

**TECHNICAL NOTE**

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**ANTHROPOLOGY**

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## Introducing Human Mandible Identification [(hu)MANid]: A Free, Web-Based GUI to Classify Human Mandibles

**ABSTRACT:** Statistical programs have revolutionized the way in which forensic anthropologists conduct casework by allowing practitioners to use computationally complex analytics at the click of a button. Importantly, the products of these statistical programs are reproducible and contain measures of error or uncertainty, thereby strengthening conclusions. This paper is an introduction to (hu)MANid, a free, web-based application that uses linear and mixture discriminant function analyses to classify human mandibles into one of many worldwide and/or periodic reference groups. The mechanics, development, and use of the application will be discussed. Further, the program was tested against other software to compare model performances and classifications. Total correct classifications among the test cases and programs were identical. Ten mandibles were tested using both statistical procedures. Mixture discriminant analysis improved classification by an average of 9.3% and correctly identified three more mandibles than LDA. Therefore, we believe (hu)MANid will be an asset to the anthropological community.

**KEYWORDS:** forensic science, forensic anthropology, mandibular morphology, graphical user interface, linear discriminant function analysis, mixture discriminant analysis

Over the last 30 years, a myriad of new methodological or statistical-based research papers have been published in the literature or presented at scientific meetings. For most of the early years, many new methodologies were not easily operationalized for practical application—they required complex calculations, graphs, tables, expensive computing programs/power, complex data gathering tools (e.g., CT or digitization capabilities), and were somewhat nonintuitive. As software and computing power have become more widely available, multiple programs for human skeletal biological analysis have become available for problems such as sex and ancestry determination, general skeletal recording, or trauma documentation. The best known software is arguably FORDISC (1), although several other programs such as CRANID (2), 3D-ID (3), and OSTEOWARE (4) have come into the fore.

In addition to the needs of the practitioner, the needs of science in terms of reliability and repeatability must be met. There has been a huge spike in papers and presentations testing older methods for reliability and repeatability (inter- and intra-observer error studies) following the Daubert decision (5) and the follow-on National Academy of Science (NAS) report (6). Additional callings from the Scientific Working Group Anthropology (SWGANTH) and follow-on NIST/OSAC committees will continue to force older methods into newer, testable, reliable, and repeatable formats. Part of the way forward is through

standardized computer-aided analysis, which allows for easy replicability among practitioners, regardless of geographic location. While FORDISC (1) has been at the forefront of this effort since its inception, there are other avenues and routes open for new additions to the scientific community.

Research regarding the human mandible has received little attention compared to the cranium. Berg (7) examined worldwide metric and morphological variation of the mandible, particularly as it is used in forensic applications. He applied linear discriminant function analysis to the datasets in order to classify both sex and ancestry in unknown individuals. He found low intra-observer error associated with this approach, although he did not specifically test interobserver error. His work was further published in a volume on new methodological approaches for determining ancestry (8). Other authors also have examined the mandible, albeit for limited population sets (9–13). Recently, Byrnes et al. (14) examined the interobserver error associated with mandibular morphological and metric data, finding high observer agreement in nearly all studied variables. As little interobserver error was documented, they determined that mandibular data, both morphological and metric, were well suited for use in forensic applications, as well as for theoretical applications.

While Berg (8) did provide discriminant functions for a wide variety of populations, a limitation to his paper was the lack of the ability for the practitioner to create their own functions. The solution was to offer all data available for importation into a program such as FORDISC (1) to any practitioner requesting it. Some limitations to this solution were the cost, availability, and operational knowledge of FORDISC by the end user, who would have to be proficient in creating custom functions within that program. Therefore, in terms of operationalizing the method, little was gained. We seek to rectify that problem with the creation

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and free distribution of (hu)MANid. (hu)MANid contains a worldwide sample of mandibular morphology and metric data that will allow analysts to classify mandibles for sex and ancestry determination. It is ideal for use in forensic casework, bioarchaeological analyses, and theoretical research. The backbone of this program is R, and it operates through a web application called *Shiny*. It is available either through download to a host's computer, if R is installed, or through the worldwide web.

