A56 A Test of the (hu)MANid Classification Software on a Sample of United States White and Black Mandibles

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After attending this presentation, attendees will understand how the newly created (hu)MANid software performed when classifying sex and ancestry on a large sample of mandibular data.

This presentation will impact the forensic science community by testing the performance of this new software to evaluate its utility in forensic cases and by providing documented accuracy rates.

A recent publication by Berg and Kenyhercz describes a newly available statistical software program that can be utilized by practitioners to estimate sex and ancestry from the human mandible.[1] The software program, (hu)MANid, is available through the web or can be downloaded to be run with the statistical program R. It allows the researcher to input a combination of metric and morphoscopic variables from the mandible, from which either a Linear Discriminant Analysis (LDA) or Mixture Discriminant Analysis (MDA) can be performed to compare and classify the unknown mandible into one of the 15 reference groups within the program's database (total *n*~1750). Given the recent release of this software, there are not yet any published validation studies analyzing the accuracy of the assigned classifications.

In this study, morphoscopic and metric data were collected from a sample of 230 adult mandibles from United States White and Black males and females, and analyzed using the (hu)MANid web-based software program. Bigonial width, bicondylar width, and mandibular length had previously been collected from the physical specimens. The remaining metric variables (mandibular body height, chin height, minimum ramus breadth, maximum ramus height, and dental arcade width) and five morphoscopic variables (chin shape, shape of the lower border of the mandible, ascending ramus profile, gonial angle flare, and posterior ramus inversion) were collected following the descriptions provided in the "Definitions and Diagrams" tab of the software program from 3D virtual models of the specimens. The virtual mandibular models were created from 3D surface scans collected with a NextEngine® desktop scanner from individuals in the Hamann-Todd, Terry, and Bass Donated skeletal collections. All metric and morphoscopic data were collected using GeoMagic® Studio. The data collected from each specimen were run through the (hu)MANid program using the two different methods (LDA and MDA), first with all variables included, then using a Forward Wilks stepwise procedure, and both were compared to all 15 modern comparison groups and also to only the United States White and Black 20th-century samples. Altogether, eight separate analyses were run on each of the 230 specimens. The resultant group classifications were compared to the actual sex, ancestry, and combined ancestry/sex of the individual, and percentage of correct classifications was calculated.

In all cases, the MDA analyses outperformed the LDA analyses, and slightly better accuracy rates were obtained when all variables were entered (compared to using a Stepwise procedure). When performing an MDA on all available variables and comparing to all 15 modern reference groups, sex was assigned correctly in 76% of individuals, ancestry was correct in 52%, and both sex and ancestry were correctly estimated in 40%. Although these values may appear low, when considering that they were compared to 15 groups and the *a prior* classification rate would be less than 7%, 40% is a major improvement. An accuracy rate of 76% for sex estimation is also higher than most reports of sex estimation from the mandible, although lower than reported values for sex estimation from other regions of the skeleton. When the comparisons were limited to the United States White and Black reference groups, accuracy rates did not increase significantly: MDA on all variables resulted in 75% correct sex, 57% correct ancestry, and 41% correct sex/ancestry group. United States Blacks were much more likely to be assigned to the correct sex/ancestry group (77% correct, compared to only 7% correct for the United States White individuals). Overall, the (hu)MANid program performed relatively well, considering that all input variables are from the mandible. Although the program still needs to be tested on a sample of modern forensic cases, it exhibits great potential as a sex and ancestry classification tool.

Reference(s):

1. Berg G.E., Kenyhercz M.W. Introducing Human Mandible Identification [(hu)MANid]: A free, web-based GUI to classify human mandibles. *J Forensic Sci.* 2017: early view doi: 10.111/1556-4029.13479.

Sex Estimation, Ancestry Estimation, Mandible