ANCESTRY-SPECIFIC VARIATION FOR ROGERS' METHOD OF SEX ESTIMATION

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Controlling for biological ancestry, I conducted a blind test of Rogers' (1999, 2009) method of sex estimation from the distal humerus. Results show that the odds for correct sex estimation are 2.027 times higher for a white individual than for a black individual.

INTRODUCTION

Is the accuracy of Rogers' sex estimation method using the distal humerus dependent on biological ancestry?

Rogers' (1999, 2009) visual method for sex estimation relies on sexual dimorphism in the following four traits of the distal posterior humerus: trochlear constriction, trochlear symmetry, olecranon fossa size/shape, and angle of the medial epicondyle.

Figure 1. Trochlear constriction (Rogers, 1999)

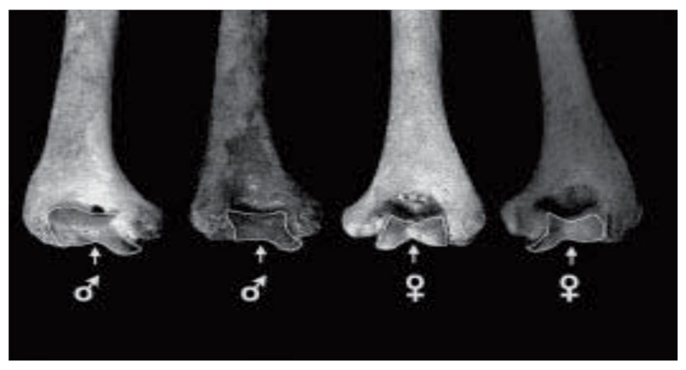
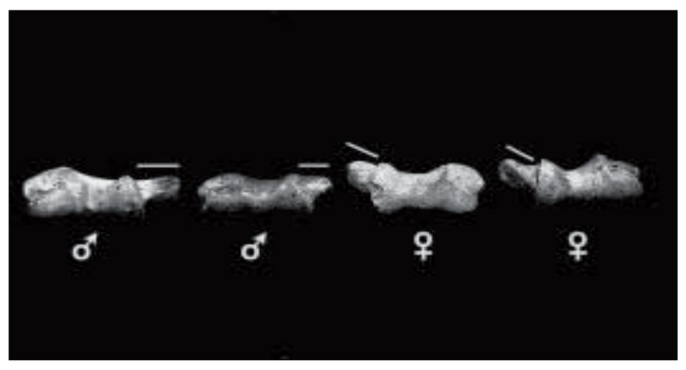


Figure 2. Trochlear symmetry and olecranon fossa size/shape (Rogers, 1999)

Figure 3. Angle of the medial epicondyle (Rogers, 1999)



This method has the potential for widespread applicability on adults and juveniles. In situations of fragmentation or commingled remains, use of the dominant pelvic and cranial methods may not always be possible, making sex estimation from other bones necessary. Furthermore, visual methods tend to be quicker and easier to apply than metric methods, which is beneficial when time and funding is limited.

However, Rogers' (1999) initial accuracy rate of 92% has not been replicated by subsequent tests (Wanek, 2002; Falys et al., 2005; Vance et al., 2011; Watkinson, 2012; Harrison, 2017. Furthermore, the method was designed from a sample of exclusively white individuals, and many of the tests have also used samples of white individuals (e.g., Falys et al., 2005, Rogers, 2009, Watkinson, 2012). This is problematic, as sex estimation methods are often population-specific (Wright & Yoder, 2003), a point that Rogers (1999:60) herself acknowledges. While Vance et al.'s (2011) and Harrison's (2017) studies have used samples of individuals of varied backgrounds, so far, only Wanek's (2002) study has controlled for biological ancestry. Wanek found variation in the accuracy of the method among groups of different ancestral backgrounds (e.g., 78% accuracy for black individuals vs. 85% accuracy for white individuals), but she concludes that the method can still be used on all human populations.

I set out to test Wanek's conclusion by conducting an additional study evaluating the population-specificity of Rogers' method but I employed slightly different methods of data collection and analysis.