## Methods and Materials

R is a free, open-source statistical program wherein users can download premade packages of statistical tests to employ on their own datasets. In 2003, there were approximately 200 available packages (15) in R. Today, there are over 9000 available packages ranging from basic summary statistics to state-of-the-art algorithms, all constantly updated and at no cost to the user (16). The main advantage to R, over other statistical programs, is that the user can control every aspect of their data analysis, thereby removing the "black box" of premade statistical programs. Additionally, all of the source code is freely available so that a user can write novel functions, or fine-tune premade analyses. Conversely, R has a steep learning curve, wherein the user must become familiar with the R programming language. However, given newer software developments, R can be used to build web-based applications to perform specific tasks without the need to understand programming, or even have R installed on one's computer.

In 2012, RStudio developed a framework to build web applications with R called *Shiny*. *Shiny* allows for users to create interactive web-based applications using R and associated packages as a backbone. *Shiny* was developed with a reactive programming model. Simply put, reactivity allows for a user to interact with the application (i.e., enter data) and generate a result from the program (i.e., output that changes with a change in new input). Reactivity can be static or dynamic (but likely a combination of both). *Shiny* does not require any advanced programming skill to create web applications, although a thorough understanding of the R language and writing basic functions is certainly beneficial.

A *Shiny* application is built from two basic files: a user interface file (ui.R) and a server file (server.R). The ui.R is used to create the overall esthetic of the graphical user interface (GUI), which dictates how the user interacts with the application (entering data, adjusting different settings, controlling how output is displayed, etc.). The server.R file contains all of the backend operations. The server.R file details what should be performed to the data to get the desired results, which includes data subsetting, different statistical operations and transformations, and the generation of graphs and plots. The ui.R and server.R files work in tandem with one another to coordinate analyses in real time. The manipulation of data can be visualized as a pipeline. The pipe starts with data entry and operation settings (ui.R) that is then sent downpipe to the server.R file that takes the newly entered data and performs the requisite statistical operations. The products of the statistical operations are then sent further downpipe to do additional analyses or generate output be it numerical, textual, or graphical. Individual outputs are then specified in the server.R file. Back on the ui.R file, the outputs can be organized and formatted. Each time a user enters new data, the data pipeline is refreshed and the functions recalculate all analyses.

Additionally, *Shiny* applications may contain data files that can be used as reference databases for analyses, such as linear

discriminant analysis, and images such as figures, diagrams, logos. Once the GUI has been programmed, the ui.R, server.R, and other associated files can be deployed to the internet to be hosted on a website, or used as an R package. If accessed on the web, users do not require any programming ability or even have R installed on their computer; they simply need an internet connection. If the application is accessed through R, it will be displayed through the user's default web browser. We offer both of these options for using (hu)MANid.

## (hu)MANid Build Specifications

*Shiny* version 0.13.2 (17) was used to build (hu)MANid. Data subsetting was performed with the "dplyr" package version 0.5.0 (18). The "dplyr" functions used are *select* and *filter*. The *select* function was used to create reactive dataframes that only include variables in the analysis that are entered by the user. The *filter* function further refines the dataframe by subsetting the dataset to only include reference groups chosen by the user.

Summary statistics are calculated with the *describeBy* function from the "psych" package (19). The *describeBy* function generates several summary measures for each group selected in the analysis. The following summary statistics are generated for each variable tested: mean, standard deviation (sd), median, median absolute deviation (mad), minimum (min), maximum (max), skew, kurtosis, and standard error (se). Lastly, positive (PPV) and negative (NPV) predictive values are calculated with the "caret" package function *confusionMatrix* (20). The equations for PPV and NPV are taken from Altman (21).

