

Is the (hu)MANid Program Valid in a Pediatric Population?

BY

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SUMMARY

This study aims to determine whether the (hu)MANid forensic identification program can accurately identify sex and ancestry of older children and adolescents, using measurements from Cone Beam Computer Tomography (CBCT) scans from the diverse pediatric population seen at the University of Illinois College of Dentistry (UIC COD). The (hu)MANid program was established in 2017 by Berg and Kenyhercz. It uses morphometric analysis to classify adults mandibles based on ancestry, age, and sex.

One hundred and ten eligible CBCTs were used in our sample. Our sample included patients ages 8-17 with a CBCT taken between January 2008 and January 2019 and race/ethnicity recorded. Subjects were categorized to ancestry groups matching (hu)MANid ancestry designations. Patients that identified as non-Hispanic White/Caucasian were of White ancestry. Patients that identified as Hispanic were of Hispanic ancestry and lastly, non-hispanic Black/African- Americans were considered Black ancestry. 3D Slicer software (BHW, Boston, MA, USA) was used to measure morphoscopic and morphometric data and input into the (hu)MANid program to estimate the likelihood that an individual is a certain sex and ancestry.

Results show low overall prediction accuracy of the (hu)MANid program in our pediatric population. The program provides an estimated likelihood that an individual is M/F and White/Hispanic/Black, identifying a most-likely sex/ancestry assignment White (n= 29) subjects were most likely to be assigned to the correct group, followed by Black (n=32), and then Hispanic (n=45). The highest percent likelihood score an individual received for ancestry was slightly more likely to match that individual's actual ancestry

($p < 0.05$) than either of the other two groups. Accuracy of ancestry estimation showed no appreciable changes when older adolescents (>14 y.o. girls, >16 y.o. boys) were examined separately.

The application struggled to predict both sex and ancestry for a given individual. For ancestry prediction only, Whites were identified at a rate consistent with prior literature. For sex prediction only, females reached this threshold. In contrast with our expectations, estimations did not appreciably improve when older adolescents (>14 y.o. girls, >16 y.o. boys) were examined separately. When predicting ancestry, (hu)MANid was slightly more likely to assign an individual to the correct group than to either incorrect group, but the frequency of correct assignment is not forensically valuable except for in the White sample. In our diverse pediatric sample, we were unable to validate the (hu)MANid application for ancestry or sex prediction in older children and adolescents.

INTRODUCTION

I.1 Background

The oral cavity, teeth and oral structures are being used more regularly in Forensic Anthropology for forensic identification. Due to variable size, morphology and individual dental anomalies, analysis of the dentition and surrounding structures can contribute to identification of individuals and human remains by predicting expected age, sex, and ancestry.¹ Research regarding the mandible in forensic identification is less common in comparison to the cranium.² The mandible is an important structure to consider for forensic identification and biological affinity due to the fact that it is a durable bone that tends to remain intact and often well preserved.³ Many times the mandible can survive conditions that other bones in the human body cannot due to its robust nature.⁴ Studies have either used mandibular morphometric or morphoscopic data to determine age, sex or ancestry.⁴

I.2 Forensic Sex Estimation

Sex estimation in forensics is often performed by analysis of the pelvis as a preferred method due to high degree of reliability. Looking at the pelvis for accuracy was developed by Phenice in 1969.⁵ The second best indicator of sex estimation is the skull.⁶ There are limited studies using mandibular measurements to determine sex. Measuring and comparing certain parameters in the mandible, such as coronoid height, projective height, condylar height, and maximum and minimum breadth, determined sexual dimorphisms with an accuracy of 80.2% in a Northern Indian population.⁷ According to this study, coronoid height was the single best parameter, providing an

accuracy rate of 74.1% in determining sex in their population. Using similar mandibular measurements from CBCT scans in a Brazilian population yielded rates of over 90% accuracy in determining sex in 18 to 60- year-old individuals. ⁸ In an Iranian population under 20 years of age, eight mandibular anthropometric measurements were taken and analyzed to determine sex. The symphysial height and bigonial breadth in the 12 to19- year-old group deemed to be accurate 69% and 86.2%, respectively. No statistical difference was noted in the values between the sexes under the age of 12 years. ⁹

I.3 Age Estimation

The most accurate means of estimating age in children is through an analysis of dental development. There are numerous dental age estimation methods, which broadly can be categorized as tooth scoring methods (e.g., Demirjian and Goldstein, 1973; Moorrees et al., 1963) and dental atlas methods (e.g., the London Dental Atlas; the Schour and Massler Dental Atlas; the Ubelaker Dental Atlas).^{10–14} Mandibular morphology has shown to be able to predict age by using ramus height as an alternative or adjunct to dentition. In this case, geometric morphologies were deemed to be more accurate when adolescents were included in the sample ¹⁵. In determining age, measuring the length of the mandibular ramus on lateral cephalometric radiographs can be used to predict whether an individual is older than 18 years with a high level of accuracy, although sexual dimorphism may not be observed until age 16.¹⁶ It is important to note that certain methods should be validated for different populations due to the fact that different ancestries give rise to different phenotypic aspects.

I.4 Ancestry Estimation

Ancestry can be estimated by analysis of standard measurements and geometric analyses that measure distance between different cranial landmarks.¹⁷ The mandible has been used for ancestry estimation by analyzing twelve major traits. These non-metric traits that are commonly examined are ramus inversion, location of the inversion, gonial eversion, mandibular tori, mandibular border form, robusticity of muscle attachments, mylohyoid bridging, accessory mandibular foramen, chin prominence, chin shape, number of mental foramina and the position of the mental foramen.¹⁸

I.5 Acceptable Accuracy in Identification

Methods involving physical and forensic anthropology that have an accuracy of over 75% are deemed suitable for determining the identification of a human, whether it be sex, age, or ancestry.¹⁹ For example, inversion of the middle third of the posterior edge of the mandibular ramus is a valid ancestry trait due to the fact that for both sexes inversion is lacking in 70% of Caucasian/Whites and in 5% African Americans/ Blacks; African Americans can be distinguished from Caucasians and American Indians two-thirds of the time just using this trait.²⁰

I.6 (hu)MANid Program

The Human Mandible Identification (hu)MANid program was established in 2017 by Berg and Kenyhercz to be used in adults. The program has a worldwide sample of mandibular morphology and metric data that allow the classification of mandibles for ancestry, age and sex determination for forensic, bio-archeological and medico-legal applications.² By using morphometrosopic analysis, the creators argue that it is

possible to attain better accuracy rates than just morphoscopic or morphometric measurements alone. However, there is no data validating its use in a pediatric population. The populations used in this application are of measured skulls from unidentified and identified human remains. The unidentified remains had osteological testing done to verify their ancestry. Many samples come from anthropologic and forensic collections at various institutions such as the University of Tennessee Forensic collection, William W. Bass Donated (WBD) collection, Central Identification Laboratory, Pima County Office of the Medical Examiner (PCOME), Guatemalan Foundation of Anthropology (FAFG) and the Hawaii (CILHI) collection.

I.7 Study Objectives

This study has the following key aims:

- 1) To validate the (hu)MANid program in our diverse pediatric population
- 2) To determine if (hu)MANid can be used to identify the sex and ancestry of children and adolescents, using CBCT measurements of the pediatric population seen at the UIC COD
- 3) To contribute to the forensic field to better identify children from fragmentary skeletal remains

I.8 Hypotheses

H₀₁: The (hu)MANid application is not accurate in sex estimation in a diverse population in Chicago

H₀₂: The (hu)MANid application is not accurate in ancestry estimation in a diverse population in Chicago

I. MATERIALS AND METHODS

II.1 Study Approval

This study was approved for exemption by the Institutional Review Board of the University of Illinois at Chicago (IRB #2019-0399), Chicago, IL (Appendix A).

II.2 Sample Collection

A retrospective cross-sectional review of electronic dental charts performed to identify all patients with Cone Beam Computerized Tomography scans (CBCT) taken in the Departments of Pediatric Dentistry, Orthodontics and Oral Surgery in the UIC College of Dentistry. These charts were reviewed based on the inclusion and exclusion criteria to select the final sample.

Inclusion Criteria:

- One of the following dental charge codes for CBCT was present in the dental electronic health record (D0355, D0360, D0365, D0364, D0367, D0372, D0373) between January 2008 and January 2019.
- Subjects were between 8 and 17 years old at the time of their scan
- The race and ethnicity were recorded in the COD electronic dental record.
- The mandible was completely captured in the CBCT

Exclusion Criteria:

- Patients who reported multiple races or ethnicities which made determination of ancestry impossible.
- Patients with trauma to the mandible.
- Patients with craniofacial abnormalities that affect the mandible.

- Patients with medical and/or dental conditions that influence jaw shape.
- Gross image distortion of mandible in the CBCT.
- Subjects who met all other criteria, but when categorized into ancestry groups lacked sufficient numbers for comparison were also excluded.

