Fordisc Help file version 1.53
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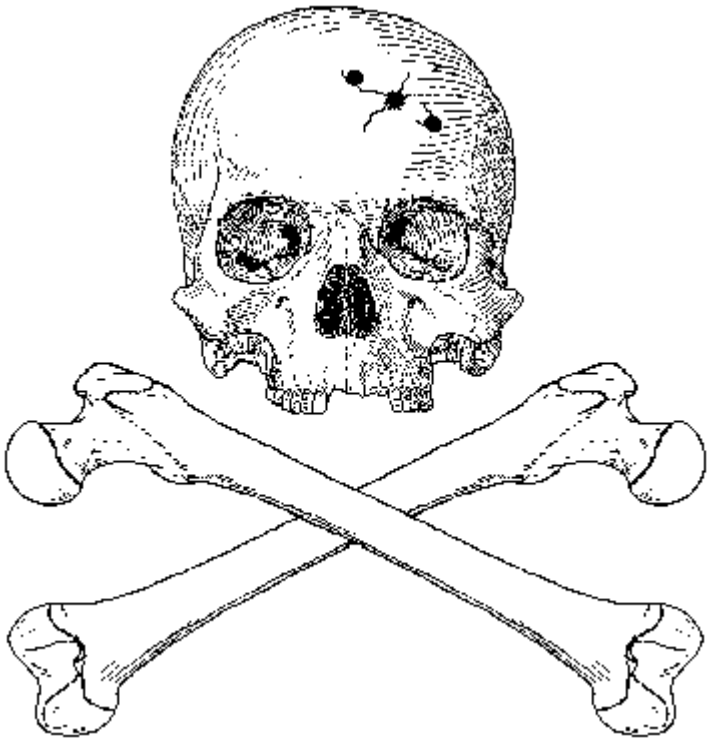
Fordisc 3

Main Help Page



Case Folder

A case folder is made up of three tabbed pages. The first has modern groups with craniometric and mandibular measurements, the second has Howells groups and groups collected by the University of Tennessee Department of Anthropology, and the third page has postcranial metrics and case notes. To select groups, click on the group box or group name to toggle using the group in an analysis.

To move between fields, press [TAB] or click the mouse on a field. To move between pages, press the [Page Up] or [Page Down] keys or click on the tab of the page you want to go to.

The first page has cranial measurements and mandibular measurements for the FDB groups. To select a group, click on the name. An **x** in the box means the group will be included in the analysis. The first page also has angles that are automatically calculated based on the measurements entered.

The second page has the Howells measurements, Howells groups, and 19th and 20th century American groups selection. In this case, the analysis will be based on the Howells cranial measurements selected.

The third page has postcranial measurements and FDB group selection for postcranial measurements. The page also has an area for entry of Case Notes. There is virtually no limit to the amount of text that can be entered into the Case Notes field. The third page also has a button for performing stature estimation.

The Case Number field, above the case folder, accepts up to 15 characters. There is also a field for the entry of a **HEADER** for the statistical output. This header can be particularly informative when you run make multiple analyses of the same individual.

Running an Analysis

If you like, you can initially enter all case information into the different pages of the case folder. To run an analysis, click on the Process button or press F8. **The page displayed when the analysis is started determines which measurements will be used and which group comparisons will be made.** If you run an analysis with none of the group pages selected, the analysis will be run based on the last selected page. The data set to be used is indicated just to the left of the Process button.

Information on Populations
Discriminant Function Analysis

Stature Estimation

Tutorial

Measurement Definitions

Cranial measurements (Page 1)
Mandibular Measurements (Page 2)
Postcranial Measurements (Page 3)

Files

Fordisc 3 stores case information in the Advantage database (*.ad*) format. It can import case files from Fordisc 2 and other data to be analyzed from Paradox and dBase files. Many database and spreadsheet programs can save files in dBase format.

Fordisc can also import case file data in comma-separated format (*.csv), semicolon-separated format (*.ssv), or tab-separated format (*.tsv).

File Operations

Options

The options page has various selections that determine how the analysis is run.

Options Page

Results

Text Results Screen

Histograms (2 groups)

Canonical plots (more than 2 groups)

When citing results from Fordisc, please use this reference: Jantz, RL, Ousley SD (2005) FORDISC 3: Computerized Forensic Discriminant Functions. Version 3.1. The University of Tennessee, Knoxville.

Program Notes

Be sure to read the licensing agreement. Note that you can install FORDISC on up to two computers that you use, but only if each copy will not be running concurrently.

FORDISC was designed to look its best at 1024 x 768 resolution, though it can run in a resolution as low as 640 x 480 as long as you have a desktop size of at least 800 x 600.

Fordisc 3 is written in Borland Delphi and incorporates various numerical routines and components from Software Development Lohninger. Several program features were adapted from routines available at delphi.about.com, maintained by Zarko Gajic. Advantage Local Server version 10 from Extended Systems is used for database access.

What's New in Version 3

Larger reference group sample sizes, specially for Hispanic males from the Southwestern US. We hope to add a sample of Hispanic females soon.

An additional group - Guatemalan males - has been added to the forensic samples.

More measurements, including nearly all from (Howells 1973). Minimum cranial breadth and a few others were not included due to high interobserver errors.

The basic FDB measurements have been expanded to include two Howells measurements, biasterionic breadth (ASB) and zygomaxillary breadth (ZMB), as well as mid-orbital width (MOW), from Woo and Morant (1934). **At this time, analyses using these measurements in the forensic samples will limit sample sizes somewhat.**

An expanded help file with updated measurement definitions, illustrations, and images.

Typicality probabilities based on the F distribution. Fordisc 3 also provides probabilities based on the chi-square distribution (as in Fordisc 2) and ranks for comparison.

Stepwise selection (forward, exhaustive) of variables using Wilks' Lambda (a multivariate measure) or classification accuracy using cross-validation, resubstitution, or a hybrid approach termed Turbo mode.

Transformations of measurements into shape variables (Darroch and Mosimann 1985) or natural logs of measurements.

Two-dimensional plots of canonical variate axes with scatter plots of individuals, identification of individuals, and confidence ellipses for groups.

Three-dimensional scatter plots that can be rotated and sized.

Selection of measurements using checkboxes, rather than by erasing measurements as in Fordisc 2. This allows you to store all case data and choose which measurements are used in an analysis more easily.

Automatic elimination of measurements not present in all groups, rather than showing a message. The removed measurements are indicated in the Fordisc output.

Faster calculation of statistical parameters and more analysis options.

Electronic submission of all case information to the FDB.

A test for the homogeneity of variance-covariance matrices.

A running log of all analyses in each session.

A notes page for multiple uses.

Importing, conversion, and analysis of data in different database formats.

A map and list of abbreviations for the Howells population samples.

Most importantly, Fordisc can be updated via an internet connection. **New features and options will be added to the program based on feedback from you.** Additionally, this help file will be modified and expanded.

A list of program revisions is below.

Fordisc 3 Program Revisions

264
Fordisc 3.0 released
265
Added significance test for two-way DFs

MOW added to FDB measurements
266
Run one instance added
Const code optimizations
Database optimizations
267
Use of mandibular measurements fixed
268
USB version enabled
269
Printing Results added
271
Improved Program Updating via the Internet
International support
272
Improved Program Updating via the Internet (Again!)
273
Faster measurement checking
Fixed angle calculation bug.
Program Updating timeout added.
Updated file button images and functions.
Added link to FDB forms in PDF file.
274
FDB case submission
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275
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277
Modified Size Output in Shape Analysis
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279
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280
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281
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282
Fixed Email bugs
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Fixed Howells 19th century groups selection bug
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283
Larger fonts
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Fixed log-stepwise bug
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Custom DB field display improvements
284
Improved and fixed report printing
285
Added compiled help support for Vista and Windows 7 users
Added more designations for multivariate outliers
Improved custom file importing
Modified regression plot
Fixed graphics printing bugs and graph buttons
Fixed stature captions
286
Fixed stature sort and exhaustive listing
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287
Added additional site license features
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Added table fix for missing memo file.
288
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289
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Relocated ini file
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290
Improved small-screen resizing
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Added subscription option
Added **COLOR** indicators of reference file outliers in extended results
Added digits to stature estimation equations output
Added sort by R-square or Prediction Interval to stature estimation
Improved HTML help file integration for Vista and Windows 7
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291
Added comma-delimited text importing
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292
Fixed importing bug
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293
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Added updating of contact information
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Fordisc now allows analysis of groups alone, without case classification
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Added link to html help file
294
Fixed chi-squared typicality probability error
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Fixed trace and determinant of group VCVMs
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297
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298
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300
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301
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302
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303
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Additional Canonical Variates axes restored
Individual scores output formatted better for copying and pasting into a spreadsheet
More text importing feedback provided
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Incorporated more robust and powerful calculation of *F* typicality probabilities following Hawkins (1981)
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Fixed proportional printing bug
Improved automatic update checking

Improved case file saves
306
Enhanced one measurement analyses
Stepwise steps improved
Forced stepwise improved
307
Fordisc updating improved using API
Dates stored in local format
308
When > 20 groups analyzed, closest 20 groups displayed in canonical variates plot
Changed Canonical variates group symbols and colors for clarity
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309
Fixed ranked probability error
Fixed freezing after check for updates
310
Updating process streamlined
311
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312
Added percentage or counts option in classification matrix
Added additional classification statistics (Sensitivity, specificity, etc.)
313
Added alternate update server location option
Redundant updates fixed
Added reference results to RefDBs
314
Added No Information Rate
Use ALL now includes ASB and ZMB
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Fixed column alignments in extended results
Added Cohen's Kappa stepwise selection
Adjusted default stepwise values
315
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Added version and build information to all output
Fixed graphical printing issues
Site license enhancements
Import of case files in csv, ssv, and tsv formats
316
Improved program updating
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Added geometric mean to output using shape
Added count of outliers on main results screen
317
Added No Information Rate to two-group analysis extended results
Added estimated contribution of each measurement to group separation
Improved defective file handling and updating Fordisc case file format
Allow extended results in up to 9 digits
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Fixed plot of groups when more than 25 groups chosen
318
Added birth years to stature estimation
Added estimated stature when plot is copied to clipboard
Several bug fixes and improvements

Help File Revisions

1.08
Reorganized program and help file revisions, added Kachigan (1991) reference
1.09

Added extra FDB measurements explanation, measurement file revision logs
1.10
Minor changes
1.11
Minor changes
1.12
More references, Printing Results help
1.13
Internet Updating
International Support
1.14
Internet Updating
1.15
Updated Internet addresses
Added link to FDB forms in PDF file
1.16
Added Huberty and Olejnik (2006) reference
1.17
Added Automatic Update information
RTF available
1.18
Expanded probabilities discussion
Expanded Statistical Glossary
Updated and expanded tutorial
Updated Options Page descriptions
1.19
Updated Email address
Updated Save file on the Results Page
1.20
Added Howells Abbreviations
Added Howells Map
1.21
Corrected postcranial measurements from the FDB; selected by birth year after 1929
Updated Trotter tibia mismeasurement information
1.23
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1.24
Updated sample descriptions, tutorial files
1.25
Updated descriptions
1.26
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Support for Vista and Windows 7 help added
1.27
Updated tutorial
1.28
Updated several sections
Corrected errors in numbered landmark list
1.29
Fixed small errors
Some preparation for transition to html help (chm)
1.30
Further integration, formatting, and preparation for html help
Added many topic headings
Updated stature section
Improved flat manual output
Added information for Vista and Windows 7 users
1.31
Added import text file help
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Updated import text file help
Updated tutorial
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Minor editorial changes
1.35
Minor editorial changes
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1.36
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1.40
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1.43
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1.46
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1.47
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149
Added importing case file information from text files
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150
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152
Added explanation of variable contributions to multi-group analyses
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Updated stature estimation page

Measurement File Revisions

Cranial

1.07
Added ASB and ZMB data to Japanese and American Indian samples
1.08
Mandibular measurement field names fixed

1.10
Indices updated
1.13
Added Hispanic females
1.15
Corrected several errors
1.17
Corrected several errors
1.19
Reindexed
1.20
Several outliers corrected
1.21
Several additional individuals added, some individuals removed
1.22
Replaced former Japanese sample with Japanese data collected by Beatrix Dudzik
Optimized data table
1.23
Replaced former Chinese sample with Chinese data collected by Beatrix Dudzik and Ousley
1.24
Changed format somewhat

PC
1.06
Two measurement corrections
1.07
Measurement correction
1.08
Measurement corrections
1.09
Indices updated
1.10
Measurement corrections
1.11
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Belatedly adjusted Trotter tibia measurements to compensate for her mismeasurement (Jantz et al. 1995)
Indices added
1.12
Added postcranial data from FDB
Measurement corrections
1.13
Corrected several errors
1.14
Corrected several errors
1.15
Reindexed
1.16
Reindexed
1.17
Numerous outlying values corrected or removed
1.18
Several outlying values corrected or removed
1.19
Changed format somewhat

Population Samples

Forensic Data Bank Groups

Our 13 population samples consist of individuals born after 1930, except for many of the American Indians. Almost all are positively identified, but some were assigned race and sex based on soft tissue features. The numbers given represent the total number of individuals with at least one measurement. Not all individuals have the complete craniometrics or postcranial measurements recorded, so depending on the measurements used, the number for each group in any particular analysis will be different.

American Blacks: 224 males, 137 females (Postcranial: 110 males, 58 females)

These are African-Americans from 27 different states around the country. Most come from the southeast and mid-Atlantic region. A good number come from the Terry Collection.

Excluded measurements: None.

American Indians: 59 males, 32 females

This sample consists of forensic cases (15 males, 5 females) mostly from the Southwest. Sample numbers were augmented by using mid to late 19th century Amerindian remains, most of which were known individuals and positively identified.

Excluded measurements: All mandibular measurements. UFBR was estimated from FMB.

American Whites: 737 Males, 454 Females (Postcranials: 309 males, 167 females)

This is a sample of Euro-American Whites and a few that were European born. These come from all over the country.

Excluded measurements: None.

Chinese Males: 80

The Chinese sample comes from Hong Kong University cadavers of individuals who died in the 1970's, digitized by Beatrix Dudzik and Stephen Ousley.

Excluded measurements: None.

Guatemalan Males: 83

The Guatemalan data are from recent forensic cases from Guatemala, digitized by Kate Spradley.

Excluded measurements: Four mandibular measurements (MRL, XRH, MLT, and MAN).

Hispanics: 281 males, 74 females (Postcranials: 56 males)

This ethnic group has been the most problematic as far as "race" is concerned, and includes individuals born in the US, Mexico and Central America. **There are no individuals born in the Caribbean area, who more often classify as Black (Slice and Ross 1994).** Most of the Fordisc Hispanics come from New Mexico and many of their identifications are based on context. Special thanks for many of these go to Bruce Anderson and the Pima County Medical Examiner's Office.

Excluded measurements: All mandibular measurements.

Japanese: 84 males, 58 females.

The Japanese sample includes individuals born in the 20th century, digitized by Beatrix Dudzik.

Excluded measurements: None.

Vietnamese Males: 51

The Vietnamese sample comes from a "Killing Fields" massacre site in Viet Nam near the Cambodian border. The data are courtesy of Michael Pietrusewsky.

Excluded measurements: UFBR, FOB, all mandibular measurements.

19th Century Groups

The 19th century groups come from the Terry and Hamann-Todd collections.

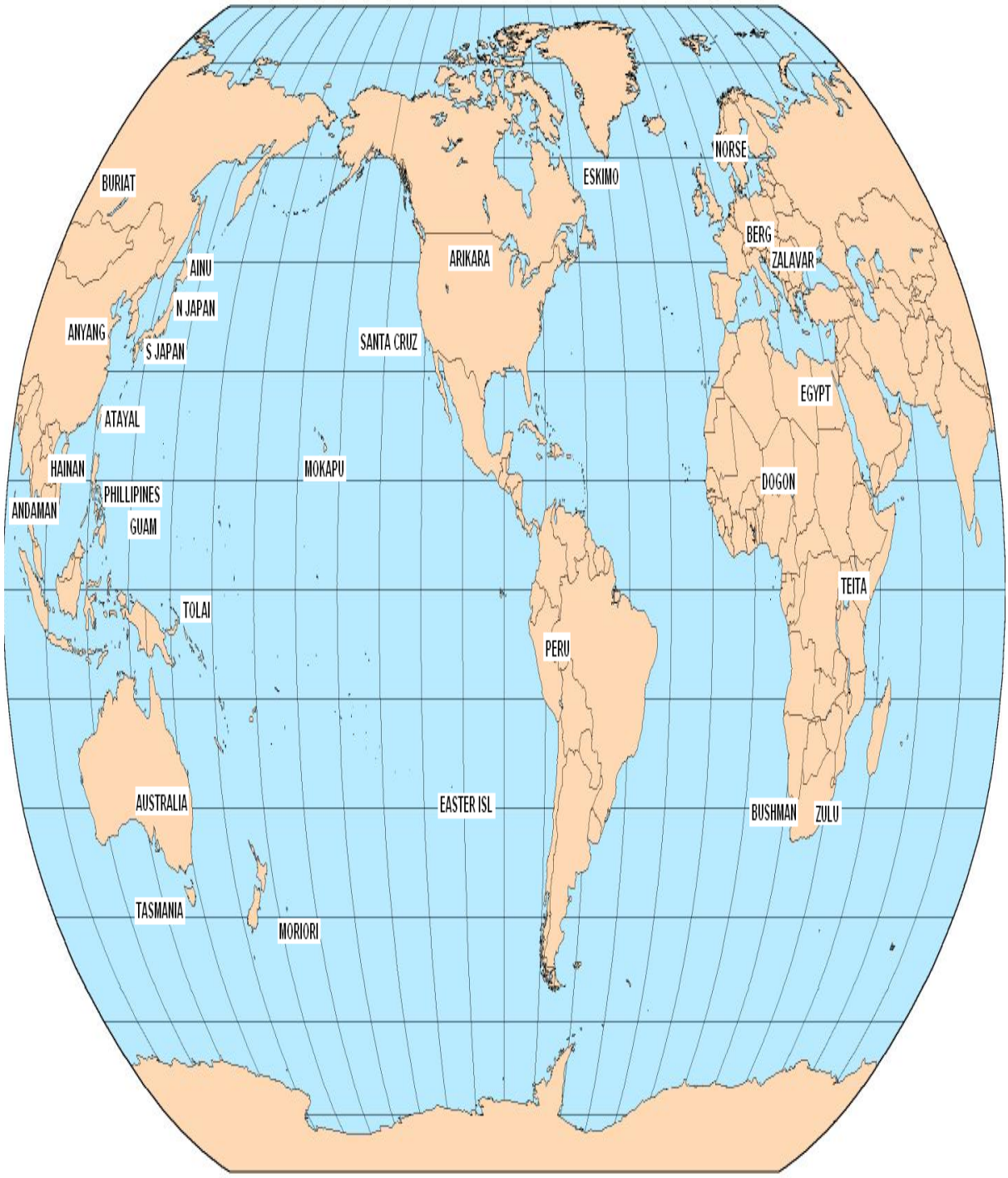
American Blacks - 75 males, 75 females

Excluded measurements: None.

American Whites: - 99 males, 75 females

Excluded measurements: None.

Howells Groups



The Howells groups have been outlined in W.W. Howells' publications *Cranial Variation in Man* (1973) and *Skull Shapes and the Map* (1989). Group abbreviations in FORDISC are composed of the first three letters of the group and a letter for the sex of the sample. For example, Arikara Males are abbreviated as ARIM. **See table below for additional information.**

Several measurements are excluded automatically without warning. Excluded measurements: MAL, WFB, FOB, and all mandibular measurements. UFHT was estimated from NPH, and UFBR was estimated from FMB.

Name	Abbreviation	AREA
AINU	AIN	Hokkaido, Japan
ANDAMAN ISLAND	AND	Andaman Islands
ANYANG	ANY	China
ARIKARA	ARI	South Dakota, USA
ATAYAL	ATA	Taiwan
AUSTRALIA	AUS	Lower Murray River
BERG	BER	Austria
BURIAT	BUR	Siberia, Russia
BUSHMAN	BUS	South Africa
DOGON	DOG	Mali
EASTER ISLAND	EAS	Easter Island
EGYPT	EGY	Gizah
ESKIMO	ESK	Greenland
GUAM	GUA	Guam
HAINAN	HAI	China
MOKAPU	MOK	Hawaii
MORIORI	MOR	Chatham Islands
NORSE	NOR	Oslo, Norway
NORTH JAPAN	NJA	Hokkaido, Japan
PERU	PER	Peru
PHILIPPINES	PHI	Philippines
SANTA CRUZ	SAN	California, USA
SOUTH JAPAN	SJA	Kyushu, Japan
TASMANIA	TAS	Tasmania
TEITA	TEI	Kenya
TOLAI	TOL	New Britain
ZALAVAR	ZAL	Hungary
ZULU	ZUL	South Africa

The Forensic Data Bank

The Forensic Data Bank (FDB) was started in 1986 with a grant from the National Institute of Justice. The FDB contains extensive demographic information for many cases, including place of birth, medical history, occupation, stature, and weight. The skeletal information for cases includes cranial and postcranial metrics, suture closure information, various aging criteria scores, non-metric cranial information, perimortem trauma, congenital traits, and dental observations.

The data were initially used to test forensic methods developed from the Terry and Hamann-Todd collections, primarily composed of 19th century indigents. The inadequacy of these collections for modern forensic cases has necessitated new statistical methods based on more recent data. FORDISC is a logical extension of the need to develop new forensic discriminant functions, and combines years of dedicated data collection and statistical expertise with the capabilities of personal computers. FDB data have also been useful in detecting and analyzing secular changes from earlier populations to recent war dead to more recent forensic cases.

A significant part of the FDB is made up of Terry Collection individuals born after 1900, who are much more similar to other individuals in the FDB born in the 20th century. This data source is nearly exhausted, however, because nearly all Terry Collection individuals born after 1900 are now in the FDB. Data from modern cases are needed to keep up with the changing populations of the United States.

At this writing, the FDB has over 2400 cases. Almost 900 of these are from cases with definite sex and race. Of these, 625 are positively identified individuals. The FDB has received contributions from around the country, but 400 forensic cases analyzed by J. Lawrence Angel over a 25 year time period, make up the largest part of contributions. We thank all FDB contributors, but especially Douglas Ubelaker and Ted Rathbun, for their numerous and continued contributions to the FDB. We also thank William Bass and Jan Simek for securing funding for computer hardware and software for the FDB.

We would like to hear from you about this program and your recent forensic cases. If you have data, please send electronically through Fordisc or complete the forensic data forms and Email, FAX, or mail them to:

Dr. Richard Jantz
Forensic Anthropology Center
Department of Anthropology
502 Strong Hall
1621 Cumberland Avenue
Knoxville, TN 37996-1525

voice (865) 974-4408
FAX (865) 974-2686

Email: rjantz@utk.edu

Any additional inquiries about the Forensic Data Bank are welcome and should be sent to the address above.

Discriminant Function Analysis

Discriminant Function Analysis (DFA) is a family of statistical procedures for the optimal separation of groups and classification of unknowns using measurements. All DFAs involve reference groups with known membership in some category such as language family, ethnicity, sex, or tribe. The known reference groups form the basis for the classification of new individuals of unknown group membership. The most commonly used DFA is the Linear Discriminant Function (LDF). The LDF converts measurements into discriminant function scores using a linear combination of the original measurements that maximizes inter-group differences. The discriminant score of an individual of unknown group membership is then compared to the mean DFA score for each reference group; it is simply classified into the group with the closest mean. If there are more than two groups ($g > 2$), more than one DFA score can be calculated, and multiple axes are used for ascertaining group differences. This procedure is known as Canonical Variates Analysis, and because more than one dimension is involved, the group mean scores are called centroids. In this case, an unknown is simply classified into the reference group it is closest to based on the overall distance to each group's centroid using all axes.

In general, discriminant analyses should be run initially using all possible groups that an unknown may classify into, and in some cases, this may mean using many groups. Then, the most dissimilar groups should be removed after repeated runs. Classifications into two to five groups are expected to be more accurate than those involving many more groups, but the classifications involving more groups need to come first, in order to establish the best candidate groups. Thus, the forensic anthropologist is faces with a Goldilocks dilemma: Good separation and classification of many groups requires many measurements, and encompasses more morphological variation; yet using too many measurements produces overfitting and lower accuracy. So a **target number of variables** needs to be anticipated. The maximum number of variables that should be used cannot be stated emphatically. Tabachnick and Fidell (2001) acknowledge that while the number of variables used can be nearly equal to the smallest group sample size in LDFs, having sample sizes of at least four times the number of variables used is necessary for reliability. Huberty (1994) recommends sample sizes of at least three times the number of measurements used, and we followed that criterion in the past. No more. Further details are found in the **Sample Sizes** section under **Statistical Procedures**. The smallest group sample size minus one is our current recommended upper limit for the target number of measurements. Ideally, for reliable comparisons, a reasonable minimum would be 10 measurements, but depending on the measurements and group separation, fewer measurements may at times be necessary and justifiable, depending on accuracy. We are investigating alternate analytical methods that should allow more measurements to be used.

Certain **assumptions** for LDFs must be met in order for the LDF solution to be an optimal one. These assumptions are covered in other parts of this help file, but are briefly mentioned here. The most important assumption is that the **samples are sufficiently large and representative.** This is especially true in multivariate analysis, where the estimation of parameters is affected by the number of measurements compared to sample sizes for each group. Also, the nature of human data from the United States shows that standards derived from the 19th century are not appropriate, or at a minimum do not provide the best reference data for the assessment of 20th century group affinities. Another assumption is that **the data show a multivariate normal distribution.** In general, craniometric measurements are more or less normally distributed, and when combined in a LDF, their normality is even more likely. Another assumption is that the level of variation in each group is relatively similar, e.g. statistically, that **the VCVMs are relatively homogeneous**. While there are several tests for homogeneity, and each test has strengths and weaknesses, this latter assumption is tested in Fordisc using the Kullback (1959) test for homogeneity. Further tests for group variance-covariance matrix homogeneity will likely be investigated and added. If groups show very different levels of variability, other statistical procedures, including quadratic discriminant functions, logistic regression, or non-parametric methods, may produce more reliable results.

Additionally, certain questions must be asked of the analysis: **Are there enough measurements in the analysis?** A few measurements may perform well at classification but do not adequately represent enough of cranial morphology for reliable group classification. **Are there too many measurements in the analysis?** Estimating reliable multivariate parameters requires relatively large sample sizes. **Are there outliers in the data?** Outliers can drastically affect the estimation of multivariate parameters and lower the accuracy and reliability of an LDF. These questions are covered in various sections of this help file, including the tutorial.

As long as the assumptions of the particular method are not grossly violated, a DFA is best judged by its classification accuracies. The most often recommended estimate of classification accuracy is **leave-one-out-cross-validation** (LOOCV; Lachenbruch and Mickey 1968). LCOOV avoids the upward bias of error rate estimation when using resubstitution, in which each member of all reference groups is classified using all N members of all reference groups, one of which includes that member. In LCOOV, the first individual in the

reference groups is removed from his or her reference group, the parameters are recalculated using the remaining N-1 individuals, and that individual is then classified into one of the reference groups using DFA. That individual is then added back into his or her group and the next individual is removed from his or her group and classified, and so on. When all have been classified in this manner, the total number of correctly classified individuals is the expected unbiased classification accuracy. While this method has a low bias, the estimated error rates have a high variance. Other approaches show lower variances and are of low bias or are unbiased. One of these is similar to LCOOV and is called *k*-fold cross-validation. Instead of removing an individual, as in LCOOV, this method removes a proportion of the total sample (say, 5 or 10%), and classifies it against the remaining individuals.

After evaluating the classification accuracy, two statistics provide information about the unknown being classified. **Posterior probabilities** (PPs) are the probability of membership for the unknown in each group based on the relative distances to each group, and they sum to 1. PPs are calculated as in the two-group case, but with more distances to groups involved. One major assumption for both of these procedures is that the variation within each group is more or less the same; the procedure exploits differences in means and estimates distances based on standardized variances. Another major assumption is that the unknown actually belongs to one of the reference groups. DFA will classify any measurements, even those from another species. An indication of group membership is fortunately given by the **typicality probabilities** (TPs). TPs represent how likely an unknown belongs to a particular group, based on the average variability of all the groups in the analysis. Absolute distances are evaluated, rather than relative distances as in calculating PPs. However, Fordisc 3 calculates TPs in three different ways. See the entry for **typicality probability** in the statistical glossary for more information. A TP is the multivariate equivalent of a probability based on a univariate *t* test and is also similar to the percentile of a univariate measurement. An individual's TP of 0.33 for a group means that 33% of the total sample from that group would be expected to be as far or farther from that group's centroid, or in other words, more different from the group's mean morphology. In practice, TPs below 0.05 (5%), or certainly 0.01 (1%) for a group (similar to *p* values of statistical significance), indicate questionable probability of membership in that group or the possibility of measurement error.

Recent publications that cover the use of Fordisc, statistical background, and approaches to classifying human remains, are found in Ousley and Jantz (2012) and Jantz and Ousley (2012, 2017).

Importing Data

Fordisc can import Fordisc 3 (AdvantageDB ; *.adt), Paradox (*.db), and dBase (*.dbf) database tables, and comma-delimited files (*.csv or *.txt). The main benefit of having data in database files is that the data types (string, numeric, integer) are consistent.

Import Data Button

This button is the right-most button underneath the menu. It opens the **CustomDB** page.

Import Data Page

Click the "Import" button at the top left of the CustomDB page to open a data file. Choose the file type at the bottom of the open dialog box. The default directory is \CustomDBs. If you import a file, the data will automatically be copied into the Advantage data format.

Any numeric fields can be used in a Fordisc analysis, and any text field can be used as a classification variable. When the data are imported, the numeric variables fill the page below. To classify the data using a particular variable, choose it in the "Grouping Variable" window and the grouping variables will be listed in the box at the top middle of the page. All unique grouping values from that field will be displayed. The particular groups to be included are selected by clicking on the group name. The ID variable at the upper left determines what values are displayed if individual scores are selected (See Results Pages).

Note: If you have difficulty importing a numeric field, it may have been given a text field attribute due to stray spaces or characters. Double-check the format and data of the file you are trying to import.

If the numeric variable names in the imported file match the standard Fordisc measurement abbreviations, the data from the current case will automatically be filled in for analysis. Likewise, if you open another case file, the measurement fields in the **CustomDB** page that match the Fordisc measurement names will be filled in. You can also start with a blank record. If you enter measurements for custom database analysis, values will be filled in on all Fordisc screens if the field names match. For instance, if you analyze GOL (glabello-occipital length), the fields will be filled in on the FDB and Howells screens. You can save all measurements you enter in the customDB page that have the same field names as the Fordisc case table. Those matching measurements will also be checked for measurement errors if measurement error checking is selected.

Importing comma-delimited files

Comma-delimited files are easier to import but data inconsistencies will produce unexpected results. **Be sure your comma-delimited data are consistently entered before importing.** It is relatively easy to displace columns in spreadsheets and mix text and numeric data. When comma-delimited files are imported, Fordisc checks all values in all columns for data consistency and if there is a text value in a column, the entire column is treated as a text field and it cannot be analyzed.

A preview of the table is given in the left upper half of the import page, and the structure of the table is given in the upper right half. Double-check that the numeric and string fields were correctly read. To start over, press the "Cancel" button.

Text fields cannot be analyzed as numbers. All text fields can be used as sample group fields.

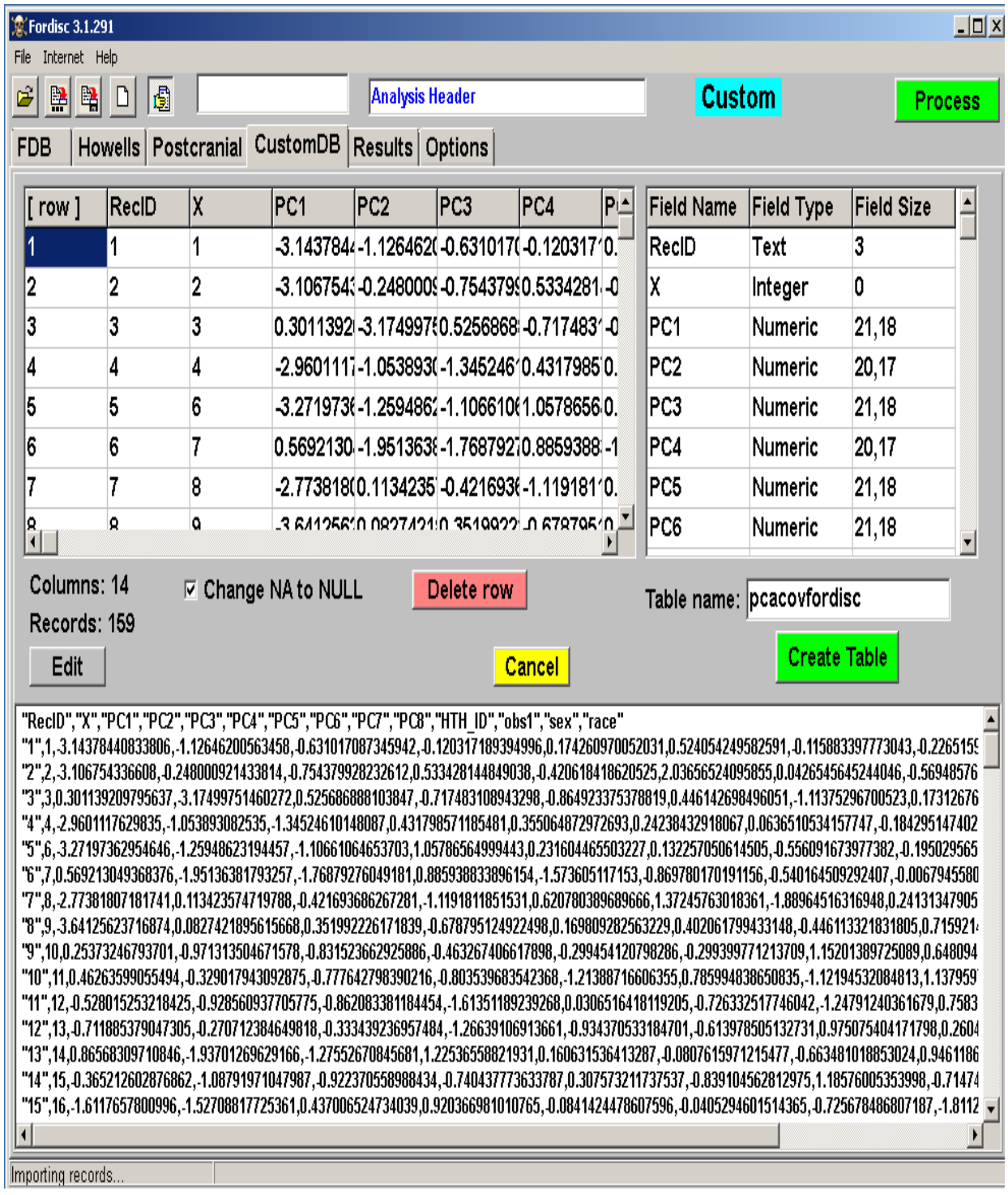
Integer fields are whole numbers.

Numeric fields are used for numbers with decimals. Numeric field formats are given as [total number of digits] , [number of decimal places]. For example, numeric data with a format of 5,3 means that there is a total of 5 digits read, three of which may be to the right of the decimal point.

If you find an incorrect record, you can prevent it from being added to the table by pressing the "Delete row" button.

The raw text data can be seen in the bottom of the screen. If you want to directly edit the file, press the "Edit" button, edit text as necessary, and then press the "Save" button. You will then need to press the "Cancel" button and re-open the file.

Once you are satisfied that the data values have been read correctly, press the "Create Table" button on the right. The data will be saved in an Advantage table with the name given above the button in a text box, which you can change. **The new table will be saved in the CustomDBs folder.**


Fordisc 3.1.291
File Internet Help
Analysis Header
Custom
Process
FDB Howells Postcranial CustomDB Results Options
[row] RecID X PC1 PC2 PC3 PC4 P
1 1 1 -3.143784 -1.126462 -0.631017 -0.120317 0.
2 2 2 -3.106754 -0.248000 -0.754379 0.533428 -0
3 3 3 0.301139 -3.174997 0.525686 -0.717483 -0
4 4 4 -2.960111 -1.053893 -1.345246 0.431798 0.
5 5 6 -3.271973 -1.259486 -1.106610 1.057865 0.
6 6 7 0.569213 -1.951363 -1.768792 0.885938 -1
7 7 8 -2.773818 0.113423 -0.421693 -1.119181 0.
8 8 9 -3.641256 0.082742 1.351992 -0.678795 0
Field Name Field Type Field Size
RecID Text 3
X Integer 0
PC1 Numeric 21,18
PC2 Numeric 20,17
PC3 Numeric 21,18
PC4 Numeric 20,17
PC5 Numeric 21,18
PC6 Numeric 21,18
Columns: 14
Records: 159
Change NA to NULL
Delete row
Table name: pcacovfordisc
Edit
Cancel
Create Table
"RecID","X","PC1","PC2","PC3","PC4","PC5","PC6","PC7","PC8","HTH_ID","obs1","sex","race"
"1",1,-3.14378440833806,-1.12646200563458,-0.631017087345942,-0.120317189394996,0.174260970052031,0.524054249582591,-0.115883397773043,-0.2265159
"2",2,-3.106754336608,-0.248000921433814,-0.754379928232612,0.533428144849038,-0.420618418620525,2.03656524095855,0.042654564524404 6,-0.56948576
"3",3,0.301139209795637,-3.17499751460272,0.525686888103847,-0.717483108943298,-0.864923375378819,0.446142698496051,-1.113752967005 23,0.17312676
"4",4,-2.9601117629835,-1.053893082535,-1.34524610148087,0.431798571185481,0.355064872972693,0.24238432918067,0.0636510534157747,-0.184295147402
"5",6,-3.27197362954646,-1.25948623194457,-1.10661064653703,1.05786564999443,0.231604465503227,0.132257050614505,-0.556091673977382,-0.195029565
"6",7,0.569213049368376,-1.95136381793257,-1.76879276049181,0.885938833896154,-1.573605117153,-0.869780170191156,-0.540164509292407,-0.0067945580
"7",8,-2.77381807181741,0.113423574719788,-0.421693686267281,-1.1191811851531,0.620780389689666,1.37245763018361,-1.889645163169 48,0.24131347905
"8",9,-3.64125623716874,0.0827421895615668,0.351992226171839,-0.678795124922498,0.169809282563229,0.402061799433148,-0.446113321831805,0.715921
"9",10,0.25373246793701,-0.971313504671578,-0.831523662925886,-0.463267406617898,-0.299454120798286,-0.299399771213709,1.152013897250 89,0.648094
"10",11,0.46263599055494,-0.329017943092875,-0.777642798390216,-0.803539683542368,-1.21388716606355,0.785994838650835,-1.121945320848 13,1.137959
"11",12,-0.528015253218425,-0.928560937705775,-0.862083381184454,-1.61351189239268,0.030651641811 9205,-0.726332517746042,-1.24791240361679,0.7583
"12",13,-0.711885379047305,-0.270712384649818,-0.333439236957484,-1.26639106913661,-0.934370533184701,-0.613978505132731,0.975075404171798,0.2604
"13",14,0.86568309710846,-1.93701269629166,-1.27552670845681,1.22536558821931,0.160631536413287,-0.080761597121 5477,-0.663481018853024,0.9461186
"14",15,-0.365212602876862,-1.08791971047987,-0.922370558988434,-0.740437773633787,0.307573211737537,-0.839104562812975,1.185760053539 98,-0.71474
"15",16,-1.6117657800996,-1.52708817725361,0.437006524734039,0.920366981010765,-0.084142447860 7596,-0.040529460151 4365,-0.725678486807187,-1.8112
Importing records...

File Operations

Fordisc 3 uses the Advantage database file format for the case file, but can import Paradox and dBase database files as well as text-based files. Any imported database files are automatically converted into the Advantage database format and given the same file name as the imported Paradox or dBase file but with a different extension (ad*). Therefore, you should only need to convert a file once from a different format as long as you save it.

Case Folder File Menu items and buttons

Open File

[Alt-F-O]

To open a data file, choose this and select a file or enter a file name at the prompt. The default file type for Fordisc 3 is an Advantage data table with the extension adt; the memo field text is stored in a file with the adm extension.

You can also open Fordisc 2 files, which are Paradox files with the db extension, or dBase files, with the dbf extension. When you open one of these file types, the file is automatically converted into the Advantage file type and data structure, and all measurement fields are automatically filled in based on matching field names. **Be sure to SAVE an opened Fordisc 2 file as a Fordisc 3 file.**

You can also open case files in several text formats. The first line of the file should have the field (column) names corresponding to Fordisc field names separated by a delimiter (comma, semicolon, or tab); the second line should have the corresponding values for each field separated by the same delimiter. Double and single quotation marks will be ignored. See the examples below. After importing, it would be best to save case data using Fordisc in Advantage format.

Fordisc has example files named CranDat1.* that will be correctly read into case information.

Comma-separated format (*.csv)

Contents of CranDat1.csv:

```
catkey,sex,"race",popsex,birthyear,eage,gol,bnl,bbh,xcb,zyb,aub,"bpl",nlh,"nl
b","nph",dkb,"frc",pac,occ
  143gerg,F,B,BF,1951,33,171,92,122,130,117,112,"96",50,25,68,21,102,110,85
```

Semicolon-separated format (*.ssv)

Contents of CranDat1.ssv:

```
catkey;sex;"race";popsex;birthyear;eage;gol;bnl;bbh;xcb;zyb;aub;"bpl";nlh;"nl
b";"nph";dkb;"frc";pac;occ
143gerg;F;B;BF;1951;33;171;92;122;130;117;112.2;"96.4";50;25;68;21;102;110;85
```

Tab-separated format (*.tsv)

Contents of CranDat1.tsv (copy and paste into a spreadsheet to see that they are indeed correctly aligned):

```
            catkey          sex             "race"          popsex          birthyear
eage        gol             bnl             bbh             xcb             zyb             aub
"bpl"       nlh             "nlb"           "nph"           dkb             "frc"           pac
occ
            143gerg         F               B               BF              1951
33          171             92              122             130             117             112.2
"96.4"      50              25              68              21              102             110
85
```

Reopen File [Alt-F-R]

To reopen a data file you've recently opened, select this and a list of the last 5 files you have accessed appears. Select a file using the mouse, using the arrow keys and pressing ENTER, or by pressing the number key corresponding to the file name.

Save As.. [Alt-F-A]

Select this if you want to save the current case data to a different file. You will be prompted to type in a different file name.

Save [Alt-F-S]

If you have opened a file or have saved this file already, the file will automatically be saved. If not, type in a file name at the prompt. If you want to save the current information in a different file, choose **Save As** from the File menu. If you make changes to a data file, including choosing different groups, and then exit Fordisc, you will be prompted to save the changes you made.

Save metric data in PDF form [Alt-F-P]

If you have opened a file or have saved this file already, this selection will save the case data to an Adobe PDF file in the Cases folder. There are additional fields that can be filled in as necessary, such as your name and the number of sacral segments. You should have Adobe reader or a similar program installed on your computer, which will try to fill in the PDF form with data from your file. You may be asked to "trust the document" or verify that the form should be filled in with data in order for all data fields to be populated. Be sure to save the PDF file after all information is entered. You can rename the PDF file or keep the default name, which is "FDB_Metrics_" plus the case file name.

New File [Alt-F-N]

This selection clears the current case folder of all data, and **all unsaved data will be lost**. FORDISC is then ready for new data.

Options Page

The options page provides many choices as to how an analysis is run and what information from an analysis is available.

Transformations

Transformations can be used to change the data distribution or bring out different aspects of the data. **Log** transforming generally makes the data more normally distributed. The logged measurements will be multiplied by 100 for readability. **Shape** transformation uses the Darroch and Mosimann (1985) method of conversion into shape variables whereby all original measurements are scaled by their geometric mean. As you might expect, removing size results in a decrease in accuracy in DFA between the sexes. The default is **None**.

Sort Groups

The default is to sort groups after an analysis by their **Distance** to the unknown. The most similar group will be listed first. Classifications can sometimes involve many groups and getting an idea of overall similarities to many groups can be valuable. You can also sort groups by **Group Name**.

Save

Analyzed Data

If this selection is checked, Fordisc saves the data that are analyzed in a tab-delimited text file named FD3ProcData.txt in the Results subdirectory. If the data were transformed, the transformed data are saved. If a shape transformation is chosen, the geometric mean is also included.

Jackknifed VCVMs

When cross-validation is chosen as well as stepwise selection, N-1 VCVMs are calculated. Examination of these VCVMs can help identify outliers and provide additional statistics based on sample composition. The jackknifed VCVMs are saved to the \Results subdirectory.

Show Results

Basic Results include the classification matrix, D-square to reference groups, measurements of the unknown, reference group means, and the determinant of the VCVM.

Extended

The extended results page has group means and standard deviations, the pooled within-group VCVM and its determinant, a test for homogeneity of VCVMs, the pooled within-group correlation matrix, mean canonical axis scores for each group, structural coefficients, eigenvalues and percentage of total variation, Mahalanobis D-square matrix, significance matrix of D-squares, and the D-square, posterior probability, and typicality probabilities to each reference group in the analysis.

Group VCVMs

If selected, the VCVM of each group will be displayed.

Individual Scores

This selection lists the classification results of each individual in the reference groups, including the individual ID, the group classified into, the Mahalanobis distance, posterior probability, and typicality probabilities to each group. If LOO cross-validation was selected, the individual values are jackknifed values, which are much more reliable for detecting outliers because each individual was excluded from the calculation of the group parameters (Penny 1996). Notation is provided for reference group outliers, whether they were correctly classified (++, +++, and ++++) or incorrectly classified (**,***, or ****), with associated p values < 0.05, 0.01, and 0.005. **Extreme outliers (**** or ++++) in reference data should certainly be removed and the data should be reanalyzed.** Outliers are listed by default before the listing of individuals. You can exclude individuals used in an a analysis by typing the ID, one ID per line, into the text box under the *Exclude IDs (one per line):* heading. To

save time, you can copy each line from the outliers list above the individual scores and paste into the Exclude ID text box. The excluded individuals will be listed on the Basic Results page.

Outliers at Typ F < 0.01

If this selection is checked, a list of individuals with typicality probabilities less than 0.01 for all groups will be displayed on the Extended Results page at the bottom. You can copy each line from the outliers list above the individual scores and paste into the Exclude IDs text box. The excluded individuals will be listed on the Basic Results page.

Classification Table

Extra Statistics

This selection provides additional classification measures such as sensitivity, specificity, and Cohen's Kappa, which can be especially useful in many cases. Further details are in Results.

Classification Matrix shows

This presents a choice between presenting the classification matrix using sample counts or percentages. Sometimes, classification patterns are more easily discerned when percentages are used.

Check for Measurement Errors

When checked, Fordisc will check the measurement of the unknown case based on "normal" univariate minimum and maximum values from a variety of populations. The default is to check for measurement errors, and this should not be changed. **Generally, if a measurement is outside these minimums or maximums, it should be left out of an analysis.** A measurement outside the normal values may be one affected by a pathological condition or taphonomic factors, and should not be expected to reflect group membership.

Classify Case

When checked, Fordisc will classify an individual using the entered measurements. Classification can only be done using the measurements that are present. However, if you wish to compare groups without classifying an individual, you can uncheck this box.

Classify only if Typ F >

This selection is a safeguard against trying to classify a highly unusual individual. Remember, DFA will classify any combination of values, whether measurements from adult humans, from another species, or a combination of random numbers. When selected, Fordisc will not indicate a classification if all Typ F are greater than the entered value. No classification is to be trusted when all typicality probabilities are that low. Since Fordisc 3.1.304, the default value is 0.005 because a more sensitive F-typicality is used (Hawkins 1981).

Classification Rate Estimation

The value of a discriminant function is best assessed in practical terms, by its accuracy, which is measured by the error rates of its classifications.

Resubstitution (N, N) If Resubstitution is chosen, the classification accuracy rate for each group is evaluated using every individual in the analysis (N). Resubstitution provides estimates that are biased upwards because each individual is evaluated in a function that was calculated using that individual.

LOOCV (1, N-1) Cross-validation is essential in estimating the real-world error rates of a discriminant function. Cross-validated error rates dramatically reveal the problem of overfitting the data, i.e. using too many measurements for the group sample sizes (Flury 1997; Huberty 1994; Huberty and Olejnik 2006). When too many measurements are used, resubstitution error rates may be zero, but cross-validated error rates may be as bad, or worse, than random assignment (Flury 1997; Ousley and McKeown 2003). Leave-one-out-cross-validation (MacLachlan 1968) removes one individual at a time from the total sample,

calculates a discriminant function based on the remaining individuals (N-1), and records whether or not the classification of the removed individual was correct; this is performed for each individual in the reference groups. LOO cross-validation is unbiased for error prediction but it does have a large variance.

Note: If LOOCV is chosen as well as stepwise variable selection, then the stepwise procedure will proceed using cross-validated error rates. While theoretically the best way of selecting measurements, this combination is particularly computationally expensive because Fordisc calculations using LOOCV have not been fully optimized.

Typicality Probabilities

Fordisc provides three typicality probabilities: **Typ F** gives the probability based on the *F* and Hotelling's *T* distributions (Hawkins 1981); **Typ Chi** gives the probability based on the Chi-square distribution; and **Typ R** provides the ranked probability. Each calculation has advantages and disadvantages depending on the number of variables used, the number of groups involved, and the sample size of each group. **Typ F** takes into account the Mahalanobis distance and sample size; Typ Chi is based on the Mahalanobis distance alone; and **Typ R** is based on ranking the Mahalanobis distance of the unknown compared to the reference group. **Typ R** also includes the rank of the unknown (in parentheses) as if it were a member of each sample. All three are important in evaluating an unknown, depending on the number of measurements used, group sample sizes, and the individual being analyzed. In our experience, **Typ F** tends to indicate fewer unknowns as atypical, while **Typ Chi** tends to indicate more unknowns as atypical. **Typ R** provides an estimate with fewer statistical assumptions, but a small sample size may produce an unusual **Typ R**.

Exclude IDs

When an outlier is suspected or identified through various means, including examination of canonical variates plots or reference group classifications in the extended results, an individual can be excluded in an a analysis by typing the ID, one ID per line, into the text box. You can paste in multiple values, such as the list of outliers on the extended results page, as long as the first value is the individual ID and other values are separated by tabs. The excluded individuals will be listed on the Basic Results page.

Stepwise

For many practical reasons, the number of measurements used in an analysis should be limited, generally following the $3m <= n$ rule. Stepwise selection of measurements can be used to determine the measurements that best classify the reference groups.

Stepwise Method

If you choose **Forward Mean %**, measurement selection will be based on the mean correct classification percentage, and if you choose **Forward min %**, measurement selection will be based on the highest minimum correct classification percentage for any group. Under **#Variables**, **Min** determines the minimum number of measurements to start with, and **Max** determines the maximum number of measurements to evaluate in combination. At each round of analysis, an additional variable is considered an improvement if the classification percentage improves by at least the **Step** amount. The default for **Step** is different for the different methods and is a proportion, so 0.002 = 0.2% for the percentage methods. If this amount of improvement is not seen in adding another variable, the procedure stops and the number of measurements may be lower than the maximum. Setting the **Step** value lower generally results in more measurements selected, and setting it higher will generally produce fewer measurements. At every step, only those individuals who have ALL candidate measurements will be used in the comparisons. This is to avoid drastic changes in sample compositions, but does limit the number of individuals used to find the best measurements. When ***Turbo*** is selected, however, a final query of reference groups uses only the stepwise-selected measurements, so sample sizes are as high as they can be.

Setting **Min** to 1 will find the single best measurement and then additional measurements will be added one at a time, up to the **Max** number of measurements, and

the best combination derived will be used in the final analysis. This is the usual forward stepwise method used in many statistical packages. However, selecting measurements this way will not necessarily find the best possible combination of multiple measurements because after a variable is selected, it remains in all further combinations (Huberty 1994). Different combinations of measurements can produce different error rates that may have little relation to their individual univariate error rates.

Based on our experience, starting with one measurement and then adding them one at a time, when selecting a maximum of 8 or more measurements, produces slightly different variable combinations and at a lower classification accuracy than when starting with six or seven measurements. In order to get the best possible combination of measurements, **Min** and **Max** must be set to the same value. Only then will each unique combination (permutation) of the number of measurements be evaluated. This can take considerable time because the number of permutations increases rapidly with the total number of measurements to be tested. The formula is $(N!)/(N-n)!n!$ where N is the maximum number of measurements and n is the minimum. For example, there are 1,140 permutations using 3 out of 20 measurements, 15,504 permutations using 5 out of 20 measurements, and 184,756 permutations using 10 out of 20 measurements. **You will be warned if the number of permutations will exceed 100,000.** If you change your mind about running the stepwise procedure you can press the **STOP** button to halt it.

In order to speed up stepwise selection, version 3.1.296 added a ***Turbo*** selection feature. When ***Turbo*** is selected and a percentage method is chosen, the best measurements are selected using resubstitution, which runs quite fast but is biased. After the best measurements are found, Fordisc then runs the final query of reference groups using only the stepwise-selected measurements and uses LOO cross-validation if that was chosen.

During stepwise selection using Forward Percent, the default error rate calculation is an **Unweighted** percentage. When sample sizes are quite imbalanced, using a weighted percentage correct can sacrifice accuracy in the smaller group for a better classification rate in the larger group. For instance, if group A has a sample size of 270 and group B has a sample size of 30, a function that classifies everyone into group A will be 90 percent correct on the whole, even though no classifications are correct from group B. Choosing **Weighted** stepwise selection results in calculating the overall percentage of correct classifications.

Forward Wilks' L is currently the default option for choosing the best measurements in a discriminant function. When this option is selected, measurements are selected according to the value of Wilks' Lambda, a multivariate measure of within-group variation compared to among-group variation. The lower the value of Wilks' Lambda, the lower the relative within-group variation and the higher the relative among-group variation, meaning that the measurements should separate groups better. Wilks' Lambda calculations are based on assumptions of multivariate normality and equal VCVMs, which are never perfectly realized. Using Wilks' Lambda will not always find variable combinations that are as accurate as choosing measurements using the Forward Mean % method. However, the difference in error rates may be quite small. Also, the Forward Wilks method using the default **W Step** value tends to select more measurements than the Forward Mean % method, and can in certain circumstances produce a higher classification accuracy with those additional measurements.

Forward Cohen's Kappa is another option for stepwise variable selection. Kappa is calculated from the classification matrix and compares classification accuracy (sensitivity) to the prevalence of each group. It may perform better when classes are imbalanced. You can choose to run stepwise selection using weighted or unweighted mean group Cohen's Kappa.

Future additions

There are various data transformations that can be valuable in answering different questions. The possible transformations will increase. Methods of error estimation besides LOO cross-validation, such as K-fold cross-validation and the .632+ estimator (Efron and

Tibshirani 1993, 1997) are being investigated for incorporation into later editions of Fordisc. Options for saving additional information from many procedures will be added. Robust discrimination, whereby outliers are reweighted or eliminated, will be incorporated into future editions of Fordisc.

Results Pages

The Results pages include **Basic** results, **Extended** results, **Steps** (if stepwise selection was selected), a **Log** of all analyses in the current session, and a **Notes** page that can be used as a scratch pad. Pressing the **Copy** button will copy the text of the current Results page to the clipboard. **If you paste the text into a word processing program, you should format the text using a `Courier` (fixed width) font** so the text is lined up properly. Clicking on the **Print** button (or pressing Alt-P) will bring up a print preview of the results. Clicking the **Save** button brings up a file save dialog for the text of the current Results page.

Basic

The variables used in the function are indicated at the top of the result screen. Not all groups have every measurement recorded. Any removed measurements based on groups selected are listed in results under "Variables removed:".

Group Means

In all analyses, measurements from the current case and the mean measurements for each reference group are shown at the top of the basic results page. Pay attention to the **Chk** column. This column indicates deviations from the group means, indicated by a plus (+) or minus (-) sign. If the unknown's measurement is simply lower than all group means, there will be a single symbol indicating whether it is lower (-) or higher (+). If the unknown's measurement deviates by one to two standard deviations (using the pooled VCVM) from all groups, it will show two symbols. If the unknown's measurement deviates by two to three standard deviations from all groups it will show three symbols, and if it deviates by at least three standard deviations from all groups it will show four symbols. **Values at least 2 standard deviations from all groups will be in bold text in blue if very high, and in red if very low.** These indicators may be measurement or data entry errors, or they may merely represent shape differences in the unknown individual. These shape differences may be due to disease or pathological changes. A mixture of pluses and minuses, especially large differences, indicates major shape differences compared to the groups chosen. The unknown may belong to a different group.

The significance of the Mahalanobis distance is also shown in a two-group analysis. As a general rule, a significance figure greater than 0.05 indicates that the measurements do not separate the groups well and the classification is likely unreliable. Non-significant separation is more often encountered when using custom data sets that have small sample sizes. The classification percentage correct will also be relatively low in most of these cases, another indicator that the classification is not reliable.

The natural log of the determinant of the variance-covariance matrix (VCVM) is also shown. In general, it should be a positive number. It indicates the amount of information in the VCVM compared to the sample sizes of each group.

Classification Table

The classification table or matrix shows how the reference groups were assigned among themselves using the variables selected as well as the correct classification percentages and overall percentage correct. With more groups selected, correct classification rates can be expected to decline. The **Total Counts** for each reference group are indicated as well, and is an important piece of information. **Generally, the more measurements selected, especially the blue-colored measurements, the smaller the reference groups become.** A discriminant function based on a small reference group will not be as reliable as indicated over the long run.

Classification of the Unknown

The group labels are printed in the left hand column and the group that FORDISC classifies the unknown into is indicated by asterisks. The Mahalanobis Distance{linkID=maldistance}, or D-square, from the unknown to each reference group is also shown, along with the posterior and typicality probabilities. The reference groups can be sorted by name or by D-square to the unknown on the options page under **Sort Groups**.

Posterior probabilities evaluate the probability that the unknown individual comes from each reference group under the assumption that the unknown actually does belong to one of the groups in the function (Tatsuoka 1971, p. 228 230). Thus, the sum of the posterior probabilities equals 1. Posterior probabilities can vary a great deal depending on which groups are part of an analysis. Posterior probabilities are related to the confidence that can be placed in the classification. A high posterior probability (> 0.9)

indicates the individual is much more similar to that group than to any other and hence is more likely to be correct than a low posterior probability (<0.7). If posterior probabilities are spread out more or less evenly among the chosen groups, less confidence can be placed in the classification (but also see typicality probabilities below).

Typicality probabilities represent how likely the unknown belongs to each group, based on the distances to each group and the average variability of all the groups in the analysis. They may indicate that an unknown could belong to several reference groups, or none of the reference groups in the analysis (Tatsuoka 1971, pp. 218-222; Van Vark and Schaafsma 1992, pp. 245-246). Because the typicality probabilities are based on the pooled variance-covariance matrix, which is based on which reference groups and measurements are selected, ***typicality probabilities for an unknown can vary for the same group among analyses involving different combinations of groups.*** But typicality probabilities should in general be less variable than posterior probabilities.

Fordisc provides three typicality probabilities: **Typ F** gives the probability based on the F distribution; **Typ Chi** gives the probability based on the Chi-square distribution; and **Typ R** provides the ranked probability. Each calculation has advantages and disadvantages depending on the number of variables used, the number of groups involved, and the sample size of each group. **Typ F** takes into account the Mahalanobis distance and sample size; Typ Chi is based on the Mahalanobis distance alone; and **Typ R** is based on ranking the Mahalanobis distance of the unknown compared to the reference group. **Typ R** evaluates the rank of the unknown (in parentheses) as if it were a member of each sample. All three are important in evaluating an unknown, depending on the number of measurements used, group sample sizes, and the individual being analyzed. In our experience, **Typ F** tends to indicate fewer unknowns as atypical, while **Typ Chi** tends to indicate more unknowns as atypical. **Typ R** provides an estimate with fewer statistical assumptions, but a small sample size will produce an unusual **Typ R**.

From our experience, typicality probabilities are often misunderstood. They are analogous to the univariate *p* value, usually based on the *Z* score, or difference in standard deviation units, from an individual to the group mean. **The typicality probability can be thought of as the probability of the null hypothesis that the individual comes from a particular group. In general, typicality probabilities above 0.05 can be ignored, because we do not have statistical grounds to reject the null hypothesis.** Typicality probabilities below 0.01 for all groups generally indicate that the individual has some measurements in error, does not belong to any of the groups, or has been distorted due to disease, trauma, deformation, or postmortem taphonomic processes. The typicality probabilities are very important in evaluating the "fit" of an individual to a classification, so special attention to low values is necessary. To aid in recognizing important values, **typicality probabilities between 0.05 and 0.01 are in bold text, and typicality probabilities below 0.01 are indicated in red.** ***When all typicality probabilities are very low, the posterior probabilities, and thus the most similar (classified) group indicated should be ignored. The classification cannot be trusted.*** Run again using fewer measurements; you may want to consider using stepwise selection of measurements.

In a two-group analysis, the **DF (discriminant function) weights** are also shown for each variable. Multiplying each measurement from the unknown by its DF weight and adding the constant gives the DF score for the unknown. The mean score for each reference group (Class means) is also indicated. The **Relative Weight** of each variable helps identify the relative discriminating power of each variable in a D.F between two groups, expressed as a percentage. The sum of the relative weights equals 100%. The relative weight for each measurement is calculated as the absolute value of the difference in group means times the DF weight divided by the sum of all such products, which is the Mahalanobis distance. High relative DF weights generally indicate very useful measurements in DFA. **Generally, measurements with low relative weights in a two group D.F. can be eliminated without loss in classification accuracy. In fact, classification accuracy often increases.** The relationships between measurements can be complex, however, and "hidden" contributions from some measurements are likely. **Also, using fewer measurements usually increases reference group sample sizes.** However, measurement errors may be compounded if they are present in the fewer measurements that are used.

Extended Results

The *Extended Results* page has many statistical results if *Extended Results* is selected (the default) on the Options page: Group means and standard deviations, the pooled within-group VCVM and its determinant, pooled within-group correlation matrix, a test for the homogeneity of VCVMs, mean canonical axis scores for each group, discriminant (if a two-way classification) or canonical (if more than two-way

classification) structure coefficients, eigenvalues and percentage of total variation, Mahalanobis D-square matrix, significance matrix of D-squares, and the D-square, posterior probability, and typicality probabilities of the unknown to each reference group in the analysis are shown.

Under *Classification Table*, if the *Extra Statistics* box is checked (the default), additional classification statistics are then shown, such as sensitivity, specificity, positive predictive value, negative predictive value, prevalence, detection rate, detection prevalence, balanced accuracy, and Cohen's kappa. Some information is provided below, but far more can be learned by consulting publications such as Klepinger and Giles (1998) or Kuhn and Johnson (2013), the R caret package pdf found at: https://cran.r-project.org/web/packages/caret/caret.pdf, and Wikipedia pages associated with the topics. These measures are especially valuable when classifying into groups with very different sample sizes.

Sensitivity is the proportion of individuals correctly classified into the group divided by the total number from the group. This is the "accuracy" that is most often used.

Specificity is the proportion of individuals correctly classified into other groups divided by the total number of individuals from other groups.

Positive Predictive Value is the proportion of individuals correctly classified into the group divided by the total number of individuals classified into the group.

Negative Predictive Value is the proportion of individuals correctly classified into other groups divided by the total number of individuals classified into other groups.

Prevalence is the proportion of individuals from a group divided by the total sample size.

Detection Rate is the proportion of individuals correctly classified into the group divided by the total sample size.

Detection Prevalence is the proportion of all individuals classified into the group divided by the total sample size.

Balanced Accuracy is (Sensitivity + Specificity) / 2. The balanced accuracy is given for each group as well as the mean balanced accuracy.

Cohen's Kappa (Cohen 1960) is a measure of classification performance that takes into account the probability of randomly classifying correctly (the prevalence of each group). For instance, 50% accuracy in a 5-way DFA with equal sample sizes is far better than chance but 50% accuracy is not better than chance in a 2-way DFA. Cohen's kappa comes from studies of interrater agreement. Cohen's kappa for each group are provided as well as the mean Cohen's kappa. General guidelines for interpreting kappa are as follows:

Kappa	Classification performance
0.00 - 0.20	poor
0.20 - 0.40	fair
0.40 - 0.60	moderate
0.60 - 0.80	good
0.80 - 1.00	very good

No Information Rate is the prevalence of the largest group. It is the accuracy you get from calling every member in the sample the most common group. This is especially important when group sample sizes are imbalanced.

By default, outliers with the highest typicality probability to any group less than 0.005 are listed at the bottom of the Extended Results page.

On the options page, if *Individual Scores* is selected, the classification results of each individual in the reference groups are shown, including the individual IDs, the group classified into, and the D-square, posterior probability, and typicality probabilities to each group. Misclassified individuals in the reference samples are designated by an asterisk (*). **NOTE:** If LOO cross-validation was selected, the individual values are jackknifed values, which are much more reliable for detecting outliers because each individual was

excluded from the calculation of the group parameters (Penny 1996). Notation is provided for reference group outliers, whether they were correctly classified (++, +++, and ++++) or incorrectly classified (**,***, or ****), with associated p values < 0.05, 0.01, and 0.005. Whether reference individuals are classified or not, having extreme outliers (**** or ++++) should be removed and the data should be reanalyzed. You can exclude individuals used in an a analysis by typing the ID, one ID per line, into the text box under the *Exclude IDs (one per line):* heading. The excluded individuals will be listed on the Basic Results page.

Commands

Copy [Alt + C]

This selection copies the current text results to the Windows paste buffer. You can then switch to another application and paste the text into a file by pressing [CTL + V] or choosing Paste from a menu selection. Printing text directly is supported but if you want to have all results from analyses involving many groups or many variables you can copy and then paste the text into a word processing program and select a small Courier font (or another fixed-width font) and it will be correctly lined up and may fit within the printed page, as in the results window. Pasting into a spreadsheet is another convenient way of saving especially wide results because spreadsheets have additional printing options. **You can also copy any portion of the text results by selecting it with the mouse and pressing [CTL + C].**

Print [Alt + P]

This selection sends formatted text to the printer depending on which results window is showing. The print format depends on the number of groups in the analysis. For fewer than 9 groups, the output will be in portrait layout and have all results output. For 9 to 12 groups, the format will be landscape. For more than 12 groups, the layout will be portrait but only the variable list, percentage correct, and classification probabilities for all groups will be printed.

Save [Alt + S]

This selection saves the current result sheet to a Rich Text (*.rtf) file (default) or plain text file (*.txt). Rich Text files retain text formatting information and can be read by a large number of programs. The default directory is \Results\.

Internet

If you experience problems with Fordisc, check the Fordisc web page for the latest solutions: http://statsmachine.net/software/Fordisc

Submit case to the FDB

This selection will Email FDB craniometric data from the current case to the FDB for inclusion. Be sure to save your file before submitting your case. After filling out a case submission form with additional information, an Email message will be started using your default Email application. The Email message will contain information on the identified remains and case notes and any comments entered. You can edit and enter additional comments in the Email message itself. Please attach any electronic files that contain important information if you wish. The data from the case file including metrics will be sent in a text file using ftp (file transfer protocol). You will see a confirmatory message if the case information transmission was successful.

Check for Program Updates

You can update Fordisc 3 through an Internet connection. As of build 281, Fordisc uses an improved method of retrieving files that should bypass institutional firewalls. Check any firewall or security settings on your PC if you cannot make a connection. Fordisc checks for updates to the program itself, the reference database files, and the help files. **NOTE: It may take up to 30 seconds to determine that a connection is not working.** After 30 seconds, the update attempt will stop. Please be sure that you are connected to the Internet before attempting to update files. One way to make sure of this is to have a web browser open.

NOTE: You may need administrative rights under Windows to update Fordisc.

Vista, Windows 7,8, and 10 users should run Fordisc 3 as an Administrator. To do so, locate Fordisc 3 on the Start menu, or find the FD3.exe file on your computer. Right-click the application menu item or file, and then click Properties. In the Properties dialog box, click the Compatibility tab. Then do one of the following:

1) To apply the setting to the currently logged-on user, select the *Run This Program As An Administrator* check box, and then click OK.

2) To apply the setting to all users on the computer and regardless of which shortcut is used to start the application, click *Change Setting For All Users* to display the Properties dialog box for the application's .exe file, select the *Run This Program As An Administrator* check box, and then click OK twice.

For Windows XP/Vista/Windows 7 users, the Windows Firewall may be blocking attempts to install or update Fordisc 3. For security reasons, Windows firewall blocks incoming network connections to most programs except those included in an exception list. You will need to add Fordisc to the exception list to be able to install and update Fordisc. To add Fordisc to the exception list,choose Control Panel | Security Center | Windows Firewall, then click the "Exceptions" tab. Click the "Add Program" button and then the Browse button to add C:\Program Files\Fordisc3\FD3.exe (the default installation location) to the list as well.

NOTE: The Windows Firewall should be set to notify you when a program tries to communicate through the Internet. On the Exceptions tab, it is recommended that you make sure

"Display a notification when Windows Firewall blocks a program" is checked. However, feedback from Windows about firewall activities seems to be inconsistent. Each time Fordisc is updated, you may need to approve internet access for the new program to check for updates. With each build, we try to improve the method for updating using an Internet connection, so this may not always be necessary.

Visit Fordisc Support Website

Clicking this should open your browser and send it to http://statsmachine.net/software/Fordisc/.

Email Fordisc support

Choosing this selection will bring up your default Email program and fill in the address so you can send questions, comments, or general feedback. **The further development of Fordisc depends on your feedback** on how we can make the program provide more and better information to aid you in analyzing remains. **You can also send an Email to** fordisc-support@roadrunner.com **.**

Automatic Updates

You can have Fordisc check for updates every 15 or 30 days. The default is every 15 days.

Forced Update

This selection can be used when the Fordisc files have somehow become corrupted or unsynchronized, or a recent update was not successful. You may be advised to select this in an Email from Fordisc Support. The forced update will begin automatically after an internet connection is detected.

Review/Update Registration

Please update your contact information if it is out of date! With this build, you can update your contact information. We will use this information only to inform you of important Fordisc-related matters and will not share it with anyone else.

Some Words of Caution

Discriminant analysis has become a fact of life in biological anthropology in general and forensic anthropology in particular. Consequently, most forensic anthropologists are familiar with its limitations as well as its capabilities. Nevertheless, it may be well to emphasize some of the limitations placed on users of the software. These might best be illustrated by situations that might arise while using FORDISC:

1. **Classification of an individual whose race or ethnic group is not represented in the reference samples.** Every function will classify an unknown into one of the reference groups, regardless of what its actual ethnic group or sex may be. For example, an Asian Indian cranium will be closest to one of the FORDISC groups. The typicality probabilities may provide some guidance here, but are by no means foolproof, since the variation within groups produces some overlap between groups.

2. **Classification using hybrid groups.** Genetic exchange among the various populations of *Homo sapiens* means that there will always be overlaps in distributions, resulting in some degree of misclassification. American Blacks and Hispanics are known to incorporate genes from at least two ancestral populations. One can observe that in most analyses involving all groups, Hispanics assume a central position. This in turn means that **misclassifications from all other groups may more often classify as Hispanic. In fact, experience has shown this to be true (Jantz).**

3. **Classification of hybrid individuals.** Here it should be emphasized that FORDISC can only return answers based on metric information, but the questions are often phrased in social terms. The progeny of a Black-White couple may have been known socially as Black, but may possess more genes from White than Black sources. Similarly, someone known in life as Hispanic may have all or nearly all of his/her genes from Native American sources. Because a person's social race is not based on objective metric criteria, metric traits are an imperfect method for assessing probable social race.

4. **Aberrant values affected by disease, disuse, treatment, or trauma.** Various measurements affected by such conditions as an edentulous maxilla or mandible, hydrocephaly, scaphocephaly, fractured or distorted bones, dysmorphic syndromes, reconstructive surgery, etc. cannot be expected to reflect the population affinities of the individual (Mulhern et al. 2000). We have included rudimentary error trapping routines to identify obvious outliers and typographical errors. However, an individual may still possess one or more unusual values that can have a drastic effect on results. **We strongly recommend that the unknown's values be compared to the reference group means to identify values that may have drastically affected the classification.** If such values are found, running again without the aberrant value is recommended.

5. **Classification of non-adults.** FORDISC should be used ideally on individuals at least 18 years old. However, examination of some subadults as young as 14 or 15 seem to classify as expected (Jantz). In fact, infants and children from different continents appear to show differences (Buck and Vidarsdottir 2004; Vidarsdottir 2003), but these differences do not necessarily correspond to adult differences.

6. **Classification of archaeological populations.** Due to population differences and secular changes, data from the **FDB** is only appropriate for the analysis of individuals born in the 20th century. The Howells populations may be more appropriate for older specimens. Analyzing remains from the 19th century is aided by the addition of 19th century American Whites and Blacks, but comparing earlier American groups, such as from the 17th century (Williams et al. 2001), to 20th century Americans should probably be avoided.

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Cranial Measurements

FORENSIC DATABANK MEASUREMENTS

Click on the abbreviation below to see the measurement definition and illustration.

Special thanks go to Kaitlyn Sanders for her help with photography.