Linear discriminant function (LDA) analysis is taken from the "MASS" package (22) *lda* function. The *lda* function in the "MASS" package is based on the discriminant procedure presented by Ripley (23). The LDA model in (hu)MANid uses leave-one-out cross-validation (LOOCV) to avoid upward bias in model performance. Further, the (hu)MANid LDA model also sets equal group prior probabilities as opposed to proportionate prior probabilities. While LDA was not envisioned to handle morphoscopic data, previous research has shown that it can be successfully employed (7,8). However, if a user is uncomfortable mixing morphoscopic and metric data, only metric data may be entered into the program.

Mixture discriminant analysis (MDA) is taken from the "mda" package's *mda* function (24). Unlike LDA, MDA does not assume one Gaussian, or normal, distribution for each of the response classes, but instead assumes a mixture of several distributions within each response class (25). Further, MDA makes use of adaptive nonparametric regression, which can "hinge" the regression line to optimize total correct classification in each case. Given the use of nonparametric regression, non-normal data can be used without violating assumptions.

The distance from group centroid is calculated through Euclidean distance with the *rdist* function from the "fields" package (26). If more than two groups are selected for analysis, the Euclidean distance is calculated from the first two discriminant functions for each of the reference groups selected and also the newly entered data. The Euclidean distance from the new individual to each of the reference group centroids is calculated and presented to act as a general measure of similarity or dissimilarity. For two-group analyses, just the first (and only) discriminant function score is used.

Chi-square typicality probabilities are calculated using the *typprobClass* function from the "Morpho" package (27). The chi-square typicality procedure also uses LOOCV. Additionally, a

robust minimum covariance determinant (MCD) estimator for the variance–covariance matrix (VCVM) is used. The MCD estimation reduces the impact of outliers to the VCVM, which is inherently sensitive to the outlier effect.

All plots are created using the “ggplot2” package (28). For two-group analyses, a histogram is generated with each group assigned a different color and the new individual is represented with a solid, black line. For analyses involving more than two groups, a scatter plot is generated with the first two discriminant function scores. Each point is assigned a color based on group membership. The newly entered data are displayed as a black asterisk. However, if a two-group analysis is performed using MDA, a scatterplot will be displayed due to MDA’s particular procedures.

### Input Variables

Currently, (hu)MANid accepts up to eleven metric variables and six morphoscopic variables. The metric variables include chin height (GNI), height of the mandibular body at the mental foramen (HML), bigonial width (GOG), bicondylar width (CDL), minimum ramus breadth (WRB), maximum ramus height (XRH), mandibular length (MLT), mandibular angle (MAN), mandibular body breadth at the mental foramen (TML), mandibular body breadth at the M2/M3 junction (TML23), and dental arcade width at the third molar (XDA). The morphoscopic variables include chin shape (CS), lower border of the mandible (LBM), ascending ramus shape (ARS), gonial angle flare (GAF), mandibular torus (MT), and posterior ramus edge inversion

(PREI). Definitions and images for the variables are available within the (hu)MANid program.

### Reference Database

The reference database for (hu)MANid is primarily composed of data collected by the first author (GEB) for his dissertation research (7). This dataset has been augmented over time with the inclusion of several new populations as well as additional data for existing reference groups. Reference data contributed by the second author (MWK) were generated over the last year, primarily gathered in conjunction with an interobserver error study on mandibular metrics and morphology (14). Both datasets were combined based on the strength of that study’s results (14).

The current sample size for (hu)MANid is approximately 1750 individuals representing 15 main populations (Table 1). Reference groups broadly span the globe, both in space and time, and represent modern, historic, and prehistoric groups. Composite groups and pooled sex groups are also available for comparison. Both sexes are present in the data, but several populations have limited amounts of females due to the nature of the collections. Group names within the program (and here) are self-explanatory. For the sake of publication space, individual population descriptions and collection origins, locations, and limitations are provided in the About section of (hu)MANid and are not repeated here.