II.3 Methodology

A complete listing of patients who met the inclusion criteria was created using the dental EHR. The listing was reviewed and potential subjects missing information were excluded. The race and ethnicity data were reviewed to determine ancestry groups comparable to those used in the (hu)MANid program. Ancestry groupings with insufficient numbers for comparison (e.g., Asian) were excluded. The scans were reviewed and images showing trauma, conditions that would alter mandibular shape, or unreadable imaging were excluded. Duplicate scans from the same patient on different dates were also excluded. For each record assigned to a group, the age at the time of the CBCT, the ancestry and the sex were recorded from the electronic dental record. The CBCTs were examined using 3D Slicer Freeware (BHW, Boston, MA, USA) to record 11 Morphometric measurements and 6 Morphoscopic measurements (See Appendix B). The mandibles were isolated from the original scan with 3D Slicer Freeware functionality. The following morphometric measurements were taken: chin height, height of the mandibular body at the mental foramen, bicondylar width, minimum ramus height, maximum ramus height, mandibular length, mandibular angle, mandibular body breadth at the mental foramen, mandibular body breadth at the M2/M3 junction, dental arcade width at the third molar. These measurements were taken following the

descriptions provided by the (hu)MANid application and can be found in the following table.

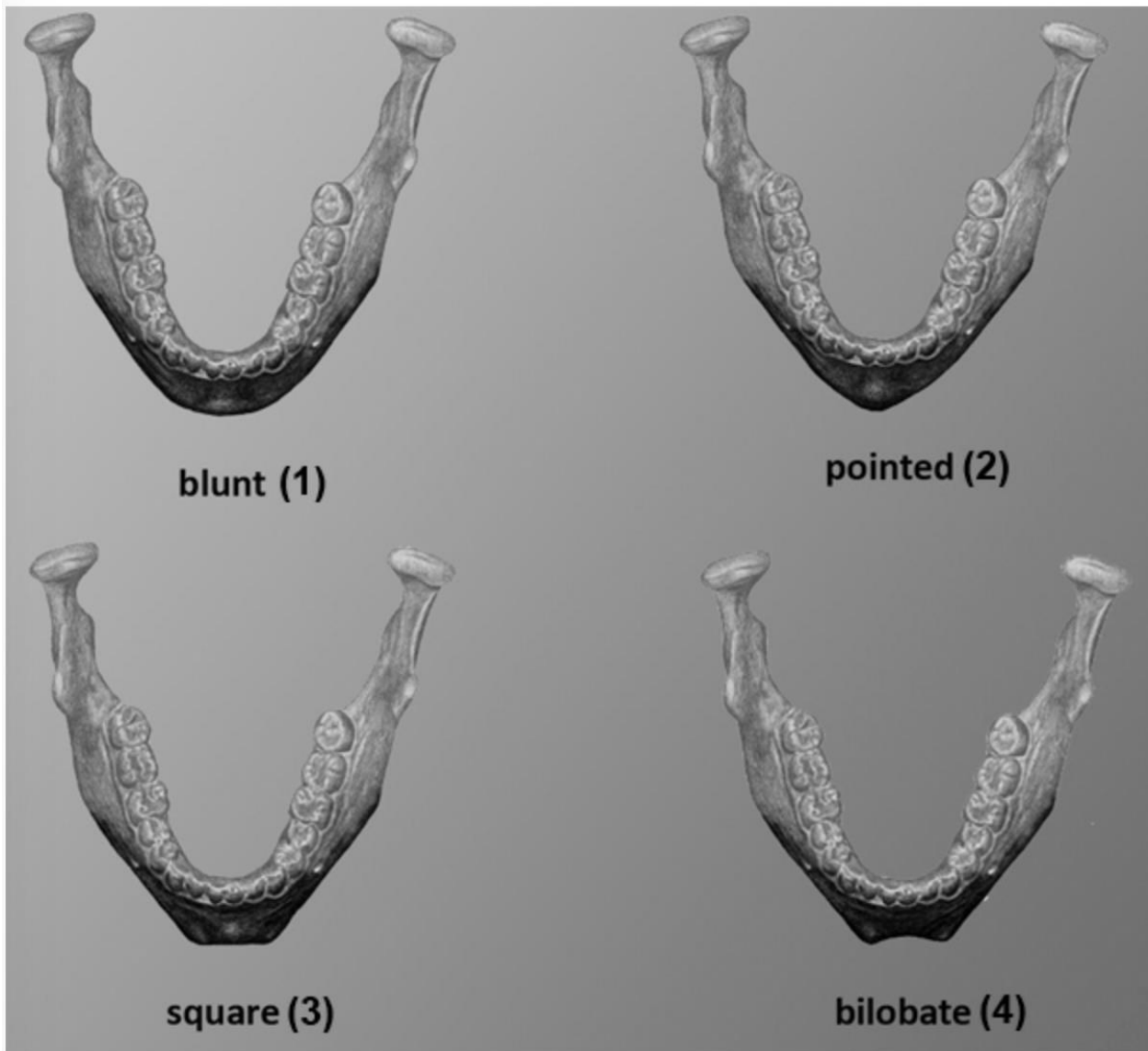
Table 1—Metric Definition Table ²¹

Variable (ABR)	Type	Definition
Chin Height (GNI) †	Metric	The direct distance from infradentale to gnathion.
Height of Mandibular Body at the Mental Foramen (HML) †	Metric	The direct distance from the alveolar process to the inferior border of the mandible perpendicular to the base at the mental foramen.
Bigonial Width (GOG) †	Metric	The direct distance between the right and left gonions.
Bicondylar Width (CDL) †	Metric	The direct distance between the most laterally projecting points on the two condyles.
Minimum Ramus breadth (WRB) †	Metric	The smallest breadth of the mandibular ramus measured perpendicularly to the height of the ramus.
Maximum Ramus Height (XRH) †	Metric	The direct distance from the highest point on the mandibular condyle to gonion.
Mandibular Length (MLT) †	Metric	The distance from the anterior margin of the chin to a center point on the projected straight line placed along the posterior border of the two mandibular angles.
Mandibular Angle (MAN) †	Metric	The angle formed by the inferior border of the corpus and the posterior border of the ramus.
Mandibular Body Breath at the Mental Foramen (TML)*	Metric	The maximum width of the mandibular body taken at the mental foramen. The measurement is typically taken from a superior-to-inferior direction and the caliper arm should be parallel to the flat surface on which the mandible is resting.
Mandibular Body Breath at the M2/M3 Junction (TML23)*	Metric	The maximum mediolateral breadth of the corpus taken at the level of the articulation between the second and third molars. The sliding caliper arm should be parallel to the surface upon which the mandible rests. The measurement location usually corresponds to a medial-lateral thickening of the mandible at that location.
Dental Arcade Width at the Third Molar (XDA)*	Metric	The maximum breadth of the dental arcade at the level of the most posterior points of the third molar crypt on the lingual surface. If necessary, a line should be drawn perpendicular to the ramus body and the tooth crypt to mark the measurement locations. If the third molars are absent, the measurement could be taken at the location of the second molar position, but should be annotated

The morphoscopic descriptions described chin shape, lower border of the mandible, ascending ramus profile, gonial angle flare and posterior ramus edge inversion, as well as the presence of mandibular tori. These morphoscopic descriptions were given a value (1-4) associated with the schematic attached provided by the (hu)MANid application which are listed and described in the following figures.

