Forensic Science International 259 (2016) 59–68

Contents lists available at ScienceDirect

Forensic Science International

journal homepage: www.elsevier.com/locate/forsciint

An alternative approach for estimating stature from long bones that is not population- or group-specific

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ARTICLE INFO

Article history:
Received 20 June 2015
Received in revised form 2 September 2015
Accepted 2 December 2015
Available online 19 December 2015

Keywords:
Forensic Anthropology
Stature equations
Non-specific
Terry Collection
Lisbon Collection

ABSTRACT

An accurate and precise estimate of stature can be very useful in the analysis of human remains in forensic cases. A problem with many stature estimation methods is that an unknown individual must first be assigned to a specific group before a method can be applied. Group membership has been defined by sex, age, year of birth, race, ancestry, continental origin, nationality or a combination of these criteria. Univariate and multivariate sex-specific and generic equations are presented here that do not require an unknown individual to be assigned to a group before stature is estimated. The equations were developed using linear regression with a sample ($n = 244$) from the Terry Collection and tested using independent samples from the Forensic Anthropology Databank ($n = 136$) and the Lisbon Collection ($n = 85$). Tests with these independent samples show that (1) the femur provides the best univariate results; (2) the best multivariate equation includes the humerus, femur and tibia lengths; (3) a generic equation that does not require an unknown to first be assigned to a given category provides the best results most often; (4) a population-specific equation does not provide better results for estimating stature; (5) sex-specific equations can provide slightly better results in some cases; however, estimating the wrong sex can have a negative impact on precision and accuracy. With these equations, stature can be estimated independently of age at death, sex or group membership.

1. Introduction

An estimate of stature, along with other information, can be used by a forensic anthropologist to assist with identification of an unknown individual when human skeletal remains are recovered. Stature has been considered a critical biometric associated with identification and has been investigated for more than a century. After Pearson [1] laid the foundation for the methodology to develop all modern stature estimation equations, Trotter and Gleser's research in the early 1950s set the benchmark as one of the most significant and influential updates to stature estimation methods, and for the methodology for developing new methods [2,3]. A key aspect of their approach was to developed sex- and race-specific equations for estimating stature using various bones [4–6].

Since the 1990s, a number of studies have been published proposing various options for estimating stature that followed Trotter and Gleser's group-specific approach. These methods fall into several major categories. First, some methods have been developed for specific geo-political populations or nationalities (for example, [7–14]). Second, some methods follow Trotter and Gleser's approach and develop race-specific equations (for example, [15–17]). Third, some methods have been developed for various birth cohorts, typically 19th versus 20th Century [15], and pre- versus post-World War II [17]. Fourth, some methods are size-specific and provide equations for short, medium and tall populations (for example, [18–20]).

The fundamental assumption for all these methods is that group-specificity will increase the precision of the estimate, but they all have the same limiting methodological problem in common: group membership must be determined before an equation can be applied. Furthermore, in many cases the

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http://dx.doi.org/10.1016/j.forsciint.2015.12.011
0379-0738/

parameters of a given group are based on assumptions which make assigning an unknown to a group at best problematic and at worst impossible. For example, Mendonça [7] developed equations from a Portuguese cadaver sample that could be applied to "Portuguese" people. Portuguese is a specific political category but a vague category for investigating human variation, and there are no independent markers that could be used to identify someone as Portuguese, or any other nationality from the skeleton. Furthermore, given the open borders among European Union member states, it is likely that skeletonized remains found in Portugal can be from a person of another nationality. Other methods that rely on different approaches to group membership have similar problems. Variation does exist in *Homo sapiens* but that variation does not necessarily cluster into racial categories or continental origin, and there are problems with using these categories for investigating human variation through time and space. However, even assuming that ancestry is a biological or statistical category, determining race is problematic, particularly from infra-cranial elements which are most often used to estimate stature [21].

