



TIPZOO: a Touchscreen Interface for Paleolithic Zooarchaeologists Manual for TIPZOO-FMP (FileMaker interface)

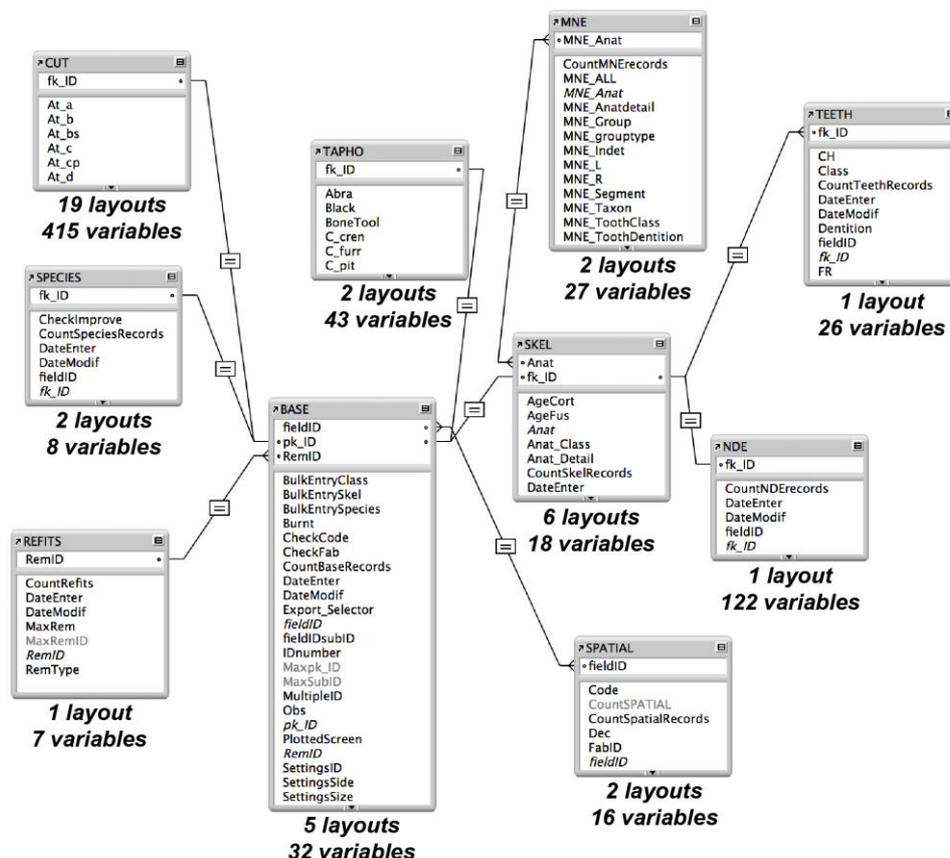
!! Disclaimer: I apologize for the English of the following text... I'm not a native speaker and couldn't afford the services of a professional for this manual. I would be glad to edit any unproper term, grammatical error, typo, etc: if you see any, please contact me at ediscamps@gmail.com.

This manual gives a step-by-step overlook of how to use the TIPZOO-FMP FileMaker interface, but the interface is designed so that you should be able to deduce, in most cases, what you should record and how to do it, without the need to systematically go back to this manual. While recording, look for the yellow buttons if you want to go the next step; and look for red contours if you are stuck (red contours relate to variables that should be recorded before going on).

TIPZOO is organised with several tables and layouts:

- **Main menu** layout, for settings and general information;
- **SPATIAL** table & layout, for importing field information (XYZ coordinates, layer, etc.);
- **BASE** table & layout, for basic information on a fragment (field ID number, size, etc.), as well as refits between fragments (with the associated **REFITS** table);
- **SKEL** table & layouts, for recording skeletal identification and information (associated with **NDE** and **TEETH** tables);
- **SPECIES** table & layout, for recording taxonomic identification;
- **TAPHO** table & layout, for recording taphonomic observations;
- **CUT** table & layouts, for recording taphonomic observations;
- **MNE** table & layouts, for recording minimal number of elements.

The following image gives an overlook of the database structure (tables with numbers of layouts and variables), but it is not necessary to know or understand it to use TIPZOO:



In this manual, texts marked in blue and green refers to **AUTOFILL** and **AUTOCHECK** features.

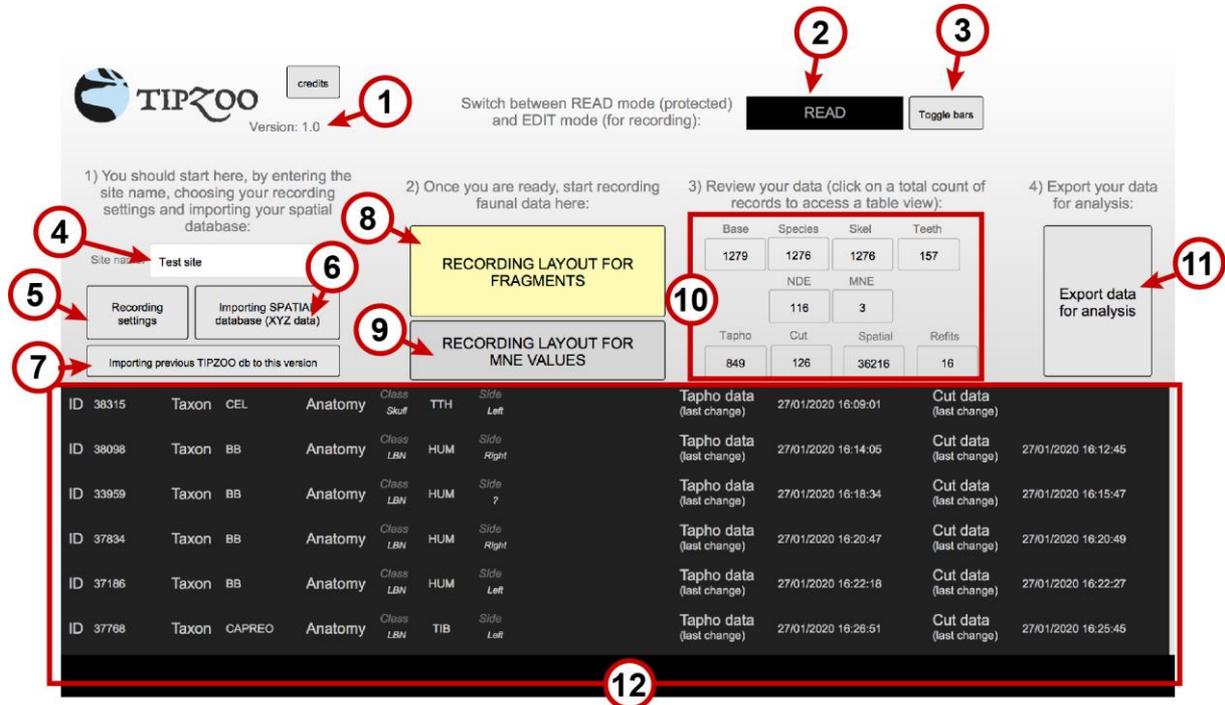
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I. Starting with TIPZOO: FileMaker main menu

