

MaMD Analytical Tool Helpfile

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Research Collections

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Drs. Bruce Anderson and Jennifer Vollner – Pima County Office of the Medical Examiner, AZ
Drs. David Hunt and Christopher J. Dudar – National Museum of Natural History, Smithsonian Institution, Washington D.C.
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Research Contributors

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INTRODUCTION

Ancestry estimation is an integral part of establishing a biological profile on unknown human skeletal remains. Ancestry, or geographic origin, can be estimated through a variety of methods, including macromorphoscopic trait analysis (Dunn et al., 2020; Hefner, 2009; Plemons and Hefner, 2016). Macromorphoscopic traits are quasicontinuous morphological traits of the cranium, which Brues (1958) describes as reflective of soft-tissue differences in the living. Macromorphoscopic traits are divided into five classes of observations: 1) assessing bone shape; 2) bony feature morphology; 3) suture shape; 4) presence or absence of a feature; and lastly, 5) feature prominence or protrusion (Hefner, 2009).

Traditionally, these traits were included within trait lists (Rhine, 1990) in which ancestry was assigned to a cranium through ad-hoc assessment and comparison to an arbitrary type specimen chosen to reflect certain ancestral groups. Standardization of the traits, as well as the implementation of statistical approaches to macromorphoscopic trait data (Hefner, 2009; Hefner and Linde, 2018; Hefner and Ousley, 2014) allows for accurate assessment against all human variation captured within a given population. Further, this approach allows for consistency and objectivity in assessing macromorphoscopic traits across different users.

To enhance Hefner's (2009) method, the Macromorphoscopic data collection software was created to allow the user to assess and collect macromorphoscopic data from various specimens (<https://macromorphoscopic.com/mms-software/>) (User Guide for MMS v1.61, 2018). This system was designed to reduce observer error and increase objectivity through standardized descriptions of traits and scoring procedures. Further, this data allowed for the creation of the Macromorphoscopic Databank (MaMD). The MaMD contains a large dataset ($n \sim 7,397$) of modern individuals from within and outside of the United States in order to complement shifts in population demographics within the United States (Hefner, 2018). The MaMD allows for the creation of larger and more appropriate reference samples, as an effort to abandon the trait list approach.

The latest step in this process has been the creation of the MaMD Analytical Tool. This software was created using a subset of modern data from the MaMD and is designed to aid with future research into ancestry estimation and macromorphoscopic trait variation across populations. With the public release of the software, users will be able to adopt this method of analysis for forensic casework applications. Currently, this software allows users to classify an unknown individual from one of seven reference groups (Dunn et al., 2020; Hefner and Byrnes, 2019).

This HelpFile has been adapted from the User Guide for MMS v1.61 (2018) and includes some of the same trait images and descriptions. New information includes specific instructions on how to operate the MaMD Analytical Tool. Users should refer to this HelpFile for application questions and for proper instructions on trait scoring for the ten traits included in the MaMD Analytical Tool.

MaMD ANALYTICAL TOOL

Setting up MaMD Analytical

After users have downloaded the desktop application for MaMD Analytical (available at: <https://macromorphoscopictraitanalysis.shinyapps.io/MaMDAnalytical/>), users can open the program locally on their computer.

Upon opening MaMD Analytical, a “Welcome to MaMD Analytical” page will appear. Users must click the “Get Started” button at the bottom of the application screen, which will allow the program to check the user’s computer for R and several required packages. Users do not have to download R and the associated packages personally, as the MaMD Analytical tool will do so for them. Note, this process may take several minutes to complete.

After the tool has finished processing, the MaMD Analytical Tool will be ready for use. The application will automatically check for updates when opened.

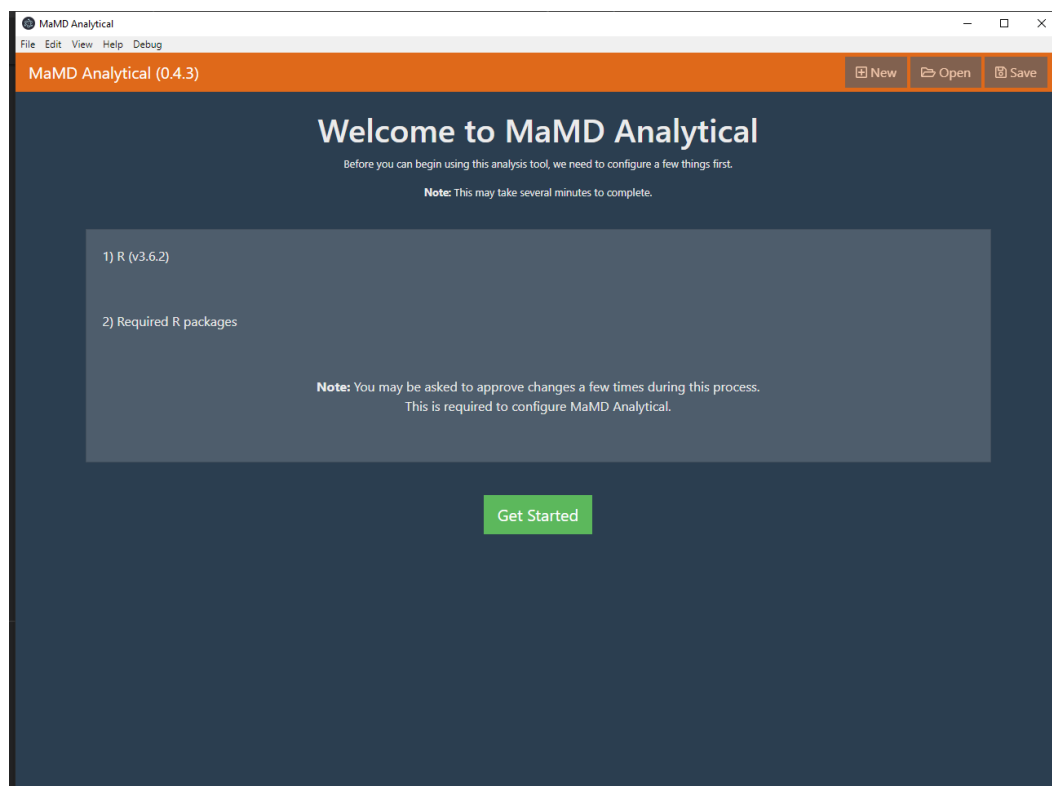


Figure 1. 1. Welcome to MaMD Analytical page in app with “Get Started” button.

Entering a new case.