Figure 1—Morphoscopic Descriptions: Chin Shape

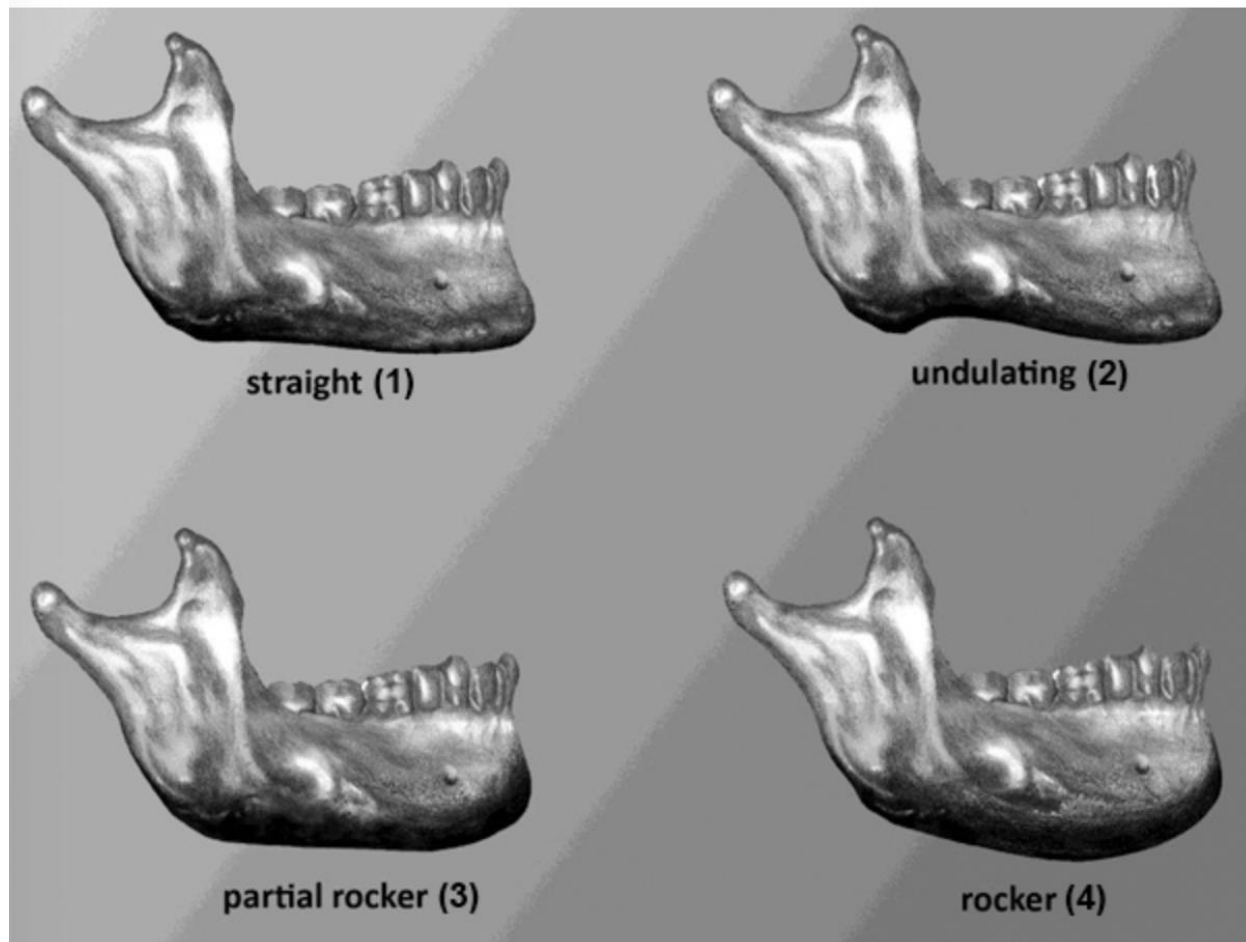
Chin Shape



Chin shape (CS). The chin shape is viewed from above (superiorly) and scored as either blunt (smoothly rounded), pointed (the chin comes to a distinct point), square (the chin has a nearly straight front) or bilobate (the chin has a distinct central sulcus). Using a straight-edge is helpful for distinguishing between the traits, and, in particular, diagnosing the square and bilobate forms²²

Figure 2—Morphoscopic Descriptions: Lower Border of Mandible

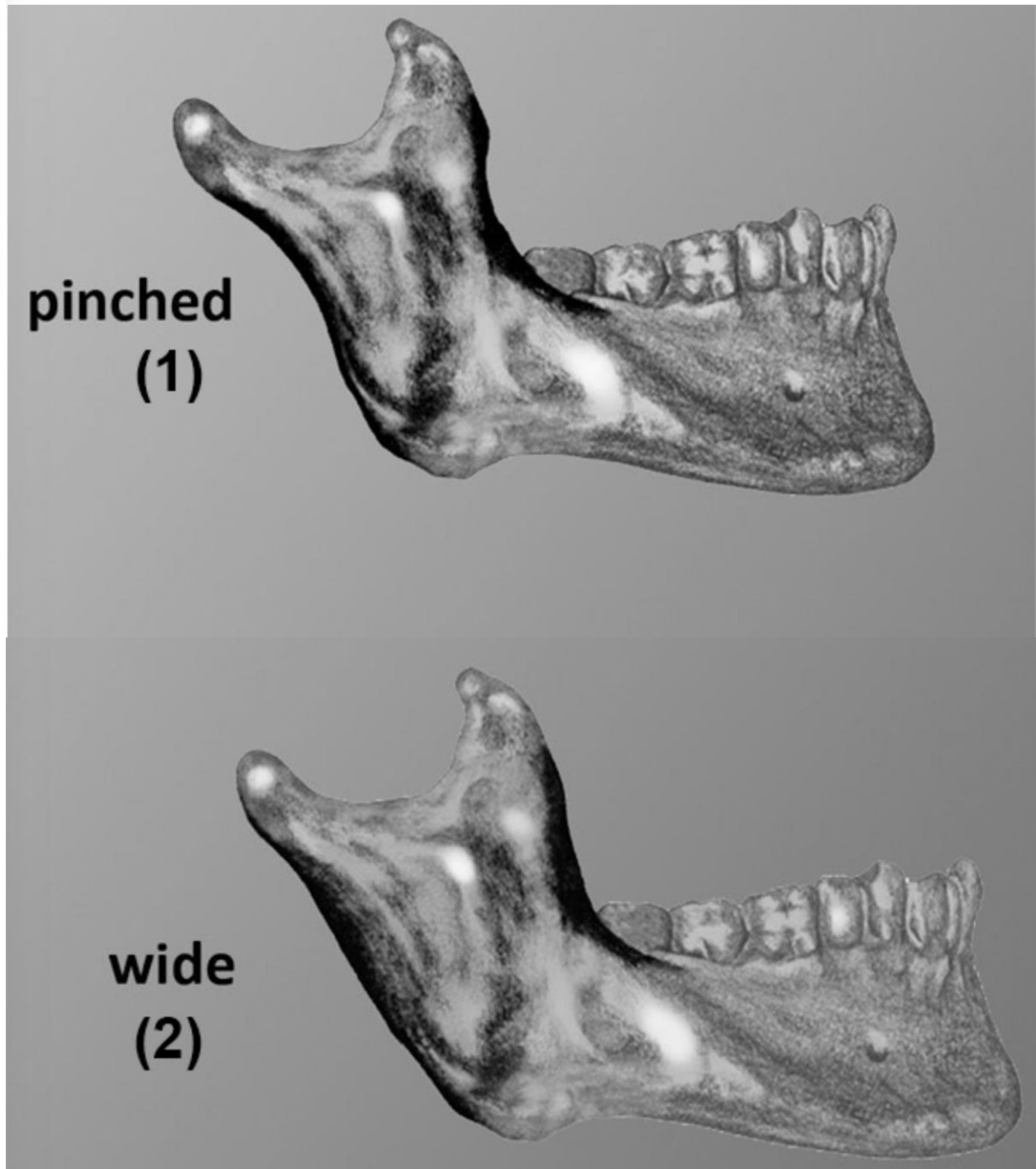
Lower Border of Mandible



Lower border of the mandible (LBM). Four categories are recognized for this trait, and it is easiest to score the trait by placing the mandible on a flat surface. If the majority of the lower border of the mandible is flush against the surface, it is scored as straight. If there is a deviation of the border upward, typically in the region of the lower second to third molars, it is scored as undulating. If the mandible inclines near the chin (and is somewhat rounded in the gonial region), and it rocks forward when gentle pressure is applied to the anterior dentition, it is scored as a partial rocker, and finally, if the mandible is sufficiently rounded on the bottom, such that pressure on the anterior teeth causes it to rock forward and back, it is scored as a rocker.²²

Figure 3 – Morphoscopic Descriptions: Ascending Ramus Profile

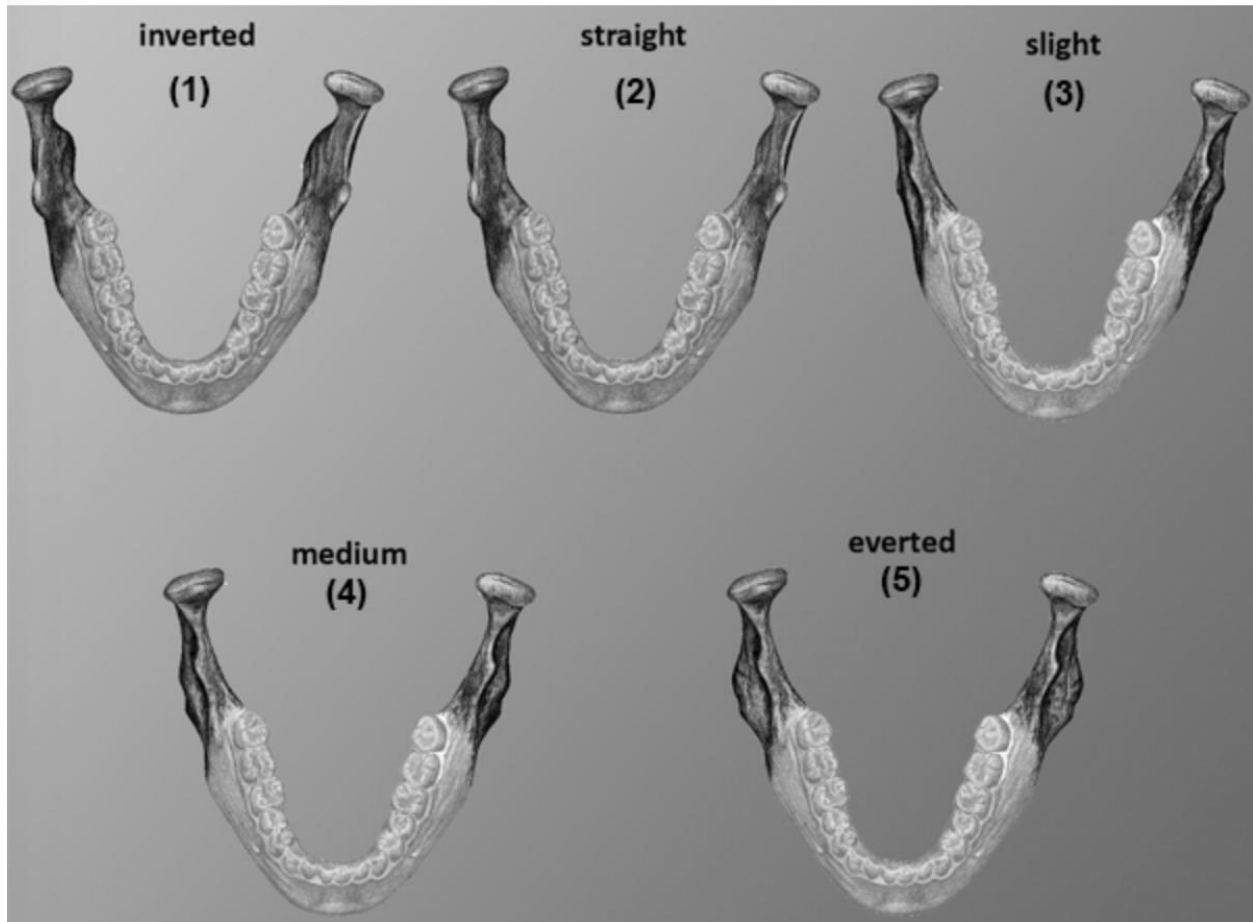
Ascending Ramus Profile



Ascending ramus shape (ARS). This trait is scored as pinched if the ascending ramus noticeably narrows about its midpoint, or wide if it is a relatively uniform width. ²²