Maximum Cranial Length **(GOL)**
Nasal Height **(NLH)**
Maximum Cranial Breadth **(XCB)**
Nasal Breadth **(NLB)**
Bizygomatic Breadth **(ZYB)**
Orbital Breadth **(OBB)**
Basion-Bregma Height **(BBH)**
Orbital Height **(OBH)**
Cranial Base Length **(BNL)**
Biorbital Breadth **(EKB)**
Basion-Prosthion Length **(BPL)**
Interorbital Breadth **(DKB)**
Max. Alveolar Breadth **(MAB)**
Frontal Chord **(FRC)**
Max. Alveolar Length **(MAL)**
Parietal Chord **(PAC)**
Biauricular Breadth **(AUB)**
Occipital Chord **(OCC)**
Upper Facial Height **(UFHT)**
Foramen Magnum Length **(FOL)**
Minimum Frontal Breadth **(WFB)**
Foramen Magnum Breadth **(FOB)**
Upper Facial Breadth **(UFBR)**
Mastoid Height **(MDH)**
Biasterionic Breadth **(ASB)**
Midorbital Width **(MOW)**
Zygomaxillary Breadth **(ZMB)**

Landmarks with images:

AsterionBasion
Bregma
Dacryon
Ectoconchion
GlabellaLambda
Prosthion
Radiculare
Zygoorbitale

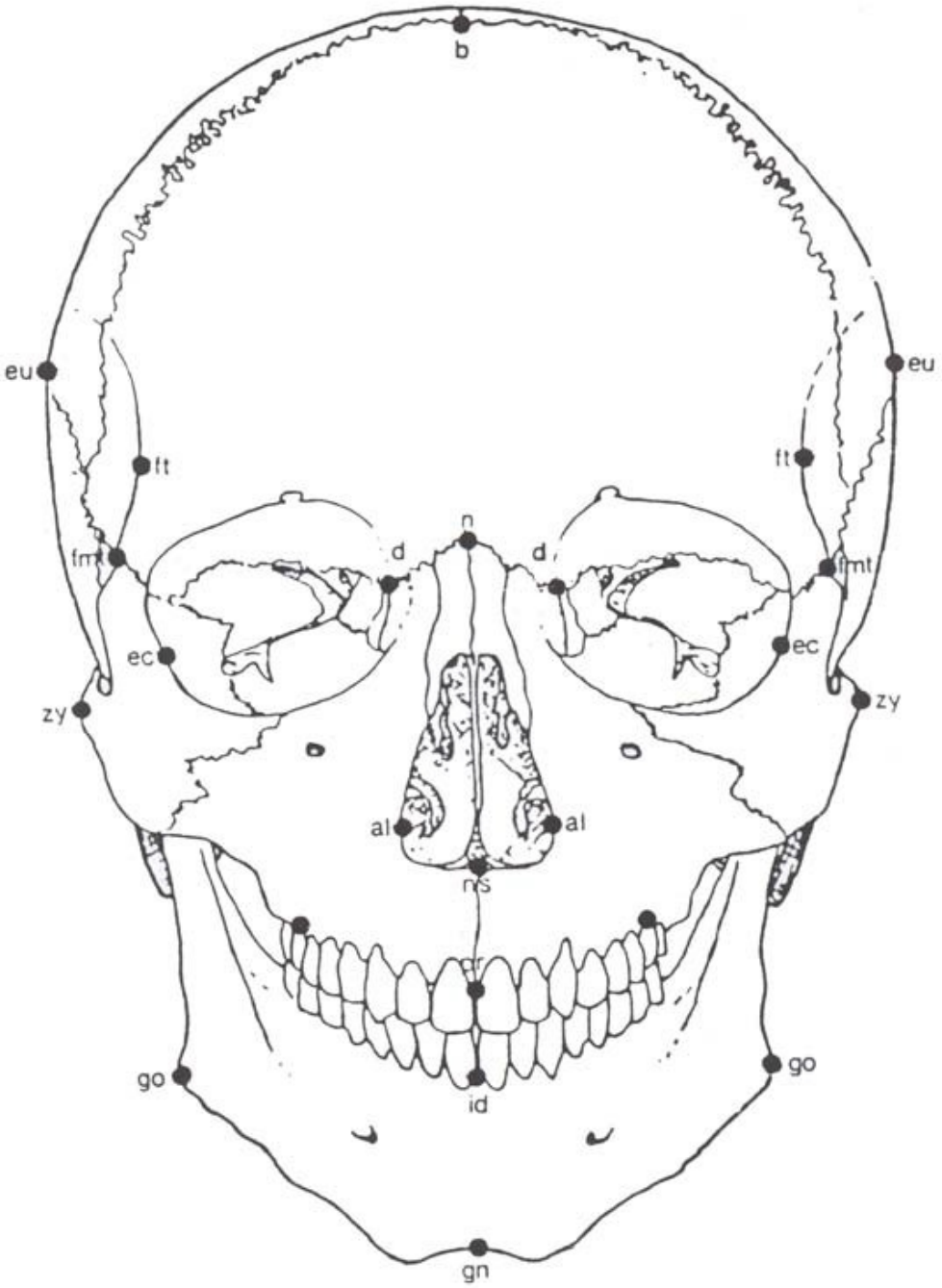
HOWELLS (1973) MEASUREMENTS

Measurement	Abbrev	Reference
1 Glabello-occipital length	GOL	H:170-71
34 Malar length maximum	XML	H:180
2 Nasio-occipital length	NOL	H:171
35 Malar subtense	MLS	H:180
3 Basion-nasion length	BNL	H:171-72
36 Cheek height, minimum	WMH	H:180
4 Basion-bregma height	BBH	H:172
37 Supraorbital projection	SOS	H:180
5 Maximum cranial breadth	XCB	H:172
38 Glabella projection	GLS	H:181
6 Maximum frontal breadth	XFB	H:172
39 Bistephanic breadth	STB	H:173
7 Minimum frontal breadth	WFB	M # 9
40 Stephanic subtense	STS	Key 1983:140
8 Bizygomatic breadth	ZYB	H:173
41 Frontal chord	FRC	H:181
9 Biauricular breadth	AUB	H:173
42 Frontal subtense	FRS	H:181
10 Minimum cranial breadth	WCB	H:173-74
43 Frontal fraction	FRF	H:181-82
11 Biasterionic breadth	ASB	H:174
44 Parietal chord	PAC	H:182
12 Basion-prosthion length	BPL	H:174
45 Parietal subtense	PAS	H:182
13 Nasion-prosthion height	NPH	H:174
46 Parietal fraction	PAF	H:182
14 Nasal height	NLH	H:175
47 Occipital chord	OCC	H:182
15 Bijugal breadth	JUB	H:175-76
48 Occipital subtense	OCS	H:182-83
16 Nasal breadth	NLB	H:176
49 Occipital fraction	OCF	H:183
17 External palate breadth	MAB	H:176
50 Foramen magnum length	FOL	H:181
18 External palate length	MAL	M # 60
51 Foramen magnum breadth	FOB	M # 16
19 Mastoid height	MDH	H:176-77
52 Nasion radius	NAR	H:183
20 Mastoid width	MDB	H:177
53 Subspinale radius	SSR	H:183
21 Orbit height	OBH	H:175
54 Prosthion radius	PRR	H:183
22 Orbit breadth	OBB	H:175
55 Dacryon radius	DKR	H:183
23 Interorbital breadth	DKB	H:178
56 Zygoorbitale radius	ZOR	H:183
24 Naso-dacryal subtense	NDS	H:178-79
57 Frontomalare radius	FMR	H:183
25 Simotic chord	WNB	H:179
58 Ectoconchion radius	EKR	H:184
26 Simotic subtense	SIS	H:179
59 Zygomaxillare radius	ZMR	H:184
27 Bimaxillary breadth	ZMB	H:177
60 Molar 1 Alveolus radius	AVR	H:184
28 Zygomaxillary subtense	SSS	H:177
61 Bregma radius	BRR	Key 1983:140
29 Bifrontal breadth	FMB	H:177-78
62 Vertex radius	VRR	H:183
30 Nasio-frontal subtense	NAS	H:178
63 Lambda radius	LAR	Key 1983:140

31 Biorbital breadth		EKB	H:178
64 Opisthion radius	OSR	Key 1983:140	
32 Dacryon subtense		DKS	H:178
65 Basion radius	BAR	Key 1983:140	
33 Malar length inferior		IML	H:179-80

H: refers to Howells (1973)
M: refers to Rudolf Martin (1928) measurements in Martin and Knussmann (1988)

Illustrated landmarks from Moore-Jansen et al.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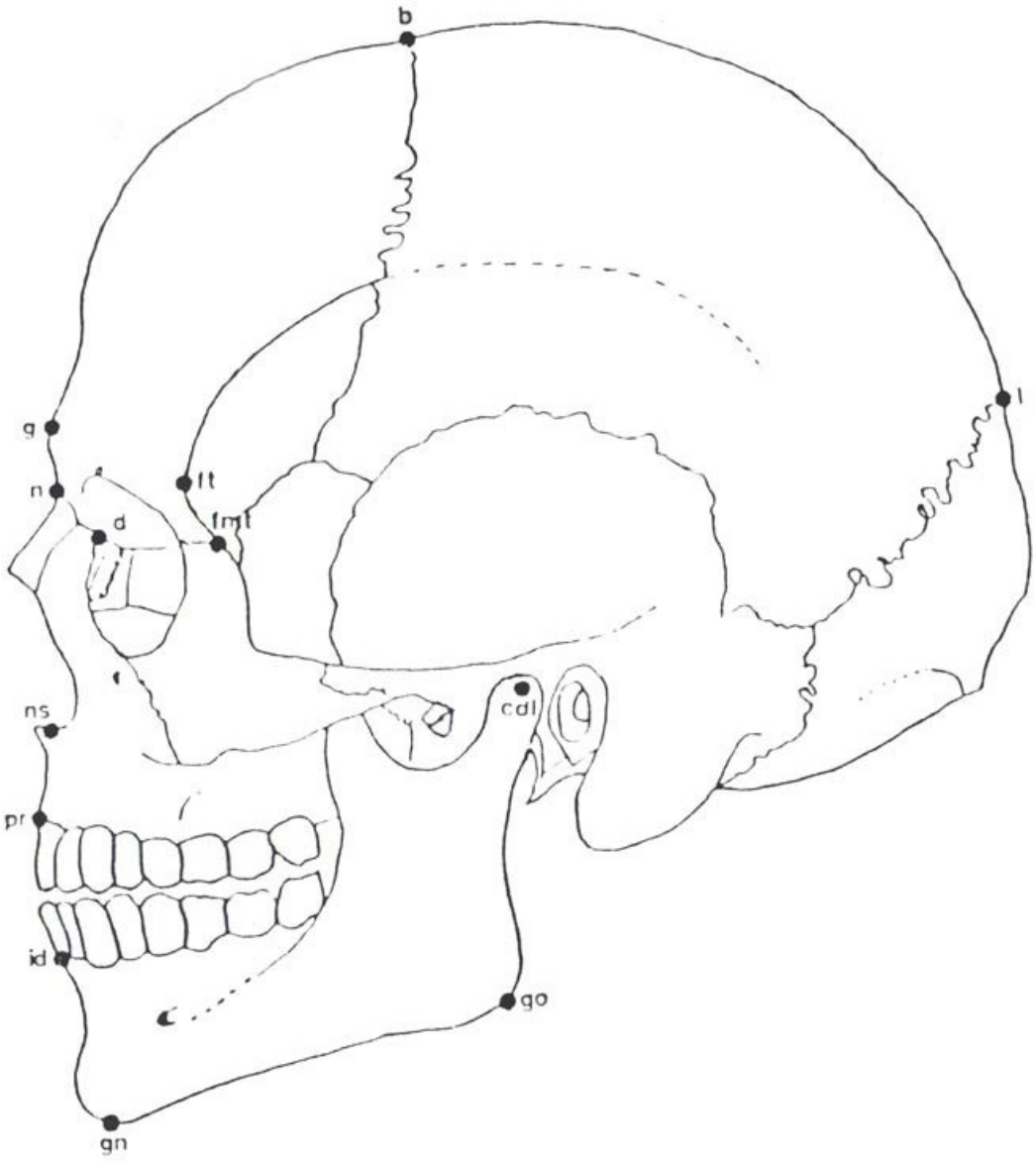
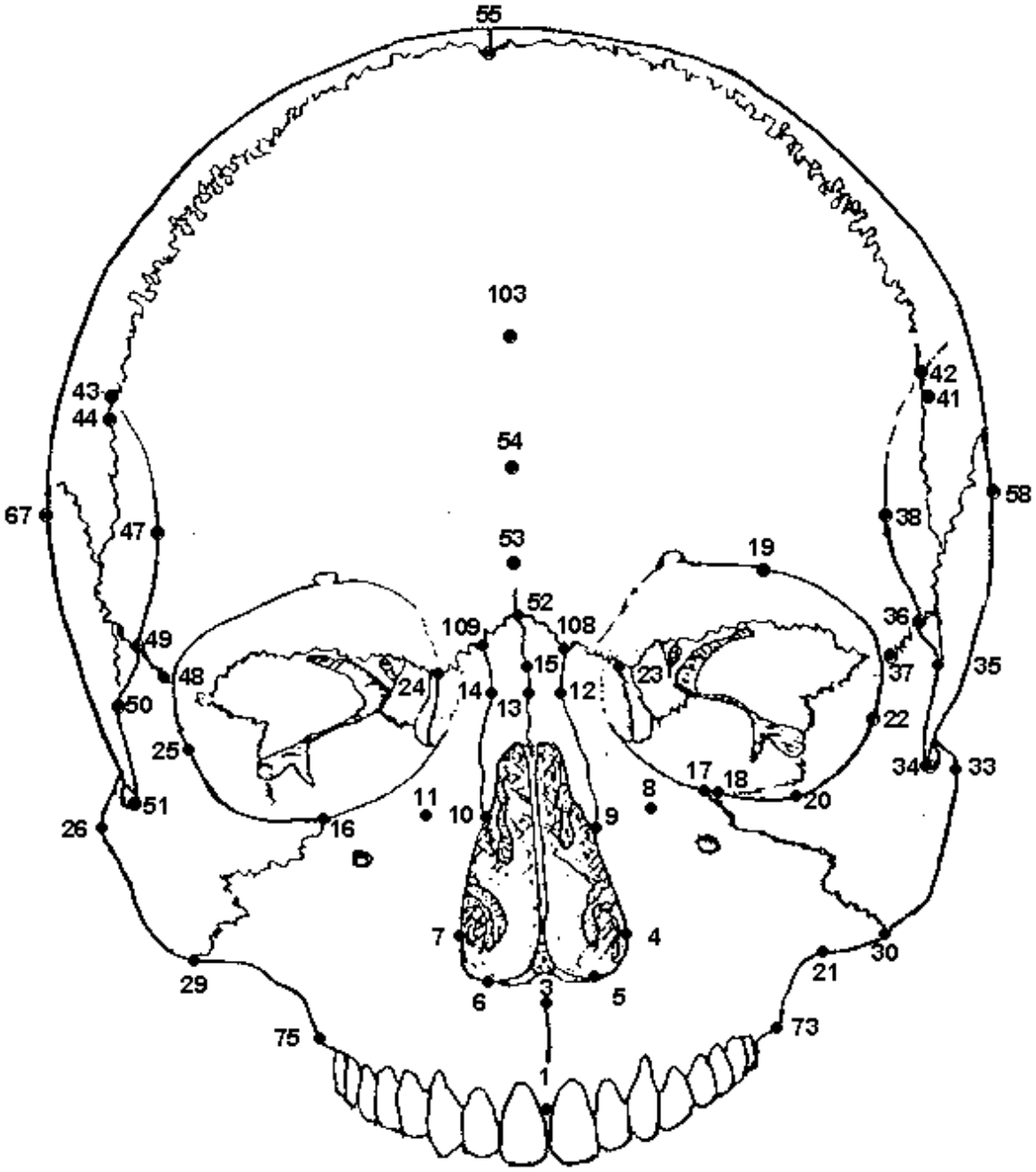


Illustrated landmarks from Ousley and McKeown (2001)

Anterior Cranial Landmarks

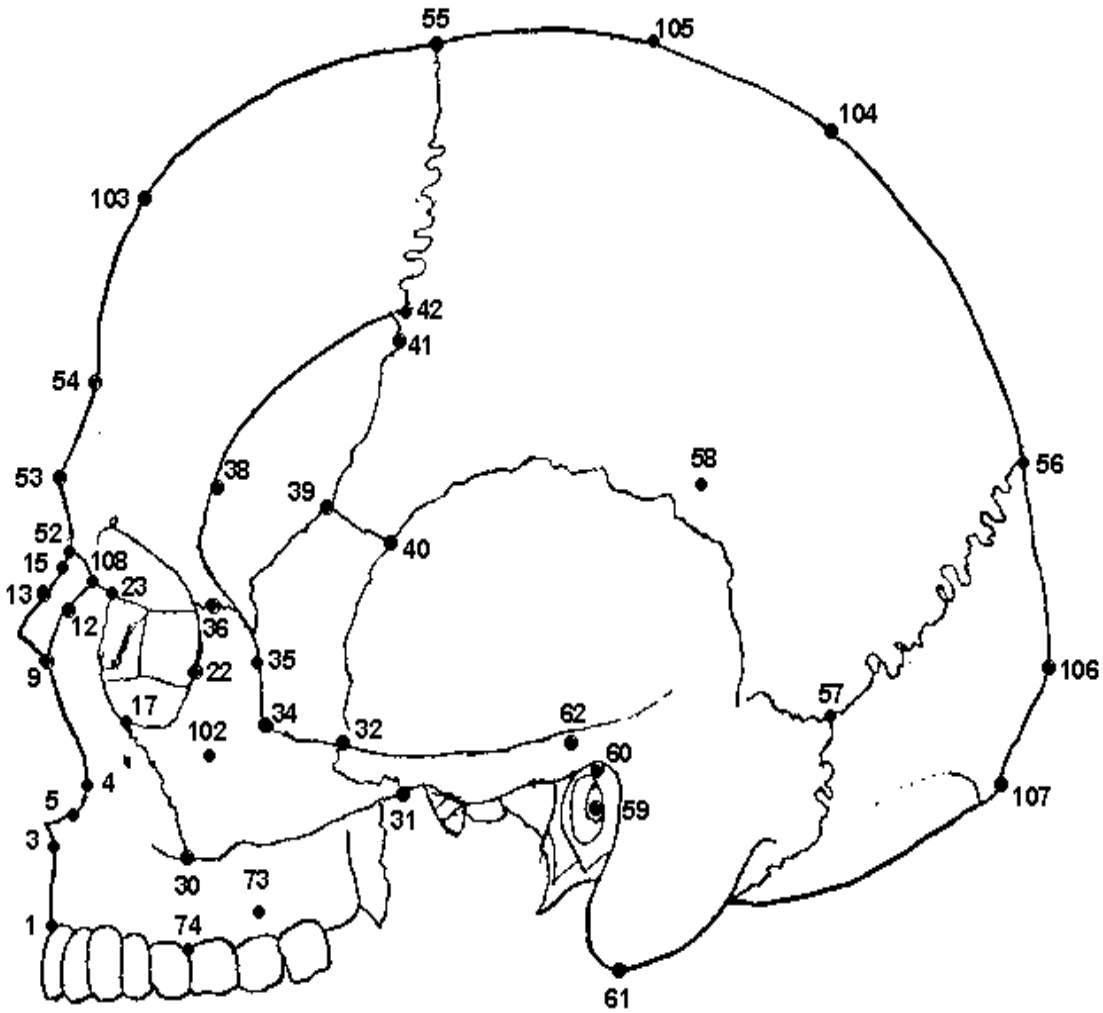


Index	Landmark	Associated Measurement
1	prosthion	BPL, NPH
3	subspinale	SSR, SSS
4	alare L	NLB
5	most inferior nasal border L	NLH
6	most inferior nasal border R	NLH
7	alare R	NLB
9	nasale inferius L	
10	nasale inferius R	
12	nasomaxillary suture pinch L	WNB
13	nasal bone elevation	SIS, SIA
14	nasomaxillary suture pinch R	WNB

15	deepest point on nasal bone profile	NDS, NDA
16	zygoorbitale R	MOW, IML, XML
17	zygoorbitale L	MOW, IML, XML
18	lower orbital border L/R	OBH (inferior point)
19	upper orbital border L/R	OBH (superior point)
20	cheek height sup point L/R	WMH
21	cheek height inf point L/R	WMH
22	ectoconchion L	OBB, EKB
23	dacryon L	OBB, DKB
24	dacryon R	DKB
25	ectoconchion R	EKB
26	zygion R	ZYB
29	zygomaxillare R	ZMB
30	zygomaxillare L	ZMB, IML
33	zygion L	ZYB
34	jugale L	JUB
36	frontomalare temporale L	Upper facial breadth (UFBR)
37	frontomalare anterior L	FMB, NAS
38	frontotemporale L	WFB
39	sphenion L	-
40	krotaphion L	-
41	Maximum frontal point L	XFB
42	stephanion L	STB, STS
43	stephanion R	STB, STS
44	Maximum frontal point R	XFB
47	frontotemporale R	WFB
48	frontomalare anterior R	FMB, NAS
49	frontomalare temporale R	UFBR
51	jugale R	JUB
52	nasion	NOL, NLH, NAS, etc.
53	glabella	GOL
54	supraglabellare	GLS
55	bregma	FRC, PAC, BBH, etc.
56	lambda	PAC, OCC
57	asterion L	ASB
58	eurion L	XCB
59	radiometer point L	radii (NAR, BRR, etc.)
60	porion L	MDH
61	mastoideale L	MDH
62	radiculare L	AUB
63	radiculare R	AUB
64	radiometer point R	radii (NAR, BRR, etc.)
65	porion R	MDH
66	mastoideale R	MDH
67	eurion R	XCB
68	asterion R	ASB
69	opisthion	FOL
70	basion	BBH, BNL, etc.
71	FOB point R	FOB
72	FOB point L	FOB
73	ectomolare L	MAB
74	M1 anterior point L	AVR
75	ectomolare R	MAB
76	hormion	
77	alveolon (use rubber band)	MAL
78	staurion	
79	pogonion (vertical projection)	XRL
80	gnathion	GNI
81	infradentale	GNI
82	HMF inferior point	HMF
83	HMF superior point	HMF
84	TMF buccal point	TMF

85	TMF lingual point	TMF
86	gonion L	GOG
88	coronion L	
89	condylion laterale L	bicondylar breadth
96	condylion laterale R	bicondylar breadth
97	coronion R	
99	gonion R	GOG
100	WRB posterior point	WRB
101	WRB anterior point	WRB
102	max malar projection point L/R	MLS
103	metopion	FRF, FRS
104	parietal subtense point	PAF, PAS
105	vertex radius point	VRR
106	opisthocranion (use instrument)	GOL
107	occipital subtense point	OCF, OCS
108	nasale superius L	
109	nasale superius R	

Lateral Cranial Landmarks



Mandibular Measurements

Click on the abbreviation to read the measurement definition and see a measurement illustration.

GNI

at Mental Foramen - HMF

Thickness at Mental Foramen - TMF

Breadth - GOG

Breadth - CDL

Ramus Breadth -WRB

Length - MLN

Ramus Height - XRH

Angle - MAN

25. Chin Height -

26. Body Height

27. Body

28. Bigonial

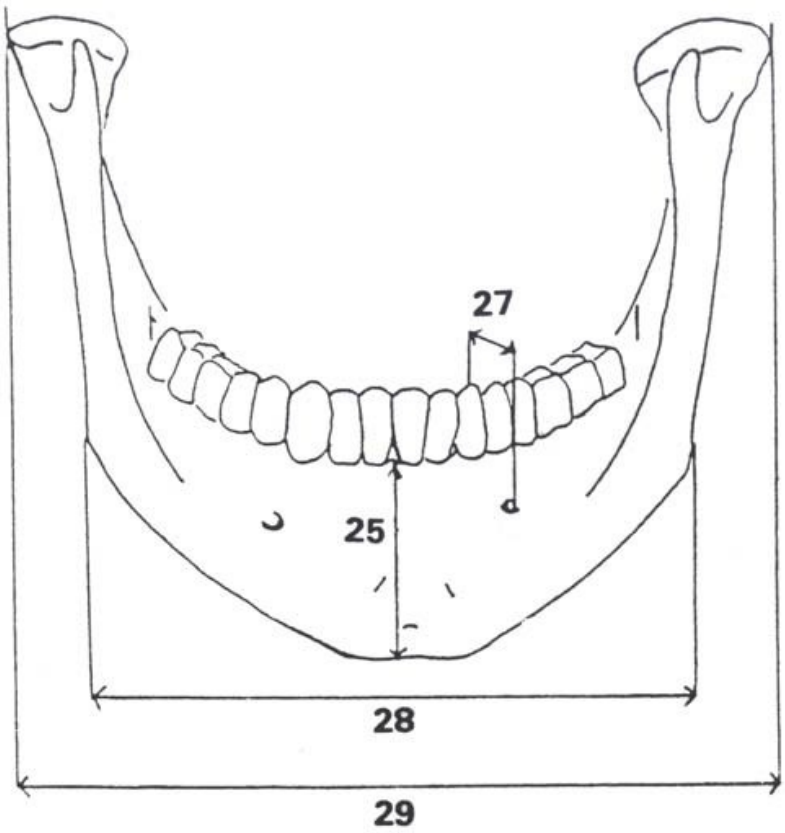
29. Bicondylar

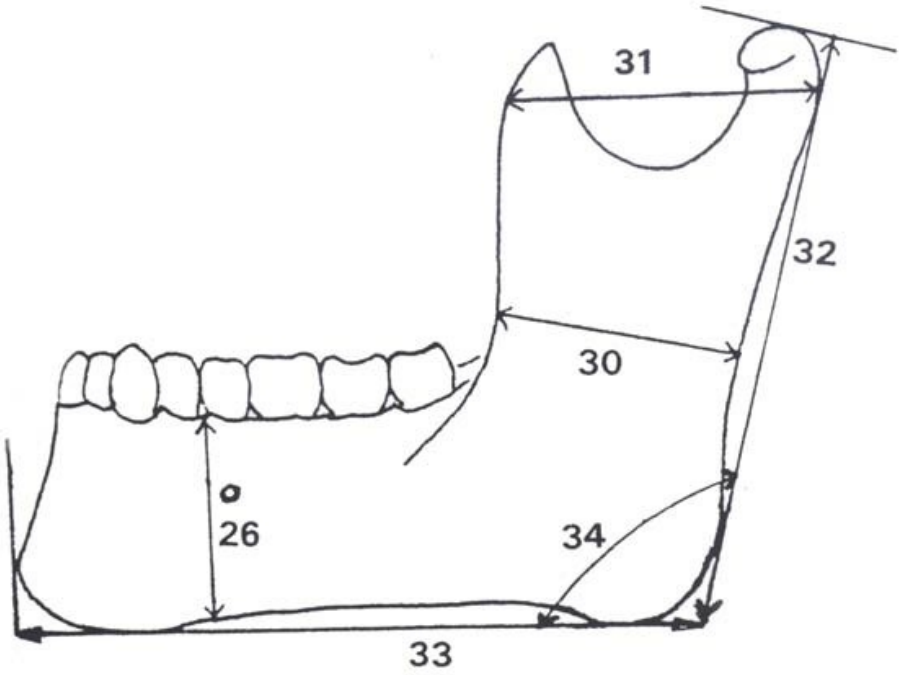
30. Minimum

33. Mandibular

32. Maximum

34. Mandibular

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Postcranial Measurements

These numbers refer to the older FDB measurement numbers and will not agree with the numbers on the most recent version of the FDB data forms. The measurements and the FDB data manual are being revised.

Clavicle

Innominate

35. Maximum Length of Clavicle

56. Innominate Height

36. Anterio-Posterior Diameter at Midshaft

57. Iliac Breadth

37. Vertical Diameter at Midshaft

58. Pubis Length

59. Ischium Length

Scapula

38. Height of Scapula

Femur

39. Breadth of Scapula

60. Maximum Length of Femur

61. Bicondylar Length of Femur

Humerus

62. Epicondylar Breadth of Femur

40. Maximum Length of Humerus

63. Maximum Diameter of Femur Head

41. Epicondylar Breadth of Humerus

64. Anterio-Posterior Subtrochanteric Diameter

42. Maximum Vertical Diameter of Head

65. Transverse Subtrochanteric Diameter

43. Maximum Diameter at Midshaft

66. Anterio-Posterior Diameter at Femur Midshaft

44. Minimum Diameter at Midshaft

67. Transverse Diameter at Femur Midshaft

68. Circumference at Midshaft

Radius

45. Maximum Length of Radius

Tibia

46. Anterio-Posterior Diameter at Midshaft

69. Condylo-Malleolar Length

47. Transverse Diameter at Midshaft

70. Maximum Proximal Epiphyseal Breadth

71. Distal Epiphyseal Breadth

Ulna

72. Maximum Diameter at Nutrient Foramen

48. Maximum Length of Ulna

73. Transverse Diameter at Nutrient Foramen

49. Dorso-Volar Diameter

74. Circumference at Nutrient Foramen

50. Transverse Diameter of Ulna

51. Physiological Length

Fibula

52. Minimum Circumference

75. Maximum Length of Fibula

76. Maximum Diameter at Fibula Midshaft

Sacrum

53. Anterior Height

Calcaneus

54. Anterior Surface Breadth

77. Maximum Length of Calcaneus

55. Transverse Breadth of S1

78. Middle Breadth

Clavicle

35. Clavicle: Maximum Length: maximum distance between the most extreme ends of the clavicle.

Instrument osteometric board (Figure 47).

36. Clavicle: Anterior-Posterior Diameter at Midshaft: distance from the anterior to the posterior surface at midshaft.

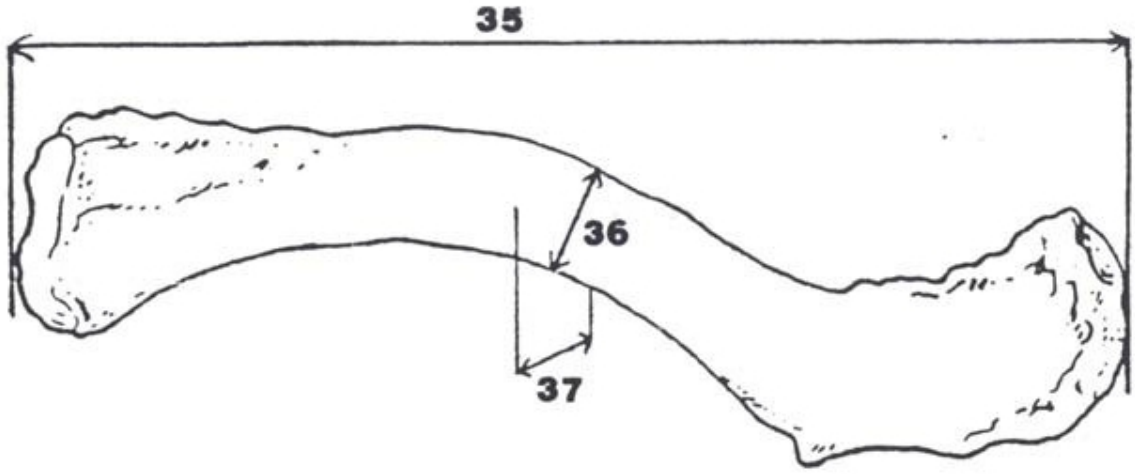
Instrument: sliding caliper

Comment: determine the midpoint of the diaphysis on the osteometric board and mark it with a pencil. Then determine sagittal diameter (Figure 47).

37. Clavicle: Superior-Inferior Diameter at Midshaft: distance from the superior to the inferior surface at midshaft.

Instrument: sliding caliper.

Comment: taken perpendicular to sagittal diameter (Figure 47).



Scapula

38. Height of the Scapula: The direct distance from the most superior point of the cranial angle to the most inferior point on the caudal angle (Figure 30).

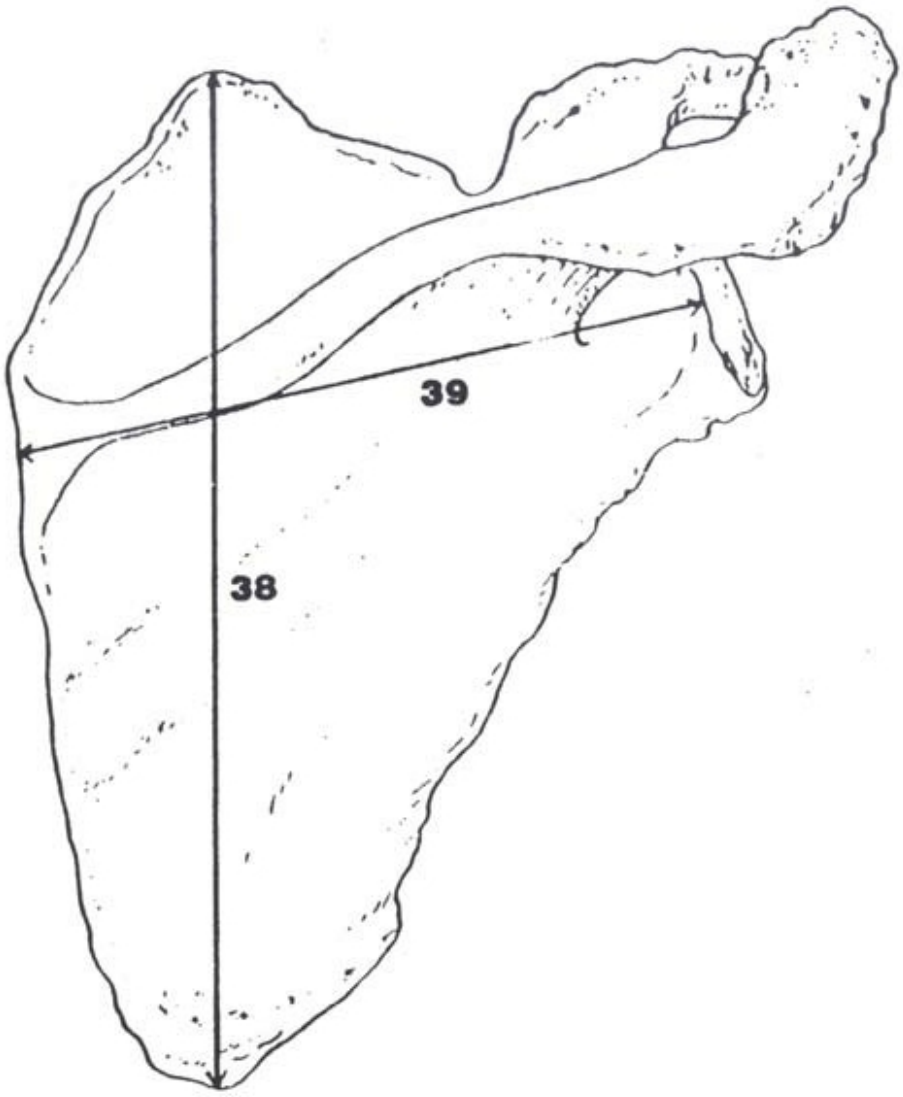
Instrument: sliding caliper

Comment: (Bass 1971 :94; Hrdlicka 1952: 170; Martin 1957:528 #I ; Montagu 1960:68; Olivier 1969:219).

39. Breadth of the Scapula: The distance from the midpoint on the dorsal border of the glenoid fossa to midway between the two ridges of the scapular spine on the vertebral border (Figure 30).

Instrument: spreading caliper

Comment: Project a line through the obtuse angle of a triangle formed by the vertebral border and the two ridges of the spine, dividing it into two equal halves. The medial measuring point is located where this line intersects the vertebral border (Bass 1971 :95; Hrdlicka 1952; Martin 1957:528 #2; Montagu 1960:70).



Humerus

40. Maximum Length of the Humerus: The direct distance from the most superior point on the head of the humerus to the most inferior point on the trochlea (Figure 31).

Instrument: osteometric board

Comment: Place the humerus on the osteometric board so that its long axis parallels the instrument. Place the head of the humerus against the vertical endboard and press the movable upright against the trochlea. Move the bone up, down and sideways to determine the maximum distance (Bass 1971 : 1 14; Hrdlicka 1952: 168; Martin 1957:532 #1; Olivier 1969:226).

41. Epicondylar Breadth of the Humerus: The distance of the most laterally protruding point on the lateral epicondyle from the corresponding projection of the medial epicondyle (Figure 31).

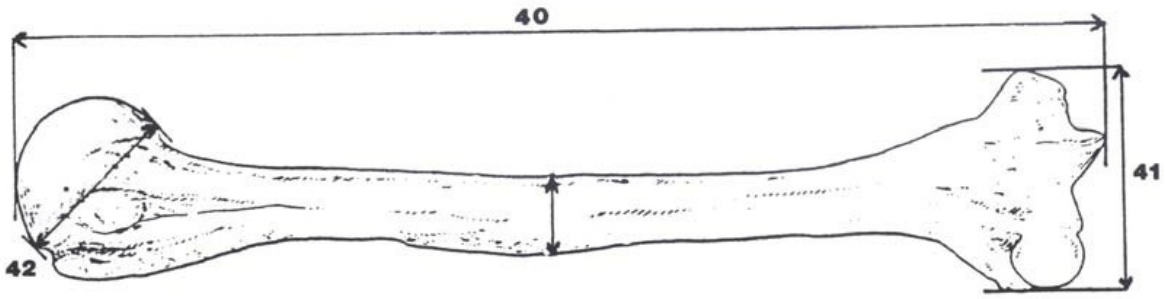
Instrument: osteometric board or sliding calipers

Comment: Place the bone with its posterior surface resting on the osteometric board. Place the medial epicondyle against the vertical endboard and apply the movable upright to the lateral epicondyle (Martin 1957:532 #4).

42. Maximum Vertical Diameter of the Head of the Humerus: The direct distance between the most superior and inferior points on the border of the articular surface (Figure 31).

Instrument: sliding caliper

Comment: Measure the vertical distance perpendicular to the transverse diameter of the head of the humerus. Do not include arthritic lipping which may be present on the perimeter of the joint surface. This diameter is not necessarily the maximum diameter overall (Martin 1957:533 #10).



43. Maximum Diameter of the Humerus at Midshaft: (Figure 31).

Instrument: sliding caliper

Comment: Determine the midpoint of the diaphysis on the osteometric board and mark with a pencil. Where the ends are broken off, the midpoint may frequently be approximated by visual estimation. The midpoint is generally located a few millimeters below the inferior margin of the deltoid tuberosity. Turn the bone until the maximum diameter is obtained. This measurement is different from that presented by others (Bass 1971 :115; Hrdlicka 1952:168) as it is not necessarily in an anterio-posterior plane (Martin 1957:532-533 #5).

44. Minimum Diameter of the Humerus at Midshaft: (Figure 31).

Instrument: sliding caliper

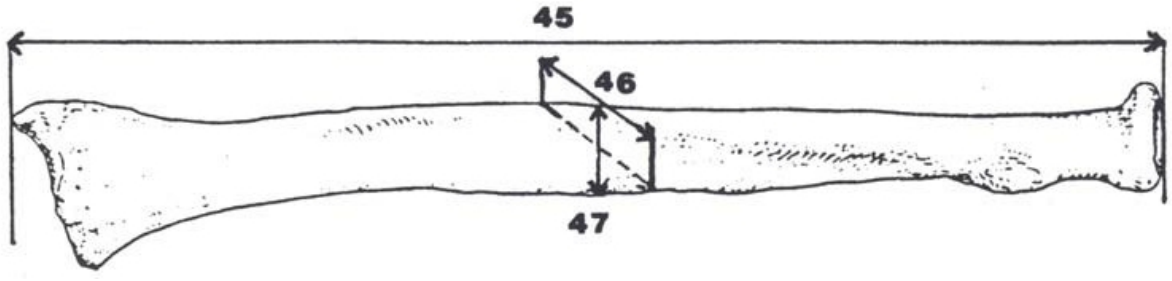
Comment: Determine the midpoint of the humerus on the osteometric board and mark with a pencil. Turn the bone until the minimum diameter is determined (Martin 1957:533 #6).

Radius

45. Maximum Length of the Radius: The distance from the most proximally positioned point on the head of the radius to the tip of the styloid process without regard to the long axis of the bone (Figure 32).

Instrument: osteometric board

Comment: Place the proximal end against the vertical upright of the osteometric board and press the movable upright against the distal end. Move the bone up, down and sideways to obtain the maximum length (Bass 1971:124; Hrdlicka 1952:169; Martin 1957:535-536 #I; Olivier 1969:235).



46. Sagittal Diameter of the Radius at Midshaft: The anterio-posterior diameter of the midshaft (Figure 32). This measurement is almost always less than the transverse diameter (number 47).

Instrument: sliding caliper

Comment: The anterio-posterior diameter is measured perpendicular to the transverse diameter (Martin 1957536 #5a).

47. Transverse Diameter of the Radius at Midshaft: The distance between the maximum medial and lateral bone surfaces at the midshaft (Figure 32).

Instrument: sliding caliper

Comment: (Martin 1957:536 #4a).

Ulna

48. Maximum Length of the Ulna: The distance between the most superior point on the olecranon and the most inferior point on the styloid process (Figure 33).

Instrument: osteometric board

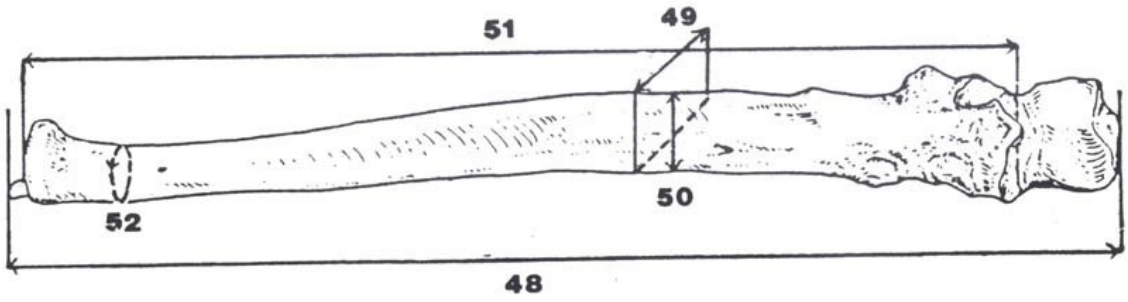
Comment: Place the proximal end of the ulna against the vertical endboard. Press the movable upright against the distal end while moving the bone up, down and sideways to obtain the maximum length (Bass 1971 : 130; Hrdlicka 1952:169; Martin 1957:539 #1; Olivier 1969:2351.

49. Dorso-Volar Diameter of the Ulna: The maximum diameter of the diaphysis where the crest exhibits the greatest development (Figure 33).

Instrument: sliding caliper

Comment: Place the arms of the instrument against the anterior and posterior bone surfaces (Martin 1957541 #11). This measurement is almost always less than the transverse diameter (number 50).

50. Transverse Diameter of the Ulna: The diameter measured perpendicular to the
Dorso-Volar diameter at the level of greatest crest development (Figure 33). Instrument: sliding caliper
Comment: Place the arms of the instrument against the lateral and medial surfaces of the bone (Martin 1957:541 #12).



51. Physiological Length of the Ulna: The distance between the deepest point on the surface of the coronoid process and the lowest point on the inferior surface of the distal head of the ulna (Figure 33).

Instrument: spreading caliper

Comment: Do not include the styloid process or the groove between the styloid process and the distal surface of the head when determining physiological length (Bass 1971:130; Martin 1957:539 #2; Olivier 1969:235).

52. Minimum Circumference of the Ulna: The least circumference near the distal end of the bone (Figure 33).

Instrument: tape

Comment: (Martin 1957:539 #3; Olivier 1969:236).

Sacrum

Record the number of segments composing the sacrum, disregarding the coccyx. Also, disregard the coccyx when measuring anterior height.

53. Anterior Height of the Sacrum: The distance from a point on the promontory in the midsagittal plane to a point on the anterior border of the tip of the sacrum (the sacral-coccyx junction) measured in the midsagittal plane (Figure 34). Do not measure if the sacrum is not complete.

Instrument: sliding caliper

Comment: Place the pointed tips of the caliper on the promontory and the anterior inferior border of the fifth sacral vertebra. If a sacrum exhibits more than five segments indicate the number of segments on the recording form and measure to the bottom segment (Bass 1971 :88; Hrdlicka 1952: 172; Martin
1957:523 #2; Montagu 1960:75; Olivier 1969:244).

54. Anterior Breadth of the Sacrum: The maximum transverse breadth of the sacrum at the level of the anterior projection of the auricular surfaces (Figure 34).

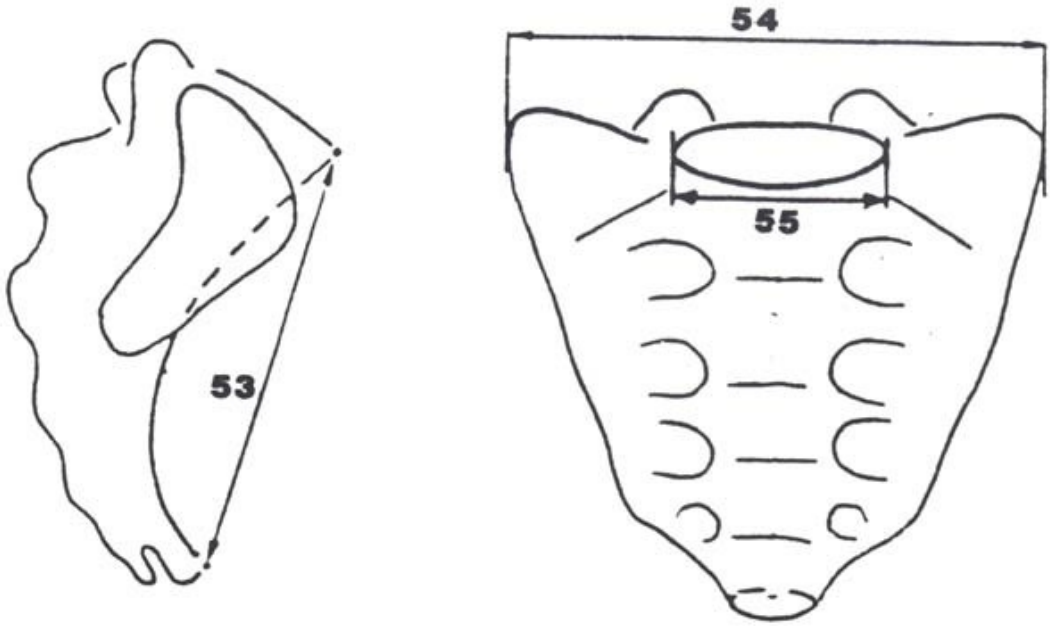
Instrument: sliding caliper

Comment: (Martin 1957:523 #5).

55. Transverse Diameter of Sacral Segment 1: The distance between the two most lateral points on the superior articular surface measured perpendicular to the midsagittal plane (Figure 34). When lipping of the articular surface is present, approximate the original articular borders.

Instrument: sliding caliper

Comment: (Martin 1957:524 #19).



Innominate

56. Height of the Innominate: The distance between the maximally distant points on the innominate, usually located on the iliac crest and the ischium (Figure 35).When using an osteometric board, place the ischium against the vertical endboard and press the movable upright against the iliac crest. **Move the ilium sideways and up and down to obtain the maximum distance** (**Hrdlicka 1920:135)**.

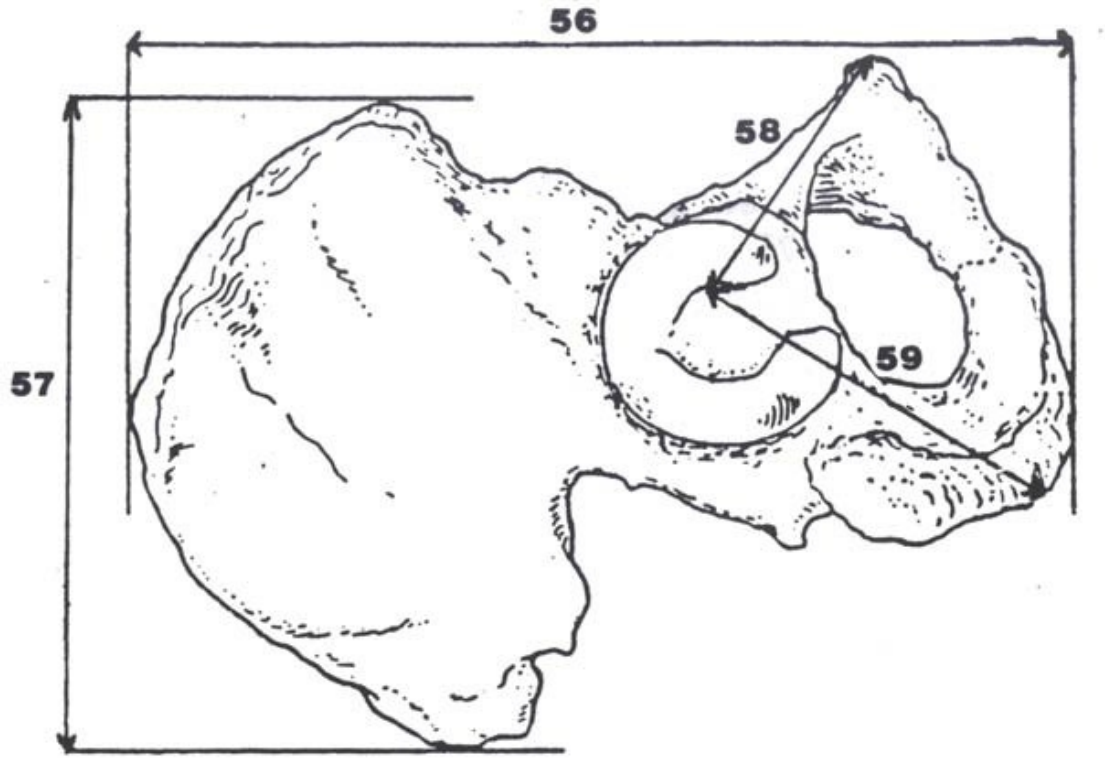
Instrument: spreading caliper or osteometric board (easiest)

Comment: Avoid including arthritic lipping. Note that this is a MAXIMUM measurement.

57. Iliac Breadth: The distance from the anterior superior iliac spine to the posterior superior iliac spine (Figure 35).

Instrument: spreading caliper

Comment: Martin (1957:556 #2)



~~58. Pubis Length: The distance from the point in the acetabulum where the three elements of the innominate meet to the upper end of the pubic symphysis (Figure 35).~~

~~Instrument: sliding caliper~~

~~Comment: The measuring point in the acetabulum may be identified in the adult because: 1) frequently there is an irregularity there, both in the acetabulum and inside the pelvis; 2) there is a change in thickness which may be seen by holding the bone up to a light; 3) often there is a notch in the border of the articular surface in the acetabulum. In measuring the pubis care should be taken to hold the caliper parallel to the long axis of the bone (Bass 1971 : 154; Montagu 1960:76-77; Olivier 1969:250; Schultz 1930:346-347; Washburn 1948:200).~~

~~59. Ischium Length: The distance from the point in the acetabulum where the three elements forming the innominate meet to the deepest point on the ischial tuberosity (Figure 35).~~

~~Instrument: sliding caliper~~

~~Comment: The measuring point in the acetabulum is defined above (see Pubis Length). Ischium length should be measured approximately perpendicular to pubis length (Bass 1971 :154; Montagu 1960:76-77; Olivier 1969:249; Schultz 1930:346-347; Washburn 1948:200).~~

Femur

60. Maximum Length of the Femur: The **MAXIMUM** distance from the head of the femur to a point on either condyle (Figure 36). Place the femur parallel to the long axis of the osteometric board and resting on its posterior surface. Press the medial condyle against the vertical endboard while applying the movable upright to the femoral head. **Raise the bone up and down and shift sideways until the maximum length is obtained** (Hrdlicka 1920:128; Trotter and Gleser 1952:473).

Instrument: osteometric board

Comment: Avoid including arthritic lipping. **Note that this is a MAXIMUM measurement.**

61. Bicondylar Length of the Femur: The distance from the distal borders of the femoral condyles to a proximal point on the femur head (Figure 36).Place the femur on the osteometric board so that the bone is resting on its posterior surface. Press both distal condyles against the vertical endboard while applying the movable upright to the head of the femur (Martin 1957:561-562 #2; Montagu 1960:70; Trotter and Gleser 1952:473).

Instrument: osteometric board

Comment:

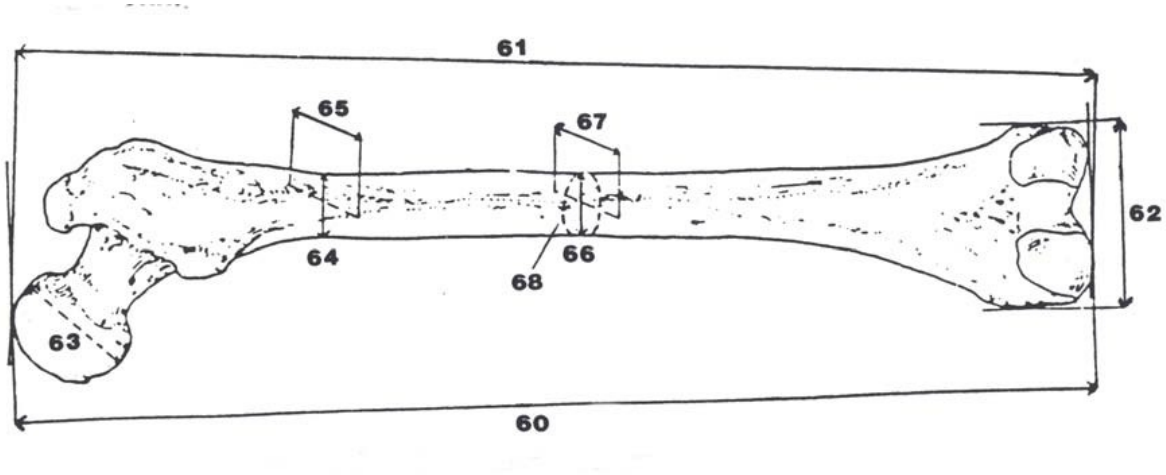
62. Epicondylar Breadth of the Femur: The distance between the two most projecting points on the epicondyles perpendicular to the shaft (Figure 36). Place the femur on the osteometric board so that it is resting on its posterior surface and the long axis of the bone is perpendicular to the long axis of the board. Place one epicondyle against the vertical endboard while applying the movable upright to the other condyle. **Do not include joint surfaces or edges, which can be prominent in individuals with arthritic lipping** (Martin 1957:565 #21).

Instrument: osteometric board

63. Maximum Diameter of the Femur Head: The maximum diameter of the femur head measured on the border of the articular surface (Figure 36).

Instrument: sliding caliper

Comment: Rotate the arms of the caliper around the femur head to find the maximum diameter. This measurement differs from the separate vertical and transverse diameters recommended by Martin (1928: #18 and #19) (Bass 1971: 168; Montagu 1960:70).



64. Anterio-posterior Subtrochanteric Diameter of the Femur: The anterio- posterior diameter of the proximal end of the diaphysis measured perpendicular to the transverse diameter at the point of the greatest lateral expansion of the femur below the lesser trochanter (See definition #65 and Figure 36)

Instrument: sliding caliper

Comment: This diameter is oriented perpendicular to the anterior surface of the femur neck. (Bass 1971 : 169; Martin 1957:564 #I 0; Montagu 1960:70; Olivier
1969:263).

65. Transverse Subtrochanteric Diameter of the Femur: The transverse diameter of the proximal portion of the diaphysis at the point of its greatest lateral expansion below the base of the lesser trochanter. In cases where this cannot be determined (e.g. where the lateral surfaces remain parallel), this measurement is recorded within 2-5 cm below the lesser trochanter (Figure 36).

Instrument: sliding caliper

Comment: The transverse diameter is oriented parallel to the anterior surface of the femur neck (Bass 1971 : 169; Martin 1957:564 #9; Montagu 1960:70; Olivier
1969:263).

66. Anterio-posterior Diameter of the Femur at Midshaft: The anterio-posterior diameter measured approximately at the midpoint of the diaphysis, at the highest elevation of the linea aspera. This measurement is taken perpendicular to the ventral surface (Figure 36).

Instrument: sliding caliper

Comment: (Martin 1957:563 #GI.

67. Transverse Diameter of the Femur at Midshaft: The distance between the medial and lateral margins of the femur from one another measured perpendicular to and at the same level as the sagittal diameter (Figure 36).

Instrument: sliding caliper

Comment: The transverse diameter is oriented parallel to the anterior surface of the femur neck. (Martin 1957:563 #7)

68. Circumference of the Femur at Midshaft: The circumference measured at the midshaft at the same level of the sagittal and transverse diameters. Note that if the linea aspera is strongly accentuated at the midshaft and not across a larger part of the diaphysis, this measurement should be recorded approximately 10 mm above the midshaft (Figure 36).

Instrument: tape

Comment: (Martin 1957:564 #81

Tibia

69. Length of the Tibia: The distance from the superior articular surface of the lateral condyle of the tibia to the tip of the medial malleolus (Figure 37).

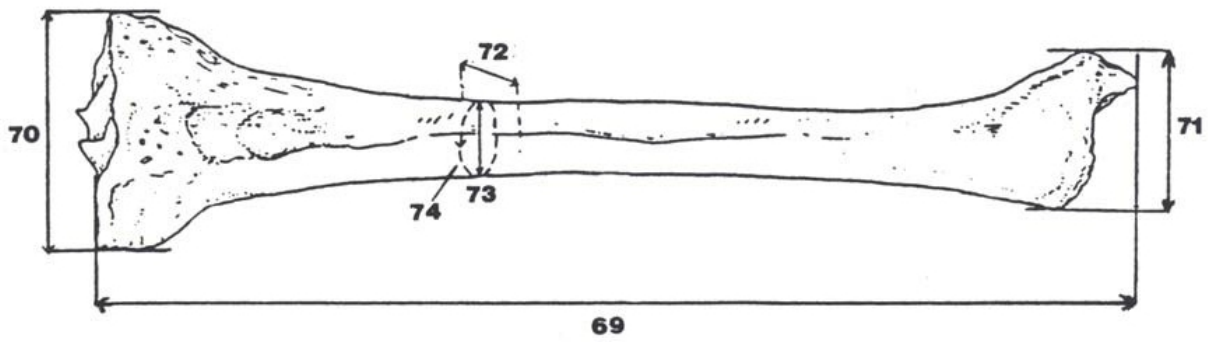
Instrument: osteometric board
Comment: This measurement is much easier using a board with a hole for the intercondylar eminence. Place the tibia on the osteometric board resting on its posterior surface with the longitudinal axis of the bone parallel to the board. Place the lip of the medial malleolus on the vertical endboard and press the movable upright against the proximal articular surface of the lateral condyle (Bass 1971 :187; Martin 1957:572 #1; Montagu 1960:72; Trotter and Gleser 1952:473).

70. Maximum Epiphyseal Breadth of the Proximal Tibia: The maximum distance between the two most projecting points on the medial and lateral condyles of the proximal epiphysis (Figure 37). Place the lateral condyle against the vertical endboard of the osteometric board, and place the movable upright against the medial condyle. Rotate the tibia to obtain the maximum breadth, but do not include the occasionally prominent articular surface for the fibula (Martin 1957:572 #3). **Do not include joint surfaces or edges, which can be prominent in individuals with arthritic lipping.**

Instrument: osteometric board

71. Epiphyseal Breadth of the Distal Tibia: The distance between the most medial point on the medial malleolus and the most lateral points of the distal epiphysis (Figure 37). Place the two lateral protrusions of the distal epiphysis against the fixed side of the osteometric board and move the sliding board until it contacts the medial malleolus. (Martin 1957:573 #6). **This is NOT a maximum.**

Instrument: osteometric board



72. Maximum Diameter of the Tibia at the Nutrient Foramen: The distance between the anterior crest and the posterior surface at the level of the nutrient foramen (Figure 37).

Instrument: sliding calipers

Comment: Rotate the caliper arms around the bone to get a maximum reading
(Bass 1971:187; Martin 1957:573 #8a).

73. Transverse Diameter of the Tibia at the Nutrient Foramen: The straight line distance of the medial margin from the interosseous crest (Figure 37).

Instrument: sliding calipers

Comment: This is taken perpendicular to #72 (Martin 1957:573 #9a).

74. Circumference of the Tibia at the Nutrient Foramen: The circumference measured at the level of the nutrient foramen (Figure 37).

Instrument: tape

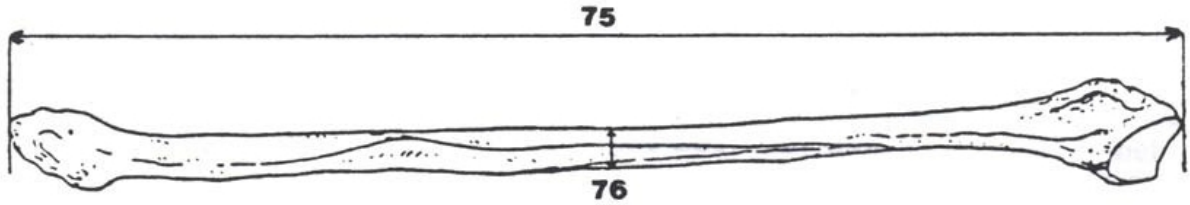
Comment: (Martin 1957:574 #10a).

Fibula

75. Maximum Length of the Fibula: The maximum distance between the most superior point on the fibular head and the most inferior point on the lateral malleolus (Figure 38).

Instrument: osteometric board

Comment: Place the fibula on the osteometric board and place the tip of the lateral malleolus against the vertical endboard. Press the movable upright against the proximal end of the bone while moving it up and down and sideways to obtain the maximum length (Bass 1971:187; Martin 1957:576 # 1).



76. Maximum Diameter of the Fibula at Midshaft: The maximum diameter at the midshaft (Figure 38).

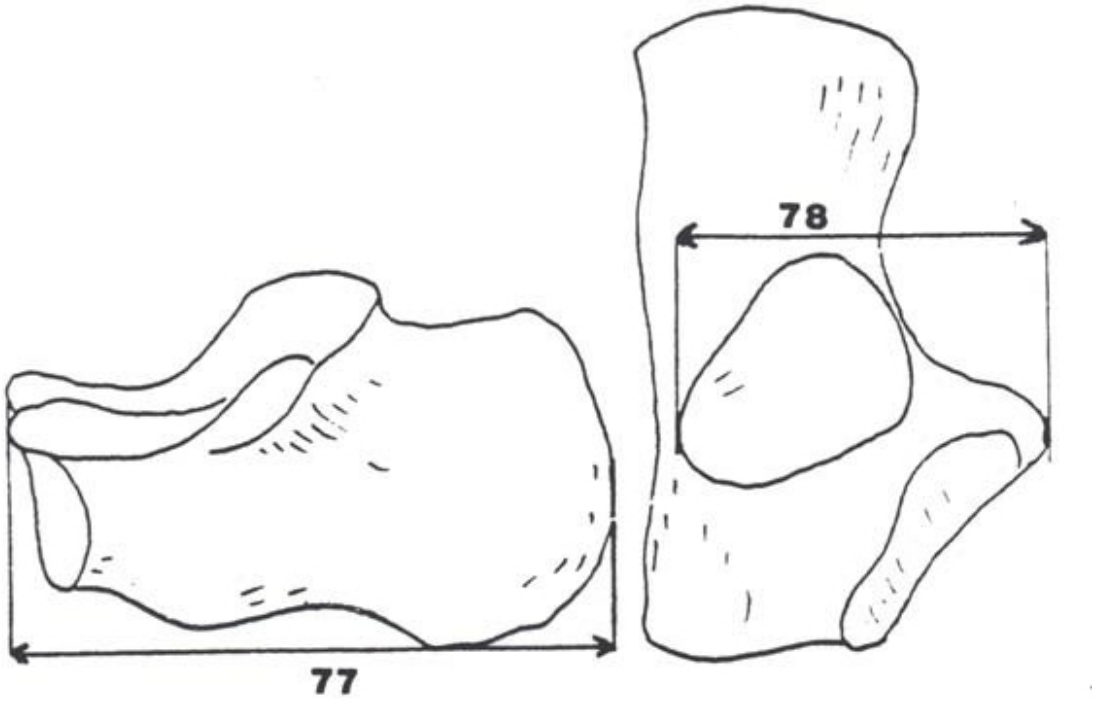
Instrument: sliding caliper

Comment: Find the midpoint on the osteometric board and mark with a pencil. Place the diaphysis of the fibula between the two arms of the caliper while turning the bone to obtain the maximum diameter (Martin 1957:576 #2).

Calcaneus

77. Length of the Calcaneus: The distance between the most posteriorly projecting point on the calcaneal tuberosity and the most anterior point on the superior margin of the articular facet for the cuboid projected onto the anterio-posterior axis (Figure 39). Position the calcaneus on the osteometric board with the anterior and superior edge of the articular facet for the cuboid against the fixed upright. Keep the anterior portion raised slightly so the long axis of the bone is perpendicular to the upright. Slide the movable upright against the posterior calcaneus (Martin 1957:582-583 # 1; Olivier 1969:279; Stewart 1979:126). Do not include arthritic lipping if present.

Instrument: osteometric board



78. Middle Breadth of the Calcaneus: The distance between the most laterally projecting point on the dorsal articular facet and the most medial point on the sustentaculum tali (Figure 39).

Instrument: sliding caliper

Comment: The two measuring points lie at neither the same height nor in a plane perpendicular to the sagittal plane. Accordingly, the measurement is projected in both dimensions. Span the calcaneus from behind with the blunt arms of the caliper so that the caliper is positioned in a flat and transverse plane across the bone (Martin 1957:583 #2; Stewart 1979: 126).

Statistical Procedures and Assumptions

Discriminant Function Analysis

Discriminant Function Analysis (DFA) is a family of statistical procedures for the optimal separation of groups and classification of unknowns using measurements. DFA involves reference groups with known membership in some category such as language family, sex, or tribe. The known reference groups form the basis for the classification of new individuals of unknown group membership. The most commonly used DFA is the Linear Discriminant Function (LDF). Measurements are converted into LDF scores using a linear combination of the original measurements, known as the **Mahalanobis Distance**. The LDF score of the unknown individual is then compared to the mean LDF score for each reference group; it is classified simply into the group with the closest mean score, which also has the smallest Mahalanobis distance. The most similar group will also have the highest **posterior probability**. Posterior probabilities are the relative probabilities of membership in each group based on the distances to each group, assuming that the unknown comes from one of the groups, and they sum to one. If there are more than two groups, more than one Linear Discriminant Analysis score can be calculated, and multiple axes are used for ascertaining group differences. This procedure is known as Canonical Variates Analysis, and because more than one dimension is involved, the group mean scores are called centroids, and groups can be plotted along multiple axes. Once again, an unknown is simply classified into the reference group it is most similar to based on the overall distance to each group's centroid along all axes.

FORDISC currently uses one of two procedures based on the LDF. For two groups, LDF methods are given in various texts; our computational procedure follows that outlined in Sneath and Sokal (1973, pp. 401 and 402). This procedure has the advantage of computational simplicity and speed. It yields a LDF, LDF scores for each group, and a sectioning point. The unknown is classified by comparing its score to the sectioning point. When more than two groups are compared the program uses a procedure described by Tatsuoka (1971, pp. 218 22). For quality control, we have compared FORDISC results to output from SAS PROC DISCRIM (SAS Institute 2002), using pooled covariance matrices and equal prior probabilities, and the posterior probabilities and classification rates are identical. Other statistical procedures have been compared to output in R (R Foundation for Statistical Computing, 2011).

For optimal estimation of parameters and thus performance, LDF methods make three assumptions: (1) the data are "multivariate normal"; (2) the variance-covariance matrix of each group is roughly the same; and (3) an unknown individual has an equal prior probability of belonging to each group. None of these assumptions is likely to be strictly true in all situations, and tests for multivariate normality and equal variance-covariance matrices can be misleading. However, these assumptions should be critically evaluated, and Fordisc 3 provides a test of the homogeneity of the reference group VCVMs. If any of these assumptions are violated, there are several alternatives to the LDF that do not require all of these assumptions, some of which will be options in future versions of Fordisc. However, the performance of the linear discriminant function -- and the simple classification rule based on overall similarity to each group -- can work remarkably well even when the assumptions are violated.

Another major assumption of Discriminant Function Analysis is that the unknown actually belongs to one of the reference groups. Discriminant Function Analysis will classify any set of measurements, even those from another species. An independent indicator of group membership is fortunately given by the **typicality probabilities**. Typicality probabilities represent how likely an unknown belongs to a particular group using the absolute distances to each group in the analysis. Here, absolute distances are evaluated, rather than relative distances as in calculating posterior probabilities. A typicality probability is the multivariate equivalent of a univariate t test probability and is also related to the percentile ranking of a univariate measurement. An individual's typicality probability of 0.33 for a group means that 33% of the total sample from that group would be expected to be as far or farther from that group's centroid, in other words, more different from the group's mean morphology. In practice, typicality probabilities below 0.01 (1%) for a group (similar to *p* values of statistical significance), may indicate measurement error or questionable membership in that group. **As a general rule of thumb, typicality probabilities above 0.05 are acceptable.** When all typicality probabilities are low, this indicates that an unknown probably does not belong to any of the groups in the analysis, and/or measurement errors are great. Frequently in such cases, the posterior probability for one group will be 0.99. **The posterior probabilities for each group and the classification itself should be ignored when all typicality probabilities are low.**

Evaluating Discriminant Functions

Discriminant Function Analysis is a practical undertaking. As such, the various methods of DFA are best judged by their classification accuracies. Multivariate criteria of group separation (such as F tests and Wilks' lambda) can be used to infer ideal classification rates, but the ultimate arbiter is how well it performs at classification of the reference samples. Further, the most recommended estimate of classification accuracy is called leave-one-out-**cross-**

validation (LOOCV). LOOCV avoids the bias of a lower estimated error rate inherent when a reference group member is tested against all reference groups, in one of which he or she is a member, as in Fordisc 2. In LOOCV, the first individual in the reference groups is removed from his or her reference group, the parameters are recalculated for each group using the remaining N-1 individuals, and that individual is then classified into one of the reference groups using the LDF. That individual is then added back into his or her group and the next individual is removed from his or her group and classified, and so on. When all have been classified in this manner, the total number of correctly classified individuals is the expected classification accuracy. There are other methods of cross-validation, notably k-fold cross-validation and various bootstrapping methods (Efron and Tibshirani 1993, 1997), that Fordisc will incorporate in future versions.

Testing assumptions goes hand-in hand with the classification accuracy; no matter how good the apparent classification is, if assumptions are violated, there are reasons to doubt such performance when applied to new cases. The crucial questions are:

1. Are the samples sufficiently large and representative?
2. Do the data show a multivariate normal distribution?
3. Is the level of variation in each group relatively similar? In other words, are the VCVMs relatively similar?
4. Are there enough measurements in the model?
5. Are there too many measurements in the model?
6. Are there outliers in the data?

These questions are covered in various sections of this help file, including the tutorial.

Sample Sizes

Sample sizes are extremely important, both the total sample size and the sample size of each group in an analysis. Sufficient sample sizes are necessary for accurate calculations of multivariate parameters such as means, variances, and covariances, and are necessarily related to the number of measurements to be analyzed. An unanswered question is how many individuals are sufficient given the number of measurements analyzed. More measurements will record more of the variation in groups, but require larger sample sizes. Additionally, after a certain number of measurements are used, as more measurements are added, there is a tendency for the classification accuracy to plateau and then decrease. This is likely due to redundant information, the introduction of greater noise, as well as poorer estimates of group parameters.

An extreme minimum requirement is that the total sample size (N) must be larger than the number of measurements (m). A more stringent but basic criterion is that the minimum sample size of each group (n) must be larger than m. But higher ratios of n to m produce more reliable parameter estimates (Tabachnick and Fidell 2001). Huberty (1994) suggests that the minimum sample size of each group (n) must be larger than $3m$. Another suggested minimum sample size is $(m*(m+1))/2 + m$, the number of means, variances, and covariances estimated for m measurements. For example, five measurements would require a sample size of 20, and ten measurements would require a sample size of 65. A more demanding suggested sufficient sample size is $10m$, so five measurements would require a sample size of 50, and ten measurements would require 100. Some of the suggested values relate to total sample size (N), while some are applied to the minimum sample size among all groups. Published craniometric analyses rarely meet the latter two suggested sufficient sample sizes. Further, these sample size recommendations are for LDA. Quadratic Discriminant Analysis (QDA) is an approach that can accommodate greater differences in group VCVMs, but has more demanding sample size requirements for optimal performance. In most cases, LDA will outperform QDA, even though the assumptions are clearly violated. **NOTE: We have recently (Spring 2018) conducted numerous simulations and feel confident in relaxing our former recommendations for the relationship between *m* and *n*. We now recommend a limit to *m* of min(*n*)-1, that is, the smallest group sample size minus one. The previous recommendations by many authors were actually for multiple regression, which resembles DFA but has important differences as well. Overfitting is no longer a primary concern based simply on the number of measurements and sample sizes. Better indicators of overfitting are a very low determinant of the pooled VCVM, failing the Kullback test for homogeneity of VCVMs, or producing many atypical reference individuals to their own group. Also, using more and more measurements unnecessarily can produce significant differences among groups and can lower the typicality of classified cases as well as the case being analyzed.**

One approach to the problem of overfitting in DFA is to find the measurements that show the greatest intergroup differences. This can be accomplished by performing **stepwise selection**, either forward, choosing the best variable combination by adding one variable at a time; backward, starting with all measurements and eliminating the variable that shows the least inter-group differences one at a time; or exhaustively, whereby each possible combination of measurements is evaluated. The group differences expressed in these variable combinations can be estimated using multivariate statistics such as Wilks' Lambda or assessed directly through classification accuracies,

though the latter is computationally more intensive. **We have recently set the default method to Wilks' Lambda and lowered the step levels to allow more measurements to be used in classification.**

Outliers

A major concern in multivariate analysis is the presence of outliers. Outliers are individuals that are so unusual that they stick out from the total sample or from other members of their particular group. Outliers can be due to recording errors, encoding errors, mismeasurement, pathological anomalies, the fact that an individual may actually belong to a different group with a different morphology, or any combination of these reasons. Removing outliers, especially in multivariate analyses, is recommended when there are large enough sample sizes, because outliers can drastically affect estimated multivariate parameters. Some researchers advise that removing outliers, up to 5% of a sample, will only bring a neutral or positive effect. The presence of one outlier can mask the presence of other outliers, so any tests are re-run after the removal of initial outliers. Discovering outliers is straightforward using one variable at a time (univariate) using the familiar ideas of the bell-shaped (normal density) curve and a standardized distance (the standard deviation) to the mean. When analyzing more measurements (multivariate), the univariate tests are not as robust in detecting outliers and can indicate outliers that are not; however, an outlier in one measurement can also be masked by other normal measurements in multivariate tests. Additionally, multivariate analyses produce an overall multivariate distance figure, most frequently the Mahalanobis D-square, which is the multivariate analog of the z score. Multivariate procedures take into account the relationships of measurements to each other and produce significance tests for outliers. Methods for detecting outliers will be incorporated into future version of Fordisc, but for the present, outliers can be detected in the canonical plots as members of a group that are far from the group centroid or by examining the typicality probabilities of each reference individual on the Extended Results page. Outliers can be removed one at a time by typing the ID into the "Exclude ID" field (one per line) on the options page. The excluded individuals will be listed on the Basic Results page. Automatically removing outliers will be an option in future versions of Fordisc.

Transformations

Transformations are generally performed on original measurements for two reasons. Transformations are more commonly performed to give the original data a more normal distribution. Univariate and multivariate normality of the data is an important requirement for the correct estimation of parameters and probabilities. For instance, logging measurements is common, especially in linear regression. Other transformations are constructed so they emphasize certain qualities of the data. On such example is converting the original measurements into shape variables, removing size. Size is useful in DFA for classifying males and females of the same group, who generally show little shape variation. In fact, DFA of two groups using both males and females tends to misclassify females into males of the same group and vice versa. As a result, shape analysis can be useful if you suspect that an unknown individual comes from a group not represented by females (such as Chinese). Depending on the variables, in comparisons across groups of the same sex, size can be a confounding factor that is best left out. Shape variable calculation in Fordisc follows Darroch and Mosimann (1985), in that the geometric mean for all measurements of an individual is calculated and this size factor is subtracted from each variable, producing the shape variables. The size factor is not used in analyses.

Two Group Plots

Multivariate normality is a requirement for finding optimal group separation using DFA. While each individual measurement may not be normally distributed, sums of measurements, as in linear DFA, will more often be normal due to the central limit theorem. So the distribution of scores from each group should appear approximately normal, depending on what bin width or interval is chosen. Another requirement for a best solution using linear DFA is that the level of variation in each group is approximately the same. This can also be "eyeballed" by looking at the two-group plot. Keep in mind that if one group has a much larger sample size, it will be taller than the other. It is the horizontal spread of each group that should appear roughly the same.

Histogram

A Histogram is displayed when a two-group DFA is run. The horizontal axis represents the DF scores for individuals in the reference groups, and the vertical axis represents the counts for each score interval. The default bin width of the histogram is 1.5 and can be changed by typing a different value into the bin width box. The **X** indicates the DF score of the current case.

Print Graph

Click this button to print the graph. A printer dialog box will appear.

Copy Graph

Clicking this button will copy the current graph to the clipboard. You can paste the graph into another program by pressing Ctrl-V or choosing Edit|Paste in most Windows programs.

Multiple Group Plots

Two Dimensional Canonical Axis Plots

A two-dimensional canonical plot is displayed in a multiple group DF when the Graph tab is selected. A Canonical plot distills the information expressed by many (often correlated) measurements from many groups into fewer uncorrelated variables, the canonical axes, which are linear functions of the original measurements. The dimensions of the canonical space are determined by differences in group means and the pooled within-groups VCVM, which is a weighted average. The first canonical axis is the function with the most among-group variation, the second canonical axis represents the function showing the next highest among-group variation, and so on. The number of possible canonical axes calculated is either the number of measurements or the number of groups minus one, whichever is less. By default, the horizontal axis represents the first canonical axis, and the vertical axis represents the second canonical axis. The amount of variation in each axis is displayed as well. The centroids of each group is located by the group abbreviation and the position of the unknown is represented as a white X in a black box. The scores of each member of each group are shown on each axis, and the confidence ellipse for each group is calculated from the individual scores in each group with a sample size of at least four. The size of the ellipse and the theoretical proportion of the group members contained in them can be adjusted. The default setting is for a 90% confidence ellipse. You can choose which centroids, ellipses, and scatter of each group that will be displayed. Toggle their display by clicking on the boxes to the right of the graph.

Be sure to examine the confidence ellipses and keep in mind one of the assumptions in a linear discriminant function, that the level of variation in each group is roughly the same. The size and orientation of the confidence ellipses should be roughly the same for each group in the canonical axis plots, at least for the first few canonical axes. You can select which canonical axes are displayed using the drop-down lists in the middle of the x and y axes.

Also, remember that DFA can be drastically affected by outliers. Such outliers should be noticeable in the first few canonical axis if they are far outside their corresponding confidence ellipse. You can right-click on an outlier to get its identification number. To exclude an outlying individual, type the identification number into the Exclude IDs text box on the options page. The excluded individuals will be listed on the Basic Results page.

To zoom in on an area, hold down the left mouse button and draw a box on the area to be enlarged. The graph will fill the entire graph with your selection. This can be especially useful if the unknown is obscured by a group centroid label. To reset the zoom, press the **Autoscale** button.

Three Dimensional Canonical Axis Plots

A three-dimensional canonical plot is displayed when the **3DGraph** page is selected. Three dimensions represent more of the total variation in the analysis because of the additional canonical axis. The graph can be rotated manually by left-clicking and dragging an area of the graph. You can zoom in or out of the graph by right-clicking and dragging on the graph. You can also choose to display the axes or not, and rotate the graph automatically or not. Rotations occur in the x,y, and z axes. The first two axes shown will be the same axes shown by default in the two-dimensional canonical axis plot.

Stature Estimation

FORDISC should only be used for stature estimation of an individual whose long bone epiphyses have fused. When viewing the Postcranial Measurements page of the Case Folder, pressing the **Stature** button or [Alt-S] brings up the stature estimation screen. If you have run an analysis, the group classified according to FORDISC will be highlighted. Otherwise, choose a group, prediction interval (PI), and stature type (forensic, measured, or cadaver) by clicking on your preferences. A list of estimated statures based on the group and stature type will appear, sorted by prediction interval. Only statures that can be estimated based on the available bone measurements will be displayed. You may find that there are many possible equations for a given case if many bones are present. You can click on an equation and scroll through all equations by using the arrow keys.

You can copy all available equations to the Windows clipboard by pressing the **Copy Nums** button, which will copy the table header and each row of values separated by tabs, or you can press the **Copy Text** button, which will copy explanatory text integrated with each row's values. To exit, click the Stature button again or press [Alt-S].

Materials and Methods

Stature prediction equations are calculated on the fly based on the available data. Adding various measurements generally improves the precision of stature estimation, so all combinations of summed measurements are tested in predicting stature. All bone combination estimates and all individual bone estimates are displayed. The sample sizes given below are totals and the sample sizes using different measurements will vary. FORDISC uses equations calculated using least-squares regression based on one of three data sources.

NOTE: In this application of linear regression methods, the prediction interval is far more important than the point estimate of stature.

Forensic Statures

Forensic statures are those on a driver's license, police record, or other official records. They have several advantages over measured statures, among which are widespread availability and no need to adjust for age-related stature loss. See Ousley (1995) for further details. Sample sizes may be rather small for some groups, and Blacks and Hispanic males in the FDB, with smaller sample sizes, required the addition of cadaver lengths converted to expected forensic stature. In general, estimates with the same prediction interval and a larger sample size are preferred over those with a significantly smaller sample size.

Black females N = 54, mean stature = 64.7" (164.4 cm)
Black males N = 87, mean stature = 69.0" (175.3 cm)
Hispanic males N = 31, mean stature = 66.0" (167.7 cm)
White females N = 99, mean stature = 64.6" (164.1 cm)
White males N = 153, mean stature = 69.4" (176.3 cm)

Use Any Group Estimation (Forensic Statures)

If you have no idea of what group an individual comes from, you can still make reasonably precise estimates of stature. The Fully method (1956,1960; Lundy 1988) should always give the best estimate of stature in terms of accuracy and precision. However, if all of the necessary skeletal elements are not available, stature estimates based on long bone lengths can be used. In general, when the group membership / ancestry is not known, estimates involving lower and upper limbs produce more precise estimates. Such estimates will always be less than precise than those involving group-specific estimators, but data for every possible group are not available.

Measured Statures

For Black and White males, Trotter and Gleser's (1952) data from World War II soldiers are used. Please note that **Trotter's measurements of the tibia have been adjusted in FORDISC for the CORRECT measurement of the tibia** based on the results of Jantz et al. (1994) and should give more accurate results than the published equations. Trotter and Gleser's original tibia equations were based on an incorrect measurement technique. For more details, see Jantz et al. (1995).

White males N = 1126, mean stature = 68.6" (174.2 cm)

Black males N = 86, mean stature = 67.8" (172.2 cm)

Cadaver Statures

For 19th century individuals, stature estimates based on the Terry collection cadaver lengths are used.

Black females N = 41, mean stature = 62.8" (159.6 cm)
Black males N = 48, mean stature = 66.9" (170.0 cm)
White females N = 39, mean stature = 62.9" (159.7 cm)
White males N = 32, mean stature = 67.2" (170.8 cm)

PI (Prediction interval)

In linear regression, the prediction interval includes the lower and upper bounds for a predicted dependent variable based on a single independent variable. The PI is wider (it has a larger range, which is the upper bound minus the lower bound), than the better known confidence interval because it is used for a single random variable that does not come from the same sample that the estimate is based on. The PI incorporates sample-to-sample distribution differences as well as differences in estimates of the mean in each sample (Neter *et al*. 1985). In FORDISC, the PI for the estimated stature of an unknown individual is based on bone measurements. A 90% PI means that in the long run, 90% of the estimated statures will be within the prediction interval, so the actual stature will be outside the interval 10% of the time. Using 95% PIs, the actual stature will be outside the interval 5% of the time. The PI becomes slightly larger as a bone measurement gets further from the mean bone length due to the error terms of the regression slope (especially) and intercept. With a large sample size, the parameters are better estimated and the differences in the PI may be negligible across the distribution.

Estimate Stature using Birth Years

You can limit the estimated statures from the forensic groups based on birth year. Fill in any value except 1930 (the default) for the minimum and you will get only those individuals born in that year or later. Any value in the maximum birth year box will limit individuals to those born that year or earlier. **Strict** limits the selection to individuals with confirmed birth years.

Statistical DOs and DON'Ts

DO check for any outliers in reference samples. Remember, outliers can be present for many different reasons and can drastically affect test results and classifications. You can exclude outliers on the **Options** page.

DO check for obvious differences in levels of within-group variation. Differences can be due to outliers or inherently greater variation among groups. Check the homogeneity of VCVM tests that Fordisc provides to test differences in within-group variation.

DO double-check measurements of the unknown individual you want to classify. Fordisc provides some basic univariate checks, but significant measurement errors or even one unusual measurement could drastically affect results. You should also check the measurements of the unknown against the group means in your analysis.

DO use enough measurements to take enough morphological variation into account, but

DON'T use too many measurements for your samples sizes. Check the determinant of the VCVM and the Kullback test p value. Various stepwise procedures can help determine the best measurements to use.

DON'T test an unknown against inappropriate samples. Fordisc will only classify an unknown into a reference group that is part of an analysis. Fordisc, and any other discriminant function analysis will classify a gorilla, a dog, a gerbil, or even a soccer ball into a group (Freid *et al.* 2005).

Finally,

DO read about multivariate analysis. An easy first read is Kachigan (1991). Chapters in Tabachnick and Fidell (2001) provide numerous explanations and examples, as do Afifi and Clark (1997), Legendre and Legendre (1998) Krzanowski (2000), and Manly (2005). Johnson and Wichern (2002) provide many exercises and worked-through examples.

Recent publications that cover the use of Fordisc, statistical background, and approaches to classifying human remains, are found in Ousley and Jantz (2012) and Jantz and Ousley (2012, 2017).

Statistical Glossary

Balanced Accuracy is (Sensitivity + Specificity) / 2.

