to aid in determining the differential diagnosis of certain diseases such as Alzheimer's, cancer, and osteomyelitis (Byers and Roberts 2003). In studies of genetic variations, researchers can trace geographical and cultural movements of past populations based on mtDNA variations (Richards et al. 2000, Wilson et al. 2001). In paleoanthropological studies, more plausible phylogenetic relationships can be established and new specimens of hominids can be placed in time based on genetic testing (Beerli and Edwards 2002, Edwards 1996). Finally, Bayes' theorem can be used in paleodemographic studies to estimate the age-at-death of adult skeletal remains, as well as in paleopathological studies to test the probability that a given set of osteological markers is due to a specific disease (Byers and Roberts 2003). I will test the further usefulness of this theorem in physical anthropology by applying Bayes' theorem to a collection of early and late coalescent perinatal skeletal remains from Arikara Indian sites dated between the 1600’s and the 1830’s. The application of this theorem is an attempt to determine the probability that the remains in question are at least 24 gestational weeks old. This collection is scientifically valuable due to the large amount of perinatal remains available to be analyzed. If Bayesian methods prove to be useful in predicting the viability of the fetuses in the Arikara collection, it can then be applied to more modern perinatal remains, while considering the impact of ethical issues.

The application of Bayesian methods to the study of perinatal age-at-death estimates brings many issues of ethics, cultural impact, and moral debate to the forefront of physical anthropology. Many of these issues center on the cultural meaning and value of life; however, in developed nations, government and legislative acts often conflict with individual cultural beliefs and impress generalized meanings regarding what constitutes life and its value- especially in matters concerning abortion and infanticide. One of the main issues that needs to be considered is the very definition of perinatal (mortality). “The definition of perinatal mortality has itself varied geographically and temporally, however. Jurisdictions differ in terms of the lower limits of gestational age or birth weight....” (Kramer et al. 2002: 494). The American Heritage Stedman’s Medical dictionary defines perinatal as “of, relating to, or being the period around child birth, especially the five months before and one month after birth” (www.answers.com). However, perinatal is defined differently in Finland.

> The Finnish definition of perinatal mortality differs…in two respects. Firstly, all live births that die within 7 days, regardless of birth weight or gestation length, are considered as early neonatal deaths. Secondly, both gestational age and birth weight are used in the definition: stillborn fetuses with a birth weight of at least 500g or 22 completed weeks of gestation are counted as stillbirths [Forssas et al. 1999:476]

Finally, in the United States, the definition of perinatal begins at 20 weeks gestation (Morrison and Rennie 1995:1038) whereas in Norway, perinatal can include fetuses as early as 16 weeks gestation (Olsen et al. 2002:240).

Applications involving perinatal remains currently center on the perinatal mortality rate (PNMR), a "summary statistic for evaluating the effectiveness of perinatal care" (Cartlidge and Stewart 1995:1038). The PNMR is influenced by cultural and biological factors. For example, in "developed countries the rate for babies over 1000g is usually less than 6/1000 births, whereas for developing countries the PNMR ranges from 30-200" (Pattinson 2000). Differences in medical competency, technology, and cultural beliefs probably account for the differences in the PNMR, and yet still reflect the best possible care available at that time, in that location.

The perinatal mortality rate is important to this investigation because accurate age-at-death measurements could help determine how effective perinatal care was on an individual or cultural level, or per case basis in a forensic setting. Although this method cannot determine without a doubt whether or not the fetus was born, Bayesian gestational aging techniques can aid in criminal investigations by providing a probability of whether or not a fetus was at a legally viable gestational age; or if it is too close to determine. The meaning of viable in this instance refers to the point at which a fetus is capable of living outside of the uterus (Breborowicz 2001). Fetal viability is not a uniform, or standard point in gestation; but rather, it is a function of current technological advances. For instance, in the United States, fetal viability is currently measured at approximately 24 weeks gestation (Breborowicz 2001); however, the US Supreme court adds a stipulation that states, "the viability determination of each case must be based on the judgment of the attending physician on the particular facts of the case before him" (Salihu et al. 2005).

Estimating the age-at-death of different developmental classes is accomplished by various means. For example, juvenile remains are generally estimated using osteological markers of growth and development (i.e. fusion of epiphyses or tooth eruption) and “adult age estimates are based on wear and tear indicators such as skeletal degeneration and bone remodeling” (Schmitt et al. 2002:1203). Perinatal remains have been estimated using regression-based methods of long bone lengths (Sheuer et al. 1980) as well as Bayesian age distributions (Gowland and Chamberlain 2002), among others. This analysis is expected to determine whether or not Bayes’ theorem is indeed a useful tool in determining the probability that the remains belonged to a viable fetus.

CHAPTER 2: LITERATURE REVIEW

Thomas Bayes (1702-1761) was an English theologian, whose other passions, mathematics and probability, led him to become one of the most influential contributors to the field of statistics. He is believed to be the first person to use probability inductively, and he established a mathematical basis for probability inference (mrs.umn.edu). Unfortunately for Bayes, his most well known contribution, *An Essay Towards Solving a Problem in the Doctrine of Chances* (1764) was not found and published until three years after his death. This essay contained within it a very powerful mathematical tool that revolutionized views of statistics and spread from there into numerous other academic and scientific fields. “Bayes’ theorem describes how knowledge of a prior probability can be used to calculate the probability of unknown events in many subject areas including the sciences, the humanities and even games of chance” (Byers and Roberts 2003: 3).

The Bayesian paradigm contains three main parts. The prior probability is the "initial assignment of the probability of any hypothesis being true before experimental evidence is considered," (Lucy et al. 1996:3). In this investigation, a uniform prior was used. The uniform prior states that there is an equal probability that each set of remains could belong to any age group before the evidence is considered. The likelihood is the "conditional probability of the observed information, assuming that the hypothesis is true," (Lucy et al. 1996:3). In this analysis, the posterior probability is the probability that the remains represent a certain gestational age, using both the uniform prior and the observed femur length measurements. This paradigm states that the " posterior probability is proportional to the prior probability multiplied by the likelihood," (Lucy et al. 1996:3)

Bayes' theorem is often described as a generalized method that can be manipulated to deal with any type or combination of data (Aykroyd et al. 1999). Although Bayes' theorem can be applied in many different scenarios, this investigation focuses on its utilization within the field of anthropology and skeletal biology.