Once you downloaded the .zip file on the website, first unzip it, go into the folder, rename the .fmp12 file as you want, and open it in FileMaker to start data acquisition. Note that you should create a different .fmp12 file for each collection you are analysing.

When you start TIPZOO, you automatically arrive on the main menu. This menu provides a general view of your database, as well as options to prepare data entry:



TIPZOO main menu.

In the following paragraphs, numbers in brackets - as (1) or (2) - pertain to the image above.

1. Basic TIPZOO handling

(1) This indicates the current TIPZOO version used. Be sure to check <http://tipzoo.cnrs.fr> for updates.

(2) By default, FileMaker automatically records any change to the database, without any option to go back (e.g. contrary to Excel for example). To avoid any unwanted change to your database, TIPZOO is automatically set to “READ” mode when you open it. In READ mode, you cannot change anything, but you can still explore your records (launching a script that alters records by pressing a button will thus likely cause an error message). If you wish to record a new bone fragment, you first need to press the (2) button to switch to EDIT mode. It is recommended to switch back to READ mode as soon as you have finished a data entry session.

(3) By default, the FileMaker toolbar is hidden in TIPZOO, but you can toggle them on or off by pressing this button.

(4) Using this text box, it is recommended to enter the name of the archaeological site you are analysing. For best results, a unique TIPZOO file should be created for each site you analyse.

2. Recording settings

(5) This button lets you access a submenu to set up different recording settings or “styles”, as described below.

Settings for ID numbers: TIPZOO supports two types of ID numbering for bone fragments, either unique IDs (e.g. when “435” refers to a unique bone across the entire site) or “square IDs” when it is

the combination of a square and a number that provides unique IDs for bone fragments (e.g. "H12-435" and "H13-435" are two different bones). It is extremely important to select the correct type of ID numbering according to your site.

Settings for Size: by default, TIPZOO will ask for the size of each bone fragment entered in the database. If you want to bypass this and accelerate data entry, you can set this settings mode to "No".

Settings for Side: similarly, by default, TIPZOO will ask for the side of each bone fragment entered in the database (even if it is indeterminate). If you want to bypass this and accelerate data entry, you can set this settings mode to "No".

Settings for taphonomic analyses: TIPZOO will ask for taphonomic data (e.g. bone surface modifications, other than burnt degree) for each fragment that is above a certain size limit, in centimetres. You can change this size limit here, or select "None" if you do not want to record any taphonomic data and accelerate data entry.

Settings for ID numbers: if two people are doing data acquisition for the same collection, you should create two .fmp12 files, and then use this button to modify the unique ID numbers created by TIPZOO. For example, one person can start with "1" ID numbers and the other with "10000" ID numbers. This will facilitate merging the datasets together (using the import records button of the Main menu), making sure that ID numbers do not overlap between the two persons.

3. Importing a field spatial database

(6) To fully exploit TIPZOO features, it is recommended to import the field database if it exists. This "spatial database", as it is called in TIPZOO, is the database that is often created on the field during excavation: it traditionally includes all the X, Y, Z data as well as layer attributions for each plotted artefact or bucket. Pressing this button will give you access to a sub-menu for importing a spatial database from a spreadsheet file.

The "Import new spatial records" button will show you the FileMaker assistant for importing your spreadsheet dataset. A template is available for download at <http://tipzoo.cnrs.fr> in order to convert your spatial database in a format that is easily imported in TIPZOO, but you can bypass this step if you wish to. It is recommended to import all spatial data, including other types of artefacts (flint, quartz, etc) and not only bone fragments.

A spatial database in TIPZOO can include the following variables:

- Year (year of excavation),
- fieldID (ID number of each artefact, cf. below),
- Code (type of artefact, for instance SILEX or FAUNA; for best results in TIPZOO, use either "FAUNE" or "FAUNA" for faunal fragments, not any other code),
- Square_field (the square as indicated on the field),
- Square_true (the square as calculated from XY coordinates, sometimes different from Square_field),
- Dec (the "décapage" or spit number),
- USfield (the stratigraphic unit, or layer, attributed during excavation),
- FabID (the fabric ID number, for pieces on which orientation and dip was noted during excavation),
- X (X coordinate), Y (Y coordinates), Z (Z coordinates),
- Group1, Group2, Group3.

The last three variables (Group1, Group2, Group3) are additional variables only intended to allow grouping pieces together during analysis (e.g. for using archaeostratigraphic units that are different from the USfield layers). **You should be extra careful with the fieldID variable:** if you use "unique IDs" setting, it should be the artefact number (e.g. 435), but if you use the "squares IDs" setting, it should be a unique IDnumber for each artefact, in the following format "Square_Number", as "H12_435" or "H13_435". In the latter case, you can use the CONCATENATE formula in Excel to quickly create these fieldID texts (i.e. =CONCATENATE(Square;"_";Number) replacing Square and Number by the appropriate columns' references).

When you reimport a spatial database, it is recommended to first delete existing records to avoid duplicates. Use the “Delete existing spatial records” button for that. The current number of spatial records imported in TIPZOO is indicated on the left of this button.