Cohen's kappa is a measure of classification performance that takes into account the probability of randomly classifying correctly (the prevalence). For instance, 50% accuracy in a 5-way DFA is far better than chance, but not in a 2-way DFA. Cohen's kappa comes from studies of interrater agreement. Cohen's kappa for each group are provided as well as the mean Cohen's kappa. General guidelines for interpreting kappa are as follows:

Kappa	Classification performance
0.00 - 0.20	poor
0.20 - 0.40	fair
0.40 - 0.60	moderate
0.60 - 0.80	good
0.80 - 1.00	very good

Curse of Dimensionality As more and more measurements are added to a model, more of the variation is explained but the model becomes more complex and the danger of overfitting arises. For instance, a curvilinear distribution with ten points can be fit perfectly with a model using ten parameters and a ninth degree polynomial, but a simpler model with some error is a better model that will be more appropriate for future predictions. To paraphrase Yogi Barra, we are more concerned with predicting the future, which is more difficult than predicting the past. Using more measurements is more likely to bring out significant group differences and higher classification accuracies, but using too many can make their VCVMs too different, making accurate classification more difficult. Group samples in multivariate space become more and more sparse, i.e. less and less dense, as more dimensions are added and the distances among individuals increase. **Using far too many measurements relative to a group's sample size can reduce accuracy and make a fairly normal individual highly atypical**. For this reason, we are stressing that a **target number of measurements (below)** is necessary, based on classification accuracy and the typicality probability of the present case.

Cross-Validation A DFA is best judged by its classification accuracies. The most often recommended estimate of classification accuracy is **leave-one-out-cross-validation** (LOOCV; MacLachlan 1968). LOOCV avoids the upward bias of error rate estimation when using resubstitution, in which each member of all reference groups is classified using all members of all reference groups, one of which includes that member. In LOOCV, the first individual in the reference groups is removed from his or her reference group, the parameters are recalculated, and that individual is then classified into one of the reference groups using DFA. That individual is then added back into his or her group and the next individual is removed from his or her group and classified, and so on. When all have been classified in this manner, the total number of correctly classified individuals is the expected unbiased classification accuracy. While this method has a low bias, the estimated error rates have a high variance. Other error rate estimation methods show lower variances and are of low bias or are unbiased. One of these is similar to LOOCV and is called *k*-fold cross-validation. Instead of removing an individual, as in LOOCV, this method removes a proportion of the total sample (say, 5 to 10%, or N/k), and classifies it against the remaining individuals. The selection and testing is performed repeatedly *k* times without replacement to get a mean error rate as well as error variance, which will be lower than for LOOCV. Bootstrapping methods, such as the .632+ estimator (Efron and Tibshirani 1993, 1997) can provide unbiased and minimally variable error estimates.

Determinant: The determinant of a matrix is calculated basically by multiplying all the diagonals (variances) and subtracting the products of the off-diagonals (covariances). The determinant is a rough indicator of how reliably a matrix can be inverted, a necessary operation in determining the **Mahalanobis Distance**. A determinant of zero means that the matrix is singular, that the matrix components are not independent of each other, that the matrix cannot be inverted, and that the analysis cannot proceed. The log of the determinant is used so that small numbers are better represented. A negative value for the log of the determinant implies a small value, meaning that the matrix is nearly singular, Mahalanobis distances based on the VCVM may not be reliable, and that the discriminant function may not be the optimal solution.

Mahalanobis Distance, or D-square A multivariate distance among individuals or groups that results from the conversion of univariate differences using the variance-covariance matrix. The univariate differences in measurements are scaled by their variances and summed, then are adjusted (usually reduced, because the covariances are positive) by the covariances. Large univariate differences in two measurements are adjusted downwards if they have a high covariance, i.e. if they are highly correlated to each other; Large univariate differences in two measurements are summed if they are completely independent. In this way differences among all measurements -- some of which will be positively correlated, some of which will be uncorrelated, and some of which will be negatively correlated -- can be reduced to one number best expressing overall similarity between individuals or groups.

Negative Predictive Value is the proportion of individuals correctly classified into other groups divided by the total number of individuals classified into other groups.

Outliers Outliers are individuals that are so unusual that they stick out from their group, or all groups. Outliers can be due to recording errors, encoding errors, mismeasurement, pathological anomalies, the fact that an individual may actually belong to a different group with a different morphology, or any combination of these reasons. Removing outliers, especially in multivariate analyses, is recommended when there are large enough sample sizes, because outliers can drastically affect estimated multivariate parameters. Methods for detecting outliers will be incorporated into future version of Fordisc, but for the present, outliers can be detected in the canonical plots as members of a group that are far from the group centroid or by examining the typicality probabilities of each individual on the Extended Results page, if "Individual Scores" is selected in the Results section of the Options page.

Positive Predictive Value is the proportion of individuals correctly classified into the group divided by the total number of individuals classified into the group.

Posterior Probability Posterior probabilities evaluate the probability of membership in each group under the assumption that the unknown belongs to one of the groups in the function (Tatsuoka 1971, p. 228-230). Posterior probabilities are based on the relative distances to all groups, and the sum of the posterior probabilities equals 1. Posterior probabilities can vary a great deal depending on which groups are part of an analysis.

Sensitivity is the proportion of individuals correctly classified into the group divided by the total number from the group. This is the accuracy that is most often provided.

Specificity is the proportion of individuals correctly classified into other groups divided by the total number of individuals from other groups.

Structure Coefficients (Discriminant or Canonical) Discriminant structure coefficients are the correlations of the original measurements with the discriminant function scores in two-group classification, or with the canonical variates scores in multi-group classification. They help reveal the contribution of each measurement to separating groups on a particular axis.

Target Number of Variables The forensic anthropologist is faced with a Goldilocks dilemma: Good separation and classification of many groups require many measurements, which encompass more morphological variation; yet using too many measurements produces overfitting and lower accuracy. **Based on recent simulations, a reasonable recommended maximum number of measurements seems to be the minimum sample size among all groups minus one.** An absolute reasonable minimum may be ten measurements for reliable comparisons, but depending on the case measurements and group separation, fewer measurements may at times be necessary and justifiable. But three or four stepwise-selected measurements, no matter how apparently accurate they are, should be avoided in favor of using more measurements, even if stepwise-selected. Variation among human groups is usually too complex to be encompassed by only four measurements.

Typicality Probability Typicality probabilities represent how likely the unknown belongs to any particular group, based on the absolute distances to each group in an analysis. They are interpretively similar to the univariate *p* value based on the normal distribution. **The typicality probability can be thought of as the probability of the null hypothesis that the individual comes from a particular group. In general, a typicality probability above 0.05 for the most similar group are accepted, because we do not have statistical grounds to reject the hypothesis that the unknown comes from that particular group.** Typicality probabilities may indicate that an unknown belongs to several or none of the groups in question (Tatsuoka 1971, pp. 218-222; Van Vark and Schaafsma 1992, pp. 245-246). Because the typicality probabilities are based on the pooled variance-covariance matrix, which can change based on the groups and measurements selected, **typicality probabilities for an individual will vary for the same group in analyses involving different combinations of groups and measurements.** Typicality probabilities for a group from a number of analyses should in general be less variable than posterior probabilities.

Fordisc calculates the typicality probabilities three ways, using the F distribution, the Chi-square distribution, and on ranked Mahalanobis distances. Each calculation has advantages and disadvantages depending on the number of measurements used, the number of groups involved, and the sample size of each group. Using the **F distribution** takes into account the Mahalanobis distance and sample size, and provides a statistically justified figure. However, in our experience, the typicality probabilities can often be relatively high for many groups in an analysis, even if the groups are quite different from the unknown individual. Also, as the number of measurements approaches a group's sample size, the F ratio typicality probability becomes more and more inflated. Thus, there is practical justification for examining the typicality probabilities using the Chi-square distribution, which are based on Mahalanobis distance alone. The **Chi-square** typicality probabilities are based on infinite sample sizes, and are therefore almost always significantly lower than the typicality probabilities based on the F distribution. Chi-square typicality probabilities also tend to call more individuals atypical than F typicality probabilities. Chi-square typicality probabilities may be justified biologically if one believes that a larger sample

would not change group parameters significantly. Typicality probabilities based on **Ranked** Mahalanobis distances to group centroids are also provided. These probabilities are objective rather than theoretical but require adequate sample sizes for reliability. Large and especially homogeneous samples may have group members that are not very far from the group mean (in comparison to other groups) but have very low ranked probabilities. All three probabilities converge as group sample sizes approach infinity.

Variance-Covariance Matrix (VCVM) A *p* by *p* matrix used in calculating the **Mahalanobis Distance**. The variance is the standard deviation squared; therefore it is always positive. The covariance is the amount of variation in one variable that can be accounted for by variation in another variable. Variables with large (positive or negative) covariances are more highly correlated to each other: The covariance of two variables divided by their pooled variance is the correlation coefficient. In discriminant function analysis, one assumption necessary in finding the best linear function, and thus, the best separation among groups, is that the VCVMs of all groups are relatively similar. Fordisc provides a test of this assumption from Kullback (1959), cited in Legendre and Legendre (1998).

Race, Races, and "Biological Race"

This text was written many years ago, though the points are still valid. An updated exploration of human races and craniometric variation can be found in:

Ousley SD, Jantz RL, Freid DL (2009) Understanding Race and Human Variation: Why Forensic Anthropologists are Good at Identifying Race. *American Journal of Physical Anthropology* 139: 68-76.

and:

Ousley SD, Jantz RL, Hefner JT (2018) From Blumenbach to Howells: The Slow, Painful Emergence of Theory Through Forensic Race Estimation. In: *Forensic Anthropology: Theoretical Framework and Scientific Basis*, CC Boyd and DC Boyd, eds. pp 67-97.

The issue of race, in particular what forensic anthropologists are up to when they use the concept for identification purposes, is subject to considerable ongoing debate (e.g. Brace 1995; Kennedy 1995; Sauer 1992). It may be useful to state explicitly how we treat the issue and explore the biological significance of results from discriminant functions and FORDISC.

Racial classifications are deeply embedded in U. S. society: Until recently, many states had laws forbidding marriage outside one's race; one only has to fill out a federal form to learn that a racial designation is asked for. Hence, we are accustomed to self-designating our "race". Americans have a fairly limited concept of race in that socially, the vast majority of persons encountered in the US would be classified as either "Black", "White", or "Oriental". The NCIC missing persons data base classifies humanity into four races, adding only "American Indian", lumping "Pacific Islander" with "Asian" (Sauer 1992).

The racial/ethnic identification of individuals comprising the reference samples in FORDISC might have been a self-designation, i.e. hospital records the decedent filled out, a designation by close relatives, as in a missing person report, or a classification by law enforcement officials. In any of these cases, race is socially and/or forensically designated. **FORDISC does not define, redefine, or justify any racial classifications**, but merely tests the relationship between these cultural categories and metric variation. There are no individuals in the FORDISC reference samples whose race has been assigned based on *post hoc* tests using morphology or metrics.

The non-existence of races, as expressed in "There are no races, there are only clines" (Livingstone 1962:279) does not mean that classifying unknown crania for forensic purposes is an exercise in futility. Howells (1996a:103) has rephrased the idea as follows: "There are no races, only populations", and his monograph provides a broader illustration of the effectiveness with which crania can be placed via their metrics. However, human populations can be defined based on any combination of cultural, historical, geographical, biological, and other criteria. We should also remember that populations, however defined, are rarely compared, but rather, samples from populations.

What FORDISC estimates may be termed "ancestry" in the sense that it identifies population differences resulting from the different origins of each reference population's ancestors. Using 25 or so cranial measurements, a DF can discriminate between American black and white males with 95% accuracy. At least for these samples in the FDB, social race and skeletal metrics are highly correlated. These results probably reflect the disparate origins of their ancestral populations (despite the estimated ~20% white admixture in Blacks) of each social race as well as the limited number of persons of non-West African ancestry in the US: There are relatively few Egyptians, Moroccans, New Guineans, Australian Aborigines, and other peoples in the US, who would likely be socially classified as "black", but who are very different genetically from most African-Americans.

Social race is assigned based on phenotypes, which in the US, appears largely based on skin color. However, skin color is not the entire basis for the racial classifications, for there is considerable overlap between groups. It is likely that additional factors such as hair form, nose shape, and face/head shape are part

of the phenotypic racial classification system in the US. This is suggested because barring extensive pleiotropy or linkage, skin color is not represented in craniometric or postcranial metrics, which separate American Blacks and Whites very well.

Phenotypic classifications are in the eye of the beholder. The Japanese, Chinese, and Vietnamese are grouped together in the NCIC database, reflecting the US racial classification system. Using many of the same measurements that separate American Blacks and Whites, samples of Japanese, Chinese, and Vietnamese in two-group DFs can be separated with 85-92% accuracy. In a three-way function, the accuracy is 80%. This likely reflects somewhat disparate origins and largely separate development of each population, whether or not they are considered the same "race" in the US view.

Good separation between two groups says little about their relationships to other groups, and a multiple-group analysis is necessary to ascertain overall relationships. Using 21 craniometric measurements, a four-way DF between white, black, American Indian, and Chinese males is 96% accurate. These groups trace ancestry to widely different parts of the world (Africa, Europe, Native America, Asia), and the morphometric variation remains considerable. But there are clearly other factors: A four-way DF with white, black, American Indian, and Japanese samples is only 84% correct, with a good number of Japanese classifying as Black and vice-versa.

Using many of the same cranial measurements, a DF can separate regional samples of modern Japanese males from Nagasaki and Tohoku with 94% accuracy. When two-group discrimination is possible at this level, its practical value may be great (if one is interested in DFs among Japanese) but its biological significance may remain unclear.

This is further illustrated by secular changes within populations. Using 8-10 craniometrics, a DF between American white adult males born 1840-1890 can be separated from American white adult males born 1930-1980 with 88-96% accuracy. Modern white males have longer, narrower, and higher heads than 19th century white males. In fact, in the last century, white males seem to have undergone the most dramatic changes among American white and black males and females (Ousley and Jantz 1997). In this case the relationship between "ancestry" and metric variation is further obscured.

Note that when samples have been divided up into "races", and differences have been seen, it was believed that the samples represented different "races". There is an assumed causal connection here, but it is actually the result of tautological reasoning. Correlation is not causation. Using the same logic, the differences between the 19th and 20th century White male samples are simply due to being born roughly 90 years apart *per se*, rather than to differences in nutrition, sanitation, overall health, etc. between the different time periods. **Thus, good separation between two human groups, however defined, does not justify the conclusion that they belong to different biological races.**

Indeed, it is likely that any two nonrandom (culturally / geographically / temporally defined) skeletal samples of humans will show significant metric differences. This is a continuation of the general pattern of much smaller variation within human groups and much larger variation among groups when looking at metric as opposed to genetic variation. Whatever the causes, this pattern can serve the needs of forensic identification very well. Biological justifications are not needed.

Imagine an objective, purely biological classification of a large worldwide sample of crania. Biological groupings might have descriptive labels such as "Dolichocephalic-Chamaecranic-Metriometopic-Euryprosopic-Mesenic-Mesorhinic-Hypsichonchic-Mesuranic- ..." or other designations such as "M645" to represent the many cranial configurations that would be present. Even if some fixed number of categories could be agreed upon, which is doubtful, each biological category would show a diverse membership from several cultural populations. In other words, many biological classes would have members from several "races". If the categories were so rigidly defined as to have no "racial" overlap, classes may consist of only one or very few members, but more importantly, the classifications would be biased: They would be judged by cultural standards, not scientific ones. One "objective" study of American Indian crania from a Pueblo site in New Mexico, in which geography, nationality, and social races (and within-sample variability) were ignored, has produced the biological varieties of "Pseudo-Negroids", "Pseudo-Australoids", and "Pseudo-Alpines" (Hooton 1930). Hooton justified his categories, which were based on visual morphological assessments, on the significant metric differences between them. Such was the tautological reasoning of racial anthropologists. In a more recent study, differences among villages on Hvar Island, roughly 41 miles long and 4 miles wide, are better explained by the differing population histories of the villages (Rudan et al. 1986).

Even if there were a consistent biological classification of humans, it would be of little use in a forensic setting. The proportions of each social "race", nationality, or some other cultural designation represented in each biological category would be necessary to enable probabilistic identification, since living persons are classified culturally, not metrically or genetically. Forensic identification involves cultural designations and would gain nothing by purely biological classifications. It makes perfect sense to record the skeletal measurements and the decedent's particular racial designation if we are interested in predicting the latter from the former. Indeed, all skeletal reference collections have materials that are classified by social race and/or nationality, or geographically, temporally, or using other cultural criteria, so there have never been any reference materials classified based solely on biology.

Forensic race identification, in sum, involves "a prediction, based upon skeletal morphology, that a particular label would have been assigned to an individual when that individual was alive." (Sauer 1992:110). In this respect, "social race" is actually an advantage of US anatomical skeletal collections and the FDB since all recorded races are social races, and identifications involve social races. **It is extremely practical to proceed with forensic identification using a social race label, which need not be objective, but merely be correlated with some biological criteria in order to be useful.** There is a parallel here between biological (measured) and forensic (recorded) stature in that biological stature, with diurnal and temporal changes, is in a constant state of flux and largely unavailable for missing persons, but forensic stature is available from a driver's license. Whether precise or not, driver's license statures are highly correlated with long bone measurements and can be accurately predicted (Ousley 1995).

It is clear that for humans, "biological race" will be subjective and ambiguous. Any particular biological classification can be contradicted by another one just as legitimate, and is thus scientifically untenable. It would also be impractical for forensics. In the past, differences between large-scale "racially" defined samples were tautologically explained as due to "racial" differences. While DFs may reveal high correlations to population criteria, correlation is not causation: There are biological differences between population samples, but these are not explained in a racial framework. Rather, these differences reflect the different origins and separate histories of each group, which can be highly correlated with many social, geographic, temporal, historical, or linguistic groupings of populations. These correlations form the basis of the study of human variation and of forensic anthropology.

Tutorial Part I

Some examples will illustrate what the program produces and offer some guidelines for interpreting the results. The results may vary somewhat depending on the reference database used. A recent publication that covers statistical background and approaches to classifying human remains is found in Ousley and Jantz (2012) and Ousley and Jantz (2012, 2017).

Suppose we have a cranium which we want to compare to white males and black males. To do so, choose File |Open and choose Example1. Click the Use All button (or press Alt + U) to analyze all measurements, and click Process or F8 to analyze. You will then see a progress indicator during the data extraction, calculation of the discriminant functions, and during the classification of the calibration sample.

First, the results page shows the measurements of the cranium, the variable Check (Chk) column, the means for the two groups, and the discriminant function weights and relative weights for each variable. In this case, the measurements most effective at separating the two groups are BPL, NLB, AUB, and BNL. Notice that some measurements apparently contribute little or nothing to group separation. The last row of the table gives the mean discriminant scores for each group and the score for the unknown. Note that in two-group DFs the sectioning point is always zero. The unknown shows a score on the negative side of the sectioning point; hence it is classified as white in this two group function. While many measurements are above or below the means for each groups, none is more than 2 standard deviations (++) further from the mean of each. The natural log of the determinant is a positive number and relatively large, indicating that the pooled variance-covariance matrix showed enough structure to have well-estimated parameters.

Next, we see how well the twelve measurements we have chosen discriminate the calibration or reference samples in the classification matrix. From this we observe that about 89% of black males and 90% of white males were correctly classified, about 89% overall, when cross-validated.

Finally, the bottom of the result screen indicates that the unknown has been classified as white, and provides some probabilities to assess how much confidence might be placed on the classification. The posterior probabilities show that the unknown is slightly more likely to be black than white, and the typicality probabilities tells us that the unknown would not be atypical in either population. Similar to the p-value calculated from the normal distribution, the typicality probabilities (Typ F) can be read as the probability for the null hypothesis that the unknown is a member of each group in question. Values less than roughly 0.010 could be considered atypical, indicating that only 1% of that population, 1 in 100, would be expected to have such a differing morphology (i.e., to have scores further away from the population centroid) as this unknown. Also, the Chi-square and ranked typicality probabilities do not indicate that this is an unusual individual compared to these groups. The high typicality probabilities are also reflected in the small deviations shown in the Chk column above.

```
--------------------------------------------------------------------------------
FORDISC 3.1 Analysis of Demo file 1
Using cranial data file version 1.23

DFA results using 12 measurements:
AUB   BBH   BNL   BPL   FRC   GOL   NLB   NLH   OCC   PAC
XCB   ZYB
--------------------------------------------------------------------------------
Measurement Checks, Group Means, and Discriminant Function Coefficients

--------------------------------------------------------------------------------
Demo file 1  Chk             BM             WM          DF      Relative
                             114            403       Weights     Weights
--------------------------------------------------------------------------------
  AUB   127     +           120.8          123.4      -0.316      13.3 %
  BBH   134     -           137.6          141.2       0.005       0.3 %
  BNL   102     -           104.4          105.7      -0.463       9.7 %
  BPL    95     -           104.0           97.4       0.389      42.3 %
  FRC   108     -           112.8          115.0      -0.042       1.5 %
  GOL   186     -           187.1          187.9       0.070       0.9 %
  NLB    25                  26.2           24.0       0.458      16.9 %
  NLH    53     +            52.5           52.9       0.013       0.1 %
  OCC    94     -            98.8          100.8      -0.047       1.5 %
  PAC   114     -           117.2          118.0      -0.041       0.6 %
  XCB   135     -           135.5          140.6      -0.114       9.5 %
  ZYB   136    ++           130.5          129.8       0.314       3.3 %

           Constant                                   11.122
--------------------------------------------------------------------------------
             Scores         2.942         -2.942       0.310
                               (Group means)          (Case)

              Mahalanobis Distance = 5.883
--------------------------------------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs
--------------------------------------------------------------------------------
```

Natural Log of VCVM Determinant = 32.4289

Classification Matrix

From Group	Group Counts	Into Group (counts) BM	WM	Percent Correct
BM	114	101	13	88.6 %
WM	403	42	361	89.6 %
Total Correct:	462 / 517 (89.4 %) *** CROSS-VALIDATED ***			

Two Group Discriminant Function Results

Group	Classified into	Distance from	Probabilities Posterior	Typ F	Typ Chi	Typ R
BM	**BM**	12.2	0.577	0.462	0.431	0.461 (63/115)
WM		12.8	0.423	0.409	0.383	0.406 (241/404)

On the extended results page, the Kullback test for homogeneity of variance-covariance matrices is almost one. p values lower than 0.0001 may be a strong indicator of significant variance-covariance homogeneity, and different measurements and/or a smaller number of them should probably be used.

Next, click on the graph tab. You will see a histogram of the discriminant scores of the calibration samples and the unknown represented by an X at its score (Figure 1). Note that the legend for each group is in the top right corner of the screen, and most of the black sample is on the right side of the screen, while most of the white sample is on the left side of the screen. What you are looking at are two more or less normally distributed scores that overlap. If these scores are normally distributed, then one of the assumptions for the LDF is met. Keep in mind that the heights of each will depend on the sample sizes in each, but the spread should be more or less the same in each. The sectioning point, at zero, is indicated in the middle of the screen. The plot shows that the unknown falls on the black side of the sectioning point but within the range of white scores, a reflection of the typicality probabilities viewed earlier.

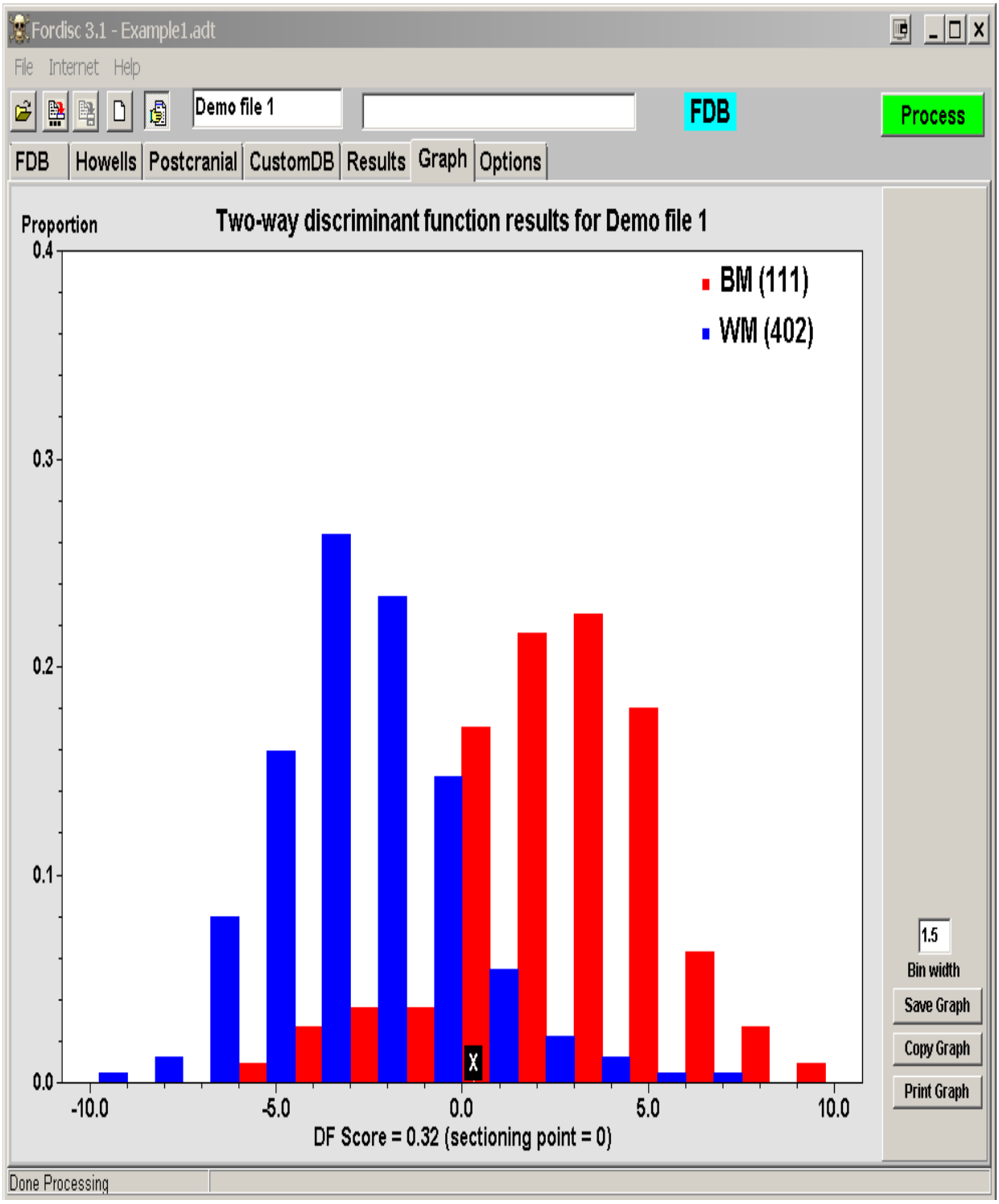


Figure 1. Histogram based on example1.db

We believe that the stepwise-selected procedure often removes "noisy" measurements that do not contribute to discrimination, but keep in mind that stepwise selection is needed the most when the samples sizes are relatively small compared to the number of available measurements, a condition known as overfitting. This example is for demonstration purposes only. **For most forensic cases you should not need to use stepwise selection.** Click the Options tab and click on the

Stepwise option, and be sure that "Forward Mean %" is selected. Click the Process button or press F8 to run an analysis. Stepwise variable selection tries to discover the best measurements that separate groups. Notice that fewer measurements were needed to achieve correct classification (89.0 %) nearly as good as using all measurements (89.9 %). Each step of the stepwise selection of measurements is shown on the Steps page. You can double-check all previous runs by clicking on the Log tab on the Results page. A good analysis tries to include enough measurements to encompass important morphological variation, while avoiding using too many redundant, or "noisy" measurements.

```
------------------------------------------------------------------------------
FORDISC 3.1.315 Analysis of Demo file 1
Using cranial data file version 1.23

DFA results using 6 Forward Mean % selected (min: 1 max: 20, out of 12) measurements:
NLB   XCB   BPL   BNL   ZYB   BBH
-------------------------------------------------------------------------------
Measurement Checks, Group Means, and Discriminant Function Coefficients

-------------------------------------------------------------------------------
Demo file 1  Chk             BM             WM          DF      Relative
                             128            435       Weights     Weights
-------------------------------------------------------------------------------
  NLB    25                  26.2           24.0       0.500      21.2 %
  XCB   135     -           135.5          140.5      -0.192      18.0 %
  BPL    95     -           104.0           97.4       0.382      47.2 %
  BNL   102     -           104.5          105.7      -0.414       9.7 %
  ZYB   136    ++           130.5          129.8       0.103       1.3 %
  BBH   134     -           137.6          141.3      -0.036       2.5 %

            Constant                                  10.715
-------------------------------------------------------------------------------
             Scores         2.660         -2.660       0.426
                               (Group means)          (Case)

              Mahalanobis Distance = 5.319
-------------------------------------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs
-------------------------------------------------------------------------------
Natural Log of VCVM Determinant =  16.5284

-------------------------------------------------------------------
Classification Matrix

-------------------------------------------------------------------
     From         Group        Into Group (counts)     Percent
     Group        Counts          BM          WM       Correct
-------------------------------------------------------------------
        BM         128           114          14        89.1 %

        WM         435            48         387        89.0 %
-------------------------------------------------------------------
     Total Correct:      501 / 563 ( 89.0 %) *** CROSS-VALIDATED ***

-------------------------------------------------------------------------------------------
Two Group Discriminant Function Results

-------------------------------------------------------------------------------------------
    Group         Classified     Distance        Probabilities
                     into          from      Posterior  Typ F   Typ Chi  Typ R
-------------------------------------------------------------------------------------------
        BM         **BM**           7.3        0.605    0.311    0.298   0.271 (95/129)
        WM                          8.1        0.395    0.239    0.231   0.248 (329/436)
-------------------------------------------------------------------------------------------
```

Next, under stepwise selection, click on the Forward Wilks option. This is another way of selecting the best measurements that separate groups. Generally, more measurements will be selected using the default values and the classification accuracy is slightly higher than the Forward Mean % selected measurements, and is often nearly the same as using all 12 measurements. The values for % Step and W Step control how much improvement is required in order for the selection procedure to keep going.

```
------------------------------------------------------------------------------
FORDISC 3.1.315 Analysis of Demo file 1
Using cranial data file version 1.23

DFA results using 6 Forward Wilks selected (min: 1 max: 20, out of 12) measurements:
BPL   BNL   NLB   XCB   ZYB   AUB
-------------------------------------------------------------------------------
Measurement Checks, Group Means, and Discriminant Function Coefficients

-------------------------------------------------------------------------------
Demo file 1  Chk             BM             WM          DF      Relative
                             118            417       Weights     Weights
```

```
-------------------------------------------------------------------------------------
  BPL    95     -           104.0           97.3       0.386      44.5 %
  BNL   102     -           104.5          105.7      -0.435       9.0 %
  NLB    25                  26.2           24.0       0.459      17.8 %
  XCB   135     -           135.5          140.5      -0.129      11.2 %
  ZYB   136    ++           130.5          129.8       0.325       4.1 %
  AUB   127     +           120.8          123.3      -0.311      13.5 %

           Constant                                    8.806
-------------------------------------------------------------------------------------
            Scores         2.904         -2.904      -0.165
                              (Group means)          (Case)

             Mahalanobis Distance = 5.807
-------------------------------------------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs
-------------------------------------------------------------------------------------
Natural Log of VCVM Determinant =  15.2254

-----------------------------------------------------------------
Classification Matrix

-----------------------------------------------------------------
     From         Group        Into Group (counts)     Percent
     Group        Counts          BM          WM       Correct
-----------------------------------------------------------------
        BM         118           104          14        88.1 %

        WM         417            40         377        90.4 %
-----------------------------------------------------------------
     Total Correct:      481 / 535 ( 89.9 %) *** CROSS-VALIDATED ***

-------------------------------------------------------------------------------------------
Two Group Discriminant Function Results

-------------------------------------------------------------------------------------------
    Group         Classified     Distance        Probabilities
                     into          from      Posterior  Typ F   Typ Chi  Typ R
-------------------------------------------------------------------------------------------
        WM         **WM**           7.9        0.541    0.255    0.245   0.256 (312/418)
        BM                          8.2        0.459    0.234    0.222   0.227 (93/119)
-------------------------------------------------------------------------------------------
```

Notice that the classification into WM is different from the other analyses. This case is quite near the sectioning point, so this is to be expected under many circumstances.

Another example will illustrate the value of the probabilities, and possible pitfalls in many other discriminant functions. Open Example2 and click off the stepwise selection of measurements. Use all measurements and press F8 to analyze. Scroll down the text results and you can see that the function performs pretty well on the sample groups, classifying 81% correctly. Remember, a random allocation to groups for a four group function would be 25% correct.

```
-----------------------------------------------------------------------------
FORDISC 3.1 Analysis of Example 2
Using cranial data file version 1.23

DFA results using 18 measurements:
AUB   BBH   BNL   BPL   DKB   FRC   GOL   MAB   MAL   MDH
NLB   NLH   OCC   PAC   UFHT  WFB   XCB   ZYB
-------------------------------------------------
Measurement Checks and Group Means
                         Group Means
                          BF     BM     WF     WM
Example 2       Chk       68    102    173    287
-------------------------------------------------
  AUB      126     +    115.6  120.6  116.8  123.2
  BBH      138          131.7  137.8  134.2  141.7
  BNL       94    --     98.6  104.6   99.2  106.2
  BPL       96           99.0  104.3   92.2   98.3
  DKB       20     -     22.4   23.7   19.9   21.2
  FRC      108     -    108.2  112.9  109.2  114.8
  GOL      168    --    178.5  186.7  177.5  188.1
  MAB       67     +     62.7   66.1   58.1   61.6
  MAL       53           56.0   58.0   51.1   54.4
  MDH       25     -     28.1   32.3   27.6   32.4
  NLB       26           25.0   26.2   22.5   23.8
  NLH       54     +     48.2   52.5   48.9   52.9
  OCC       94     -     97.4   98.4   97.7  101.0
  PAC      114          112.9  117.2  112.6  118.4
UFHT       71           66.8   72.7   66.8   71.9
  WFB       94           93.4   96.1   93.9   96.9
  XCB      144     +    133.1  135.5  135.6  140.2
  ZYB      138    ++    121.9  130.5  120.7  129.7
-------------------------------------------------
```

```
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- deviates at least 3 STDEVs
--------------------------------------------------
Natural Log of VCVM Determinant =  44.2848

-------------------------------------------------------------
Classification Table

-------------------------------------------------------------
From     Total            Into Group (counts)
Group    Number     BF     BM     WF     WM    Correct
-------------------------------------------------------------
     BF     68       51      5     10      2     75.0 %
     BM    102        9     82      1     10     80.4 %
     WF    173       18      1    137     17     79.2 %
     WM    287        2     23     20    242     84.3 %
-------------------------------------------------------------
Total Correct:  512 out of 630 (81.3 %) *** CROSS-VALIDATED ***

-----------------------------------------------------------------------------------------
Multigroup Classification of Example 2

-----------------------------------------------------------------------------------------
   Group      Classified      Distance          Probabilities
                 into           from     Posterior   Typ F   Typ Chi   Typ R
-----------------------------------------------------------------------------------------

     BM         **BM**          29.3        0.892    0.063    0.045    0.184 (84/103)
     WM                         34.1        0.078    0.018    0.012    0.035 (278/288)
     BF                         36.4        0.025    0.011    0.006    0.058 (65/69)
     WF                         40.1        0.004    0.004    0.002    0.006 (173/174) ----------------------------
-------------------------------------------------------
  Example 2 is closest to BMs
-----------------------------------------------------------------------------------------
```

Click on the Graph tab. The first canonical axis, the axis that shows the greatest differences (55.5 %) among means, separates males on the left from females on the right. The second axis, representing 42.9% of the differences among group means, separates white Americans above from black Americans below. There is very little variation left to display on the third canonical axis. The position of the unknown is indicated by the X. The unknown appears closest to the black male centroid.

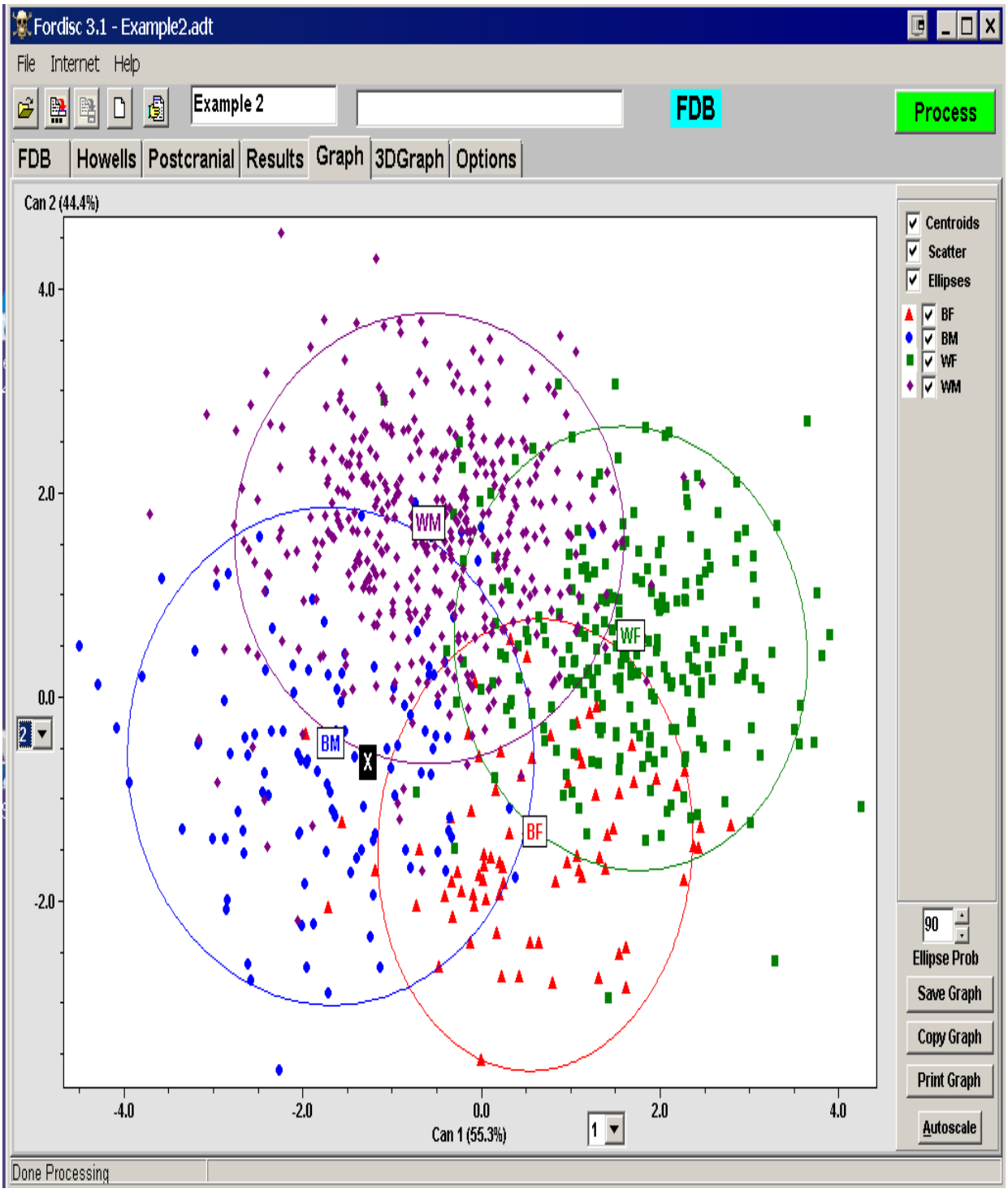


Figure 2. Canonical Plot of Example2 with four groups.

Move back to the text results. The unknown is closest to black males based on these measurements, and very strongly so, based on the high posterior probability for black males. These results are similar to the results of other published discriminant functions, that is, indicating to which reference group the unknown is closest. The posterior probability is high for black males and low for the other groups. The bolded typicality probabilities are a reminder that the probability is less than 0.05; the bolded red probabilities are less than 0.01. These are most important when the most similar group is

atypical. Take a look at the F typicality probabilities. According to the F typicality probabilities, this is an unusual skull if it is of a modern White, but the most similar group is the most important one to compare. The Chi-square typicality probability is low for Black males, the group it was classified into. Perhaps we can see why. Scroll up and look at the Chk column and the measurement means and the group means. The unknown cranium shows a shorter head length (GOL), a wider cranial breadth (XCB), wider zygomatic arches (ZYB), a relatively wide palate (MAB), and a low cranial base length (BNL) relative to these four groups, especially to the Whites. The mixture of lower and higher measurements are indicative of shape differences expressed in these measurements. It may not be a member of the four groups we tested against, and that is one reason why Fordisc presents the measurement checks first. An analysis using all groups is in order.

Click "All Females" and "All Males" to include all the other groups, and press F8. This function using all groups will take longer to process than the four group function. In examining the measurement checks and group means, the unknown's measurements are no longer so unusual and all are close to the Vietnamese means.The results screen shows that the correct classification rates have fallen to 57% overall. With more groups, correct classification rates can be expected to decline, but the rate is still much higher than random assignment (1/13 = 7.7 %). Maybe the classification matrix can tell us why. It reveals that many of the East Asian groups tend to classify into other East Asian groups using these measurements. Also, a good number of white males are classified as white females, Hispanic males, and Japanese males. This time, FORDISC indicates that the unknown is closest to Vietnamese males, with a high posterior probability, and all three typicality probabilities are also high. It is also not atypical of many other populations. The typicality probabilities show that the unknown is closer to the Vietnamese centroid than 92% of the rest of the theoretical distribution of Vietnamese, and 57% of the Vietnamese in the sample. Also, the second and third groups most similar are the Chinese and Japanese males. The skull shows general East Asian similarities. The posterior probability for black males is now quite close to zero.

```
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----
FORDISC 3.1 Analysis of Example 2
Using cranial data file version 1.23

DFA results using 18 measurements:
AUB   BBH   BNL   BPL   DKB   FRC   GOL   MAB   MAL   MDH
NLB   NLH   OCC   PAC   UFHT  WFB   XCB   ZYB
--------------------------------------------------------------------------------------------------------------------------------
-------
Measurement Checks and Group Means
                                                    Group Means
                          AF     AM     BF     BM    CHM    GTM     HF     HM     JF     JM     VM     WF     WM
Example 2       Chk       28     51     68    102     73     67     42    174    115    183     48    173    287
--------------------------------------------------------------------------------------------------------------------------------
-------
  AUB      126          126.0  132.1  115.6  120.6  123.6  124.0  119.0  124.1  117.2  123.2  122.8  116.8  123.2
  BBH      138          129.6  133.4  131.7  137.8  139.5  133.3  131.5  136.8  131.9  138.2  137.8  134.2  141.7
  BNL       94      -   100.1  103.0   98.6  104.6  100.6   98.5   95.6  101.1   95.5  101.6   97.6   99.2  106.2
  BPL       96           96.8  100.1   99.0  104.3   96.0   97.7   92.9   98.7   93.6   97.4   95.4   92.2   98.3
  DKB       20      -    22.4   22.5   22.4   23.7   22.1   21.6   20.5   21.2   20.5   21.4   21.3   19.9   21.2
  FRC      108          107.9  110.8  108.2  112.9  112.8  106.6  106.6  111.2  107.2  110.8  112.1  109.2  114.8
  GOL      168      -   177.7  180.1  178.5  186.7  179.4  173.1  170.9  178.4  171.7  179.2  172.4  177.5  188.1
  MAB       67      +    62.9   66.2   62.7   66.1   64.2   64.6   62.6   65.4   60.3   63.9   66.4   58.1   61.6
  MAL       53           53.2   54.8   56.0   58.0   52.8   55.2   52.4   55.4   50.5   52.7   52.2   51.1   54.4
  MDH       25           24.8   29.5   28.1   32.3   29.5   31.1   26.2   28.5   26.2   30.1   26.5   27.6   32.4
  NLB       26           25.4   26.1   25.0   26.2   26.2   25.5   24.0   24.9   25.0   25.5   26.2   22.5   23.8
  NLH       54      +    51.6   53.8   48.2   52.5   52.4   52.0   49.1   52.1   48.7   51.4   53.1   48.9   52.9
  OCC       94           93.8   93.9   97.4   98.4   98.3   95.8   95.8   97.3   96.7  100.1   98.4   97.7  101.0
  PAC      114          107.7  110.1  112.9  117.2  115.3  112.1  108.8  112.0  108.9  113.3  110.4  112.6  118.4
UFHT       71           70.8   73.4   66.8   72.7   73.1   71.8   67.3   73.1   68.4   72.1   71.5   66.8   71.9
  WFB       94           91.9   97.1   93.4   96.1   91.7   93.0   92.4   94.3   90.0   93.0   94.7   93.9   96.9
  XCB      144      +   137.3  143.0  133.1  135.5  139.5  136.8  135.5  138.4  134.0  138.3  140.5  135.6  140.2
  ZYB      138          132.1  141.2  121.9  130.5  132.9  131.9  123.5  131.2  124.8  133.2  130.0  120.7  129.7
--------------------------------------------------------------------------------------------------------------------------------
-------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- deviates at least 3 STDEVs
--------------------------------------------------------------------------------------------------------------------------------
-------
Natural Log of VCVM Determinant =  43.9485

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Classification Table

--------------------------------------------------------------------------------------------------------------------------------
------------------
From     Total            Into Group (counts)
Group    Number     AF     AM     BF     BM    CHM    GTM     HF     HM     JF     JM     VM     WF     WM
Correct
--------------------------------------------------------------------------------------------------------------------------------
------------------
     AF     28       12      6      1      0      2      1      2      2      0      0      1      1      0
42.9 %
```

AM	51	2	32	0	4	4	2	1	1	0	2	1	0	2
62.7 %														
BF	68	1	0	41	5	1	1	5	3	3	0	1	6	1
60.3 %														
BM	102	1	1	7	65	2	5	0	5	1	2	2	1	10
63.7 %														
CHM	73	3	1	0	4	35	1	2	4	5	13	5	0	0
47.9 %														
GTM	67	1	2	1	4	2	40	4	4	2	4	2	1	0
59.7 %														
HF	42	1	0	5	0	0	1	18	1	7	0	4	4	1
42.9 %														
HM	174	13	4	5	14	5	22	10	47	7	16	13	1	17
27.0 %														
JF	115	2	0	3	1	4	5	12	3	71	8	4	2	0
61.7 %														
JM	183	4	10	0	6	29	14	2	12	18	80	3	0	5
43.7 %														
VM	48	0	0	0	0	3	2	5	1	4	0	33	0	0
68.8 %														
WF	173	1	0	11	1	0	1	18	2	4	0	2	119	14
68.8 %														
WM	287	4	7	0	11	8	2	3	8	0	12	0	19	213
74.2 %														

Total Correct: 806 out of 1411 (57.1 %) *** CROSS-VALIDATED ***

Multigroup Classification of Example 2

Group	Classified into	Distance from	Probabilities Posterior	Typ F	Typ Chi	Typ R
VM	**VM**	12.0	0.834	0.864	0.845	0.714 (14/49)
CHM		17.4	0.057	0.526	0.495	0.392 (45/74)
GTM		17.9	0.045	0.497	0.464	0.397 (41/68)
HM		19.0	0.026	0.415	0.392	0.520 (84/175)
JM		19.1	0.025	0.410	0.389	0.261 (136/184)
AM		21.4	0.008	0.297	0.262	0.481 (27/52)
JF		22.5	0.005	0.234	0.212	0.103 (104/116)
HF		25.6	0.001	0.136	0.109	0.302 (30/43)
AF		28.6	0.000	0.077	0.054	**0.034 (28/29)**
BM		28.6	0.000	0.065	0.054	0.204 (82/103)
WM		35.1	0.000	**0.011**	**0.009**	**0.031 (279/288)**
BF		35.7	0.000	**0.011**	**0.008**	0.058 (65/69)
WF		40.1	0.000	**0.003**	**0.002**	**0.006 (173/174)**

Example 2 is closest to VMs

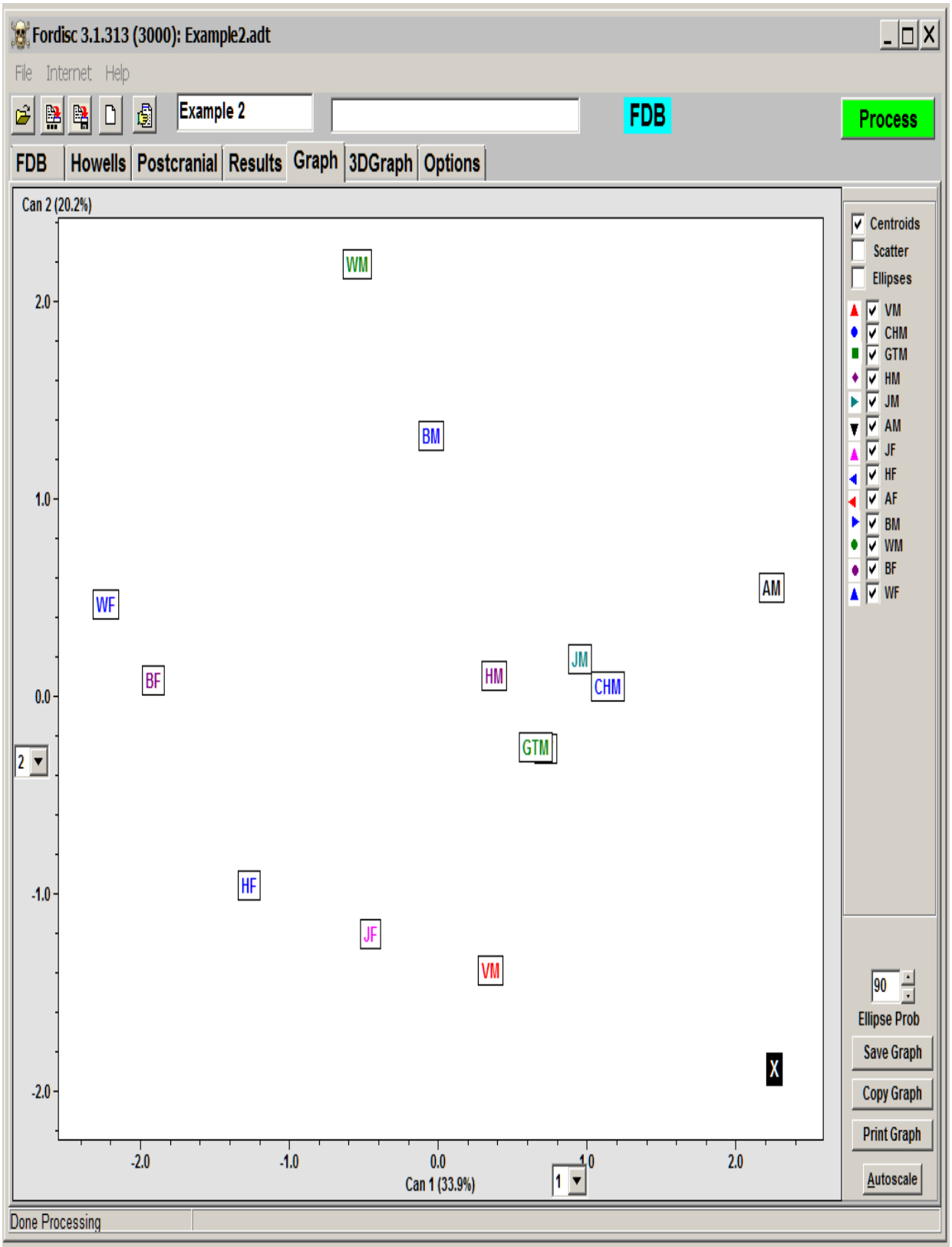

Figure 3. Canonical Plot of Example2 with twelve groups.

Click on the Graph tab. It may be more clear if you click off the Scatter and Ellipses, and just view the centroids (Figure 3). The unknown appears to be about equidistant to Guatemalan and Vietnamese males. But this plot is more distorted than the four group plot because the first two axes only represent about 20.2 + 33.9 = 54 % of the total variation among group means. This distortion becomes less pronounced with fewer measurements and groups. The general procedure we recommend for classification is to repeatedly classify, after removing the most dissimilar group each time, until all groups have posterior probabilities of at least 0.10, or there are only two groups left. We will take a shortcut here. To see the effects of fewer groups, analyze Example 2 again with the same data using the three closest groups based on the text results: Guatemalan males, Chinese males, and Vietnamese males. Click on the Scatter and Ellipses boxes. This time, the two-dimensional canonical plot will better express the closer relationship between the unknown and the Vietnamese sample, because it can display 100% of the variation (Figure 4). These measurements are from a University of Tennessee forensic case positively identified as a Laotian male. Even though the confidence ellipses of the three groups have slightly different orientations and shapes, no heterogeneity in the variance-covariance matrices is indicated by the Kullback test.

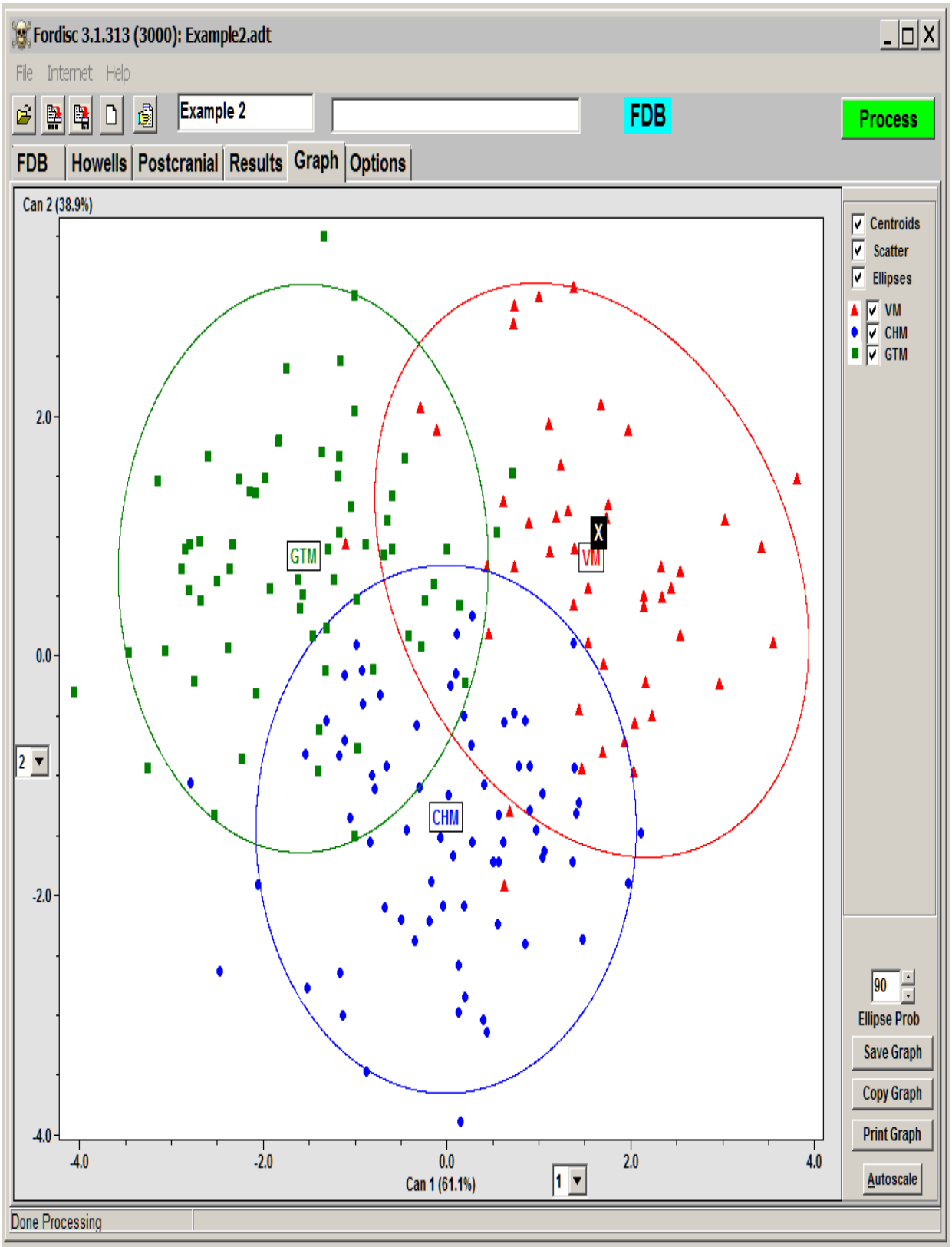

Figure 4. Canonical Plot of Example2 with the three most similar groups.

FORDISC 3.1 Analysis of Example 2
Using cranial data file version 1.23

DFA results using 18 measurements:
AUB BBH BNL BPL DKB FRC GOL MAB MAL MDH
NLB NLH OCC PAC UFHT WFB XCB ZYB

Measurement Checks and Group Means

			Group Means		
			CHM	GTM	VM
Example 2	Chk		73	67	48
AUB	126	+	123.6	124.0	122.8
BBH	138		139.5	133.3	137.8
BNL	94	--	100.6	98.5	97.6
BPL	96		96.0	97.7	95.4
DKB	20	-	22.1	21.6	21.3
FRC	108		112.8	106.6	112.1
GOL	168	-	179.4	173.1	172.4
MAB	67	+	64.2	64.6	66.4
MAL	53		52.8	55.2	52.2
MDH	25	-	29.5	31.1	26.5
NLB	26		26.2	25.5	26.2
NLH	54	+	52.4	52.0	53.1
OCC	94	-	98.3	95.8	98.4
PAC	114		115.3	112.1	110.4
UFHT	71	-	73.1	71.8	71.5
WFB	94		91.7	93.0	94.7
XCB	144	+	139.5	136.8	140.5
ZYB	138	++	132.9	131.9	130.0

+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- deviates at least 3 STDEVs

Natural Log of VCVM Determinant = 40.8723

Classification Table

From Group	Total Number	Into Group (counts) CHM	GTM	VM	Correct
CHM	73	54	10	9	74.0 %
GTM	67	8	54	5	80.6 %
VM	48	6	3	39	81.3 %

Total Correct: 147 out of 188 (78.2 %) *** CROSS-VALIDATED ***

Multigroup Classification of Example 2

Group	Classified into	Distance from	Probabilities Posterior	Typ F	Typ Chi	Typ R
VM	**VM**	13.1	0.979	0.857	0.783	0.837 (8/49)
CHM		21.4	0.016	0.393	0.260	0.378 (46/74)
GTM		23.5	0.006	0.295	0.173	0.309 (47/68)

Example 2 is closest to VMs

Proceed to Part II

Tutorial Part II

Next, open Example3 and run a postcranial analysis on American black and white males and females by choosing the postcranial tab and selecting all groups and measurements. Click on "Process" or press F8 to analyze the data. The measurement checks have many plus signs, including some triple signs in blue (**+++**), meaning that this individual has relatively large measurements. The mean classification accuracy is 94%, and Example 3 classifies strongly as a black male, with a posterior probability of 0.94. But all F typicality probabilities are zero, and the Chi-square typicality probabilities are all zero too. The ranked typicality probabilities place this individual dead last in each group. These results illustrate the problems with using too many measurements compared to sample sizes, known as the curse of dimensionality, or overfitting mentioned above. To avoid an overfitted function with 36 measurements, we would want a minimum sample size of 37. The smallest sample size comes from black females and is 18. Disregard the classification!

```
--------------------------------------------------
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FORDISC 3.1 Analysis of Example 3
Using postcranial data file version 1.18

DFA results using 36 measurements:
CALCBR  CALCXL  FEMBLN  FEMCIR  FEMEBR  FEMHDD  FEMMAP  FEMMTV
FEMSAP  FEMSTV  FEMXLN  FIBMDM  FIBXLN  HUMEBR  HUMHDD  HUMMWD
HUMMXD  HUMXLN  ILIABR  INNOHT  RADXLN  SACABR  SACAHT  SACS1B
SCAPBR  SCAPHT  TIBCIR  TIBDEB  TIBNFX  TIBPEB  TIBXLN  ULNCIR
ULNDVD  ULNPHL  ULNTVD  ULNXLN
--------------------------------------------------
Measurement Checks and Group Means
                           Group Means
                            BF     BM     WF     WM
Example 3         Chk       18     47    107    284
--------------------------------------------------
CALCBR        42            38.3   43.8   38.9   43.9
CALCXL        76     -      75.9   85.6   78.6   87.0
FEMBLN       518    ++     427.6  485.6  432.4  468.2
FEMCIR        98     +      79.8   92.5   82.6   92.7
FEMEBR        88     +      71.9   82.6   75.5   85.6
FEMHDD        52    ++      40.8   46.9   42.2   48.3
FEMMAP        33     +      27.2   31.5   27.7   31.1
FEMMTV        29     +      23.3   27.6   25.1   28.3
FEMSAP        33    ++      24.4   28.2   25.3   28.3
FEMSTV        37    ++      28.6   31.7   29.1   32.5
FEMXLN       521    ++     431.8  488.9  436.4  471.7
FIBMDM        18     +      13.8   15.6   14.5   16.1
FIBXLN       435    ++     351.4  403.0  351.8  386.2
HUMEBR        71    ++      53.3   64.2   55.3   64.7
HUMHDD        46            40.1   46.8   42.5   49.0
HUMMWD        23    ++      16.1   19.3   15.2   18.7
HUMMXD        28   +++      20.1   23.5   19.8   23.4
HUMXLN       390   +++     302.3  341.0  305.0  334.5
ILIABR       169     +     141.2  154.3  156.3  162.3
INNOHT       232     +     187.8  211.7  202.9  224.5
RADXLN       284    ++     229.6  268.7  227.1  253.6
SACABR        86    --      97.5  102.8  109.0  108.8
SACAHT        89    --     102.8  106.1  109.1  112.7
SACS1B        51            44.1   50.8   46.0   51.1
SCAPBR       117     +      93.1  111.2   96.1  108.4
SCAPHT       180    ++     135.1  161.8  141.7  163.3
TIBCIR       112    ++      86.0  100.6   84.5   97.0
TIBDEB        55    ++      44.2   50.7   45.1   51.2
TIBNFX        43    ++      31.0   37.1   31.6   36.6
TIBPEB        81     +      67.8   78.9   69.7   79.5
TIBXLN       440    ++     357.7  411.4  358.6  392.5
ULNCIR        44    ++      32.2   36.6   31.8   36.4
ULNDVD        18    ++      12.4   15.1   11.6   14.3
ULNPHL       271    ++     220.8  256.6  216.0  240.3
ULNTVD        21    ++      13.6   16.7   14.3   17.5
ULNXLN       303    ++     247.8  287.2  243.3  271.5
--------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- deviates at least 3 STDEVs
--------------------------------------------------
```

Natural Log of VCVM Determinant = 77.9867

Classification Table

From Group	Total Number	Into Group (counts) BF	BM	WF	WM	Correct
BF	18	16	0	2	0	88.9 %
BM	47	2	43	0	2	91.5 %
WF	107	6	0	100	1	93.5 %
WM	284	0	7	6	271	95.4 %

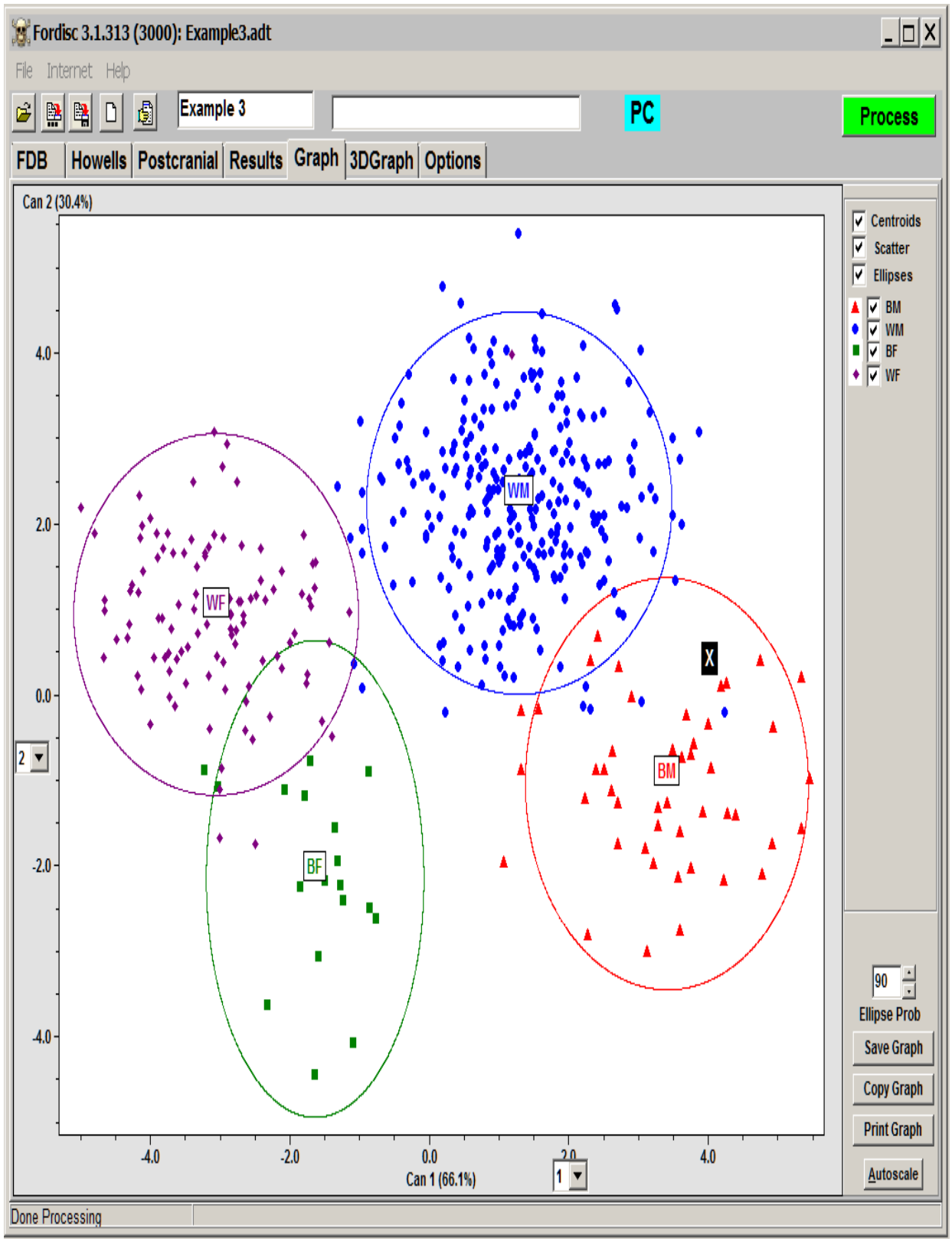
Total Correct: 430 out of 456 (94.3 %) *** CROSS-VALIDATED ***

Multigroup Classification of Example 3

Group	Classified into	Distance from	Probabilities Posterior	Typ F	Typ Chi	Typ R
BM		95.4	0.941	**0.000**	**0.000**	**0.021 (47/48)**
WM		101.0	0.059	**0.000**	**0.000**	**0.004 (284/285)**
BF		127.5	0.000	**0.000**	**0.000**	0.053 (18/19)
WF		144.6	0.000	**0.000**	**0.000**	**0.009 (107/108)**

Example 3 is too dissimilar to all groups; all TPs < 0.01

Click on the Graph tab. The plot illustrates that the unknown is far closer to the male groups than to the female groups, but also that the groups are being separated at an unrealistically high rate.



Due to small sample sizes and many measurements available, we want to use stepwise selection of measurements to reduce the total number of measurements in the analysis so our case is not too

atypical for classification. On the Options tab, click on the Stepwise box, be sure Forward Wilks is selected, and run another analysis with a maximum of 20 measurements. There should be more than 18 black females this time because it will use fewer measurements. Click on "Process" or press F8 to analyze the data. The measurement checks show many measurements with two or more plus signs. This is a consistent pattern for a male of above average stature and overall size. The stepwise procedure used the maximum of six measurements for classification, and example 3 now classifies as a black male. The F- and chi-squared typicality probabilities are zero for the female groups. With such large measurements, it is no wonder that the typicality probabilities for females are so low. Click on the Graph tab and notice the overlap among groups. The unknown is still far closer to the male groups than to the female groups.

```
-----------------------------------------------------------------
------------
FORDISC 3.1 Analysis of Example 3
Using postcranial data file version 1.18

DFA results using 12 Forward Wilks selected (min: 1 max: 20, out of 36) measurements:
HUMEBR  INNOHT  ULNXLN  ILIABR  TIBPEB  HUMMWD  HUMHDD  SCAPBR
SCAPHT  FEMBLN  FEMEBR  SACABR
-------------------------------------------------
Measurement Checks and Group Means
                            Group Means
                             BF     BM     WF     WM
Example 3          Chk       26     85    161    395
-------------------------------------------------
HUMEBR       71    ++     54.4   64.5   55.2   64.7
INNOHT      232     +    191.6  212.3  202.8  224.5
ULNXLN      303    ++    251.2  285.5  243.2  271.4
ILIABR      169     +    145.3  154.3  156.3  161.9
TIBPEB       81     +     68.7   79.3   69.7   79.6
HUMMWD       23    ++     15.9   19.6   15.2   18.8
HUMHDD       46           40.7   47.0   42.6   49.1
SCAPBR      117    ++     94.9  110.5   95.8  108.4
SCAPHT      180    ++    136.4  161.1  141.6  163.5
FEMBLN      518    ++    438.0  484.3  432.3  468.8
FEMEBR       88     +     73.0   83.7   75.5   85.7
SACABR       86    --    100.4  102.3  110.0  109.1
-------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- deviates at least 3 STDEVs
-------------------------------------------------
Natural Log of VCVM Determinant =  36.1211

-----------------------------------------------------------
Classification Table

-----------------------------------------------------------
From     Total            Into Group (counts)
Group    Number     BF     BM     WF     WM    Correct
-----------------------------------------------------------
     BF     26       20      0      6      0     76.9 %
     BM     85        0     80      0      5     94.1 %
     WF    161       14      0    146      1     90.7 %
     WM    395        6     22      8    359     90.9 %
-----------------------------------------------------------
Total Correct:  605 out of 667 (90.7 %) *** CROSS-VALIDATED ***

-------------------------------------------------------------------------------------------
Multigroup Classification of Example 3

-------------------------------------------------------------------------------------------
   Group      Classified      Distance          Probabilities
                 into           from     Posterior   Typ F   Typ Chi   Typ R
-------------------------------------------------------------------------------------------

     BM         **BM**          23.6        0.999    0.030    0.023    0.093 (78/86)
     WM                         37.1        0.001    0.000    0.000    0.008 (393/396)
     BF                         57.2        0.000    0.000    0.000    0.037 (26/27)
     WF                         74.2        0.000    0.000    0.000    0.006 (161/162)
-------------------------------------------------------------------------------------------
  Example 3 is closest to BMs
-------------------------------------------------------------------------------------------
```

It seems clear that the individual is probably a black male, but the typicality probabilities are rather low. We have a good classification rate and can probably use fewer measurements to exclude some groups. Go to the options page

and change the Max value for # Variables to 10 and run again.

```
------------------------------------------------------------------
------------
FORDISC 3.1 Analysis of Example 3
Using postcranial data file version 1.18

DFA results using 10 Forward Wilks selected (min: 1 max: 10, out of 36) measurements:
HUMEBR  INNOHT  ULNXLN  ILIABR  TIBPEB  HUMMWD  HUMHDD  SCAPBR
SCAPHT  ULNTVD
-----------------------------------------------------
Measurement Checks and Group Means
                            Group Means
                             BF     BM     WF     WM
Example 3         Chk        31     88    182    451
-----------------------------------------------------
HUMEBR        71    ++      54.5   64.5   55.3   64.7
INNOHT       232     +     191.2  212.4  202.5  224.5
ULNXLN       303    ++     251.9  285.8  243.7  271.1
ILIABR       169     +     144.6  154.4  156.5  162.1
TIBPEB        81     +      68.8   79.2   69.7   79.5
HUMMWD        23    ++      16.3   19.5   15.3   18.8
HUMHDD        46            40.6   47.1   42.6   49.0
SCAPBR       117    ++      94.5  110.5   95.8  108.4
SCAPHT       180    ++     137.3  161.3  141.7  163.5
ULNTVD        21    ++      14.0   17.0   14.2   17.4
-----------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- deviates at least 3 STDEVs
-----------------------------------------------------
Natural Log of VCVM Determinant =  26.8517

------------------------------------------------------------
Classification Table

------------------------------------------------------------
From     Total            Into Group (counts)
Group    Number     BF     BM     WF     WM    Correct
------------------------------------------------------------
     BF     31       27      0      4      0     87.1 %
     BM     88        0     83      0      5     94.3 %
     WF    182       14      0    167      1     91.8 %
     WM    451        6     29     10    406     90.0 %
------------------------------------------------------------
Total Correct:  683 out of 752 (90.8 %) *** CROSS-VALIDATED ***

-------------------------------------------------------------------------------------------
Multigroup Classification of Example 3

-------------------------------------------------------------------------------------------
   Group      Classified      Distance          Probabilities
                 into           from     Posterior   Typ F   Typ Chi   Typ R
-------------------------------------------------------------------------------------------

     BM          **BM**          14.4        0.992    0.174    0.157    0.247 (67/89)
     WM                          24.0        0.008    0.009    0.008    0.022 (442/452)
     BF                          42.2        0.000    0.000    0.000    0.031 (31/32)
     WF                          55.2        0.000    0.000    0.000    0.005 (182/183)
-------------------------------------------------------------------------------------------
  Example 3 is closest to BMs
-------------------------------------------------------------------------------------------
```

These results make it seem reasonable to classify again using only white and black males. The sample size of 47 for black males from before means we can use all 36 measurements. Turn stepwise selection off and run another analysis using only white and black males.

```
-------------------------------------------------------------------------------------------
FORDISC 3.1 Analysis of Example 3
Using postcranial data file version 1.18

DFA results using 36 measurements:
CALCBR  CALCXL  FEMBLN  FEMCIR  FEMEBR  FEMHDD  FEMMAP  FEMMTV
FEMSAP  FEMSTV  FEMXLN  FIBMDM  FIBXLN  HUMEBR  HUMHDD  HUMMWD
HUMMXD  HUMXLN  ILIABR  INNOHT  RADXLN  SACABR  SACAHT  SACS1B
SCAPBR  SCAPHT  TIBCIR  TIBDEB  TIBNFX  TIBPEB  TIBXLN  ULNCIR
ULNDVD  ULNPHL  ULNTVD  ULNXLN
-------------------------------------------------------------------------------------------
Measurement Checks, Group Means, and Discriminant Function Coefficients

-------------------------------------------------------------------------------------------
Example 3      Chk             BM             WM          DF      Relative
                                47             284      Weights     Weights
-------------------------------------------------------------------------------------------
CALCBR    42     -            43.8           43.9       0.073       0.0 %
CALCXL    76    --            85.6           87.0      -0.136       0.8 %
```

FEMBLN	518	++	485.6	468.2	0.054	3.8 %
FEMCIR	98	+	92.5	92.7	-0.112	0.1 %
FEMEBR	88	+	82.6	85.6	-0.540	6.6 %
FEMHDD	52	++	46.9	48.3	-0.049	0.3 %
FEMMAP	33	+	31.5	31.1	0.479	0.9 %
FEMMTV	29	+	27.6	28.3	0.580	1.7 %
FEMSAP	33	++	28.2	28.3	-0.424	0.3 %
FEMSTV	37	++	31.7	32.5	-0.053	0.2 %
FEMXLN	521	++	488.9	471.7	-0.001	0.1 %
FIBMDM	18	+	15.6	16.1	-0.617	1.2 %
FIBXLN	435	++	403.0	386.2	-0.128	8.7 %
HUMEBR	71	++	64.2	64.7	-0.007	0.0 %
HUMHDD	46	-	46.8	49.0	-0.411	3.7 %
HUMMWD	23	++	19.3	18.7	0.528	1.4 %
HUMMXD	**28**	**+++**	23.5	23.4	0.225	0.1 %
HUMXLN	**390**	**+++**	341.0	334.5	-0.099	2.6 %
ILIABR	169	+	154.3	162.3	-0.150	4.8 %
INNOHT	232	+	211.7	224.5	-0.396	20.4 %
RADXLN	284	++	268.7	253.6	0.154	9.4 %
SACABR	86	--	102.8	108.8	-0.035	0.9 %
SACAHT	89	--	106.1	112.7	-0.039	1.0 %
SACS1B	51		50.8	51.1	0.194	0.2 %
SCAPBR	117	+	111.2	108.4	0.314	3.6 %
SCAPHT	180	++	161.8	163.3	-0.010	0.1 %
TIBCIR	112	++	100.6	97.0	0.448	6.3 %
TIBDEB	55	++	50.7	51.2	0.131	0.3 %
TIBNFX	43	++	37.1	36.6	-0.638	1.3 %
TIBPEB	81	+	78.9	79.5	0.613	1.5 %
TIBXLN	440	++	411.4	392.5	0.100	7.7 %
ULNCIR	44	++	36.6	36.4	-0.083	0.1 %
ULNDVD	18	++	15.1	14.3	-0.046	0.1 %
ULNPHL	271	++	256.6	240.3	0.017	1.1 %
ULNTVD	21	++	16.7	17.5	-0.006	0.0 %
ULNXLN	303	++	287.2	271.5	0.141	8.9 %

Constant			1.064
Scores	8.277	-8.277	2.195
	(Group means)		(Case)

Mahalanobis Distance = 16.553

+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs

Natural Log of VCVM Determinant = 77.3961

Classification Matrix

From Group	Group Counts	Into Group (counts) BM	WM	Percent Correct
BM	47	44	3	93.6 %
WM	284	9	275	96.8 %

Total Correct: 319 / 331 (96.4 %) *** CROSS-VALIDATED ***

Two Group Discriminant Function Results

Group	Classified into	Distance from	Probabilities Posterior	Typ F	Typ Chi	Typ R
BM		96.4	0.900	0.000	0.000	**0.021 (48/48)**
WM		100.8	0.100	0.000	0.000	0.007 (284/285)

Example 3 is too dissimilar to all groups; all TPs < 0.01

Wow, we can get high classification accuracy using all the measurements, but they still make our individual quite atypical. We must use fewer measurements. Turn on stepwise selection choose Forward Mean %, change the % Step to 0.005, and change the maximum variables allowed to 30. This time, only three measurements were selected, they are not as deviant compared to the group means, and Example 3 classifies once again as a black male. Most importantly, the typicality probabilities are higher, which often happens when fewer measurements are used.

```
-------------------------------------------------
------------------------------
FORDISC 3.1.315 Analysis of Example 3
Using postcranial data file version 1.18

DFA results using 3 Forward Mean % selected (min: 1 max: 30, out of 36) measurements:
ULNPHL  INNOHT  FEMMAP
-------------------------------------------------------------------------------------
Measurement Checks, Group Means, and Discriminant Function Coefficients

-------------------------------------------------------------------------------------
Example 3      Chk             BM             WM          DF      Relative
                                94            482       Weights     Weights
-------------------------------------------------------------------------------------
ULNPHL   271    ++           254.8          240.2       0.207      43.6 %
INNOHT   232     +           212.9          224.6      -0.309      51.8 %
FEMMAP    33     +            31.9           31.0       0.381       4.6 %

              Constant                                    4.307
-------------------------------------------------------------------------------------
               Scores         3.475         -3.475       1.383
                                 (Group means)          (Case)

                Mahalanobis Distance = 6.950
-------------------------------------------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs
-------------------------------------------------------------------------------------
Natural Log of VCVM Determinant =  10.8567

-----------------------------------------------------------------
Classification Matrix

-----------------------------------------------------------------
     From         Group        Into Group (counts)      Percent
     Group        Counts          BM          WM        Correct
-----------------------------------------------------------------
        BM          94            86           8        91.5 %

        WM         482            44         438        90.9 %
-----------------------------------------------------------------
     Total Correct:      524 / 576 ( 91.0 %) *** CROSS-VALIDATED ***

-------------------------------------------------------------------------------------------
Two Group Discriminant Function Results

-------------------------------------------------------------------------------------------
    Group         Classified     Distance        Probabilities
                     into          from      Posterior  Typ F   Typ Chi  Typ R
-------------------------------------------------------------------------------------------
        BM         **BM**           3.8         0.800    0.289    0.281   0.347 (63/95)
        WM                          6.6         0.200    0.089    0.086   0.070 (450/483)
-------------------------------------------------------------------------------------------
```

Notice that using stepwise selection can result in only three measurements being selected. Whether or not three measurements classify well or not, it is worthwhile to contemplate whether three measurements can capture enough meaningful variation for a classification that applies to this new case. Change the % Step value to 0.001 and run again.

```
-------------------------------------------------------------------------------------------
FORDISC 3.1.315 Analysis of Example 3
Using postcranial data file version 1.18

DFA results using 7 Forward Mean % selected (min: 1 max: 30, out of 36) measurements:
ULNPHL  INNOHT  FEMMAP  FIBMDM  ULNXLN  FEMMTV  FEMXLN
-------------------------------------------------------------------------------------
Measurement Checks, Group Means, and Discriminant Function Coefficients

-------------------------------------------------------------------------------------
Example 3      Chk             BM             WM          DF      Relative
                                91            449       Weights     Weights
-------------------------------------------------------------------------------------
ULNPHL   271    ++           255.0          240.3      -0.027       4.4 %
INNOHT   232     +           213.2          224.8      -0.375      49.1 %
FEMMAP    33     +            31.8           31.1       0.331       2.8 %
FIBMDM    18     +            15.7           16.1      -0.211       0.9 %
ULNXLN   303    ++           286.5          271.6       0.224      37.6 %
FEMMTV    29     +            28.0           28.4       0.302       1.2 %
FEMXLN   521    ++           488.9          472.3       0.022       4.1 %

              Constant                                    0.267
```

```
-------------------------------------------------------------------------------
               Scores         3.959         -3.959       1.044
                                 (Group means)          (Case)

                Mahalanobis Distance = 7.918
-------------------------------------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs
-------------------------------------------------------------------------------
Natural Log of VCVM Determinant =  20.7128

-------------------------------------------------------------------
Classification Matrix

-------------------------------------------------------------------
     From         Group        Into Group (counts)      Percent
     Group        Counts          BM          WM        Correct
-------------------------------------------------------------------
        BM          91            87           4        95.6 %

        WM         449            36         413        92.0 %
-------------------------------------------------------------------
     Total Correct:      500 / 540 ( 92.6 %) *** CROSS-VALIDATED ***

-----------------------------------------------------------------------------------------
Two Group Discriminant Function Results

-----------------------------------------------------------------------------------------
    Group         Classified     Distance        Probabilities
                     into          from      Posterior  Typ F   Typ Chi  Typ R
-----------------------------------------------------------------------------------------
        BM         **BM**           5.4        0.740    0.622    0.607   0.630 (35/92)
        WM                          7.5        0.260    0.388    0.377   0.358 (290/450)
-----------------------------------------------------------------------------------------
```

Using seven measurements is probably more reliable than using three measurements. This looks like a consistent classification. Change stepwise selection back to Forward Wilks' Lambda. set maximum measurements to 10, and run again.

```
-------------------------------------------------
-----------------------------
FORDISC 3.1.315 Analysis of Example 3
Using postcranial data file version 1.18

DFA results using 10 Forward Wilks selected (min: 1 max: 10, out of 36) measurements:
ULNPHL  INNOHT  TIBCIR  SCAPBR  HUMHDD  FIBMDM  HUMMWD  ILIABR
SACS1B  ULNXLN
-------------------------------------------------------------------------------
Measurement Checks, Group Means, and Discriminant Function Coefficients

-------------------------------------------------------------------------------
Example 3      Chk             BM             WM          DF      Relative
                                62             352       Weights     Weights
-------------------------------------------------------------------------------
ULNPHL   271    ++           256.4          240.0       0.035       4.4 %
INNOHT   232     +           212.0          224.5      -0.396      38.0 %
TIBCIR   112    ++           101.5           97.0       0.260       8.9 %
SCAPBR   117    ++           110.8          108.4       0.237       4.4 %
HUMHDD    46     -            46.8           49.1      -0.437       7.4 %
FIBMDM    18     +            15.7           16.1      -0.380       1.0 %
HUMMWD    23    ++            19.5           18.8       0.400       2.2 %
ILIABR   169     +           154.7          162.2      -0.126       7.3 %
SACS1B    51                  50.7           51.2       0.114       0.4 %
ULNXLN   303    ++           287.8          271.2       0.204      25.8 %

              Constant                                   2.506
-------------------------------------------------------------------------------
               Scores         6.476         -6.476       5.480
                                 (Group means)          (Case)

                Mahalanobis Distance = 12.952
-------------------------------------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs
-------------------------------------------------------------------------------
Natural Log of VCVM Determinant =  27.3976

-------------------------------------------------------------------
Classification Matrix

-------------------------------------------------------------------
     From         Group        Into Group (counts)      Percent
```

```
     Group        Counts           BM           WM       Correct
-------------------------------------------------------------------
        BM           62            61            1        98.4 %

        WM          352            14          338        96.0 %
-------------------------------------------------------------------
     Total Correct:      399 / 414 ( 96.4 %) *** CROSS-VALIDATED ***

-------------------------------------------------------------------------------------
Two Group Discriminant Function Results

-------------------------------------------------------------------------------------
    Group         Classified     Distance        Probabilities
                     into          from      Posterior  Typ F   Typ Chi  Typ R
-------------------------------------------------------------------------------------
        BM          **BM**          10.5        0.996    0.437    0.401   0.429 (37/63)
        WM                          21.4        0.004    0.024    0.018   0.051 (336/353)
-------------------------------------------------------------------------------------
```

Notice that more measurements were selected using Wilks lambda and the classification accuracy improved. But the sample size for black males became rather small. When using postcranial measurements, it is best to remove certain measurements if the sex is pretty certain, such as those from the calcaneus, fibula, and sacrum by unchecking them because sample sizes will be larger: stepwise is performed using only individuals with all selected measurements present. Click the boxes to deselect those measurements and run again.

```
-------------------------------------------------------------------------------------
FORDISC 3.1 Analysis of Example 3
Using postcranial data file version 1.18

DFA results using 10 Forward Wilks selected (min: 1 max: 10, out of 29) measurements:
INNOHT  ULNXLN  TIBCIR  ILIABR  SCAPBR  HUMHDD  TIBPEB  FEMEBR
RADXLN  ULNTVD
-------------------------------------------------------------------------------------
Measurement Checks, Group Means, and Discriminant Function Coefficients

-------------------------------------------------------------------------------------
Example 3      Chk             BM             WM          DF      Relative
                                78            417       Weights     Weights
-------------------------------------------------------------------------------------
INNOHT   232     +           212.3          224.4       -0.370      38.3 %
ULNXLN   303    ++           286.2          271.0        0.069       9.0 %
TIBCIR   112    ++           101.2           97.3        0.201       6.8 %
ILIABR   169     +           154.4          162.2       -0.149       9.8 %
SCAPBR   117    ++           110.6          108.3        0.230       4.5 %
HUMHDD    46     -            47.1           49.0       -0.326       5.4 %
TIBPEB    81     +            79.0           79.5        0.412       1.7 %
FEMEBR    88     +            83.5           85.5       -0.252       4.4 %
RADXLN   284    ++           267.7          252.9        0.153      19.4 %
ULNTVD    21    ++            16.9           17.4        0.163       0.6 %

-------------------------------------------------------------------------------------
+/- measurement deviates higher/lower than all group means; ++/-- deviates 1 to 2 STDEVs
+++/--- deviates two to three STDEVs; ++++/---- at least 3 STDEVs
-------------------------------------------------------------------------------------
              Constant                                    1.750
               Scores         5.582         -5.582        4.083
                                 (Group means)          (Case)

                Mahalanobis Distance = 11.164

F-ratio significance of Mahalanobis Distance between groups: p <=   0.001
Natural Log of VCVM Determinant =  27.7110
-------------------------------------------------------------------
Classification Matrix

-------------------------------------------------------------------
     From         Group        Into Group (counts)      Percent
     Group        Counts           BM           WM       Correct
-------------------------------------------------------------------
        BM           78            73            5        93.6 %

        WM          417            23          394        94.5 %
-------------------------------------------------------------------
     Total Correct:      467 / 495 ( 94.3 %) *** CROSS-VALIDATED ***

-------------------------------------------------------------------------------------
Two Group Discriminant Function Results

-------------------------------------------------------------------------------------
    Group         Classified     Distance        Probabilities
```

	into	from	Posterior	Typ F	Typ Chi	Typ R
BM	**BM**	11.7	0.983	0.331	0.302	0.405 (48/79)
WM		19.9	0.017	**0.037**	**0.030**	0.065 (392/418)

This time using only ten stepwise-selected measurements, Example 3 again classifies quite strongly as a black male, in a highly accurate function, and the typicality probability for black males is acceptable, while those for white males are rather low. We can be quite comfortable with a classification of black male in this case.