To enter a new case into MaMD Analytical, click on the “Case Info” tab. First, enter the case number assigned to the specimen (or individual ID for a collection) in the “Case #” box. This box should not be left blank. While MaMD Analytical does not retain any individualizing information from user case analysis, this identifier information is included on saved .mamd files and PDFs of analysis results for user records. Next, enter the observation date. Finally, include analyst name/initials in the “Analyst” box. Once all necessary information is entered into the appropriate text boxes, press the “Analysis” tab to transition to the application screen where users can select MMS trait scores.

Note: clicking the “New” button at the top right of the screen will automatically bring you to the Analysis tab. However, this will erase all information previously entered into the “Case Info” and “Analysis” tabs. The “New” button should only be clicked after analysis is complete and the user plans to enter a new case into the MaMD Analytical Tool.

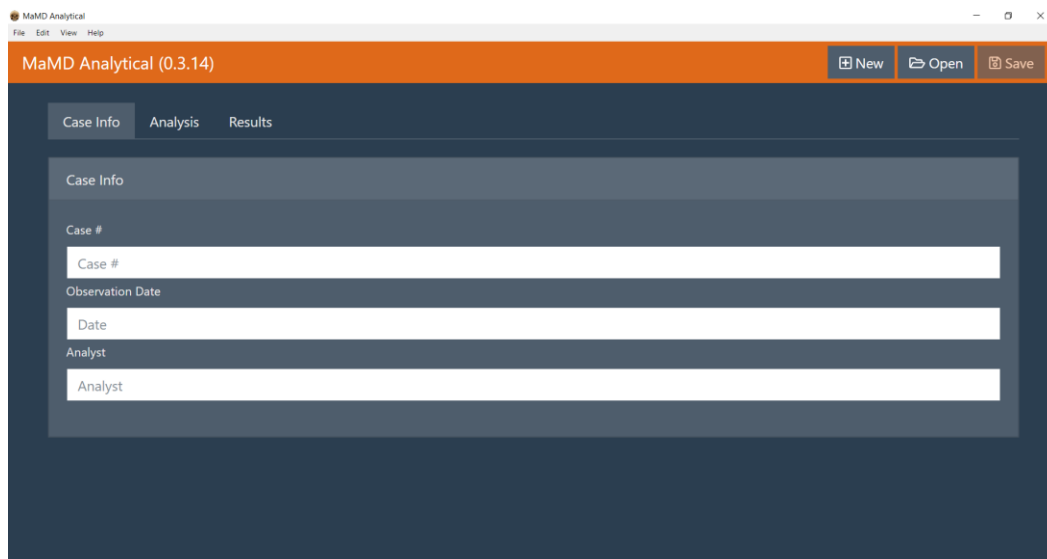
The image shows a screenshot of the MaMD Analytical software interface. At the top, there is a title bar with the text "MaMD Analytical" and a menu bar with "File", "Edit", "View", and "Help". Below the menu bar is an orange header bar with the text "MaMD Analytical (0.3.14)" and three buttons: "New", "Open", and "Save". The main content area has three tabs: "Case Info", "Analysis", and "Results". The "Case Info" tab is selected and highlighted. It contains a form with four input fields: "Case #", "Observation Date", "Analyst", and "Analyst". Each field has a label above it and a text input box below it. The "Case #", "Observation Date", and "Analyst" fields are currently empty, while the "Analyst" field at the bottom contains the text "Analyst".

Figure 2. MaMD Analytical Case Info tab.

Analysis

The analysis tab is composed of a user friendly interface where users can score up to 10 macromorphoscopic traits guided by depictions of each trait expression. Traits are listed vertically in alphabetical order with their associated abbreviation (e.g., ANS) and trait expressions are provided horizontally in order of expression (e.g., 1-3). To select a score for each trait, click the image associated with the correct score/level of expression; the program indicates that a trait expression has been selected by highlighting the image in orange (Figure 3.1). Users are not locked into the first image they click and are able to change their selected scores prior to analysis if necessary. Traits do not have to be selected in alphabetical order, and to access all traits, users must simply scroll down. Traits can also be selected via keyboard shortcuts:

- Tab: progresses through traits from left to right
- Shift + tab: progresses through traits from right to left
- Enter: selects trait expression

Not all traits are required for analysis and if a trait in question is unobservable, it is best practice to not select a score for that trait. Once all traits scores are selected, click the “Run Analysis” button at the bottom of the screen (Figure 3.2). The application will automatically redirect to the “Results” tab.

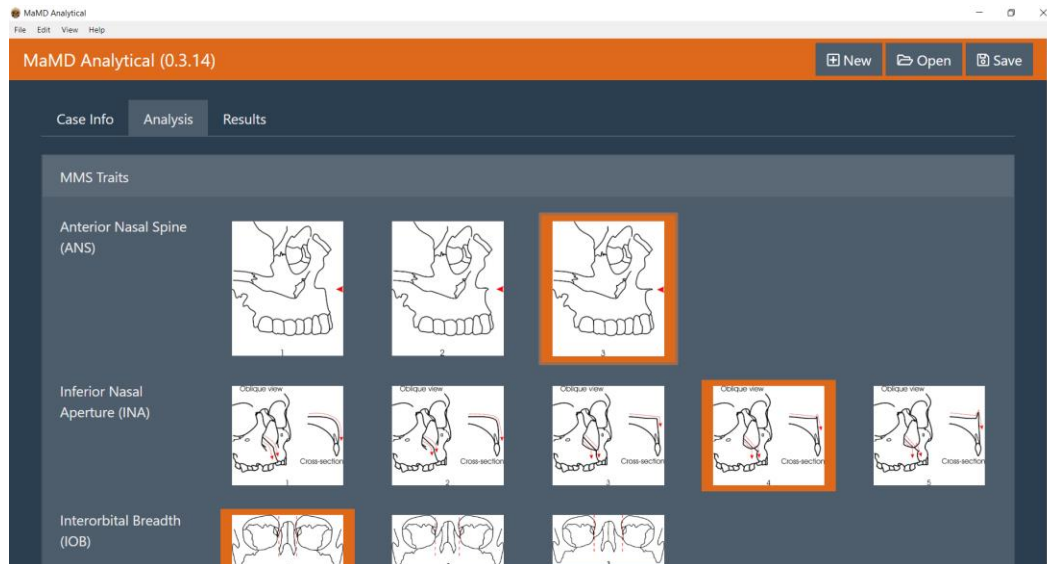


Figure 3.1. Sample image of scores selected in MaMD Analytical Analysis tab.