The “Back to Main Menu” button lets you go back to the main menu at any time.

4. Importing records from another TIPZOO database

(7) You can use this button to import records from another TIPZOO database (e.g. if two people did data acquisition on the same bone collection, cf. *supra*), or to transfer your records to a newly released version of TIPZOO (after checking that it is compatible). First, create a copy of the TIPZOO database that you want to import, rename it “OLD.fmp12” and place it in the same folder as the TIPZOO database in which you want to import the records. Then open this file, click this button, and all the records should be automatically imported.

5. Records: data entry, record reports, and export

(8) and (9) give you access to recording layouts for bone fragments and for minimal number of elements, respectively.

(10) provides total record counts for each TIPZOO table. If you click on the total number, you can access a basic table view of each table.

(11) opens up the export submenu. This will notably allow exporting all your data in a preformatted form for analysis with the TIPZOO R scripts. Faunal data (as entered in TIPZOO) and spatial data (from the field spatial database) are automatically linked according to the ID number of each fragment: this will save you a lot of time for the spatial analysis of your faunal data. Click:

- “Export Species DATA” for preformatted export of identified specimens by taxa for analysis with the TIPZOO-R “SPECIES_script”, or for spatial analysis;
- “Export Tapho DATA” for preformatted export of taphonomic observations for analysis with the TIPZOO-R “TAPHO_script”, or for spatial analysis;
- “Export CUT DATA” for preformatted export of cut-mark codes (for a given taxon) for analysis of butchering activities with the TIPZOO-R “CUT_script”;
- “Export NDE DATA” for preformatted export of NDE landmarks (for a given taxon) for analysis of skeletal-part representation with the TIPZOO-R “NDE_script” and TIPZOO-QGIS;
- “Export Teeth DATA” for preformatted export of a summary table of all teeth recorded (either isolated or included in a cranium/mandible fragment) for a given taxon, for MNI calculation and analysis of mortality profiles.

(12) provides a quick overview of some of the bone fragments previously recorded.

II. Data entry for bone fragments: the BASE table

Accessing the recording layout for fragments let you first enter data for the “BASE” table:

The screenshot shows the TIPZOO BASE table recording layout. The interface is divided into several sections:

- Top Panel (1):** A black header bar containing record information: ID 38549, Taxon CEL, Anatomy, Class LBN, TIB, Side ?, Last record modif 27/01/2020 16:28:51, and Observations.
- Navigation (3, 4):** Buttons for 'previous record', 'next record', 'READ mode', and 'Toggle bars' are in the top left. A 'BACK TO MAIN MENU' button is on the left side.
- Record Creation (5):** Two yellow buttons: 'NEW RECORD (plotted)' and 'NEW RECORD (screen)'. A 'delete' button is also present.
- Field Entry (6):** A text box for 'Field ID number' containing '38549'. Below it is a checkbox for 'Normal that multiple remains with the same field number?'.
- CheckCode (7):** A section with 'CheckCode ok' and a red warning 'ELONGATED BONE? (check for fabric)' with 'X' checked under 'Yes'.
- Table (8):** A table with columns: Year, CODE, fieldID, Square_field, Dec, USfield. A row shows: 2019, FAUNE, 38549, C49d, B_39, B6.
- Size class (11):** Radio buttons for size classes from 0-1 to 13-14, plus 'Autre...'. The '5-6' class is selected.
- Burnt degree (10):** Radio buttons for 'No', 'Partially', 'Mostly black', 'Mostly grey', and 'Mostly white'. 'No' is selected.
- Bulk Entry (13):** A yellow box with a dropdown menu and a 'reset' button.
- Skull bones and teeth (12):** A list of categories: 'Skull bones and teeth', 'Long Bones (including phalanges)', 'Flat bones (+ vertebrae)', and 'Small bones (+ patella, malleolus)'. 'Long Bones' is selected.
- Buttons (14):** A 'NEW REFIT' button at the bottom left.
- Bottom Panel (2):** A black bar with 'Go to' buttons for BASE, SKEL, SPECIES, TAPHO, and CUT. It also shows 'DateEnter', 'DateModif', 'Site name: Test site', and 'pk_ID rec'.

Example of a record in the TIPZOO BASE layout.

In the following paragraphs, numbers in brackets - as (1) or (2) - pertain to the image above.

(1): the top black panel shows basic info on the current record (fieldID, species identified, anatomy, last record modification) as well as a text box for observations that cannot be recorded elsewhere.

(2): the lower black panel provides “Go to” buttons to access the recording layouts for fragments (BASE, SKEL, SPECIES, TAPHO and CUT) when data was already entered. They are either shown in white when data was recorded (and thus accessible), or in grey when data is absent (the button is thus deactivated).

(3) are navigation buttons (previous and next record, switch for EDIT/READ mode, “toggle bars” button, and a lens for finding a specific record) and (4) brings you back to the main menu.

1. Creating a new record

(5) To create a new record, you should press the correct button depending on whether the fragment was plotted or found in a sieve residue (screen). TIPZOO will then ask for the unique fieldID number (if you use the “unique IDs” setting), or you Square and IDnumber (if you use the “squares IDs” setting).

AUTOCHECK: TIPZOO automatically checks that the fieldID is not left empty, and that it is unique (no duplicates when considering both fieldID and SudID, cf. below). If it is normal that two fragments have the same fieldID (for example, if two fragments of two different bones were by mistake plotted with the same fieldID number), you should check the (6) box. A SubID box will then appear: it provides a quick and easy way to keep track of duplicates, by giving fragments with an identical fieldID number (e.g. 435) unique SubID numbers (e.g. 435-1 and 435-2). It is especially useful for fragments extracted from screens. The “next subID?” button will automatically calculate the next available subID number for a given fieldID number.

When a new record is created, it is directly linked with the spatial database:

- **AUTOCHECK: (7)** checks in the spatial database that the fragment is marked as “FAUNE” or “FAUNA” for plotted specimens, or “SEAU” or “BUCKET” for screen records (a red “PROBLEM” box will otherwise appear);
- **AUTOCHECK: (8)** if the “FabID” field is not empty in the spatial database (i.e. if a fabric measurement was taken for this artefact on the field), TIPZOO asks to check if the object is elongated or not, which is not useful to keep track of artefacts whose orientation and dip were measured by mistake on the field;
- **(9)** shows a list of all the linked records from the spatial database, updated in real-time (FileMaker portal feature).