Click the Graph tab. The histogram looks more or less like two distributions with similar dispersion, as in Figure 1.

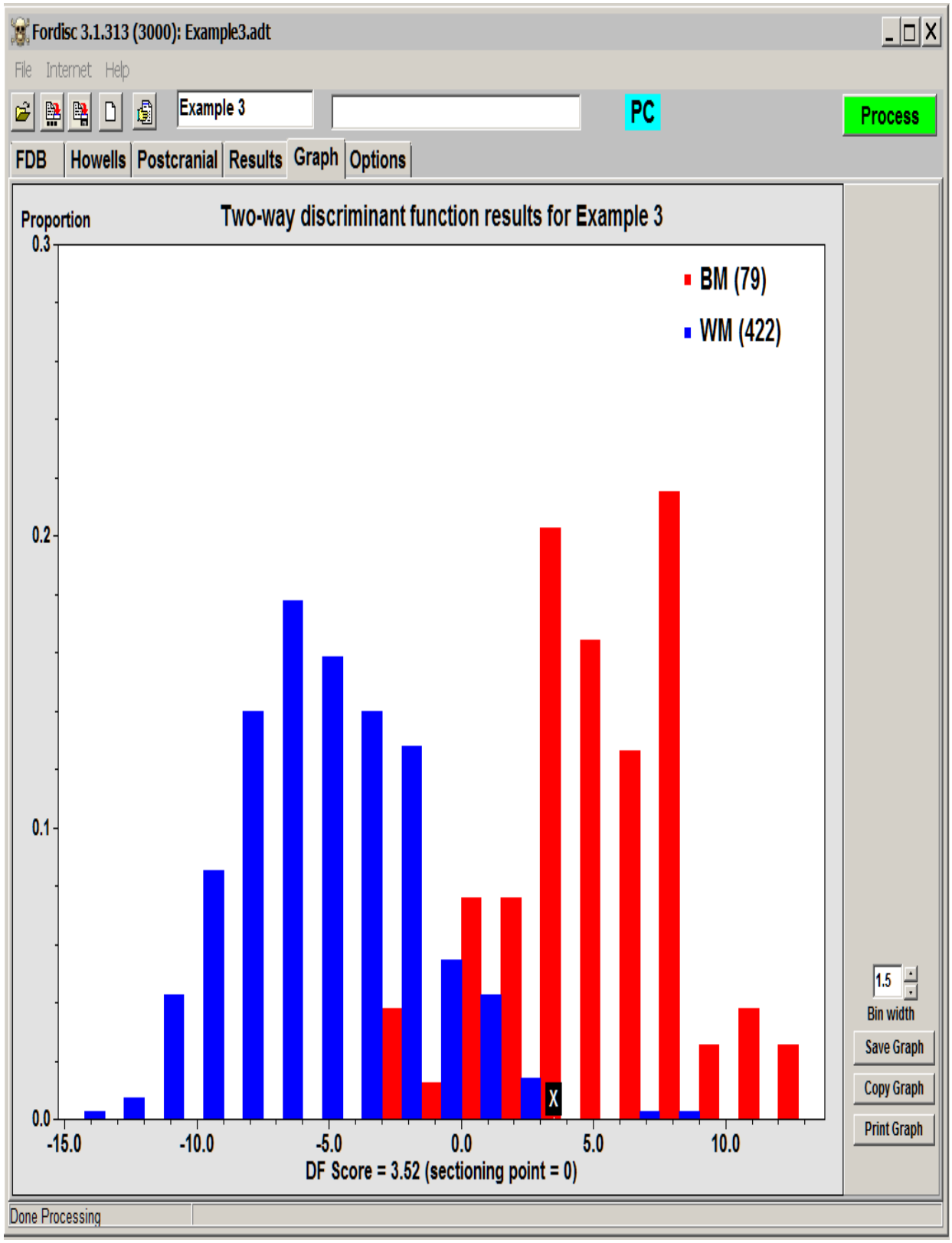
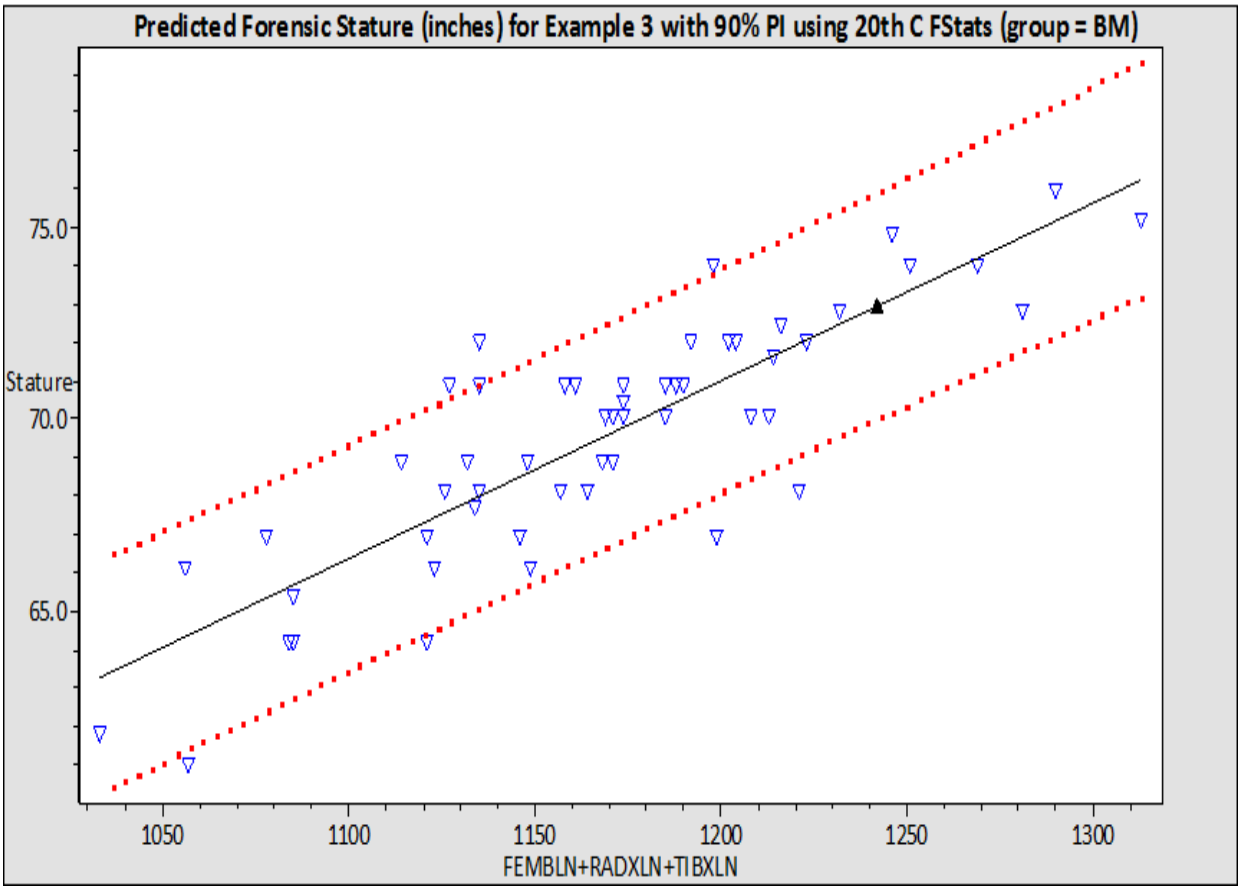


Figure 5. Histogram based on example3.db after stepwise selection

Proceed to Part III

Tutorial Part III

Next, move to the postcranial page and click the Stature button or press Alt+S to bring up the stature estimation window. Click the **Use All** button to include all measurements in stature estimations. Because you ran an analysis and the unknown was classified into one of the four forensic stature groups, BM is selected. The 20th century forensic statures are the most appropriate statures to use in this case. In other cases, click on the sample and group you wish to calculate stature for, and press the **Estimate** button. Fordisc calculates equations on the fly using many different measurement combinations. The equations are sorted by R-squared, the goodness of fit of the measurements to the statures, but you can also sort by the size of the prediction interval (PI). You can highlight the equation you wish to use or scroll through the equations by highlighting one and then using the arrow keys.



You can look through the equations and get a general sense of stature estimations, or you can press the **Copy Nums** button to the right of the copy all applicable numeric information to the clipboard. This text is formatted for pasting into a spreadsheet, with tabs between adjacent items.

PI	Measurement	Value	Point Est	L 90%	U 90%
N	Slope	Intrcpt	R-Square		
	FEMBLN+RADXLN+TIBXLN				
3.0		1242	73.0	70.0	75.9
54	0.04627	15.49	0.723		

	FIBXLN+HUMXLN+TIBXLN					
3.0		1265	74.3	71.4	77.3	
53	0.04352	19.26	0.731			
3.0	RADXLN+TIBXLN	724	72.7	69.8	75.7	
54	0.07466	18.67	0.721			
	INNOHT+TIBXLN+ULNPHL					
3.0		943	73.2	70.2	76.1	
44	0.06118	15.48	0.733			
	FIBXLN+TIBXLN+ULNPHL					
3.0		1146	72.8	69.8	75.7	
46	0.04548	20.66	0.745			
	FIBXLN+RADXLN+TIBXLN					
3.0		1159	72.9	70.0	75.9	
51	0.04566	20.03	0.728			
	FEMBLN+FIBXLN+ULNPHL					
3.0		1224	72.9	69.9	75.9	
48	0.04659	15.89	0.742			
	CALCXL+TIBXLN+ULNPHL					
3.0		787	71.5	68.5	74.5	
38	0.05765	26.10	0.594			
	FEMXLN+RADXLN+TIBXLN					
3.0		1245	72.9	69.9	75.9	
54	0.04623	15.38	0.715			
	FEMBLN+TIBXLN+ULNPHL					
3.0		1229	72.8	69.8	75.8	
47	0.04578	16.53	0.735			
	HUMXLN+RADXLN+TIBXLN					
3.0		1114	74.4	71.4	77.4	
53	0.05218	16.24	0.722			
	INNOHT+RADXLN+TIBXLN					
3.0		956	73.3	70.3	76.3	
47	0.06114	14.83	0.723			
	CALCXL+RADXLN+TIBXLN					
3.0		800	71.6	68.6	74.6	
41	0.05766	25.48	0.591			
	FEMBLN+FIBXLN+RADXLN					
3.0		1237	73.1	70.1	76.1	
53	0.04684	15.18	0.726			
	FIBXLN+INNOHT+TIBXLN					
3.0		1107	73.3	70.3	76.4	
49	0.04853	19.62	0.709			
3.0	TIBXLN+ULNPHL	711	72.6	69.6	75.6	
47	0.07416	19.85	0.729			
3.0	FIBXLN+ULNPHL	706	72.9	69.8	75.9	
49	0.07633	18.98	0.736			
3.0	FIBXLN+RADXLN	719	73.1	70.0	76.1	
54	0.07626	18.23	0.722			
	RADXLN+SCAPHT+TIBXLN					
3.0		904	73.5	70.5	76.6	
50	0.06592	13.95	0.727			
	FIBXLN+INNOHT+ULNPHL					
3.0		938	73.4	70.3	76.4	
46	0.06212	15.09	0.724			
	SCAPHT+TIBXLN+ULNPHL					
3.0		891	73.4	70.3	76.4	
47	0.06541	15.08	0.729			
	FEMXLN+FIBXLN+ULNPHL					
3.0		1227	72.9	69.9	76.0	
48	0.04667	15.64	0.733			
3.1	INNOHT+TIBXLN	672	73.4	70.4	76.5	
49	0.08339	17.39	0.703			
	CALCXL+INNOHT+TIBXLN					
3.1		748	72.1	69.0	75.2	
40	0.06250	25.36	0.572			
	FEMXLN+TIBXLN+ULNPHL					
3.1		1232	72.8	69.7	75.8	
47	0.04575	16.41	0.724			
	FIBXLN+HUMXLN+RADXLN					
3.1		1109	74.7	71.6	77.7	
54	0.05407	14.71	0.726			
	FEMXLN+FIBXLN+RADXLN					
3.1		1240	73.1	70.0	76.2	
53	0.04691	14.93	0.718			
	FEMBLN+FIBXLN+HUMXLN					
3.1		1343	74.4	71.4	77.5	
55	0.04417	15.12	0.713			
	FEMBLN+HUMXLN+TIBXLN					
3.1		1348	74.1	71.1	77.2	
56	0.04250	16.86	0.695			
3.1	FIBXLN+HUMXLN	825	75.2	72.2	78.3	
56	0.07083	16.81	0.716			
	HUMXLN+TIBXLN+ULNPHL					
3.1		1101	74.2	71.1	77.3	
47	0.05212	16.85	0.727			
	FIBXLN+SCAPHT+ULNPHL					
3.1		886	73.7	70.6	76.8	
49	0.06748	13.87	0.728			
	FIBXLN+INNOHT+RADXLN					
3.1		951	73.5	70.4	76.6	
49	0.06201	14.52	0.710			
	RADXLN+TIBXLN+ULNPHL					
3.1		995	72.5	69.4	75.6	
47	0.05414	18.67	0.716			
	FIBXLN+HUMXLN+ULNPHL					
3.1		1096	74.5	71.4	77.6	
49	0.05392	15.40	0.733			

3.1	HUMXLN+TIBXLN	830	74.7	71.6	77.8
56	0.06674	19.31	0.695		
	FIBXLN+RADXLN+ULNPHL				
3.1		990	72.7	69.6	75.8
49	0.05531	17.98	0.723		
	FEMBLN+INNOHT+TIBXLN				
3.1		1190	73.3	70.2	76.4
49	0.04786	16.32	0.692		
	FIBXLN+RADXLN+SCAPHT				
3.1		899	73.9	70.8	77.0
52	0.06780	12.91	0.721		
	FEMXLN+FIBXLN+HUMXLN				
3.1		1346	74.4	71.3	77.5
55	0.04420	14.93	0.706		
	HUMXLN+SCAPHT+TIBXLN				
3.1		1010	75.4	72.2	78.5
50	0.06120	13.55	0.724		
	CALCXL+FIBXLN+ULNPHL				
3.1		782	71.7	68.6	74.9
41	0.06135	23.77	0.591		
	CALCXL+SACAHT+TIBXLN				
3.1		605	70.0	66.8	73.1
38	0.07109	26.95	0.548		
	FEMXLN+HUMXLN+TIBXLN				
3.1		1351	74.1	71.0	77.2
56	0.04240	16.85	0.686		
	FIBXLN+TIBXLN+ULNXLN				
3.1		1178	72.9	69.8	76.0
49	0.04501	19.89	0.713		
	HUMXLN+INNOHT+TIBXLN				
3.1		1062	74.9	71.8	78.0
49	0.05592	15.52	0.699		
	CALCXL+FIBXLN+RADXLN				
3.1		795	71.9	68.8	75.0
44	0.06104	23.36	0.585		
	FEMXLN+INNOHT+TIBXLN				
3.1		1193	73.3	70.1	76.4
49	0.04792	16.09	0.686		
	CALCXL+FIBXLN+TIBXLN				
3.1		951	71.9	68.8	75.0
41	0.04390	30.14	0.557		
	FEMBLN+TIBXLN+ULNXLN				
3.1		1261	72.9	69.8	76.1
50	0.04535	15.75	0.704		
	CALCXL+TIBXLN+ULNXLN				
3.1		819	71.6	68.5	74.8
40	0.05606	25.71	0.560		
	FEMBLN+SACAHT+TIBXLN				
3.1		1047	71.9	68.8	75.0
44	0.05415	15.22	0.680		
	FEMBLN+FIBXLN+SACAHT				
3.1		1042	72.1	69.0	75.3
45	0.05726	12.46	0.691		
	FEMBLN+FIBXLN+TIBXLN				
3.1		1393	73.1	69.9	76.2
54	0.03961	17.88	0.707		
	FEMBLN+FIBXLN+INNOHT				
3.2		1185	73.5	70.3	76.6
51	0.04910	15.27	0.687		
3.2	FEMBLN+TIBXLN	958	72.9	69.7	76.0
58	0.05836	16.98	0.691		
	INNOHT+TIBXLN+ULNXLN				
3.2		975	73.3	70.1	76.4
46	0.06020	14.57	0.700		
3.2	FIBXLN+INNOHT	667	73.8	70.6	76.9
51	0.08613	16.33	0.689		
3.2	FEMBLN+RADXLN	802	72.9	69.8	76.1
58	0.07366	13.87	0.678		
	FEMBLN+FIBXLN+ULNXLN				
3.2		1256	73.1	69.9	76.2
51	0.04617	15.08	0.709		
	INNOHT+SCAPHT+TIBXLN				
3.2		852	74.2	71.0	77.3
46	0.07186	12.96	0.704		
	FEMXLN+FIBXLN+TIBXLN				
3.2		1396	73.1	69.9	76.2
54	0.03964	17.71	0.701		
3.2	FEMBLN+FIBXLN	953	73.2	70.0	76.4
56	0.06007	15.94	0.703		
	CALCXL+SCAPHT+TIBXLN				
3.2		696	72.1	68.9	75.3
40	0.06694	25.53	0.555		
	FEMXLN+TIBXLN+ULNXLN				
3.2		1264	72.9	69.7	76.1
50	0.04536	15.59	0.696		
	FEMXLN+FIBXLN+INNOHT				
3.2		1188	73.5	70.3	76.6
51	0.04923	14.96	0.681		
	FIBXLN+SACAHT+TIBXLN				
3.2		964	71.8	68.6	75.0
43	0.05343	20.33	0.678		
	HUMXLN+TIBXLN+ULNXLN				
3.2		1133	74.3	71.1	77.5
50	0.05151	15.97	0.703		
	FEMXLN+SACAHT+TIBXLN				
3.2		1050	71.9	68.7	75.1
44	0.05425	14.93	0.671		

3.2	TIBXLN+ULNXLN	743	72.7	69.5	75.9
50	0.07248	18.83	0.693		
	FEMXLN+FIBXLN+SACAHT				
3.2		1045	72.1	68.9	75.3
45	0.05750	12.03	0.682		
3.2	FEMXLN+RADXLN	805	72.9	69.7	76.1
59	0.07346	13.77	0.665		
	TIBXLN+ULNXLN+ULNPHL				
3.2		1014	72.5	69.3	75.7
47	0.05326	18.49	0.696		
	SCAPHT+TIBXLN+ULNXLN				
3.2		923	73.5	70.3	76.7
49	0.06449	13.94	0.701		
	RADXLN+TIBXLN+ULNXLN				
3.2		1027	72.7	69.5	75.9
50	0.05349	17.74	0.690		
	FEMXLN+FIBXLN+ULNXLN				
3.2		1259	73.1	69.9	76.3
51	0.04627	14.80	0.701		
	FIBXLN+HUMXLN+SCAPHT				
3.2		1005	75.8	72.6	79.0
52	0.06384	11.61	0.717		
3.2	FEMXLN+TIBXLN	961	72.9	69.7	76.1
58	0.05821	16.92	0.680		
	FIBXLN+HUMXLN+INNOHT				
3.2		1057	75.2	72.0	78.4
51	0.05808	13.83	0.690		
3.2	FEMXLN+FIBXLN	956	73.2	70.0	76.4
56	0.06023	15.60	0.695		
	FIBXLN+ULNXLN+ULNPHL				
3.2		1009	72.7	69.5	75.9
49	0.05434	17.85	0.700		
	FEMBLN+HUMXLN+RADXLN				
3.2		1192	74.4	71.2	77.6
56	0.05118	13.40	0.678		
	FIBXLN+HUMXLN+ULNXLN				
3.2		1128	74.6	71.4	77.8
52	0.05329	14.51	0.706		
	CALCXL+FEMBLN+TIBXLN				
3.2		1034	71.8	68.5	75.0
42	0.04396	26.31	0.534		
3.2	FEMBLN+ULNPHL	789	72.7	69.5	75.9
50	0.07297	15.13	0.688		
	FEMBLN+FEMXLN+TIBXLN				
3.2		1479	72.9	69.7	76.1
58	0.03852	15.94	0.676		
	FEMBLN+RADXLN+ULNPHL				
3.2		1073	72.6	69.4	75.9
50	0.05352	15.20	0.686		
	FIBXLN+RADXLN+ULNXLN				
3.2		1022	72.9	69.6	76.1
52	0.05461	17.06	0.693		
	CALCXL+FEMBLN+RADXLN				
3.2		878	71.7	68.4	74.9
44	0.05674	21.85	0.544		
3.2	FIBXLN+ULNXLN	738	73.0	69.8	76.2
52	0.07445	18.05	0.694		
	HUMXLN+SACAHT+TIBXLN				
3.2		919	73.3	70.1	76.5
44	0.06193	16.38	0.669		
	RADXLN+SACAHT+TIBXLN				
3.2		813	71.3	68.1	74.6
44	0.06628	17.46	0.657		
	CALCXL+FEMBLN+ULNPHL				
3.2		865	71.5	68.2	74.7
41	0.05637	22.73	0.541		
	FEMBLN+FEMXLN+FIBXLN				
3.2		1474	73.1	69.9	76.4
56	0.03939	15.04	0.690		
	FEMXLN+HUMXLN+RADXLN				
3.2		1195	74.4	71.1	77.6
57	0.05104	13.38	0.667		
	FEMBLN+FEMXLN+RADXLN				
3.2		1323	72.9	69.7	76.2
58	0.04423	14.43	0.661		
3.2	CALCXL+TIBXLN	516	71.1	67.8	74.3
42	0.07959	29.99	0.521		
3.3	TIBXLN	440	72.5	69.2	75.8
59	0.11136	23.50	0.663		
3.3	FIBXLN+TIBXLN	875	72.9	69.6	76.1
55	0.05734	22.69	0.679		
	FEMBLN+SCAPHT+TIBXLN				
3.3		1138	73.6	70.3	76.8
51	0.05361	12.58	0.705		
	CALCXL+INNOHT+RADXLN				
3.3		592	71.9	68.6	75.1
43	0.08899	19.19	0.533		
	FEMBLN+INNOHT+ULNPHL				
3.3		1021	73.1	69.9	76.4
47	0.05878	13.12	0.673		
	FIBXLN+RADXLN+SACAHT				
3.3		808	71.6	68.4	74.9
46	0.07091	14.34	0.667		
	FIBXLN+INNOHT+ULNXLN				
3.3		970	73.5	70.2	76.7
48	0.06092	14.37	0.685		

	CALCXL+HUMXLN+TIBXLN				
3.3		906	73.1	69.9	76.4
42	0.05199	26.02	0.542		
	CALCXL+FEMBLN+FIBXLN				
3.3		1029	72.0	68.8	75.3
43	0.04656	24.12	0.553		
	FEMBLN+RADXLN+SCAPHT				
3.3		982	73.7	70.4	76.9
53	0.06488	9.94	0.683		
	CALCXL+FEMXLN+TIBXLN				
3.3		1037	71.7	68.5	75.0
42	0.04379	26.32	0.523		
	FEMBLN+SCAPHT+ULNPHL				
3.3		969	73.4	70.2	76.7
50	0.06433	11.11	0.684		
	CALCXL+FIBXLN+ULNXLN				
3.3		814	71.9	68.6	75.2
43	0.05926	23.65	0.551		
	FEMBLN+INNOHT+RADXLN				
3.3		1034	73.3	70.0	76.6
50	0.05884	12.45	0.664		
	FIBXLN+INNOHT+SCAPHT				
3.3		847	74.5	71.2	77.8
48	0.07394	11.85	0.686		
	CALCXL+INNOHT+ULNPHL				
3.3		579	71.7	68.4	75.0
40	0.09033	19.38	0.523		
	FIBXLN+SCAPHT+ULNXLN				
3.3		918	73.8	70.5	77.0
51	0.06623	12.95	0.694		
	CALCXL+FIBXLN+INNOHT				
3.3		743	72.3	69.0	75.6
42	0.06559	23.60	0.540		
	FEMXLN+SCAPHT+TIBXLN				
3.3		1141	73.6	70.3	76.9
51	0.05373	12.27	0.698		
	CALCXL+FEMXLN+FIBXLN				
3.3		1032	72.0	68.7	75.3
43	0.04654	23.96	0.544		
	CALCXL+FEMXLN+RADXLN				
3.3		881	71.6	68.3	74.9
44	0.05624	22.08	0.528		
	FEMBLN+FIBXLN+SCAPHT				
3.3		1133	73.8	70.5	77.1
52	0.05495	11.54	0.704		
	FIBXLN+SACAHT+ULNPHL				
3.3		795	71.5	68.2	74.8
43	0.07073	15.23	0.660		
	FEMBLN+HUMXLN+ULNPHL				
3.3		1179	74.2	70.9	77.5
50	0.05110	13.98	0.682		
	FEMXLN+RADXLN+ULNPHL				
3.3		1076	72.6	69.3	75.9
50	0.05337	15.18	0.672		
	FIBXLN+HUMXLN+SACAHT				
3.3		914	73.7	70.4	77.0
46	0.06647	12.94	0.669		
	SACAHT+TIBXLN+ULNPHL				
3.3		800	71.2	67.9	74.5
41	0.06592	18.46	0.646		
3.3	FIBXLN	435	73.1	69.8	76.4
58	0.11696	22.22	0.670		
	CALCXL+FEMXLN+ULNPHL				
3.3		868	71.4	68.1	74.8
41	0.05579	23.01	0.519		
3.3	FEMXLN+ULNPHL	792	72.7	69.4	76.0
50	0.07287	14.96	0.670		
	FEMBLN+FEMXLN+ULNPHL				
3.3		1310	72.7	69.4	76.0
50	0.04360	15.60	0.670		
	FEMXLN+INNOHT+ULNPHL				
3.3		1024	73.1	69.8	76.4
47	0.05883	12.87	0.660		
	FEMBLN+ULNXLN+ULNPHL				
3.3		1092	72.6	69.3	75.9
50	0.05276	14.98	0.669		
	INNOHT+SACAHT+TIBXLN				
3.3		761	71.9	68.5	75.2
43	0.07495	14.84	0.649		
3.3	CALCXL+FIBXLN	511	71.5	68.2	74.8
44	0.08679	27.16	0.529		
	FEMXLN+RADXLN+SCAPHT				
3.3		985	73.6	70.3	76.9
53	0.06479	9.80	0.669		
	CALCXL+FIBXLN+HUMXLN				
3.3		901	73.6	70.3	76.9
44	0.05658	22.64	0.554		
	CALCXL+FIBXLN+SACAHT				
3.3		600	70.2	66.8	73.5
41	0.07975	22.31	0.518		
	FEMBLN+RADXLN+ULNXLN				
3.3		1105	72.8	69.5	76.2
54	0.05316	14.09	0.659		
	FEMXLN+INNOHT+RADXLN				
3.3		1037	73.3	69.9	76.6
50	0.05887	12.22	0.654		

		FEMXLN+FIBXLN+SCAPHT				
3.3		1136	73.8	70.4	77.1	
52	0.05517	11.12	0.697			
		FEMBLN+RADXLN+SACAHT				
3.4		891	71.6	68.3	75.0	
47	0.06778	11.24	0.632			
		FEMXLN+SCAPHT+ULNPHL				
3.4		972	73.4	70.1	76.8	
50	0.06424	10.98	0.668			
3.4	FEMBLN	518	72.9	69.5	76.2	
63	0.10949	16.17	0.637			
3.4	CALCXL+RADXLN	360	70.4	67.0	73.8	
45	0.13269	22.63	0.501			
		CALCXL+RADXLN+ULNPHL				
3.4		631	71.0	67.7	74.4	
42	0.07295	25.02	0.503			
		FEMXLN+HUMXLN+ULNPHL				
3.4		1182	74.2	70.8	77.6	
50	0.05112	13.78	0.670			
		FIBXLN+SCAPHT+TIBXLN				
3.4		1055	73.5	70.2	76.9	
50	0.05289	17.73	0.689			
3.4	FEMBLN+ULNXLN	821	72.9	69.5	76.3	
54	0.07185	13.91	0.652			
		FEMBLN+FEMXLN+HUMXLN				
3.4		1429	74.0	70.6	77.4	
59	0.04054	16.08	0.631			
		CALCXL+FEMBLN+ULNXLN				
3.4		897	71.7	68.3	75.0	
43	0.05509	22.24	0.511			
3.4	FEMBLN+HUMXLN	908	74.7	71.3	78.1	
59	0.06447	16.14	0.635			
		INNOHT+RADXLN+ULNPHL				
3.4		787	72.9	69.5	76.3	
47	0.07422	14.49	0.645			
		FIBXLN+INNOHT+SACAHT				
3.4		756	72.2	68.8	75.6	
45	0.07968	11.96	0.643			
		FEMXLN+ULNXLN+ULNPHL				
3.4		1095	72.6	69.2	76.0	
50	0.05265	14.91	0.655			
3.4	INNOHT+ULNPHL	503	73.4	70.0	76.8	
47	0.12277	11.63	0.648			
		FEMXLN+RADXLN+ULNXLN				
3.4		1108	72.8	69.4	76.2	
54	0.05306	14.00	0.648			
		CALCXL+FIBXLN+SCAPHT				
3.4		691	72.5	69.1	75.9	
43	0.07195	22.77	0.528			
		FEMBLN+HUMXLN+ULNXLN				
3.4		1211	74.4	71.0	77.8	
53	0.05066	13.01	0.661			
3.4	FEMBLN+FEMXLN	1039	72.9	69.5	76.3	
63	0.05475	15.97	0.628			
		CALCXL+RADXLN+ULNXLN				
3.4		663	71.2	67.8	74.6	
44	0.07250	23.17	0.502			
3.4	SCAPHT+TIBXLN	620	73.8	70.3	77.2	
51	0.09408	15.43	0.678			
3.4	INNOHT+RADXLN	516	73.5	70.1	76.9	
50	0.11985	11.66	0.641			
		FEMBLN+SCAPHT+ULNXLN				
3.4		1001	73.6	70.2	77.0	
52	0.06360	9.90	0.658			
3.4	HUMXLN+RADXLN	674	75.2	71.7	78.6	
58	0.08766	16.08	0.639			
		FEMBLN+FEMXLN+ULNXLN				
3.4		1342	72.9	69.5	76.3	
54	0.04352	14.51	0.643			
		CALCXL+HUMXLN+RADXLN				
3.4		750	73.4	70.0	76.8	
45	0.06914	21.57	0.517			
		FEMBLN+INNOHT+ULNXLN				
3.4		1053	73.3	69.8	76.7	
49	0.05807	12.11	0.643			
3.4	FEMXLN	521	72.8	69.4	76.2	
64	0.10896	16.05	0.616			
		FEMBLN+SACAHT+ULNPHL				
3.4		878	71.4	68.0	74.9	
44	0.06705	12.57	0.616			
3.4	FEMXLN+HUMXLN	911	74.6	71.2	78.1	
60	0.06407	16.25	0.618			
		CALCXL+INNOHT+ULNXLN				
3.4		611	71.9	68.4	75.3	
42	0.08630	19.13	0.490			
		CALCXL+FEMXLN+ULNXLN				
3.4		900	71.6	68.2	75.0	
43	0.05470	22.37	0.495			
3.4	SACAHT+TIBXLN	529	70.7	67.2	74.1	
44	0.09281	21.56	0.612			
		FEMBLN+FEMXLN+INNOHT				
3.4		1271	73.1	69.6	76.5	
53	0.04458	16.41	0.611			
3.4	FEMXLN+ULNXLN	824	72.9	69.4	76.3	
54	0.07190	13.62	0.638			

	FEMXLN+RADXLN+SACAHT				
3.4		894	71.6	68.1	75.0
47	0.06733	11.40	0.612		
	CALCXL+FEMBLN+INNOHT				
3.4		826	72.0	68.6	75.5
43	0.05823	23.93	0.481		
	SACAHT+TIBXLN+ULNXLN				
3.5		832	71.3	67.9	74.8
43	0.06431	17.81	0.620		
	FEMXLN+HUMXLN+ULNXLN				
3.5		1214	74.3	70.9	77.8
53	0.05067	12.83	0.650		
3.5	FEMBLN+INNOHT	750	73.3	69.9	76.8
53	0.07734	15.33	0.609		
	FEMBLN+FEMXLN+SACAHT				
3.5		1128	71.9	68.5	75.4
48	0.05149	13.86	0.602		
	FEMBLN+HUMXLN+SCAPHT				
3.5		1088	75.3	71.8	78.7
53	0.05910	10.97	0.657		
	SACAHT+SCAPHT+TIBXLN				
3.5		709	71.9	68.4	75.4
43	0.07735	17.05	0.619		
	FEMXLN+INNOHT+ULNXLN				
3.5		1056	73.2	69.8	76.7
49	0.05821	11.76	0.633		
3.5	FIBXLN+SACAHT	524	71.1	67.6	74.5
46	0.10232	17.44	0.618		
	FEMXLN+SCAPHT+ULNXLN				
3.5		1004	73.5	70.1	77.0
52	0.06361	9.67	0.645		
	FEMBLN+HUMXLN+INNOHT				
3.5		1140	74.7	71.3	78.2
52	0.05318	14.11	0.626		
	CALCXL+FEMBLN+SACAHT				
3.5		683	70.1	66.6	73.6
41	0.07120	21.47	0.459		
	CALCXL+ULNXLN+ULNPHL				
3.5		650	71.0	67.6	74.5
42	0.07091	24.94	0.469		
	INNOHT+SCAPHT+ULNPHL				
3.5		683	74.2	70.7	77.7
47	0.09712	7.89	0.638		
	CALCXL+FEMBLN+SCAPHT				
3.5		774	72.2	68.7	75.7
43	0.06643	20.76	0.488		
	HUMXLN+RADXLN+ULNPHL				
3.5		945	74.3	70.8	77.8
51	0.06169	15.98	0.648		
3.5	RADXLN	284	72.3	68.8	75.8
60	0.18185	20.65	0.598		
	CALCXL+FEMXLN+INNOHT				
3.5		829	72.0	68.5	75.5
43	0.05814	23.79	0.467		
	FIBXLN+SACAHT+ULNXLN				
3.5		827	71.6	68.1	75.1
45	0.06855	14.90	0.625		
3.5	CALCXL+FEMBLN	594	71.2	67.7	74.7
45	0.07790	24.91	0.465		
3.5	FEMXLN+INNOHT	753	73.3	69.8	76.8
53	0.07761	14.87	0.599		
	HUMXLN+INNOHT+RADXLN				
3.5		906	75.2	71.7	78.7
50	0.06949	12.24	0.638		
	CALCXL+FEMBLN+FEMXLN				
3.5		1115	71.7	68.2	75.2
45	0.04112	25.82	0.466		
	FEMXLN+HUMXLN+SCAPHT				
3.5		1091	75.2	71.7	78.8
53	0.05919	10.68	0.647		
	CALCXL+RADXLN+SCAPHT				
3.5		540	71.9	68.4	75.4
44	0.09623	19.96	0.476		
	INNOHT+RADXLN+ULNXLN				
3.5		819	73.0	69.5	76.5
49	0.07291	13.30	0.622		
	INNOHT+ULNXLN+ULNPHL				
3.5		806	72.8	69.3	76.3
47	0.07251	14.39	0.617		
	HUMXLN+RADXLN+SCAPHT				
3.5		854	75.8	72.3	79.3
54	0.07705	10.03	0.649		
	INNOHT+RADXLN+SCAPHT				
3.5		696	74.4	70.9	77.9
49	0.09632	7.34	0.634		
	FEMXLN+HUMXLN+INNOHT				
3.5		1143	74.7	71.2	78.2
52	0.05324	13.87	0.617		
	CALCXL+FEMBLN+HUMXLN				
3.5		984	73.1	69.6	76.6
45	0.05078	23.13	0.485		
	FEMBLN+HUMXLN+SACAHT				
3.5		997	73.4	69.9	76.9
47	0.06080	12.78	0.608		
3.5	CALCXL+ULNPHL	347	70.1	66.6	73.7
42	0.13130	24.59	0.450		

	FEMXLN+SACAHT+ULNPHL					
3.5		881	71.4	67.9	74.9	
44	0.06658	12.74	0.593			
	CALCXL+FEMXLN+SCAPHT					
3.5		777	72.1	68.6	75.7	
43	0.06619	20.69	0.471			
	FEMBLN+SACAHT+ULNXLN					
3.5		910	71.6	68.0	75.1	
46	0.06595	11.57	0.596			
	FEMBLN+FEMXLN+SCAPHT					
3.6		1219	73.5	69.9	77.0	
54	0.05059	11.79	0.644			
	HUMXLN+RADXLN+ULNXLN					
3.6		977	74.4	70.8	77.9	
54	0.06055	15.20	0.629			
	FEMBLN+INNOHT+SACAHT					
3.6		839	72.1	68.5	75.6	
47	0.07349	10.41	0.588			
	CALCXL+FEMXLN+SACAHT					
3.6		686	70.0	66.5	73.6	
41	0.07029	21.83	0.435			
3.6	FIBXLN+SCAPHT	615	74.2	70.6	77.8	
53	0.09714	14.47	0.658			
3.6	CALCXL+FEMXLN	597	71.1	67.6	74.7	
45	0.07736	24.94	0.443			
	CALCXL+HUMXLN+ULNPHL					
3.6		737	73.2	69.6	76.8	
42	0.06772	23.30	0.476			
3.6	FEMBLN+SACAHT	607	71.0	67.5	74.6	
48	0.09508	13.33	0.569			
	CALCXL+HUMXLN+ULNXLN					
3.6		769	73.4	69.8	77.0	
44	0.06771	21.32	0.482			
	CALCXL+FEMXLN+HUMXLN					
3.6		987	73.0	69.5	76.6	
45	0.05035	23.34	0.469			
3.6	FEMBLN+SCAPHT	698	73.9	70.3	77.5	
54	0.09165	9.95	0.641			
	HUMXLN+INNOHT+ULNPHL					
3.6		893	75.0	71.5	78.6	
47	0.06924	13.21	0.627			
	HUMXLN+ULNXLN+ULNPHL					
3.6		964	74.2	70.6	77.8	
51	0.06054	15.83	0.626			
	FEMXLN+HUMXLN+SACAHT					
3.6		1000	73.4	69.8	77.0	
47	0.06067	12.69	0.593			
3.6	HUMXLN+ULNPHL	661	75.0	71.4	78.6	
51	0.08851	16.53	0.632			
	FEMBLN+INNOHT+SCAPHT					
3.6		930	74.0	70.4	77.6	
49	0.06723	11.49	0.613			
3.6	CALCXL+ULNXLN	379	70.4	66.8	74.1	
44	0.12558	22.84	0.432			
	FEMXLN+INNOHT+SACAHT					
3.6		842	72.0	68.4	75.7	
47	0.07368	10.00	0.574			
	FEMXLN+SACAHT+ULNXLN					
3.6		913	71.5	67.9	75.2	
46	0.06567	11.58	0.578			
	CALCXL+SCAPHT+ULNPHL					
3.6		527	71.6	68.0	75.2	
42	0.09254	22.85	0.432			
3.6	RADXLN+ULNPHL	555	72.1	68.5	75.8	
51	0.09154	21.32	0.602			
	FIBXLN+SACAHT+SCAPHT					
3.6		704	72.2	68.6	75.9	
45	0.08267	14.05	0.599			
	RADXLN+SCAPHT+ULNPHL					
3.6		735	73.2	69.5	76.8	
51	0.07897	15.12	0.609			
3.6	INNOHT+ULNXLN	535	73.4	69.8	77.1	
49	0.11655	11.06	0.597			
	HUMXLN+SCAPHT+ULNPHL					
3.7		841	75.6	72.0	79.3	
51	0.07601	11.68	0.629			
	FEMXLN+INNOHT+SCAPHT					
3.7		933	74.0	70.3	77.6	
49	0.06747	11.04	0.602			
	HUMXLN+INNOHT+ULNXLN					
3.7		925	75.1	71.5	78.8	
49	0.06856	11.71	0.614			
3.7	FEMXLN+SCAPHT	701	73.9	70.2	77.5	
54	0.09189	9.47	0.625			
3.7	FEMXLN+SACAHT	610	71.0	67.3	74.7	
48	0.09471	13.22	0.545			
3.7	HUMXLN+ULNXLN	693	75.1	71.4	78.8	
54	0.08616	15.39	0.608			
	HUMXLN+SCAPHT+ULNXLN					
3.7		873	75.7	72.0	79.4	
53	0.07521	10.02	0.619			
3.7	ULNPHL	271	72.0	68.3	75.7	
51	0.18147	22.83	0.584			
	INNOHT+SCAPHT+ULNXLN					
3.7		715	74.2	70.5	77.9	
49	0.09320	7.60	0.593			

	RADXLN+ULNXLN+ULNPHL					
3.7		858	72.1	68.4	75.8	
51	0.05974	20.84	0.584			
3.7	RADXLN+SCAPHT	464	73.9	70.2	77.7	
54	0.13326	12.11	0.592			
	FEMBLN+SACAHT+SCAPHT					
3.7		787	72.1	68.4	75.9	
46	0.07767	11.02	0.562			
	RADXLN+SCAPHT+ULNXLN					
3.7		767	73.3	69.5	77.0	
53	0.07765	13.70	0.593			
3.7	RADXLN+ULNXLN	587	72.3	68.6	76.0	
55	0.08923	19.92	0.573			
	CALCXL+SCAPHT+ULNXLN					
3.7		559	71.8	68.1	75.5	
44	0.08919	21.95	0.413			
	CALCXL+RADXLN+SACAHT					
3.8		449	68.9	65.1	72.7	
42	0.08974	28.64	0.365			
	SCAPHT+ULNXLN+ULNPHL					
3.8		754	73.0	69.2	76.8	
51	0.07610	15.66	0.574			
3.8	ULNXLN+ULNPHL	574	72.0	68.2	75.8	
51	0.08821	21.40	0.566			
	CALCXL+HUMXLN+INNOHT					
3.8		698	73.7	69.9	77.5	
43	0.06892	25.58	0.414			
	FEMXLN+SACAHT+SCAPHT					
3.8		790	72.1	68.3	75.9	
46	0.07725	11.07	0.541			
	HUMXLN+RADXLN+SACAHT					
3.8		763	73.0	69.2	76.9	
48	0.07316	17.21	0.536			
3.8	SCAPHT+ULNPHL	451	73.6	69.8	77.5	
51	0.13074	14.66	0.569			
	CALCXL+INNOHT+SCAPHT					
3.9		488	72.5	68.6	76.3	
42	0.10324	22.08	0.373			
3.9	CALCXL+INNOHT	308	71.0	67.1	74.9	
43	0.14018	27.82	0.334			
3.9	ULNXLN	303	72.2	68.3	76.1	
55	0.17051	20.53	0.533			
3.9	HUMXLN+INNOHT	622	75.9	72.0	79.8	
52	0.09606	16.19	0.555			
	INNOHT+RADXLN+SACAHT					
3.9		605	71.2	67.3	75.1	
46	0.09297	14.94	0.506			
3.9	HUMXLN	390	75.9	72.0	79.8	
64	0.13049	25.00	0.506			
	CALCXL+HUMXLN+SCAPHT					
4.0		646	74.1	70.1	78.0	
44	0.07727	24.16	0.398			
4.0	CALCXL+HUMXLN	466	73.3	69.3	77.3	
46	0.09412	29.43	0.368			
	HUMXLN+INNOHT+SCAPHT					
4.0		802	76.3	72.4	80.3	
49	0.08102	11.37	0.567			
	CALCXL+SACAHT+ULNXLN					
4.0		468	69.1	65.1	73.1	
41	0.08275	30.34	0.309			
	CALCXL+SACAHT+ULNPHL					
4.0		436	68.8	64.8	72.8	
39	0.08076	33.63	0.293			
4.0	SCAPHT+ULNXLN	483	73.7	69.7	77.7	
53	0.12524	13.18	0.535			
	HUMXLN+SACAHT+ULNPHL					
4.0		750	72.8	68.8	76.8	
45	0.07202	18.81	0.497			
	CALCXL+HUMXLN+SACAHT					
4.0		555	71.3	67.3	75.3	
42	0.06824	33.46	0.301			
	HUMXLN+SACAHT+ULNXLN					
4.0		782	72.9	68.9	77.0	
47	0.07105	17.38	0.498			
4.0	HUMXLN+SCAPHT	570	76.7	72.6	80.7	
55	0.10804	15.10	0.551			
	INNOHT+SACAHT+ULNPHL					
4.0		592	70.9	66.9	75.0	
43	0.09156	16.73	0.474			
	RADXLN+SACAHT+ULNPHL					
4.1		644	70.4	66.3	74.6	
45	0.07155	24.37	0.445			
	RADXLN+SACAHT+ULNXLN					
4.1		676	70.6	66.5	74.7	
47	0.07054	22.92	0.445			
	HUMXLN+INNOHT+SACAHT					
4.2		711	73.5	69.3	77.6	
46	0.07791	18.08	0.473			
	INNOHT+SACAHT+ULNXLN					
4.2		624	71.1	66.9	75.3	
45	0.08795	16.22	0.452			
4.2	INNOHT	232	73.7	69.5	77.9	
53	0.23029	20.28	0.437			
	CALCXL+INNOHT+SACAHT					
4.2		397	69.3	65.0	73.5	
41	0.07879	38.00	0.205			

	SACAHT+ULNXLN+ULNPHL				
4.3		663	70.4	66.1	74.6
45	0.06777	25.45	0.404		
4.3	INNOHT+SCAPHT	412	74.9	70.6	79.2
49	0.15146	12.53	0.480		
4.3	CALCXL+SCAPHT	256	70.8	66.5	75.1
44	0.13562	36.10	0.199		
	RADXLN+SACAHT+SCAPHT				
4.4		553	71.1	66.7	75.4
47	0.08603	23.49	0.385		
4.4	RADXLN+SACAHT	373	69.5	65.1	73.9
48	0.10403	30.70	0.346		
4.4	HUMXLN+SACAHT	479	72.6	68.1	77.0
48	0.09412	27.50	0.378		
	HUMXLN+SACAHT+SCAPHT				
4.4		659	73.5	69.1	77.9
47	0.07847	21.78	0.406		
	SACAHT+SCAPHT+ULNPHL				
4.5		540	70.7	66.2	75.3
45	0.07974	27.68	0.330		
	SACAHT+SCAPHT+ULNXLN				
4.6		572	70.9	66.4	75.5
47	0.07843	26.07	0.328		
	CALCXL+SACAHT+SCAPHT				
4.6		345	69.5	64.9	74.1
41	0.04727	53.21	0.076		
4.7	SACAHT+ULNPHL	360	69.3	64.6	74.0
45	0.09561	34.87	0.281		
4.7	SACAHT+ULNXLN	392	69.5	64.8	74.2
47	0.09279	33.14	0.280		
	INNOHT+SACAHT+SCAPHT				
4.8		501	71.3	66.6	76.1
45	0.08938	26.56	0.295		
4.9	INNOHT+SACAHT	321	69.8	64.9	74.7
47	0.09860	38.13	0.202		
5.0	CALCXL+SACAHT	165	69.0	64.1	74.0
42	0.03286	63.60	0.019		
5.0	CALCXL	76	67.9	62.8	72.9
46	0.18885	53.50	0.059		
5.3	SCAPHT	180	73.1	67.8	78.4
57	0.20572	36.07	0.214		
5.4	SACAHT+SCAPHT	269	69.6	64.3	75.0
47	0.05558	54.68	0.066		
5.5	SACAHT	89	69.4	63.9	75.0
49	0.00133	69.31	0.000		

Press the **Copy Text** button to copy the equations to the clipboard in a format for pasting into a word processor document. The data set used and PIs are indicated in the text output. Sometimes the output can be extensive, as the example output illustrates for this case.

Predicted Forensic Stature (inches) for Example 3 with 90% PI using 20th C FStats (group = BM) for Example 3 with 90% PI

Estimated stature with 90% PI: 70.0 to 75.9 (73.0 +/- 3.0); Formula is: 0.04627 * FEMBLN+RADXLN+TIBXLN (1242 mm) + 15.49.
Estimated stature with 90% PI: 71.4 to 77.3 (74.3 +/- 3.0); Formula is: 0.04352 * FIBXLN+HUMXLN+TIBXLN (1265 mm) + 19.26.
Estimated stature with 90% PI: 69.8 to 75.7 (72.7 +/- 3.0); Formula is: 0.07466 * RADXLN+TIBXLN (724 mm) + 18.67.
Estimated stature with 90% PI: 70.2 to 76.1 (73.2 +/- 3.0); Formula is: 0.06118 * INNOHT+TIBXLN+ULNPHL (943 mm) + 15.48.
Estimated stature with 90% PI: 69.8 to 75.7 (72.8 +/- 3.0); Formula is: 0.04548 * FIBXLN+TIBXLN+ULNPHL (1146 mm) + 20.66.
Estimated stature with 90% PI: 70.0 to 75.9 (72.9 +/- 3.0); Formula is: 0.04566 * FIBXLN+RADXLN+TIBXLN (1159 mm) + 20.03.
Estimated stature with 90% PI: 69.9 to 75.9 (72.9 +/- 3.0); Formula is: 0.04659 * FEMBLN+FIBXLN+ULNPHL (1224 mm) + 15.89.
Estimated stature with 90% PI: 68.5 to 74.5 (71.5 +/- 3.0); Formula is: 0.05765 * CALCXL+TIBXLN+ULNPHL (787 mm) + 26.10.
Estimated stature with 90% PI: 69.9 to 75.9 (72.9 +/- 3.0); Formula is: 0.04623 * FEMXLN+RADXLN+TIBXLN (1245 mm) + 15.38.
Estimated stature with 90% PI: 69.8 to 75.8 (72.8 +/- 3.0); Formula is: 0.04578 * FEMBLN+TIBXLN+ULNPHL (1229 mm) + 16.53.
Estimated stature with 90% PI: 71.4 to 77.4 (74.4 +/- 3.0); Formula is: 0.05218 * HUMXLN+RADXLN+TIBXLN (1114 mm) + 16.24.
Estimated stature with 90% PI: 70.3 to 76.3 (73.3 +/- 3.0); Formula is: 0.06114 * INNOHT+RADXLN+TIBXLN (956 mm) + 14.83.
Estimated stature with 90% PI: 68.6 to 74.6 (71.6 +/- 3.0); Formula is: 0.05766 * CALCXL+RADXLN+TIBXLN (800 mm) + 25.48.
Estimated stature with 90% PI: 70.1 to 76.1 (73.1 +/- 3.0); Formula is: 0.04684 * FEMBLN+FIBXLN+RADXLN (1237 mm) + 15.18.
Estimated stature with 90% PI: 70.3 to 76.4 (73.3 +/- 3.0); Formula is: 0.04853 * FIBXLN+INNOHT+TIBXLN (1107 mm) + 19.62.
Estimated stature with 90% PI: 69.6 to 75.6 (72.6 +/- 3.0); Formula is: 0.07416 * TIBXLN+ULNPHL (711 mm) + 19.85.
Estimated stature with 90% PI: 69.8 to 75.9 (72.9 +/- 3.0); Formula is: 0.07633 * FIBXLN+ULNPHL (706 mm) + 18.98.
Estimated stature with 90% PI: 70.0 to 76.1 (73.1 +/- 3.0); Formula is: 0.07626 * FIBXLN+RADXLN (719 mm) + 18.23.
Estimated stature with 90% PI: 70.5 to 76.6 (73.5 +/- 3.0); Formula is: 0.06592 * RADXLN+SCAPHT+TIBXLN (904 mm) + 13.95.
Estimated stature with 90% PI: 70.3 to 76.4 (73.4 +/- 3.0); Formula is: 0.06212 * FIBXLN+INNOHT+ULNPHL (938 mm) + 15.09.
Estimated stature with 90% PI: 70.3 to 76.4 (73.4 +/- 3.0); Formula is: 0.06541 * SCAPHT+TIBXLN+ULNPHL (891 mm) + 15.08.
Estimated stature with 90% PI: 69.9 to 76.0 (72.9 +/- 3.0); Formula is: 0.04667 * FEMXLN+FIBXLN+ULNPHL (1227 mm) + 15.64.
Estimated stature with 90% PI: 70.4 to 76.5 (73.4 +/- 3.1); Formula is: 0.08339 * INNOHT+TIBXLN (672 mm) + 17.39.
Estimated stature with 90% PI: 69.0 to 75.2 (72.1 +/- 3.1); Formula is: 0.06250 * CALCXL+INNOHT+TIBXLN (748 mm) + 25.36.
Estimated stature with 90% PI: 69.7 to 75.8 (72.8 +/- 3.1); Formula is: 0.04575 * FEMXLN+TIBXLN+ULNPHL (1232 mm) + 16.41.
Estimated stature with 90% PI: 71.6 to 77.7 (74.7 +/- 3.1); Formula is: 0.05407 * FIBXLN+HUMXLN+RADXLN (1109 mm) + 14.71.
Estimated stature with 90% PI: 70.0 to 76.2 (73.1 +/- 3.1); Formula is: 0.04691 * FEMXLN+FIBXLN+RADXLN (1240 mm) + 14.93.
Estimated stature with 90% PI: 71.4 to 77.5 (74.4 +/- 3.1); Formula is: 0.04417 * FEMBLN+FIBXLN+HUMXLN (1343 mm) + 15.12.
Estimated stature with 90% PI: 71.1 to 77.2 (74.1 +/- 3.1); Formula is: 0.04250 * FEMBLN+HUMXLN+TIBXLN (1348 mm) + 16.86.
Estimated stature with 90% PI: 72.2 to 78.3 (75.2 +/- 3.1); Formula is: 0.07083 * FIBXLN+HUMXLN (825 mm) + 16.81.
Estimated stature with 90% PI: 71.1 to 77.3 (74.2 +/- 3.1); Formula is: 0.05212 * HUMXLN+TIBXLN+ULNPHL (1101 mm) + 16.85.
Estimated stature with 90% PI: 70.6 to 76.8 (73.7 +/- 3.1); Formula is: 0.06748 * FIBXLN+SCAPHT+ULNPHL (886 mm) + 13.87.
Estimated stature with 90% PI: 70.4 to 76.6 (73.5 +/- 3.1); Formula is: 0.06201 * FIBXLN+INNOHT+RADXLN (951 mm) + 14.52.
Estimated stature with 90% PI: 69.4 to 75.6 (72.5 +/- 3.1); Formula is: 0.05414 * RADXLN+TIBXLN+ULNPHL (995 mm) + 18.67.

Estimated stature with 90% PI: 71.4 to 77.6 (74.5 +/- 3.1); Formula is: 0.05392 * FIBXLN+HUMXLN+ULNPHL (1096 mm) + 15.40.
Estimated stature with 90% PI: 71.6 to 77.8 (74.7 +/- 3.1); Formula is: 0.06674 * HUMXLN+TIBXLN (830 mm) + 19.31.
Estimated stature with 90% PI: 69.6 to 75.8 (72.7 +/- 3.1); Formula is: 0.05531 * FIBXLN+RADXLN+ULNPHL (990 mm) + 17.98.
Estimated stature with 90% PI: 70.2 to 76.4 (73.3 +/- 3.1); Formula is: 0.04786 * FEMBLN+INNOHT+TIBXLN (1190 mm) + 16.32.
Estimated stature with 90% PI: 70.8 to 77.0 (73.9 +/- 3.1); Formula is: 0.06780 * FIBXLN+RADXLN+SCAPHT (899 mm) + 12.91.
Estimated stature with 90% PI: 71.3 to 77.5 (74.4 +/- 3.1); Formula is: 0.04420 * FEMXLN+FIBXLN+HUMXLN (1346 mm) + 14.93.
Estimated stature with 90% PI: 72.2 to 78.5 (75.4 +/- 3.1); Formula is: 0.06120 * HUMXLN+SCAPHT+TIBXLN (1010 mm) + 13.55.
Estimated stature with 90% PI: 68.6 to 74.9 (71.7 +/- 3.1); Formula is: 0.06135 * CALCXL+FIBXLN+ULNPHL (782 mm) + 23.77.
Estimated stature with 90% PI: 66.8 to 73.1 (70.0 +/- 3.1); Formula is: 0.07109 * CALCXL+SACAHT+TIBXLN (605 mm) + 26.95.
Estimated stature with 90% PI: 71.0 to 77.2 (74.1 +/- 3.1); Formula is: 0.04240 * FEMXLN+HUMXLN+TIBXLN (1351 mm) + 16.85.
Estimated stature with 90% PI: 69.8 to 76.0 (72.9 +/- 3.1); Formula is: 0.04501 * FIBXLN+TIBXLN+ULNXLN (1178 mm) + 19.89.
Estimated stature with 90% PI: 71.8 to 78.0 (74.9 +/- 3.1); Formula is: 0.05592 * HUMXLN+INNOHT+TIBXLN (1062 mm) + 15.52.
Estimated stature with 90% PI: 68.8 to 75.0 (71.9 +/- 3.1); Formula is: 0.06104 * CALCXL+FIBXLN+RADXLN (795 mm) + 23.36.
Estimated stature with 90% PI: 70.1 to 76.4 (73.3 +/- 3.1); Formula is: 0.04792 * FEMXLN+INNOHT+TIBXLN (1193 mm) + 16.09.
Estimated stature with 90% PI: 68.8 to 75.0 (71.9 +/- 3.1); Formula is: 0.04390 * CALCXL+FIBXLN+TIBXLN (951 mm) + 30.14.
Estimated stature with 90% PI: 69.8 to 76.1 (72.9 +/- 3.1); Formula is: 0.04535 * FEMBLN+TIBXLN+ULNXLN (1261 mm) + 15.75.
Estimated stature with 90% PI: 68.5 to 74.8 (71.6 +/- 3.1); Formula is: 0.05606 * CALCXL+TIBXLN+ULNXLN (819 mm) + 25.71.
Estimated stature with 90% PI: 68.8 to 75.0 (71.9 +/- 3.1); Formula is: 0.05415 * FEMBLN+SACAHT+TIBXLN (1047 mm) + 15.22.
Estimated stature with 90% PI: 69.0 to 75.3 (72.1 +/- 3.1); Formula is: 0.05726 * FEMBLN+FIBXLN+SACAHT (1042 mm) + 12.46.
Estimated stature with 90% PI: 69.9 to 76.2 (73.1 +/- 3.1); Formula is: 0.03961 * FEMBLN+FIBXLN+TIBXLN (1393 mm) + 17.88.
Estimated stature with 90% PI: 70.3 to 76.6 (73.5 +/- 3.2); Formula is: 0.04910 * FEMBLN+FIBXLN+INNOHT (1185 mm) + 15.27.
Estimated stature with 90% PI: 69.7 to 76.0 (72.9 +/- 3.2); Formula is: 0.05836 * FEMBLN+TIBXLN (958 mm) + 16.98.
Estimated stature with 90% PI: 70.1 to 76.4 (73.3 +/- 3.2); Formula is: 0.06020 * INNOHT+TIBXLN+ULNXLN (975 mm) + 14.57.
Estimated stature with 90% PI: 70.6 to 76.9 (73.8 +/- 3.2); Formula is: 0.08613 * FIBXLN+INNOHT (667 mm) + 16.33.
Estimated stature with 90% PI: 69.8 to 76.1 (72.9 +/- 3.2); Formula is: 0.07366 * FEMBLN+RADXLN (802 mm) + 13.87.
Estimated stature with 90% PI: 69.9 to 76.2 (73.1 +/- 3.2); Formula is: 0.04617 * FEMBLN+FIBXLN+ULNXLN (1256 mm) + 15.08.
Estimated stature with 90% PI: 71.0 to 77.3 (74.2 +/- 3.2); Formula is: 0.07186 * INNOHT+SCAPHT+TIBXLN (852 mm) + 12.96.
Estimated stature with 90% PI: 69.9 to 76.2 (73.1 +/- 3.2); Formula is: 0.03964 * FEMXLN+FIBXLN+TIBXLN (1396 mm) + 17.71.
Estimated stature with 90% PI: 70.0 to 76.4 (73.2 +/- 3.2); Formula is: 0.06007 * FEMBLN+FIBXLN (953 mm) + 15.94.
Estimated stature with 90% PI: 68.9 to 75.3 (72.1 +/- 3.2); Formula is: 0.06694 * CALCXL+SCAPHT+TIBXLN (696 mm) + 25.53.
Estimated stature with 90% PI: 69.7 to 76.1 (72.9 +/- 3.2); Formula is: 0.04536 * FEMXLN+TIBXLN+ULNXLN (1264 mm) + 15.59.
Estimated stature with 90% PI: 70.3 to 76.6 (73.5 +/- 3.2); Formula is: 0.04923 * FEMXLN+FIBXLN+INNOHT (1188 mm) + 14.96.
Estimated stature with 90% PI: 68.6 to 75.0 (71.8 +/- 3.2); Formula is: 0.05343 * FIBXLN+SACAHT+TIBXLN (964 mm) + 20.33.
Estimated stature with 90% PI: 71.1 to 77.5 (74.3 +/- 3.2); Formula is: 0.05151 * HUMXLN+TIBXLN+ULNXLN (1133 mm) + 15.97.
Estimated stature with 90% PI: 68.7 to 75.1 (71.9 +/- 3.2); Formula is: 0.05425 * FEMXLN+SACAHT+TIBXLN (1050 mm) + 14.93.
Estimated stature with 90% PI: 69.5 to 75.9 (72.7 +/- 3.2); Formula is: 0.07248 * TIBXLN+ULNXLN (743 mm) + 18.83.
Estimated stature with 90% PI: 68.9 to 75.3 (72.1 +/- 3.2); Formula is: 0.05750 * FEMXLN+FIBXLN+SACAHT (1045 mm) + 12.03.
Estimated stature with 90% PI: 69.7 to 76.1 (72.9 +/- 3.2); Formula is: 0.07346 * FEMXLN+RADXLN (805 mm) + 13.77.
Estimated stature with 90% PI: 69.3 to 75.7 (72.5 +/- 3.2); Formula is: 0.05326 * TIBXLN+ULNXLN+ULNPHL (1014 mm) + 18.49.
Estimated stature with 90% PI: 70.3 to 76.7 (73.5 +/- 3.2); Formula is: 0.06449 * SCAPHT+TIBXLN+ULNXLN (923 mm) + 13.94.
Estimated stature with 90% PI: 69.5 to 75.9 (72.7 +/- 3.2); Formula is: 0.05349 * RADXLN+TIBXLN+ULNXLN (1027 mm) + 17.74.
Estimated stature with 90% PI: 69.9 to 76.3 (73.1 +/- 3.2); Formula is: 0.04627 * FEMXLN+FIBXLN+ULNXLN (1259 mm) + 14.80.
Estimated stature with 90% PI: 72.6 to 79.0 (75.8 +/- 3.2); Formula is: 0.06384 * FIBXLN+HUMXLN+SCAPHT (1005 mm) + 11.61.
Estimated stature with 90% PI: 69.7 to 76.1 (72.9 +/- 3.2); Formula is: 0.05821 * FEMXLN+TIBXLN (961 mm) + 16.92.
Estimated stature with 90% PI: 72.0 to 78.4 (75.2 +/- 3.2); Formula is: 0.05808 * FIBXLN+HUMXLN+INNOHT (1057 mm) + 13.83.
Estimated stature with 90% PI: 70.0 to 76.4 (73.2 +/- 3.2); Formula is: 0.06023 * FEMXLN+FIBXLN (956 mm) + 15.60.
Estimated stature with 90% PI: 69.5 to 75.9 (72.7 +/- 3.2); Formula is: 0.05434 * FIBXLN+ULNXLN+ULNPHL (1009 mm) + 17.85.
Estimated stature with 90% PI: 71.2 to 77.6 (74.4 +/- 3.2); Formula is: 0.05118 * FEMBLN+HUMXLN+RADXLN (1192 mm) + 13.40.
Estimated stature with 90% PI: 71.4 to 77.8 (74.6 +/- 3.2); Formula is: 0.05329 * FIBXLN+HUMXLN+ULNXLN (1128 mm) + 14.51.
Estimated stature with 90% PI: 68.5 to 75.0 (71.8 +/- 3.2); Formula is: 0.04396 * CALCXL+FEMBLN+TIBXLN (1034 mm) + 26.31.
Estimated stature with 90% PI: 69.5 to 75.9 (72.7 +/- 3.2); Formula is: 0.07297 * FEMBLN+ULNPHL (789 mm) + 15.13.
Estimated stature with 90% PI: 69.7 to 76.1 (72.9 +/- 3.2); Formula is: 0.03852 * FEMBLN+FEMXLN+TIBXLN (1479 mm) + 15.94.
Estimated stature with 90% PI: 69.4 to 75.9 (72.6 +/- 3.2); Formula is: 0.05352 * FEMBLN+RADXLN+ULNPHL (1073 mm) + 15.20.
Estimated stature with 90% PI: 69.6 to 76.1 (72.9 +/- 3.2); Formula is: 0.05461 * FIBXLN+RADXLN+ULNXLN (1022 mm) + 17.06.
Estimated stature with 90% PI: 68.4 to 74.9 (71.7 +/- 3.2); Formula is: 0.05674 * CALCXL+FEMBLN+RADXLN (878 mm) + 21.85.
Estimated stature with 90% PI: 69.8 to 76.2 (73.0 +/- 3.2); Formula is: 0.07445 * FIBXLN+ULNXLN (738 mm) + 18.05.
Estimated stature with 90% PI: 70.1 to 76.5 (73.3 +/- 3.2); Formula is: 0.06193 * HUMXLN+SACAHT+TIBXLN (919 mm) + 16.38.
Estimated stature with 90% PI: 68.1 to 74.6 (71.3 +/- 3.2); Formula is: 0.06628 * RADXLN+SACAHT+TIBXLN (813 mm) + 17.46.
Estimated stature with 90% PI: 68.2 to 74.7 (71.5 +/- 3.2); Formula is: 0.05637 * CALCXL+FEMBLN+ULNPHL (865 mm) + 22.73.
Estimated stature with 90% PI: 69.9 to 76.4 (73.1 +/- 3.2); Formula is: 0.03939 * FEMBLN+FEMXLN+FIBXLN (1474 mm) + 15.04.
Estimated stature with 90% PI: 71.1 to 77.6 (74.4 +/- 3.2); Formula is: 0.05104 * FEMXLN+HUMXLN+RADXLN (1195 mm) + 13.38.
Estimated stature with 90% PI: 69.7 to 76.2 (72.9 +/- 3.2); Formula is: 0.04423 * FEMBLN+FEMXLN+RADXLN (1323 mm) + 14.43.
Estimated stature with 90% PI: 67.8 to 74.3 (71.1 +/- 3.2); Formula is: 0.07959 * CALCXL+TIBXLN (516 mm) + 29.99.
Estimated stature with 90% PI: 69.2 to 75.8 (72.5 +/- 3.3); Formula is: 0.11136 * TIBXLN (440 mm) + 23.50.
Estimated stature with 90% PI: 69.6 to 76.1 (72.9 +/- 3.3); Formula is: 0.05734 * FIBXLN+TIBXLN (875 mm) + 22.69.
Estimated stature with 90% PI: 70.3 to 76.8 (73.6 +/- 3.3); Formula is: 0.05361 * FEMBLN+SCAPHT+TIBXLN (1138 mm) + 12.58.
Estimated stature with 90% PI: 68.6 to 75.1 (71.9 +/- 3.3); Formula is: 0.08899 * CALCXL+INNOHT+RADXLN (592 mm) + 19.19.
Estimated stature with 90% PI: 69.9 to 76.4 (73.1 +/- 3.3); Formula is: 0.05878 * FEMBLN+INNOHT+ULNPHL (1021 mm) + 13.12.
Estimated stature with 90% PI: 68.4 to 74.9 (71.6 +/- 3.3); Formula is: 0.07091 * FIBXLN+RADXLN+SACAHT (808 mm) + 14.34.
Estimated stature with 90% PI: 70.2 to 76.7 (73.5 +/- 3.3); Formula is: 0.06092 * FIBXLN+INNOHT+ULNXLN (970 mm) + 14.37.
Estimated stature with 90% PI: 69.9 to 76.4 (73.1 +/- 3.3); Formula is: 0.05199 * CALCXL+HUMXLN+TIBXLN (906 mm) + 26.02.
Estimated stature with 90% PI: 68.8 to 75.3 (72.0 +/- 3.3); Formula is: 0.04656 * CALCXL+FEMBLN+FIBXLN (1029 mm) + 24.12.
Estimated stature with 90% PI: 70.4 to 76.9 (73.7 +/- 3.3); Formula is: 0.06488 * FEMBLN+RADXLN+SCAPHT (982 mm) + 9.94.
Estimated stature with 90% PI: 68.5 to 75.0 (71.7 +/- 3.3); Formula is: 0.04379 * CALCXL+FEMXLN+TIBXLN (1037 mm) + 26.32.
Estimated stature with 90% PI: 70.2 to 76.7 (73.4 +/- 3.3); Formula is: 0.06433 * FEMBLN+SCAPHT+ULNPHL (969 mm) + 11.11.
Estimated stature with 90% PI: 68.6 to 75.2 (71.9 +/- 3.3); Formula is: 0.05926 * CALCXL+FIBXLN+ULNXLN (814 mm) + 23.65.
Estimated stature with 90% PI: 70.0 to 76.6 (73.3 +/- 3.3); Formula is: 0.05884 * FEMBLN+INNOHT+RADXLN (1034 mm) + 12.45.
Estimated stature with 90% PI: 71.2 to 77.8 (74.5 +/- 3.3); Formula is: 0.07394 * FIBXLN+INNOHT+SCAPHT (847 mm) + 11.85.
Estimated stature with 90% PI: 68.4 to 75.0 (71.7 +/- 3.3); Formula is: 0.09033 * CALCXL+INNOHT+ULNPHL (579 mm) + 19.38.