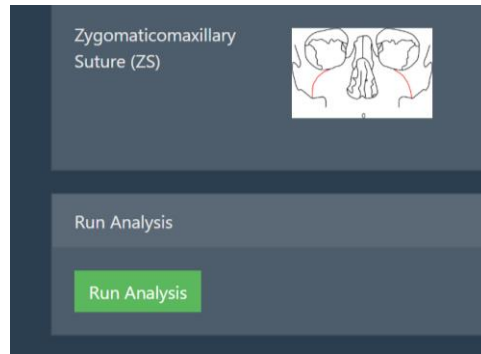


Figure 3.2. MaMD Analytical Run Analysis button.

Results

The “Results” tab provides a print out of summary statistics. The MaMD Analytical Tool uses an artificial neural network (aNN) to classify an unknown cranium into one of seven reference groups (Figure 4.1).

The summary statistics listed include the predicted ancestry and its associated posterior probability, accuracy of the model, the confidence interval, and the sensitivity and specificity of the analysis.

Furthermore, a table with all selected trait scores is provided, along with a graph of posterior probabilities for each of the reference groups used in the analysis. NA is listed by default when no trait score is selected. Finally, a classification matrix is provided, which includes the correct classifications for each reference group.

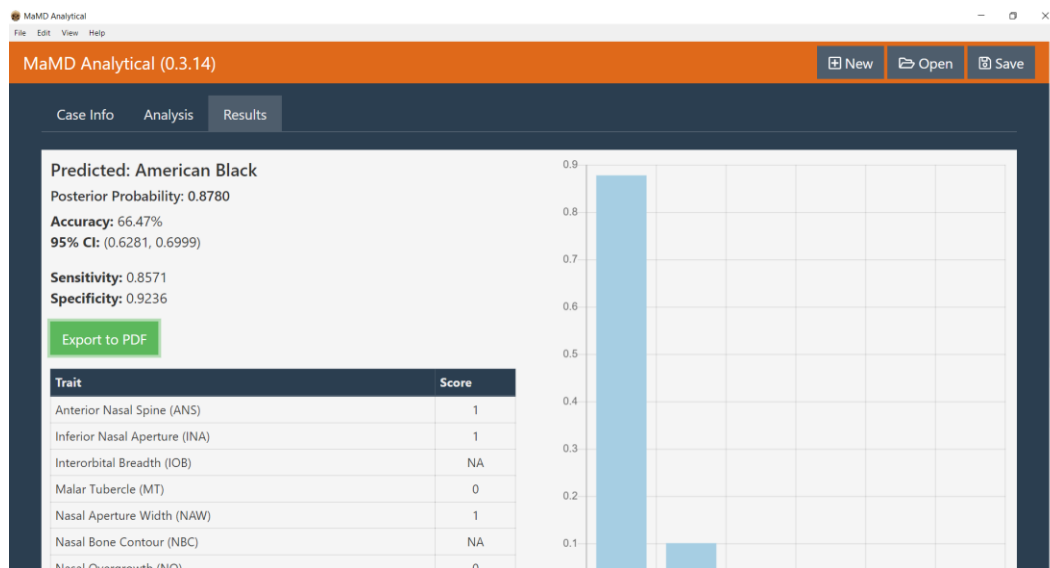


Figure 4.1. Sample printout on MaMD Analytical Results tab.

To keep a copy of this printout, click the “Export to PDF” button. A prompt will appear to choose a file name and location for the exported PDF file.

MaMD Analysis v0.3.14

Case Info

Case #:
 Observation Date:
 Analyst:
 Exported On: 2020-1-28 11:16:31

Predicted: American Black

Posterior Probability: 0.8780

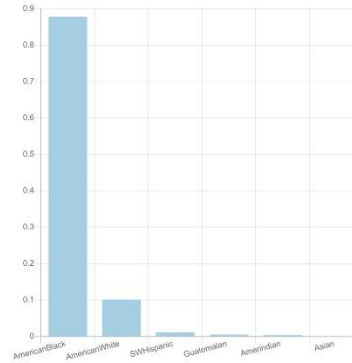
Accuracy: 66.47%

95% CI: (0.6281, 0.6999)

Sensitivity: 0.8571

Specificity: 0.9236

Trait	Score
Anterior Nasal Spine (ANS)	1
Inferior Nasal Aperture (INA)	1
Interorbital Breadth (IOB)	NA
Malar Tubercle (MT)	0
Nasal Aperture Width (NAW)	1
Nasal Bone Contour (NBC)	NA
Nasal Overgrowth (NO)	0
Postbregmatic Depression (PBD)	1
Posterior Zygomatic Tubercle (PZT)	1
Zygomaticomaxillary Suture (ZS)	NA



	American Black	American White	American Indian	Asian	Guatemalan	Southwest Hispanic
American Black	108	10	2	18	8	5
American White	4	58	3	7	7	15
American Indian	4	5	24	18	8	9
Asian	3	0	13	186	7	5
Guatemalan	4	8	4	24	34	16
Southwest Hispanic	3	9	1	7	4	48

Figure 4.2. Sample image of exported PDF from MaMD Analytical Tool.

Once analysis is complete, a new case can be processed through the MaMD Analytical Tool by selecting the “New” button in the top right corner of the application screen (Figure 4.1). This will automatically erase all previously entered data (case info and scores), as well as analysis results. Prior results will no longer be accessible.

Saving Case Files

Cases can be saved locally using the “Save” button located at the top right corner of the application screen (Figure 5.1). Upon clicking this button, a prompt will appear for choosing a file name and destination for the case file. These files are automatically saved as MaMD Analytical files (.mamd), which allow files to be reopened directly in the MaMD Analytical application.

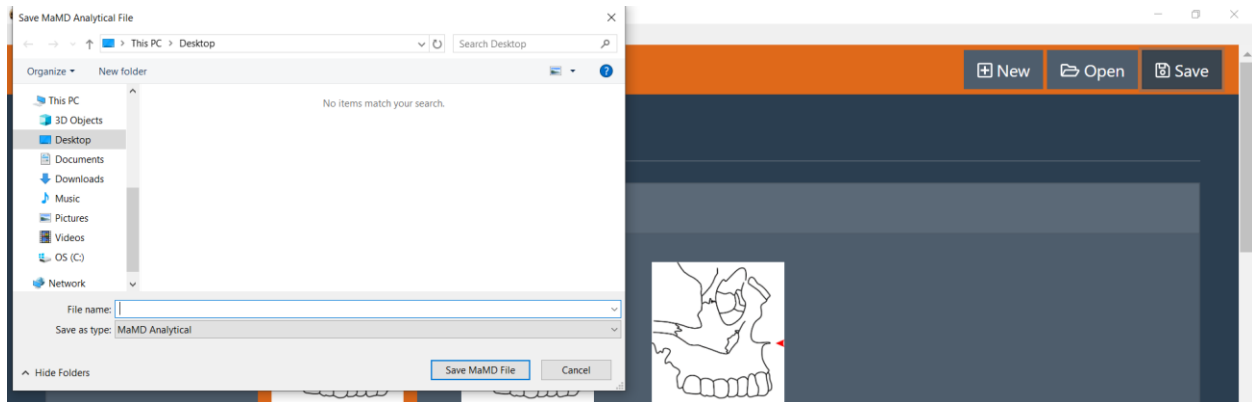


Figure 5.1. MaMD Analytical Save function.