Genetic studies in anthropology provide one platform for the application of Bayesian methods and interpretations of various problems. For example, Richards et al. (2000) have investigated the geographical and chronological movements of past populations into Europe by tracing mtDNA diversity.

> Our aim was to identify the principle founder lineages that have entered Europe and to date the times of their entry in order to quantify the contribution that the main episodes of new settlement during European prehistory have made to the modern mtDNA pool [Richards et al. 2000: 1272].

The investigation incorporated a phylogeographic approach and analysis of nonrecombining DNA sequence data. More generally, this approach is the study of the geographic distribution and diversity of genetic variation. By incorporating a Bayesian technique with an uninformative prior, the authors were able to account for recurrent mutation as well as gene flow. "We determined the probability that each founder cluster took part in each of the migration events, on the basis of the age of that cluster," (Richards et al. 2000: 1262). Their results were supported by archaeological evidence and suggested that most of the genetic variation is due to migrations during the Upper Paleolithic period (Richards et al. 2000).

In a similar examination of genetic variations, Wilson et al. (2001) probed the question of whether cultural changes in the British Isles involved the movement of cultural ideas with migrations of people, or whether the movement was of culture only. One of the core aspects of this research involved analyses of the role of gender in these cultural movements. In order to identify changes in gender roles, the source populations needed to be distinguished with respect to some sort of genetic marker, which happened to be Y-chromosomal variation, and mtDNA. Bayes' theorem was then used on X-chromosome microsatellites.

> To assess which of the two uniparentally inherited genetic systems more closely reflects the history of the genome more widely and to check that the lack of differentiation among the British and non-Basque European populations is not caused by a lack of resolution in the mtDNA data, we analyzed microsatellites on the X chromosome, [Wilson et al. 2001:5082].

Using arguments of coalescence, the authors concluded, “the identified markers of paternal Scandinavian influence in the British Isles suggest that Viking settlement…involved substitutions of genetic and cultural replacement” (Wilson et al. 2001:5083). Also, genetic continuity evidences that Neolithic, Iron-age and subsequent cultural revolutions involved mainly the movement of ideas alone, whereas comparisons of mtDNA reveal the major impact that at least one cultural revolution had on the maternal genetic heritage of these Celtic speaking peoples (Wilson et al. 2001).

Investigations of genetic diversity can be applied to heritability as well as being used to determine lines of descent. Fernandez et al. (2003) tested a maximum likelihood as well as a Bayesian approach to “investigate the role of genetic admixture in explaining phenotypic variation in obesity-related traits in African-American women” (904). The core elements of this study included the genetic effects of various ethnic mixtures of Europeans, Africans and Native Americans during periods of colonization. One of the conclusions reached by these scholars is that the descendents of these mixed groups are more likely to “inherit variants [from the parent populations] that either predispose them to disease-related traits or greater sensitivity to the environment” (Fernandez et al. 2003: 905). Both the maximum likelihood and Bayesian methods showed positive correlations between African genetic admixture and Body Mass Indices, which led these authors to conclude that increased levels of obesity in African-American women is linked to genetics.

Another area of anthropology that has benefited from the application of Bayesian methodology is paleoanthropology, specifically studies of phylogeny. According to Edwards (1996), “probabilistic reasoning implicitly replaced Ockham’s razor long ago as a scientific tool…in all but a restricted set of probability models, the naïve application of parsimony does not lead to the solution with the greatest likelihood” (81). Bayesian inference of phylogenetic trees has actually been developed into a computer program called MRBAYES, and is seen as being more advantageous than other methods. “Bayesian inference has several advantages over other methods of phylogenetic inference, including easy interpretation of results, the ability to incorporate prior information, and some computational advantages” (Huelsenbeck and Ronquist 2001:754). MRBAYES uses a variant of Markov chain Monte Carlo to extract the posterior probabilities of the trees while the conditional probabilities are derived from an alignment of DNA.

Other studies in phylogeny have also employed Bayesian methods to answer questions about our evolutionary history. One such question, addressed by Beerli and Edwards in 2002, concerns the timeline for the split between Neanderthals and modern humans. “The availability of sequences from the mtDNA hypervariable region I and II of a specimen of the Neanderthal, *Homo neanderthalensis,* permits the estimation of the time of divergence of Neanderthals and modern humans” (Beerli and Edwards 2002: 60). In this investigation the authors used a Bayesian approach based on coalescence theory to jointly estimate the ancestral population size and the divergence of the two populations where the divergence time is in generations. "This approximation can be incorporated into a Bayesian approach that integrates over that range of possible values of ? to achieve a likelihood curve for ?....[This] estimator...is based on the coalescent and includes an arbitrary prior distribution for ?," (Beerli and Edwards 2002:61).

One final example of the application of Bayes’ theorem in paleoanthropology comes from an investigation of south Asian hominid fossils led by Kennedy in 1999. This investigation centered on an analysis of ancient hominid fossils (named the Narmada woman) that exhibited a mosaic of features which were anatomically identical in part with *Homo erectus*, and in part with *Homo sapiens*. Still other cranial features were completely unique, and the bones were found with tools from the Lower Paleolithic Acheulian tradition. The question therefore became: what species do these remains belong to, and during what time did this creature live? "Given that Narmada exhibits some anatomical features of both *Homo erectus* and *Homo sapiens* as well as a variety of unique cranial features, I undertook trait comparisons with values of recognized hominid taxa," (Kennedy 1999:169). The results of these trait comparisons led to further statistical testing including bivariate plots and multivariate Bayesian analysis. These findings, along with an analysis of the tools found in the same stratigraphic level suggest that the Narmada woman belongs to early *Homo* dating to around 200,000 years ago (Kennedy 1999).

Along with genetic studies and paleoanthropological investigations, Bayes' theorem has also been applied in archaeological settings. Robertson (1999) illustrates the usefulness of Bayesian techniques in dealing with the random effects of sampling errors at sites such as Teotihuacan, Mexico. “Bayesian statistics provide a method and rationale for formally integrating prior beliefs or evidence about a population parameter with new empirical information derived from a sample of that population” (Robertson 1999:139). Robertson (1999) contends that Bayesian methods help archaeologists make the most of their data sets by facilitating the exposure of spatial and temporal relationships among data in a more clear and interpretable manner.