Two BASE variables are then recorded in this layout:

- **(10)** the burnt degree, according to Costamagno et al., 2009. **AUTOFILL:** burnt degree is set to “No” by default.
- **(11)** the size class (in cm). **AUTOCHECK:** TIPZOO automatically checks that size is recorded, except if you alter the recording settings in the main menu.

In TIPZOO 2.0, bone color was added (with modifiable modalities): it is still in development, but should work properly! If you convert a 1.X database to TIPZOO 2.0 and want to try the bone color menu, please check in the settings that “Default” is selected as a bone color group after the DB transfer.

2. Switching to the appropriate layout for skeletal data entry

The next step when you record a fragment in TIPZOO is to enter skeletal information. For this, you can either:

- **(12)** directly use one of the five buttons on the right to go to the appropriate SKEL layout (divided by classes of skeletal elements);
- **(13)** or use the bulk entry system for faster data entry. The bulk entry allows you to pre-enter anatomical and/or species identification(s) to gain time when your collection is already sorted by element and/or species: for example, if you are going to enter all your reindeer tibia fragments in one recording session, you can pre-set the bulk entry fields so that you no longer have to tell TIPZOO that the fragments you are recording are reindeer tibia. The bulk entry fields are emptied each time TIPZOO is restarted, or can be emptied at any time using the “reset” button (this will not alter the anatomical and species identification fields of a fragment, only the bulk entry settings).

If you made a mistake on the anatomical identification of a fragment, and if you click once again on one of the **(12)** buttons to correct your record, a message will appear: if you click “Yes”, all the data previously recorded for this fragment will be deleted (i.e. linked records in the SKEL, SPECIES and CUT tables), so that you can start again and record the fragment correctly.

3. Entering refits

Additionally, the BASE layout allows you to record refitting groups of bone fragments. You should:

- first of all, record all the fragments, at least in the BASE layout (that is very important!),
- then press the **(14)** “NEW REFIT” button,
- enter the fieldID of the first fragment included in the refit group (e.g. “435” if you use “unique IDs” setting, or “H12_435” if you use the “squares IDs” setting), and its SubID if it has one, then press “OK, next”,
- enter the ID details of the second fragment, press “OK, end” if the refit group includes only two fragments, or “OK, next” if it includes more.
- continue enter the ID details of other fragments one by one (by pressing “OK, next”), and press “OK, end” when finished,
- enter the type of refit (e.g. green-bone break, unknown break, articulated bones, etc).

A unique refit group ID is automatically created each time you press the “NEW REFIT” button, allowing you to easily keep track and record refits.

In TIPZOO Main menu (cf. above), you can click the total number of refits to access a specific REFIT layout that gives you a general overview of all recorded refits, allowing quick checks and corrections.

III. Data entry for bone fragments: the SKEL table

The layout you will see when recording anatomical identification (SKEL table) will depend on the element group selected in the BASE layout (cf. above).

You will be asked to enter the skeletal element by pressing a button (e.g. for skull fragments), a tab in a panel (e.g. for long bones), or a tab in a panel and then a button (e.g. carpals, tarsals, vertebrae). A list of the codes used are provided in the appendixes, but the user does not need to know these codes to use TIPZOO. Additional information is then entered (portion, segment, side, etc.).

1. General case

The following image shows the example of a tibia fragment:

*Example of a record in the TIPZOO SKEL layout (here, for a tibia fragment).
In the following paragraphs, numbers in brackets - as (1) or (2) - pertain to the image above.*

- (1) The tabs at the top of the panel allows you to choose the appropriate long bone (here, tibia).
- (2) "Frag": CO for complete element, ACO for almost complete, FR for fragmented. **AUTOFILL**: to gain time in data entry, this field is first set to "FR" for long bones and flat bones at record creation.
- (3) "Spongy": check the box if the fragment includes spongy bone (at least one complete spongy alveolus preserved). **AUTOFILL**: by default, "Spongy" is set to 0 at record creation for long bones, and to 1 for small and flat bones. **AUTOCHECK**: for long bones, TIPZOO automatically checks that "Spongy" is set to 1 if an extremity is recorded in the "Portion" field, and shows a warning message if not. You can however ignore this message if you want to, for example in the rare cases in which a fragment of a long bone extremity does not have spongy bone.
- (4) "AgeCort": age estimation on the basis of the sole observation of the cortical surface of the bone (i.e. bone texture exhibiting an open/woven or closed structure cf. Reitz and Wing, 1999), with F for foetus, J for Juvenile, A for Adult, and ? for unknown.
- (5) "Portion": portion of the fragment. Check if one portion is present. Codes differ depending on the element (for long bones, P for the proximal extremity, SH for the shaft, D for the distal extremity, and E for an unidentified extremity). A list of the codes used are provided in the appendixes, but the user does not need to know these codes to use TIPZOO. **AUTOFILL**: for long bones, the "Portion" fields are automatically filled if "Frag" is set to "CO" or "ACO".

(6) "Segment": segment of the shaft. Useful to precisely indicate the part of the shaft that is preserved, with P for proximal, M for medial, D for distal, Ant for anterior, Post for posterior, Med for medial, Lat for lateral, and NID for unidentified. **AUTOFILL**: for long bones, the "Segment" fields are automatically filled if "Frag" is set to "CO" or "ACO". **AUTOCHECK+AUTOFILL**: if "Segment" information was recorded by mistake for a long bone that does not have any shaft preserved ("SH" in Portion field), this field is emptied when going to the next layout (SPECIES).

(7) "AgeFus": age estimation on the basis of epiphyseal fusion, with P for proximal, D for distal, fus for fused, justfus for just fused (when the fusion line is still easily discernable), unfus for unfused.

(8) "SHC": shaft circumference (cf. Bunn, 1983). **AUTOCHECK+AUTOFILL**: if "SHC" information was recorded by mistake for a long bone that does not have any shaft preserved ("SH" in Portion field), the field is emptied when going to the next layout (SPECIES).

