

TA³ Installation and Software User Guide

Version 0.16

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Introduction

TA³, (Transition Analysis 3) is a system for estimating age using new trait scoring procedures coupled with statistical and machine learning methods. TA3 was funded by National Institute of Justice award number 2014-DN-BX-K007.

The TA³ team includes George Milner (University of Pennsylvania), Jesper Boldsen (University of Southern Denmark), Stephen Ousley (University of Tennessee), Svenja Weise (University of Southern Denmark), Sara Getz (University of Wisconsin-Madison), and Peter Tarp (University of Southern Denmark).

The previous version of Transition Analysis for age estimation is known as ADBOU or TA2. TA³ includes a richly illustrated trait manual and accompanying software. Be sure to read through the scoring manual thoroughly before scoring and analyzing data.

Requirements

Mac: OSX (*Coming sometime in June*)

Windows: Windows 7 or later.

Installation

For Windows users: You can download the installation file (an EXE file) from <https://github.com/rer145/ta3/releases/latest> or <https://statsmachine.net/software/TA3/>. TA³ is installed in three parts. The installation procedure will create folders and copy the necessary files to each folder, and create a desktop shortcut. You will then be prompted to complete the installation by installing a special version of R (R Development Core Team 2015) and the necessary R packages that TA³ uses. **NOTE: The installation of the R packages may take at least 5 minutes.**

Running TA³

To start the program, click on the desktop icon. Click the "Start New Case" button to record information from a skeleton or click menu items *File / Open* (or press Ctrl-O) to open a file with previously saved skeletal data.

Entering Data

In Basic Mode, you will open on the "Evaluation" tab and see "Select a section from the left to access the trait scoring". Each area of the skeleton for scoring is displayed on the left side of the window. Click on a skeletal area to show the first trait under that heading (Fig. 1).

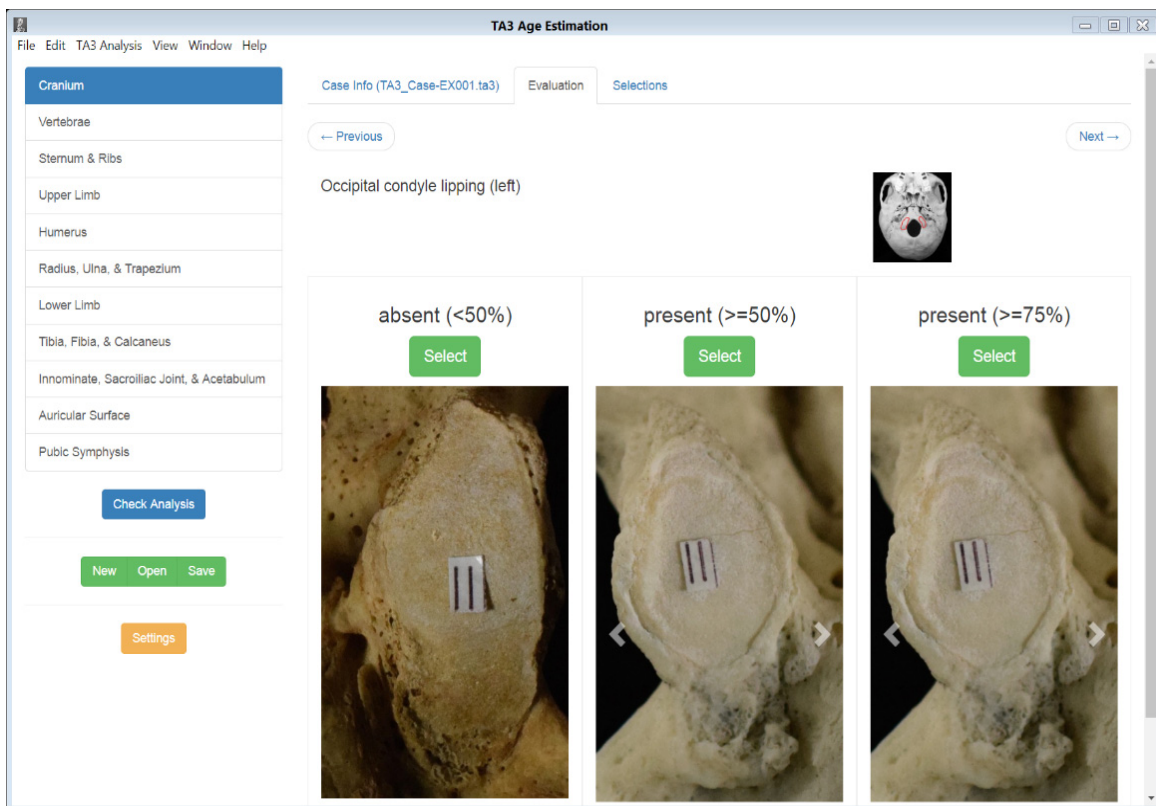


Figure 1. Data entry using basic mode.