In addition to these reference groups, (hu)MANid also contains composite reference data (pooled sexes, pooled groups) (Table 2). The pooled sex option allows the user to compare a mandible for a “sex-only” approach. Composite groups allow for broader geographic comparisons. These were formed typically based on geographic location, although time was also a factor. For example, the Southeast Asian composite group is composed of Thai, Vietnamese, and Cambodians (geographic based), while the Native American composite group is a combination of Arikara (proto/prehistoric) and Hohokam (prehistoric) reference samples (geographic and time based). Caution should be exercised when using composite groups. Berg (7) has shown that closely related geographic populations can be separated from each other using mandibular data and that groups across time have changing characteristics within the mandible (secular change and admixture). A pooled sex analysis also should be viewed with caution as well, based on the characteristics of the data employed.

### Missing Data Imputation

Given the often fragmentary nature of skeletal collections, not all observations could be measured or scored on each mandible. For the sake of adequate sample sizes, missing data were imputed within each group. Metric and morphoscopic data were

TABLE 1—Reference groups, group codes, demographics, and total samples size currently included in (hu)MANid.

Reference Population	Group Code(s)	n		
		F	M	Total
19th Century American Black	BF(19c), BM(19c)	68	70	138
19th Century American White	WF(19c), WM(19c)	6	61	67
20th Century American Black	BF(20c), BM(20c)	10	43	53
20th Century American White	WF(20c), WM(20c)	145	235	380
Arikara (Proto/pre historic)	ARKF, ARM	30	30	60
Cambodian	CAMF, CMM	29	149	178
Chinese	CHM	—	65	65
Guatemalan	GUATF, GUATM	14	89	103
Hispanic	HM	—	30	30
Hohokam (Prehistoric)	HOHF, HOHM	14	35	49
Korean	KORF, KORM	15	149	164
Nubian	NUBF, NUBM	55	55	110
Prehistoric Korean	phKORF, phKORM	60	78	138
Thai	THAIF, THAIF	59	125	184
Vietnamese	VIETM	—	41	41
Total	—	505	1140	1745

TABLE 2—Composite reference groups, group codes, demographics, and total samples sizes available in (hu)MANid.

Composite Reference Group	Group Codes	Composition	n		
			F	M	Total
American Black	BF, BM	19th Century American Black, 20th Century American Black	78	113	191
American White	WF, WM	19th Century American White, 20th Century American White	151	296	447
American Indian	AIF, AIM	Arikara, Hohokam	44	65	109
Pooled Hispanic	HISPF, HISPM	Guatemalan, Hispanic	14	119	133
Northeast Asian	NEAF, NEAM	Chinese, Korean	15	195	214
Southeast Asian	SEAF, SEAM	Cambodian, Thai, Vietnamese	88	315	403

imputed separately and with different procedures. While Berg (7) employed missing data techniques within his original study, all of those imputed data were removed prior to conducting the following approach. All metric data were imputed using kNN ( $k = 5$ ), as suggested by Kenyhercz and Passalacqua (29). The kNN imputation algorithm imputes missing values by taking the mean of the five most similar cases to the specimen in question. The morphoscopic data were imputed using a Hot Deck procedure, as recommended by Kenyhercz et al. (30). Hot Deck imputation randomly finds the most similar, complete specimen in the reference dataset (referred to as a donor) based on the combination of variables present. The particular trait values of the most similar donor are then used for the imputation. Additional discussion of missing data imputation, to include amounts of data imputed per group, can be found in Berg (7).

### Testing (hu)MANid

In order to ensure (hu)MANid functions properly, extensive testing of multiple procedures and cases across two additional platforms was conducted. First, total correct classification results using the same reference populations (both pooled sex and all composite groups) were compared to runs in FORDISC 3.0 (1) and SPSS version 22.0 (31). Identical results were produced in all three programs (total correct classifications of 83.5% for pooled sexes, 53% for composite groups). Therefore, (hu)MANid functioned with the same performance as these programs. Next, 10 cases of known sex and ancestry were entered into both (hu)MANid and FORDISC 3.0 (1) to compare group classification performance using the composite males reference groups. These cases were not included in the reference data. Again, results from this testing showed exactly the same results, to include group classifications, posterior probabilities, and total correct classifications across the platforms (see Table 4, below). These two tests indicated that (hu)MANid was performing as expected and was appropriate for use for this type of data.