Estimated stature with 90% PI: 70.5 to 77.0 (73.8 +/- 3.3); Formula is: 0.06623 * FIBXLN+SCAPHT+ULNXLN (918 mm) + 12.95.
Estimated stature with 90% PI: 69.0 to 75.6 (72.3 +/- 3.3); Formula is: 0.06559 * CALCXL+FIBXLN+INNOHT (743 mm) + 23.60.
Estimated stature with 90% PI: 70.3 to 76.9 (73.6 +/- 3.3); Formula is: 0.05373 * FEMXLN+SCAPHT+TIBXLN (1141 mm) + 12.27.
Estimated stature with 90% PI: 68.7 to 75.3 (72.0 +/- 3.3); Formula is: 0.04654 * CALCXL+FEMXLN+FIBXLN (1032 mm) + 23.96.
Estimated stature with 90% PI: 68.3 to 74.9 (71.6 +/- 3.3); Formula is: 0.05624 * CALCXL+FEMXLN+RADXLN (881 mm) + 22.08.
Estimated stature with 90% PI: 70.5 to 77.1 (73.8 +/- 3.3); Formula is: 0.05495 * FEMBLN+FIBXLN+SCAPHT (1133 mm) + 11.54.
Estimated stature with 90% PI: 68.2 to 74.8 (71.5 +/- 3.3); Formula is: 0.07073 * FIBXLN+SACAHT+ULNPHL (795 mm) + 15.23.
Estimated stature with 90% PI: 70.9 to 77.5 (74.2 +/- 3.3); Formula is: 0.05110 * FEMBLN+HUMXLN+ULNPHL (1179 mm) + 13.98.
Estimated stature with 90% PI: 69.3 to 75.9 (72.6 +/- 3.3); Formula is: 0.05337 * FEMXLN+RADXLN+ULNPHL (1076 mm) + 15.18.
Estimated stature with 90% PI: 70.4 to 77.0 (73.7 +/- 3.3); Formula is: 0.06647 * FIBXLN+HUMXLN+SACAHT (914 mm) + 12.94.
Estimated stature with 90% PI: 67.9 to 74.5 (71.2 +/- 3.3); Formula is: 0.06592 * SACAHT+TIBXLN+ULNPHL (800 mm) + 18.46.
Estimated stature with 90% PI: 69.8 to 76.4 (73.1 +/- 3.3); Formula is: 0.11696 * FIBXLN (435 mm) + 22.22.
Estimated stature with 90% PI: 68.1 to 74.8 (71.4 +/- 3.3); Formula is: 0.05579 * CALCXL+FEMXLN+ULNPHL (868 mm) + 23.01.
Estimated stature with 90% PI: 69.4 to 76.0 (72.7 +/- 3.3); Formula is: 0.07287 * FEMXLN+ULNPHL (792 mm) + 14.96.
Estimated stature with 90% PI: 69.4 to 76.0 (72.7 +/- 3.3); Formula is: 0.04360 * FEMBLN+FEMXLN+ULNPHL (1310 mm) + 15.60.
Estimated stature with 90% PI: 69.8 to 76.4 (73.1 +/- 3.3); Formula is: 0.05883 * FEMXLN+INNOHT+ULNPHL (1024 mm) + 12.87.
Estimated stature with 90% PI: 69.3 to 75.9 (72.6 +/- 3.3); Formula is: 0.05276 * FEMBLN+ULNXLN+ULNPHL (1092 mm) + 14.98.
Estimated stature with 90% PI: 68.5 to 75.2 (71.9 +/- 3.3); Formula is: 0.07495 * INNOHT+SACAHT+TIBXLN (761 mm) + 14.84.
Estimated stature with 90% PI: 68.2 to 74.8 (71.5 +/- 3.3); Formula is: 0.08679 * CALCXL+FIBXLN (511 mm) + 27.16.
Estimated stature with 90% PI: 70.3 to 76.9 (73.6 +/- 3.3); Formula is: 0.06479 * FEMXLN+RADXLN+SCAPHT (985 mm) + 9.80.
Estimated stature with 90% PI: 70.3 to 76.9 (73.6 +/- 3.3); Formula is: 0.05658 * CALCXL+FIBXLN+HUMXLN (901 mm) + 22.64.
Estimated stature with 90% PI: 66.8 to 73.5 (70.2 +/- 3.3); Formula is: 0.07975 * CALCXL+FIBXLN+SACAHT (600 mm) + 22.31.
Estimated stature with 90% PI: 69.5 to 76.2 (72.8 +/- 3.3); Formula is: 0.05316 * FEMBLN+RADXLN+ULNXLN (1105 mm) + 14.09.
Estimated stature with 90% PI: 69.9 to 76.6 (73.3 +/- 3.3); Formula is: 0.05887 * FEMXLN+INNOHT+RADXLN (1037 mm) + 12.22.
Estimated stature with 90% PI: 70.4 to 77.1 (73.8 +/- 3.3); Formula is: 0.05517 * FEMXLN+FIBXLN+SCAPHT (1136 mm) + 11.12.
Estimated stature with 90% PI: 68.3 to 75.0 (71.6 +/- 3.4); Formula is: 0.06778 * FEMBLN+RADXLN+SACAHT (891 mm) + 11.24.
Estimated stature with 90% PI: 70.1 to 76.8 (73.4 +/- 3.4); Formula is: 0.06424 * FEMXLN+SCAPHT+ULNPHL (972 mm) + 10.98.
Estimated stature with 90% PI: 69.5 to 76.2 (72.9 +/- 3.4); Formula is: 0.10949 * FEMBLN (518 mm) + 16.17.
Estimated stature with 90% PI: 67.0 to 73.8 (70.4 +/- 3.4); Formula is: 0.13269 * CALCXL+RADXLN (360 mm) + 22.63.
Estimated stature with 90% PI: 67.7 to 74.4 (71.0 +/- 3.4); Formula is: 0.07295 * CALCXL+RADXLN+ULNPHL (631 mm) + 25.02.
Estimated stature with 90% PI: 70.8 to 77.6 (74.2 +/- 3.4); Formula is: 0.05112 * FEMXLN+HUMXLN+ULNPHL (1182 mm) + 13.78.
Estimated stature with 90% PI: 70.2 to 76.9 (73.5 +/- 3.4); Formula is: 0.05289 * FIBXLN+SCAPHT+TIBXLN (1055 mm) + 17.73.
Estimated stature with 90% PI: 69.5 to 76.3 (72.9 +/- 3.4); Formula is: 0.07185 * FEMBLN+ULNXLN (821 mm) + 13.91.
Estimated stature with 90% PI: 70.6 to 77.4 (74.0 +/- 3.4); Formula is: 0.04054 * FEMBLN+FEMXLN+HUMXLN (1429 mm) + 16.08.
Estimated stature with 90% PI: 68.3 to 75.0 (71.7 +/- 3.4); Formula is: 0.05509 * CALCXL+FEMBLN+ULNXLN (897 mm) + 22.24.
Estimated stature with 90% PI: 71.3 to 78.1 (74.7 +/- 3.4); Formula is: 0.06447 * FEMBLN+HUMXLN (908 mm) + 16.14.
Estimated stature with 90% PI: 69.5 to 76.3 (72.9 +/- 3.4); Formula is: 0.07422 * INNOHT+RADXLN+ULNPHL (787 mm) + 14.49.
Estimated stature with 90% PI: 68.8 to 75.6 (72.2 +/- 3.4); Formula is: 0.07968 * FIBXLN+INNOHT+SACAHT (756 mm) + 11.96.
Estimated stature with 90% PI: 69.2 to 76.0 (72.6 +/- 3.4); Formula is: 0.05265 * FEMXLN+ULNXLN+ULNPHL (1095 mm) + 14.91.
Estimated stature with 90% PI: 70.0 to 76.8 (73.4 +/- 3.4); Formula is: 0.12277 * INNOHT+ULNPHL (503 mm) + 11.63.
Estimated stature with 90% PI: 69.4 to 76.2 (72.8 +/- 3.4); Formula is: 0.05306 * FEMXLN+RADXLN+ULNXLN (1108 mm) + 14.00.
Estimated stature with 90% PI: 69.1 to 75.9 (72.5 +/- 3.4); Formula is: 0.07195 * CALCXL+FIBXLN+SCAPHT (691 mm) + 22.77.
Estimated stature with 90% PI: 71.0 to 77.8 (74.4 +/- 3.4); Formula is: 0.05066 * FEMBLN+HUMXLN+ULNXLN (1211 mm) + 13.01.
Estimated stature with 90% PI: 69.5 to 76.3 (72.9 +/- 3.4); Formula is: 0.05475 * FEMBLN+FEMXLN (1039 mm) + 15.97.
Estimated stature with 90% PI: 67.8 to 74.6 (71.2 +/- 3.4); Formula is: 0.07250 * CALCXL+RADXLN+ULNXLN (663 mm) + 23.17.
Estimated stature with 90% PI: 70.3 to 77.2 (73.8 +/- 3.4); Formula is: 0.09408 * SCAPHT+TIBXLN (620 mm) + 15.43.
Estimated stature with 90% PI: 70.1 to 76.9 (73.5 +/- 3.4); Formula is: 0.11985 * INNOHT+RADXLN (516 mm) + 11.66.
Estimated stature with 90% PI: 70.2 to 77.0 (73.6 +/- 3.4); Formula is: 0.06360 * FEMBLN+SCAPHT+ULNXLN (1001 mm) + 9.90.
Estimated stature with 90% PI: 71.7 to 78.6 (75.2 +/- 3.4); Formula is: 0.08766 * HUMXLN+RADXLN (674 mm) + 16.08.
Estimated stature with 90% PI: 69.5 to 76.3 (72.9 +/- 3.4); Formula is: 0.04352 * FEMBLN+FEMXLN+ULNXLN (1342 mm) + 14.51.
Estimated stature with 90% PI: 70.0 to 76.8 (73.4 +/- 3.4); Formula is: 0.06914 * CALCXL+HUMXLN+RADXLN (750 mm) + 21.57.
Estimated stature with 90% PI: 69.8 to 76.7 (73.3 +/- 3.4); Formula is: 0.05807 * FEMBLN+INNOHT+ULNXLN (1053 mm) + 12.11.
Estimated stature with 90% PI: 69.4 to 76.2 (72.8 +/- 3.4); Formula is: 0.10896 * FEMXLN (521 mm) + 16.05.
Estimated stature with 90% PI: 68.0 to 74.9 (71.4 +/- 3.4); Formula is: 0.06705 * FEMBLN+SACAHT+ULNPHL (878 mm) + 12.57.
Estimated stature with 90% PI: 71.2 to 78.1 (74.6 +/- 3.4); Formula is: 0.06407 * FEMXLN+HUMXLN (911 mm) + 16.25.
Estimated stature with 90% PI: 68.4 to 75.3 (71.9 +/- 3.4); Formula is: 0.08630 * CALCXL+INNOHT+ULNXLN (611 mm) + 19.13.
Estimated stature with 90% PI: 68.2 to 75.0 (71.6 +/- 3.4); Formula is: 0.05470 * CALCXL+FEMXLN+ULNXLN (900 mm) + 22.37.
Estimated stature with 90% PI: 67.2 to 74.1 (70.7 +/- 3.4); Formula is: 0.09281 * SACAHT+TIBXLN (529 mm) + 21.56.
Estimated stature with 90% PI: 69.6 to 76.5 (73.1 +/- 3.4); Formula is: 0.04458 * FEMBLN+FEMXLN+INNOHT (1271 mm) + 16.41.
Estimated stature with 90% PI: 69.4 to 76.3 (72.9 +/- 3.4); Formula is: 0.07190 * FEMXLN+ULNXLN (824 mm) + 13.62.
Estimated stature with 90% PI: 68.1 to 75.0 (71.6 +/- 3.4); Formula is: 0.06733 * FEMXLN+RADXLN+SACAHT (894 mm) + 11.40.
Estimated stature with 90% PI: 68.6 to 75.5 (72.0 +/- 3.4); Formula is: 0.05823 * CALCXL+FEMBLN+INNOHT (826 mm) + 23.93.
Estimated stature with 90% PI: 67.9 to 74.8 (71.3 +/- 3.5); Formula is: 0.06431 * SACAHT+TIBXLN+ULNXLN (832 mm) + 17.81.
Estimated stature with 90% PI: 70.9 to 77.8 (74.3 +/- 3.5); Formula is: 0.05067 * FEMXLN+HUMXLN+ULNXLN (1214 mm) + 12.83.
Estimated stature with 90% PI: 69.9 to 76.8 (73.3 +/- 3.5); Formula is: 0.07734 * FEMBLN+INNOHT (750 mm) + 15.33.
Estimated stature with 90% PI: 68.5 to 75.4 (71.9 +/- 3.5); Formula is: 0.05149 * FEMBLN+FEMXLN+SACAHT (1128 mm) + 13.86.
Estimated stature with 90% PI: 71.8 to 78.7 (75.3 +/- 3.5); Formula is: 0.05910 * FEMBLN+HUMXLN+SCAPHT (1088 mm) + 10.97.
Estimated stature with 90% PI: 68.4 to 75.4 (71.9 +/- 3.5); Formula is: 0.07735 * SACAHT+SCAPHT+TIBXLN (709 mm) + 17.05.
Estimated stature with 90% PI: 69.8 to 76.7 (73.2 +/- 3.5); Formula is: 0.05821 * FEMXLN+INNOHT+ULNXLN (1056 mm) + 11.76.
Estimated stature with 90% PI: 67.6 to 74.5 (71.1 +/- 3.5); Formula is: 0.10232 * FIBXLN+SACAHT (524 mm) + 17.44.
Estimated stature with 90% PI: 70.1 to 77.0 (73.5 +/- 3.5); Formula is: 0.06361 * FEMXLN+SCAPHT+ULNXLN (1004 mm) + 9.67.
Estimated stature with 90% PI: 71.3 to 78.2 (74.7 +/- 3.5); Formula is: 0.05318 * FEMBLN+HUMXLN+INNOHT (1140 mm) + 14.11.
Estimated stature with 90% PI: 66.6 to 73.6 (70.1 +/- 3.5); Formula is: 0.07120 * CALCXL+FEMBLN+SACAHT (683 mm) + 21.47.
Estimated stature with 90% PI: 67.6 to 74.5 (71.0 +/- 3.5); Formula is: 0.07091 * CALCXL+ULNXLN+ULNPHL (650 mm) + 24.94.
Estimated stature with 90% PI: 70.7 to 77.7 (74.2 +/- 3.5); Formula is: 0.09712 * INNOHT+SCAPHT+ULNPHL (683 mm) + 7.89.
Estimated stature with 90% PI: 68.7 to 75.7 (72.2 +/- 3.5); Formula is: 0.06643 * CALCXL+FEMBLN+SCAPHT (774 mm) + 20.76.
Estimated stature with 90% PI: 70.8 to 77.8 (74.3 +/- 3.5); Formula is: 0.06169 * HUMXLN+RADXLN+ULNPHL (945 mm) + 15.98.
Estimated stature with 90% PI: 68.8 to 75.8 (72.3 +/- 3.5); Formula is: 0.18185 * RADXLN (284 mm) + 20.65.
Estimated stature with 90% PI: 68.5 to 75.5 (72.0 +/- 3.5); Formula is: 0.05814 * CALCXL+FEMXLN+INNOHT (829 mm) + 23.79.

Estimated stature with 90% PI: 68.1 to 75.1 (71.6 +/- 3.5); Formula is: 0.06855 * FIBXLN+SACAHT+ULNXLN (827 mm) + 14.90.
Estimated stature with 90% PI: 67.7 to 74.7 (71.2 +/- 3.5); Formula is: 0.07790 * CALCXL+FEMBLN (594 mm) + 24.91.
Estimated stature with 90% PI: 69.8 to 76.8 (73.3 +/- 3.5); Formula is: 0.07761 * FEMXLN+INNOHT (753 mm) + 14.87.
Estimated stature with 90% PI: 71.7 to 78.7 (75.2 +/- 3.5); Formula is: 0.06949 * HUMXLN+INNOHT+RADXLN (906 mm) + 12.24.
Estimated stature with 90% PI: 68.2 to 75.2 (71.7 +/- 3.5); Formula is: 0.04112 * CALCXL+FEMBLN+FEMXLN (1115 mm) + 25.82.
Estimated stature with 90% PI: 71.7 to 78.8 (75.2 +/- 3.5); Formula is: 0.05919 * FEMXLN+HUMXLN+SCAPHT (1091 mm) + 10.68.
Estimated stature with 90% PI: 68.4 to 75.4 (71.9 +/- 3.5); Formula is: 0.09623 * CALCXL+RADXLN+SCAPHT (540 mm) + 19.96.
Estimated stature with 90% PI: 69.5 to 76.5 (73.0 +/- 3.5); Formula is: 0.07291 * INNOHT+RADXLN+ULNXLN (819 mm) + 13.30.
Estimated stature with 90% PI: 69.3 to 76.3 (72.8 +/- 3.5); Formula is: 0.07251 * INNOHT+ULNXLN+ULNPHL (806 mm) + 14.39.
Estimated stature with 90% PI: 72.3 to 79.3 (75.8 +/- 3.5); Formula is: 0.07705 * HUMXLN+RADXLN+SCAPHT (854 mm) + 10.03.
Estimated stature with 90% PI: 70.9 to 77.9 (74.4 +/- 3.5); Formula is: 0.09632 * INNOHT+RADXLN+SCAPHT (696 mm) + 7.34.
Estimated stature with 90% PI: 71.2 to 78.2 (74.7 +/- 3.5); Formula is: 0.05324 * FEMXLN+HUMXLN+INNOHT (1143 mm) + 13.87.
Estimated stature with 90% PI: 69.6 to 76.6 (73.1 +/- 3.5); Formula is: 0.05078 * CALCXL+FEMBLN+HUMXLN (984 mm) + 23.13.
Estimated stature with 90% PI: 69.9 to 76.9 (73.4 +/- 3.5); Formula is: 0.06080 * FEMBLN+HUMXLN+SACAHT (997 mm) + 12.78.
Estimated stature with 90% PI: 66.6 to 73.7 (70.1 +/- 3.5); Formula is: 0.13130 * CALCXL+ULNPHL (347 mm) + 24.59.
Estimated stature with 90% PI: 67.9 to 74.9 (71.4 +/- 3.5); Formula is: 0.06658 * FEMXLN+SACAHT+ULNPHL (881 mm) + 12.74.
Estimated stature with 90% PI: 68.6 to 75.7 (72.1 +/- 3.5); Formula is: 0.06619 * CALCXL+FEMXLN+SCAPHT (777 mm) + 20.69.
Estimated stature with 90% PI: 68.0 to 75.1 (71.6 +/- 3.5); Formula is: 0.06595 * FEMBLN+SACAHT+ULNXLN (910 mm) + 11.57.
Estimated stature with 90% PI: 69.9 to 77.0 (73.5 +/- 3.6); Formula is: 0.05059 * FEMBLN+FEMXLN+SCAPHT (1219 mm) + 11.79.
Estimated stature with 90% PI: 70.8 to 77.9 (74.4 +/- 3.6); Formula is: 0.06055 * HUMXLN+RADXLN+ULNXLN (977 mm) + 15.20.
Estimated stature with 90% PI: 68.5 to 75.6 (72.1 +/- 3.6); Formula is: 0.07349 * FEMBLN+INNOHT+SACAHT (839 mm) + 10.41.
Estimated stature with 90% PI: 66.5 to 73.6 (70.0 +/- 3.6); Formula is: 0.07029 * CALCXL+FEMXLN+SACAHT (686 mm) + 21.83.
Estimated stature with 90% PI: 70.6 to 77.8 (74.2 +/- 3.6); Formula is: 0.09714 * FIBXLN+SCAPHT (615 mm) + 14.47.
Estimated stature with 90% PI: 67.6 to 74.7 (71.1 +/- 3.6); Formula is: 0.07736 * CALCXL+FEMXLN (597 mm) + 24.94.
Estimated stature with 90% PI: 69.6 to 76.8 (73.2 +/- 3.6); Formula is: 0.06772 * CALCXL+HUMXLN+ULNPHL (737 mm) + 23.30.
Estimated stature with 90% PI: 67.5 to 74.6 (71.0 +/- 3.6); Formula is: 0.09508 * FEMBLN+SACAHT (607 mm) + 13.33.
Estimated stature with 90% PI: 69.8 to 77.0 (73.4 +/- 3.6); Formula is: 0.06771 * CALCXL+HUMXLN+ULNXLN (769 mm) + 21.32.
Estimated stature with 90% PI: 69.5 to 76.6 (73.0 +/- 3.6); Formula is: 0.05035 * CALCXL+FEMXLN+HUMXLN (987 mm) + 23.34.
Estimated stature with 90% PI: 70.3 to 77.5 (73.9 +/- 3.6); Formula is: 0.09165 * FEMBLN+SCAPHT (698 mm) + 9.95.
Estimated stature with 90% PI: 71.5 to 78.6 (75.0 +/- 3.6); Formula is: 0.06924 * HUMXLN+INNOHT+ULNPHL (893 mm) + 13.21.
Estimated stature with 90% PI: 70.6 to 77.8 (74.2 +/- 3.6); Formula is: 0.06054 * HUMXLN+ULNXLN+ULNPHL (964 mm) + 15.83.
Estimated stature with 90% PI: 69.8 to 77.0 (73.4 +/- 3.6); Formula is: 0.06067 * FEMXLN+HUMXLN+SACAHT (1000 mm) + 12.69.
Estimated stature with 90% PI: 71.4 to 78.6 (75.0 +/- 3.6); Formula is: 0.08851 * HUMXLN+ULNPHL (661 mm) + 16.53.
Estimated stature with 90% PI: 70.4 to 77.6 (74.0 +/- 3.6); Formula is: 0.06723 * FEMBLN+INNOHT+SCAPHT (930 mm) + 11.49.
Estimated stature with 90% PI: 66.8 to 74.1 (70.4 +/- 3.6); Formula is: 0.12558 * CALCXL+ULNXLN (379 mm) + 22.84.
Estimated stature with 90% PI: 68.4 to 75.7 (72.0 +/- 3.6); Formula is: 0.07368 * FEMXLN+INNOHT+SACAHT (842 mm) + 10.00.
Estimated stature with 90% PI: 67.9 to 75.2 (71.5 +/- 3.6); Formula is: 0.06567 * FEMXLN+SACAHT+ULNXLN (913 mm) + 11.58.
Estimated stature with 90% PI: 68.0 to 75.2 (71.6 +/- 3.6); Formula is: 0.09254 * CALCXL+SCAPHT+ULNPHL (527 mm) + 22.85.
Estimated stature with 90% PI: 68.5 to 75.8 (72.1 +/- 3.6); Formula is: 0.09154 * RADXLN+ULNPHL (555 mm) + 21.32.
Estimated stature with 90% PI: 68.6 to 75.9 (72.2 +/- 3.6); Formula is: 0.08267 * FIBXLN+SACAHT+SCAPHT (704 mm) + 14.05.
Estimated stature with 90% PI: 69.5 to 76.8 (73.2 +/- 3.6); Formula is: 0.07897 * RADXLN+SCAPHT+ULNPHL (735 mm) + 15.12.
Estimated stature with 90% PI: 69.8 to 77.1 (73.4 +/- 3.6); Formula is: 0.11655 * INNOHT+ULNXLN (535 mm) + 11.06.
Estimated stature with 90% PI: 72.0 to 79.3 (75.6 +/- 3.7); Formula is: 0.07601 * HUMXLN+SCAPHT+ULNPHL (841 mm) + 11.68.
Estimated stature with 90% PI: 70.3 to 77.6 (74.0 +/- 3.7); Formula is: 0.06747 * FEMXLN+INNOHT+SCAPHT (933 mm) + 11.04.
Estimated stature with 90% PI: 71.5 to 78.8 (75.1 +/- 3.7); Formula is: 0.06856 * HUMXLN+INNOHT+ULNXLN (925 mm) + 11.71.
Estimated stature with 90% PI: 70.2 to 77.5 (73.9 +/- 3.7); Formula is: 0.09189 * FEMXLN+SCAPHT (701 mm) + 9.47.
Estimated stature with 90% PI: 67.3 to 74.7 (71.0 +/- 3.7); Formula is: 0.09471 * FEMXLN+SACAHT (610 mm) + 13.22.
Estimated stature with 90% PI: 71.4 to 78.8 (75.1 +/- 3.7); Formula is: 0.08616 * HUMXLN+ULNXLN (693 mm) + 15.39.
Estimated stature with 90% PI: 72.0 to 79.4 (75.7 +/- 3.7); Formula is: 0.07521 * HUMXLN+SCAPHT+ULNXLN (873 mm) + 10.02.
Estimated stature with 90% PI: 68.3 to 75.7 (72.0 +/- 3.7); Formula is: 0.18147 * ULNPHL (271 mm) + 22.83.
Estimated stature with 90% PI: 70.5 to 77.9 (74.2 +/- 3.7); Formula is: 0.09320 * INNOHT+SCAPHT+ULNXLN (715 mm) + 7.60.
Estimated stature with 90% PI: 68.4 to 75.8 (72.1 +/- 3.7); Formula is: 0.05974 * RADXLN+ULNXLN+ULNPHL (858 mm) + 20.84.
Estimated stature with 90% PI: 70.2 to 77.7 (73.9 +/- 3.7); Formula is: 0.13326 * RADXLN+SCAPHT (464 mm) + 12.11.
Estimated stature with 90% PI: 68.4 to 75.9 (72.1 +/- 3.7); Formula is: 0.07767 * FEMBLN+SACAHT+SCAPHT (787 mm) + 11.02.
Estimated stature with 90% PI: 69.5 to 77.0 (73.3 +/- 3.7); Formula is: 0.07765 * RADXLN+SCAPHT+ULNXLN (767 mm) + 13.70.
Estimated stature with 90% PI: 68.6 to 76.0 (72.3 +/- 3.7); Formula is: 0.08923 * RADXLN+ULNXLN (587 mm) + 19.92.
Estimated stature with 90% PI: 68.1 to 75.5 (71.8 +/- 3.7); Formula is: 0.08919 * CALCXL+SCAPHT+ULNXLN (559 mm) + 21.95.
Estimated stature with 90% PI: 65.1 to 72.7 (68.9 +/- 3.8); Formula is: 0.08974 * CALCXL+RADXLN+SACAHT (449 mm) + 28.64.
Estimated stature with 90% PI: 69.2 to 76.8 (73.0 +/- 3.8); Formula is: 0.07610 * SCAPHT+ULNXLN+ULNPHL (754 mm) + 15.66.
Estimated stature with 90% PI: 68.2 to 75.8 (72.0 +/- 3.8); Formula is: 0.08821 * ULNXLN+ULNPHL (574 mm) + 21.40.
Estimated stature with 90% PI: 69.9 to 77.5 (73.7 +/- 3.8); Formula is: 0.06892 * CALCXL+HUMXLN+INNOHT (698 mm) + 25.58.
Estimated stature with 90% PI: 68.3 to 75.9 (72.1 +/- 3.8); Formula is: 0.07725 * FEMXLN+SACAHT+SCAPHT (790 mm) + 11.07.
Estimated stature with 90% PI: 69.2 to 76.9 (73.0 +/- 3.8); Formula is: 0.07316 * HUMXLN+RADXLN+SACAHT (763 mm) + 17.21.
Estimated stature with 90% PI: 69.8 to 77.5 (73.6 +/- 3.8); Formula is: 0.13074 * SCAPHT+ULNPHL (451 mm) + 14.66.
Estimated stature with 90% PI: 68.6 to 76.3 (72.5 +/- 3.9); Formula is: 0.10324 * CALCXL+INNOHT+SCAPHT (488 mm) + 22.08.
Estimated stature with 90% PI: 67.1 to 74.9 (71.0 +/- 3.9); Formula is: 0.14018 * CALCXL+INNOHT (308 mm) + 27.82.
Estimated stature with 90% PI: 68.3 to 76.1 (72.2 +/- 3.9); Formula is: 0.17051 * ULNXLN (303 mm) + 20.53.
Estimated stature with 90% PI: 72.0 to 79.8 (75.9 +/- 3.9); Formula is: 0.09606 * HUMXLN+INNOHT (622 mm) + 16.19.
Estimated stature with 90% PI: 67.3 to 75.1 (71.2 +/- 3.9); Formula is: 0.09297 * INNOHT+RADXLN+SACAHT (605 mm) + 14.94.
Estimated stature with 90% PI: 72.0 to 79.8 (75.9 +/- 3.9); Formula is: 0.13049 * HUMXLN (390 mm) + 25.00.
Estimated stature with 90% PI: 70.1 to 78.0 (74.1 +/- 4.0); Formula is: 0.07727 * CALCXL+HUMXLN+SCAPHT (646 mm) + 24.16.
Estimated stature with 90% PI: 69.3 to 77.3 (73.3 +/- 4.0); Formula is: 0.09412 * CALCXL+HUMXLN (466 mm) + 29.43.
Estimated stature with 90% PI: 72.4 to 80.3 (76.3 +/- 4.0); Formula is: 0.08102 * HUMXLN+INNOHT+SCAPHT (802 mm) + 11.37.
Estimated stature with 90% PI: 65.1 to 73.1 (69.1 +/- 4.0); Formula is: 0.08275 * CALCXL+SACAHT+ULNXLN (468 mm) + 30.34.
Estimated stature with 90% PI: 64.8 to 72.8 (68.8 +/- 4.0); Formula is: 0.08076 * CALCXL+SACAHT+ULNPHL (436 mm) + 33.63.
Estimated stature with 90% PI: 69.7 to 77.7 (73.7 +/- 4.0); Formula is: 0.12524 * SCAPHT+ULNXLN (483 mm) + 13.18.
Estimated stature with 90% PI: 68.8 to 76.8 (72.8 +/- 4.0); Formula is: 0.07202 * HUMXLN+SACAHT+ULNPHL (750 mm) + 18.81.
Estimated stature with 90% PI: 67.3 to 75.3 (71.3 +/- 4.0); Formula is: 0.06824 * CALCXL+HUMXLN+SACAHT (555 mm) + 33.46.
Estimated stature with 90% PI: 68.9 to 77.0 (72.9 +/- 4.0); Formula is: 0.07105 * HUMXLN+SACAHT+ULNXLN (782 mm) + 17.38.

Estimated stature with 90% PI: 72.6 to 80.7 (76.7 +/- 4.0); Formula is: 0.10804 * HUMXLN+SCAPHT (570 mm) + 15.10.
Estimated stature with 90% PI: 66.9 to 75.0 (70.9 +/- 4.0); Formula is: 0.09156 * INNOHT+SACAHT+ULNPHL (592 mm) + 16.73.
Estimated stature with 90% PI: 66.3 to 74.6 (70.4 +/- 4.1); Formula is: 0.07155 * RADXLN+SACAHT+ULNPHL (644 mm) + 24.37.
Estimated stature with 90% PI: 66.5 to 74.7 (70.6 +/- 4.1); Formula is: 0.07054 * RADXLN+SACAHT+ULNXLN (676 mm) + 22.92.
Estimated stature with 90% PI: 69.3 to 77.6 (73.5 +/- 4.2); Formula is: 0.07791 * HUMXLN+INNOHT+SACAHT (711 mm) + 18.08.
Estimated stature with 90% PI: 66.9 to 75.3 (71.1 +/- 4.2); Formula is: 0.08795 * INNOHT+SACAHT+ULNXLN (624 mm) + 16.22.
Estimated stature with 90% PI: 69.5 to 77.9 (73.7 +/- 4.2); Formula is: 0.23029 * INNOHT (232 mm) + 20.28.
Estimated stature with 90% PI: 65.0 to 73.5 (69.3 +/- 4.2); Formula is: 0.07879 * CALCXL+INNOHT+SACAHT (397 mm) + 38.00.
Estimated stature with 90% PI: 66.1 to 74.6 (70.4 +/- 4.3); Formula is: 0.06777 * SACAHT+ULNXLN+ULNPHL (663 mm) + 25.45.
Estimated stature with 90% PI: 70.6 to 79.2 (74.9 +/- 4.3); Formula is: 0.15146 * INNOHT+SCAPHT (412 mm) + 12.53.
Estimated stature with 90% PI: 66.5 to 75.1 (70.8 +/- 4.3); Formula is: 0.13562 * CALCXL+SCAPHT (256 mm) + 36.10.
Estimated stature with 90% PI: 66.7 to 75.4 (71.1 +/- 4.4); Formula is: 0.08603 * RADXLN+SACAHT+SCAPHT (553 mm) + 23.49.
Estimated stature with 90% PI: 65.1 to 73.9 (69.5 +/- 4.4); Formula is: 0.10403 * RADXLN+SACAHT (373 mm) + 30.70.
Estimated stature with 90% PI: 68.1 to 77.0 (72.6 +/- 4.4); Formula is: 0.09412 * HUMXLN+SACAHT (479 mm) + 27.50.
Estimated stature with 90% PI: 69.1 to 77.9 (73.5 +/- 4.4); Formula is: 0.07847 * HUMXLN+SACAHT+SCAPHT (659 mm) + 21.78.
Estimated stature with 90% PI: 66.2 to 75.3 (70.7 +/- 4.5); Formula is: 0.07974 * SACAHT+SCAPHT+ULNPHL (540 mm) + 27.68.
Estimated stature with 90% PI: 66.4 to 75.5 (70.9 +/- 4.6); Formula is: 0.07843 * SACAHT+SCAPHT+ULNXLN (572 mm) + 26.07.
Estimated stature with 90% PI: 64.9 to 74.1 (69.5 +/- 4.6); Formula is: 0.04727 * CALCXL+SACAHT+SCAPHT (345 mm) + 53.21.
Estimated stature with 90% PI: 64.6 to 74.0 (69.3 +/- 4.7); Formula is: 0.09561 * SACAHT+ULNPHL (360 mm) + 34.87.
Estimated stature with 90% PI: 64.8 to 74.2 (69.5 +/- 4.7); Formula is: 0.09279 * SACAHT+ULNXLN (392 mm) + 33.14.
Estimated stature with 90% PI: 66.6 to 76.1 (71.3 +/- 4.8); Formula is: 0.08938 * INNOHT+SACAHT+SCAPHT (501 mm) + 26.56.
Estimated stature with 90% PI: 64.9 to 74.7 (69.8 +/- 4.9); Formula is: 0.09860 * INNOHT+SACAHT (321 mm) + 38.13.
Estimated stature with 90% PI: 64.1 to 74.0 (69.0 +/- 5.0); Formula is: 0.03286 * CALCXL+SACAHT (165 mm) + 63.60.
Estimated stature with 90% PI: 62.8 to 72.9 (67.9 +/- 5.0); Formula is: 0.18885 * CALCXL (76 mm) + 53.50.
Estimated stature with 90% PI: 67.8 to 78.4 (73.1 +/- 5.3); Formula is: 0.20572 * SCAPHT (180 mm) + 36.07.
Estimated stature with 90% PI: 64.3 to 75.0 (69.6 +/- 5.4); Formula is: 0.05558 * SACAHT+SCAPHT (269 mm) + 54.68.
Estimated stature with 90% PI: 63.9 to 75.0 (69.4 +/- 5.5); Formula is: 0.00133 * SACAHT (89 mm) + 69.31.

To get output based on different equations or PIs, for instance, choose Trotter MStats and 95% PI.

Example 3 is FDN 46, a black male with a forensic stature of 183 cm or 72". All but a few of the estimated stature intervals include the forensic stature of 72".

International Considerations

Language

Index files speed up queries, and the indices are sorted using the English (US) sort order for the Forensic Data. If you are using a different sort order on your computer, the indices will automatically be rebuilt when accessed.

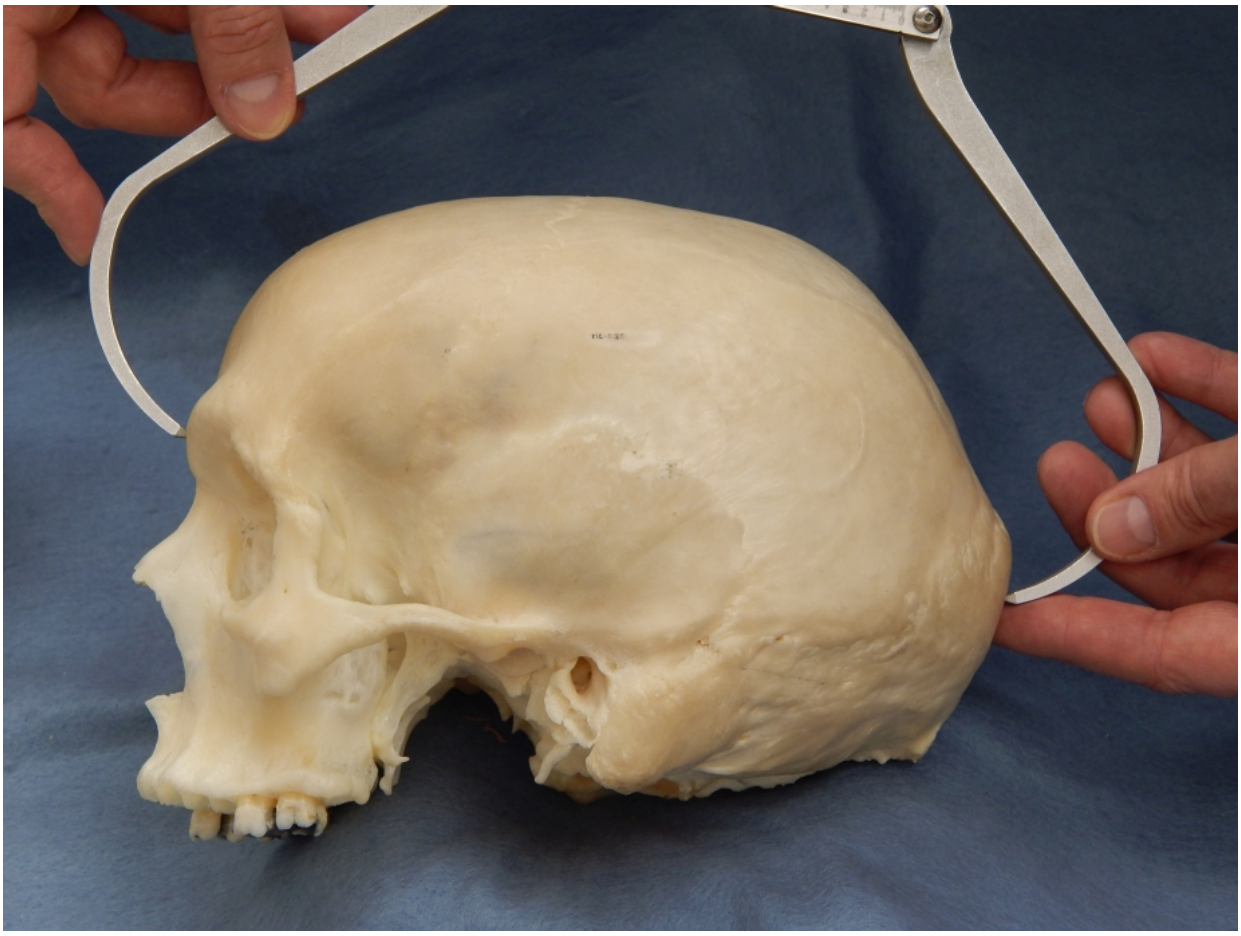
Characters

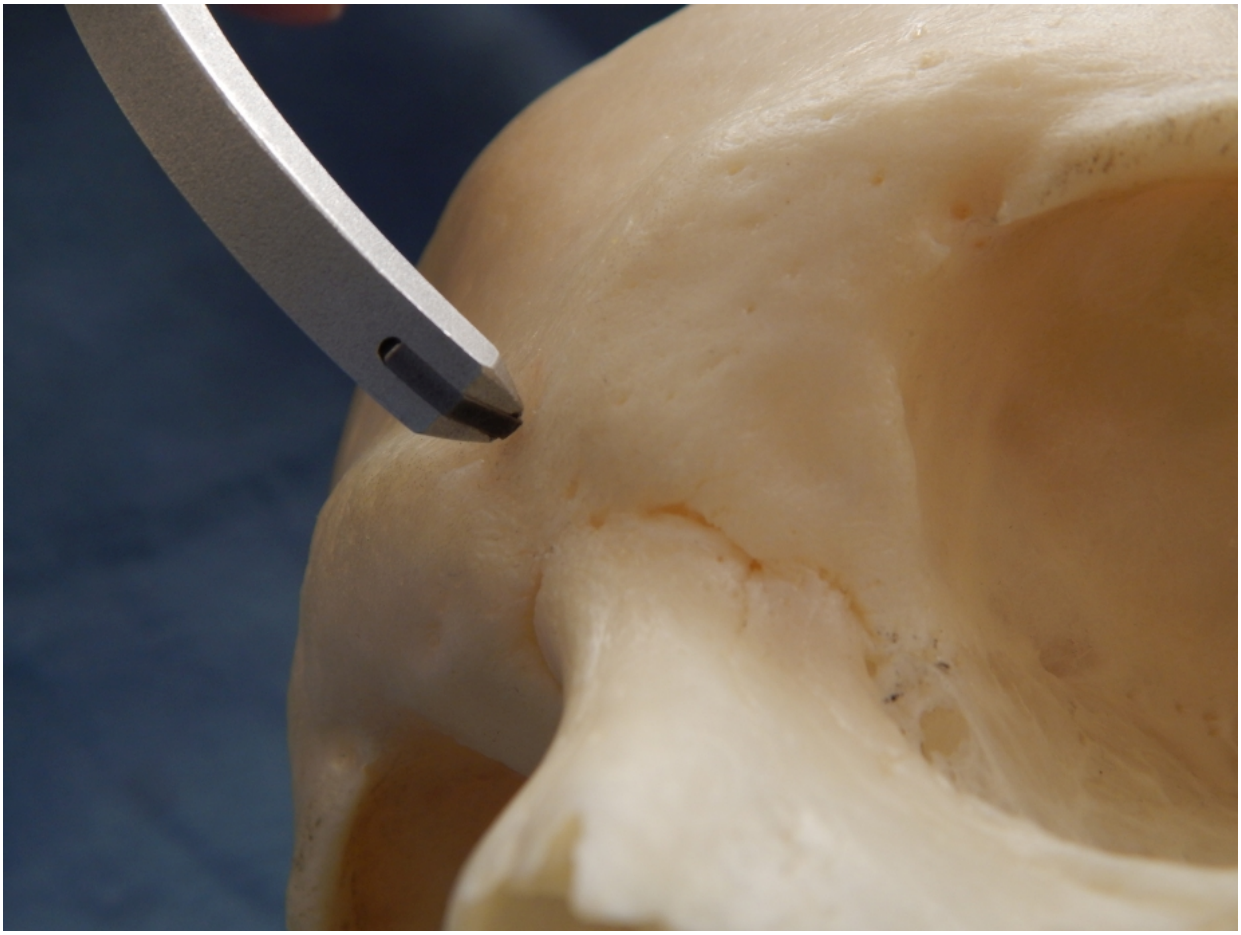
Support for the extended character set was added in build 271, so you should be able to save case information using international characters.

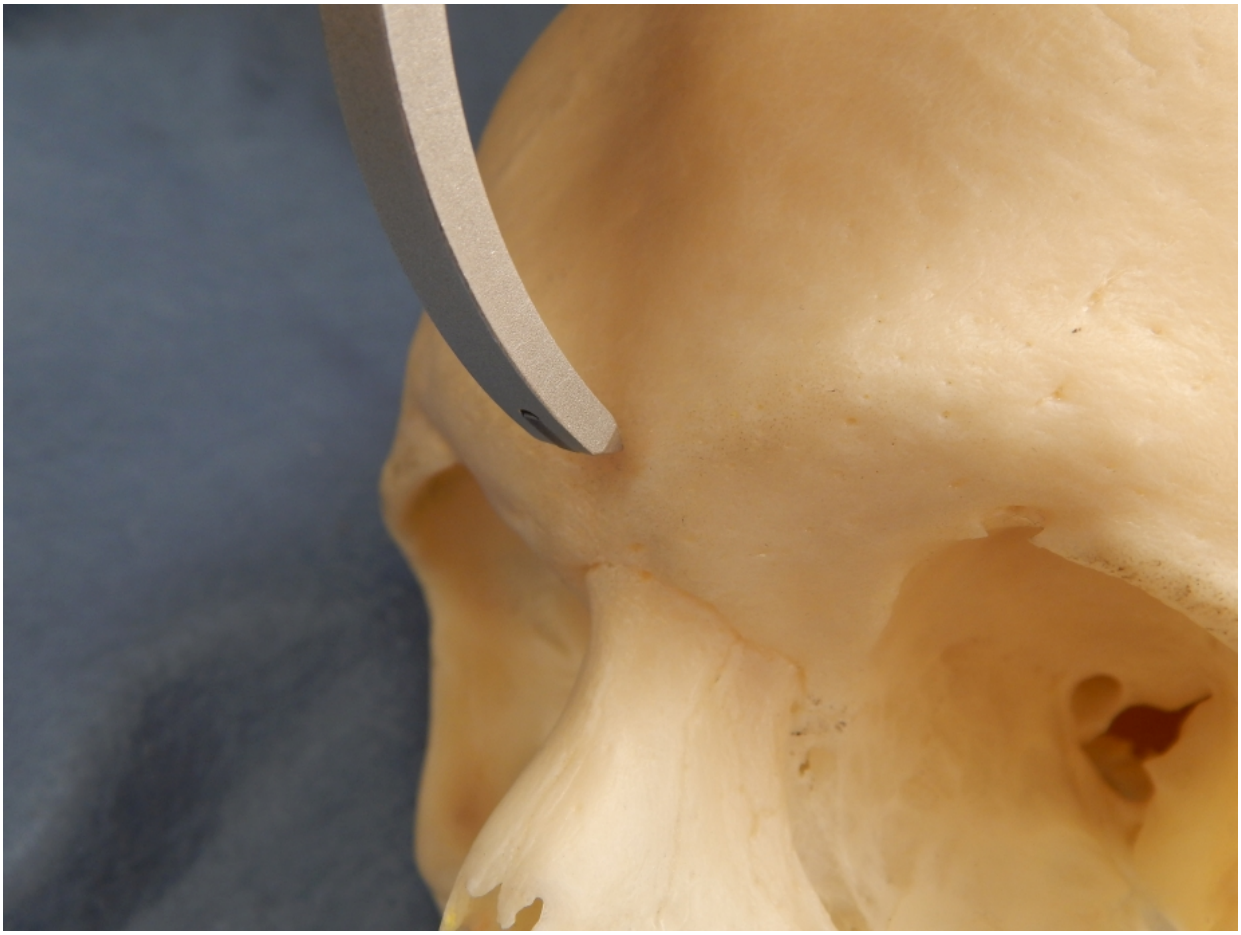
Numbers

Decimal numbers will need to be formatted using a period rather than a comma when using Fordisc.

Maximum Cranial Length (g-op, GOL): The distance from Glabella (g) to Opisthocranion (op) in the mid-sagittal plane measured in a straight line.







Nasal Height (n-ns, NLH): The distance from nasion (n) to nasospinale (ns). Nasospinale is the lowest point in the midsagittal plane on a line from the left and right inferior margins of the nasal aperture. The nasal spine often gets in the way. To measure NLH, you may prefer to measure to each side of the nasal aperture and average them. Or, you can measure indirectly from nasion to nasospinale by orienting the scale of the calipers parallel to those points. In individuals with nasal guttering and no clear anterior margin to the nasal aperture, measure to points on the floor of the nasal aperture (see figure below).

Measuring the right side

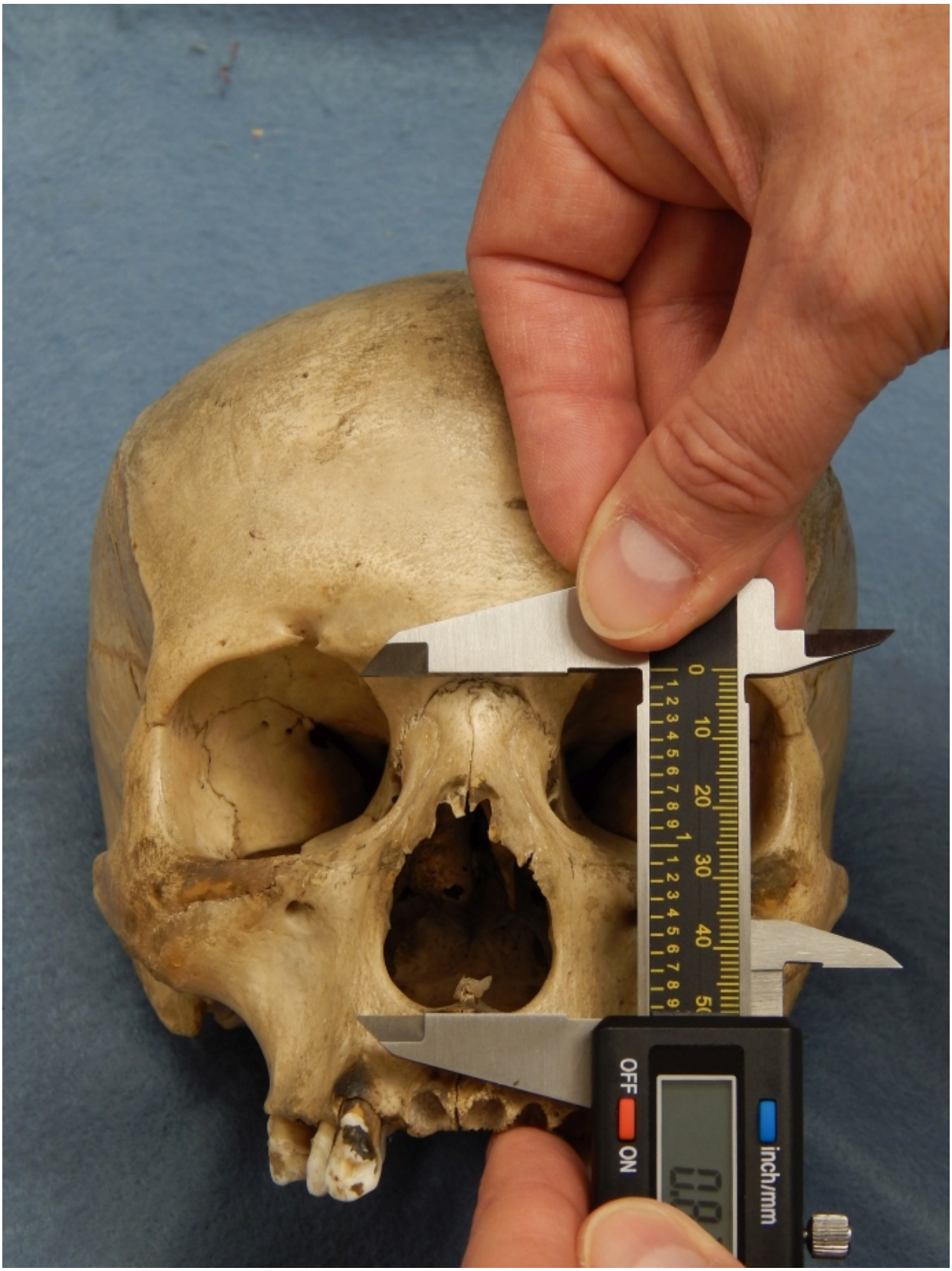

ZERO
OFF
ON
inch/mm

Measuring the left side

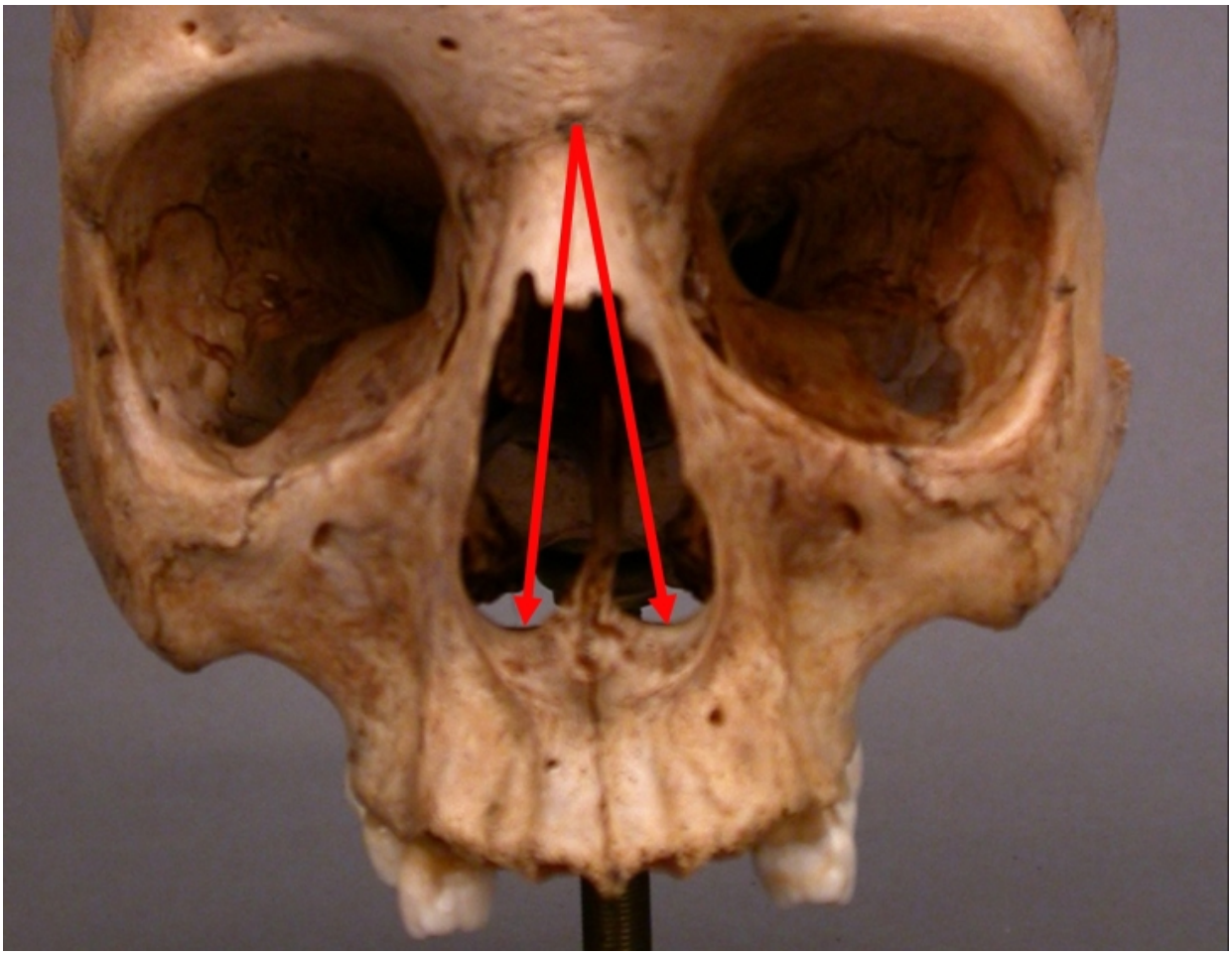
Indirectly measuring parallel


inch/mm
OFF
ON

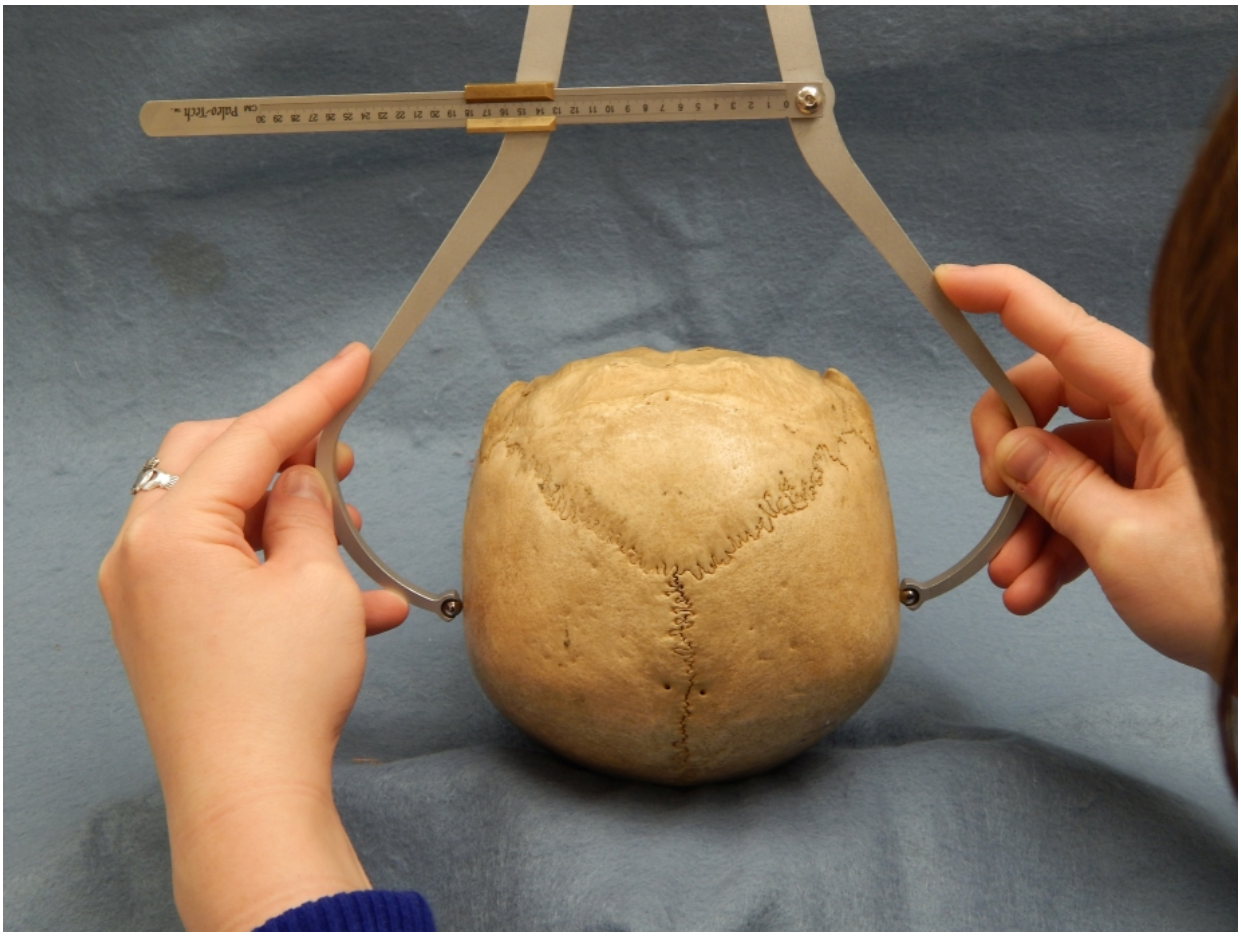
Indirectly measuring parallel



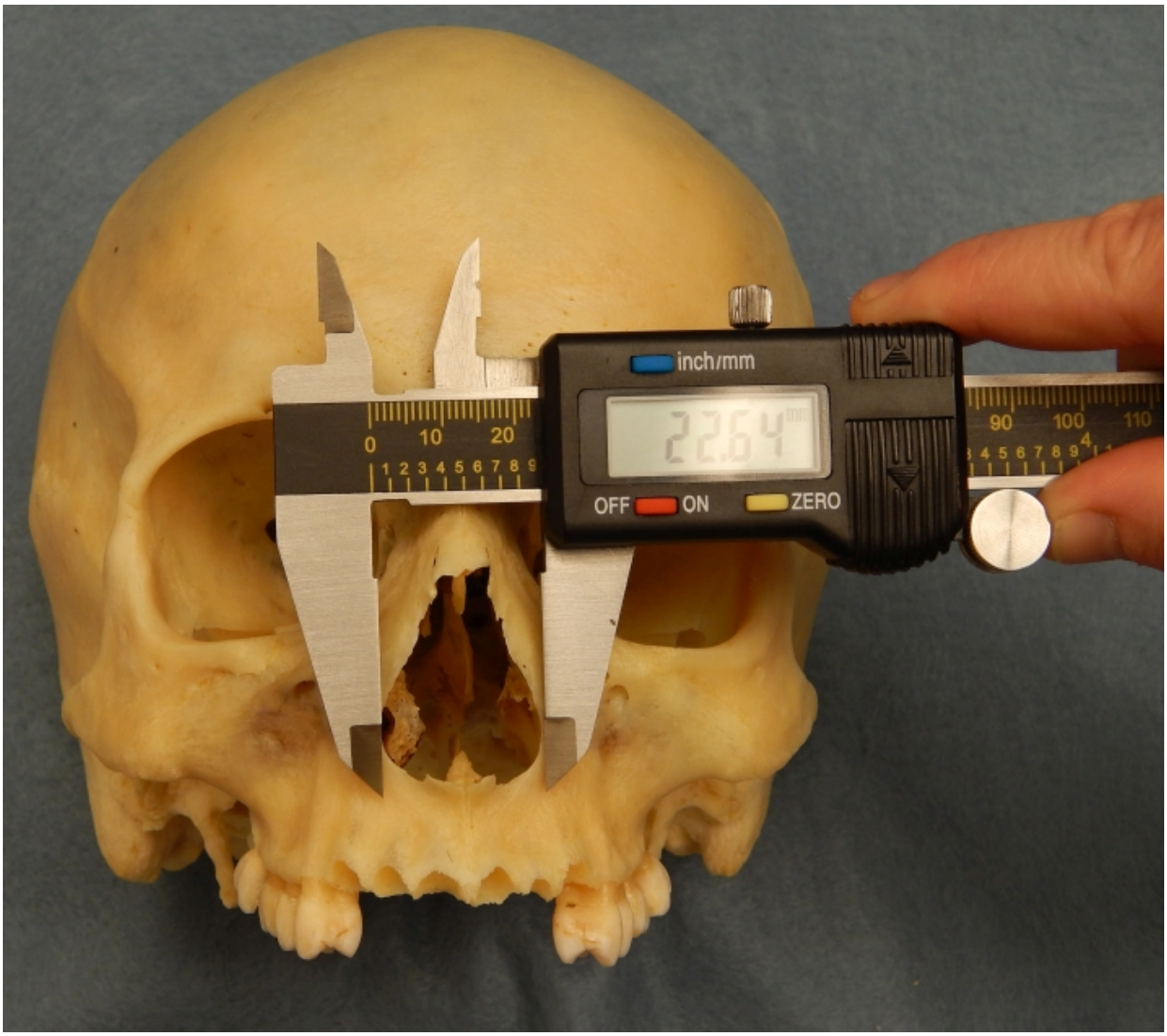
With nasal guttering



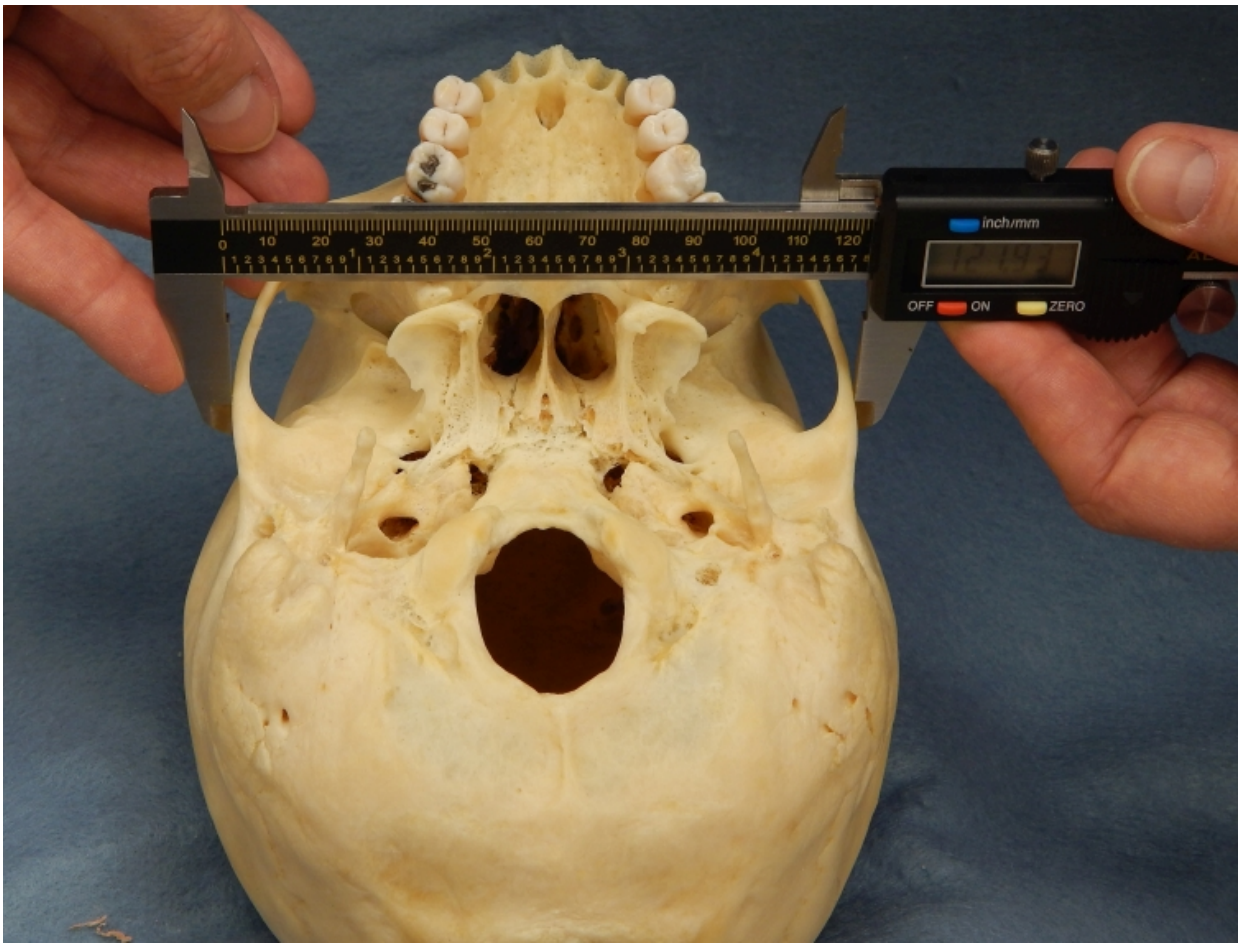
Maximum Cranial Breadth (eu-eu, XCB): The maximum width of the skull perpendicular to the mid sagittal plane; the points are left and right euryon. XCB must be taken superior to the zygomatic process and the supramastoid crest and is generally found on the parietal near the squamosal suture.

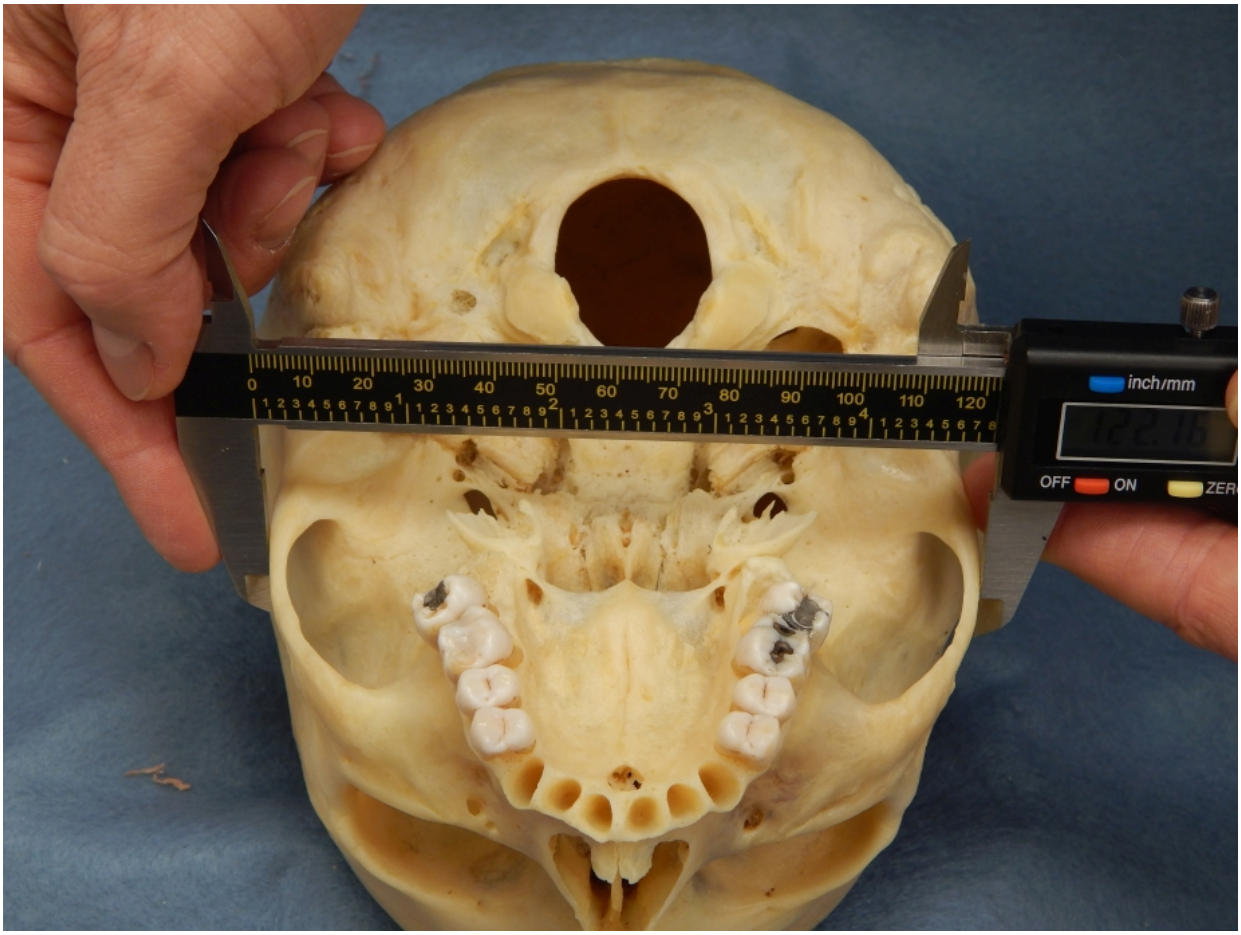


Nasal Breadth (al-al, **NLB**): The maximum breadth of the nasal aperture.



Bizygomatic Breadth (zy-zy, ZYB): The direct distance between each zygion (zy), located at the most lateral points of the zygomatic arches.