To open saved files, open the MaMD Analytical application and then click the “Open” button located at the top right corner of the application screen (Figure 5.2). A separate window will appear to choose which file to open into the MaMD Analytical program. This save function allows users to always keep a record of cases analyzed through the MaMD Analytical Tool.

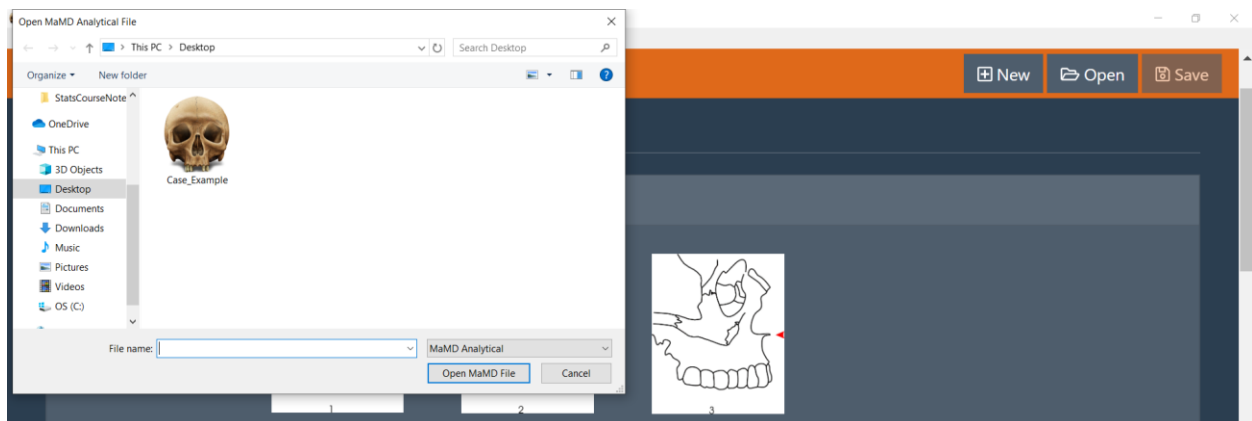


Figure 5.2. MaMD Analytical Open function.

MACROMORPHOSCOPIC TRAITS

General Macromorphoscopic Trait Locations

All traits are pictured in the line drawings within the MaMD Analytical Tool, but are also provided and described in detail below. Figures 6.1 and 6.2 depicts anterior and lateral views with all traits and their location on the cranium (some traits are shown, but not used via the MaMD Analytical Tool).

Where to Make an Observation

Bilateral traits should be observed and recorded from the left side of the cranium with the exceptions of PZT and MT. These two exceptions should be recorded for greatest expression of the trait between the two sides. If remaining traits are unobservable on the left portion of the cranium due to postmortem damage or pathology, the right side should be scored. When neither side can be observed, no score should be entered in the MaMD Analytical Tool for that trait. Trait scores should only be selected for observable traits.