(9) "Side": side (left, right, or unidentified). **AUTOCHECK**: for identified long bones, TIPZOO automatically checks that side is recorded, except if you alter the recording settings in the main menu.

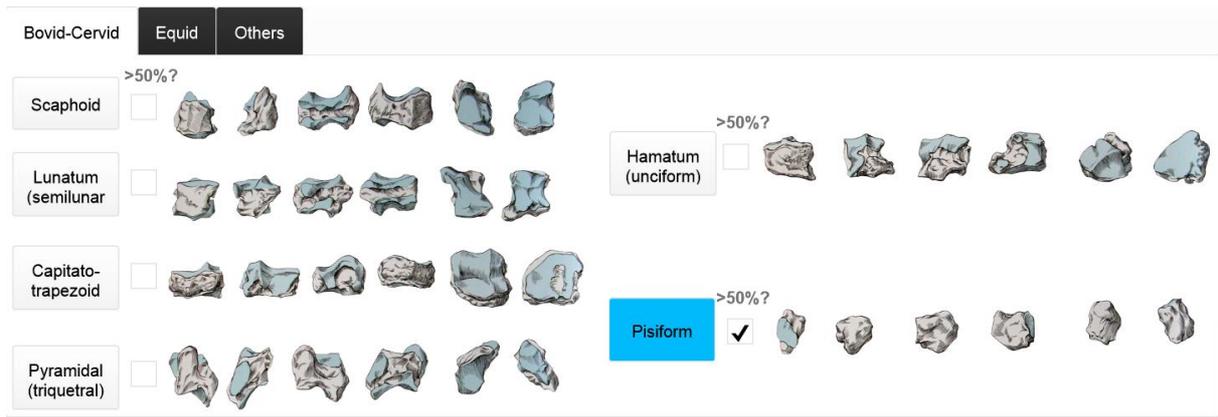
(10) This panel allows you to easily record Morin et al., 2017, 2019 "NDEs" (landmarks) using visual aids. The reader is advised to read these publications prior to using this TIPZOO feature. In the example above, the landmark 25 is recorded (marked by a red tick mark). The top part of this panel allows switching between "Bovid/Cervid" and "Equid" landmarks. NDE definitions follow Morin et al. (*ibid*), with some additions (in each case, a drawing is included in TIPZOO to better explain the new landmark):

- NDE 88 (rib measurement) is defined as the length of rib body fragments that have a circumference >50%, following Castel, 1999, p. 48;
- NDE 89 (radio-ulna measurement) is defined as the length of the radioulnar groove, following Morin, 2004, p. 125;
- NDE 90 (mandible measurement) is defined as the length of the lower part of the mandible body, inbetween the vascular incision and the P2, following Castel, 1999, p. 47;
- NDE 91 (femur measurement) is defined as the length of the linea aspera of the femur, from above the supracondylary fossa to the level of the small trochanter (cf. drawing in TIPZOO);
- NDE 92 (distal phalanx 1) is recorded as 0, 0.5 or 1 depending if none, one or both fossae of the distal condyles of the first phalange are preserved, respectively (similar to NDE 16 and 29 on metapodials);
- NDE 93 (distal phalanx 2) is recorded as 0, 0.5 or 1 depending if none, one or both fossae of the distal condyles of the second phalange are preserved, respectively (similar to NDE 16 and 29 on metapodials);
- NDE 94 (distal phalanx 3) is recorded if more than half of the distal tip of the third phalange is preserved;

(11) Once you are finished, you should click this button to enter species identification.

For phalanges, carpals, tarsals and vertebrae, TIPZOO will ask for detailed anatomical identification (Anat_Detail) and provide a graphical aid for identification (cf. example below). A list of the codes used are provided in the appendixes, but the user does not need to know these codes to use TIPZOO. **AUTOCHECK**: TIPZOO automatically checks that this information is recorded, and shows a warning message if not.

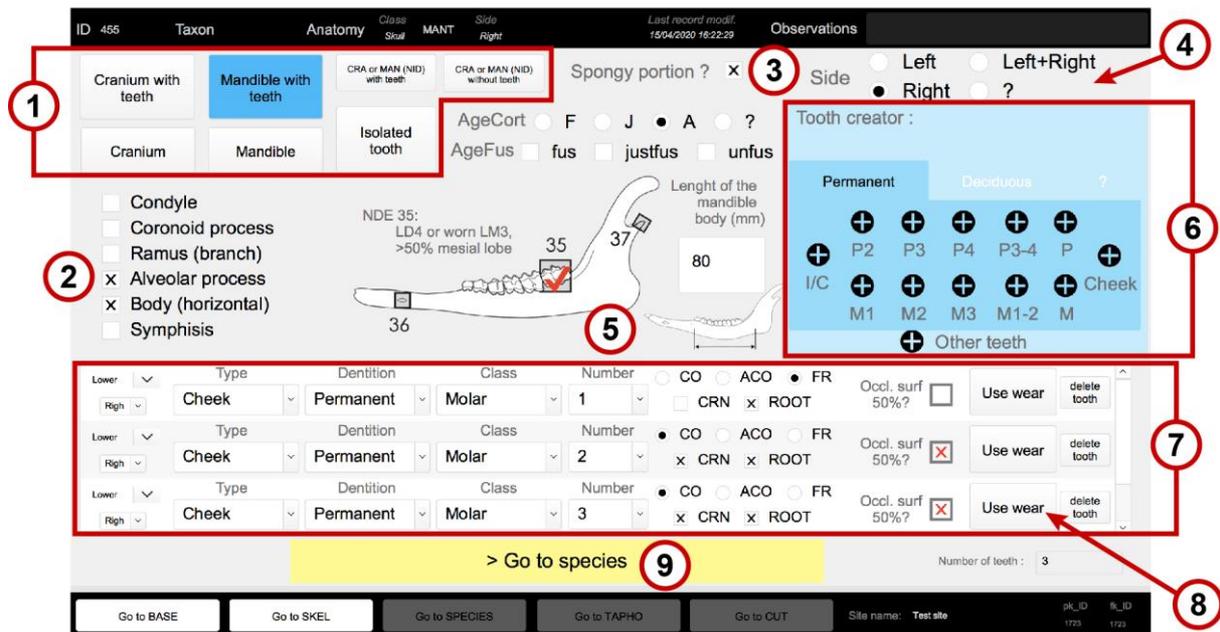
TIPZOO: a Touchscreen Interface for Paleolithic Zooarchaeologists
Manual for the FileMaker interface



Example of a TIPZOO carpal panel for the Anat_Detail variable. Pressing one of the buttons enters the detailed anatomical identification (the box turns blue if the information is correctly recorded).