From archaeology to paleopathology, Bayesian methodology has been tested and credited as a useful tool in solving applied problems in anthropology. Byers and Roberts (2003) have added their support for this argument by addressing the possible relevance of Bayes' theorem in aiding the diagnosis of osteological pathologies. Medical professionals have been using this theorem to help diagnose everything from Alzheimer's to lung cancer with a high rate of accuracy, and these authors argue that if the proper priors and likelihoods can be derived, then Bayesian techniques can also be applied to past populations. For example, in a clinical diagnosis

> the prior is equal to the prevalence of pathological conditions and the likelihood of the signs within those conditions. The prevalence is the frequency with which the pathological condition occurs in a population and the likelihood is the frequency with which the signs appear within the condition for which the prevalence is known
> [Byers and Roberts 2003: 3].

This method works nicely in the medical profession because their reference sample is their patients. In paleopathological investigations, modern populations cannot be used as reference samples due to factors such as industrialized medicine, geography, climate, diet, sex and age (Byers and Roberts 2003). Though some of the problems regarding reference populations is due to the lack of written medical histories of ancient peoples, Hoppa and Vaupel (2002) also recognized other problems in the lack of reference sample data due to scholars not publishing their raw data.

Along with the use of Bayesian techniques in fields such as genetics, archaeology, and paleoanthropology, perhaps the most well-known and widespread use of this theorem is in the fields of paleodemography and forensics. Due to the substantial amount of research in these areas, the remainder of this analysis will be devoted to illustrating the contribution of Bayesian techniques to determining more accurate age-at-death estimates within the limits used in this method. The determination of age-at-death of skeletal remains is as important in forensics as a prerequisite for identification, as it is for unbiased paleoanthropological studies that make meaningful statements about the past (Schmitt et al. 2002

Bayesian analysis for age-at-death estimations is very useful in the fields of paleodemography and forensics. Hoppa and Vaupel (2002) explored the concept of age estimations by explaining it in three steps. The first step is to assess the skeletal morphologies of the remains in question. Then one must link the morphology to a chronological age through a reference collection. Finally, the remains can be placed in an estimated age category. The second step in this process requires the use of Bayesian methodology as expressed for this analysis by Gowland and Chamberlain (2002:681) in the following formula:

$$p(A_i/L_j) = \frac{p(L_j / A_i) \times p(A_i)}{p(L_j)}$$

Where A= age and L= femur length. In this equation, the posterior probability, $p(A_i/L_j)$, represents the "probability of being in an age category $_i$ given the particular indicator state $_j$," (Gowland and Chamberlain 2002: 681). The likelihood, $p(L_j / A_i)$, is described as the "probability of possessing a particular indicator state $_j$, given a particular age category $_i$, " (681). "The overall probability of possessing a particular indicator state is represented by $p(L_j)$, calculated as the sum of $[p(L_j / A_i) \times p(A_i)]$ over all categories of A," (681).The prior probability, expressed as $p(A_i)$, "represents an opinion of the probability of being in A_i before any data is observed (681). In this analysis, we are using a uniform prior, which assumes an equal probability of death at any age.

An appropriate choice of reference sample to be used with Bayesian age estimation methods is vital to the accuracy of the technique. Oftentimes methods of aging are based on the assumption that the “underlying biological basis of the age/indicator relationship is constant across populations” (Schmitt et al. 2002). In order to create a realistic age estimate, the reference sample needs to be as large as possible; however, it may not necessarily be tied to geographic specifications such as regional background, sex, chronological age distribution, or ethnicity. In fact, Braga and colleagues (2004) used Bayesian methods in comparison to correspondence analysis and regression methods (CAR) to analyze the factors that influence the accuracy and reliability of non-adult age estimation. The main goal of these authors was to determine if age estimations are dependent on such factors as geographical background; and upon closer scrutiny of the Bayesian technique, found "a clear trend in favor of higher accuracy and reliability levels when using *non-* geographic-specific standards" (Braga et al. 2004: 271, italics added).

Bayesian statistics can be of paramount use in the aging of adult skeletal remains. There are various established gross visual techniques for aging skeletons; however, most of these techniques are only accurate when estimating the age of children and young adults. The reason for this concerns the dependence of visual methods on stages of growth and development. Many skeletal biologists and forensic anthropologists use tooth eruption patterns and the fusion of epiphyses to estimate the age of younger individuals. These methods become problematic when dealing with adult remains. After all the permanent teeth have erupted and epiphyses have fused, the skeleton begins to deteriorate at varying rates dependent on disease, diet and physical activity levels. Most age estimates of adult remains based on visual methods are fuzzy and based on a wide-range, as visual methods are limited to age ranges with regular age-related changes (Meindl and Russell 1998). In fact, Aykroyd et al. (1999) argue that many methods are not reliable past 40-50 years old, and attempting to use visual methods on adult remains often leads to a trend of underestimating the age of adults and creating a demographic profile in which no one lives past the age of fifty.

In order to combat the problems with estimating adult age-at-death, many scholars advocate the use of multiple, varied methods to account for the biases from each individual method (Aykroyd et al. 1999, Konigsberg et al. 1998, Müller et al. 2002). One of those multiple methods so highly supported uses Bayes' theorem. "A Bayesian approach to converting age indicators into estimated age-at-death can reduce this trend of underestimation at the older end" (Aykroyd et al. 1999:55).

Schmitt et al. (2002) advocate the use of Bayesian techniques in an investigation of the adult age estimation based on the auricular surface and the pubic symphysis. Two of their main arguments for the usefulness of this approach include its straightforward reproducibility and its ability to better age adults over sixty. These indicators are also practical choices because they are frequently preserved in the archaeological record. “Multiple indicators are not more outstanding than single criteria...[however] it is better to take into account the most reliable indicator” (Schmitt et al. 2002: 5). After several tests of this technique, the authors found that by applying a Bayesian prediction to the auricular surface by itself, as well as to a combination of the auricular surface and the pubic symphysis, that there were far fewer unclassified remains for older adults (Schmitt et al. 2002).