Additional testing of various procedures within (hu)MANid was conducted for comparison, performance, and ultimate inclusion into the program. Three stepwise procedures from the “klaR” package (32), forward, backward, and forward Wilks were evaluated. Each stepwise procedure was tested against an analysis that included all variables and all modern groups and was evaluated by the total correct classification. As can be seen in Table 3, poor performance was found for these procedures. No stepwise procedure exceeded the classification accuracy of using none at all. Forward stepwise selection was the most detrimental to model performance (40.1% as compared to 67.5%). Forward Wilks stepwise selection achieved comparable total correct classifications, although it only dropped one variable (GAF). Given these results, Forward Wilks was included as the only stepwise option in (hu)MANid.

TABLE 3—Results of the comparisons between stepwise and nonstepwise statistical procedures using an analysis of all modern groups, all variables.

Procedure	Total Correct Classification (%)
Forward	40.1
Backward	62.8
Forward Wilks	67.5
None	67.5

Second, as MDA analysis has received little attention in the anthropology literature, a performance test between MDA and LDA was conducted on the ten cases previously mentioned using the composite male reference groups (six group comparisons, the top three groups per test are reported in Table 4). The test was evaluated through the posterior probabilities and total correct classifications results. Noticeably, using MDA increased model performance across the entire test—all ten cases resulted in an average increase of 9.3% in total correct classification, with a range from 8.6 to 10.1%. Group classification was the same for the two procedures in seven of ten cases. In each of these, the MDA model increased the posterior probability of the assigned group over LDA posterior probabilities. In three cases, MDA assigned a different group classification (Cases 5, 7, and 9), from an incorrect to a correct answer. In the test, MDA correctly identified the appropriate group in eight of 10 test cases, while LDA correctly identified five of 10 cases. Of note, one case is abnormally small and pathologic—both procedures classified it as a SEAM, when in fact the case is a White male. Overall, these performance statistics generally match what is expected (with a slight increase), based on the total correct classifications per model. For MDA, the average correct classification is approximately 70%, while LDA is approximately 60%, representing correct classifications between 3.6 and 4.2 times chance alone (for these six group comparisons).

### Introducing the (hu)MANid program

To access (hu)MANid, go to <https://www.anthropologyapps.com> and click on the link to (hu)MANid; alternatively, the user can go directly to the hyperlink <https://anthropologyapps.shinya.pps.io/humanid/>. There are four main tabs on the (hu)MANid menu bar: Input, Definitions and Diagrams, Print Report, and About. The program automatically defaults to open in the Input tab (we encourage the reader to access the program for a visual display relating to this text section). The Input tab contains drop-down menus to select the number of comparison groups, the classification statistic, and the stepwise procedure; buttons to select reference groups for analyses; data input tables for metric and morphoscopic variables; text boxes for case ID and analyst name; an evaluate button; and a results tab (blank until an analysis is run).

Under the Definitions and Diagrams main tab are three sub-tabs: Morphoscopic Definitions, Metric Definition Table, and How Not to Read a Mandibulometer. Morphoscopic Definitions shows diagrams with associated definitions and scoring procedures for each of the morphoscopic variables. The Metric Definition Table is taken from Byrnes et al. (14) and provides descriptions for each of the measurements. How Not to Read a Mandibulometer shows a diagram and text explaining the common misreads of the device, also taken from Byrnes et al. (14). These should be used as reference prior to conducting data gathering to re-familiarize the user with the definitions and measurement characteristics.