Analyzing data

After you have completed scoring, click the *Check Analysis* button on the left. You will be presented with your Current Case Selections, showing all the traits you scored and their scores. Click the *Run Analysis* button to start the Analysis. **NOTE: You must score at least two traits to get an estimated age.**

After the analysis is finished you will see a text summary on the Results tab, including the traits used, the sample size, the point estimate and lower and upper bounds of the 95%

prediction interval, and some other useful statistics such as the standard error and the correlation between the predicted and actual ages in the reference data. All predicted ages and prediction intervals are estimated using independent validation.

IMPORTANT!

Because TA³ is currently in beta testing, some scoring and analytical aspects are still being developed. Analytical methods will be expanded and improved for quite some time. There are some traits that we already know are not useful for estimating age. The useless traits will be removed in later editions of the software, but we encourage you to at least observe them, and take note of other aspects of the skeleton that are not scored. That is because with enough practice, you will start to look at skeletons differently. We believe there are many other aspects of the skeleton that are potentially age informative, including bony features not scored in TA³, that can be identified after observing many hundreds of skeletons.

Your first goal should be to recognize the traits and score them consistently. This relates to the *Daubert* criterion of reliability, especially when you compare your scores to scores of other observers. First read pages 7 through 10 in the Trait Scoring Manual carefully.

You might feel that different thresholds separating “present” from “absent” would provide better information. In some instances, we would agree. However, the analytical procedure is based on observations scored as defined in the accompanying manual. Valid results can only be obtained if users adhere strictly to the definitions, including size thresholds and the like, which were refined by the TA³ team over the course of data collection.

TA³ currently analyzes all traits entered, but only those traits from the right side if both sides are entered. Using more scored traits in an analysis should theoretically allow more accurate age prediction, but only up to a certain point. Generally, the more traits that are entered, the smaller the reference sample size because only individuals with all entered traits are used. Some traits, such as from the second rib, restrict the sample size because not every skeleton had a scorable second rib; in such cases, use the traits from ribs 3-10. DISH (Diffuse Idiopathic Skeletal Hyperostosis) shows selective mortality effects, which complicate age estimations, and should be left out of age estimation for now. Some traits add little or no information at all and will be removed in later versions of the manual and software (Table 1).

Table 1. Traits that can be left out of any analysis.

DISH (due to selective mortality; Milner et al. 2018)
Fibula wings
Ischial spur
R1 fusion

Radius tuberosity crest
Sacral elbow
Ulna olecranon spur

Further, some traits add more information than others depending on the traits involved and the age of the individual. For instance, when analyzing an individual with many indicators of advanced age, if you include an early trait, such as a closed spheno-occipital synchondrosis or fully fused vertebral rings, it will not add useful information. But adding that trait will limit the analysis to only those with that trait scored. We are exploring sophisticated ways of dealing with issues such as the relevance of different traits in various parts of adulthood, and we encourage you to do so as well. There is much to be discovered, and continued refinements will increase age estimate accuracy and precision.

TA³ currently analyzes all individuals, males and females, from all worldwide samples. There are two consequences of using this reference sample. First, it is a global (or universal) sample, not a regional one. The sample's diversity means the procedure is broadly applicable for forensic and archaeological purposes. At this point, it is by no means certain that regional samples perform better for forensic applications than a global one, and for archaeological purposes a use of a global sample is undoubtedly the best approach. Second pooling males and females is appropriate for many traits, but not all of them. Future work where the sexes are analyzed separately will likely improve estimate accuracy and precision.

The reference data were checked for univariate and multivariate outliers and the obvious errors were corrected after consulting the original data sheets or by deleting the outlying values. One example of an obvious error is a spheno-occipital synchondrosis scored as open in a 55 year old. On the whole, we were very conservative in correcting values. We will run more checks and make corrections as we develop more methods and understand the data better, so the reference data will itself be updated as will the software and analytical methods.

Currently, TA³ uses only the random GLM method (Song et al. 2013) in the R package "randomGLM" for age estimation. But more methods have been explored, and are being explored, and will be incorporated in future versions of TA³.

If you have questions or comments about the skeletal traits or how they are scored you can contact George Milner at ost@psu.edu.

Please share any comments, bugs, questions, or concerns with the analytical methods or TA³ software by emailing Stephen Ousley at craniator@statsmachine.net.

Interface

Menu Items

There are six menu choices.

File

New: remove all scores and start again with a new skeleton

Open: open a saved file (*.TA3)

Save: saves the current file entries. Be sure to fill out the fields on the Case Info tab so you can keep track of your cases.

Save As: saves the current entries into a different file. Be sure to fill out the fields on the Case Info tab so you can keep track of your cases.

Settings: Choose between Basic entry mode (with illustrations) and Advanced entry mode (with scoring fields only; Fig. 2). Basic Mode has images and text to guide you in scoring. Advanced Mode is used when you are entering from a hard copy sheet or are quite familiar with the scoring system and would like to enter data more efficiently. Simply click on the score.

Exit: closes the program.