DATA COLLECTION

Like Wanek, I blindly tested the technique on a sample of humeri (n = 199) that had been randomly selected from the Hamann-Todd Collection at the Cleveland Museum of Natural History.

However, rather than assess all four traits for each bone simultaneously, I instead evaluated each trait independently by repeatedly seriating the entire sample collection and assigning sex on a three-point scale (male, ambiguous, or female). In between seriations, I shuffled the order of the humeri, better allowing me to evaluate each trait individually without being influenced by my assessment of the previous trait.

Figure 4. Seriation Technique *(Specimens Courtesy of the Cleveland Museum of Natural History)*

When compiling data from all four traits, I assigned an overall sex to each humerus on a five point scale (male, probable male, ambiguous, probable female, or female) based on the following criteria (Table 1).

Table 1. Criteria for Overall Sex Assignment

Assigned Sex	Criteria
Male	All four traits consistent with male sex
Probable Male	Three of four traits consistent with male sex
Ambiguous	Two traits consistent with each sex*
Probable Female	Three of four traits consistent with female sex
Female	All four traits consistent with female sex

*As proposed by Rogers (1999), olecranon fossa shape (if unambiguous itself) was given extra weight in ambiguous cases, allowing some humeri to be assigned to probable males or probable females.

DATA ANALYSIS

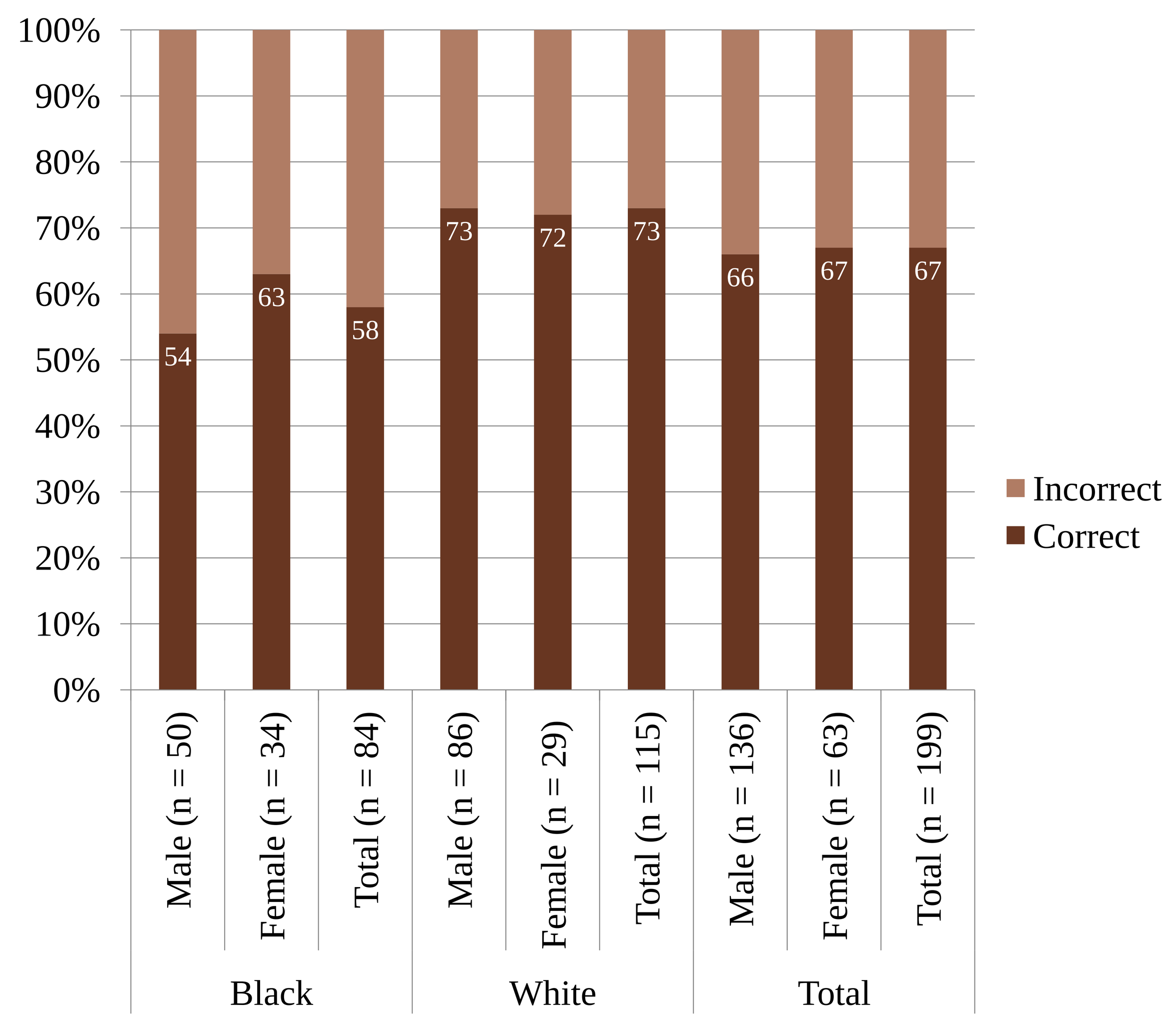
Unlike previous studies that used chi-squared tests to evaluate the statistical significance of differences between expected vs observed results of a single variable (Wanek, 2002; Falys et al., 2005, Vance et al., 2011), I used logistic regression to model the relationships between the accuracy of the method and two categorical variables of biological ancestry and sex. Logistic regression is modeled using an odds ratio, rather than standard probability, which better allows us to consider relative benefits and risks.