The Print Report tab shows a single-page summary of any run analysis. The date of the analysis is automatically added to the report. The case number and analyst are first shown, followed by the measurements entered into the analysis, and then by the two classification matrices (raw numbers and converted percentages). After the classification matrices are the total correct classification and then group prediction. Next, the posterior and typicality probabilities are listed, followed by the group means, and a table showing the difference of the group means from the

TABLE 4—Results of 10 cases used to compare group classification, posterior probabilities, and total correct classifications between FORDISC and (hu)MANid. All correct classification percentages use a LOOCV procedure.

Case	LDA*			MDA		
	Group	Posterior Probability	Total Correct Classification (%)	Group	Posterior Probability	Total Correct Classification (%)
Case 1	WM	0.949	59.2	WM	0.933	69.3
	SEAM	0.036		SEAM	0.059	
	NEAM	0.007		HISPM	0.004	
Case 2	WM	0.980	59.2	WM	0.993	69.3
	BM	0.011		AIM	0.005	
	HISPM	0.006		BM	0.001	
Case 3	BM	0.550	62.1	BM	0.700	70.7
	HISPM	0.296		HISPM	0.177	
	AIM	0.109		AIM	0.060	
Case 4	WM	0.533	62.1	WM	0.797	70.7
	AIM	0.228		NEAM	0.085	
	NEAM	0.104		BM	0.053	
Case 5	BM	0.733	62.1	WM	0.422	70.7
	NEAM	0.126		NEAM	0.405	
	WM	0.071		BM	0.088	
Case 6	SEAM	0.711	59.2	SEAM	0.853	69.3
	NEAM	0.234		NEAM	0.120	
	HISPM	0.022		WM	0.014	
Case 7	AIM	0.317	59.2	WM	0.569	69.3
	WM	0.255		AIM	0.159	
	HISPM	0.232		HISPM	0.130	
Case 8	SEAM	0.572	57.1	SEAM	0.722	66.8
	NEAM	0.353		NEAM	0.247	
	HISPM	0.058		HISPM	0.018	
Case 9	HISPM	0.357	62.1	WM	0.619	70.7
	WM	0.292		HISPM	0.236	
	BM	0.165		BM	0.123	
Case 10	NEAM	0.369	59.2	NEAM	0.430	69.3
	SEAM	0.249		SEAM	0.268	
	HISPM	0.247		WM	0.176	

LDA, linear discriminant function; MDA, mixture discriminant analysis.

\*The LDA results for each case were exactly the same when using either FORDISC or (hu)MANid, as discussed in text.

new data. Any negative numbers in the difference from the individual to the group means reflect that the new data are greater than the group mean for that variable, and positive numbers indicate that the new data are less than the group mean. Finally, the classification plot is shown. To print the report, simply push `cntrl + p` (Windows) or `command + p` (Mac), or save it as a PDF within the print option.

The About tab has three subtabs: Using (hu)MANid, Population Descriptions, and References. Using (hu)MANid describes the use of the program, and is similar to the description given here. The Population Descriptions subtab details each of the reference populations, composite groups, and lists each of the group codes. Embedded in this information are some basic characteristics about each population and references for additional information. The References subtab lists citations for presentations and publications on mandibular metrics and morphoscopy, interobserver error, population backgrounds, statistics, and R packages used in (hu)MANid.

Using (hu)MANid should be easy and intuitive for the average analyst familiar with other statistical programs. To start, the user must first select the number of reference groups they wish to compare, which will either be “Two Groups” or “More Than Two Groups.” Due to the different outputs between a two-group and more-than-two-group LDA within R, the user must specify the number of groups for the analysis to avoid any errors. This one step is critical for a correct analysis in the program. Next, a selection of either LDA or MDA can be made, although the default is always LDA. Within (hu)MANid, the individual

reference populations are listed and the user selects the desired reference groups to compare to. Besides the individual reference populations, there are 14 composite reference groups. Composite samples likely should not be used if individual groups are selected. To select a group for analysis, click on the checkbox to the left of the group code. Below the reference samples are two tables to enter in the new data (metric and morphoscopic). Not all data needs to be entered—the user can add as many, or as few variables as available, in either category. Next, the user can enter in the case number or specimen ID and their name or initials, which are used for the Print Report page. To run the analysis, click on the “Evaluate” button.