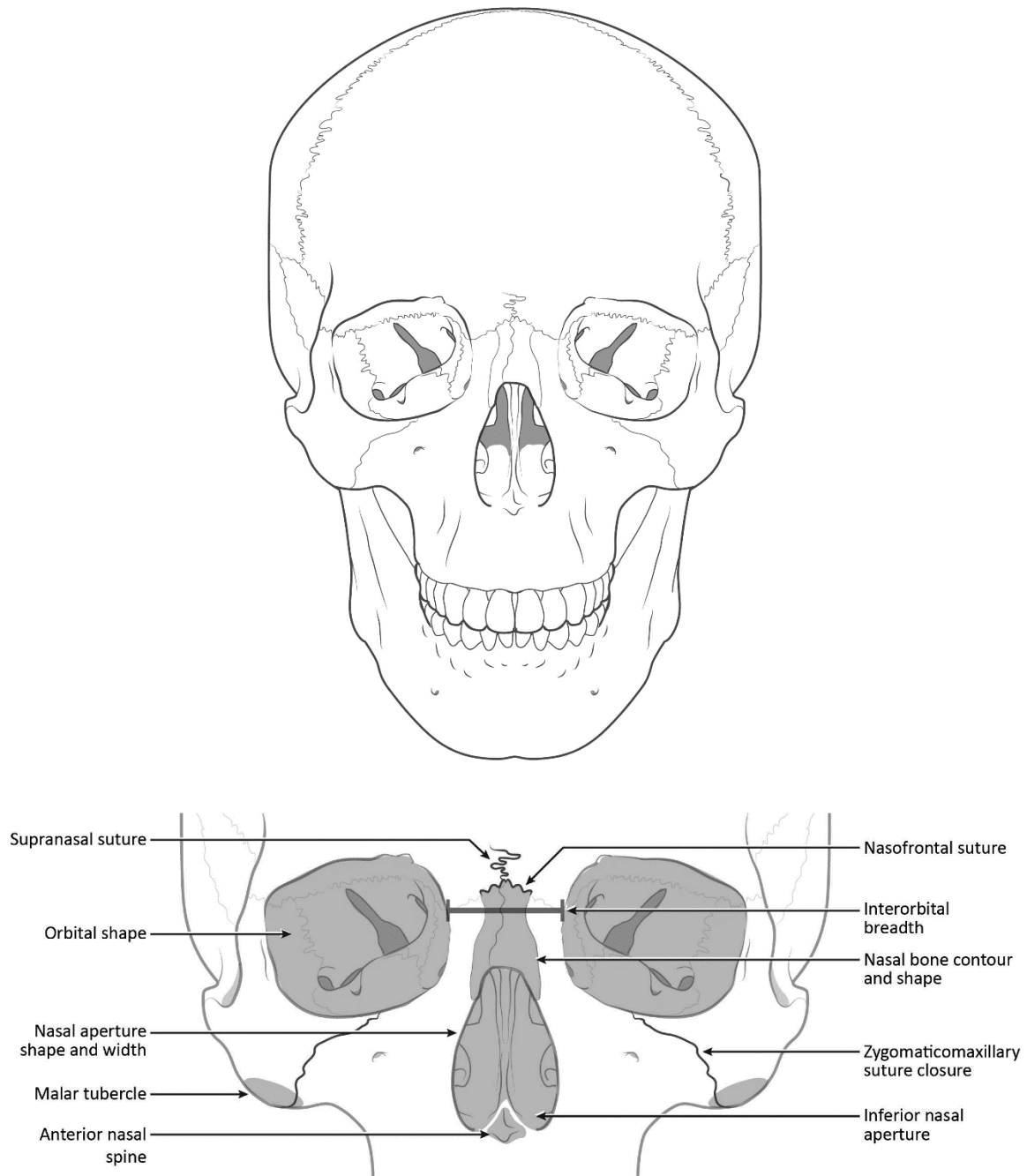


Figure 6.1. Anterior views of a cranium to demonstrate approximate location of macromorphoscopic traits (image taken from Plemons and Hefner, 2016).

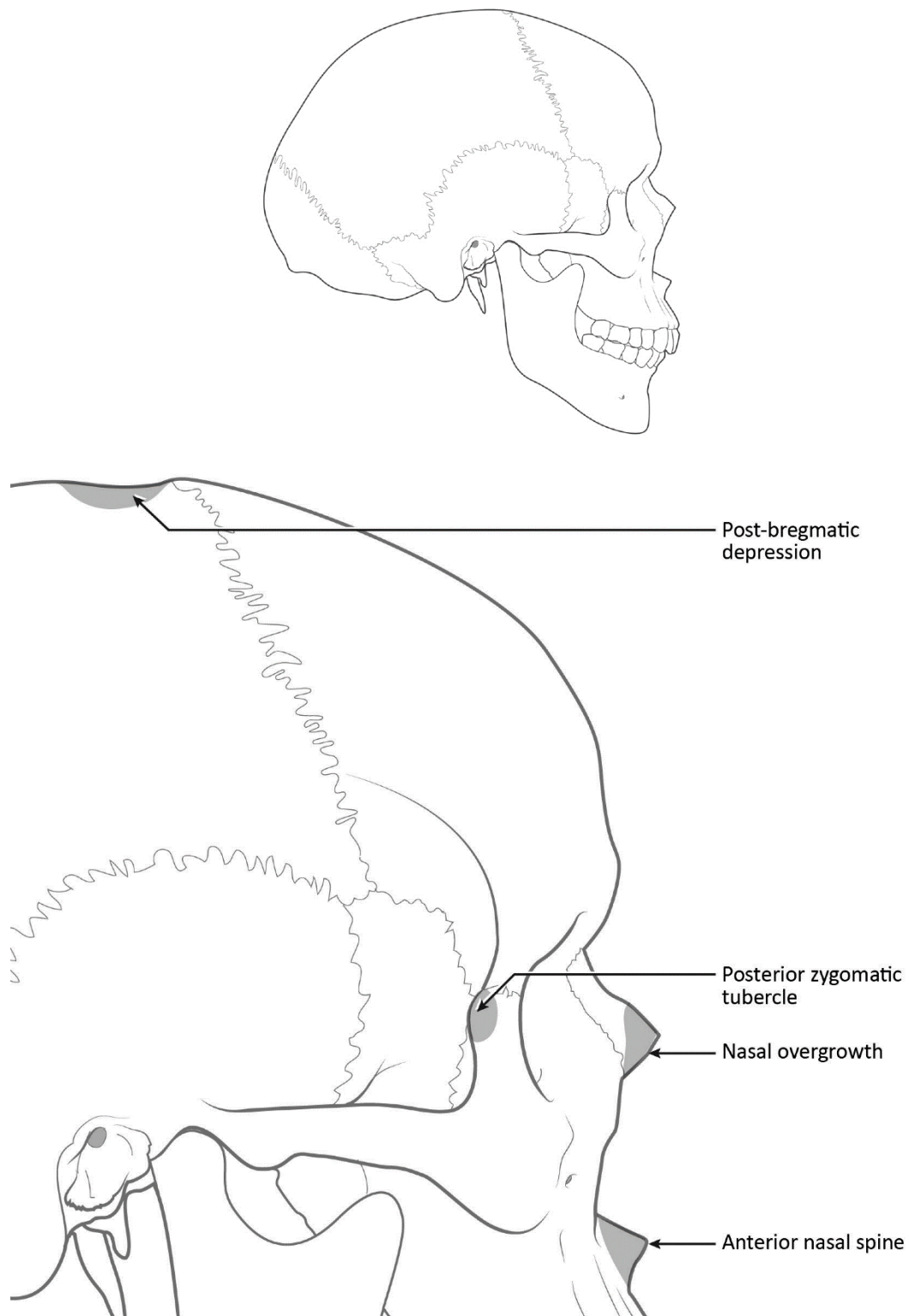


Figure 6.2. Lateral views of a cranium to demonstrate approximate location of macromorphoscopic traits (image taken from Plemons and Hefner, 2016).

Macromorphoscopic Traits and Definitions

Only the ten traits included in the MaMD Analytical Tool are provided below. The following definitions are taken from the User Guide for MMS v1.61 (2018).

Anterior Nasal Spine (ANS)

Anterior nasal spine is a small bony feature located at the inferior border of the nasal aperture. This trait exhibits the following three character states: slight, intermediate, and marked, with corresponding scores of 1, 2, and 3. Photographs of ANS for each character state and corresponding score are shown in Figure 7.1.

To score this trait, the cranium should be viewed laterally to assess the degree of projection of ANS.

1 = Slight; indicates a minimal to no projection of the anterior nasal spine beyond the inferior nasal aperture.

2 = Intermediate; indicates a moderate projection of the anterior nasal spine beyond the inferior nasal aperture.

3 = Marked; indicates a pronounced projection of the spine beyond the inferior nasal aperture.