There are currently several methods (both visual and statistical) available for estimating the age-at-death of sub-adults and adults. For example, Bayes’ theorem has been utilized in the estimation of individual adult age-at-death in archaeological samples based on age indicators such as dental wear patterns (Aykroyd et al. 1999). Obstetricians can estimate the growth rates and gestational age of fetuses through ultrasound technology (Oman and Wax 1984). There have been other studies on ultrasound estimates of gestational age (Olsen et al. 2004), more specifically on perinatal remains as a comparison to measurements of live fetuses. There has also been research conducted on skeletal measurements of perinatal remains of known ages (Olsen et al. 2002b). Owsley and Jantz (1985) applied regression formulae to Arikara perinatal remains to determine a gestational age distribution based on diaphysial lengths of long bones. The data from this analysis will form the basis of the current investigation of Bayesian methodologies of gestational aging. Finally, Gowland and Chamberlain (2002) examined the Sheuer, Musgrave, and Evans (1980) formulae used in the Owsley and Jantz analysis. In this investigation, the authors reanalyzed perinatal data from Roman-Britain using Bayesian methods with both a uniform prior and model priors to determine if the regression methods did indeed create an artificial peak. Applying the previous research on known age perinatal remains in conjunction with a collection of perinatal remains of unknown ages should illustrate whether Bayes' theorem can be as useful in this endeavor as it has been in previous studies.

The final topic to be addressed here is the application of Bayes' theorem in forensic cases. Bayesian techniques are especially valuable in a forensic setting for a variety of reasons. For example, most forensic cases (with the exception of mass disasters and cemetery disruptions) involve single sets of skeletal remains. The case-by-case basis of forensic problems is only complimented by using Bayesian techniques because the researcher is not attempting to create a demographic profile for an entire population. Another positive effect of using Bayesian techniques on forensic cases is the availability of more representative reference populations. Determining the reference sample is far less complicated when dealing with modern populations. Yet another reason that Bayesian techniques are a valuable tool in forensic cases is its ease of use. In most instances, forensic anthropologists can apply Bayes' theorem as a univariate-univariate calibration problem in which they have one predictor (i.e. features on the auricular surface) and one variable to be predicted (i.e. age)

(Konigsberg et al. 1998). This single variable formula is quick and easy to apply without requiring a lot of extra steps.

As can clearly be seen, Bayes' theorem has been adopted and used in numerous and varied ways throughout the discipline of anthropology. From genetic studies of founder lineages, to probabilities of the heritability of less desirable traits from admixture, and even studies in archaeological sampling and paleopathological diagnoses, Bayesian techniques can aid in the investigation of very diverse problems within anthropology. Perhaps the most widely recognized and comprehensively studied application of Bayesian methods; however, occurs in the fields of paleodemography and forensics through the development of more accurate, Bayesian, age-at-death estimation methods.

CHAPTER 3: MATERIALS AND METHODS

The data used in this analysis originated from two main sources. The reference sample data was generously provided by Dr. Oystein E. Olsen (2002) (See Table 1 in the Appendix). The experimental data consisted of Native American long bone lengths originally used in an analysis by Owsley and Jantz (1985). The analysis performed by Owsley and Jantz (1985) used the regression-based techniques described in Sheuer, Musgrave, and Evans (1980) on the Arikara perinatal remains, and developed a distribution of infants by age rather than individual age assessments. The Bayesian analysis was performed on these same Arikara remains in order to assess if an accurate probability of viability could be determined.

The reference sample data was originally collected and analyzed by Dr. Oystein E. Olsen and colleagues (2002, 2002b, 2004) in a systematic, population-based study of perinatal remains. The remains consisted of stillborn and aborted fetuses ranging from 16 weeks gestational age to seven days post-delivery. All of the remains originated within the Haukeland University Hospital in Bergen, Norway between 1988 and 1998 and include only non-twin fetuses. During this period, these remains were routinely radiographed and measured prior to autopsy.

The reference data consisted of 348 perinatal remains of known gestational age used in the Bayesian analysis. The mean gestational age of this sample is about 24 weeks. The relevant demographic data, including weight in grams and gestational age in weeks LMP, were obtained from the clinical health records and the Medical Birth Registry of Norway (Olsen et al. 2002b). The known gestational ages were gauged by both second trimester ultrasound and LMP. The original analysis of these remains included diaphysial lengths of the humerus, radius, tibia, and femur; however, in this analysis only the mean femoral length measurements were used.

Population-specific conditions such as nutritional status and access to health care also contribute to the overall growth of the fetus. In many cases, remarkable differences in size of individual fetuses of the same gestational age are shown to be due to growth restrictions caused by maternal malnutrition and placental abruption among other prenatal conditions. (See Figure 1). For this reason, it is more accurate to determine a population age distribution rather than

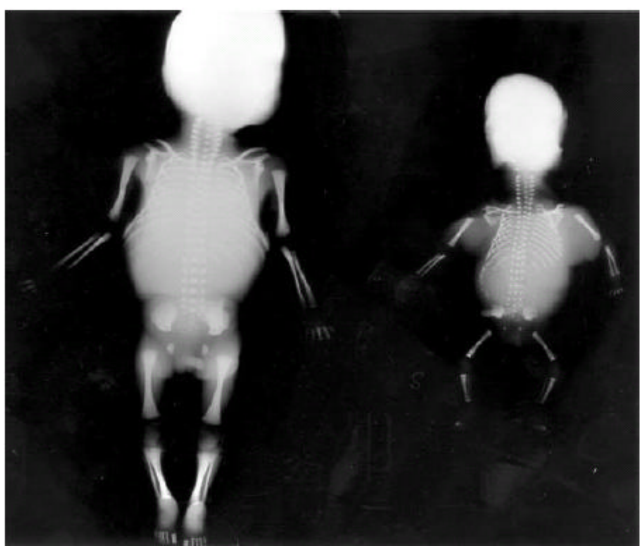

Figure 1. Differences in Size Due to Growth Restrictions
Two fetuses at 24 weeks gestational age. The fetus on the left has a femoral length measurement of 34mm while the fetus on the right has a femoral length measurement of 16mm.- (Taken from Olsen et al. 2002b: 671)

attempting to determine the gestational age of individual remains. In this analysis, growth restriction would not significantly affect the accuracy of Bayesian methodology. A Bayesian method is not meant to determine specific gestational ages, but rather to produce a probability as to whether or not the remains have reached a certain developmental stage where they could be considered viable based on the length of the femur. Growth restricted remains would measure small, and therefore produce a probability of being less than 24 weeks developed.