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inch/mm
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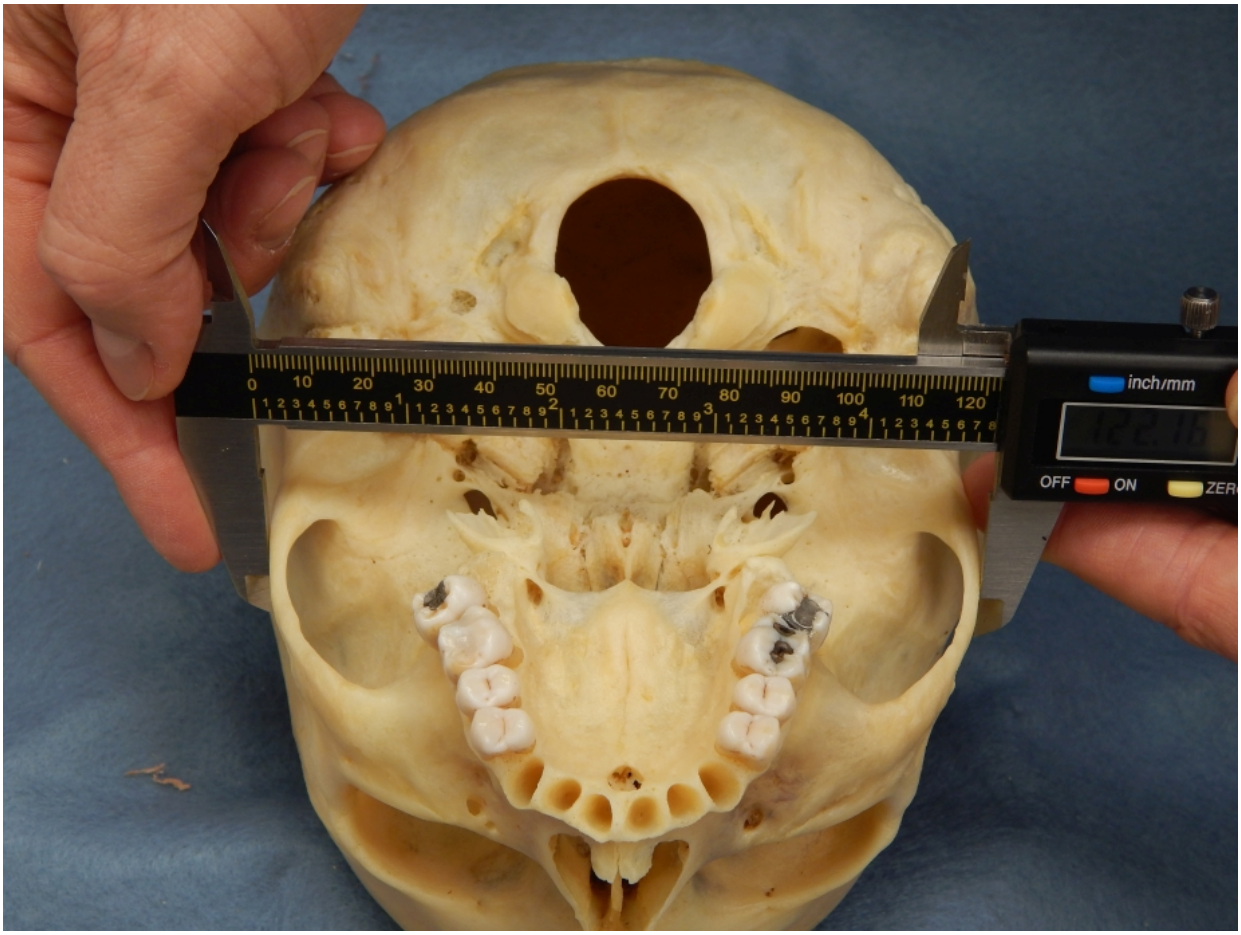
ON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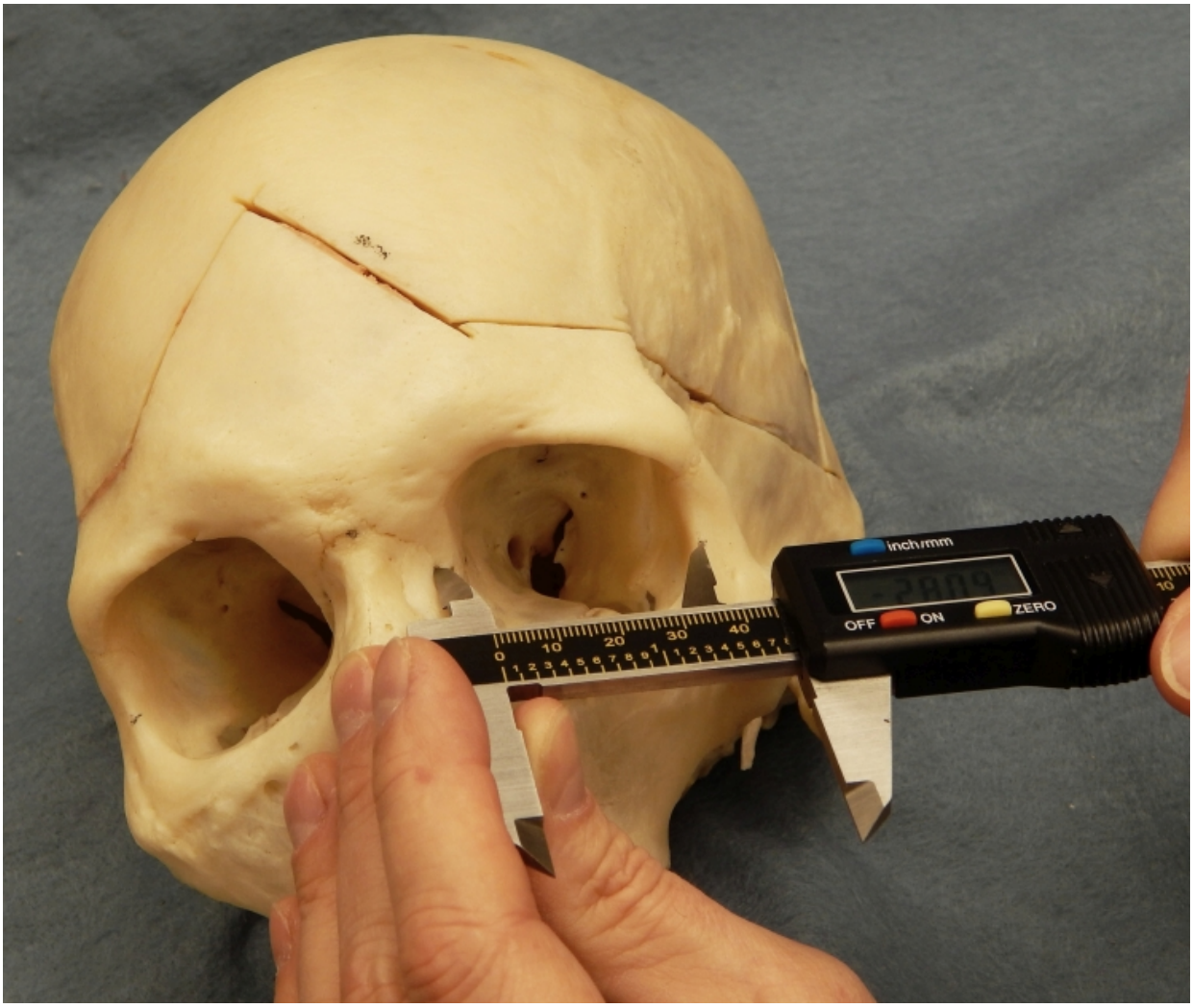
inch/mm
OFF
ON

Orbital Breadth (d-ec, OBB): The laterally sloping distance from dacryon (d) to ectoconchion (ec).


inch/mm
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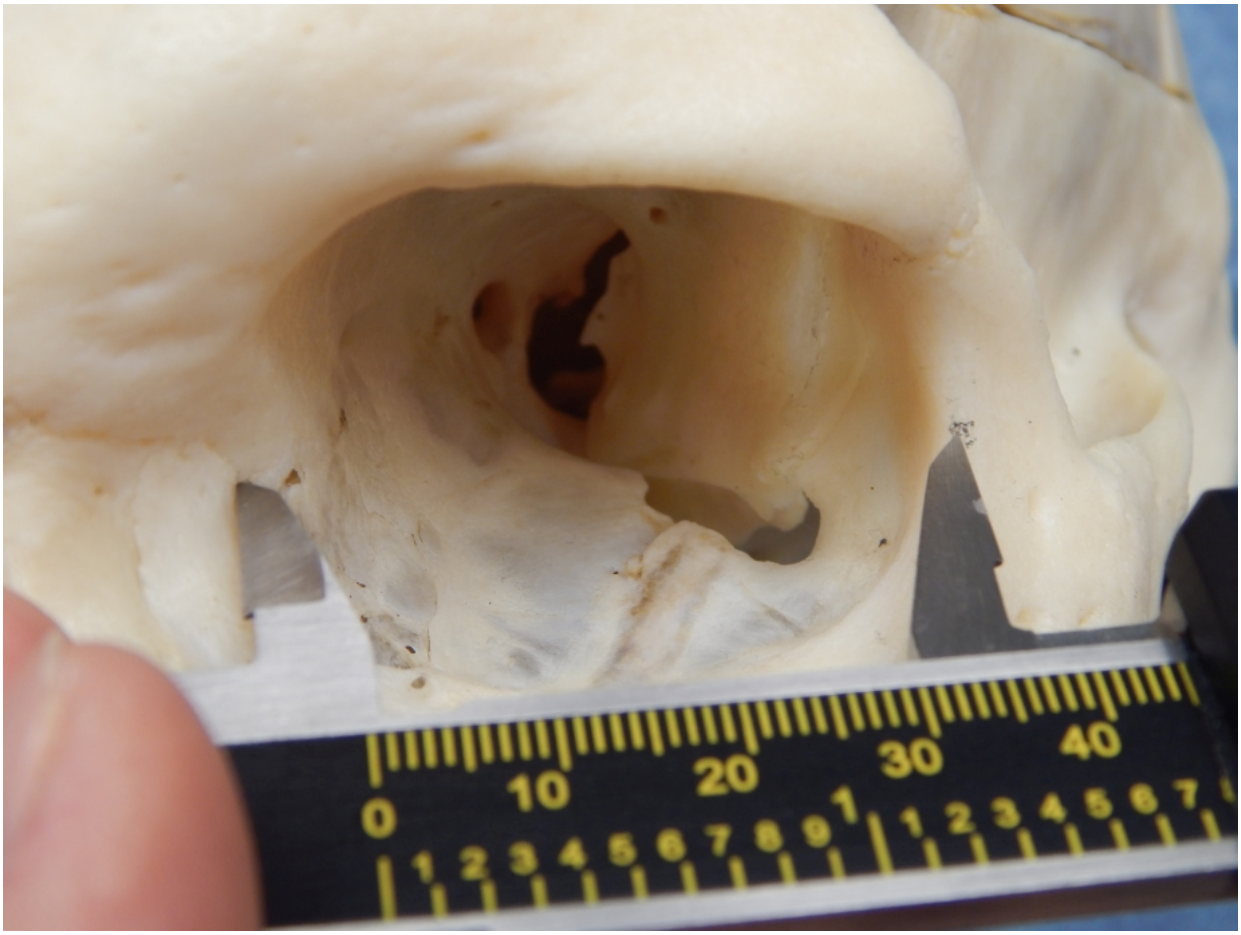
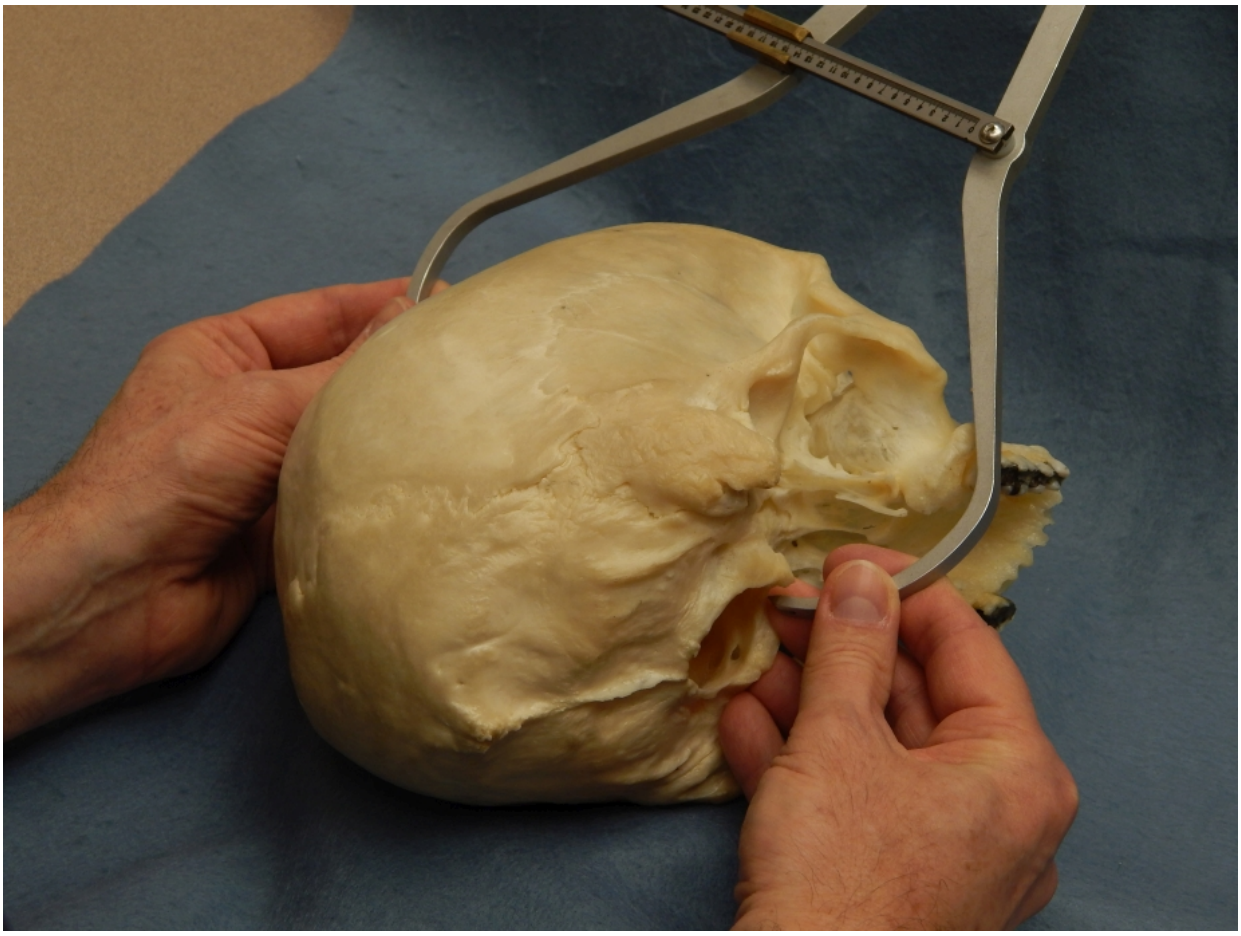
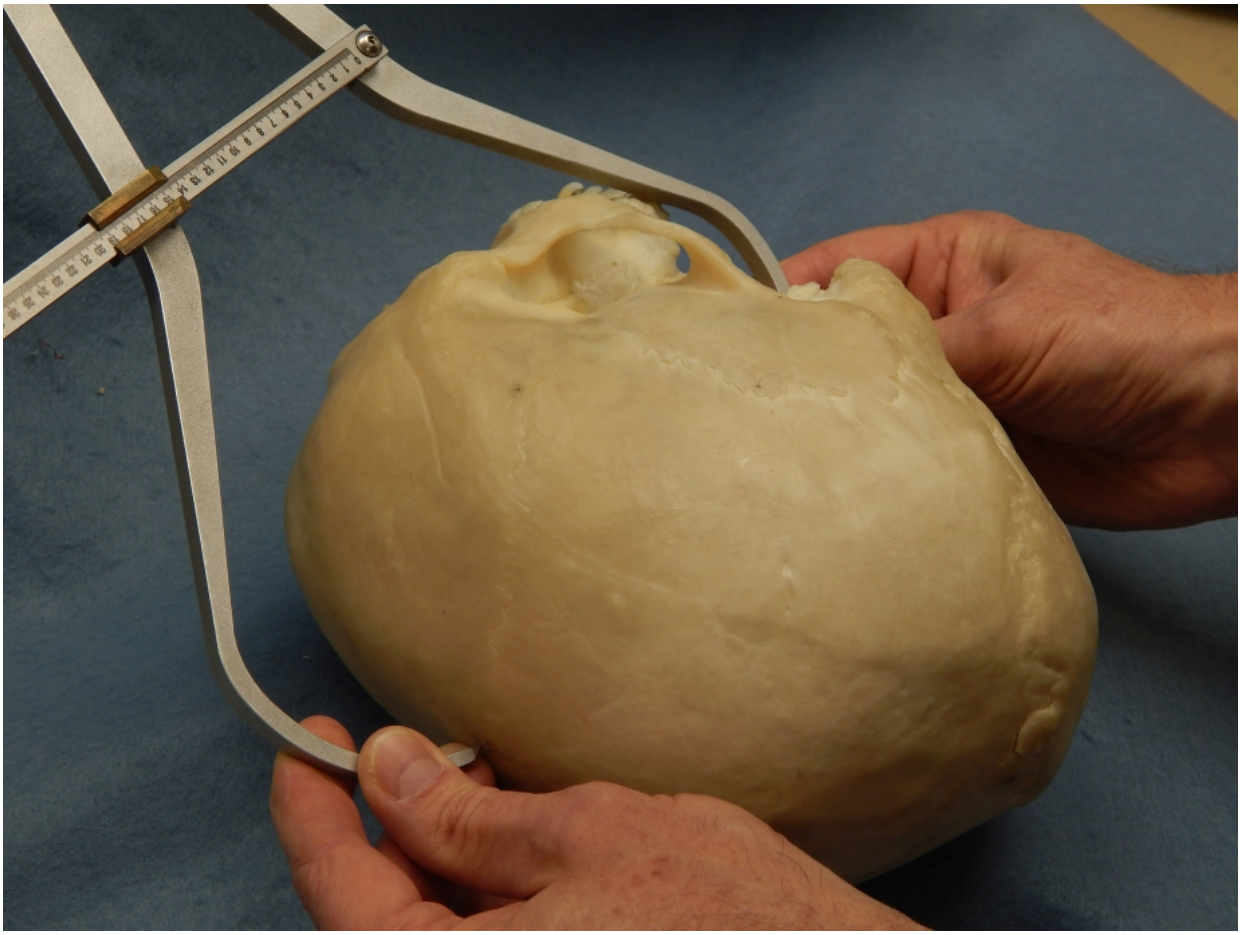
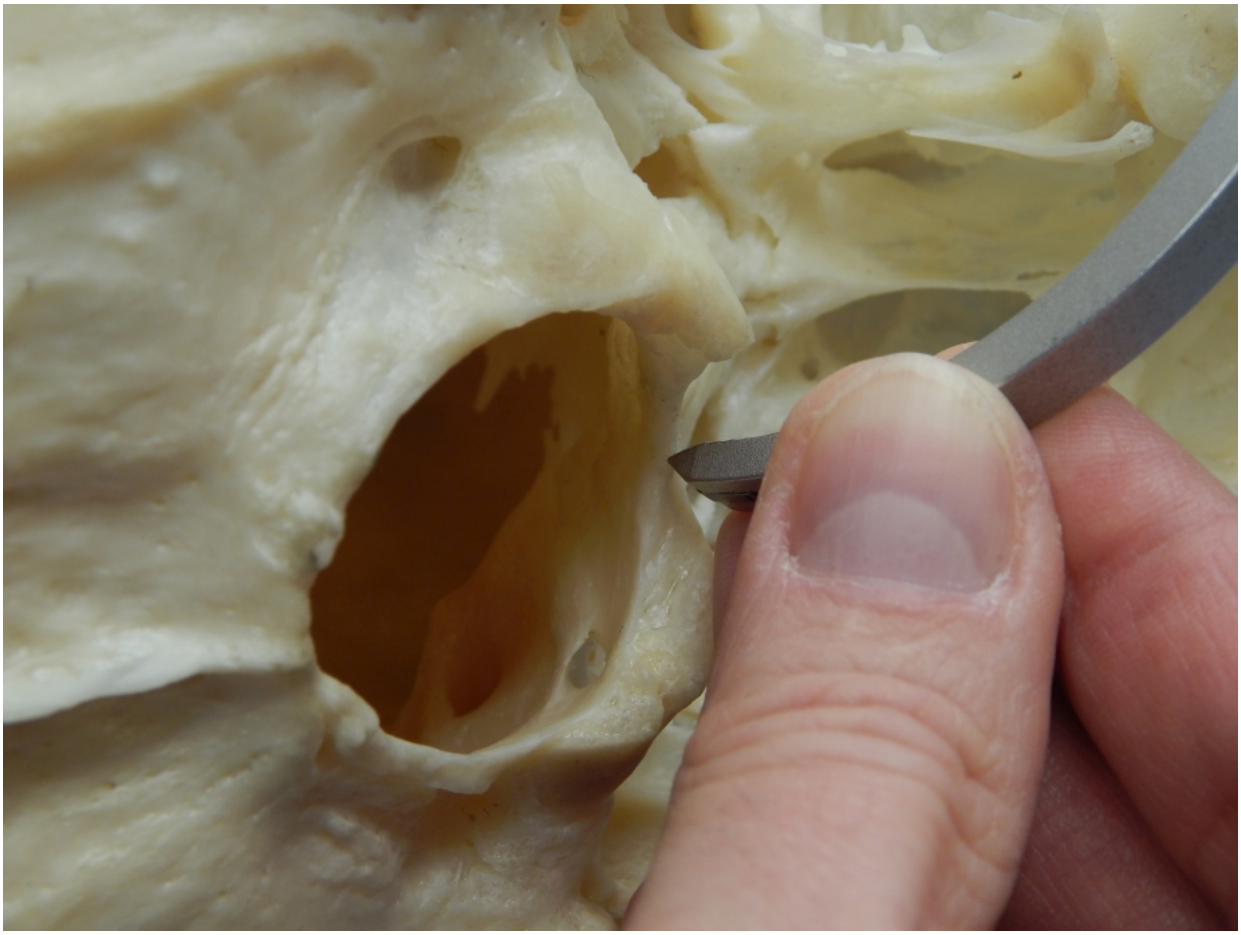
ON
ZERO


0
10
20
30
40

Basion Bregma Height (ba-b, BBH): The direct distance from the lowest point on the anterior margin of the foramen magnum, basion (hypobasion) (ba), to bregma.

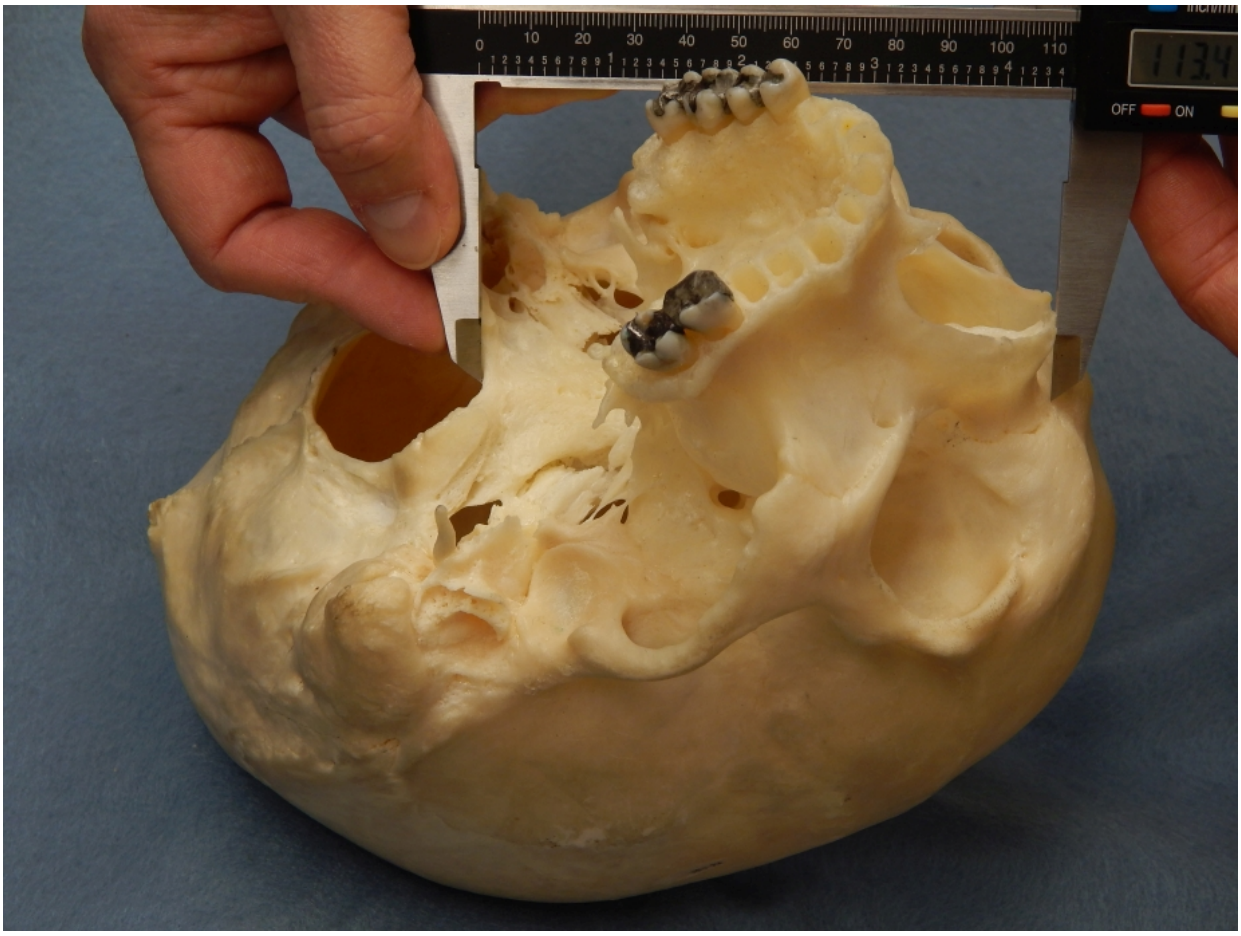


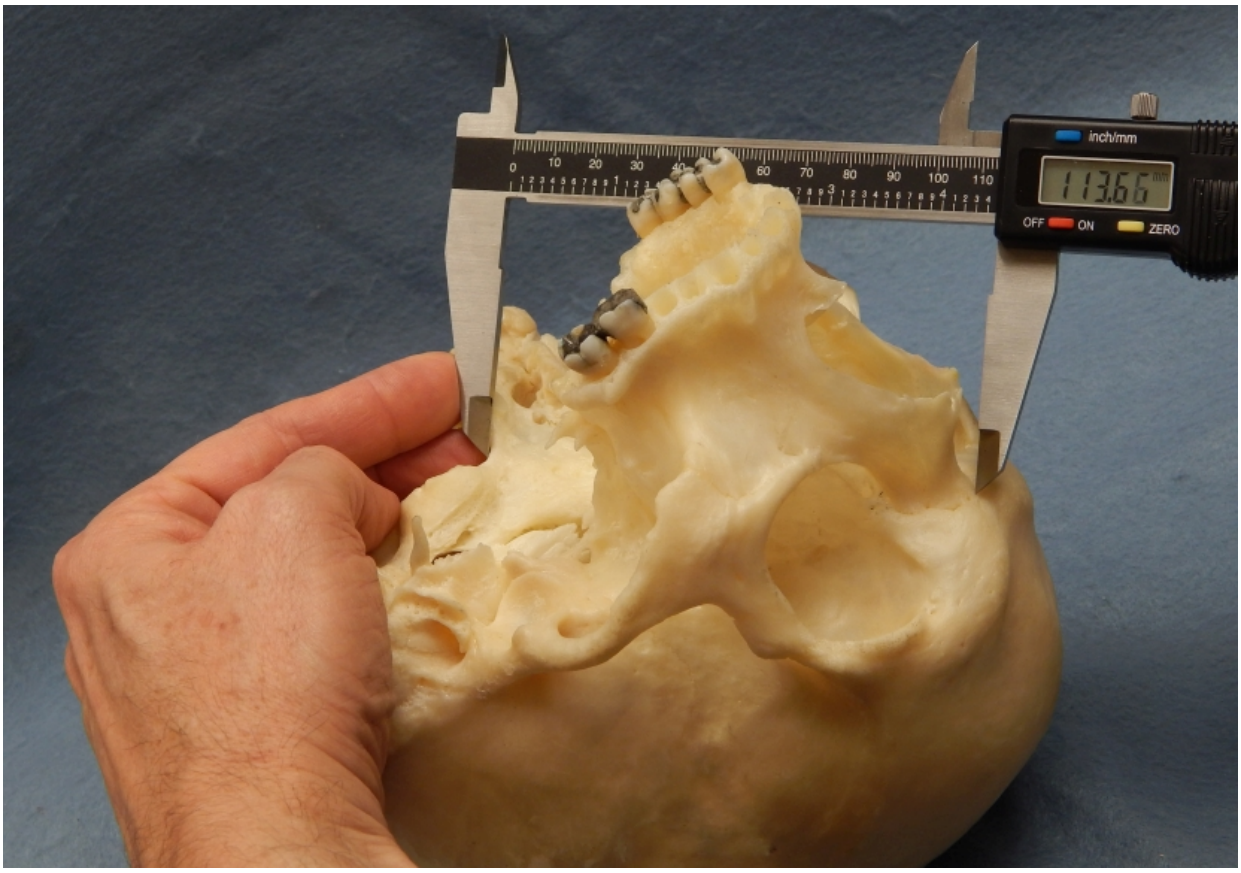




Orbital Height (OBH): The direct distance between the superior and inferior orbital margins, along a line that dives the orbit into equal halves and perpendicular to OBB. Using the inside caliper jaws makes this measurement easier to take.

Cranial Base Length (ba-n,BNL): The direct distance from nasion (n) to basion (ba). For this measurement, measure from nasion to the point opposite nasion on the anterior border of the foramen magnum.




inch/mm
113.66
OFF
ON
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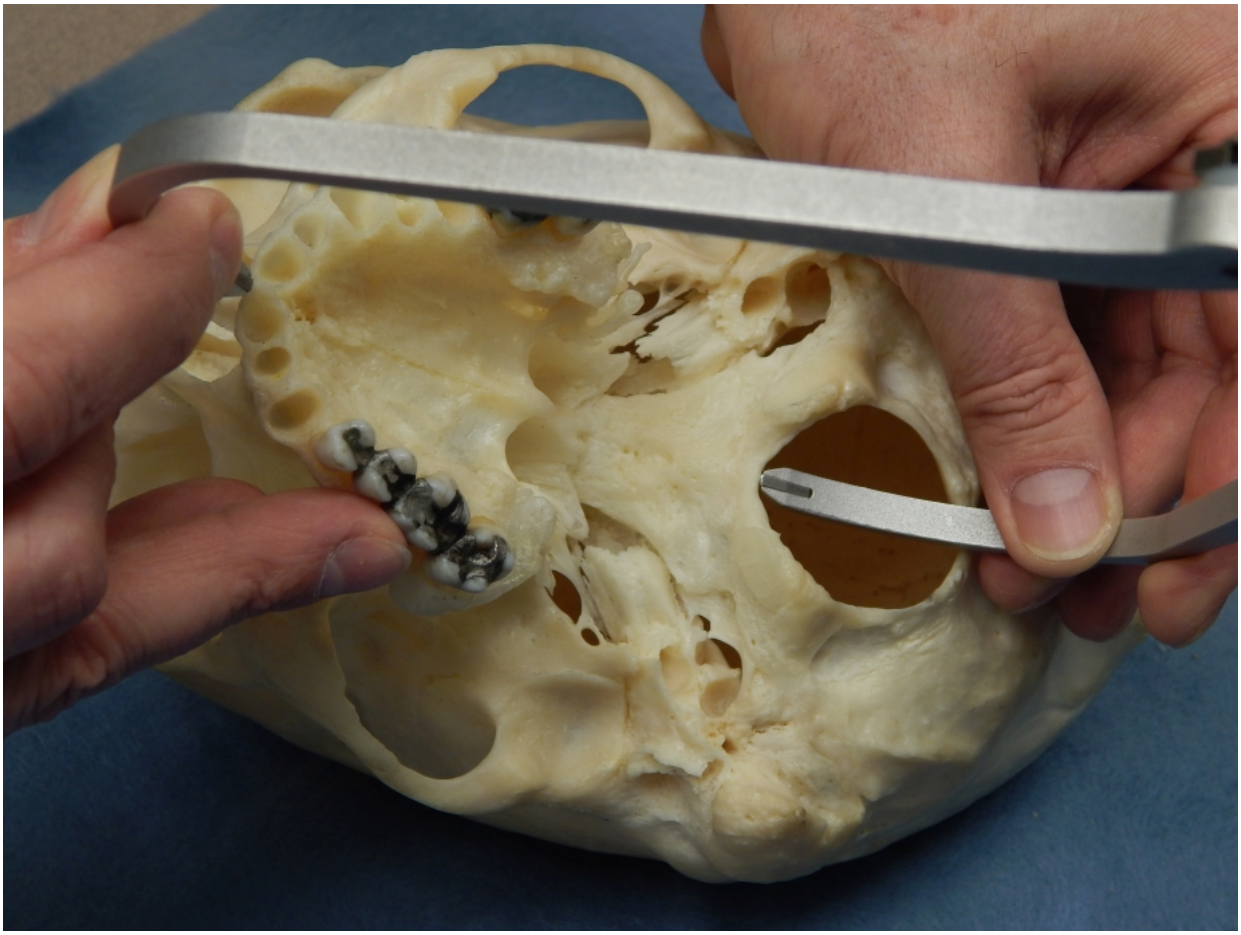
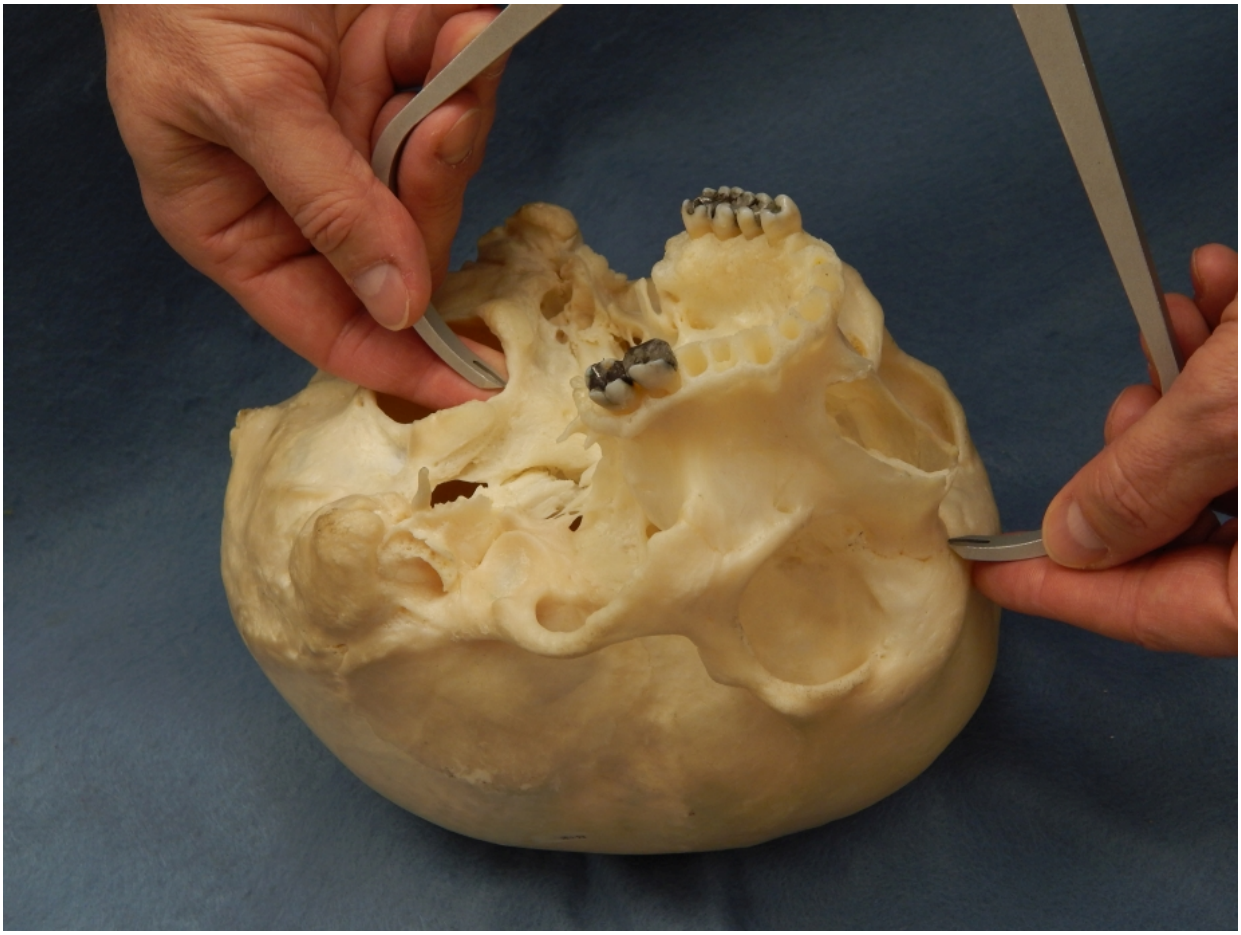
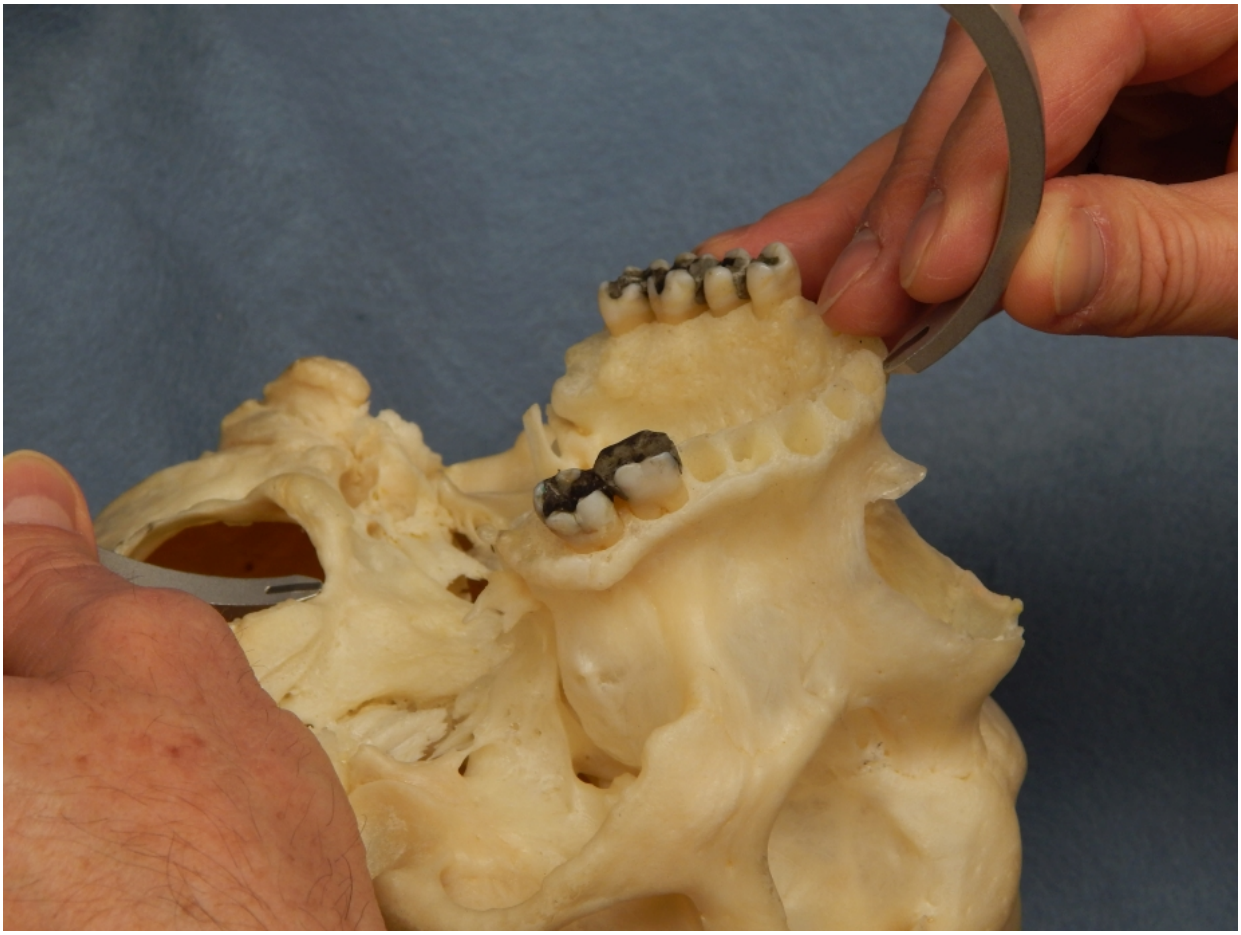
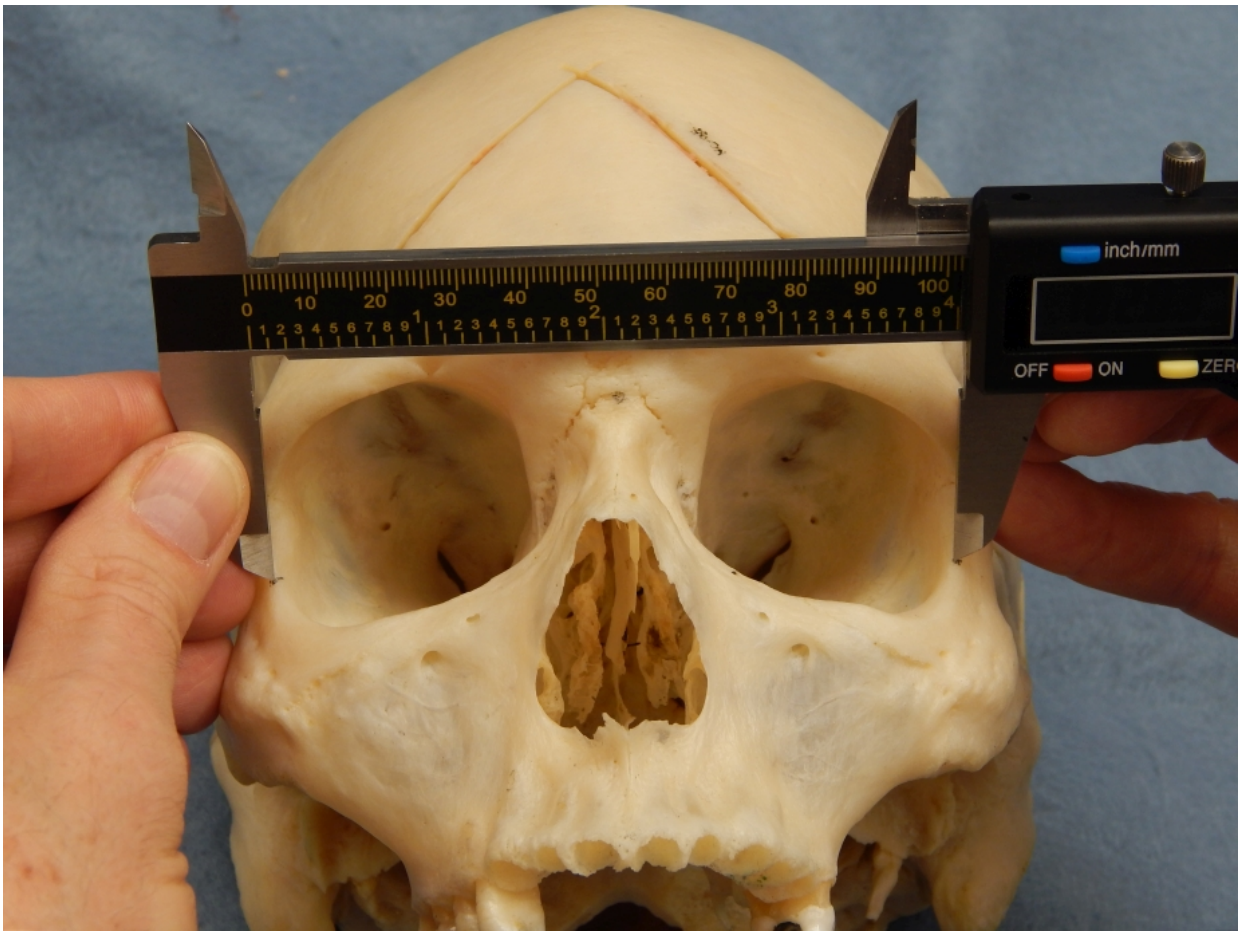


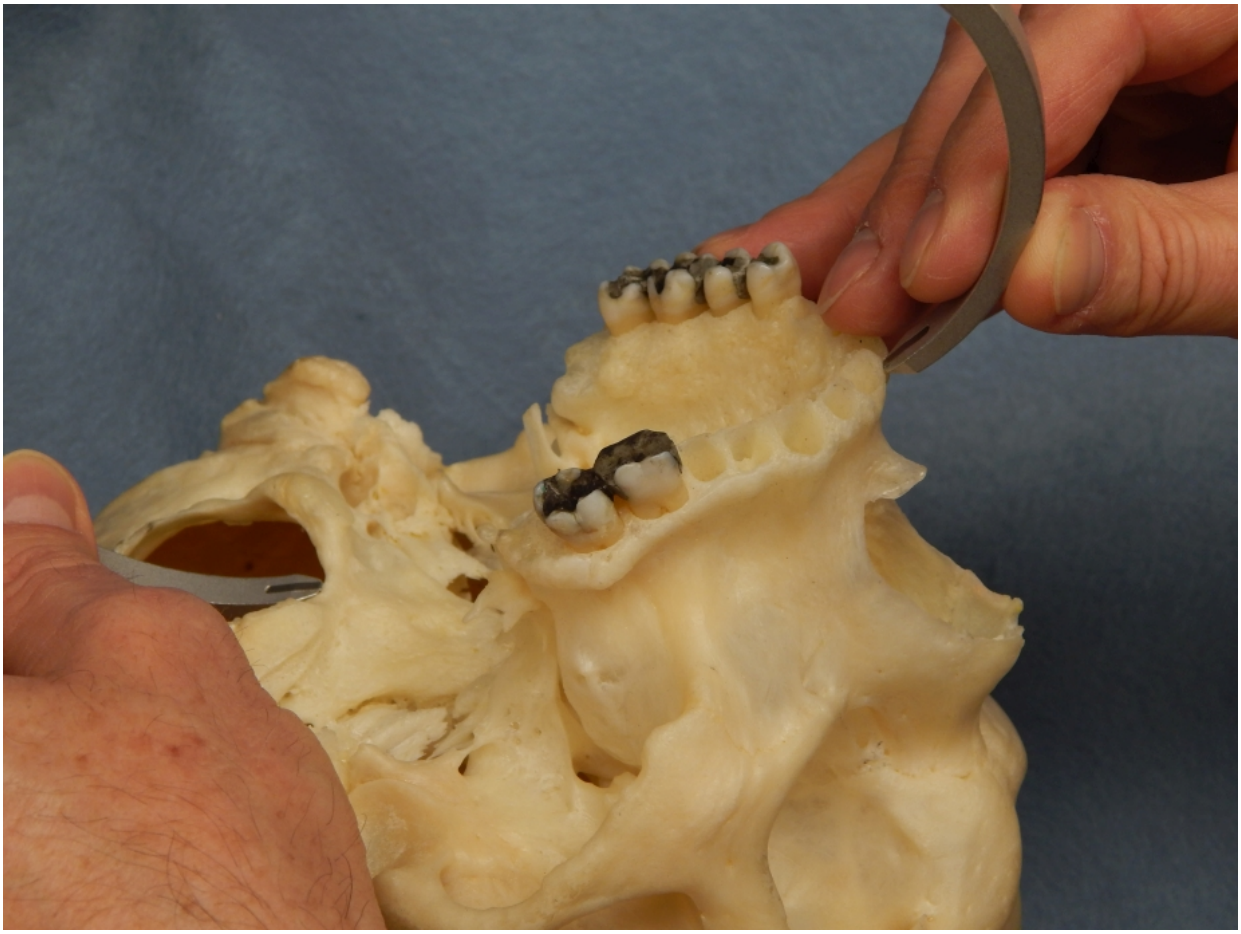




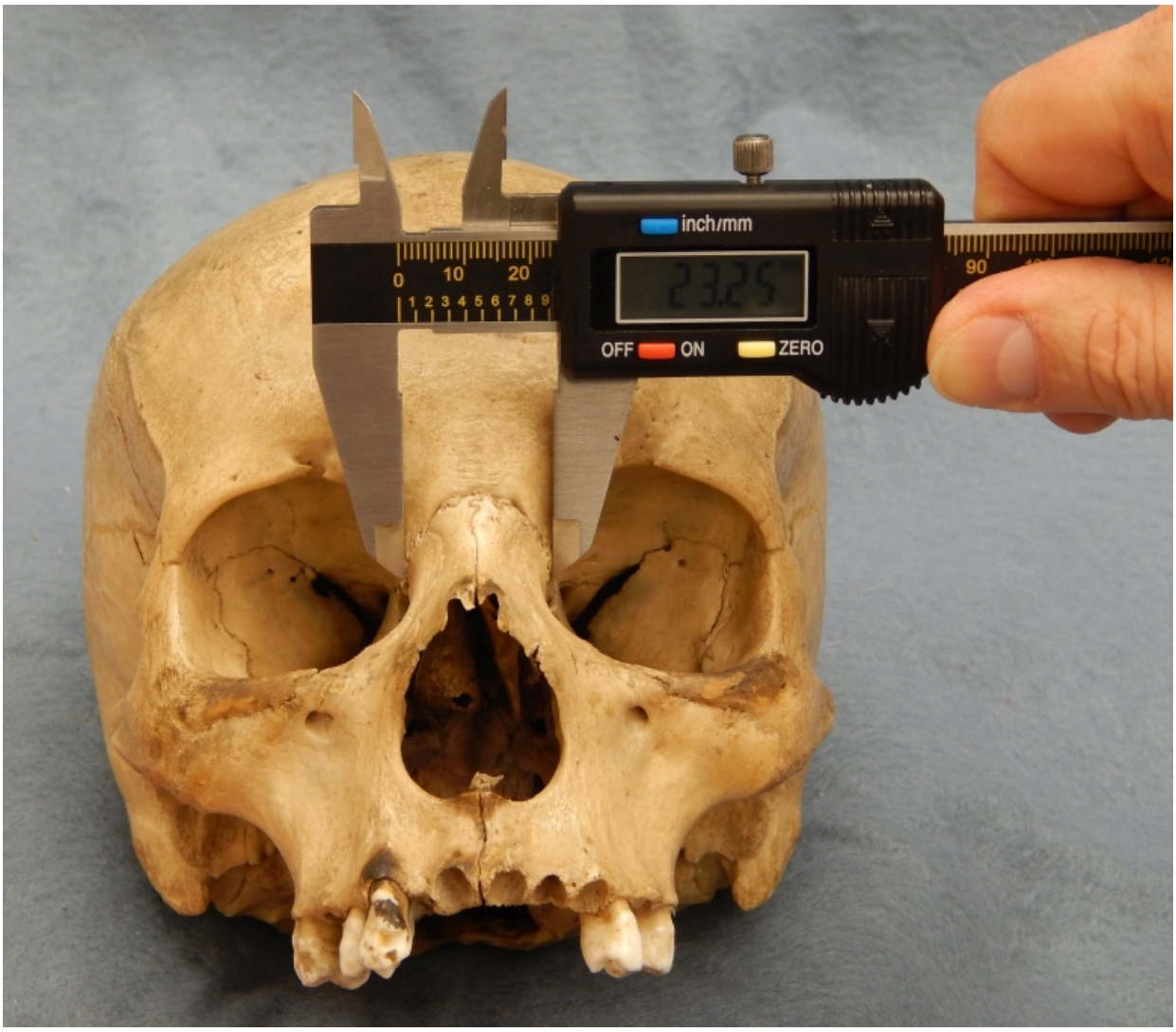
Biorbital Breadth (ec-ec, EKB): The direct distance from one ectoconchion (ec) to the other.



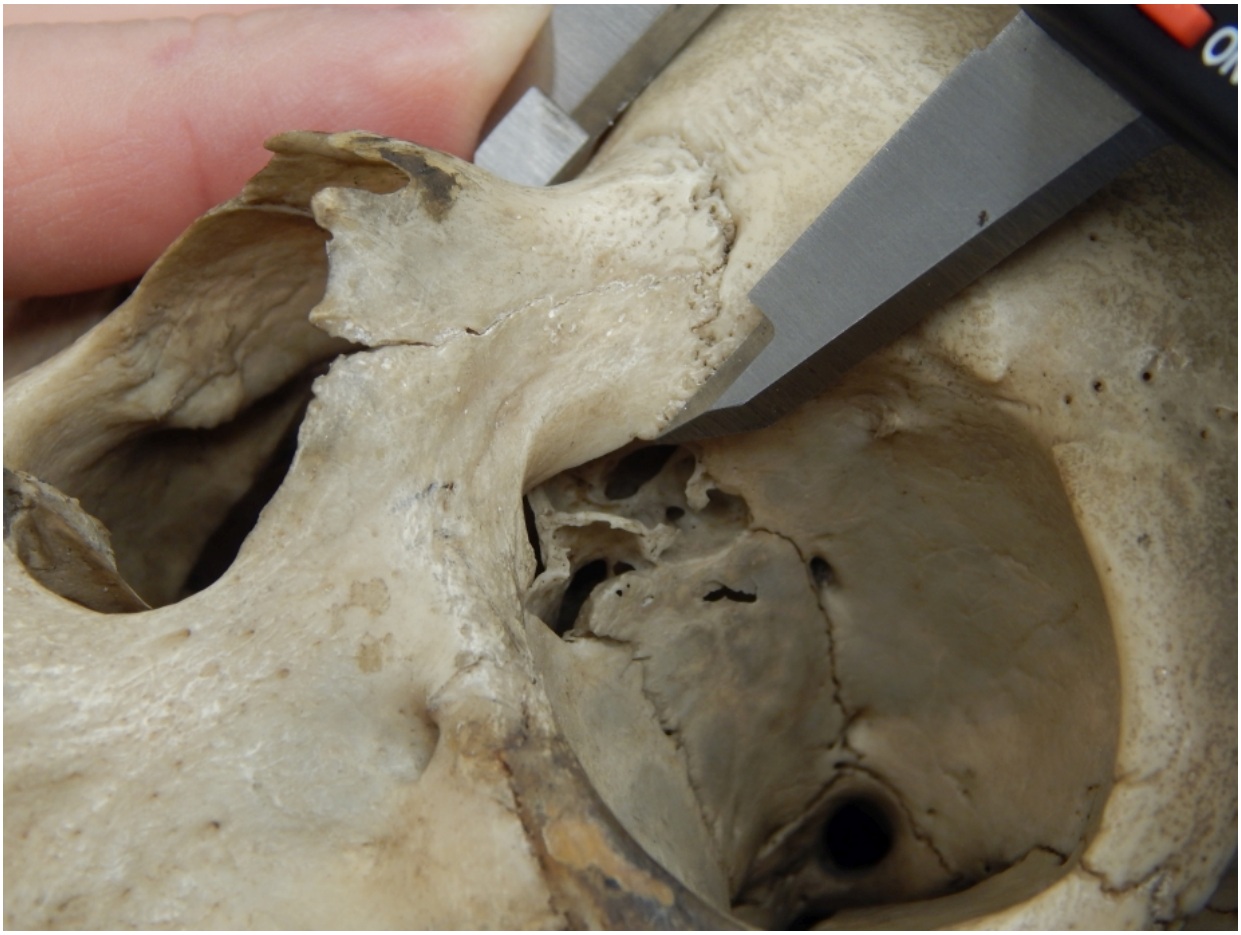
Basion Prosthion Length (ba pr, BPL): The direct distance from basion (ba) to prosthion (pr). For this measurement, measure from prosthion to the point opposite prosthion (endobasion) on the anterior border of the foramen magnum.

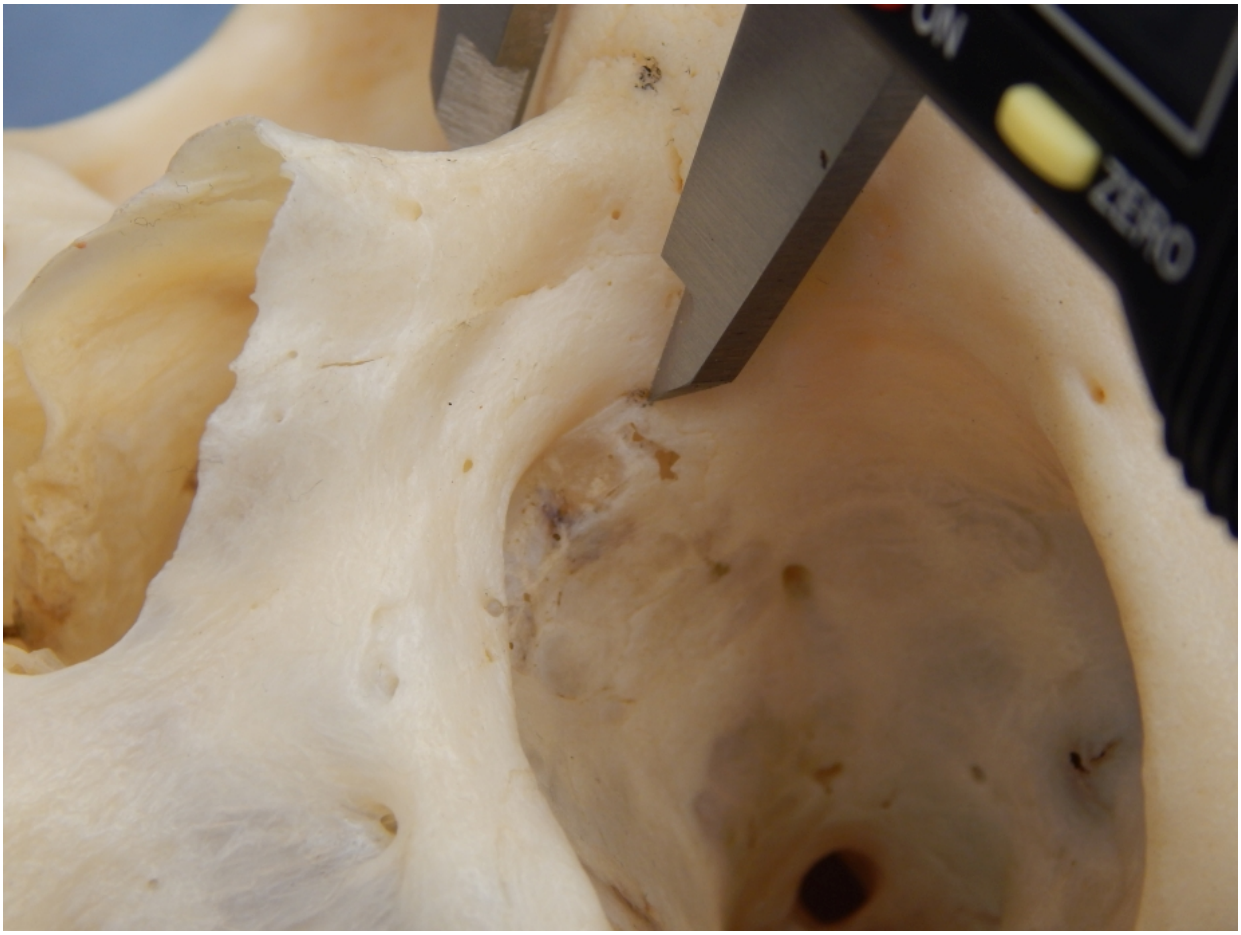


Interorbital Breadth (d-d, DKB): The direct distance between right and left dacryon.

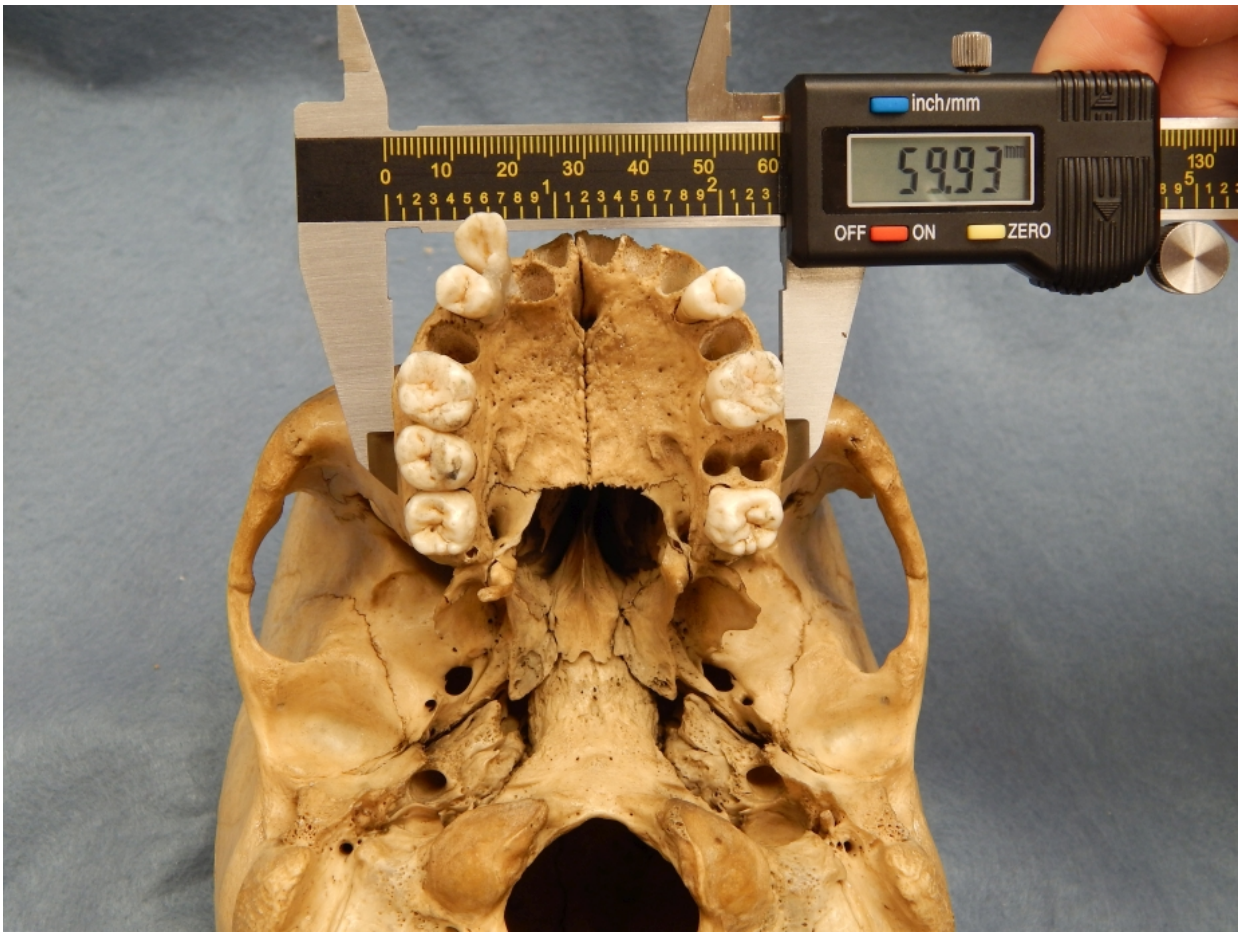



ZERO
OFF
ON



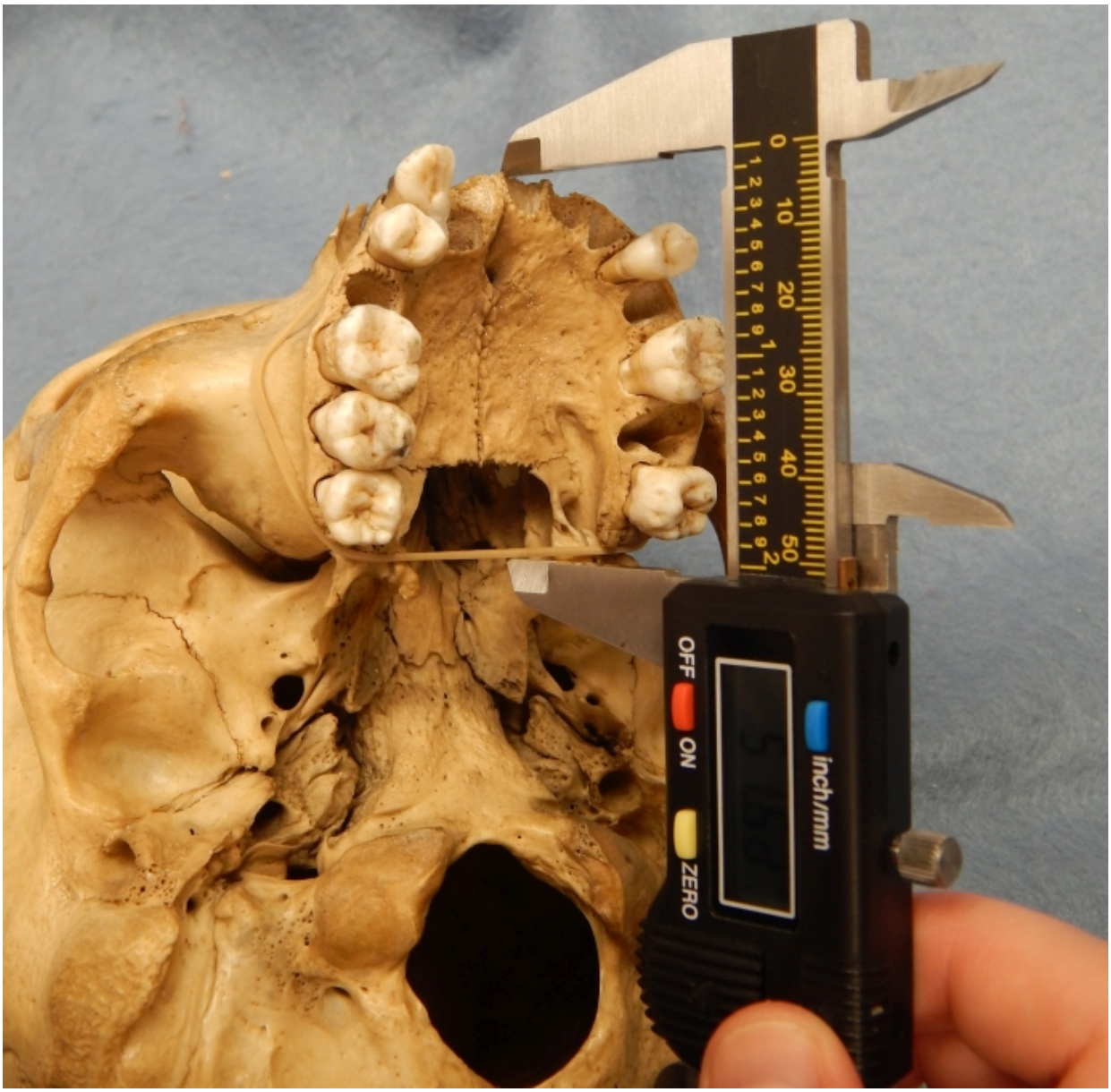

ON
ZERO

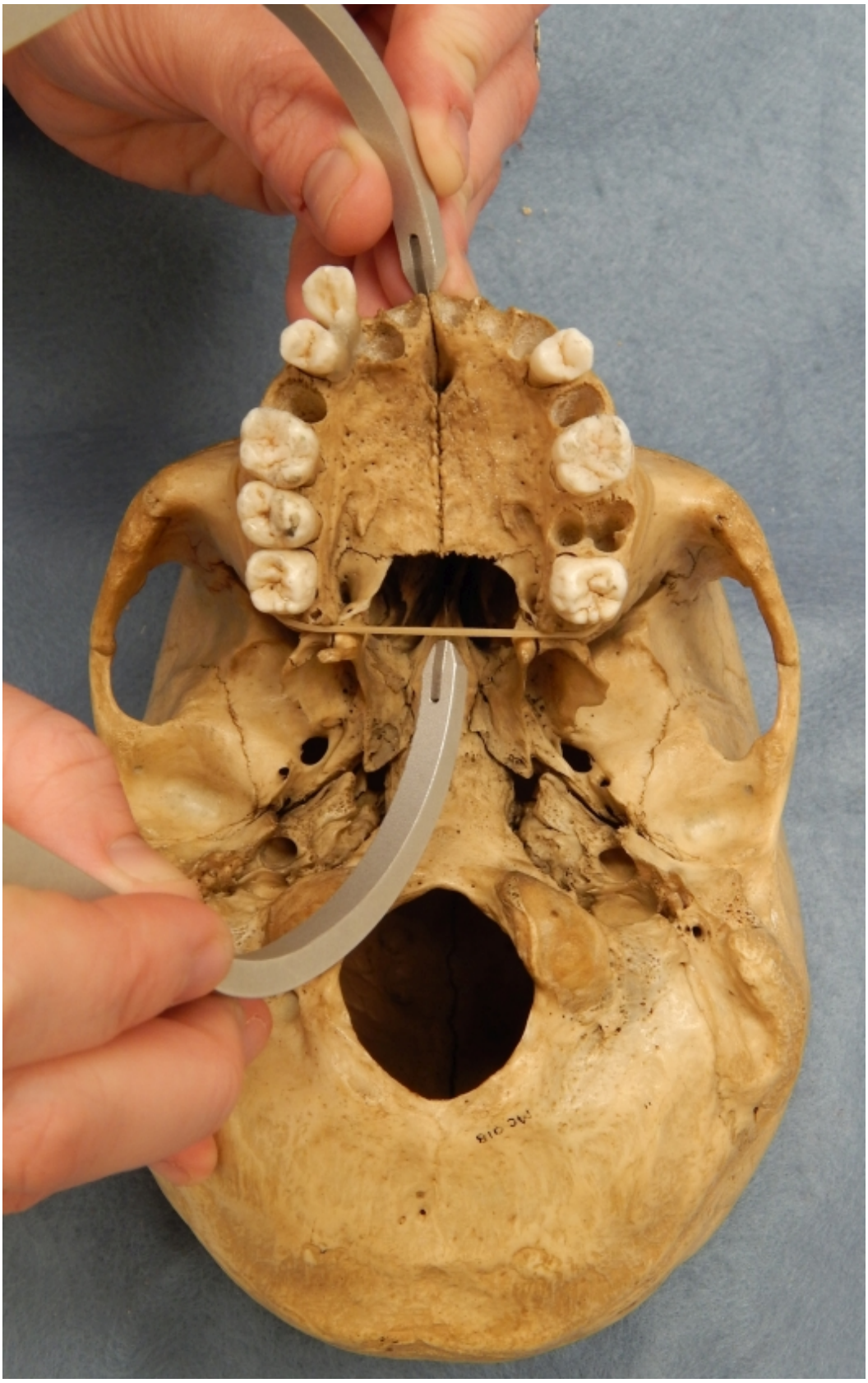
Maxillo-Alveolar Breadth, External Palate Breadth (ecm-ecm, MAB): The maximum breadth across the alveolar borders of the maxilla measured at its widest point, between each ectomolare (ecm). The maximum breadth is usually found at the level of the second molars.



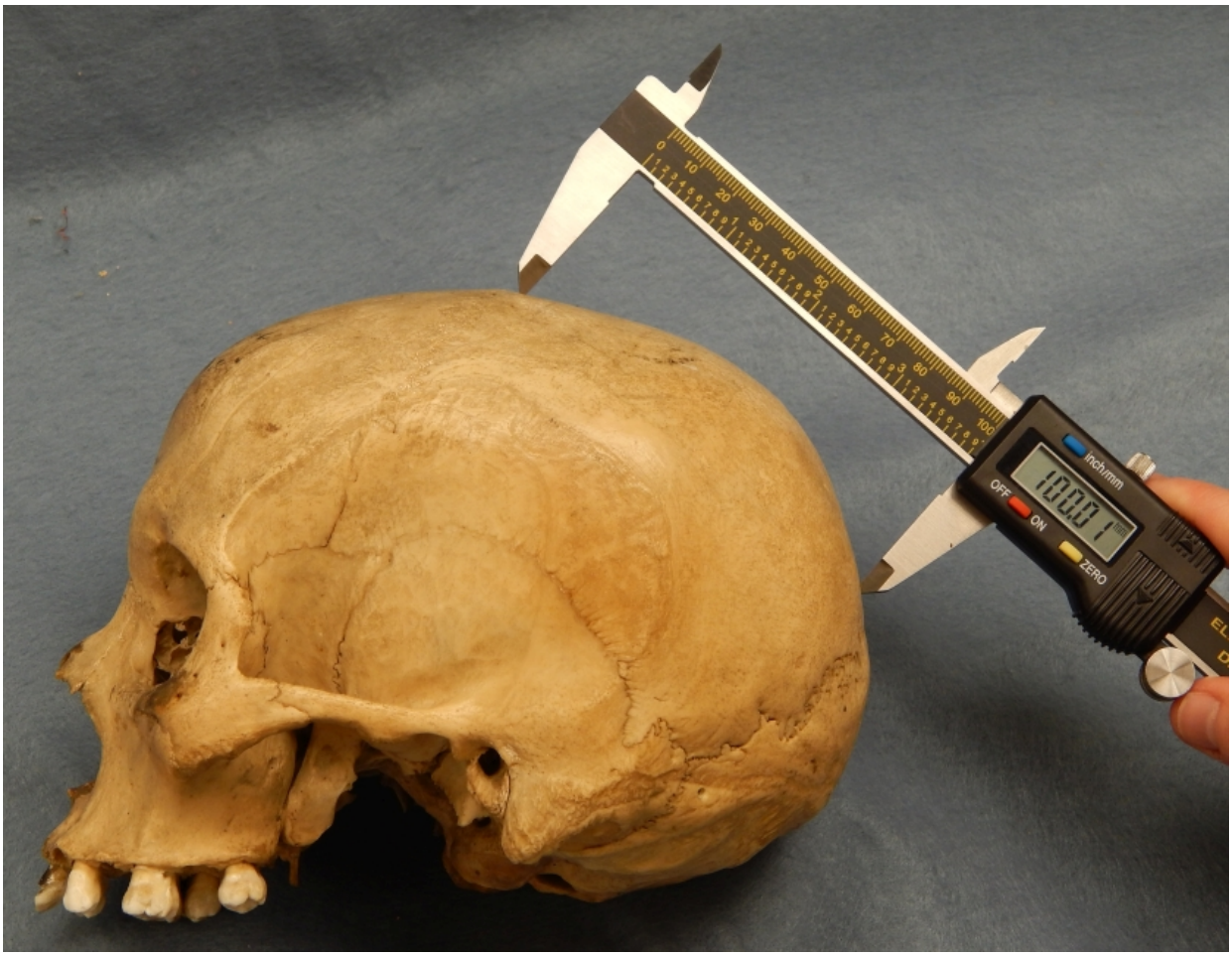
Frontal Chord (n-b, FRC): The direct distance from nasion (n) to bregma (b) taken in the midsagittal plane.

Maxillo-Alveolar Length, External Palate Length (pr-alv, MAL): The direct distance from prosthion (Hrdlicka's prealveolar point) to alveolon (alv).

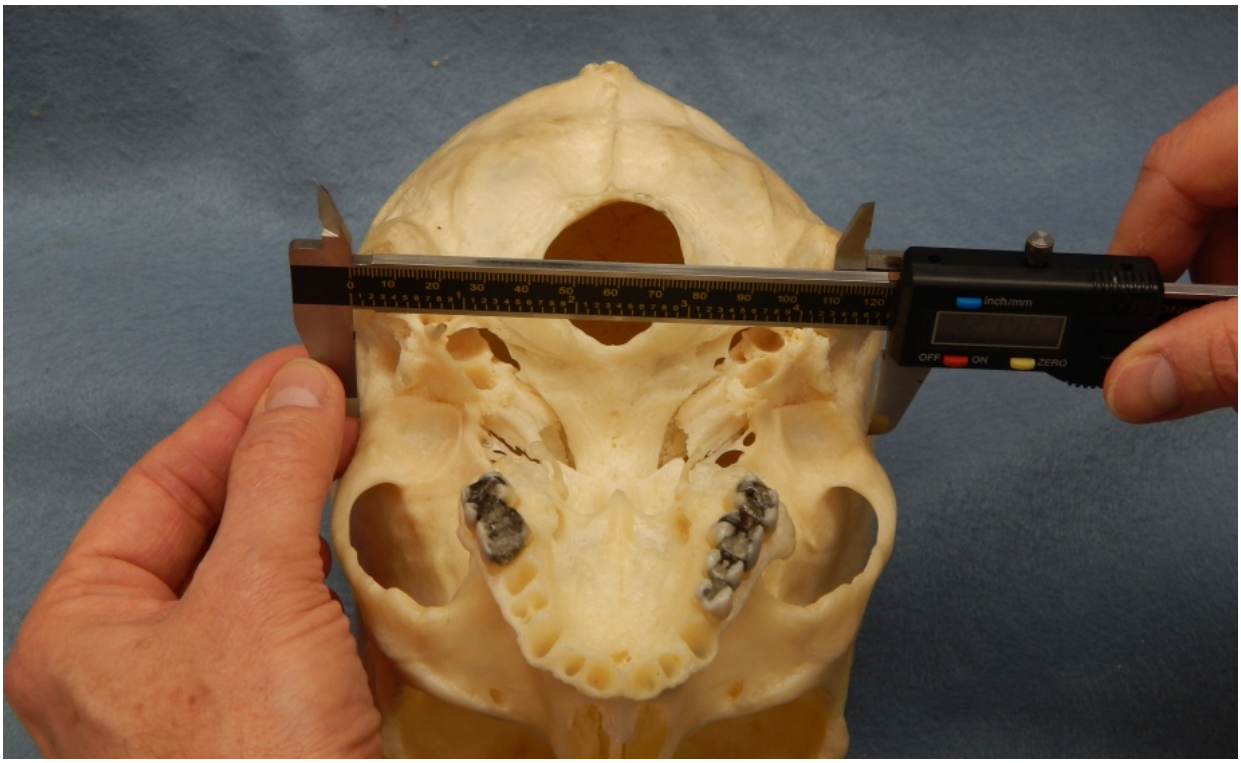


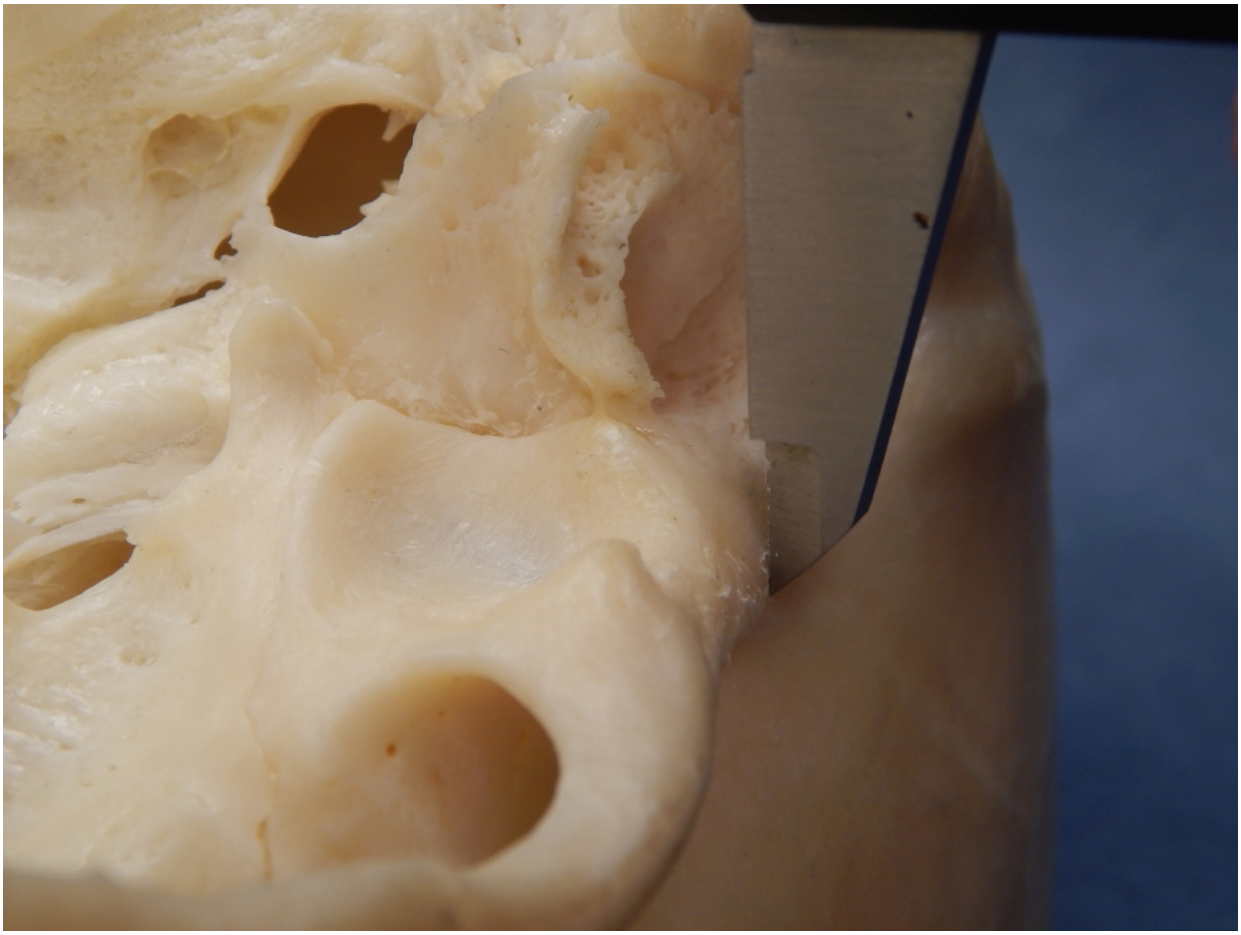


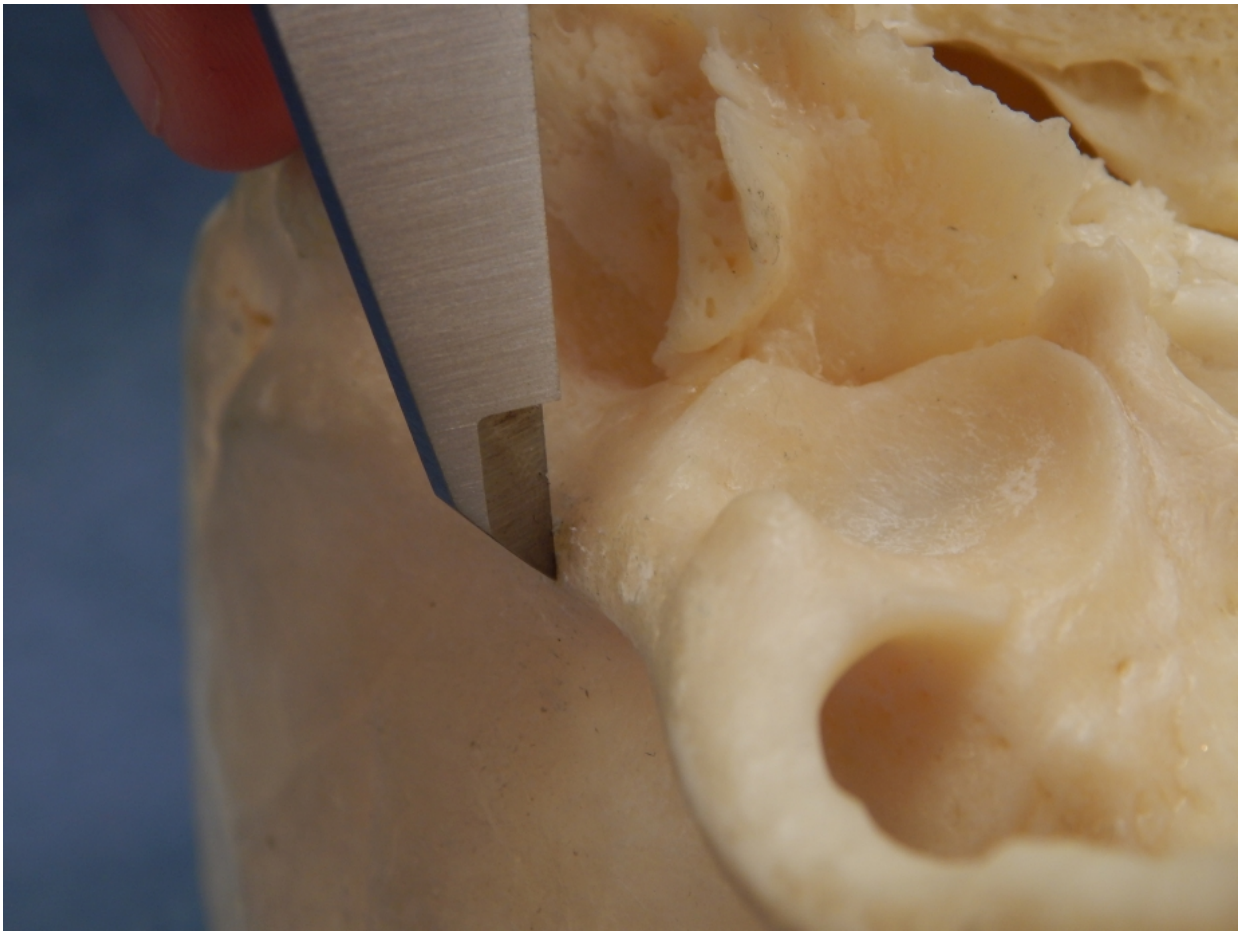
Parietal Chord (b-l, PAC): The direct distance from bregma (b) to lambda (l) taken in the midsagittal plane.



Biauricular Breadth (au-au, AUB): The least exterior breadth across the roots of the zygomatic processes, in other words, from left to right radiculare. This point will NOT be posterior to the middle of the external auditory meatus.

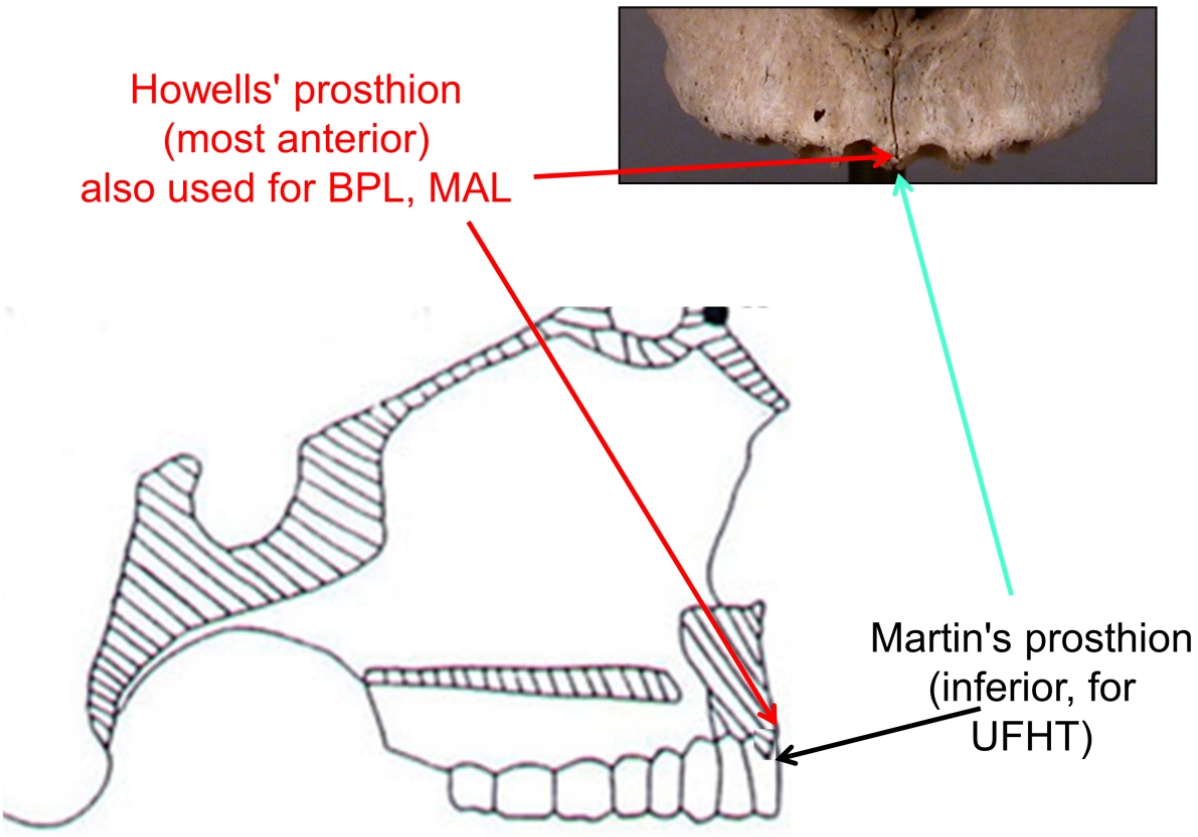




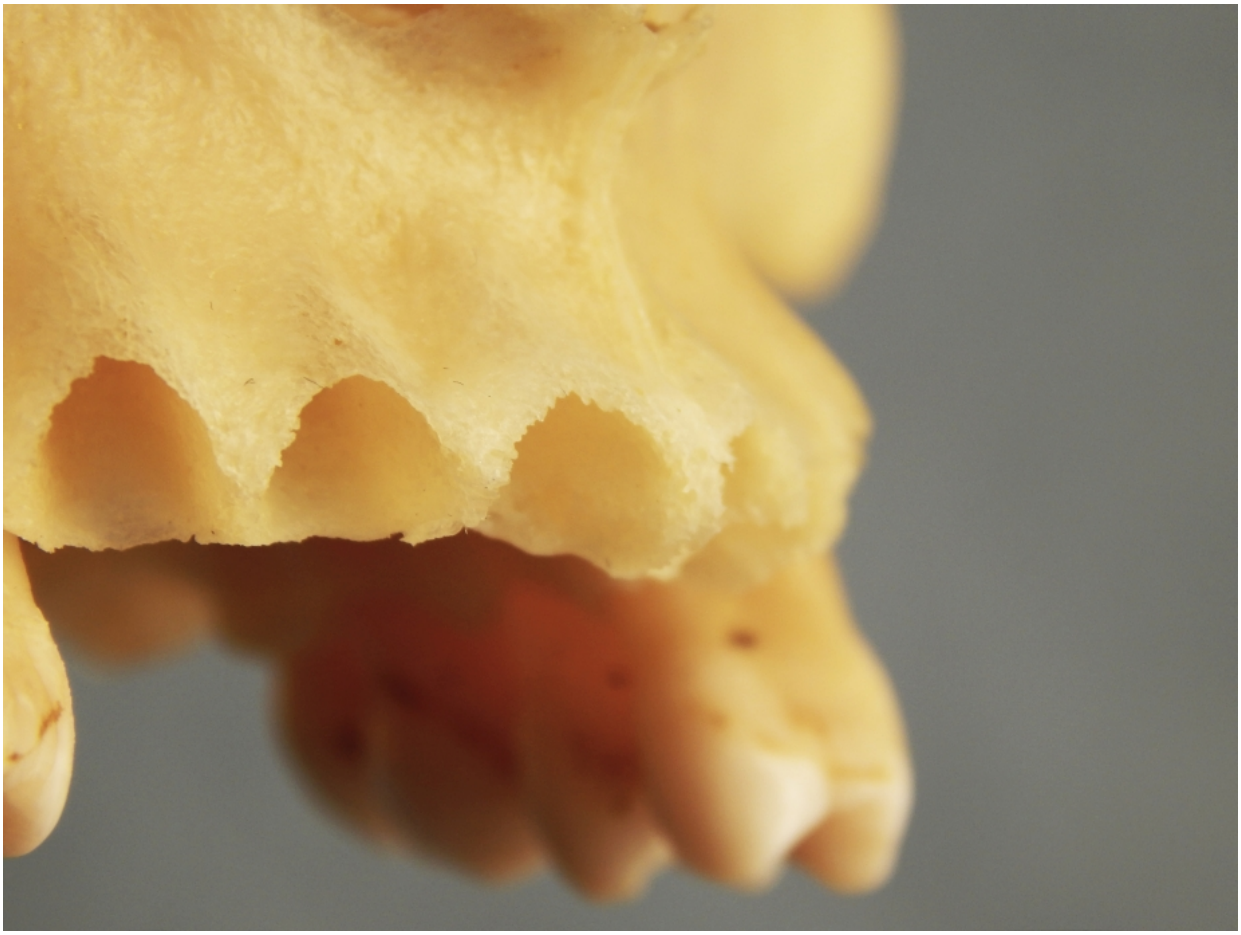


Occipital Chord (l-o, OCC): The direct distance from lambda (l) to opisthion (o) taken in the midsagittal plane.