****Note:** Do not score if the individual is edentulous.

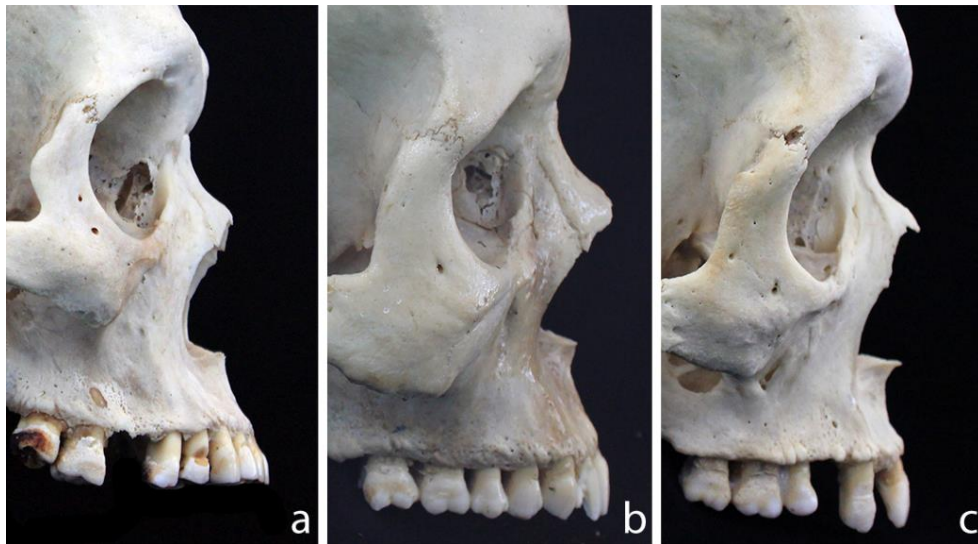


Figure 7.1. Various character states of ANS. Scores: a) 1 = slight; b) 2 = intermediate; c) 3 = marked (image taken from User Guide for MMS v1.61, 2018).

Inferior Nasal Aperture (INA)

Inferior nasal aperture assesses the shape of the inferior border of the nasal aperture. Specifically, this trait aims to assess the transition from the nasal floor to the vertical portion of the maxilla. The left portion of the inferior nasal aperture should be assessed.

This trait exhibits five character states scored as 1, 2, 3, 4, and 5, and ranges in morphology from a gentle slope with no delineation of the inferior border (1) to a sharp, pronounced vertical ridge, commonly referred to as a nasal sill (5). Photographs of INA for each character state and corresponding score are shown in Figure 7.2.

1 = A score of 1 is given to an INA that exhibits a sloping of the nasal floor which starts inside of the nasal cavity and terminates on the vertical surface of the maxilla. This gradual slope is a smooth transition between the two anatomical areas of bone.

2 = With this score, INA again exhibits a slope from the floor of the nasal cavity to the vertical surface of the maxilla. However, to differentiate from the previous state, the slope begins more anteriorly in the nasal aperture and exhibits more angulation at the opening of the nasal aperture.

3 = This state exhibits a steep transition from the nasal floor to the vertical maxilla. There is no slope, however there is no intervening projection or sill. This morphology closely resembles a right angle, although a more blunted form may be present.

4 = A score of 4 is assigned to a character state that shows any superior incline of the anterior nasal floor. This includes leads to the creation of a weak ridge of bone that crosses the anterior nasal floor perpendicularly, resulting in a partial nasal sill.

5 = This score is given to a pronounced ridge, or nasal sill, that obstructs the nasal floor to maxilla transition.

****Note:** When scoring INA, ignore subnasal grooves in the nasal floor. These grooves are indentations made by vessels in the area and are not reflective of the start of the nasal floor (Figure 7.3).

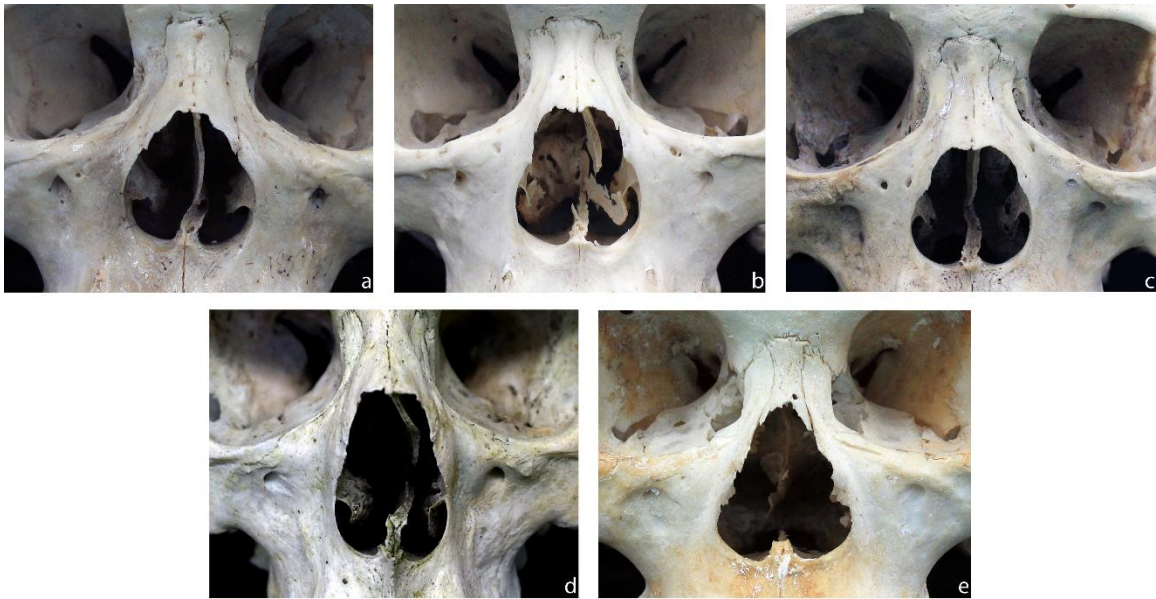


Figure 7.2. Character states of INA. Scores: a) 1 = deep, posterior sloping; b) 2 = slight, anterior sloping; c) 3 = no sloping or sill; d) 4 = weak ridge; e) 5 = pronounced ridge (image taken from User Guide for MMS v1.61, 2018).



Figure 7.3. Example of subnasal grooves, particularly on the left portion of the nasal floor (image taken from User Guide for MMS v.1.61, 2018).

Interorbital Breadth (IOB)

Interorbital breadth assesses the space between both orbits relative to the facial skeleton. The trait is assessed by using a ratio of IOB to the overall facial breadth. IOB is essentially visually observing the space between two cranial landmarks at left and right dacryon. This trait is scored using three character states (narrow, intermediate, and broad) translated numerically as 1, 2, and 3. Figure 7.4 illustrates the three character states and associated scores.

1 = A narrow IOB or 1:5 ratio of the interorbital space relative to the facial skeleton.