2. The specific case of teeth records

Recording a tooth record (i.e. an isolated tooth or a mandible or maxillary fragment with one or several teeth) follows a slightly different approach in TIPZOO. In order to easily be able to calculate the number of a given tooth in an assemblage (considering both isolated teeth and teeth inserted in a bone), the user has to create “teeth records”. This can be easily done by using what is called the “tooth creator” in TIPZOO:



Example of a TIPZOO tooth record.

In the following paragraphs, numbers in brackets - as (1) or (2) - pertain to the image above.

- (1) First, press the correct button according to your element (the box turns blue if the information is correctly recorded).
- (2) Enter Portion data, as with other elements. An option will appear for antler fragments to record if it was shed or massacred.
- (3) Enter Spongy, AgeCort and AgeFus data, as with other elements.

(4) Enter the Side. This will activate the tooth creator below.

(5) Enter NDE (landmark) data if appropriate. Please note that if you have one petrous bone, you should click 1 (this will automatically be converted to a NDE value = 0,5 in accordance with Morin et al., 2017 definition), and if you have both sides (e.g. one cranium fragment with the two petrous bones) you should click "2" (this will automatically be converted to a NDE value = 2 in accordance with the original definition). Similarly, if you have a mandible fragment with both sides and both foramens, you should click "2", that will be recorded as a NDE value = 2 (again, in accordance with the original definition by Morin et al., 2017).

(6) Using the panel of the tooth creator, add all the teeth present by pressing the dark "+" signs. Be sure to select the correct dentition (e.g. permanent, deciduous or unknown) using the tabs at the top of the panel. Each time you add a tooth, it should appear in the portal view below, (7). **AUTOFILL**: if your fragment is a "Mandible with teeth", the Tooth creator is automatically set to "Lower", and similarly to "Upper" for "Cranium with teeth" fragments.

(7) Here, you can review the recorded teeth, edit or delete them if necessary. Enter data for completeness (CO, ACO, FR) and tooth portion (CRN for crown, ROOT for root). If more than 50% of the occlusal surface is preserved, check the appropriate box. **AUTOFILL**: if you select CO or ACO, tooth portions are automatically entered.

(8) Using the "Use wear" button, you can access a submenu to record use wear information for each tooth (this TIPZOO feature is still being developed, and should get better in the future).

(9) Once you are done, you can click this yellow button to record taxonomic identification.

AUTOCHECK: TIPZOO automatically checks that at least one tooth record is created for each fragment that contains a tooth.

IV. Data entry for bone fragments: the SPECIES table

Once you entered anatomical identifications, the layout you will see is made to record taxonomic identification (SPECIES table):

The screenshot shows the 'SPECIES' table layout in a FileMaker interface. At the top, there is a header bar with fields for 'ID' (566), 'Taxon', 'Anatomy', 'Class' (LBN, HUM), 'Side' (Left, Right), 'Last record modif.' (21/09/2020 12:06:38), and 'Observations'. Below the header, there are checkboxes for 'To Check', 'To Improve', and 'Taxonomic observations'. A red box labeled '1' highlights a tab system at the top with the text 'Select a different tab to display other taxa:' and tabs for 'Old world macrofauna', 'Arctic mammals', 'Birds', 'Fish', and 'Mollusca'. Below this, there are columns for different mammal groups: 'SVERT' (Small vertebrates), 'MAM1' (CAPREO, RUPI), 'MAM2' (RANG, CAPRA, SUS, DAMA, SAIGA), 'MAM3' (CAB, CEL, HYDR), 'MAM4' (BB, MEG), and 'MAM5' (PROBO, RHINO). Red arrows labeled '2' point to sub-menu buttons for 'Small vertebrates', 'Small carnivores', and 'Large carnivores'. A red box labeled '3' highlights a section 'NID by size class' with radio buttons for 'SVERT', 'MAM1', 'MAM2', 'MAM3', 'MAM4', 'MAM5', 'MAM12', 'MAM23', 'MAM34', and 'MAM45'. Below this, there are radio buttons for 'NID' and 'Autre...'. A yellow button labeled '6' is labeled '> Go to tapho' and '> Create new record'. At the bottom, there are buttons for 'Go to BASE', 'Go to SKEL', 'Go to SPECIES', 'Go to TAPHO', and 'Go to CU'. The 'Site name' field is also visible at the bottom right.

Example of a record in the TIPZOO SPECIES layout.

In the following paragraphs, numbers in brackets - as (1) or (2) - pertain to the image above.

- (1) Since version 1.1, a tab system allows you to access different groups of species codes:
- European wild macrofauna, suited for Palaeolithic zooarchaeology in Europe (original implementation of TIPZOO). At the very top of this layout, in dark grey, the species size classes used in TIPZOO are reminded (e.g. "CAPREO" roe deer is a MAM1, "CEL" red deer a MAM2/3, "BB" auroch/bison a MAM4);
 - Domestic taxa (incomplete list, work in progress);
 - African carnivore mammals (code list by R. Hanon)
 - African herbivore mammals (code list by R. Hanon)
 - Arctic mammals (including marine mammals, code list by H. Barbel)
 - Birds (incomplete list, work in progress, code list by H. Barbel)
 - Fish (incomplete list, work in progress, code list by H. Barbel)
 - Mollusca (incomplete list, work in progress, code list by H. Barbel)

The list of codes used for mammal species is provided in Appendix 6.

Note that you can select the default SPECIES tab in Layout edit mode (right click on the tab panel to access the "Tab Control Setup" dialog box, and then change the "Default Front Tab").