The logistic regression was modelled by the equation, $logit(P) = \beta_0 + \beta_1 (Ancestry) + \beta_2 (Sex)$. A test of interaction was initially included in the model but removed when shown not to be statistically significant.

RESULTS

Overall, the method was 67% accurate, ranging from 58% accuracy for black individuals and 73% accuracy for white individuals.

Figure 5. Proportion of correct classifications of sex for black and white individuals



The logistic regression model revealed that neither sex nor the interaction between ancestry and sex are statistically significant variables in this study; however, biological ancestry is a statistically significant predictor of accuracy.

According to the regression model, the odds for a correct classification of the sex of a white individual are 2.027 times higher than the odds for a correct classification of a black individual** (Table 2)**.

Table 2. Logistic Regression Results

	Degrees of Freedom	P-Value	Odds Ratio
Ancestry	1	0.022	2.027
Sex	1	0.830	0.830
Interaction	1	0.552	1.480

DISCUSSION & CONCLUSIONS

The technique's accuracy rate established from this study is considerably lower than Rogers' (1999) initial accuracy rate of 92%, which is consistent with previous tests of the method (Wanek, 2002; Falys et al., 2005; Vance et al., 2011; Rogers, 2009; Watkinson, 2012; Harrison, 2017) (Table 3).

Table 3. Comparison of Results Across Studies

Study	Overall Accuracy (%)	Accuracy of Traits (%)
Simpson (current study)	**67**	**54–67**
Rogers (1999)	92	74–91
Wanek (2002)	83	65–77
Falys et al. (2005)	79	69–82
Rogers (2009)	81	n/a
Vance et al. (2011)	76	45–70
Watkinson (2012)	80	65–78
Harrison (2017)	n/a	60–71

These results also support Wanek's (2002) findings that there are differences in the accuracy of this method associated with biological ancestry. However, the findings that the odds for a correct classification of the sex are 2.027 times more likely for a white individual than for a black individual suggest that application of the technique to non-white populations may be more problematic than Wanek concluded.

Overall, then, while still a useful technique, bioarchaeologists and forensic anthropologists must consider the population specificity of this method within the context of their study.

Future research will examine (1) the ancestry-specific variation in the accuracy of this method in greater detail, (2) how the accuracy established from this study of each of the four traits compare to all other studies' results, and (3) how skeletal manifestations of diseases, especially osteoarthritis, contribute to misclassification of sex using this method.

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