2 = A medium IOB or 1:4 ratio of the interorbital space relative to the facial skeleton.

3 = A broad IOB or 1:3 ratio of the interorbital space relative to the facial skeleton.



Figure 7.4. Character states of IOB. Scores: a) 1 = narrow; b) 2 = medium; c) 3 = broad (image taken from User Guide for MMS v1.61, 2018).

Malar Tubercle (MT)

The malar tubercle is defined as a caudally protruding tubercle on the inferior margin of maxilla and zygomatic bones. This feature is commonly located at the inferior end of the zygomaticomaxillary suture. Size of the tubercle is assessed and scored on a 0, 1, 2, and 3 scale. The side with the greatest expression of MT should be scored. It should be noted that a completely absent MT is rare. Figure 7.5 illustrates the character states of MT.

This trait is assessed by placing a transparent ruler at a point approximately 0.5 cm lateral to the inferior terminus of the zygomaticomaxillary suture (*zygomaxillare*), extending to the deepest superior incurvature on the maxilla. A score is assigned on regarding the extent of the bone protruding past the ruler's inferior edge.

0 = There is no projection of bone.

1 = There is a trace tubercle below the ruler's edge; approximately 2 mm or less.

2 = The tubercle exhibits a medium protrusion below the ruler's edge; approximately 2 to 4 mm.

3 = There is a pronounced tubercle that protrudes approximately 4 mm or more below the ruler's edge.

****Note:** A malar tubercle might be present on either the maxilla, zygomatic, or at the zygomaticomaxillary suture. Observations should not consider any tubercles on the lateral portion of the zygomatic arch. When a tubercle is directly on or just posterior to the zygomaticomaxillary suture, the ruler should extend from the deepest incurvature of the maxilla to a point approximately 0.5 cm lateral to *zygomaxillare*.

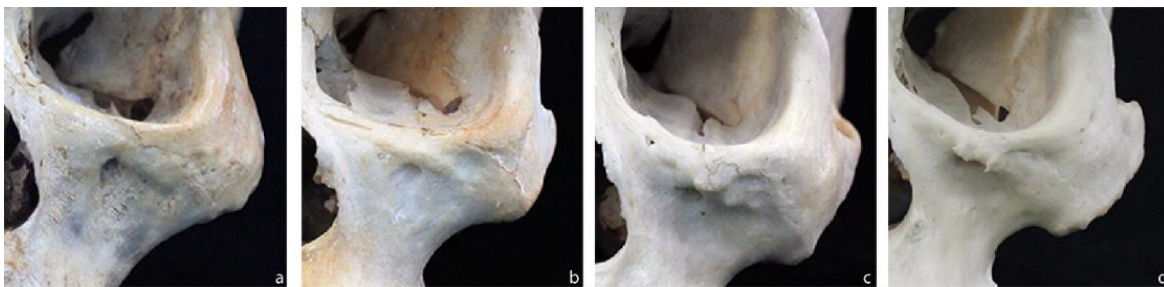


Figure 7.5. Variation in character states of MT. Scores from left to right (top to bottom): a) 0 = no projection of bone; b) 1 = trace; c) 2 = medium; d) 3 = pronounced (image taken from User Guide for MMS v1.61, 2018).

Nasal Aperture Width (NAW)

This trait is defined as the width of the nasal aperture relative to the entire facial skeleton. NAW should be assessed using a ratio of nasal aperture width to the overall width of the facial skeleton. This trait is captured in three character states, scored as 1, 2, and 3. Figure 7.6 illustrate the character states for NAW.

1 = NAW is narrow; ratio of 1:5 (NAW: width of facial skeleton).

2 = NAW is intermediate; ratio of 1:4 (NAW: width of facial skeleton).

3 = NAW is broad; ratio of 1:3 (NAW: width of facial skeleton).



Figure 7.6. Character states of NAW. Scores: a) 1 = narrow; b) 2 = medium; c) 3 = broad (image taken from User Guide for MMS v1.61, 2018).

Nasal Bone Contour (NBC)

This trait is defined as the curvature of the midfacial region, specifically the nasal bones and frontal process of both maxillae at 1 cm below the cranial landmark *nasion*. This trait presents itself as five possible character states scored as 0, 1, 2, 3, and 4. Figure 7.7 illustrates four character states for NBC.

Visual assessment of NBC is not recommended due to a high level of inter- and intra-observer error. It is recommended that this trait be scored with a contour gauge, as this tool permits a more objective assessment of NBC. To score this trait, the user should place the contour gauge directly on the nasal bones 1 cm below *nasion*. Keeping the contour gauge perpendicular to a transverse plane and parallel to the sagittal plane (Figure 5.9), the observer should apply gentle but firm, consistent pressure until the deepest points on the contour gauge are reached. This process should be repeated multiple times along the length of the contour gauge to ensure correct assessment of NBC.

0 = NBC exhibits a low and rounded nasal bone contour.

1 = NBC exhibits an oval contour with elongated, high, and rounded lateral walls.

2 = This character state exhibits steep lateral walls and a broad (approximately 7 mm or more), flat plateau. On the contour gauge, the plateau is identified by a flat cluster of seven or more needles at the same height.

3 = At this score, NBC exhibits steep-sided lateral walls and a narrow surface plateau.

4 = This character state is triangular in cross-section and lacks a surface plateau.

****Note:** Each needle on the contour gauge represent 1 mm. Make sure the needles on the gauge do not separate when pressing the instrument on the nasal bones. This will create space and inaccurately model the true shape of the nasal contour.



Figure 7.7. Character states of NBC. Scores: a) 0 = low, rounded, circular; b) 1 = high rounded, oval; c) 2 = broad plateau; d) 3 = narrow plateau; e) 4 = triangular (image taken from User Guide for MMS v1.61, 2018).



Figure 7.8. Trait assessment using the contour gauge (image taken from User Guide for MMS v1.61, 2018).

Nasal Overgrowth (NO)

Nasal overgrowth is defined as the projection of the lateral border of the nasal bones at their inferior edge beyond the maxilla at the cranial landmark *nasale inferious*. This trait exhibits two character states based on presence or absence of overgrowth. Figure 7.9 illustrates the character states of NO.

This trait is visualized by close inspection of the inferior lateral border of the left nasal bone where it articulates with the maxilla. It may be useful to gently run your finger along the border of the maxilla and nasal bones at *nasale inferious* to determine whether a projection is present.

0 = No bony overgrowth at *nasale inferious*.

1 = Any projection of bone from the lateral border of the nasal bones beyond the maxillary border at *nasale inferious*.