Figure 4—Morphoscopic Descriptions: Gonial Angle Flare

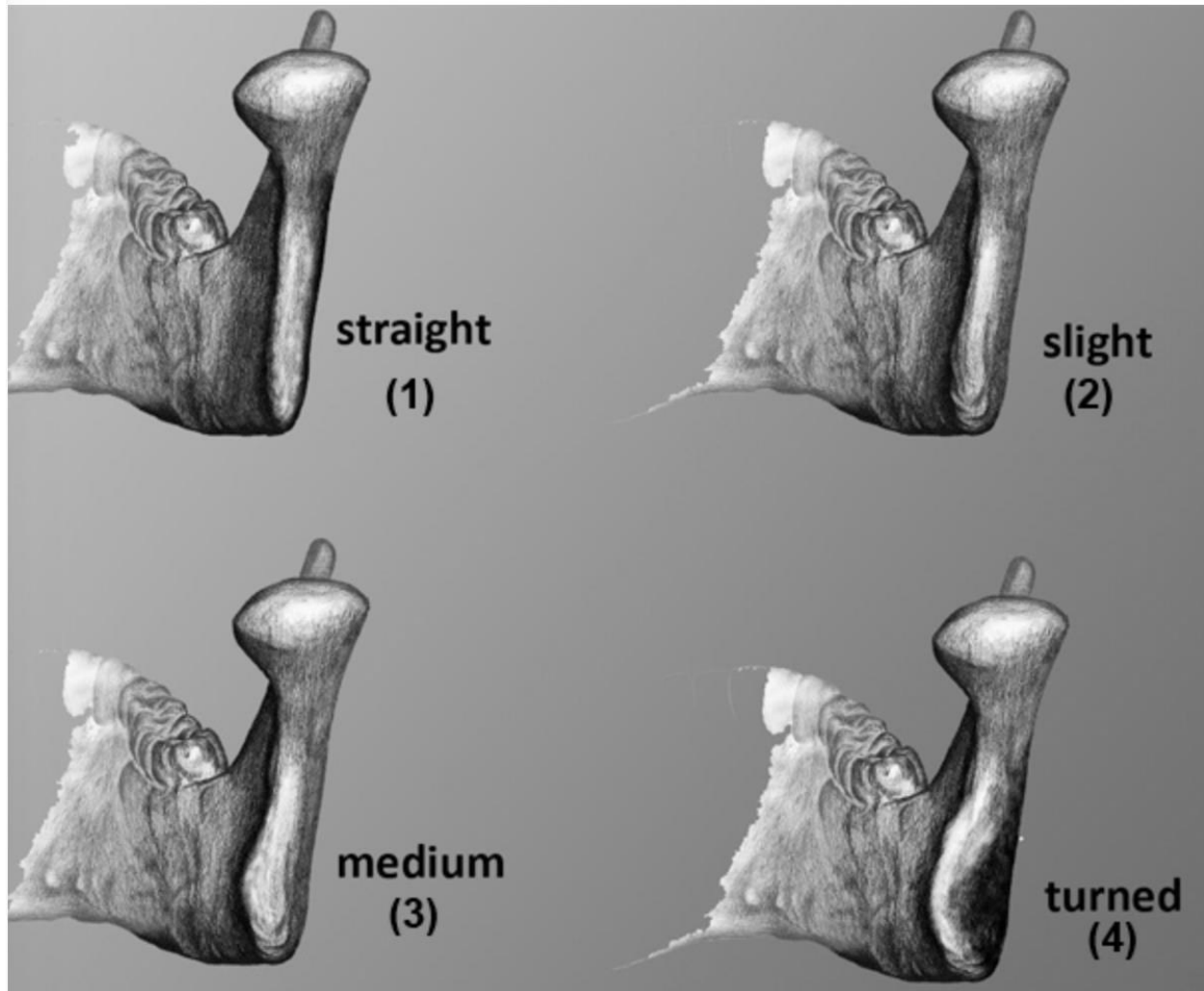
Gonial Angle Flare



Gonial angle flare (GAF). This trait is scored in five stages, the first being inverted, where the gonial process slants medially toward the midline; absent, when the gonial process is in line with the ramus; slight when the gonial process flares outward a short distance (~1-2 mm); medium, when the gonial process flares beyond slight to double that distance (~2-4 mm); and everted, which is greater than twice the distance of slight (>~4 mm). This trait is best scored in relation to the line drawings found in the above figure, and familiarity with multiple mandibles is recommended prior to scoring the trait.²²

Figure 5—Morphoscopic Descriptions: Posterior Ramus Edge Inversion

PREI



Posterior ramus edge inversion (PREI). The trait is observed on the posterior one-third of the ascending ramus. If no discernible flexure toward the midline is present, the mandible is scored as straight. If a small, but discernible flexure toward the midline is present, the trait is scored as slight. Medium is a very noticeable inward deviation, up to twice the distance of the slight category. The mandible is scored as turned when it is greater than a double expression of the slight category.²²

The morphoscopic and morphometric measurements recorded were entered into the (hu)MANid program: <https://anthropologyapps.shinyapps.io/humanid/> to generate expected ancestry, sex and posterior probability. Reference groups were chosen to match with the characteristics of the sample. Linear Discriminant Analysis (LDA) was selected in the program. The (hu)MANid's LDA reported average of correct classification is approximately 60%.²³ For this reason, our study used 60% for comparison.

II.4 Intra- examiner Reliability

Ten randomly selected CBCT scan morphometric measurements and 10 morphoscopic measurements were scored twice by the PI in an interval of one month. An intra-rater reliability test was performed.

II.5 Statistical Analysis

The percent likelihood prediction for each ancestry group was compared using Kruskal-Wallis tests.

II. RESULTS

III.1 Study Results

Seven hundred and nine total potential subjects were reviewed for selection. One hundred and ten subjects fit all inclusion and exclusion criteria. Measurements and predictions were completed for all 110 eligible subjects.

The sample contained 59 female subjects and 51 male subjects. Three ancestry groups contained sufficient numbers for comparison in our sample, White, Hispanic, and Black. Subjects who indicated Hispanic ethnicity were assigned to the Hispanic ancestry group (n=49). Subjects who reported non-Hispanic ethnicity with White/Caucasian race were assigned to White ancestry (n=29). Subjects who indicated non-Hispanic ethnicity with Black/African American race were assigned to Black ancestry (n=32). Figure 6 shows the frequency of predicted and actual ancestry and sex for each group. Figures 7-12 show the predicted ancestry and sex for each actual ancestry and sex.