The comparison data consists of 495 sets of perinatal remains of about 41 weeks gestation or less. These bones are excellently preserved and consist of two temporally defined sets of Arikara remains from seven coalescent tradition sites in South Dakota. These sites include: Four Bear (39DW2), Larson (39WW2), Leavenworth (39CO9), Leavitt (39ST215), Mobridge (39WW1), Rygh (39CA4), and Sully (39SL4) (Owsley and Jantz 1985). The early coalescent remains date from 1600-1733, and the late coalescent remains date from 1760-1835. The main distinction between these different sets of remains concerns growth restrictions due to environmental factors such as change in subsistence patterns and post-contact introduction of diseases. Increased numbers of small for gestational age (SGA) remains are found among the late coalescent remains, as indicated by earlier age assignments based on long bone lengths in the later set of remains. This distinction was not made in the following analysis for the reason previously mentioned. The small for gestational age remains would most

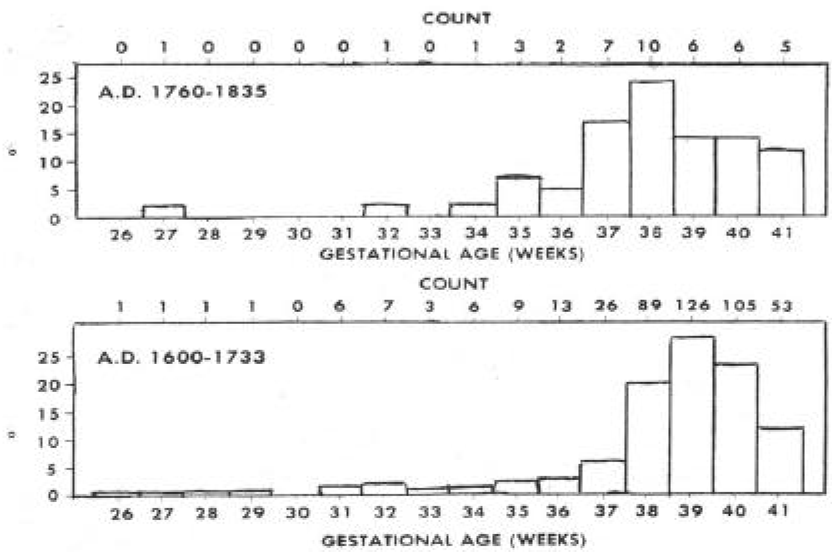

Figure 2. Differences in Age Assignments Due to Growth Restrictions
The later coalescent graph peaks earlier (38wks) than the early coalescent graph due to an increase in SGA femur length measurements. - (Taken from Owsley and Jantz 1985: 325).

likely give a probability of not being viable under a Bayesian analysis. (See Figure 2).

In the Owsley and Jantz analysis, the Arikara remains were divided into diaphysial measurements of the humerus, radius, ulna, tibia and femur from the left side; substituting the right side if needed. In this investigation; however, only the femur lengths were used in the analysis. The Owsley and Jantz (1985) analysis uses the Sheuer et al. (1980) regression formulae to determine an age distribution for the perinatal remains from the Arikara sites.

The Bayesian analysis was performed using the statistical computer program R, version 2.0.0. In the first part of the analysis, a logistic regression of femur length on age was performed on the reference data and illustrates the non-linear relationship between femur length and gestational age in weeks LMP.

The information from the logistic regression was then used to determine the log-odds that a femur measuring a certain length would correspond to a fetus at least 24 weeks developed.

In the next step, Dr. Konigsberg created a function to determine the log-likelihood using a loop across the 495 Arikara femoral measurements. A t-distribution was used to establish the probability of getting an observed femur length given a known age. In this formula, the predicted value and standard error are based on the logistic regression of femur length on age from the reference data. From this data, the posterior age distribution was created in a lognormal form, and the origin is shifted 20 weeks. The posterior probability is the product of the prior age and the likelihood at a given age. In order to find the total likelihood for each case tested, I integrated the posterior for each case across age. From this the log-likelihood was determined across all the cases by adding the log to the log-likelihood. Finally, the log-likelihood was optimized across the mean and standard deviation for the log age with the origin shifted 20 weeks.

CHAPTER 4: RESULTS

The reference data contained in the appendix presents the identification numbers used by Dr. Olsen and colleagues (2002, 2002b, 2004). Additional information included the gestational age in weeks LMP and the mean femur lengths in millimeters. The youngest remains are at eleven weeks gestation, and the oldest remains are four weeks post-partum. There is great variation in the femur length averages per age in weeks, with the smallest length being 8.88mm for remains at 19 weeks LMP. This measurement seems to illustrate a case of growth restriction. The average gestational age of the reference material is about 24 weeks LMP. (See figure 3)

The logistic regression was used to create the log-odds of viability, as seen in figure 4. The results allow for a femur of about 52mm in length being 100

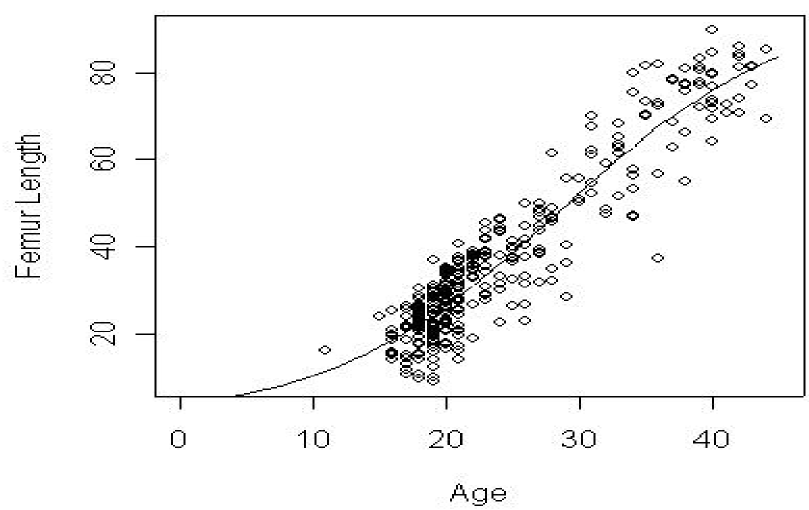

Figure 3. Logistic Regression of Femur Length on Age.
The data is clustered around the 20-week mark .