The (2) buttons will bring up sub-menus for small vertebrates, small and large carnivores.

(3) This section is intended to enter data for unidentified specimens classified by size classes. "MAM23" is the equivalent of "MAM2/3", an unidentified mammal of size class 2 or 3.

(4) is for unidentified specimens, with no size class. The "Autre..." or "Other..." button allows you to enter a code not listed above (for example, if a species you identified is not included in TIPZOO codes).

(5) The text box at the top allows you to directly edit the species code if necessary. "To Check", "To Improve" and "Taxonomic observations" can be used to mark specimens of interest.

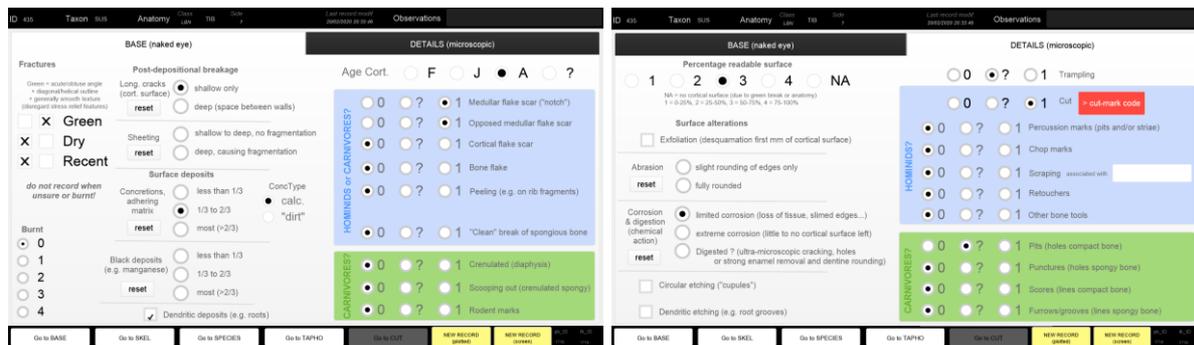
(6) Once you are done, press the yellow button to go further.

V. Data entry for bone fragments: the TAPHO table

Once anatomical and taxonomic identifications are entered, and if the fragment is above the defined size limit (cf. Settings in the Main menu), you will see access the layout for taphonomic observations (TAPHO table).

Which taphonomic variables are included in TIPZOO, how they are defined, their possible states and when they should (or should not) be recorded is provided in the (long!) table provided in the next pages. This table is however not intended to replace the thorough reading of the abundant literature available on taphonomic alterations that every zooarchaeological student should perform (starting, for example, with the book by Fernandez-Jalvo and Andrews, 2016).

Despite the apparent complexity of the following table, the TAPHO layout is conceived so that it is not necessary to frequently go back to this table: 1) variables are named in the layout in full letters, instead of their code; 2) short texts are provided for each possible value to remind the user of their definition; 3) variables that should not be coded (e.g. for a tooth, or for a burnt fragment) are by default invisible to the user. With this system, using TIPZOO to enter taphonomic data should be straightforward for an experienced zooarchaeologist. **AUTOFILL**: Note that by default, all taphonomic alterations except readability are set to “0” at record creation (or “NA” if not applicable, as in the case of teeth and carbonised fragments for certain variables). This increases data entry speed for fragments with few taphonomic alterations.



Example of a record in the TIPZOO TAPHO layout, with its two panels.

The TAPHO layout is composed of two panels:

- The “BASE (naked eye)” panel includes the recording of fractures (only for long bone fragments) and taphonomic variables that should be recorded by macroscopic (naked eye) observations (as well as the Burnt and AgeCort variables, in case you made a mistake and would like to correct it without going back to the BASE or the SKEL layouts).
- The “DETAILS (microscopic)” panel includes variables that should be recorded while looking at the fragment with an hand lens or a binocular microscope.

Variables that are binary (0 or 1) are shown as check boxes. Variables that are more complex (several options) are shown as radio buttons. For longitudinal cracks, sheeting, concretions, black deposits, abrasion and corrosion, if after pressing a button you want to go back, you can press the “reset” button close to it. Note that C_SUM is a variable automatically calculated by TIPZOO that returns 1 if at least one of type of carnivore marks (C_ variables) is set to 1, or 0 if they all equal 0. P_SUM works the same way, but for “P_” variables. These are invisible in the layout, but used in TIPZOO-R.

When a cut-mark is recorded, a red button “> cut-mark code” appears, allowing to record cut-mark codes (cf. next section of the manual). This button turns grey once a cut-mark code is recorded for the fragment.

The two yellow buttons at the very bottom-right of the layout allows for quick creation of a new record (either plotted or screen). **AUTOCHECK**: by default, TIPZOO checks that Readability is recorded before creating a new record.

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Scale obs.	Type	Code	Name	Possible states (with explanations in parentheses)	Details	Other names used in the literature (including French terms)	Elements EXCLUDED for this variable
Naked eye	Fractures	Fract1	Fracture of one end of a long bone	Green Dry Recent	Fractures are only recorded for long bones. Green-bone fractures have acute/obtuse fractures angles, diagonal/helical outlines, and a generally smooth texture (disregarding stress relief features); dry-bone fractures have right-angled fractures, transverse outlines, and irregular textures; recent fractures have a distinctive white surface (cf. Villa and Mahieu, 1991). If the fracture is hardly categorised, if the bone is unbroken or burnt, fractures are not recorded.		All except long bones. Burnt > 1 (at least carbonized).
		Fract2	Fracture of the other end of a long bone	Green Dry Recent			
	Post-dep. breakage	Crack	Longitudinal cracks	0 (absent) 1 (only shallow cracks) 2 (deeper cracks)	Cracks on the cortical surface, parallel to the bone axis. Only coded for the exterior surface of the bone. Cracks due to burning, excavation damage or green-bone breaks are not coded. Cracks are considered deep when an empty space is clearly visible between the fissure walls with the naked eye.	fissures longitudinales, craquelures	Tooth or Burnt > 1 (at least carbonized)
		Sheet	Sheeting	0 (absent) 1 (cracks only) 2 (fragmentation)	Cracks in the bone thickness, parallel to the cortical surface, or bones that have broken down into one or more sheets following these cracks.	délitement, gelifraction, piles d'assiettes, "frites"	Tooth or Burnt > 1 (at least carbonized)
	Surface deposits	Conc	Extent of concretions	0 (absent) 1 (covering <1/3) 2 (covering 1/3 to 2/3) 3 (covering >2/3)	Concretions, adhering matrix. Coded in function of the cortical surface that is covered.		
		ConcType	Type of concretions	calc. (calcareous concretions) "dirt" (adhering matrix/cemented dirt)			
		Black	Black deposits	0 (absent) 1 (covering <1/3) 2 (covering 1/3 to 2/3) 3 (covering >2/3)	Black deposits, staining, on the cortical surface. Dark spots on the enamel are not considered. Coded in function of the cortical surface that is covered.	oxydes, "manganese" staining	Tooth or Burnt > 1 (at least carbonized)
		DenD	Dendritic deposits	0 (absent) 1 (present)	Deposits that are divided into branches or sinuous.	root marks (deposits), racines depots	Burnt > 1 (at least carbonized)