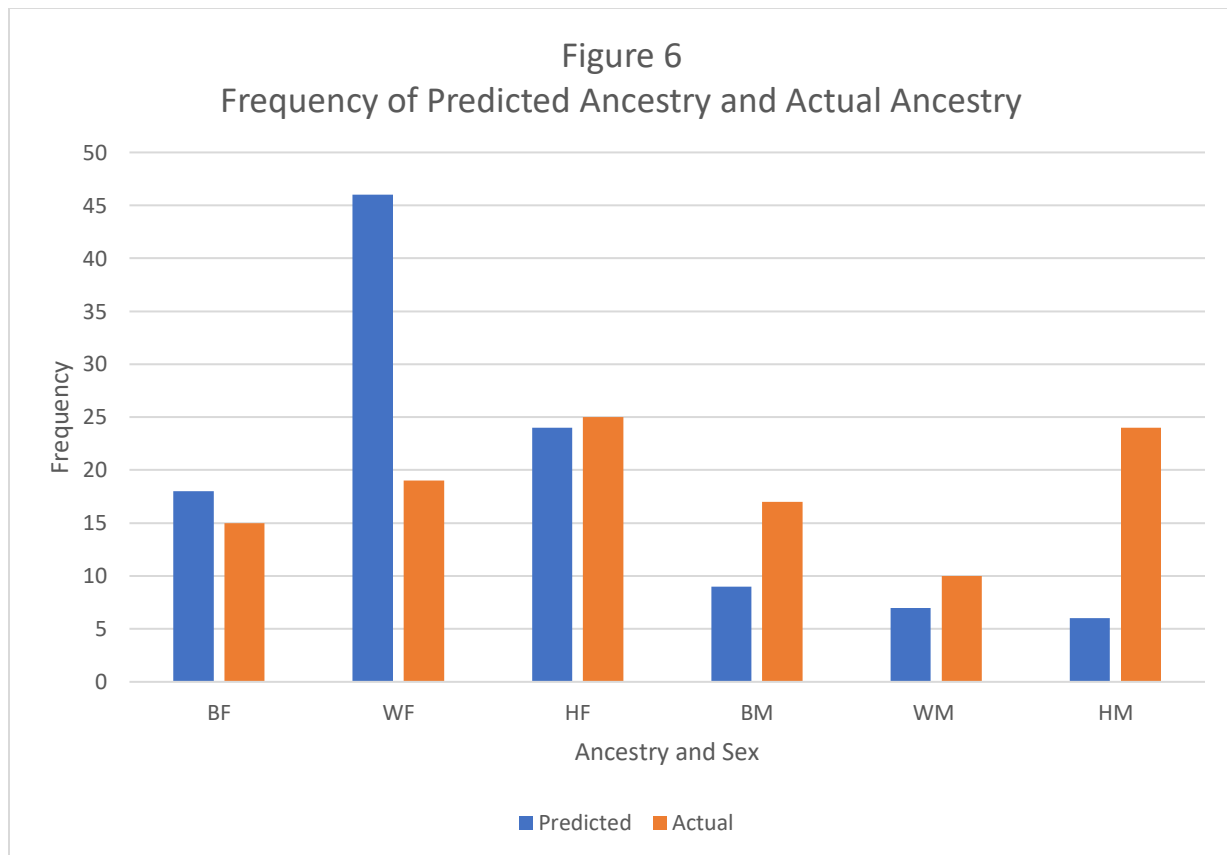


Figure 7

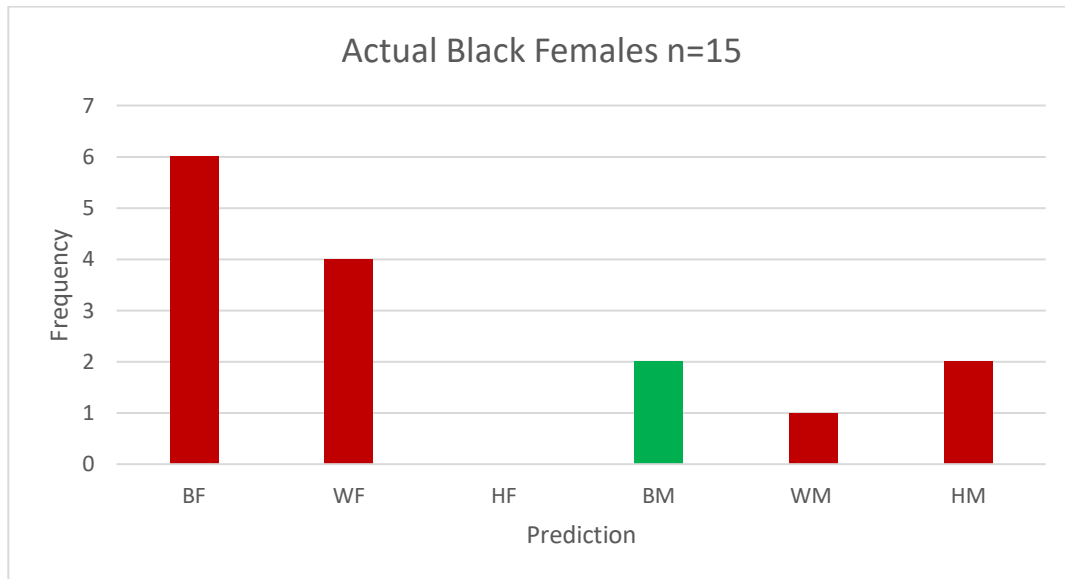


Figure 8

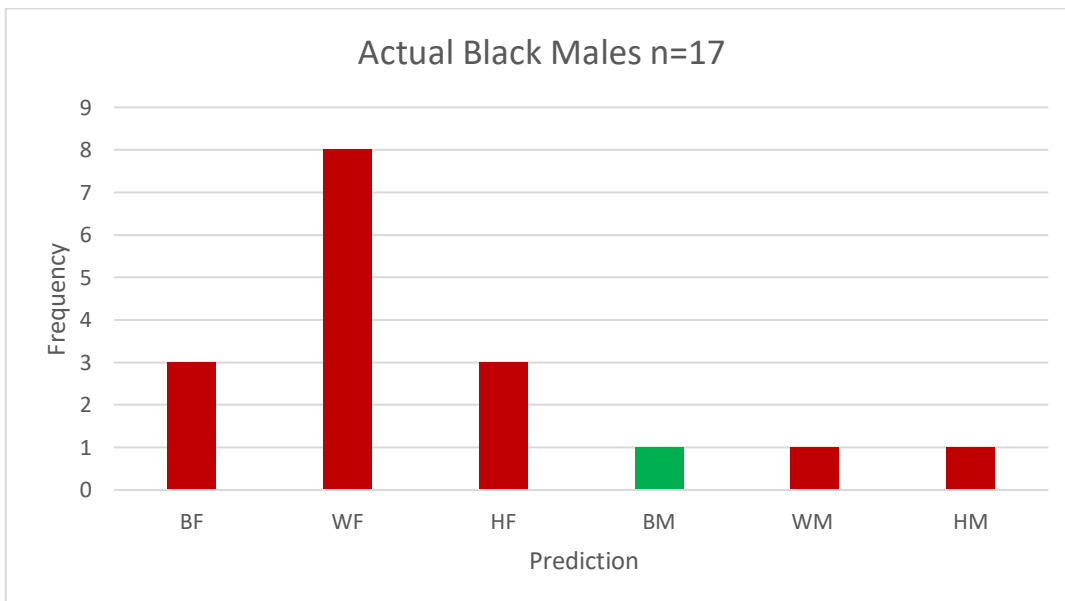


Figure 9

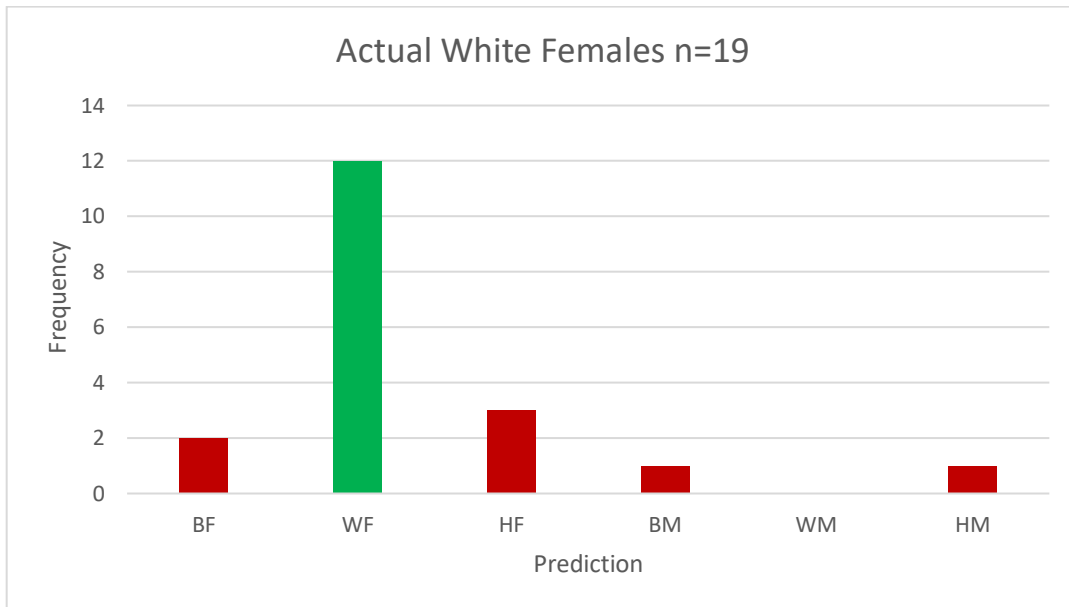


Figure 10

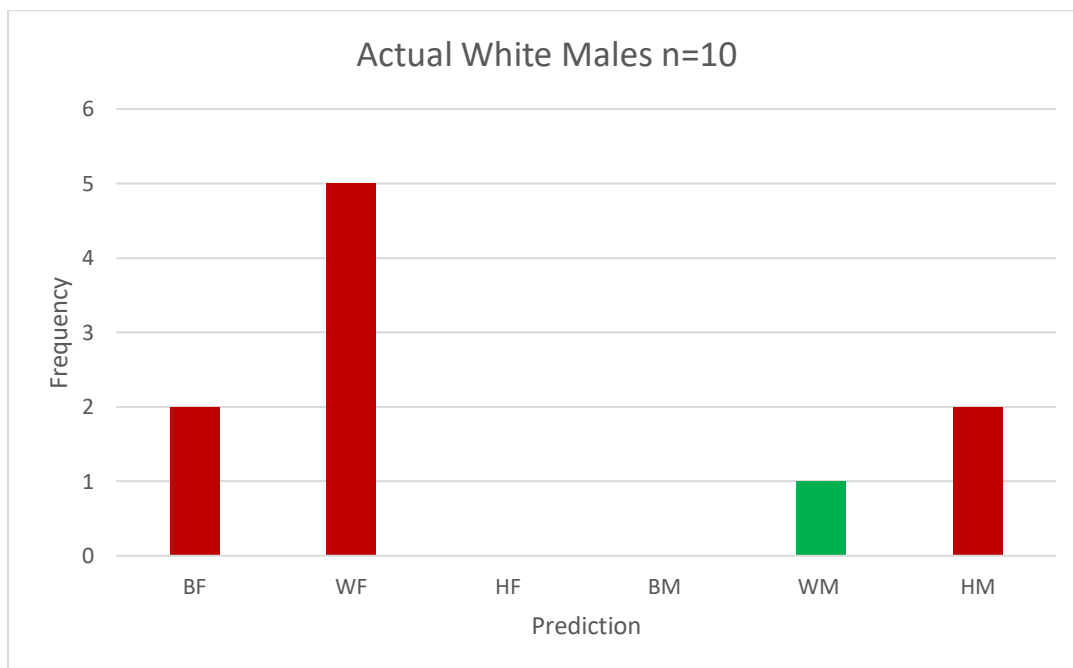


Figure 11

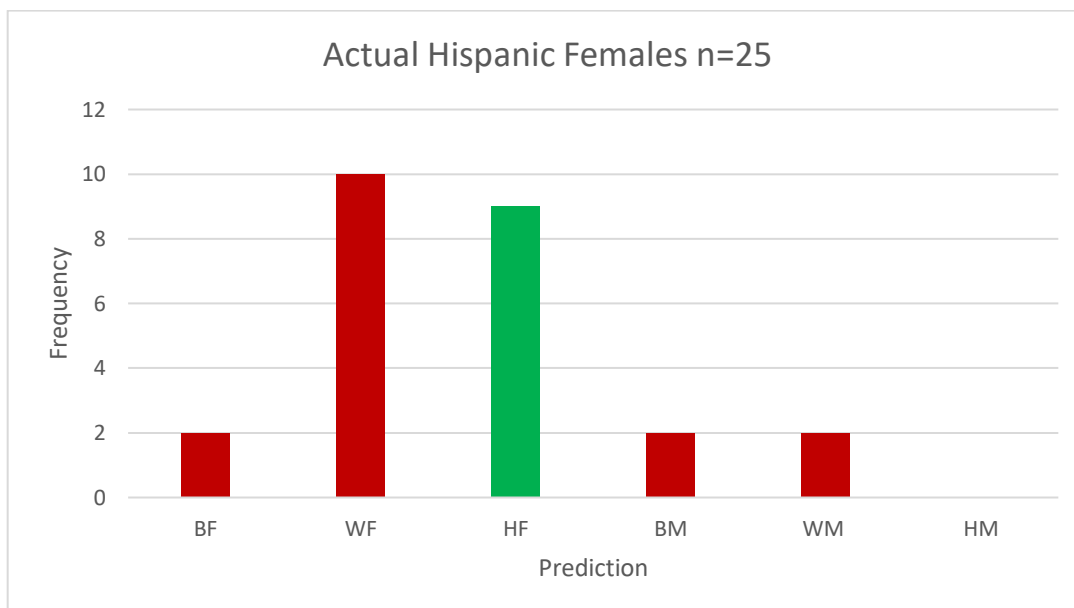


Figure 12

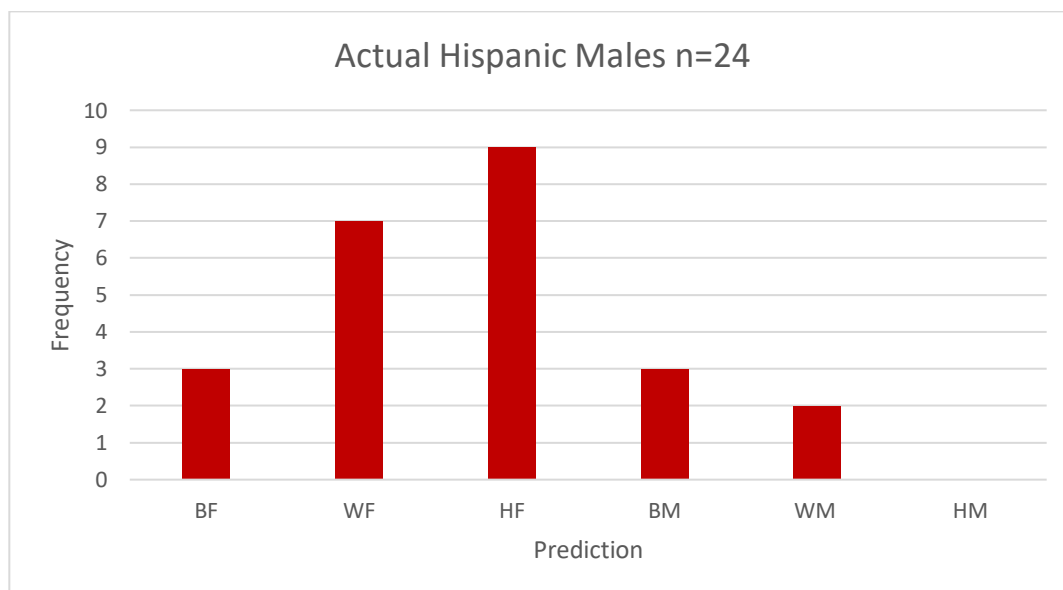


Table 2—% Correct Predictions by Ancestry, Sex, and Combined

	% Correct Ancestry	% Correct Sex	% Correct Ancestry and Sex
Black (n= 32)	37.50	43.75	21.88
White (n=29)	62.10	68.97	44.83
Hispanic (n=49)	36.70	53.06	18.37

None of the groups demonstrated the desired prediction accuracy for combined ancestry and sex (Table 2). The White ancestry group had the highest combined prediction accuracy at 44.83%. The White ancestry group was able to achieve the desired accuracy when predicting sex alone (68.97%) and ancestry alone (62.10%). The Hispanic and Black ancestry groups