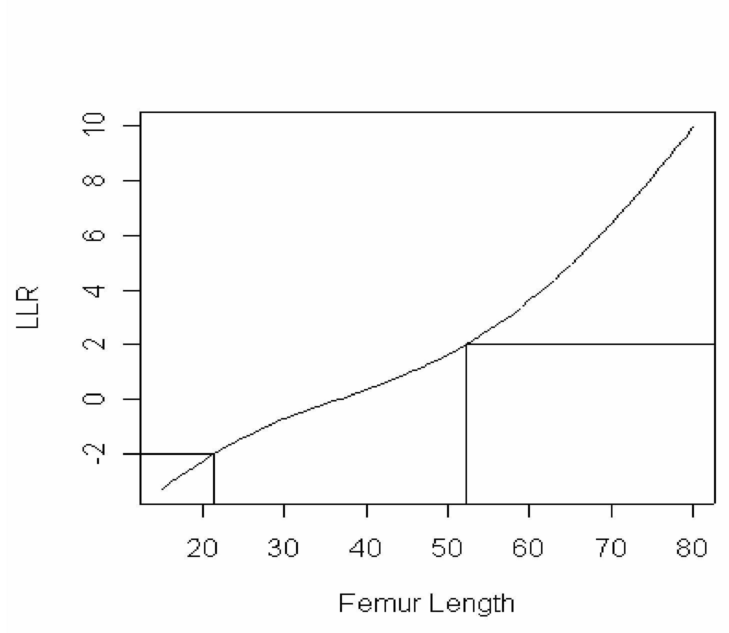

Figure 4. Log-Odds of the Viability of the Reference Sample.

times more likely to be at least 24 weeks gestation. In the same regard, a femur measuring around 21mm in length is 100 times more likely to be less than 24 weeks developed, and therefore has a higher probability of not being viable.

The raw Arikara data contains 495 sets of remains. These data were used to create a perinatal age distribution (figure 5), and a survivorship curve (figure 6). The perinatal age distribution is shifted 20 weeks at the origin in order to include only perinatal remains. The peak age range provided by the Bayesian analysis is 40 weeks LMP. The survivorship curve with a 95% confidence interval illustrates the highest probability of death being at birth, or around 40 weeks LMP.

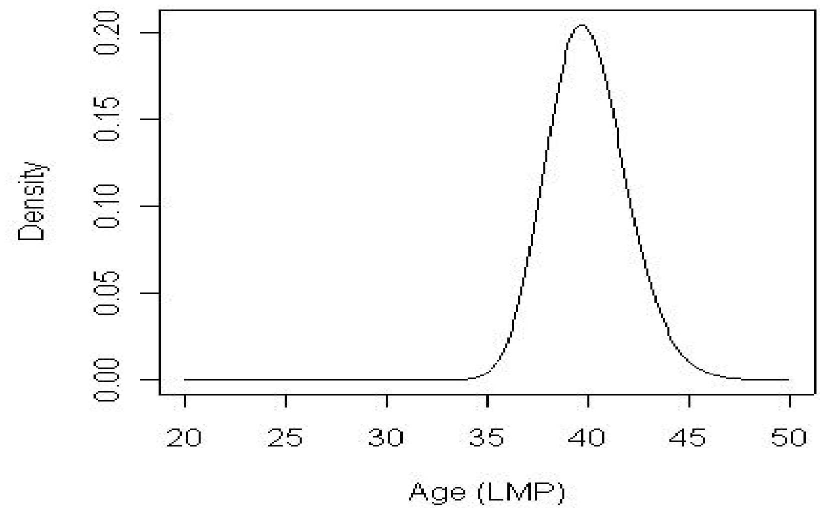

Figure 5. Arikara Perinatal Age Distribution.
The peak age is around 40 wks LMP.

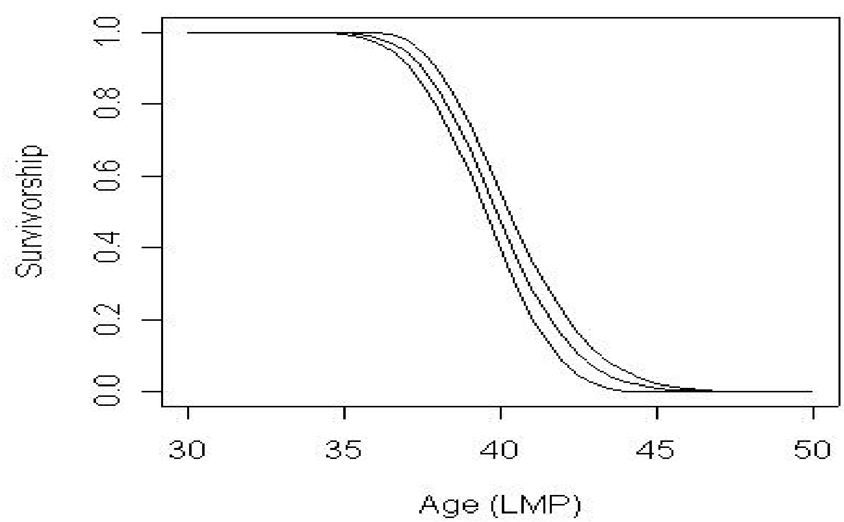

Figure 6. Arikara Survivorship Curve and 95% Confidence Interval

CHAPTER 5: DISCUSSION

The previous analysis required the use of a large reference sample and an unknown sample to be tested. One prominent problem with using Bayesian statistical analyses is the lack of published raw data. Currently there are very few sets of raw data available for use in research endeavors. I was fortunate enough to procure the reference data used in this project from a generous scholar and doctor.

The use of appropriate reference data is paramount to this type of investigation. There are several important aspects to be aware of regarding the data used in a Bayesian analysis. For instance, the reference sample should be as large as possible. In this case the data included 348 sets of remains, a fairly large sample size. Another factor to consider when choosing reference data is that it is as representative of the unknown data as possible. When analyzing perinatal remains, ultrasound measurements of femur lengths (i.e. Oman and Wax 1984), would not be appropriate because those data represent normal growth whereas perinatal remains do not represent normal growth at all. Perhaps the most constraining factor when choosing a reference sample for this investigation is the availability of raw data. Since there is not a lot of published raw data to choose from, the reference sample was decided on because it was available, it was a large sample, and it contained femur length measurements in millimeters. Unfortunately, there is a large temporal difference between the Arikara data and the reference sample.