****Note:** If the left side is damaged, the right side may be used to assess the trait. If both nasal bones are missing, fractured (ante- or peri-mortem), or damaged, do not score nasal overgrowth. Be careful to closely examine this feature for postmortem so that the individually is not incorrectly scored as having no nasal overgrowth.

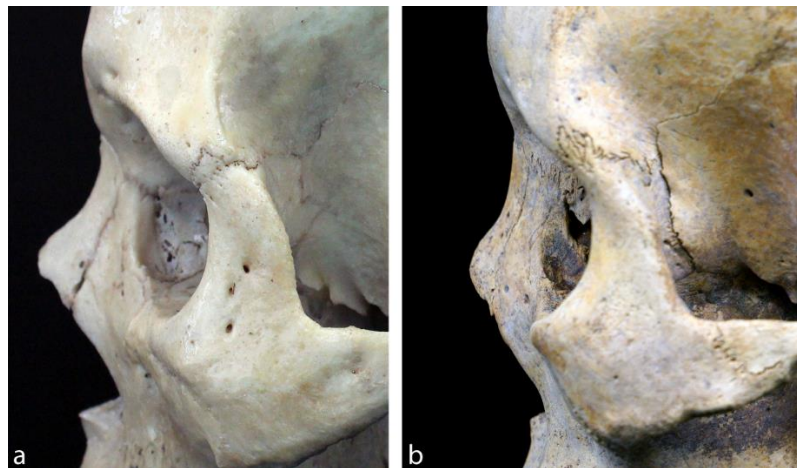


Figure 7.9. Character states of NO. Scores: a) 0 = no overgrowth; b) 1 = overgrowth (image taken from User Guide for MMS v1.61, 2018).

Postbregmatic Depression (PBD)

This trait is defined as a depression along the sagittal suture posterior to the cranial landmark, *bregma* that is not a result of pathology. This trait is scored based on its presence or absence as 0, 1. Figure 7.10 illustrates the character states of PBD.

To score this trait, hold the cranium in a lateral profile view and look for a depression posterior to *bregma*. It may be helpful to palpate the area.

0 = No depression present posterior to *bregma*.

1 = Any depression posterior to *bregma* along the mid-sagittal plane.

****Note:** PBD can be assessed using the contour gauge to detect small expressions of this trait. The gauge should be held vertically with the pins directly on the skull. The gauge should be positioned with the midpoint of the instrument superior to *bregma* and the posterior portion aligned with the sagittal suture. The anterior edge should align with the midline of the frontal bone. Press the contour gauge firmly, but gently, with consistent pressure to replicate the shape of the postbregmatic region. If the gauge exhibits any signs of postbregmatic depression, it should be scored as present (score of 1).

Be careful scoring individuals with obliterated sutures because the bone along the suture sites may be elevated, giving the appearance of a depression for the surrounding bone. The key is to determine if the sagittal suture contours just posterior to *bregma* and extends superiorly to return to the original elevation.



Figure 7.10. Character states of PBS. Scores: a) 0 = absent; b) 1 = present (image taken from User Guide for MMS v1.61, 2018).

Posterior Zygomatic Tubercle (PZT)

This trait is defined as the posterior projection of the zygomatic bone as viewed laterally on the cranium. This projection, also referred to as the marginal process, is viewed at approximately the midorbit level. This trait exhibits four character states, scored as 0, 1, 2, and 3. The side with the greatest expression is scored. Figure 7.11 illustrates the character states for this trait.

This trait is scored by viewing the cranium in lateral view. By placing a transparent ruler on the frontal process of the zygomatic that extends from the two cranial landmarks, *frontomolare posterale* to *jugale*, the degree of protrusion of the tubercle can be assessed. A score is assigned on the extent of the bone protruding past the ruler's edge.

0 = There is no projection of bone past the ruler's edge.

1 = There is a weak projection of bone that extends less than 4 mm past the ruler's edge.

2 = There is a moderate projection of bone that extends approximately 4 to 6 mm past the ruler's edge.

3 = There is a marked projection of bone extending more than 6 mm past the ruler's edge.

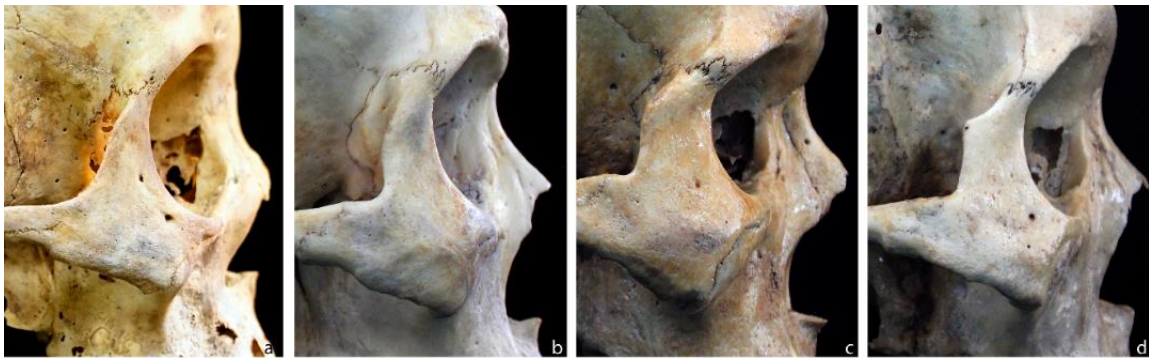


Figure 7.11. Character states of PBS. Scores: a) 0 = absent; b) 1 = present (image taken from User Guide for MMS v1.61, 2018).

Zygomaticomaxillary Suture (ZS)

This trait is defined as the suture between the maxilla and zygomatic. Observations should be based on the approximate location of the greatest lateral projection of the suture and the number of major angles present. ZS has three character states, scored as 0,1,2. Figure 7.12 illustrates the character states of ZS.

This trait is scored from viewing the cranium in the anterior view. The left side should be scored. Any infraorbital sutures should be ignored when scoring ZS.

0 = ZS has no angles, and the greatest lateral projection of the suture is at the inferior margin of the malar.

1 = ZS has one angle, and the greatest lateral projection is near the midline.

2 = ZS has two or more angles that have a jagged or S-shaped appearance. The greatest lateral projection of this character state is variable.

****Note:** Sutures with the greatest lateral projection at the inferior margin with a slight angle near the midpoint of the suture should be scored as 0.



Figure 7.12. Character states of PBS. Scores: a) 0 = absent; b) 1 = present (image taken from User Guide for MMS v1.61, 2018).

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