did not reach the desired accuracy for any categories. Sex prediction was more accurate than ancestry prediction for all ancestry groups.

Table 3— % Correct Predictions by Ancestry, Sex, and Combined, Stratified by Age

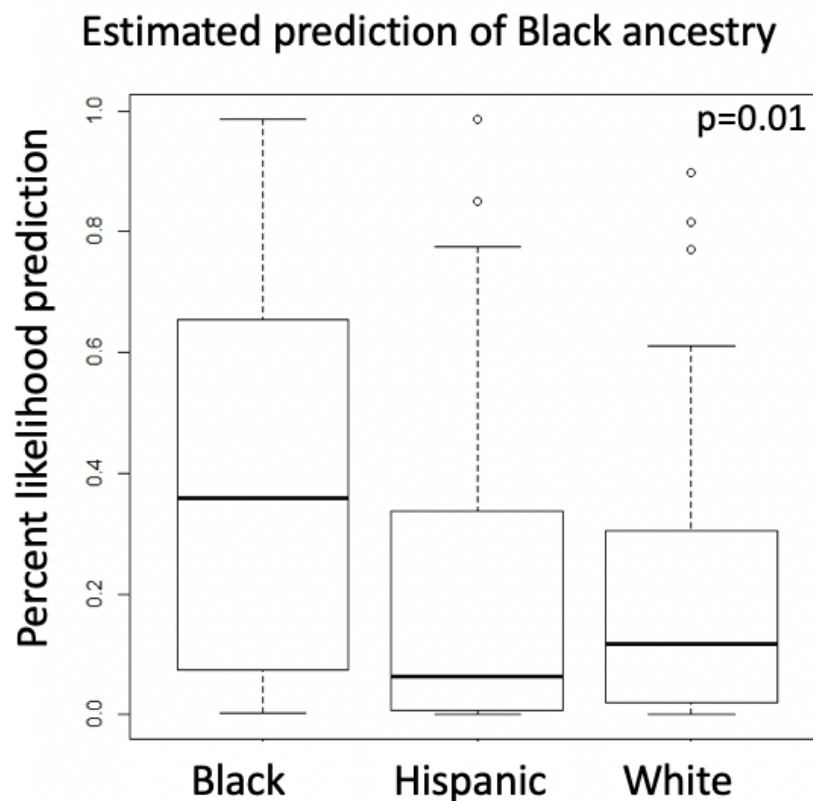
	% Correct Ancestry	% Correct Sex	% Correct Ancestry and Sex
Female (8-13) (n=28)	46.40	96.40	46.40
Female (14-17) (n=31)	51.60	67.70	45.16
Male (8-15) (n=36)	36.11	24.14	2.78
Male (16-17) (n=15)	40.00	33.30	6.67

Sex prediction for females age 8-13 was accurate 96.40% of the time (Table 3), this dropped to 67.70% for females age 14-17 years old. Sex prediction accuracy for males was low for both age categories and did not significantly change. Ancestry

prediction accuracy did not appreciably change for males or females across age categories. Combined prediction accuracy was low for all groups, particularly so for males, with minimal change across age categories.