Below the Evaluate button, the results will be generated into a series of five subtabs: Classification Results, Classification Matrix, Classification Plot, Summary Statistics, and Model Details. Once new data are evaluated, all of these tabs are populated with the results. The Classification Results tab shows the predicted group membership. Next, the posterior probabilities and chi-square typicalities are shown ordered from highest to lowest. Last, the Euclidean distance from the new data’s DF score(s) to each group centroid or mean is shown. Under the Classification Matrix tab, the classification (or confusion) matrix is shown first with the raw numbers. Below the classification matrix is the total correct classification. Next, the classification matrix converted into percentages. Finally, positive and negative predictive values are shown. The Classification Plot tab will show a scatterplot for analyses of more than two groups or a histogram for two-group analyses. The new data will be plotted as a black asterisk in the

scatterplot and a solid, black line in the histogram. Below, the plot will show the new individual's discriminant function scores and the amount of variation accounted for from each discriminant function. The Summary Statistics tab shows a variety of summary statistics for each group in the analysis. The Model Details tab shows the prior probabilities for each group in the analysis (set to equal), group means, the discriminant function coefficients, and proportion of trace for each discriminant function. Each time a new analysis is run, the results are overwritten with new data. Therefore, in order to save prior work, each run should be printed out or saved as a file (see above, Print tab).

## Discussion and Conclusion

Based on requirements not only from Daubert (5) but also from SWGANATH and the NAS report (6), the need for repeatable conclusions with known error rates is a must in forensic anthropology today. (hu)MANid allows the user to present conclusions based on strong statistical analyses with associated error or uncertainty rates. The program has a large comparison database, allowing for analyses that go beyond the traditional comparisons of U.S. Blacks and Whites. This may make it particularly interesting to those practitioners working in other areas of the world. This paper has shown that (hu)MANid produces the same results as other major programs such as FOR-DISC (1) and SPSS (32), but it has the added benefits of being a complete package without the need for expensive programs, importing data, or programming complex comparisons. Further, (hu)MANid has additional analysis choices, such as MDA, which is not typically available on other platforms.

As with any statistical program, it is for the user to decide on the parameters of each test. The underlying assumptions, procedures, and theory are ultimately the user's responsibility. Further, the user should be particularly aware of using composite datasets when examining unknown mandibles. Some sample sizes are small (particularly 20th century Black females and 19th century White females), and the user should be aware of how this may limit potential analyses. We encourage the user to understand the background statistical processes prior to performing any analyses in this program. Last, we also encourage the user to be very familiar with mandibular measurements and morphology scoring prior to undertaking an analysis (see 14). As definitions and diagrams are available in the package, we suggest using these in conjunction with active analysis to ensure proper techniques are being followed.

(hu)MANid is now available for use by the anthropological community. We believe the program is elegantly suited for forensic, medicolegal, and bioarchaeological applications. We believe this user-friendly GUI provides an excellent resource previously lacking in the literature. The user can download the program (with a request to the authors), or simply access it via the worldwide web. Updates, to include data revisions and new features, will continue for the foreseeable future. Future expansion packs for this program include dental metric data, and possibly dental morphological data. Underlying source code for building (hu)MANid is available upon request.

If you would like to submit your mandibular data to be included in (hu)MANid, we will gladly accept it. Please send to either of the authors, listing the measurements and scores, and include background population information (sex and ancestry, as well as what collection they came from). This can simply be accomplished through any standard spreadsheet file type. We will anonymize the data for future use as well as check the data

for errors prior to its inclusion in an upcoming release. Acknowledgments will be placed in the About tab of (hu)MANid.

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