Stature estimation equations that are not population- or group-specific have been proposed in the past to address some of these problems (for example, [26,22–25]). However, there are some limitations to these methods in general and specifically when applied in a forensic context. In the early 1950s, contemporaneously with Trotter and Gleser, Dupertuis and Hadden [26] published a paper in which they presented race-specific and generic equations for estimating stature. However, they did not critically assess issues regarding group parameters and presented these generic equations as only a second best option for estimating stature. The first major study to deal systematically with the issue of group-specificity since Dupertuis and Hadden was conducted by Feldesman and colleagues [23]. They used a very large sample that included widely diverse sources, but their study was a meta-analysis using only the femur and they did not provide prediction errors for use in individual cases (see also [24]). Sjøvold [22] also conducted a meta-analysis and came to similar conclusions as Feldesman and colleagues and developed methods that were not sex- or race-specific, but presented the findings within a complex description of a statistical alternative methodology and did not provide multivariate approaches drawing on data from multiple long bones. Additionally, although data corrections may be possible, a limitation of any meta-analysis dealing with skeletal metrics and stature is the compounding impact of the varying nature of the source material: skeletal measurements taken from wet bone, dry bone and X-ray; the nature of cadaveric stature; and age and year of birth bias of the sample [22]. Konigsberg et al. [25] provide one of the better examples of generic formulae, but little information is provided about sample composition and the regression equations are limited to the humerus and the femur. Although there has been some limited testing of the statistical robustness of pooling groups into a single large sample (for example, [22,24]), there has been no testing of these methods using large independent samples in realistic forensic applications to assess the efficacy of the method overall and in comparison to group-specific methods.

In this paper we (1) develop and test a series of univariate and multivariate generic equations that are accurate, precise and easy to apply for estimating stature using the humerus, radius, ulna, femur, tibia and various combinations of these bones without first having to assign an unknown to a given group, using a sample of the Terry Collection; (2) investigate the impacts on accuracy and precision of sex-specific equations; (3) assess how often the equations provide stature estimates and ranges that would be useful in a forensic context using an independent sample from the Forensic Anthropology Databank; (4) assess how well the equations estimate living stature using a sample from the Lisbon Collection; (5) test the assumption that group-specific equations provide the best results by comparing the utility of the equations developed in this paper to Mendonça's [7] Portuguese equations using an independent Portuguese sample from the Lisbon Collection.

2. Materials and methods

Data to develop the method were collected from the Terry Collection, National Museum of Natural History at the Smithsonian Institution, because it is one of the few identified skeletal collections with reliable documented stature for a large number of individuals [27]. Stature data are available for 972 individuals – and photographs or negatives are available for 947 of those individuals – who died between 1928 and 1943 [27]. Stature data were not collected from antemortem records by Terry and his assistants, but rather from a strict, standardized protocol for positioning, measuring and photographing the cadaver [28,4]. Terry [28] designed two variants of a pivoting table that positioned a cadaver in a "standing" position with the head on the Frankfurt horizontal plane, the knees extended, and with the lumbar curve in the spine. Terry [28] conducted various experiments using living subjects and cadavers that showed both tables were useful for closely recreating living stature. Despite the strict protocol established by Terry, it was not always possible to accurately reproduce living stature using the pivoting tables. Those cases were easily excluded from the sample because of Terry's thorough documentation of the collection. There are clear notes on the forms where stature is documented that state "feet off [foot] board" or "knees bent" when there were problems with positioning the cadaver. The sample was selected from those individuals who were properly positioned with their feet flat on the foot board and their knees not bent that met the sampling criteria outlined below for sex, age at death and year of birth.

Sampling is a critical issue when using any reference collection to develop identification methods. A random sample of the Terry Collection will result in a reference sample that is representative of variation in the Terry Collection, and not actually useful for developing identification methods. Statistically speaking, the entire collection should not be treated as a population. The collection is itself a biased sample of the population from which it was derived [28,27]. A random sampling of an already biased sample (the collection) will result in a biased sample being used in research [29]. Through careful sampling based on detailed knowledge of the history of a reference collection, it is possible to select a reference sample that is much more representative of human variation outside of the collection and to successfully develop accurate methods using "older collections" that are applicable in forensic contexts in the 21st Century [30].

The sample from the Terry Collection was selected to include a wide range of human variation following a modified methodology used by Albanese [30] for developing sex determination methods. The underlying assumption is that if a large range of human variation is included in the reference sample used to develop a method, then that method can be applied with confidence in a wide number of contexts. This assumption is based on the fundamental statistical concept that a model cannot be used to reliably predict something outside the range of the original reference sample used to develop the model. Expanding the range of the original reference sample by definition will expand the applicability of the method.

For this research, adults of both sexes were selected with a wide range of ages at death and years of birth to construct a reference sample that includes as much variation as possible. For the purposes of this research, adult is defined as anyone who is 18