The reference data consisted of purposefully gathered perinatal remains used in a systematic study. These remains are modern and well preserved, having never been buried. The Arikara data, on the other hand, contained remains that were several hundred years old and had been interred for nearly as long. These remains were also well preserved and in excellent condition due to the careful excavation methods used to retrieve them. The condition of the remains as well as the environment in which they are discovered will come into play in future investigations of this method because the unknown data could come from several sources including disinterred remains from a cemetery, hastily buried forensic cases, or mass burials from war crimes or such.

The way in which the Bayesian investigation was set up allows for its use in both mass remains, and individual settings. Due to the nature of this analytical method providing age estimates, Bayesian analysis of perinatal remains can be a useful tool in academic research as well as forensic applications.

CHAPTER 6: CONCLUSIONS

While the Bayesian analysis does not offer precise age estimations for perinatal remains, it does provide a useful and informative probability that can be used in several situations. For example, a Bayesian analysis of perinatal remains found in an archeological setting (i.e. a cemetery) can shed light on the type and value of the perinatal care available in a certain culture at a specific time, as well as providing evidence of such cultural practices as infanticide. One question that might be addressed in this case is the nutritional status of the mother and the prevalence of congenital diseases and growth restrictions.

This method can also be useful in mass disasters, forensic settings and cases of genocide. In these examples, Bayesian methods of perinatal age-at-death estimations can provide evidence of purposeful disregard of lives in situations of genocide (i.e. murdering the mother without regard for the fetus). Another application of this technique is the counting of individuals in mass disasters by including perinatal remains among the numbers of victims. In forensic settings, the determination of viability can be a useful tool in the establishment of charges against the accused. For instance, if a pregnant woman is found murdered, and the fetus is determined to be at least 24 weeks gestation, the accused would be charged in a double homicide and perhaps given a harsher sentence due to the nature of the crime.

In total, Bayesian age-at-death measurements are useful in a number of situations. One important factor to keep in mind, however, is the need for an appropriate reference sample. Different situations may call for a different set of reference data dependent upon the antiquity or modernity of the remains. In either case, a large sample is required for a more accurate analysis. These reference data are currently scarce; but perhaps more researchers would be willing to publish their data if advised of the urgent need and usefulness of those data. Of course this method is also in need of extensive testing and would benefit from further investigations, however, hopefully this analysis provides an adequate starting point.

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APPENDIX

Table 1. Raw Reference Data Used in Analysis

ID	Gestational Age in Weeks	Femur length mean in mm
666/90	11	16.06
273/93	15	24.09
835/93	16	13.94
14/90	16	15.06
95/91	16	15.09
211/95	16	15.31
728/92	16	15.64
62/95	16	18.64
471/95	16	18.65
173/93	16	19.63
545/92	16	19.75
307/96	16	21.02
79/95	16	25.42
189/88	17	10.50
146/97	17	11.51
197/91	17	12.87
463/97	17	14.33
141/89	17	15.03
199/96	17	15.09
649/91	17	18.52
599/93	17	21.28
421/94	17	21.32
528/91	17	21.39
122/98	17	21.43
642/93	17	21.43
175/96	17	21.95
81/97	17	23.83
358/98	17	23.90
258/90	17	25.67
501/88	17	26.42
66/97	18	9.58
214/96	18	10.80
321/89	18	13.96
117/94	18	14.98
287/96	18	15.42
240/90	18	17.47
367/95	18	17.91
131/98	18	17.92
639/91	18	19.19
63/90	18	20.47
394/96	18	20.57
99/88	18	20.66
131/95	18	21.27
359/94	18	21.47

Table 1 Continued

ID	Gestational Age in Weeks	Femur length mean in mm
184/91	18	21.63
130/98	18	21.75
289/98	18	22.37
556/89	18	22.42
47/91	18	22.60
2/91	18	22.72
58/93	18	23.01
317/92	18	23.44
470/88	18	23.55
634/92	18	24.37
792/89	18	24.72
360/97	18	24.74
154/90	18	25.12
56/91	18	25.17
678/93	18	25.33
744/93	18	25.35
177/97	18	25.57
207/95	18	25.82
665/91	18	25.84
64/92	18	26.12
652/93	18	26.45
272/96	18	26.60
443/94	18	28.07
618/91	18	28.63
659/90	18	30.45
182/90	19	8.88
327/94	19	9.87
408/93	19	12.43
516/90	19	13.90
382/90	19	15.61
148/98	19	15.91
402/95	19	16.63
408/97	19	17.33
251/96	19	18.24
23/90	19	18.31
657/93	19	18.54
290/91	19	19.03
152/88	19	19.64
56/96	19	19.70
587/93	19	19.96
606/93	19	20.00
750/91	19	20.27
618/90	19	20.27
602/93	19	20.46
473/92	19	20.77

Table 1 Continued

ID	Gestational Age in Weeks	Femur length mean in mm
278/90	19	20.79
95/90	19	21.40
158/90	19	21.95
482/97	19	22.04
435/94	19	22.05
248/94	19	22.32
609/88	19	22.67
121/91	19	24.16
622/90	19	24.38
607/90	19	24.49
587/90	19	25.14
448/95	19	25.51
571/91	19	26.26
31/95	19	26.30
655/90	19	26.41
258/92	19	27.25
318/95	19	28.15
10/94	19	28.19
468/93	19	28.34
794/88	19	28.68
430/94	19	28.73
209/90	19	28.77
664/89	19	28.84
433/97	19	29.42
433/91	19	29.42
508/92	19	29.60
434/96	19	29.67
146/95	19	30.34
152/94	19	30.57
565/90	19	30.97
568/93	19	36.91
447/98	20	16.53
713/91	20	17.37
457/98	20	17.89
281/94	20	20.40
403/97	20	20.72
206/97	20	22.25
16/89	20	22.45
654/90	20	22.71
266/89	20	23.00
109/95	20	23.20
437/93	20	24.79
109/96	20	25.14
17/94	20	25.94