Upper Facial Height (n-pr, UFHT): The direct distance from nasion (n) to prosthion (pr). With this measurement, use the LOWEST point on the alveolar bone in the midline.



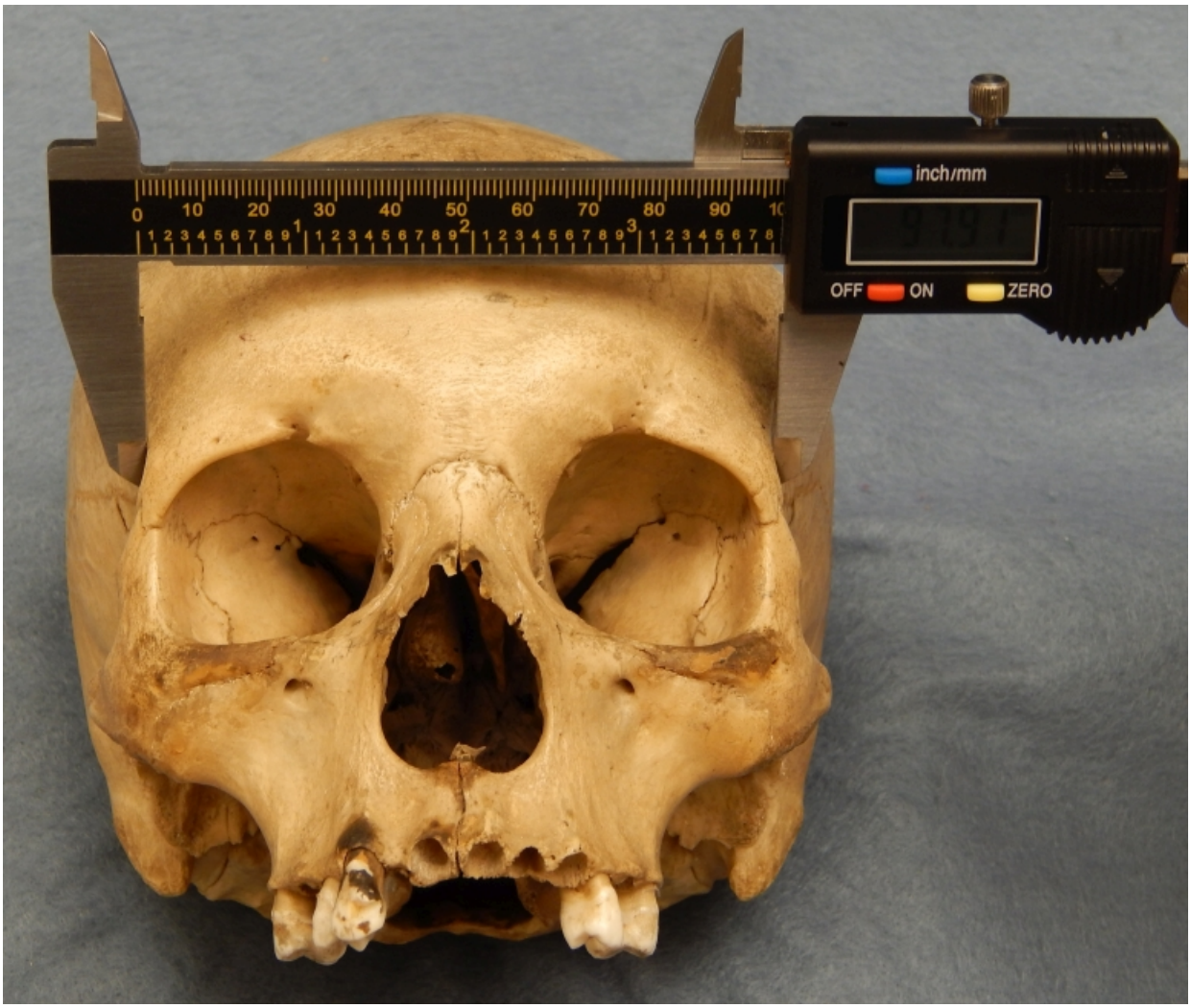

0 10 20 30 40 50 60 70
1 2 3 4 5 6 7 8 9 1 1 2 3 4 5 6 7 8 9 2 1 2 3 4 5 6 7 8 9 3
OFF

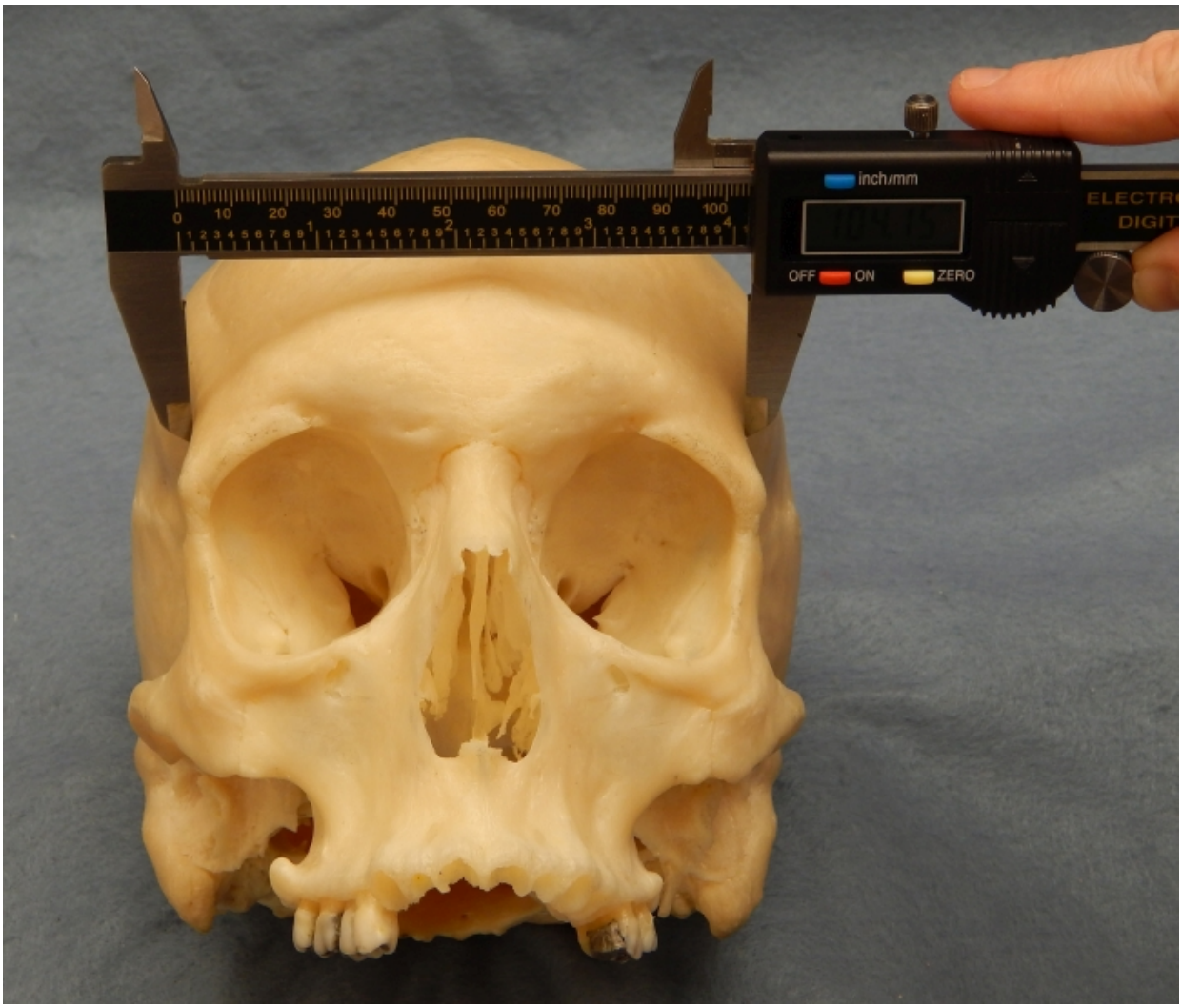


Foramen Magnum Length (ba-o,FOL): The direct distance of basion (ba) to opisthion (o).

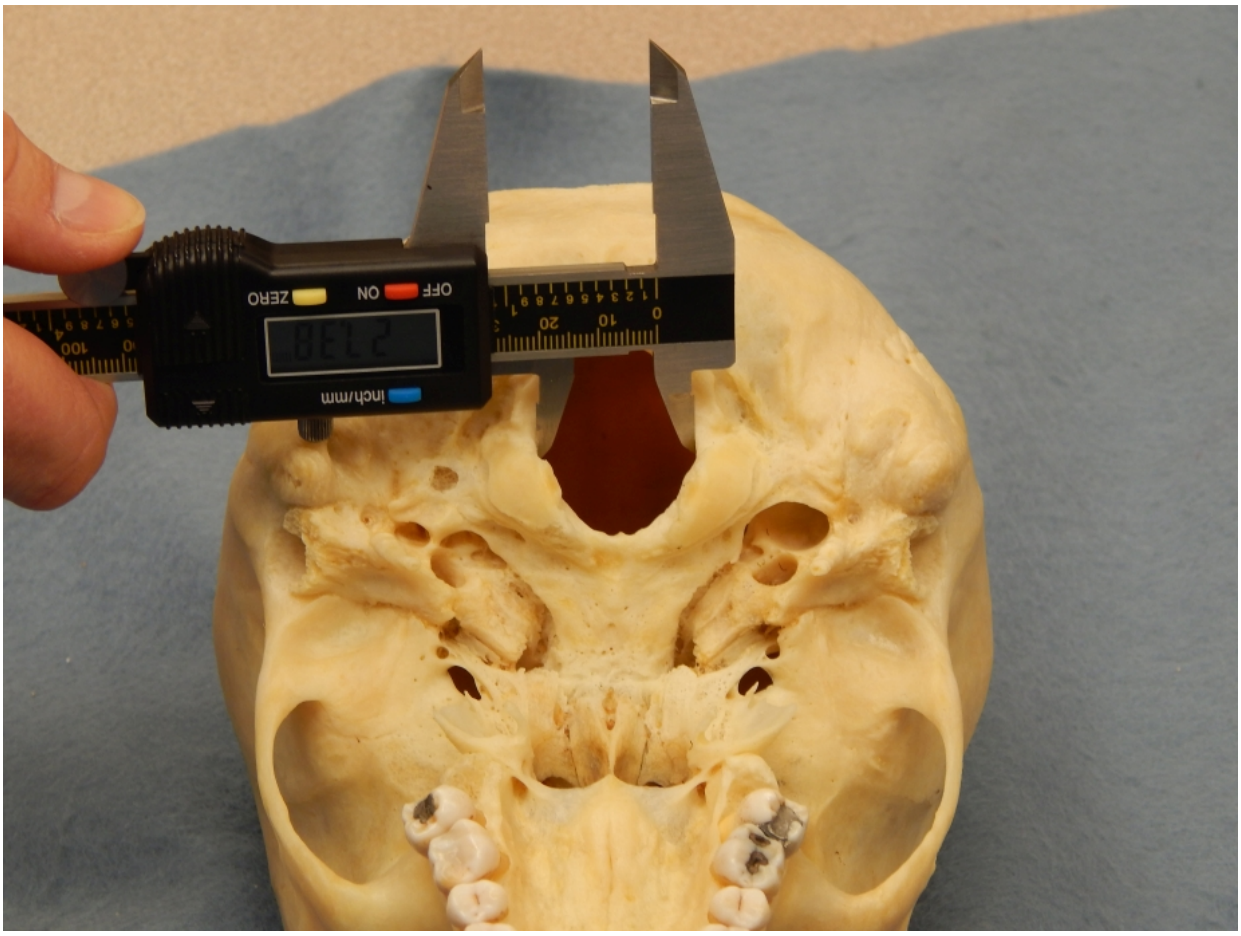

ZERO
ON
OFF
inch/mm
0 10 20 30

Minimum Frontal Breadth (ft-ft, WFB): The direct distance between left and right frontotemporale.



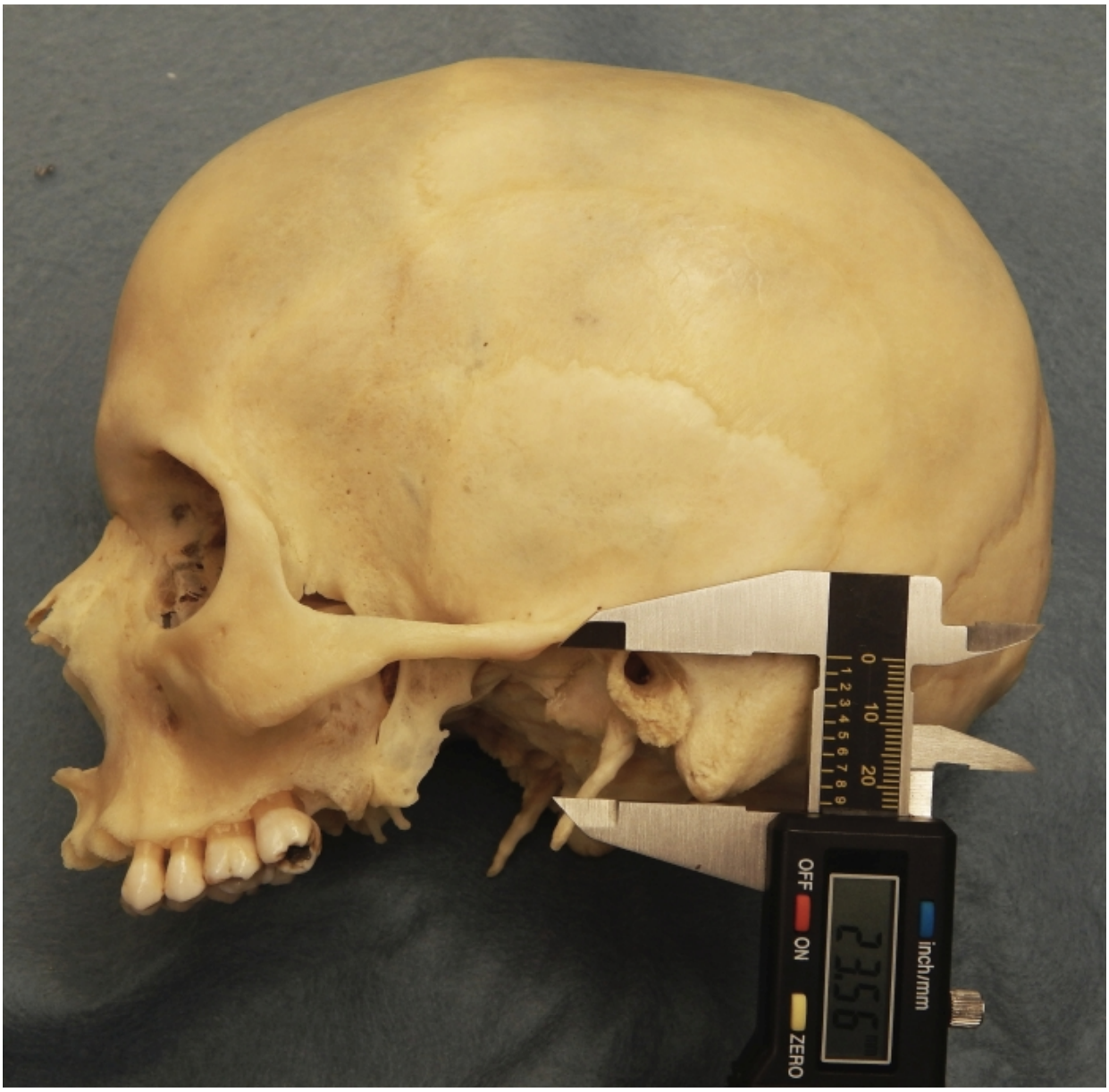

inch/mm
OFF
ON
ZERO

Foramen Magnum Breadth (FOB): The distance between the lateral margins of the Foramen magnum at the point of greatest lateral curvature. Using the inside caliper jaws makes this measurement easier to take.

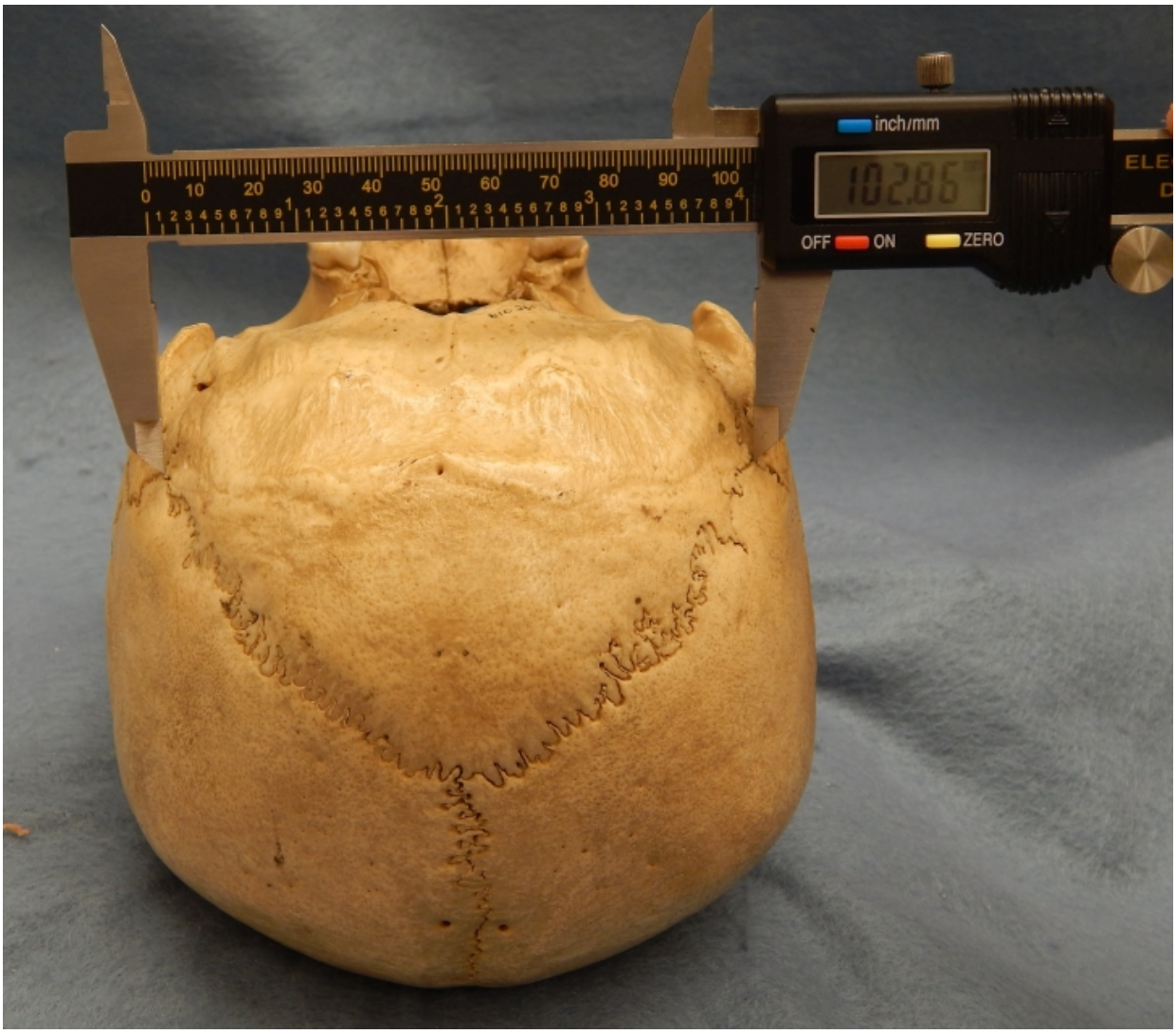


Upper Facial Breadth (fmt-fmt, UFBR): The direct distance between each frontomalare temporale.

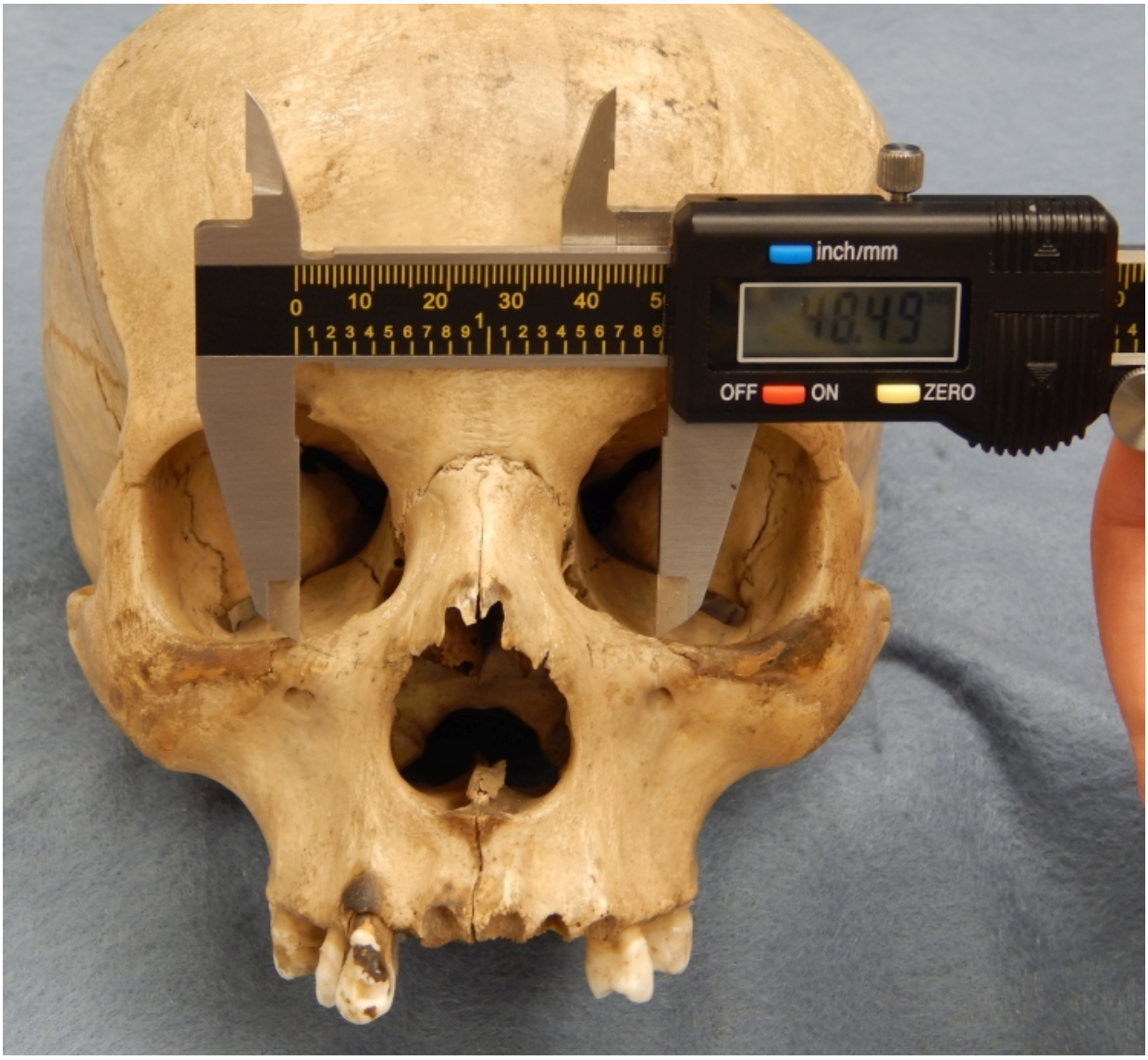
Mastoid Height (MDH): The most inferior projection of the mastoid process (mastoideale) perpendicular to the Frankfurt plane. The Frankfurt plane is defined by left and right porion (the most superior point in the external auditory meatus), and the lowest point on the left orbital border.



Biasterionic Breadth (ASB): The distance from left asterion to right asterion (Howells 1973:174).

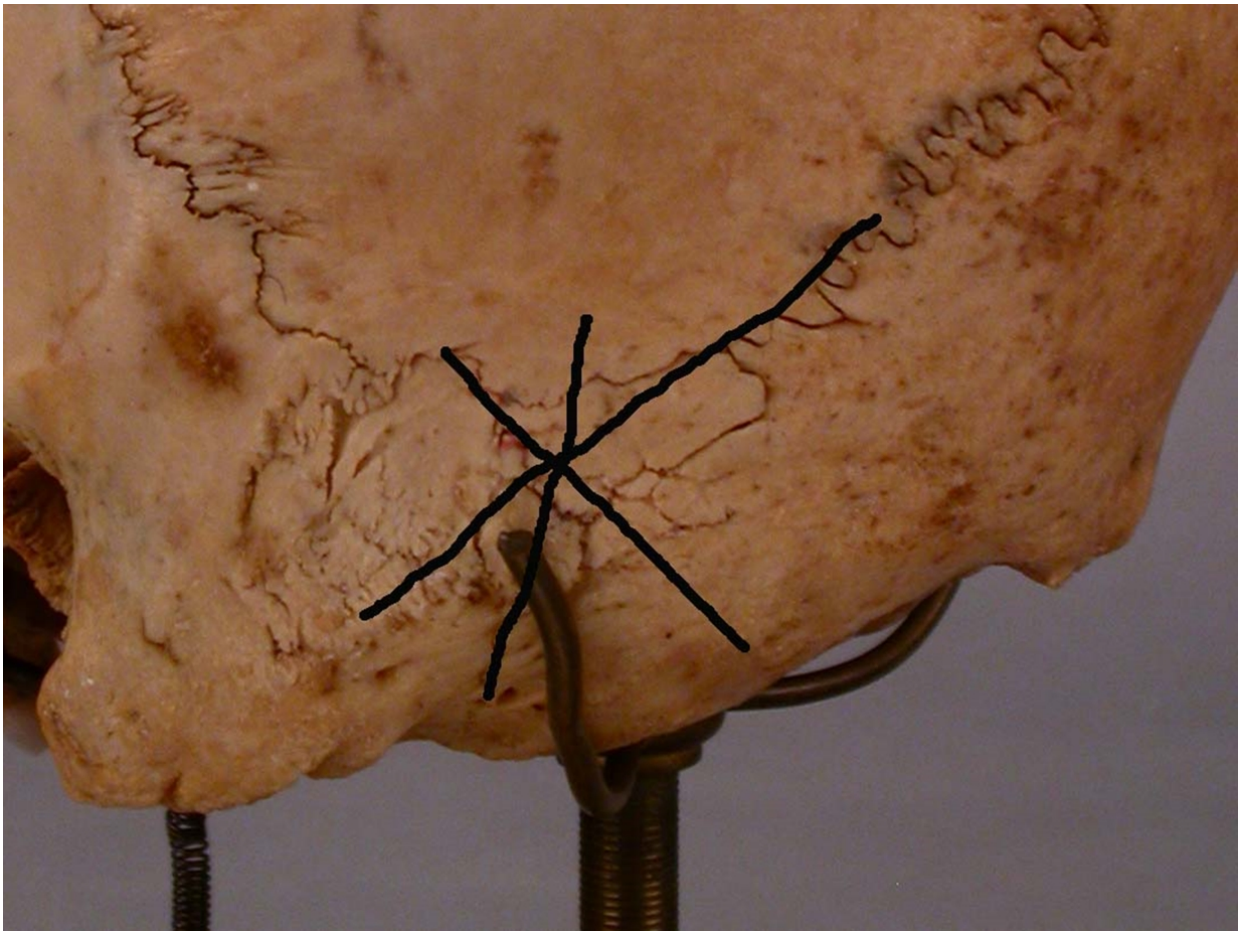


Mid-Orbital Width (MOW): The direct distance from the left zygoorbitale to the right zygoorbitale (Woo and Morant 1934:199).


inch/mm
48.49
OFF
ON
ZERO

Bimaxillary breadth (ZMB): The distance from left to right zygomaxillare anterior (Howells 1973:177).

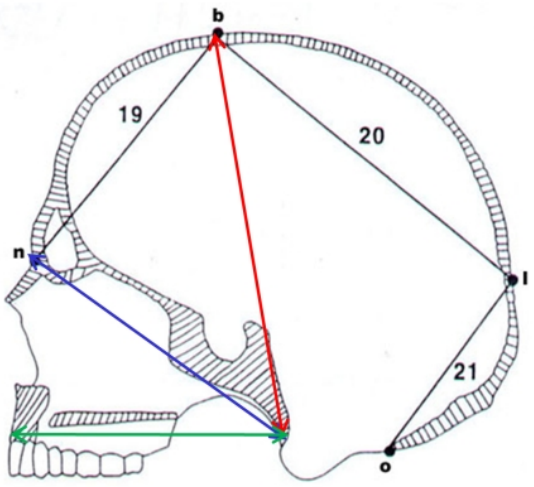
Asterion: The common meeting point of the temporal, parietal, and occipital (Howells 1973:166). When ossicles are present that obscure the point, find the main axes of each suture (temporoparietal, temporooccipital and lambdoidal) and extend them until they intersect. Their estimated intersection would be asterion (see below).

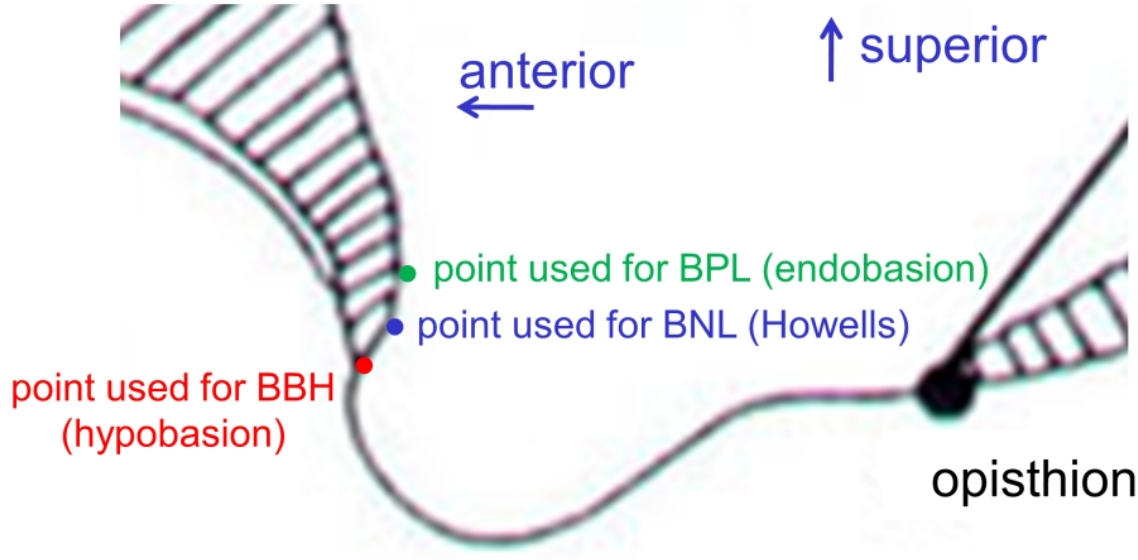


Basion (ba): The exact position of basion is determined by the measurement being taken in the Martin craniometric system.

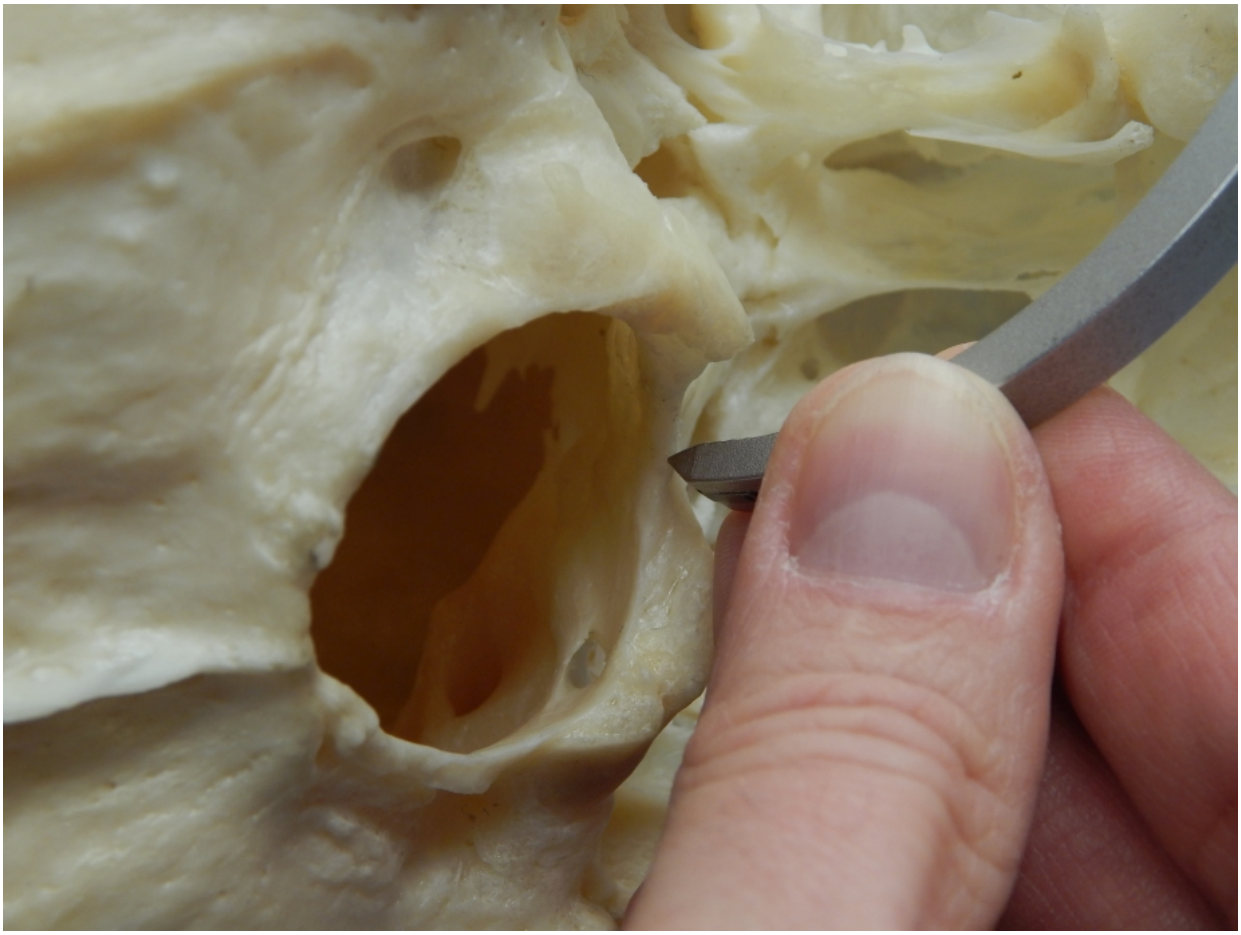
The point where the anterior margin of the foramen magnum is intersected by the mid sagittal plane. The specific point (endobasion) is located on the inner border of the anterior margin of the foramen magnum directly opposite of Opisthion. In rare cases, the determination of the position of basion may be made difficult by a thickening of the anterior margin.

In height measurements of the braincase, Basion is positioned somewhat farther onto the underside of the margin of the foramen magnum (hypobasion), so that the observer may distinguish between an inferior and a posterior basion for reasons of convenience and technical demands (Martin and Saller 1957:446).

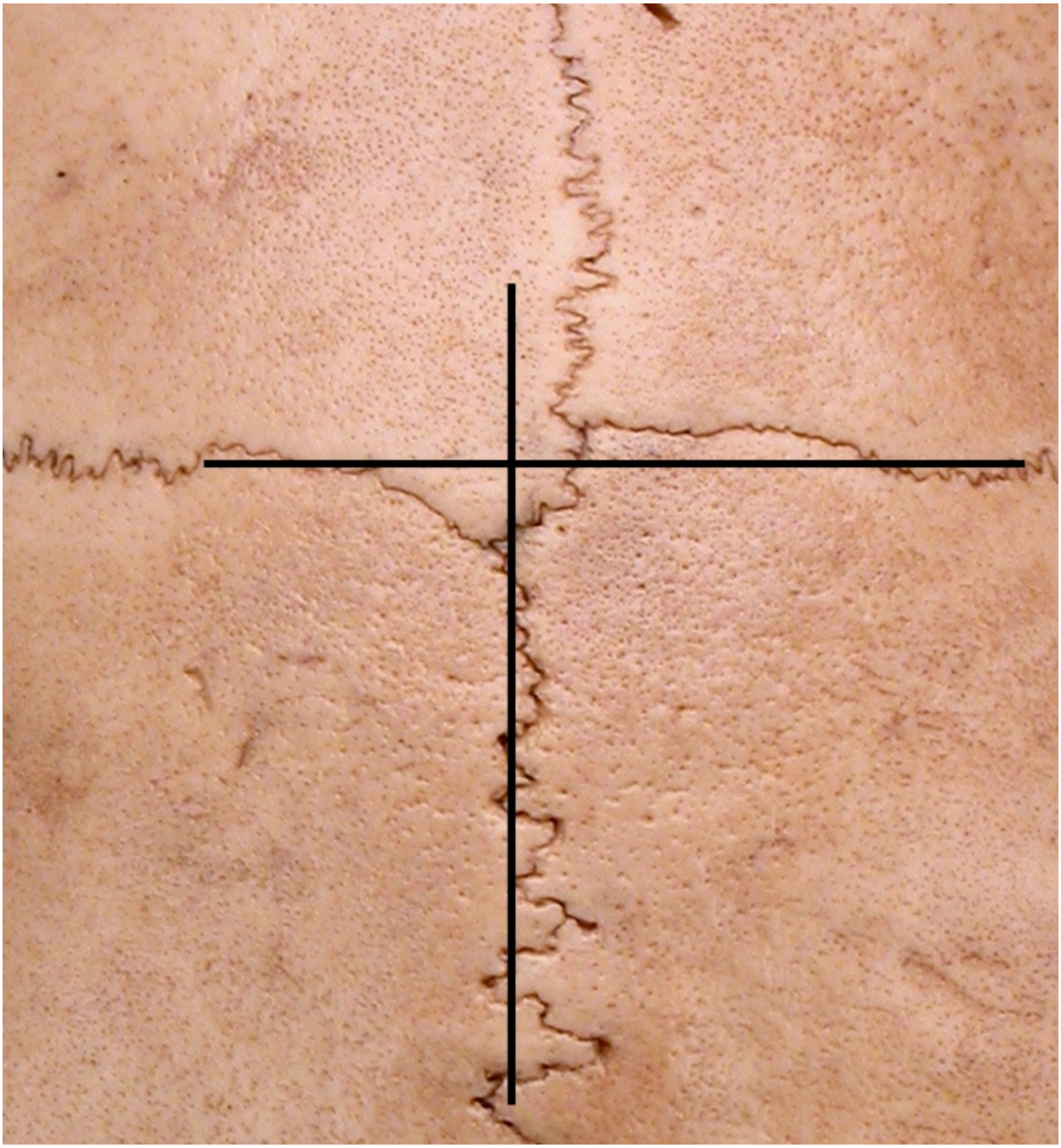


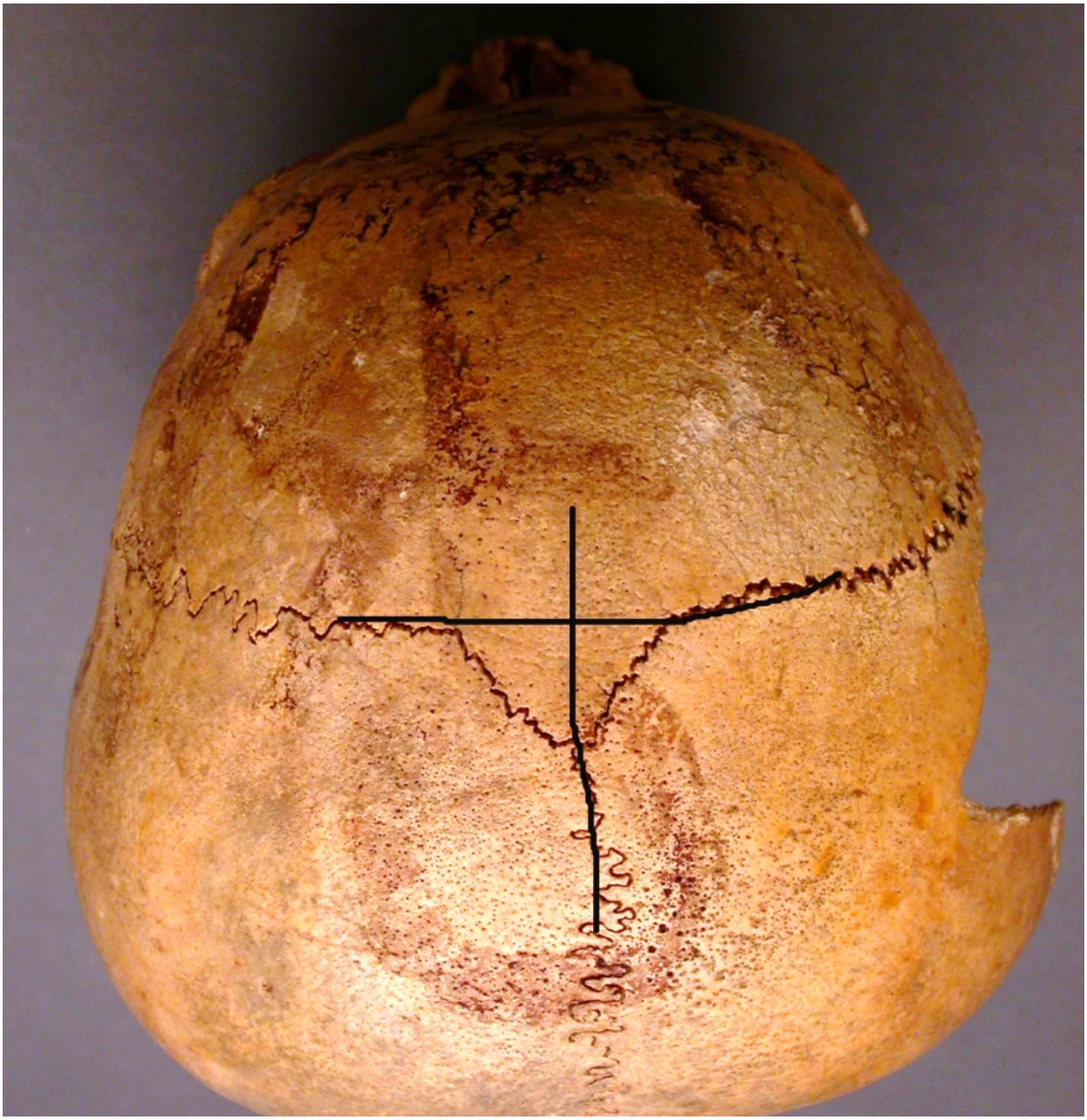


Basion when measuring BBH



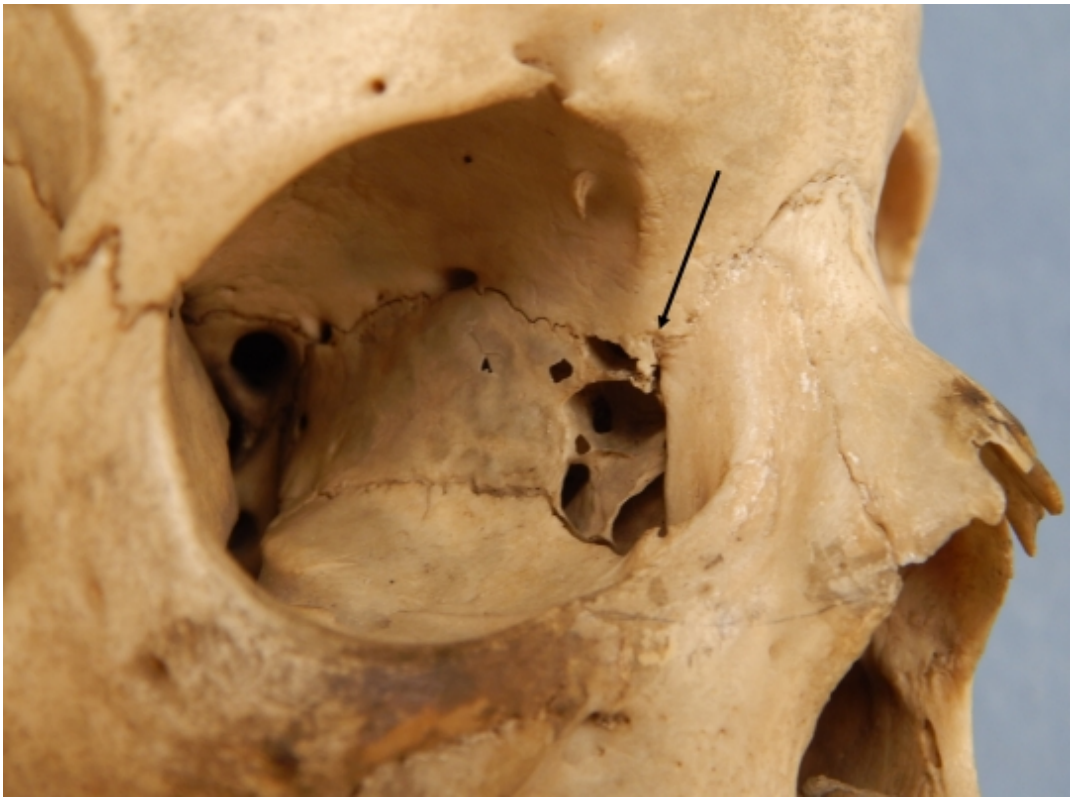
Bregma (b): The point where the sagittal and coronal sutures meet. In those cases where the most anterior segment of the sagittal suture deflects to one side, the point of the junction of the two sutures must be projected. Bregma is impossible to determine exactly on children's crania with open fontanelles, skulls with "Fontanelle" bones, and in skulls with total obliteration of the sutures. In the latter case it may be possible to see existing traces of the sutures by slightly moistening the area. In case of the presence of a "Fontanelle" bone, a straight extension of the sagittal suture is drawn across the forehead while a similar connection is drawn between the two sections of the coronal suture. Bregma is positioned at the point of intersection of these two imaginary lines or extensions (Martin and Saller 1957:444).

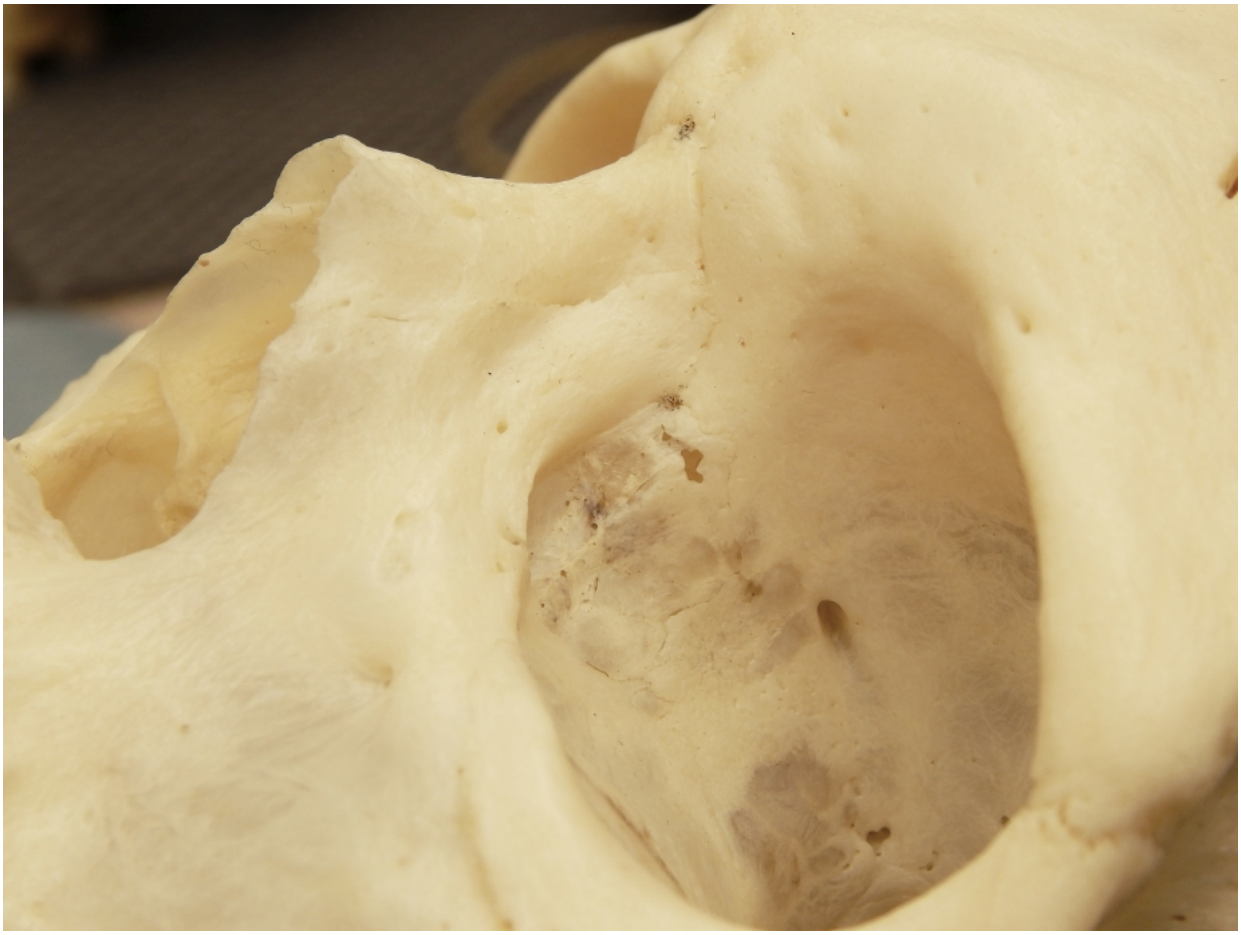


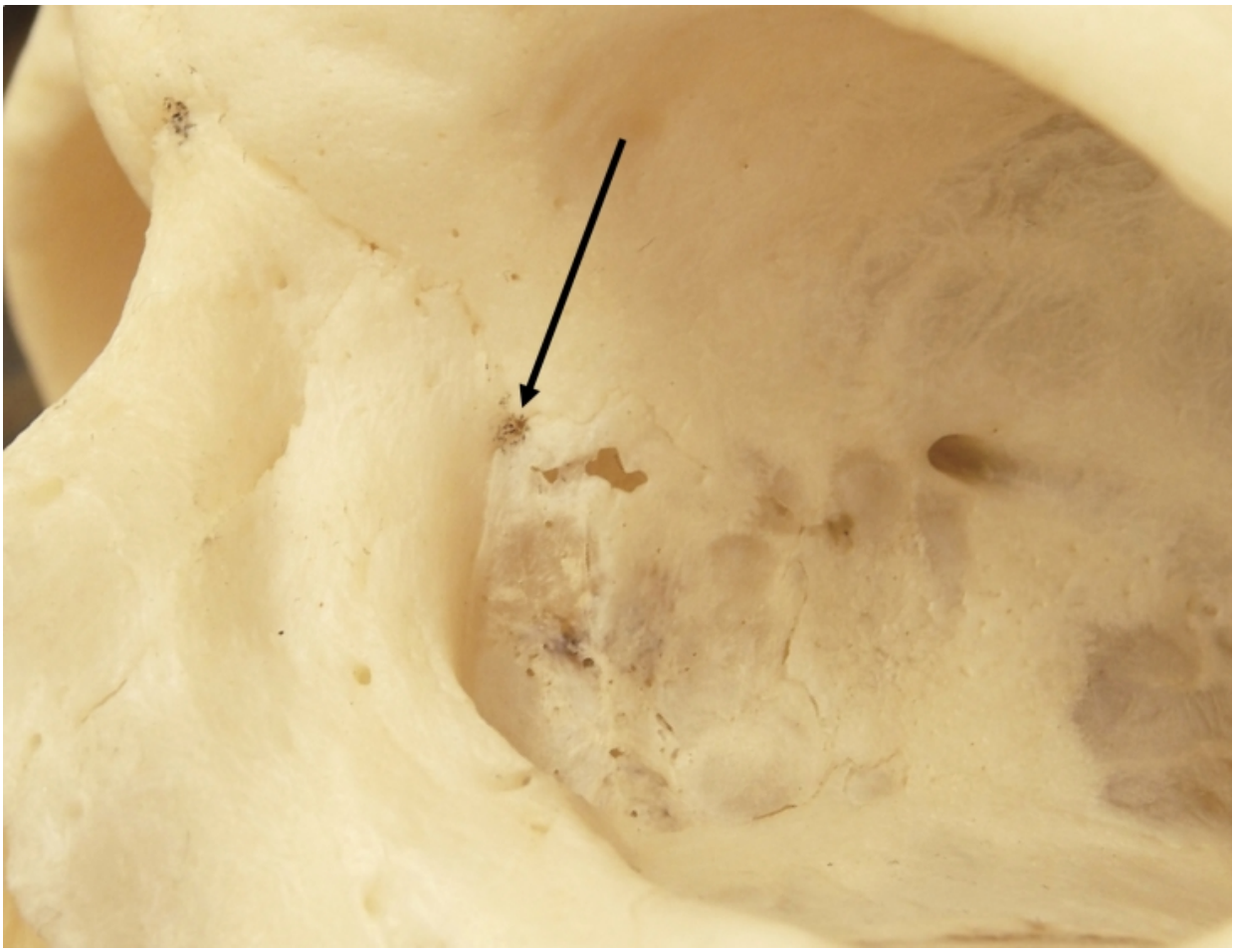


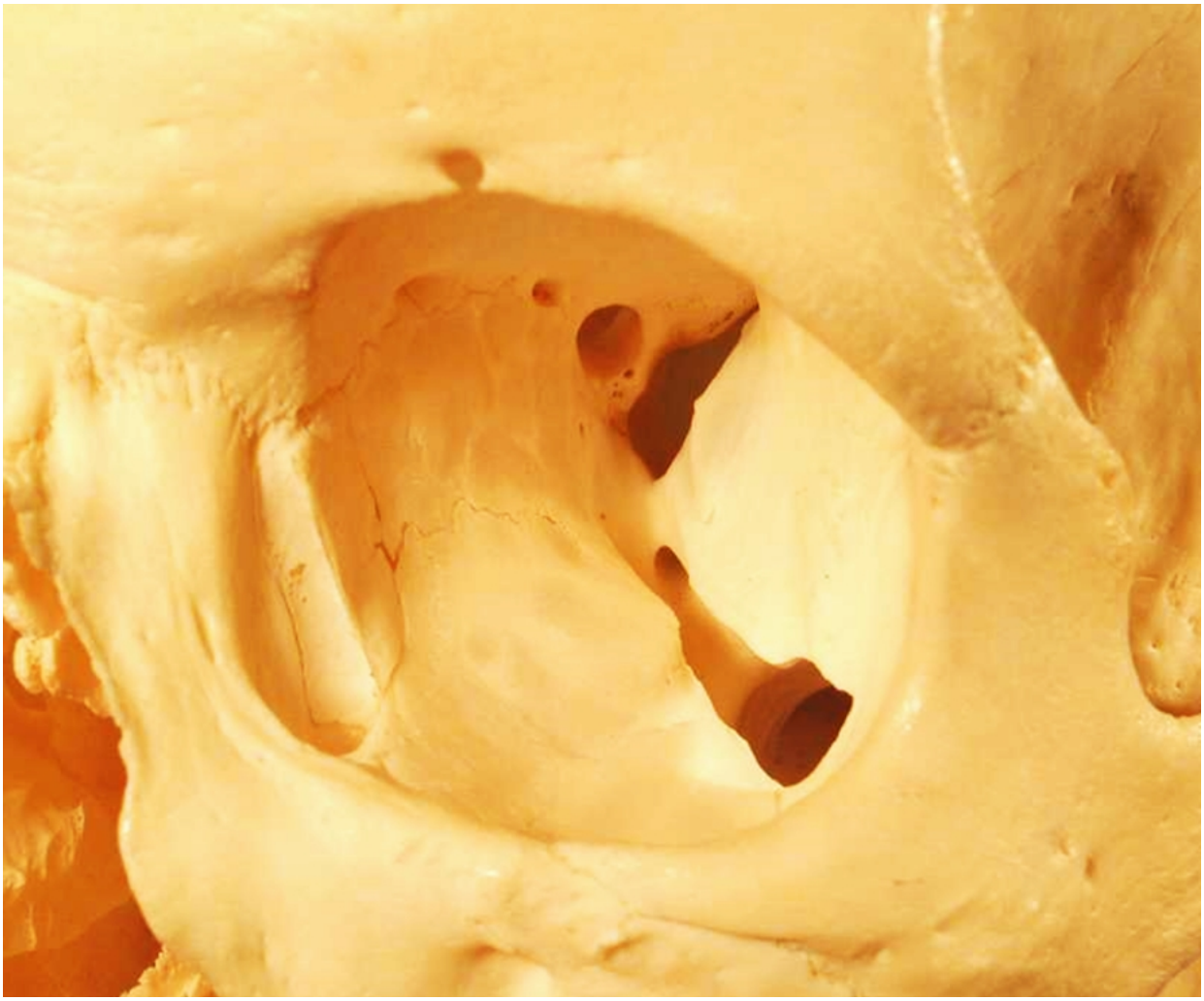
Dacryon (d): The point on the medial border of the orbit at which the frontal, lacrimal, and maxilla intersect. In other words, dacryon lies at the intersection of the lacrimomaxillary suture and the frontal bone. There is often a small foramen at this point. (Martin and Saller 1957:450).

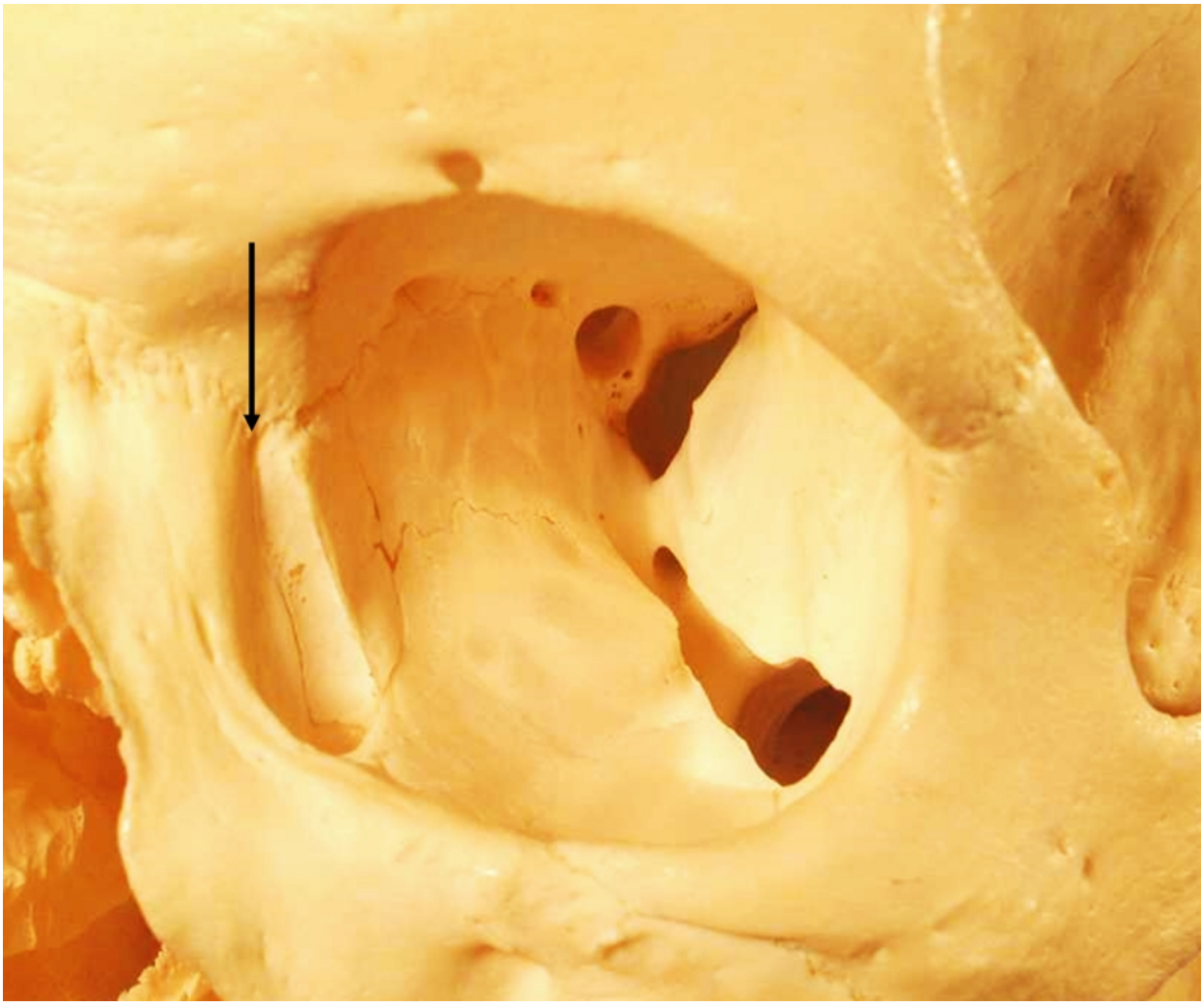
Images with dacryon





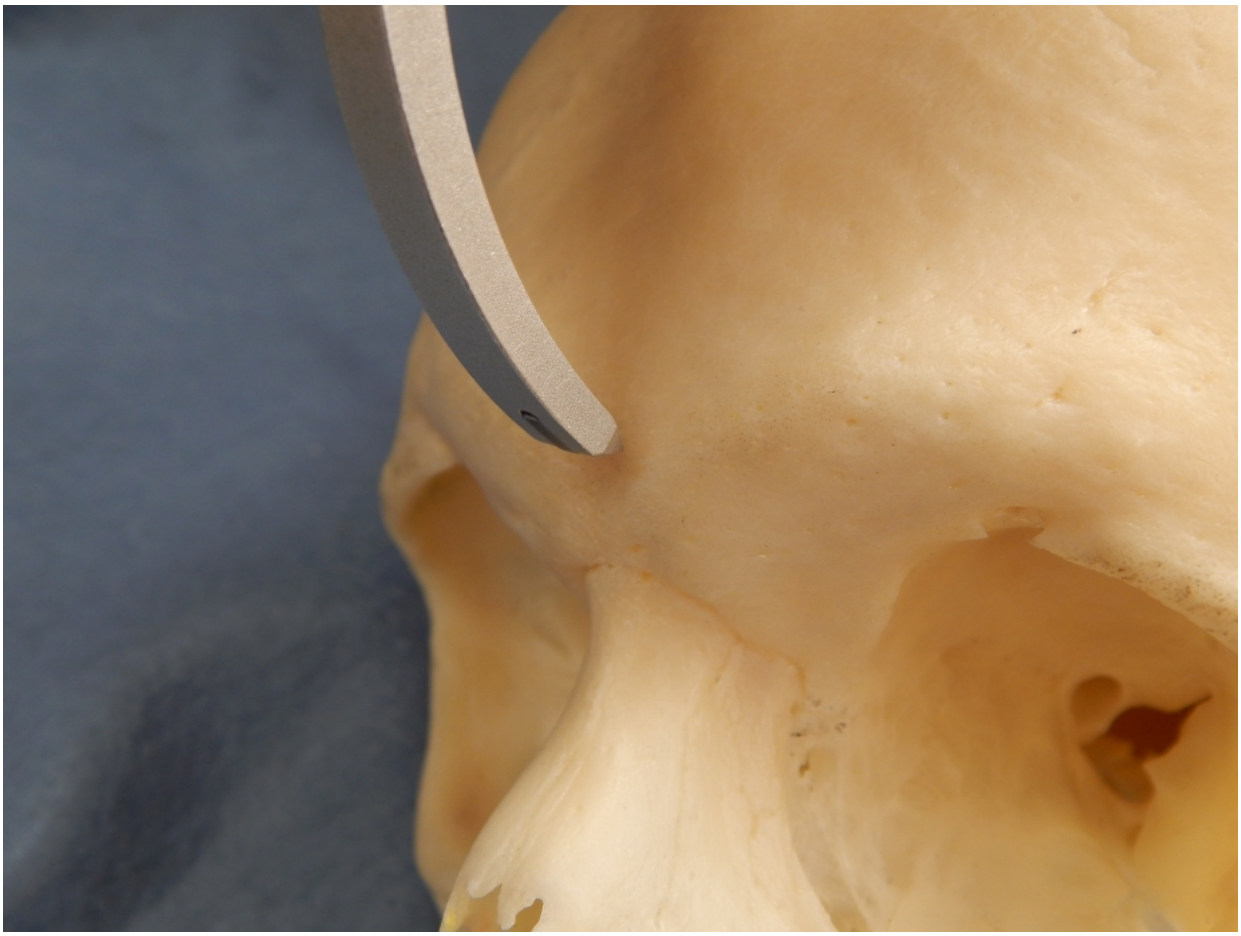






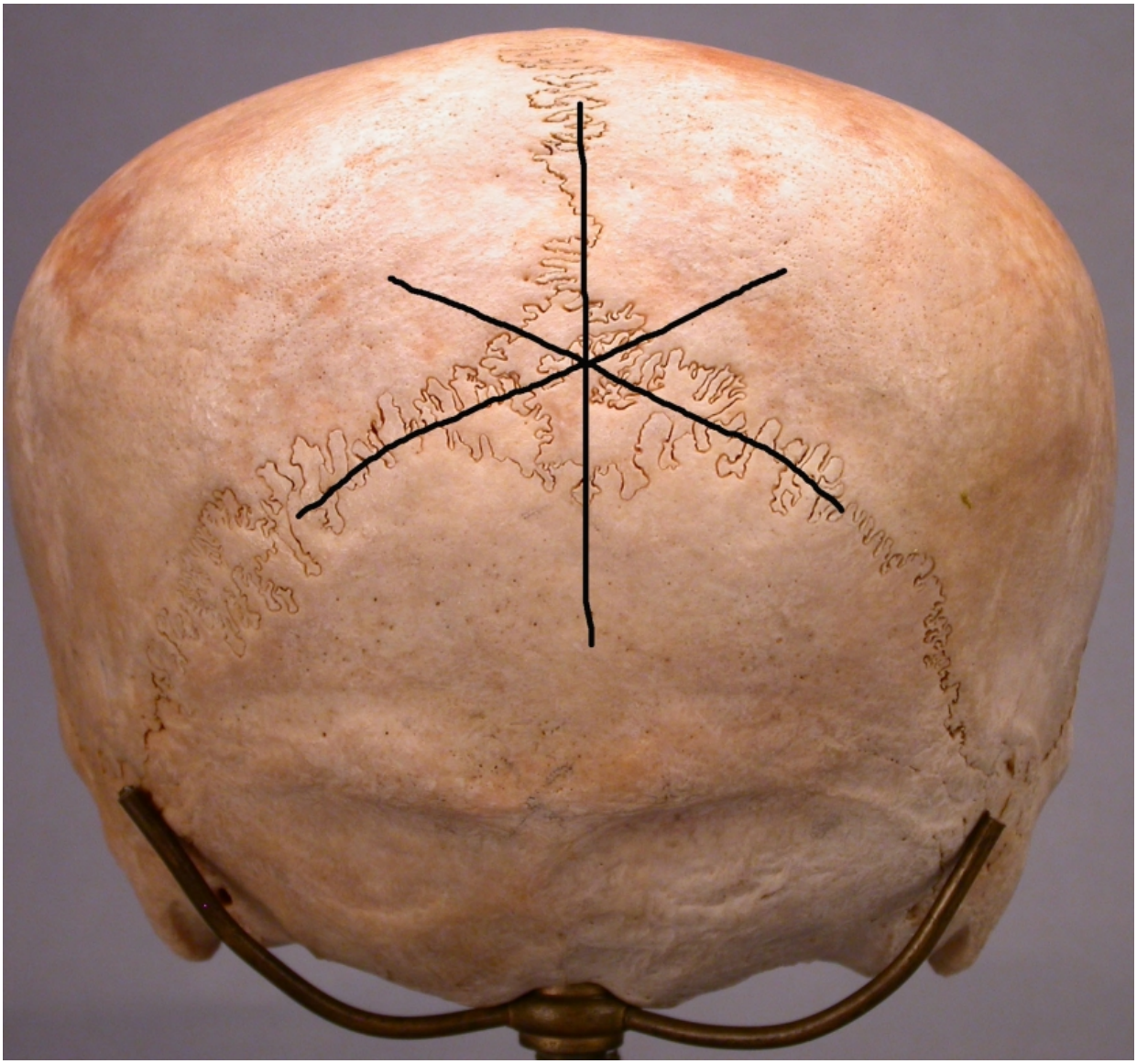
Ectoconchion (ec): The intersection of the most anterior surface of the lateral border of the orbit and a line bisecting the orbit along its long axis. To mark ectoconchion, move a toothpick or other thin straight instrument up and down, keeping it parallel to the superior orbital border, until you divide the eye orbit into two equal halves. **Ignore dacryon when determining ectoconchion.** Mark the point on the anterior orbital margin with a pencil. (Howells 1973:168).

Glabella (g): The most forwardly projecting point in the mid sagittal plane at the lower margin of the frontal bone, which lies above the nasal root and between the superciliary arches . The point of Glabella is depressed between the confining bony ridges, and is often delineated superiorly by a shallow gutter or a transversely running indentation on the surface of the frontal bone. Note that in juvenile skulls with strongly forwardly vaulted foreheads, the most projecting point of the curve of the forehead is not that of Glabella. However, its position is still possible to determine (Martin and Saller 1957:442 443).



Lambda (l): The point where the two branches of the lambdoidal suture meet with the sagittal suture . The determination of this point is uncertain in cases with strongly serrated sutures, as well as cases where sutures are totally obliterated. Locating Lambda may be further complicated in crania with Wormian or sutural bones at the apex of the occipital squama. In such cases the general direction of the two branches of the lambdoidal sutures is determined and two straight lines are projected along the branches of the suture placing Lambda at the point where these lines meet with one another and with the sagittal suture (Martin and Saller 1957:444).

Finding lambda with ossicles

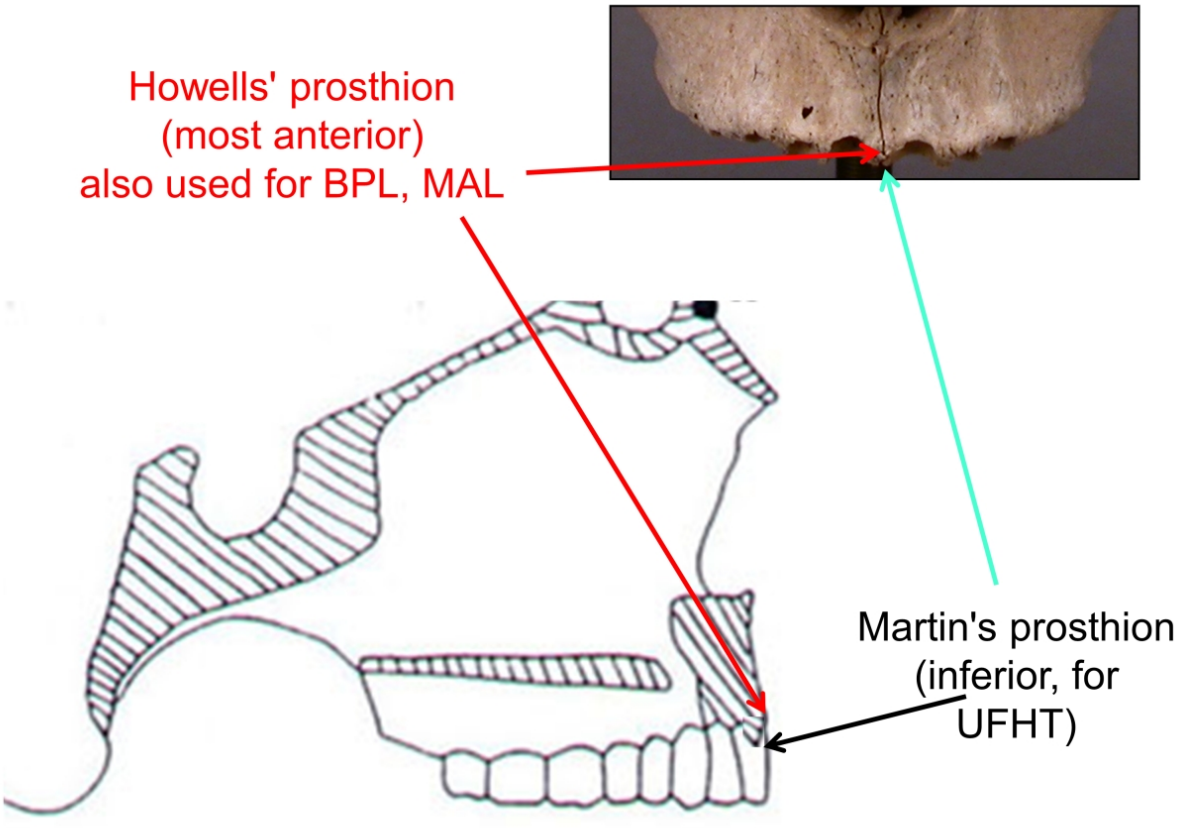


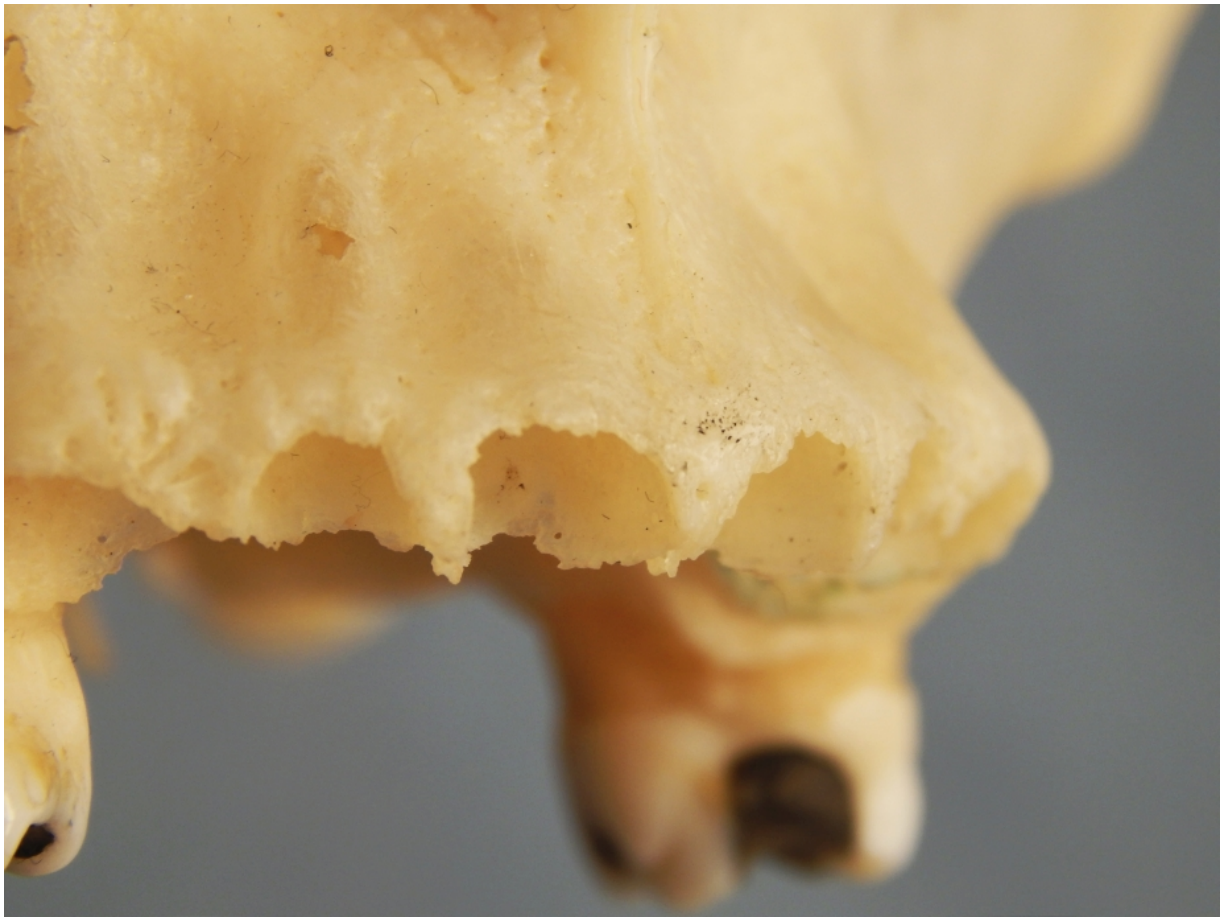
Prosthion (pr): The position of prosthion depends on the measurement being taken in the Martin measurement system (Martin and Saller 1957:449).