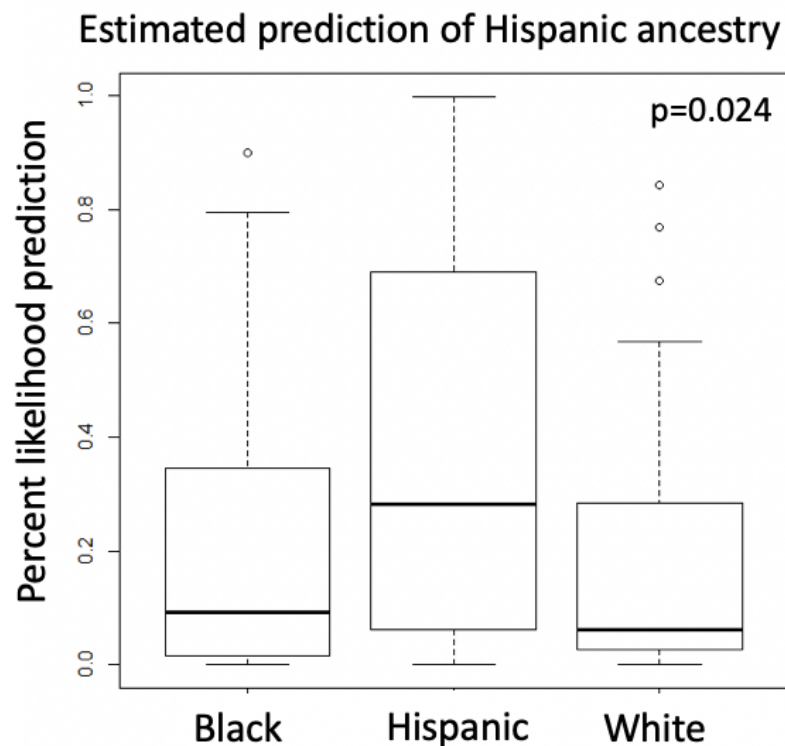
A given subject with actual Black ancestry was under 40% likely to be predicted as having Black ancestry (Figure 13). However, they were still more likely to be predicted as of Black ancestry than any other individual ancestry, and this difference was significant ($p=0.01$).

Figure 13 – Box plot of the estimated prediction of Black ancestry and their percent likelihood prediction.



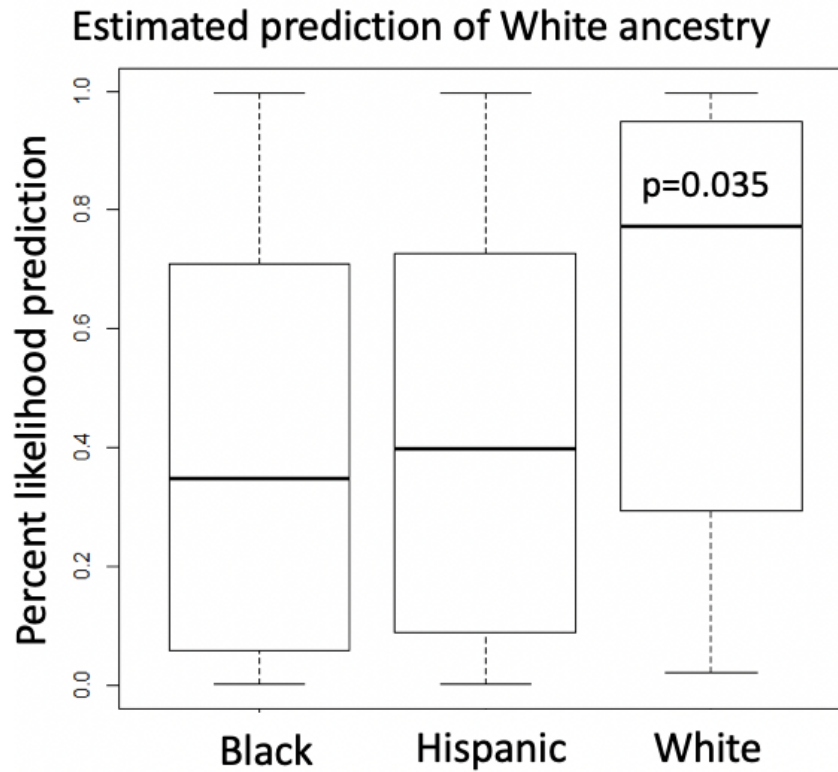
A given subject with actual Hispanic ancestry was approximately 30% likely to be predicted as having Hispanic ancestry (Figure 14). However, they were still more likely to be predicted as of Hispanic ancestry than any other individual ancestry, and this difference was significant ($p=0.024$).

Figure 14 – Box plot of the estimated prediction of Hispanic ancestry and their percent likelihood prediction.



The percent likelihood that an individual in the White ancestry group was predicted correctly as White was over approximately 68% and they are more likely to be predicted as White than being predicted as Hispanic or Black. This difference was found to be significant ($p=0.035$).

Figure 15 – Box plot of the estimated prediction of White ancestry and their percent likelihood prediction



We ran Cohen's Kappa and Interclass Correlation Coefficient tests to measure intra-rater reliability. For our categorical data we scored less than 0.80 in our Cohen's Kappa test for our measured values pertaining to Gonial Angle Flare and Posterior Edge Inversion. For our continuous data, we ran a Interclass Correlation Coefficient that yielded less than 0.80 in only one measurement that was TML23.

Table 4 – Cohen’s Kappa and Interclass Correlation Coefficient Tests for Intra-rater Reliability

Intra- rater Reliability Testing			
<u>Categorical Data</u>	<u>Cohen’s Kappa</u>	<u>Continuous Data</u>	<u>Interclass Correlation Coefficient</u>
Chin shape	0.808	GNI	0.958
Lower Border of Mandible	1	HML	0.951
Ascending Ramus	1	TML	0.957
Gonial Angle Flare	0.348	GOG	0.978
Mandibular Tori	1	CDL	0.988
Posterior Ramus Edge Inversion	0.738	WRB	0.951
		XRH	0.808
		MLT	0.97
		MAN	0.993
		XDA	0.947
		TML23	0.703

III. DISCUSSION

The application struggled to accurately predict sex and ancestry for a given child. Identification of an individual that is a complete unknown presents many challenges for any forensic identifier estimation methodology, and our results show that the (hu)MANid program was no exception. In the absence of supporting information, our results suggest the program would likely not be useful in identifying the sex and ancestry of an unknown sample of a younger individual. This is true of many identification programs, the more information available about the subject, the more accurate test results tend to be.²⁴ Our results suggest that for children and adolescents, the (hu)MANid program should not be a primary identification technique.

The program had adequate accuracy when predicting individuals of White ancestry, so it may be more useful when working with samples expected to be in that ancestry. The accuracy when predicting ancestry for the Hispanic and Black ancestry groups would not be useful in most identification scenarios. Even though the program was more likely to predict the correct ancestry than either other individual ancestry, it was still more likely to predict incorrectly for these two ancestry groups.

It was also noted that the application had a tendency to predict white females in the sample. Out of the 110 predictions, the most frequent prediction was White Female (n=46). This was not an expected finding in our study, and it is not understood why the application tended to predict White Female so often. It has been seen in previous studies such as that of Spradley et al, that “Hispanic crania are often misclassified as female because of their smaller size and more gracile nature than other groups such as American Black and Whites.”²⁵ It would be reasonable to assume that the mandible may also follow this trend. There may be some measurements that may predispose the application to choose White Female, especially in our sample of children and adolescents. It is often difficult to predict accurately in these transitional age ranges due to the mixed impacts of sex and growth.

Another unexpected finding was that as age increased, ancestry prediction did not meaningfully improve. As an adolescent approached puberty, we expected the accuracy of ancestry and sex estimation to improve due to the fact that the majority of growth has ceased and many biological elements should resemble that of an adult, but this was not the case in our study.

IV.1 Age and its effect on sex estimation

Sex estimation is usually the first component that is predicted when trying to establish a biological profile.²⁵ It was demonstrated in our study that age has a large effect on estimating sex. The younger the individuals, the more likely they were to be categorized as female. This may be due to the fact that in general, females tend to have smaller mandibular measurements in comparison to males. The (hu)MANid application had a sample size that included adult males and females, but no children, as it was made to be used in identifying adults. The application does not have sufficient samples to correctly identify the difference between the smaller mandibular measurements in predicting if the specimen was a child or female. Therefore, we noted that many of the younger males were incorrectly predicted by sex, while the younger females were being predicted more accurately. Contrary to our initial beliefs, increasing age actually decreased accuracy in females, and showed a small, non-significant increase in males. Females reach puberty sooner than males, and at ages 14-17 many women have reached their maximum growth period. The mean age for maximum growth of the ramus height in females is around 12 years old. In males it appears to be around 13 years, and their measurements are more pronounced²⁶. The age at which certain growth spurts occur can play a big role in incorrectly predicting sex based on an individual's age. According to Love et al., mandibular growth for males was statistically significant between the ages of 16-18 and 18-20 years. The 16-18 year old group had a more significant difference in growth.²⁷ For females, Foley and Mamandras determined that mandibular growth was significant as ages 14-16 and 16-20 years.²⁸ For this reason we predicted that the older females in the groups (14-17 year olds) would be correctly

identified in comparison to the younger females. This was not the case; the younger females were correctly identified by ancestry about half the time and by sex about two-thirds of the time. This application does not work well for identifying male or female children.