Table 1 Continued

ID	Gestational Age in Weeks	Femur length mean in mm
44/90	20	26.27
51/92	20	26.90
436/88	20	27.26
521/88	20	27.33
59/94	20	27.80
840/93	20	28.73
108/95	20	28.96
130/94	20	29.25
291/91	20	29.57
125/94	20	29.78
574/93	20	29.79
37/91	20	30.15
101/97	20	31.20
381/94	20	31.49
49/96	20	31.56
787/93	20	32.13
147/97	20	33.39
539/93	20	33.39
150/94	20	33.79
702/89	20	34.13
112/96	20	34.52
18/90	20	34.69
504/95	20	35.22
287/88	21	14.21
103/97	21	16.14
704/88	21	17.20
40/97	21	19.55
260/94	21	20.67
333/95	21	20.76
621/92	21	22.02
871/93	21	24.17
634/88	21	25.32
25/90	21	25.50
210/95	21	27.27
306/92	21	27.31
169/94	21	27.62
698/93	21	28.04
243/96	21	28.95
593/92	21	30.26
81/94	21	30.38
216/89	21	30.65
156/97	21	31.33
446/97	21	31.57
508/93	21	32.00

Table 1 Continued

ID	Gestational Age in Weeks	Femur length mean in mm
26/92	21	32.06
355/89	21	32.20
504/92	21	33.45
192/94	21	33.62
491/92	21	33.86
25/92	21	34.45
665/90	21	34.53
317/91	21	35.19
154/91	21	35.25
123/94	21	35.30
364/90	21	36.61
734/91	21	36.78
356/91	21	37.56
500/90	21	40.52
808/89	22	18.93
52/96	22	26.69
515/90	22	32.68
446/93	22	33.23
299/90	22	34.58
144/92	22	34.91
200/97	22	35.65
224/94	22	35.68
558/90	22	35.94
402/89	22	36.03
183/94	22	36.90
455/95	22	37.68
572/88	22	38.07
213/96	22	38.10
381/90	22	38.18
553/90	22	39.07
119/89	23	27.78
662/90	23	28.67
228/90	23	28.99
98/93	23	30.71
278/96	23	30.73
336/93	23	34.09
316/91	23	35.64
509/97	23	37.57
108/90	23	37.79
718/89	23	38.43
368/96	23	38.77
297/92	23	41.82
24/91	23	41.96
361/93	23	43.71

Table 1 Continued

ID	Gestational Age in Weeks	Femur length mean in mm
663/91	23	45.32
30/88	24	22.46
161/94	24	30.14
9/94	24	31.60
429/97	24	33.05
154/92	24	37.98
111/91	24	43.34
191/95	24	43.39
349/94	24	43.66
406/94	24	43.67
58/97	24	44.43
762/93	24	45.99
59/88	24	46.27
543/90	25	26.41
714/93	25	32.56
178/89	25	36.60
143/94	25	37.28
502/92	25	37.71
490/90	25	39.27
671/90	25	40.02
240/94	25	41.41
513/93	26	22.95
354/91	26	26.69
265/94	26	31.28
390/95	26	33.15
90/98	26	37.45
427/89	26	40.23
91/98	26	41.65
82/95	26	44.67
497/96	26	49.77
380/94	27	31.88
325/92	27	38.32
362/93	27	38.60
412/92	27	39.21
372/90	27	43.73
249/96	27	44.75
218/96	27	46.78
179/94	27	47.70
340/93	27	47.75
380/89	27	48.37
542/90	27	49.78
14/94	28	32.17
699/92	28	34.84
364/93	28	45.66

Table 1 Continued

ID	Gestational Age in Weeks	Femur length mean in mm
437/88	28	46.40
361/92	28	46.91
283/91	28	48.86
585/90	28	61.37
631/90	29	28.46
464/97	29	36.32
188/96	29	40.28
102/91	29	55.49
635/93	30	50.28
81/88	30	50.71
54/90	30	51.01
46/94	30	55.80
442/92	31	52.25
551/89	31	54.48
224/97	31	61.03
536/89	31	61.97
452/92	31	67.72
719/89	31	69.88
253/88	32	47.43
611/92	32	48.63
783/89	32	59.00
414/97	33	51.66
7/95	33	61.28
253/90	33	62.74
131/97	33	63.41
74/94	33	65.06
55/89	33	68.14
21/93	34	46.83
328/98	34	47.24
527/90	34	53.37
29/91	34	56.24
99/94	34	57.58
223/96	34	75.57
111/94	34	79.96
441/92	35	69.97
655/91	35	70.27
356/89	35	73.25
166/93	35	81.60
239/91	36	37.31
269/89	36	56.63
102/98	36	72.41
142/95	36	72.91
177/98	36	81.92
116/96	37	62.86

Table 1 Continued

ID	Gestational Age in Weeks	Femur length mean in mm
335/91	37	68.44
214/89	37	78.10
327/98	37	78.44
190/96	38	54.97
570/91	38	66.12
507/93	38	75.86
263/98	38	77.07
143/88	38	77.60
142/88	38	80.93
44/94	39	72.11
113/90	39	76.99
342/97	39	77.73
696/93	39	80.43
478/96	39	81.11
141/97	39	83.29
574/90	40	64.14
834/90	40	69.11
630/92	40	71.59
600/92	40	72.96
210/92	40	73.74
174/97	40	76.88
353/97	40	79.42
63/98	40	79.83
112/88	40	79.89
158/96	40	84.77
678/89	40	89.79
119/95	41	70.70
278/95	41	72.66
7/94	42	70.68
690/93	42	74.05
28/90	42	81.24
594/92	42	83.65
138/96	42	84.16
106/98	42	86.10
413/97	43	77.05
298/92	43	81.04
216/91	43	81.38
747/92	44	69.22
378/95	44	85.22

VITA

Tiffanie Sue Cave was born in Colorado Springs, CO on November 24, 1980. She was raised in Tiro, Ohio and went to grade school at Buckeye East Elementary and Jr. High and High school at Buckeye Central in New Washington, OH. She graduated from Buckeye Central in 1999. From there, she went to the University of Memphis in Memphis, TN and received her B.A. in anthropology in 2003. She received her M.A. in anthropology from the University of Tennessee, Knoxville in 2006.

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