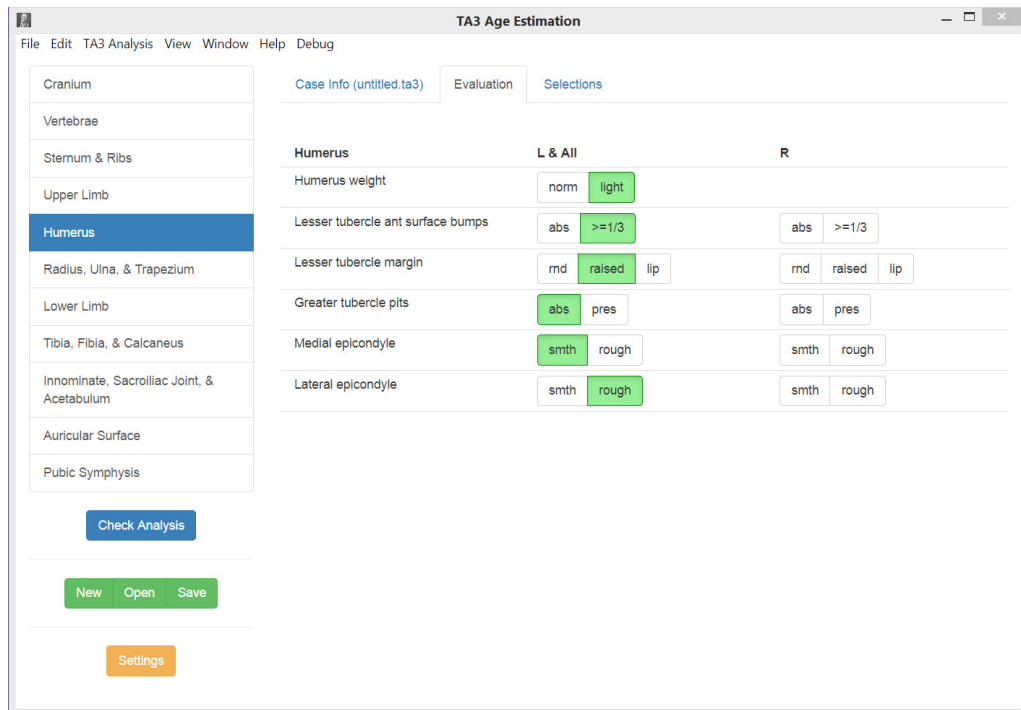


Fig.2 Entering data using advanced mode.

Edit

Copy: the usual copying function

Paste: the usual paste copied text function

Select All: select all text

TA3 Analysis

View Case Info: displays the information in the fields of the case info tab.

View Selections: shows the Current Case Selections.

Run Analysis: perform analysis using the entered data.

View Results: show the latest text results.

Radio buttons for *Use Basic Mode/Use Advanced Mode*

View

Actual Size: sets all fonts to default size.

Zoom In: makes fonts larger.

Zoom out: makes fonts smaller.

Toggle Full Screen (F11): switches in and out of full-screen mode.

Help

Data Collection Form:

User Guide: shows basic instructions on using TA³.

Trait Manual: displays the current Trait Scoring Manual in pdf format.

Website: opens <https://github.com/rer145/ta3>

Source code: opens <https://github.com/rer145/ta3>

Report an Issue: opens a feedback page on Github related to programming. You can also report issues/bugs and ask questions by emailing Steve Ousley at craniator@statsmachine.net.

Check for App Updates: checks for program updates. Data and R program updates are checked for at program start.

Data Collection and Privacy: opens an agreement form for sharing your user experience with us for understanding how users interact with TA3 and for debugging and troubleshooting. Any and all collected information is anonymized.

About Transition Analysis 3: Displays current version information.

Program Buttons (lower left)

Check Analysis: Displays all current traits scored.

New: Start a new case.

Open: Open a saved case.

Save: Save current trait scores to a file.

Settings: Use Basic Mode/Use Advanced Mode.

Case Tabs

Case Info: shows fields to enter case identifying information, recorder names, observation date, and notes on the current case. This information is saved into the case file.

Evaluation: currently blank.

Selections: shows current traits selected and their scores in plain text.

Results: shows program details including program, R code, and data versions, traits used and their numerical scores, and analytical results including sample size used in calculations, point estimate for age, lower 95% prediction bound, upper 95% prediction bound, standard error (for general comparisons), and correlation between age and predicted age.

Plots: shows analytical plot(s). Currently, it shows a plot of estimated ages using random GLM when applied to all individuals. A line of perfect agreement ($x = y$) is shown in black, a LOESS line is shown in a heavy dashed purple line, and the prediction bounds are shown in lighter dashed lines. To save a plot, right-click it and choose *Save As*, and provide a file name. To copy the current plot to the paste buffer, right-click and choose *Copy Image*.

References

Milner, G.R., Boldsen, J.L., Ousley, S.D., Getz, S.M., Weise, S., Tarp, P., Steadman, D.W. (2018). Selective mortality in middle-aged American women with diffuse idiopathic skeletal hyperostosis (DISH). *PLOS One*, 13:e0202283. [doi.org/10.1371/journal.pone.0202283].

R Development Core Team. (2015). R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing.

Song, L., Langfelder, P., Horvath, S. (2013). Random generalized linear model: A highly accurate and interpretable ensemble predictor. *BMC Bioinformatics*, 14, 5.
[https://bmcbioinformatics.biomedcentral.com/track/pdf/10.1186/1471-2105-14-5]