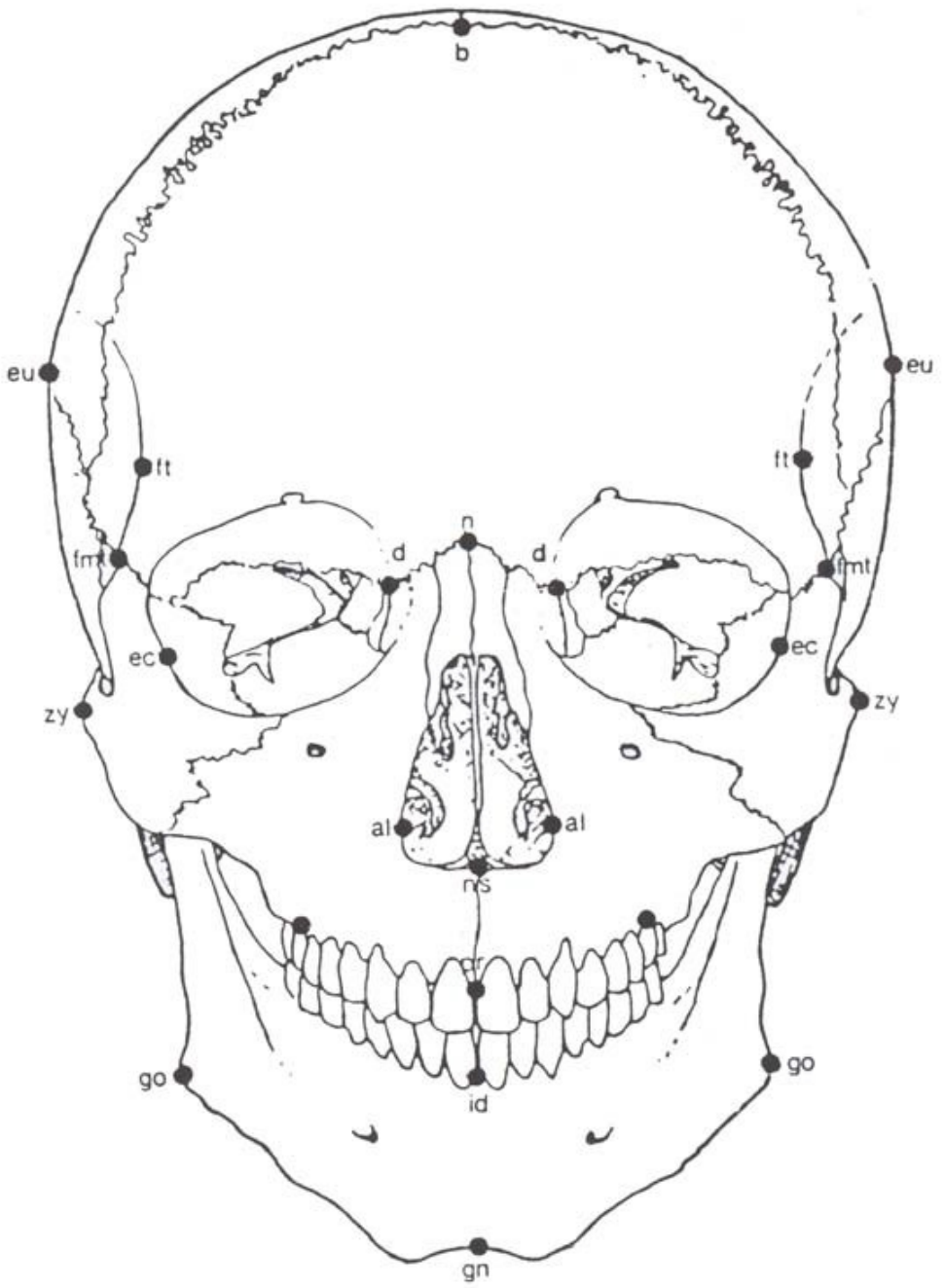
In measuring BPL and palate length (MAB), prosthion is the most anterior point on the alveolar process at the midline.

In measuring upper facial height (UFHT), prosthion is located on the most inferior point of the alveolar process in the midline. In cases of a defective or resorbed alveolar process, determination of prosthion becomes uncertain or impossible, and upper facial height cannot be measured.

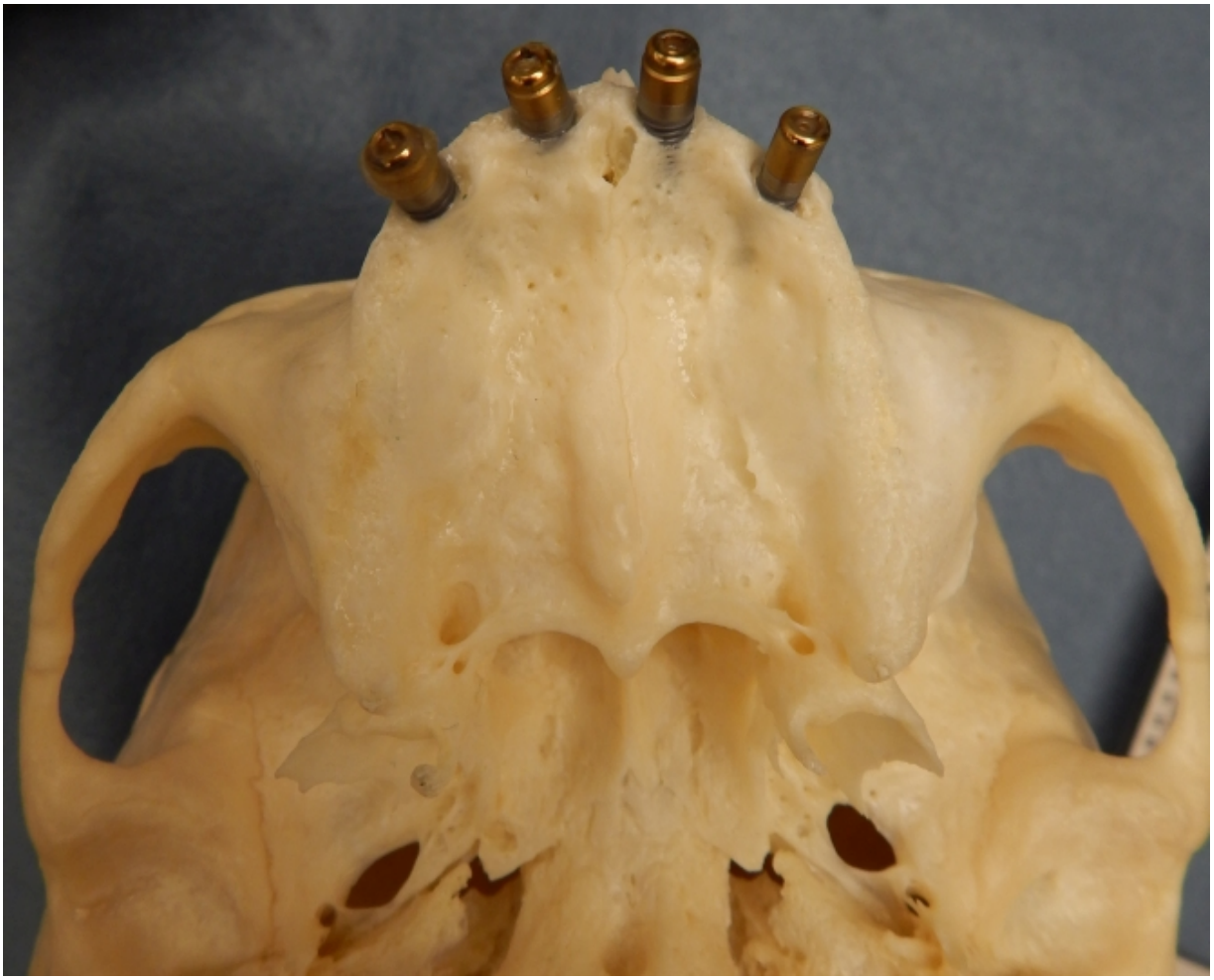
Prosthion

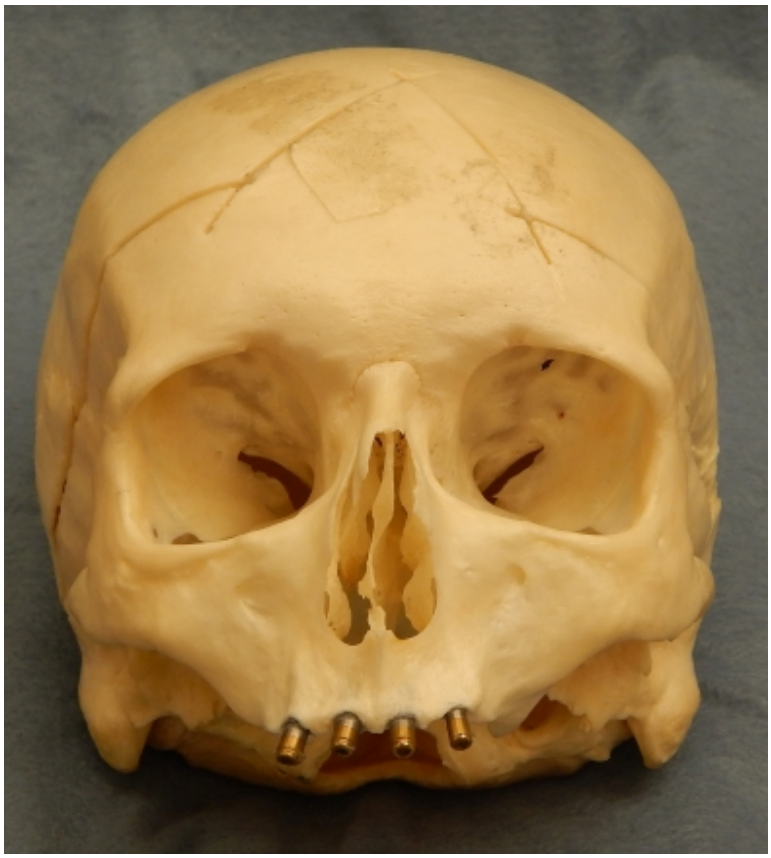




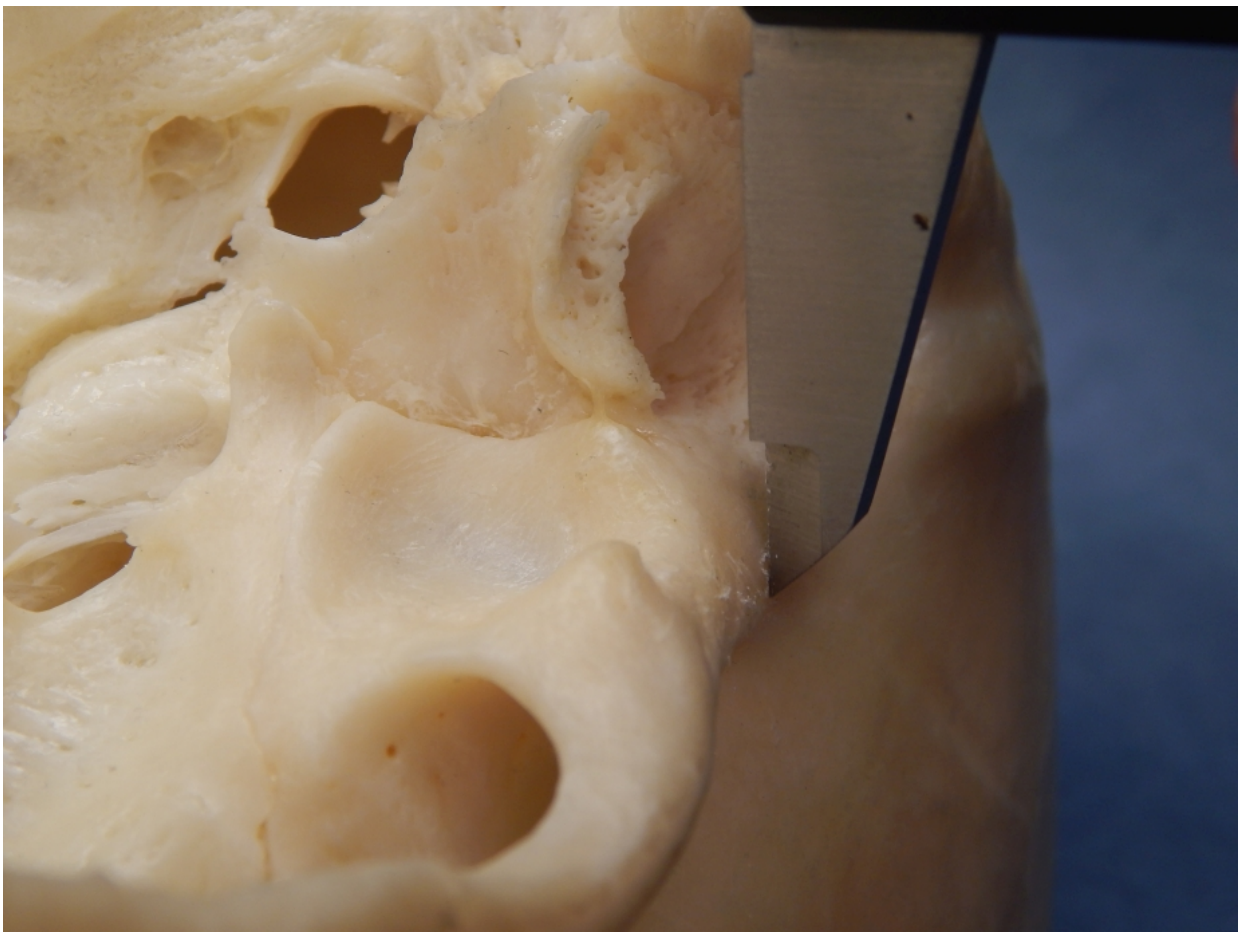


Resorbed prosthion - do not measure

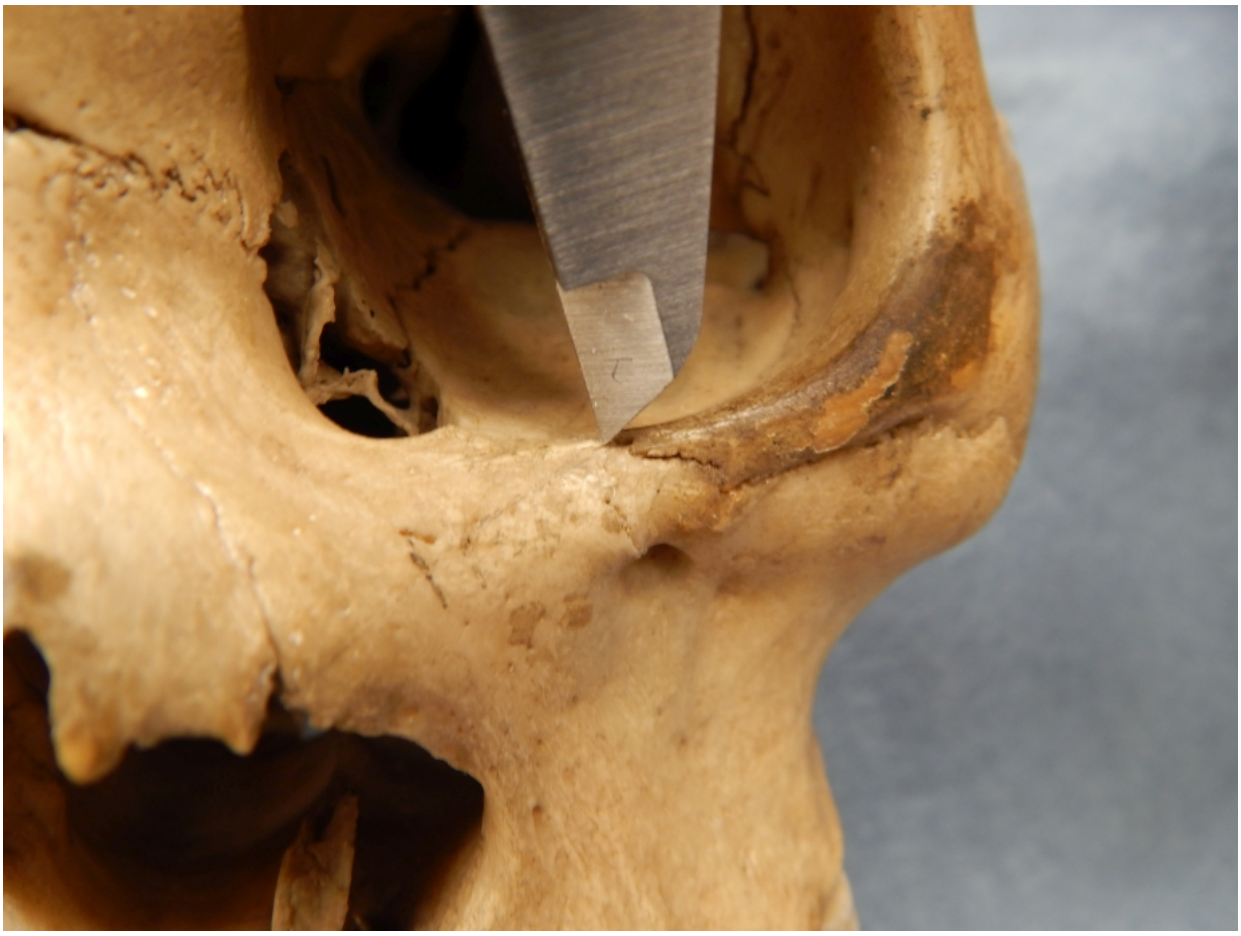




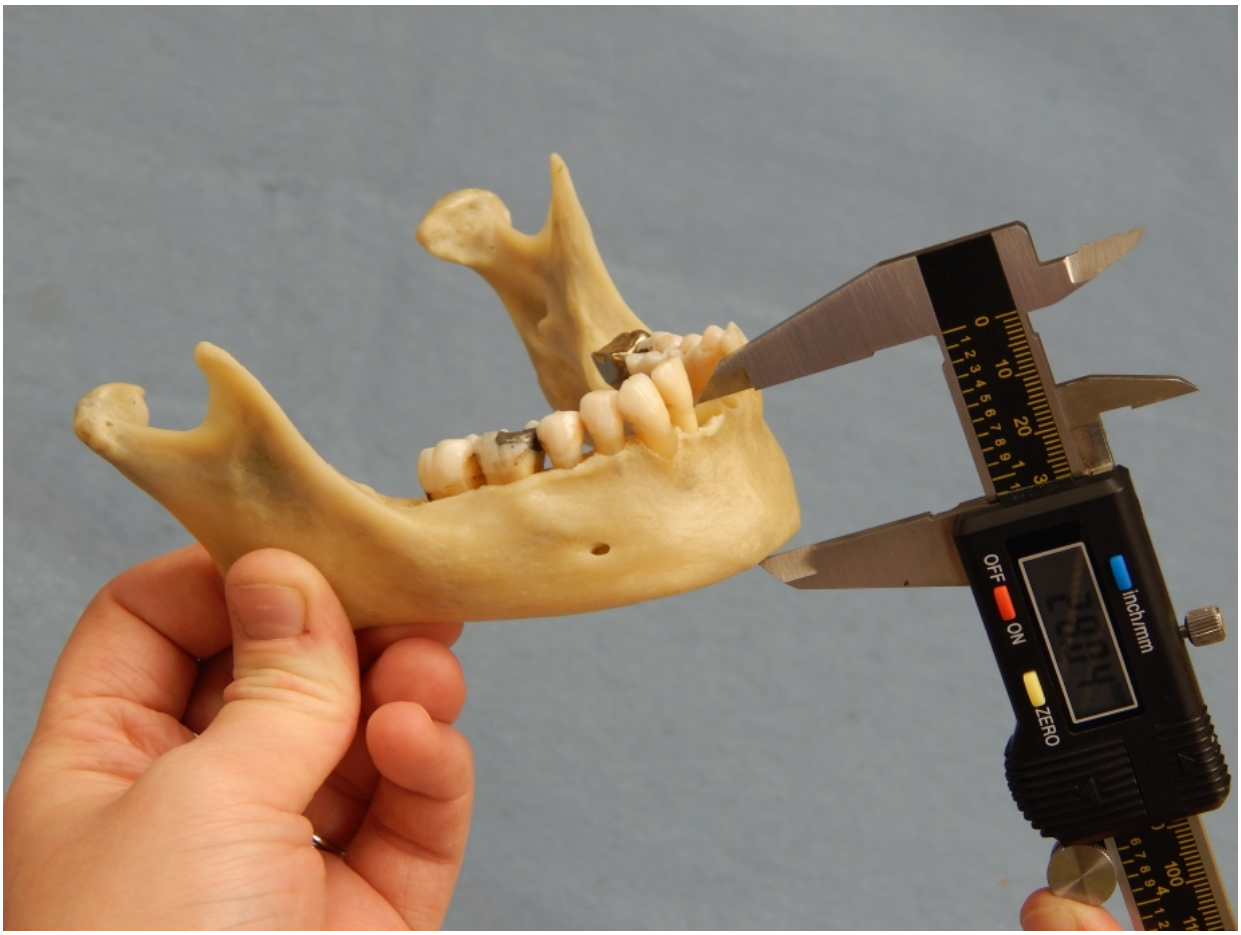
Radiculare: The point on the lateral aspect of the root of the zygomatic process at the deepest medial incurvature. Determined by instrument.



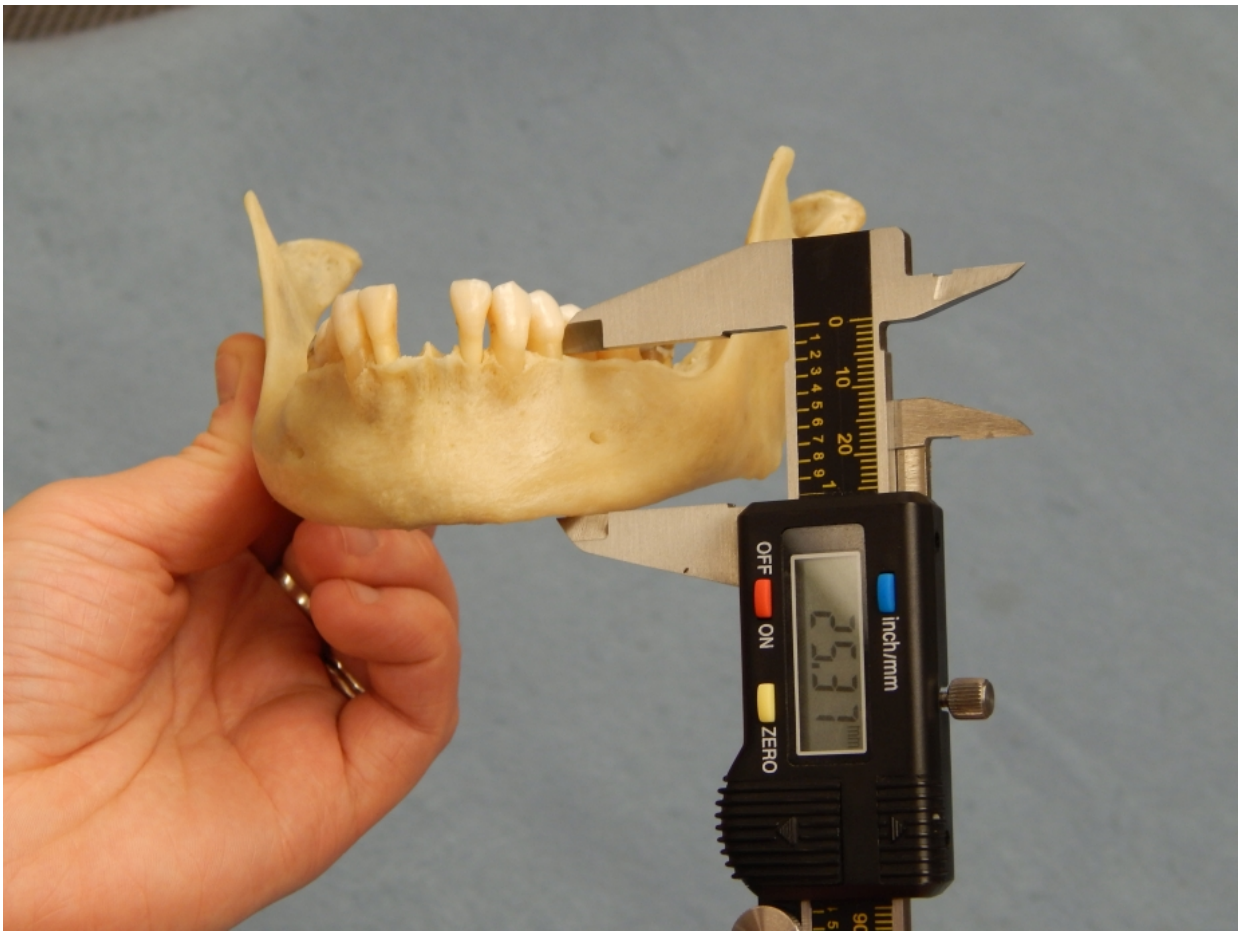
Zygoorbitale (zyo) is the intersection of the orbital margin and the zygomaxillary suture (Howells 1973). In other words, it is found at the junction of the zygomatic and the maxilla on the orbital border.



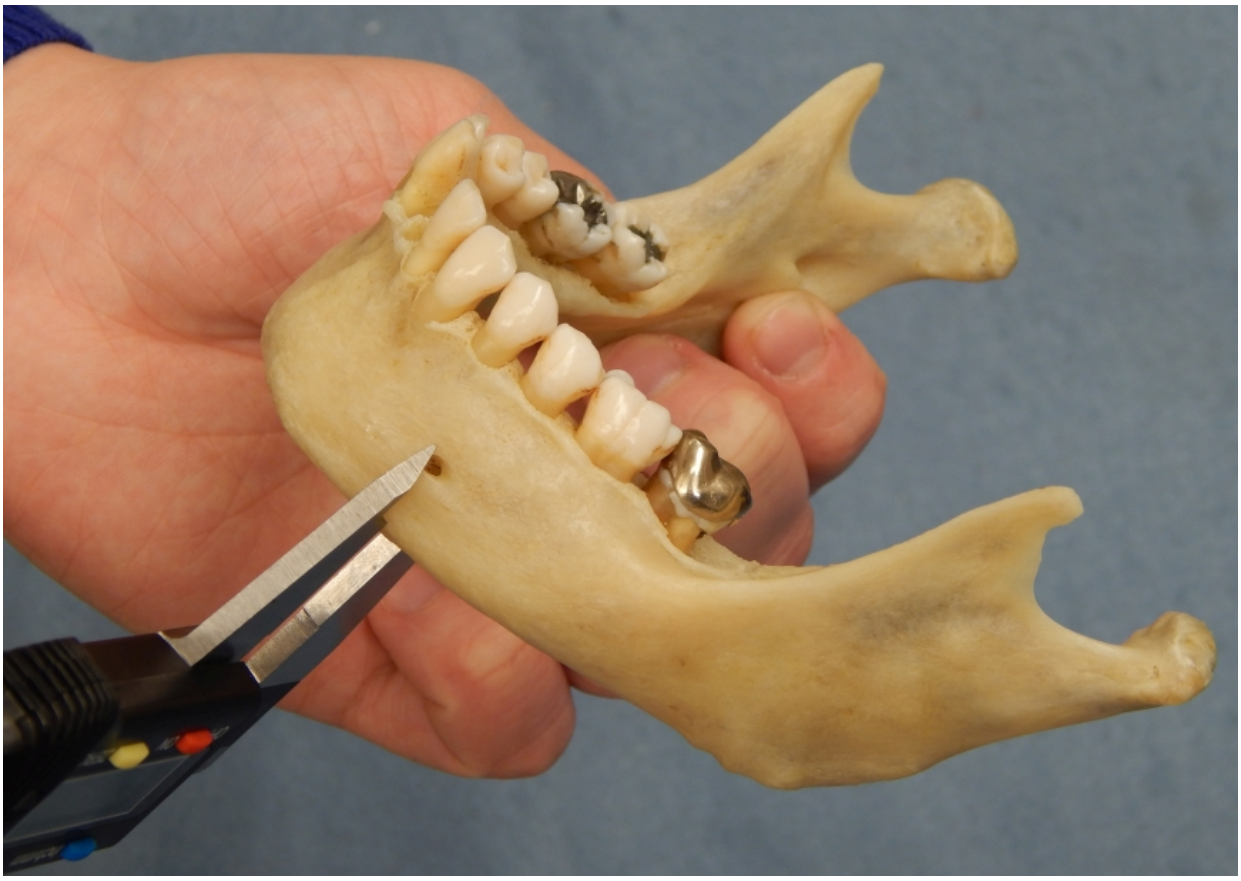
Chin Height (id-gn, GNI): The direct distance from infradentale (id) to gnathion (gn).



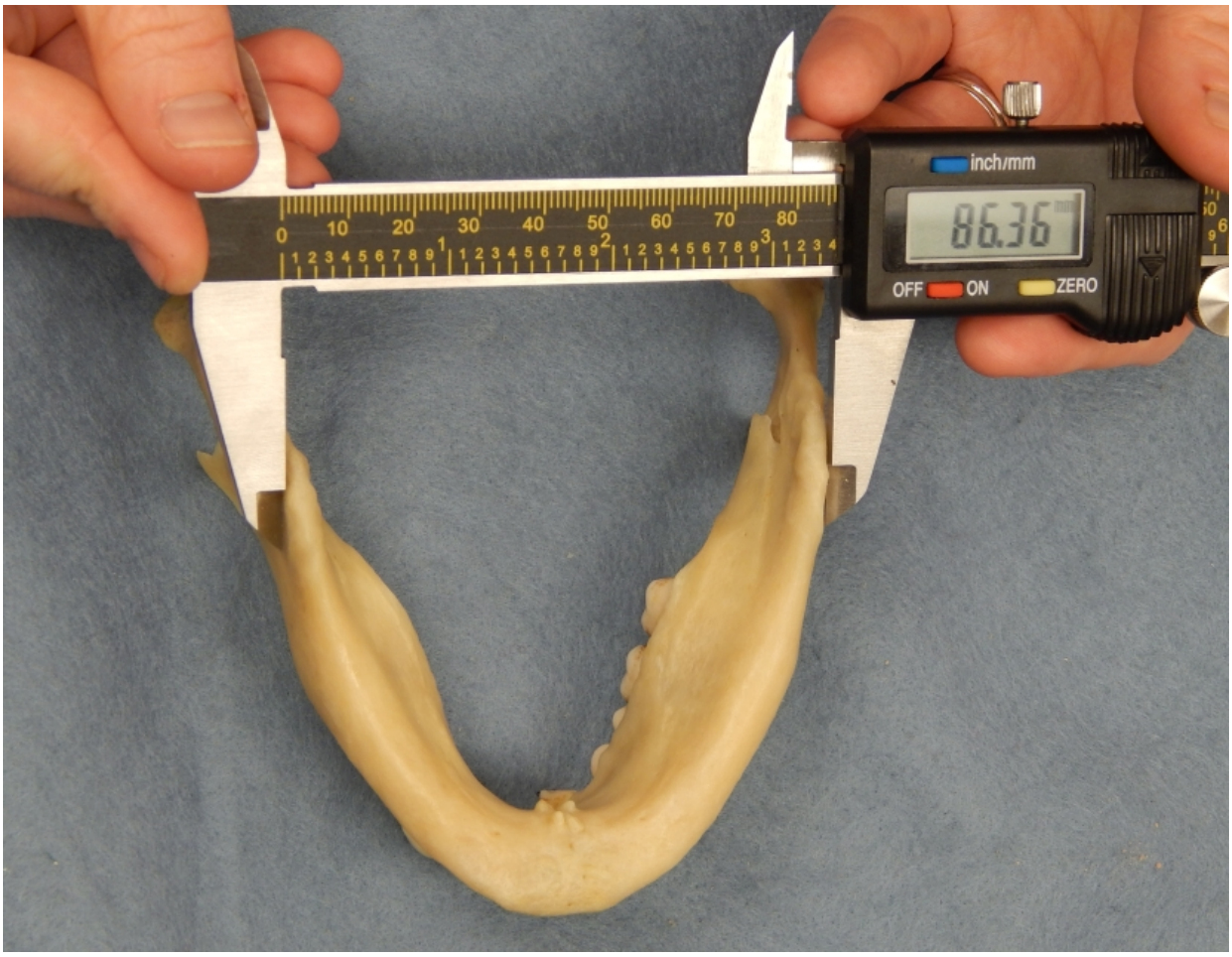
Height of the Mandibular Body at mental foramen (HMF): The direct distance from the alveolar process to the inferior border of the mandible perpendicular to the base at the level of the mental foramen.



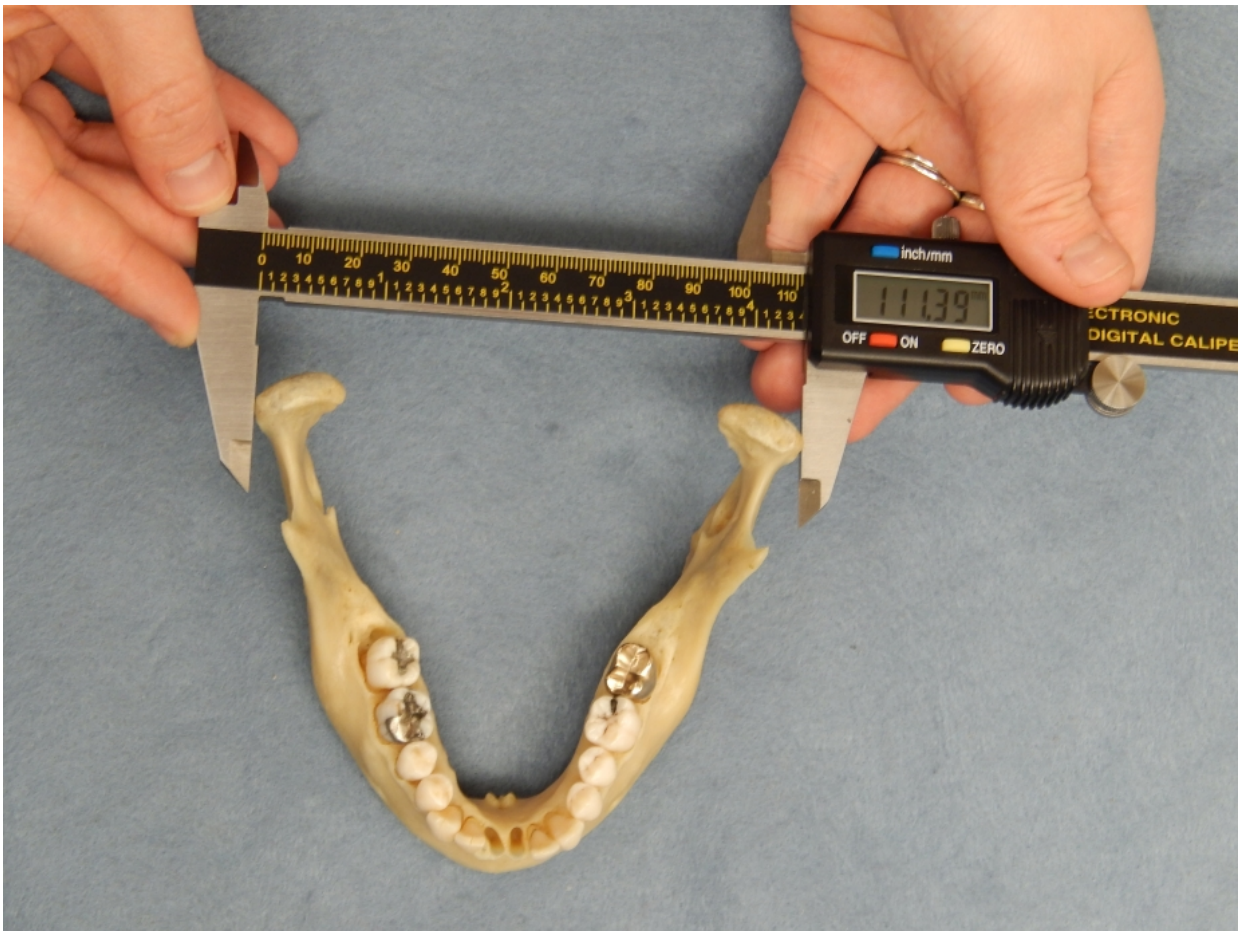
Thickness of Mandibular Body at the mental foramen (TMF): The maximum breadth measured in the region of the mental foramen perpendicular to the long axis of the mandibular body.

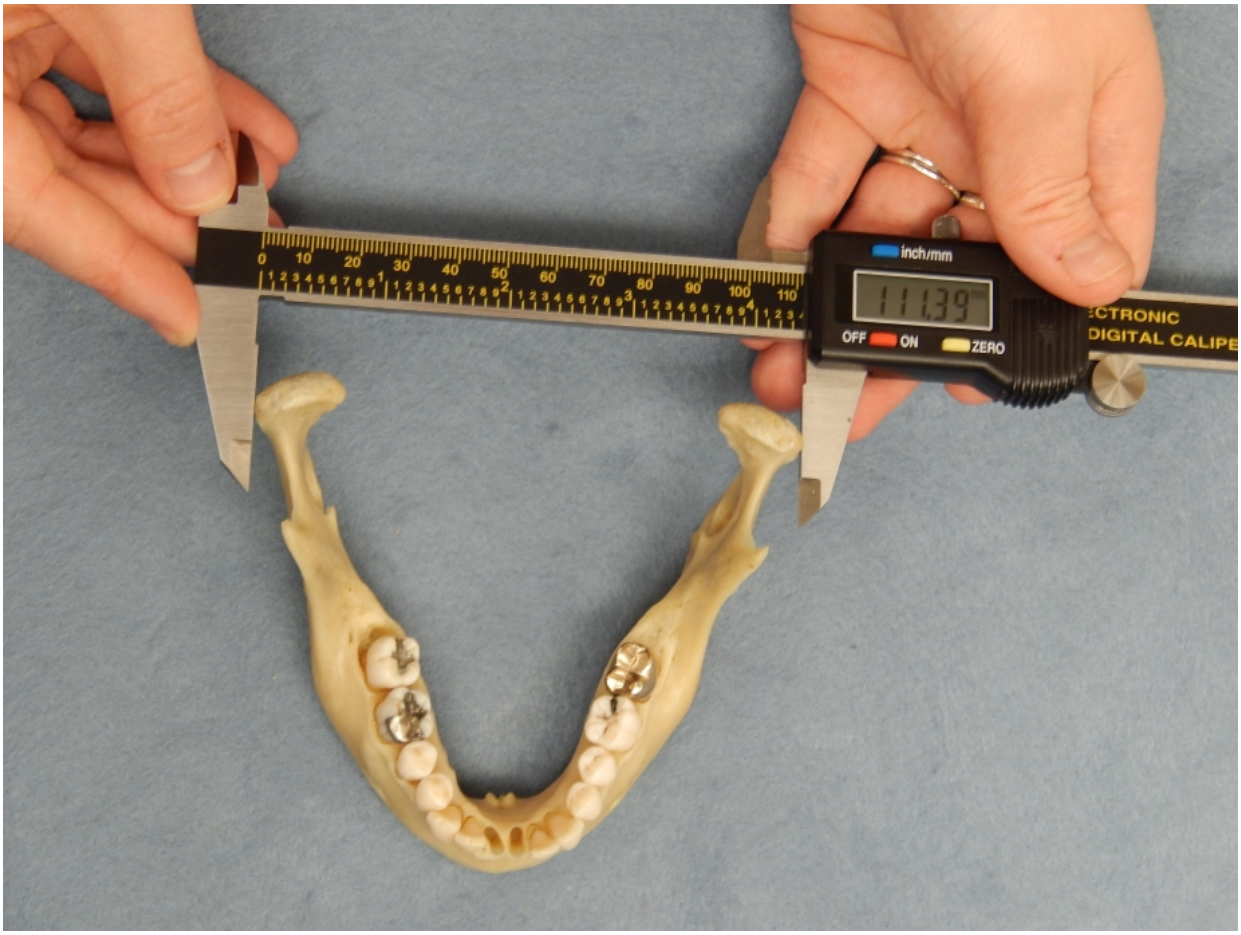


Bigonial Width (go-go, GOG): The direct distance between left and right gonion (go).



Bicondylar Breadth (cdl-cdl, CDB): The direct distance between the most lateral points on the two condyles (cdl).

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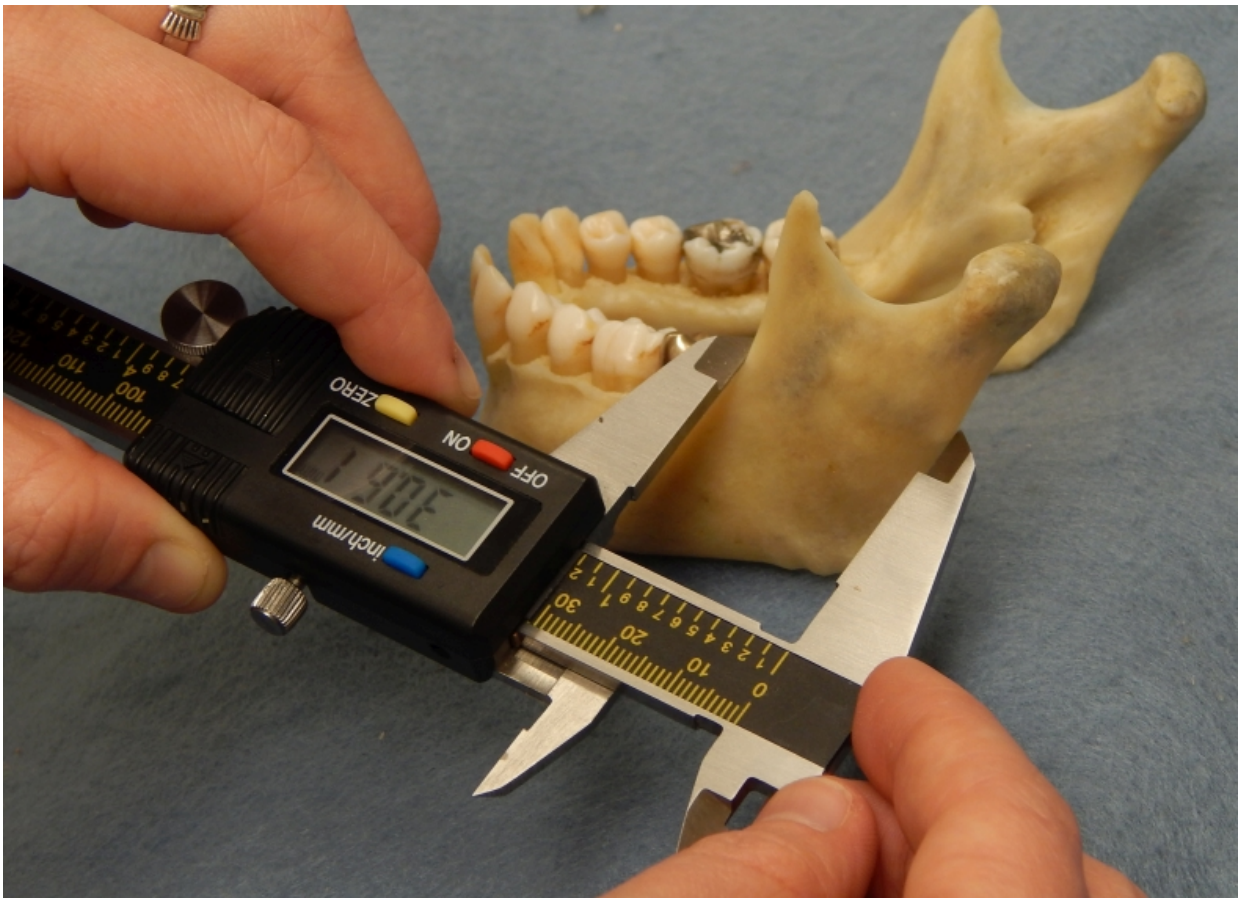
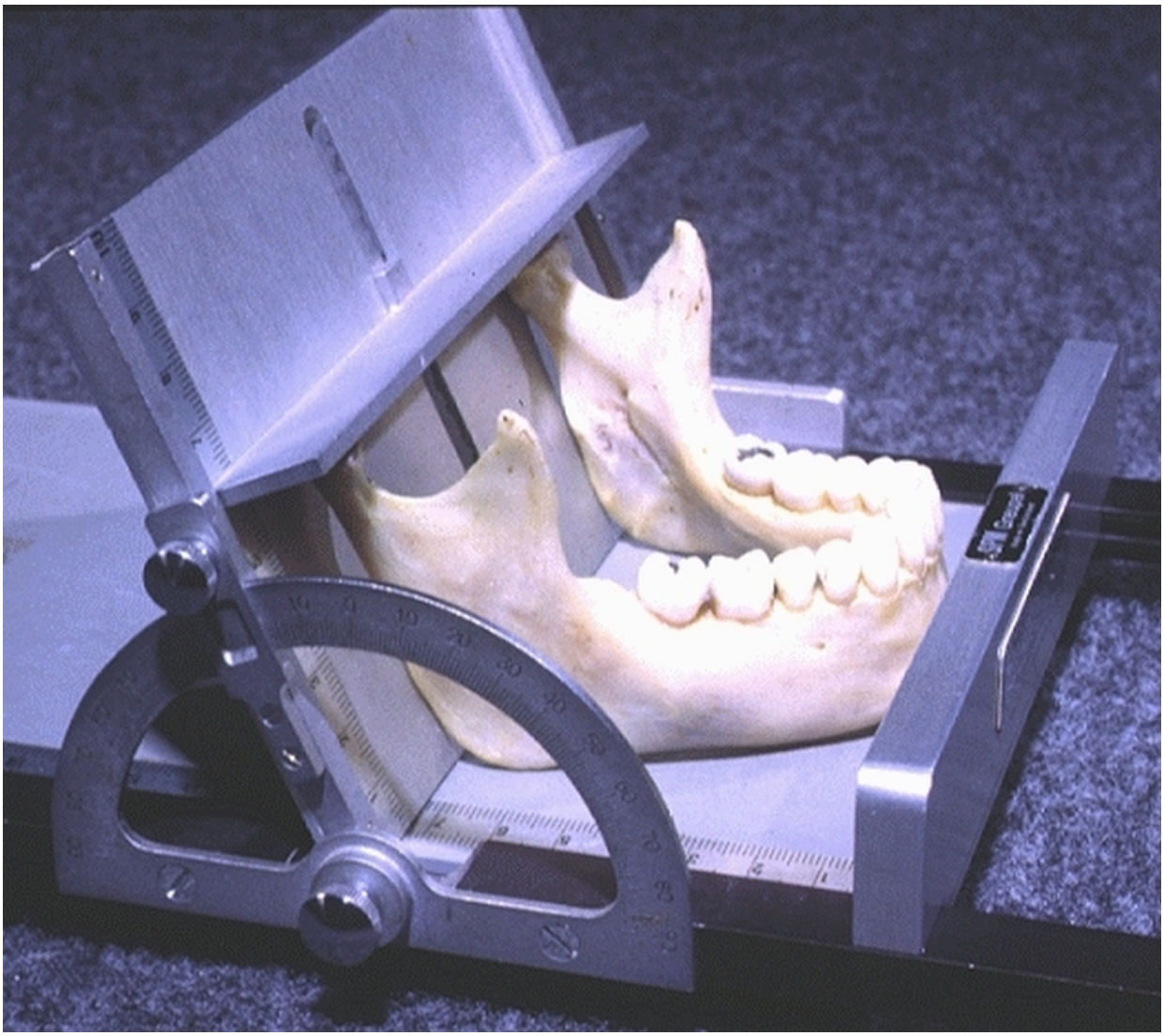
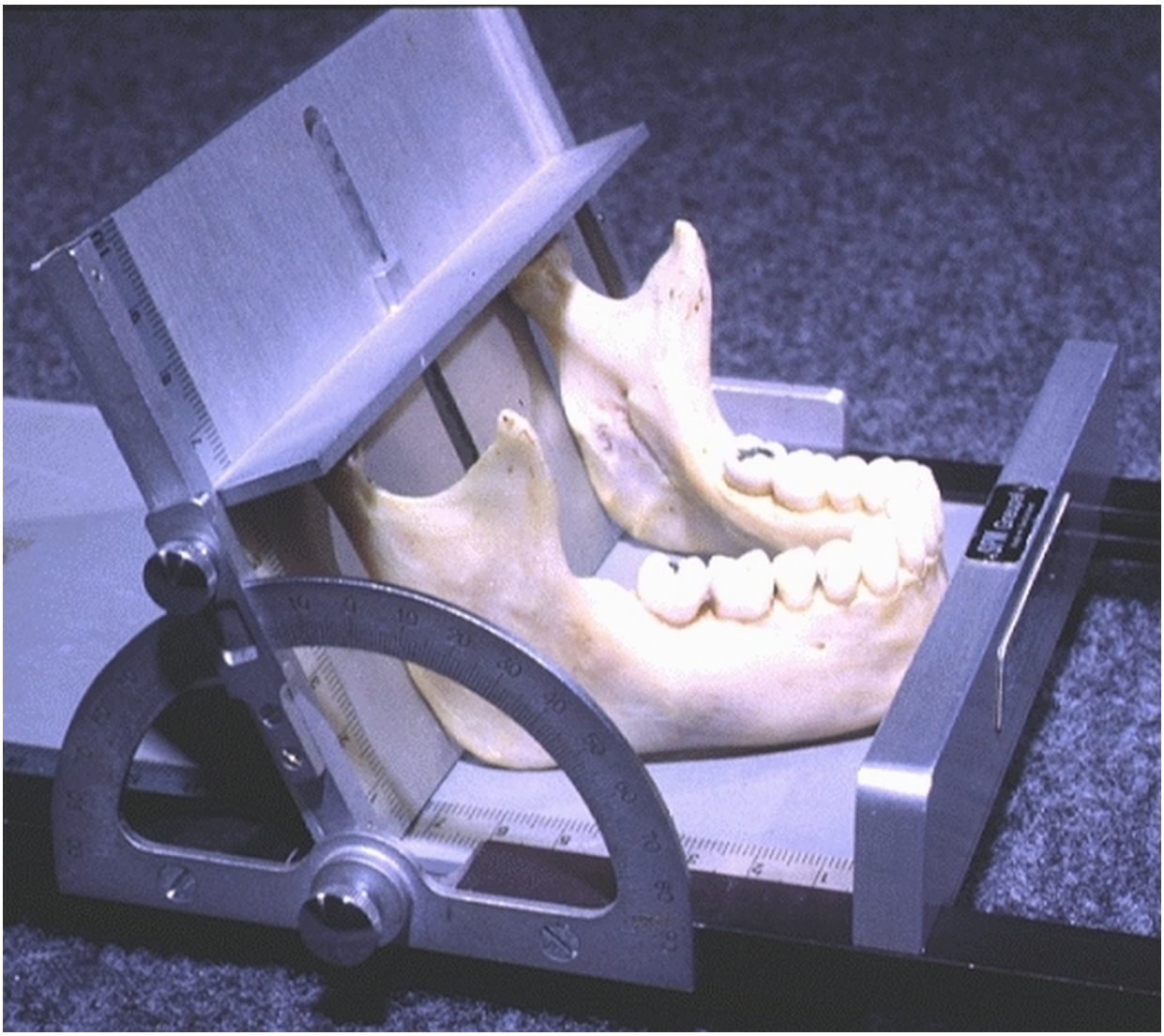
Minimum Ramus Breadth (WRB): The least breadth of the mandibular ramus measured more or less perpendicular to the posterior border of the ramus.



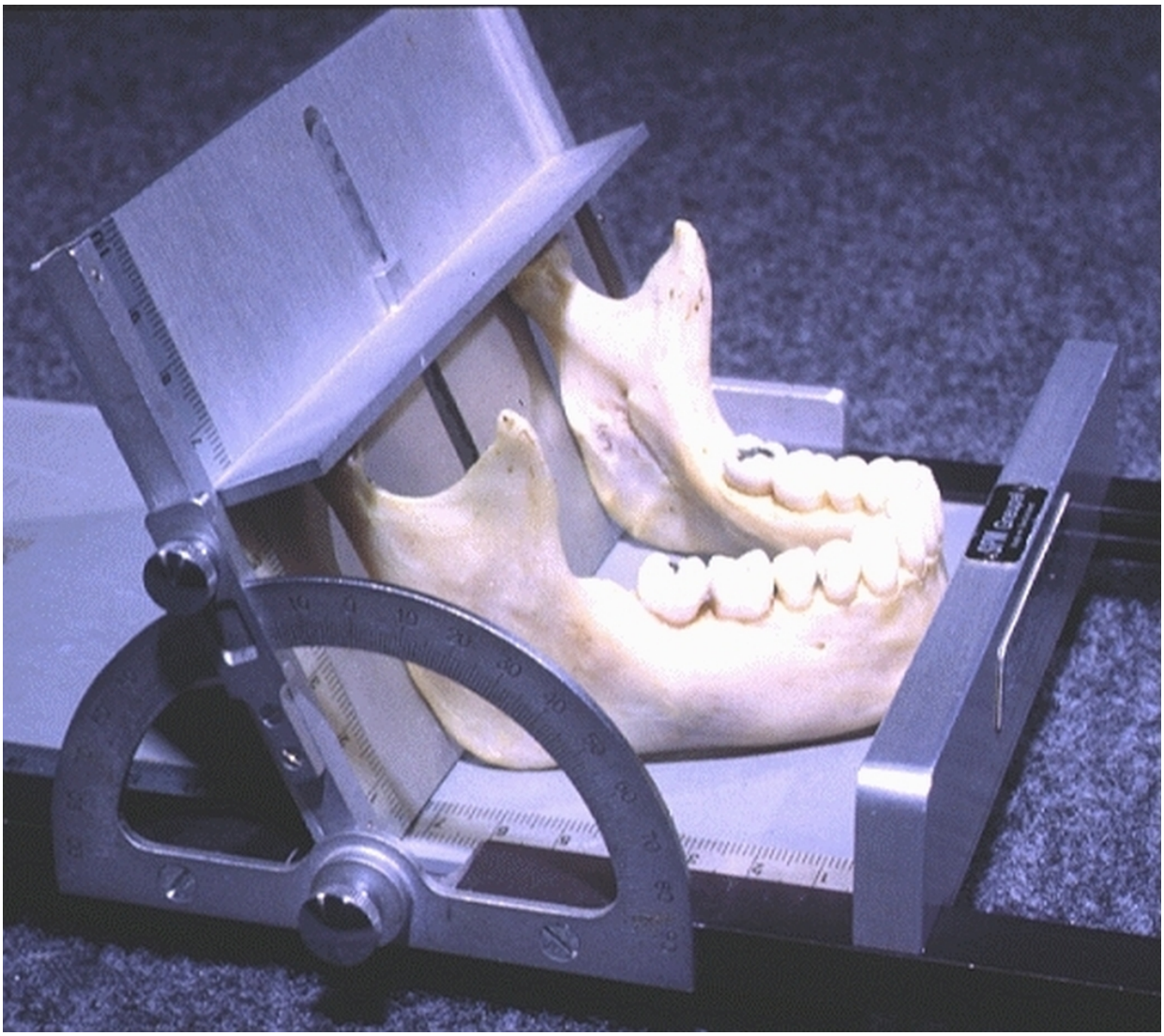
Mandibular Length (MLN): The distance of the anterior margin of the chin from a center point on a projected straight line placed along the posterior border of the two mandibular angles. Record only if a mandibulometer is used.



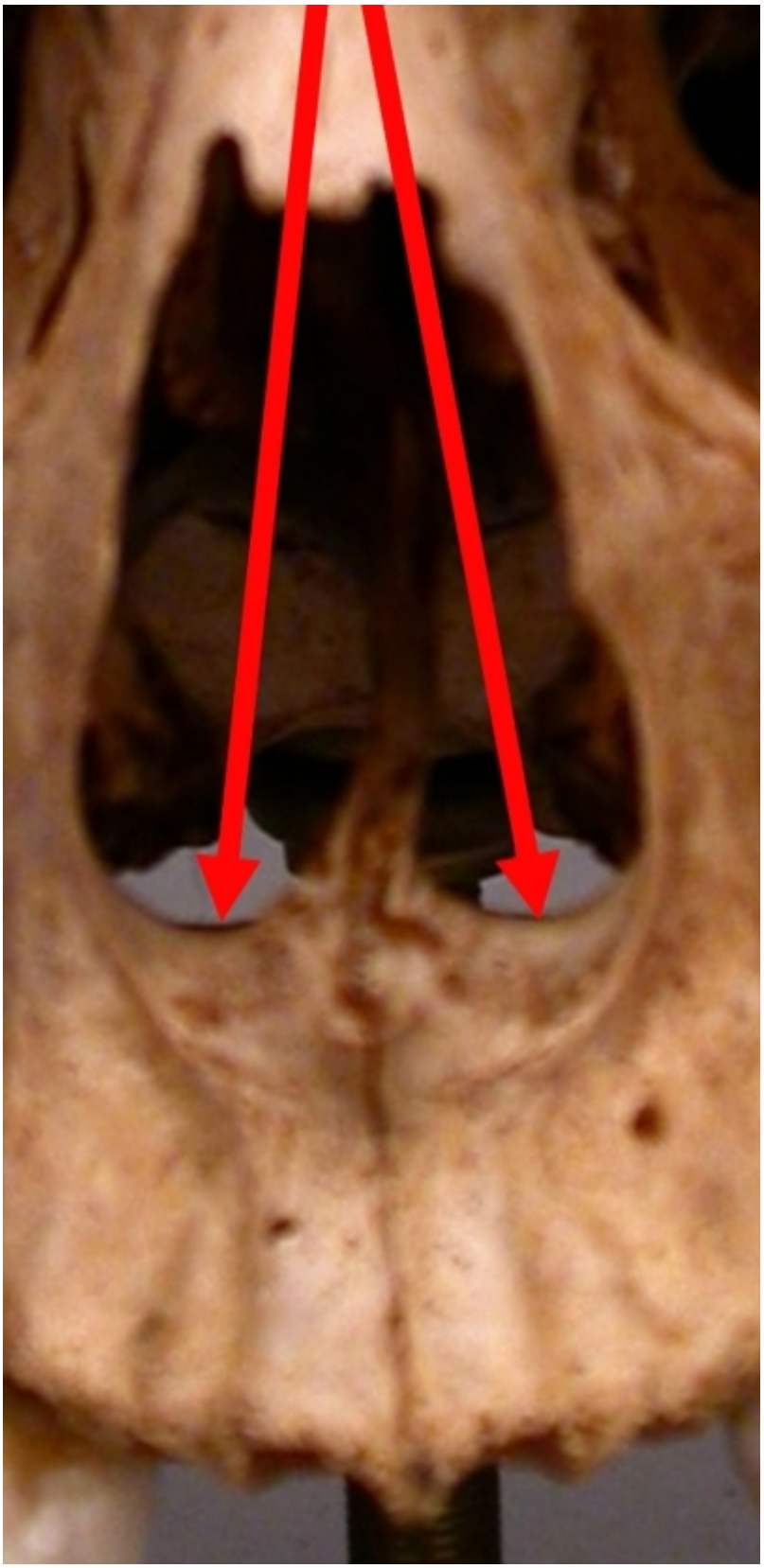
Maximum Ramus Height (XRH): The direct distance from the highest point on the mandibular condyle to Gonion. Record only if a mandibulometer is used.

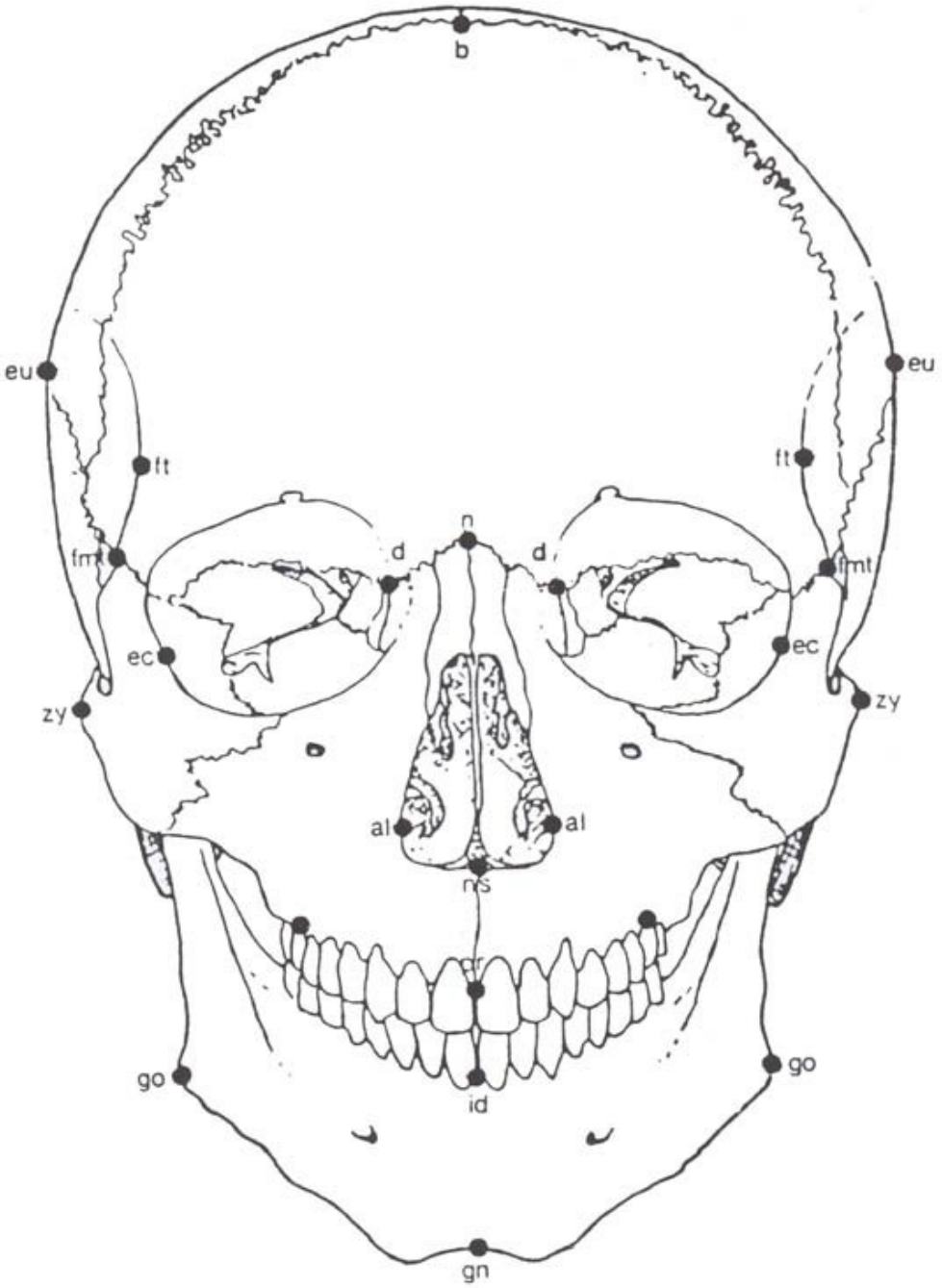


Mandibular Angle (MAN): The angle formed by inferior border of the corpus and the posterior border of the ramus. Record only if a mandibulometer is used.



Nasospinale (ns): The lowest point in the midsagittal plane on a line from the left and right inferior margins of the nasal aperture. In individuals with slight to moderate development of a nasal sill, this point is easily determined by connecting the lowest point on the inferior margin of the nasal aperture right and left of the nasal spine. Nasospinale is located wherever this line is intersected by the mid sagittal plane. **Nasospinale is not located at the tip of the nasal spine.** In an individual with nasal guttering, the points will be located more posteriorly, inside the nasal aperture. (Martin and Saller 1957:448).

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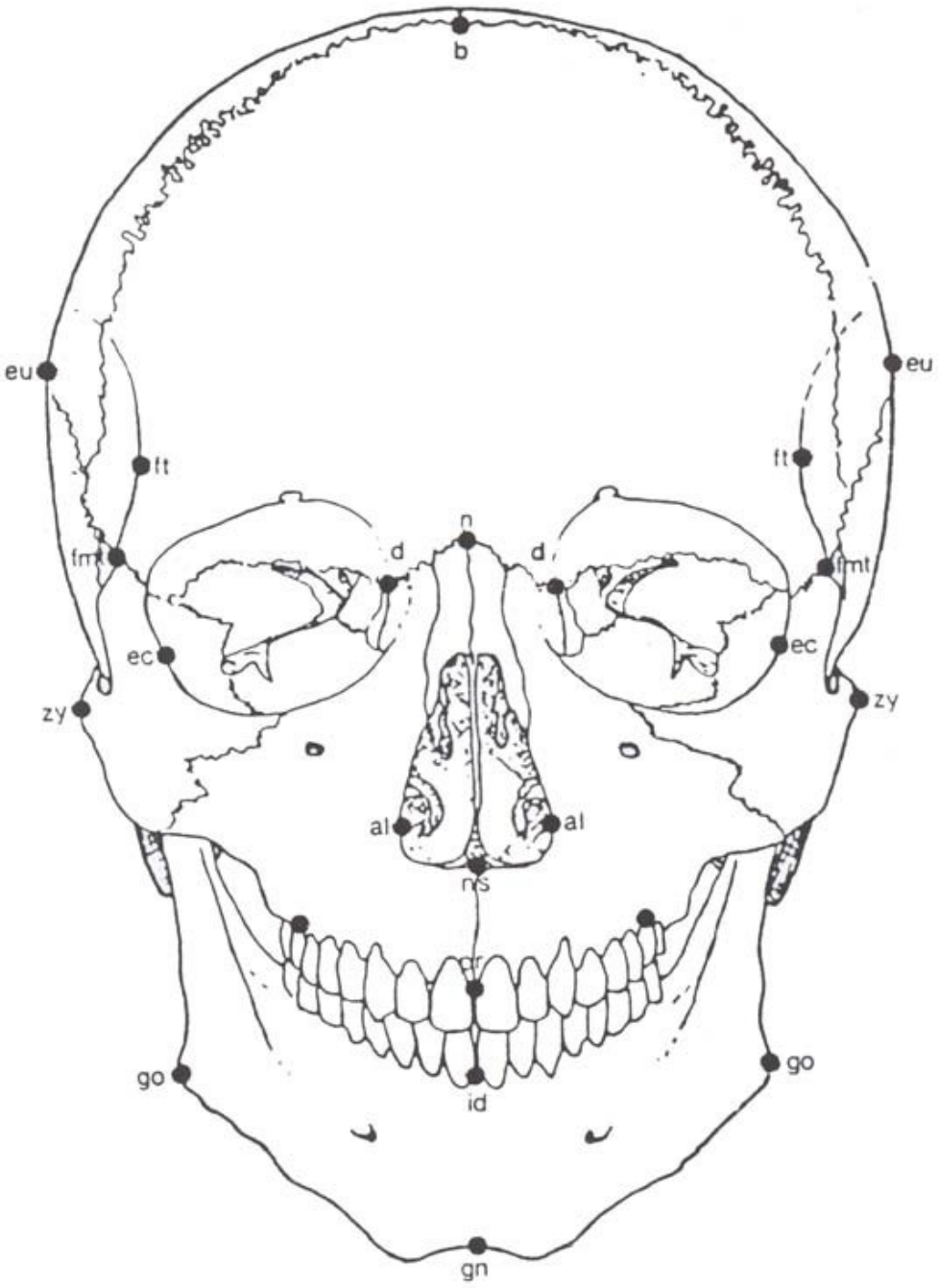
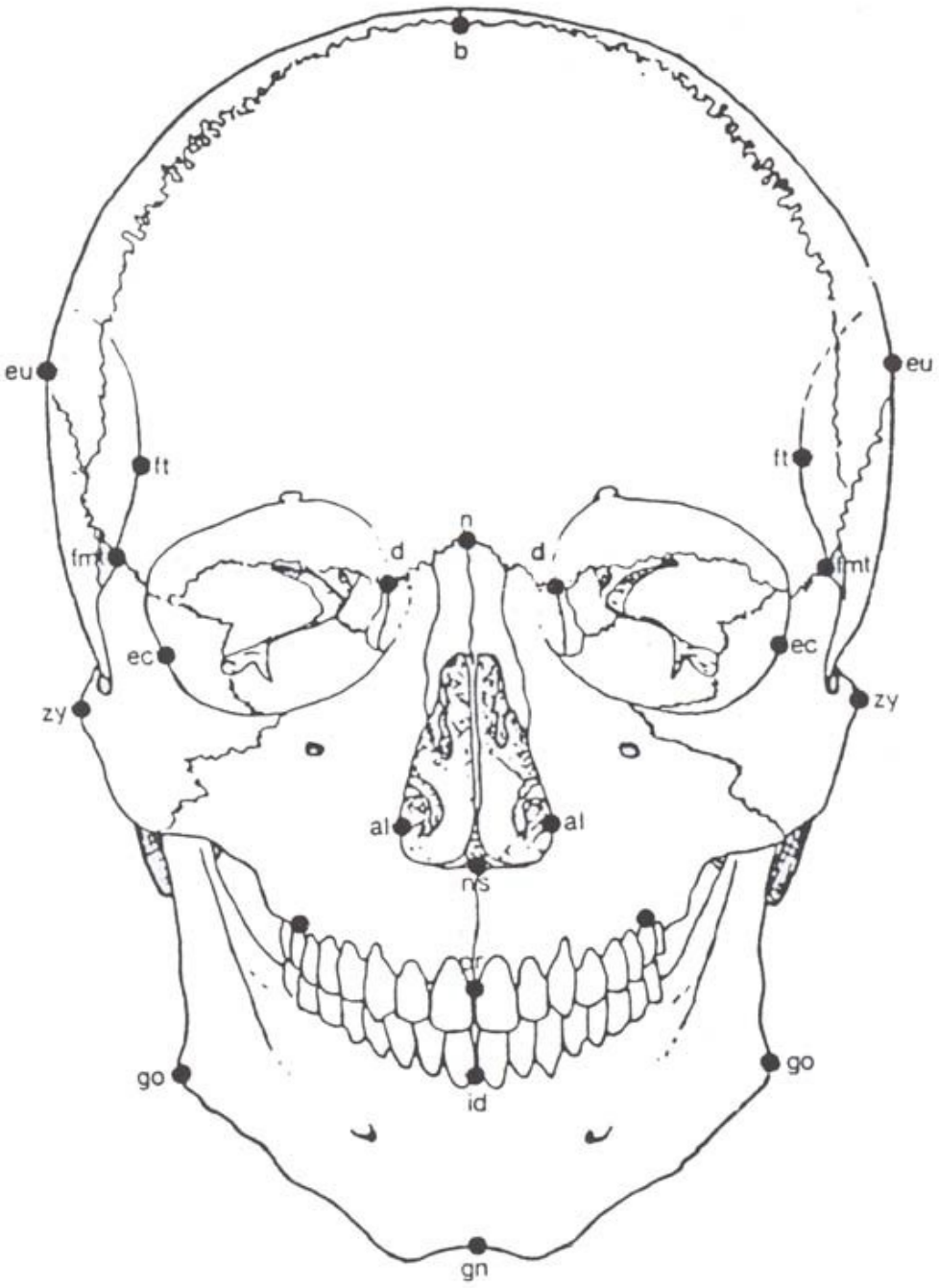
Zygion (zy): The most laterally positioned point on the zygomatic arches . The position of zygion is defined from the measurement of bizygomatic breadth (Martin and Saller 1957:450).



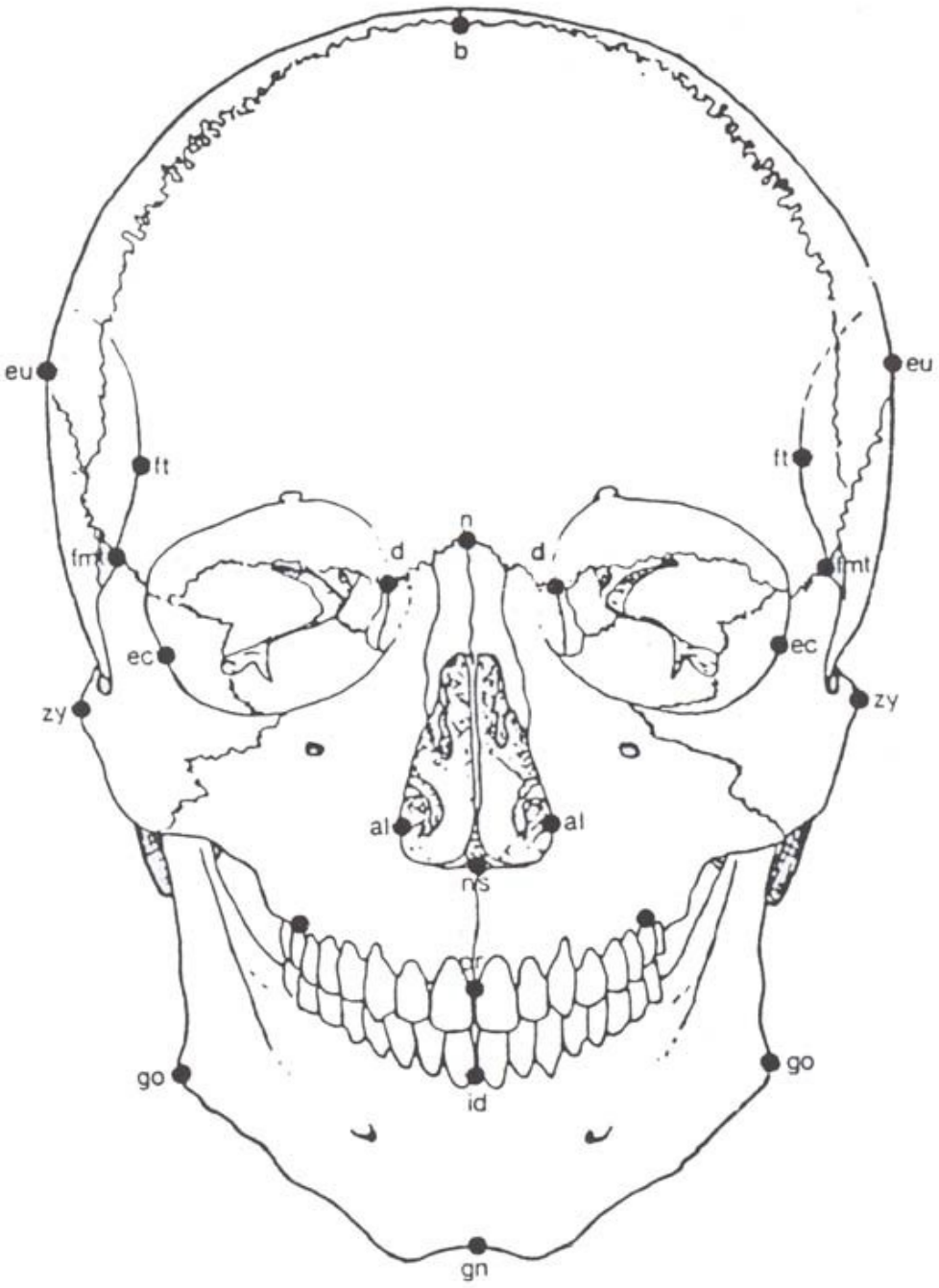
Nasion (n): The point of intersection of the Naso-Frontal suture and the mid sagittal plane. Nasion corresponds to the nasal root (Martin and Saller 1957:448).



Alveolon (alv): The point where the midline of the palate is intersected by a line connecting the posterior borders of the alveolar crests. This point is determined in practice as the point where the midsagittal plane intersects a a rubber band placed against the posterior margins of the alveolar processes of the maxilla (Martin and Saller 1957:451).

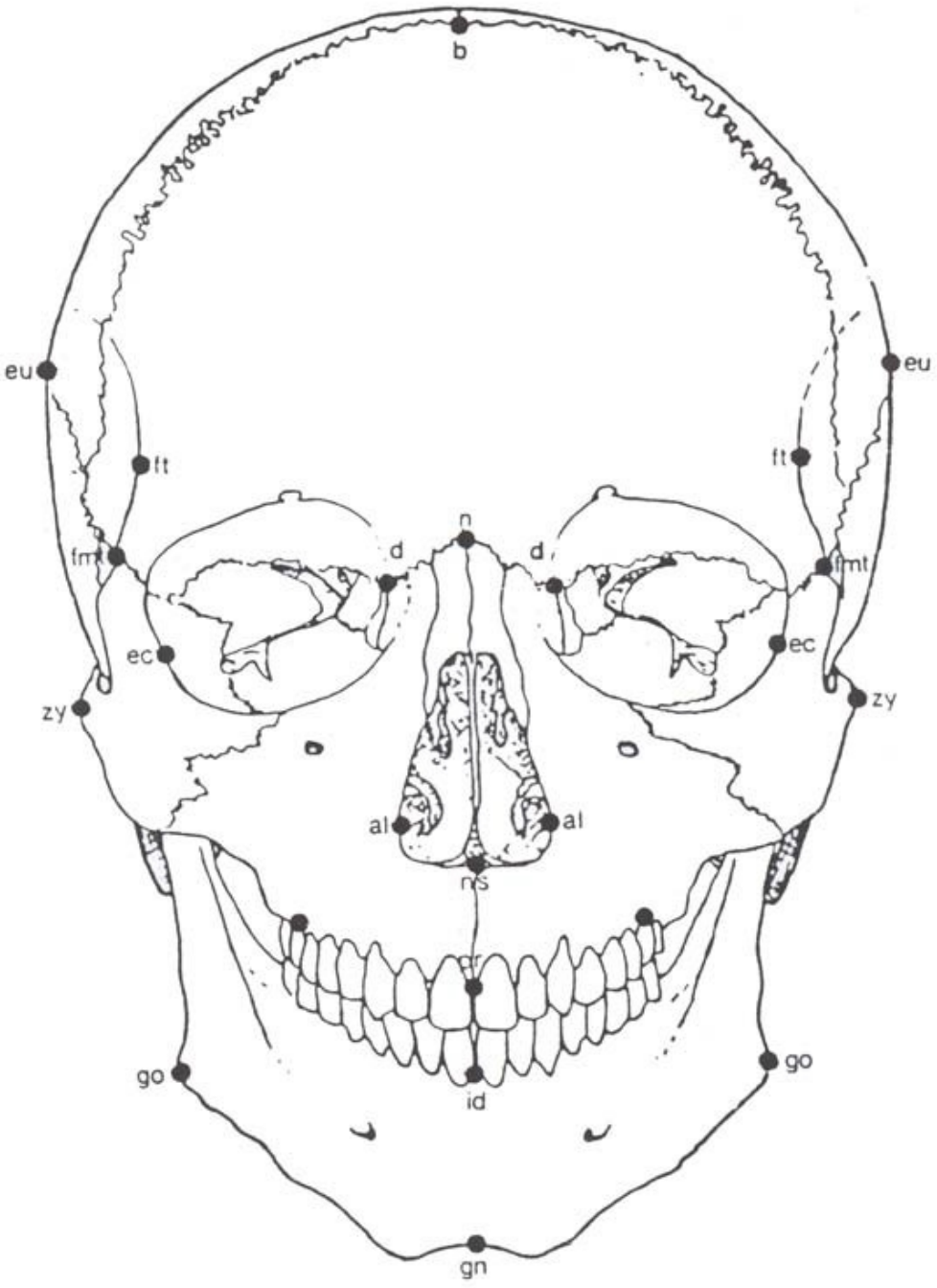
Opisthion (o): The point at which the mid sagittal plane intersects the posterior margin of the foramen magnum. Opisthion is located on the inner border of the posterior margin of the foramen magnum facing basion (Martin and Saller 1957:446).

Frontomalare temporale (fmt): The most laterally positioned point on the frontomalar suture (Martin and Saller 1957:451).



Zygomaxilare anterior (zym): The point where the zygomatic bone meets the maxilla inferiorly, at the level of the masseter attachment. (Howells 1973:170).

Infradentale (id): The point between the lower incisor teeth where the anterior margins of the alveolar processes are intersected by the mid sagittal plane . The point corresponds to the anterio-superior limit of the fetal symphyseal suture (Martin and Saller 1957:452).



Gnathion (gn): The lowest point on the inferior margin of the mandibular body in the midsagittal plane. Frequently, gnathion is not the most inferiorly located point of the mandible, as the more laterally placed elements of the mandible may be extending far more inferiorly. This is particularly the case in mandibles with broad and square chin development (Martin and Saller 1957:452).