IV.2 Age and its effect on ancestry estimation

Age also has an effect of ancestry estimation. At a young age, certain traits are not yet done developing. Many morphological traits are only obvious when an individual has undergone their pubertal growth spurt. This is particularly true for mandibular traits, as the mandible undergoes extensive size and shape changes in adolescence. In males, in particular, there may be significant development of bone in the region of the mentum osseum.²⁹

A study done by Buck and Strand Vidarsdottir used geometric morphometric analysis of the mandibles of sub-adults to estimate their ancestry. Seventeen mandibular landmarks were analyzed to determine if the subjects were correctly characterized by their ancestry. The individuals were then categorized as African Americans, Native Americans, Caucasians, Inuit and Pacific Islanders. After analysis of all 5 groups, 70.1% of individuals were estimated correctly. When the sample was reduced to three groups (African American, Native American and Caucasian), 87.6% of the individuals were assigned to the correct group. The Caucasian group had the largest of correctly identified individuals.³⁰ Our study also correctly identified more Caucasians correctly than any other group (68%). In a study done by Franklin et al, it was found that “population- specific mandibular morphology is perhaps established earlier in ontogeny, the result of inherited genetic traits”¹⁵. This study also proved the

findings of Buck and Vidarsdottir in showing that different populations can be measured using morphometric measurements³⁰.

IV.3 Study Limitations

The (hu)MANid application uses both morphometric and morphoscopic measurements to gather data and compare that data to their source populations. With this information the application predicts an individual's sex and ancestry. The samples used to reference the data for the application were physical human mandibles. A mandibulometer was used for measuring as well as other physical instruments. Since our study included living subjects, this was not available to us. Using CBCT's of the human mandible and 3D Slicer 's (BHW, Boston, MA, USA) measuring tool compared to measuring a physical mandible may therefore differ in accuracy.

The (hu)MANid application provided resources describing the 11 morphometric variables that were necessary to measure from the mandible (Appendix C). It also provided schematics and descriptions of the 6 morphoscopic variables (Appendix D). The morphoscopic descriptions could be considered subjective. In a study that examined inter and intra- reliability of metric and morphoscopic characteristics of the mandible, Berg reported that metric variables showed greater reliability than morphoscopic variables.³¹ Descriptions such as Gonial Angle Flare and Posterior Ramus Edge Inversion were not easily distinguished using a digital scan versus the physical mandible, this difficulty was noted in our Intra-rater reliability testing. Both of these morphological descriptions earned the lowest scores in our Cohen's Kappa test. Such findings were also evident in our study. Certain descriptions such as chin shape were difficult to determine due to that fact that our population is still maturing and

changing. Determining the difference between a young individual who has a chin shape of square versus bilobate was a challenge since many may be in between the two descriptions. Since the variables were viewed in a CBCT, it was difficult to determine the inversion direction and amount with descriptions such as straight, slight, medium, and turned. These variables were difficult to determine in a maturing population and without having the mandible physically available to measure and examine. A positive note about using CBCT scans was that it allowed the study to be well organized, easily reviewable and easily accessible by the PI. Future studies can be done using the digital scans and measurements.

IV.4 Study Population

It is important to note that the study population at UIC is a very diverse, urban population. Grouping ancestries into White, Black, and Hispanic has its challenges. These categories describe rather broad populations. Being Hispanic can mean anyone of Spanish origin or descent regardless of the individual's race. This includes many countries around the world that share different backgrounds, cultures, and population history. Spradley et al, describes that "the term Hispanic is a social construct with no precise genetic meaning". Although these Hispanic individuals may come from different countries and cultures, they are referred to as Hispanic, regardless of their country of origin.²⁵ Black ancestry is also a broad category that describes people of different backgrounds. Similarly, in African Americans, it is noted that "self-reported ancestry and ancestry can predict ancestral clusters but do not reveal the extent of admixture".³² In an urban, diverse population like that of Chicago, one can expect a broad range of ancestries within a given category due to admixture. The (hu)MANid application stated

that they used very specific ancestries that were included in the different categories. For example, their Hispanic category was comprised of human remains from Tucson, Arizona and the U.S./Mexico border, Mexico, and Guatemala. The Black and White samples are from human remains that are part of special collections around the U.S. and they are both from 19th and 20th century samples. We were limited in categorizing the individuals in our sample based on the (hu)MANid application.

At the UIC COD, the race/ethnicity of the patient is not always self-reported. If the patient does not self-report their ancestry, the administrative staff inputs a race/ethnicity for the patient into their Electronic Health Record chart. This may have influenced the study slightly if the person did not identify themselves directly. Patients who expressed non-Hispanic ethnicity and White/Caucasian race were classified as White ancestry. Patients who expressed non-Hispanic ethnicity and Black/African-American race were classified as Black ancestry. If patients reported a Hispanic ethnicity, they were categorized as Hispanic regardless of their race.

IV.5 Future Studies

Forensic anthropology and human identification is a growing area with many new advancements. While our study failed to find an acceptable level of accuracy in a juvenile population, future studies might add adults from the same Chicago population to determine whether age of the sample or diversity of the sample was the underlying issue. Additionally, future studies might employ other adolescent samples in order to test whether our low level of accuracy was anomalous. Finally, given the difficulties replicating some of the methods typically used with osteological specimens, a follow-up study could 3D print the mandibles and take all measuring and trait scoring from the

models. This would further allow us to control for the methodological issues and hopefully better determine the cause of our low accuracy.

IV. CONCLUSION

The application struggled to predict both sex and ancestry for a given individual. For ancestry prediction only, the White ancestry group were identified at a rate consistent with prior literature. For sex prediction only, females reached this threshold. In contrast with our expectations, estimations did not appreciably improve when older adolescents (>14 y.o. girls, >16 y.o. boys) were examined separately. When predicting ancestry, (hu)MANid was slightly more likely to assign an individual to the correct ancestry than any other individual ancestry, but the frequency of correct assignment is not forensically valuable except for in the White sample. In our diverse pediatric sample, we were unable to validate the (hu)MANid application for ancestry or sex prediction in older children and adolescents.

Appendix A



Exemption Granted

April 15, 2019

Natalie Tomas
Pediatric Dentistry

RE: **Protocol # 2019-0399**
“Can the Human Mandible Identification Program be used in a pediatric population?”

Dear Natalie Tomas:

Your application was reviewed on **April 13, 2019** and it was determined that your research meets the criteria for exemption as defined in the U.S. Department of Health and Human Services Regulations for the Protection of Human Subjects [45 CFR 46.104(d)]. You may now begin your research.

Exemption Granted Date: April 13, 2019

Funding Source/Sponsor: None

The specific exemption category under 45 CFR 46.104(d) is: 4

HIPAA Waiver:

The Board determined that this research meets the regulatory requirements for waiver of authorization as permitted at 45CFR164.512(i)(1)(i)(A). Specifically, that the use or disclosure of protected health information (PHI) meets the waiver criteria under 45CFR164.512(i)(2)(ii); the research involves no more than a minimal risk to the privacy of the individuals; the research could not practicably be conducted without the waiver; and the research could not practicably be conducted without access to and use of the PHI.

The type of protected health information (PHI) to be used in the research includes:

Age of CBCT, Sex, Ancestry, Morphometric measurements, Morphoscopic descriptions.

You are reminded that investigators whose research involving human subjects is determined to be exempt from the federal regulations for the protection of human subjects still have responsibilities for the ethical conduct of the research under state law and UIC policy.

Please remember to:

- Use your research protocol number (2019-0399) on any documents or correspondence with the IRB concerning your research protocol.
- Review and comply with the [policies](#) of the UIC Human Subjects Protection Program (HSPP) and the guidance [Investigator Responsibilities](#).

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UNIVERSITY OF ILLINOIS AT CHICAGO
Office for the Protection of Research Subjects

201 AOB (MC 672)
1737 West Polk Street
Chicago, Illinois 60612

Phone: (312) 996-1711



We wish you the best as you conduct your research. If you have any questions or need further help, please contact me at (312) 355-2908 or the OPRS office at (312) 996-1711. Please send any correspondence about this protocol to OPRS via [OPRS Live](#).

Sincerely,
Charles W. Hoehne
Assistant Director, IRB #7
Office for the Protection of Research Subjects

cc: Marcio Da. Fonseca
Ian Marion

Appendix B

Data Collection Table

<u>Subject #</u>	
<u>Age</u>	
<u>Ancestry</u>	
<u>Morphometric measurements</u>	
• Chin Height	
• Height of the Mandibular Body at the Mental Foramen	
• Bicondylar Width	
• Minimum Ramus Height	
• Maximum Ramus Height	
• Mandibular Length	
• Mandibular Angle	
• Mandibular Body Breadth at the Mental Foramen	
• Mandibular Body Breadth at the M2/M3 Junction	
• Dental Arcade Width at the Third Molar	
<u>Morphoscopic descriptions</u>	
• Chin Shape	
• Lower Border of Mandible	
• Mandibular Tori	
• Ascending Ramus Profile	
• Gonial Angle Flare	
• Posterior Ramus Edge Inversion (PREI)	

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