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Naked eye	Hominids or carnivores?	P_scar	Medullar flake scar	0 (absent) ? (uncertain) 1 (present)	Percussion "notch" on the medullar surface.	encoche, impact notch	Tooth
		P_oppo	Opposed medullar flake scar	0 (absent) ? (uncertain) 1 (present)	Percussion "notch" on the medullar surface, opposed to another "notch".	contre encoche	Tooth
		P_cort	Cortical flake scar	0 (absent) ? (uncertain) 1 (present)	Percussion "notch" on the cortical surface.		Tooth
		P_flake	Bone flake	0 (absent) ? (uncertain) 1 (present)	Bone flake with a detachment bulb. This includes bone flakes still adhering to a larger fragment.	éclat osseux	Tooth
		P_peel	Peeling fracture	0 (absent) ? (uncertain) 1 (present)	Peeling of the bone surface due to a fracture, as in rib or ulna fragments for example.	fracture par arrachement	Tooth
		P_tooth	"Clean" tooth break	0 (absent) ? (uncertain) 1 (present)	Clean oblique break of tooth, "split barrel".	"fût fendu"	No tooth
		P_spong	"Clean" break of spongy bone	0 (absent) ? (uncertain) 1 (present)	"Clean" break of spongy bone.		Tooth

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Naked eye	Carnivores?	C_cren	Carnivore crenulated	0 (absent) ? (uncertain) 1 (present)	Crenulated shafts. The abundant literature on these marks cannot be summarised up here.		Tooth
		C_scoop	Carnivore scooping out	0 (absent) ? (uncertain) 1 (present)	Crenulated epiphyses. The abundant literature on these marks cannot be summarised up here.		Tooth
		Rodent	Rodent marks	0 (absent) ? (uncertain) 1 (present)	The abundant literature on these marks cannot be summarised up here.	rongeurs	Tooth
Microscopic	Surface alterations	Read	Readability	1 (<25%) 2 (25-50%) 3 (50-75%) 4 (>75%) NA (no cortical surface)	Percentage of the cortical surface that is well-preserved (sufficiently well so that cut-marks would be preserved). Comparable to the "percentage intact" used by Olsen, 1989; White, 1992. AUTOFILL: automatically set to "NA" for teeth.	percentage of intact surface, lisibilité, severity	Tooth
		Exfo	Exfoliation	0 (absent) 1 (present)	Desquamation of the first mms of cortical bone (bone surface peeling away, like "onion peels")	desquamation	Tooth or Burnt > 1 (at least carbonized)
		Abra	Abrasion	0 (absent) 1 (slight rounding of edges) 2 (important, entirely rounded)	abraded edges, "rounding" of sharp edges and other features (such as foramen or tuberosities)	abrasion, émoussé	
		CorDig	Corrosion and digestion	0 (absent) 1 (limited corrosion, slimed edges) 2 (extreme corrosion, little to no cortical surface left) 3 (digested?)	Loss of tissue through chemical action, without cracks or flaking, not concentrated in grooves or linear marks. Digestion (?) is identified by ultra-microscopic cracking, holes or strong enamel removal and dentine rounding, cortical layer of bone has almost dissapeared leaving bone histological traits exposed, cf fernandez andrews	dissolution, altération chimique, digestion, surfaces lunaires	
		DenE	Dendritic etching	0 (absent) 1 (present)	Grooves/holes on the surface that are divided into branches or sinuous	creusement racinaire, root groove marks, root etching	
		CirE	Circular etching	0 (absent) 1 (present)	Small semi-circular holes on the surface	cupules de dissolution	

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Microscopic		Tramp	Trampling marks	0 (absent) ? (uncertain) 1 (present)	Less deep liner marks, shorter, much more frequent on one bone, often transverse, often U-shaped, randomly distributed. Trampling marks are not recorded on enamel (they can be due to feeding activities). The abundant literature on these marks cannot be summarised up here.	Piétinement	
	Hominids?	Cut	Cut marks	0 (absent) ? (uncertain) 1 (present)	Deep linear marks, often V-shaped. The abundant literature on these marks cannot be summarised up here.	Stries de découpe	
		P_mark	Percussion marks	0 (absent) ? (uncertain) 1 (present)	The abundant literature on these marks cannot be summarised up here.		
		Chop	Chop marks	0 (absent) ? (uncertain) 1 (present)	Extremely deep cut-marks.	hackmarks (Binford, 1981)	
		Scrape	Scrape marks	0 (absent) ? (uncertain) 1 (present)	The abundant literature on these marks cannot be summarised up here.		
		Scrape_Aссо	Marks associated with scrape marks	fracturation retouchoir nothing ? (uncertain)			
		Ret	Retouchers	0 (absent) ? (uncertain) 1 (present)	The abundant literature on these marks cannot be summarised up here.		
		BoneTool	Other bone tool	0 (absent) ? (uncertain) 1 (present)	Bone tool other than retouchers. The abundant literature on these marks cannot be summarised up here.		

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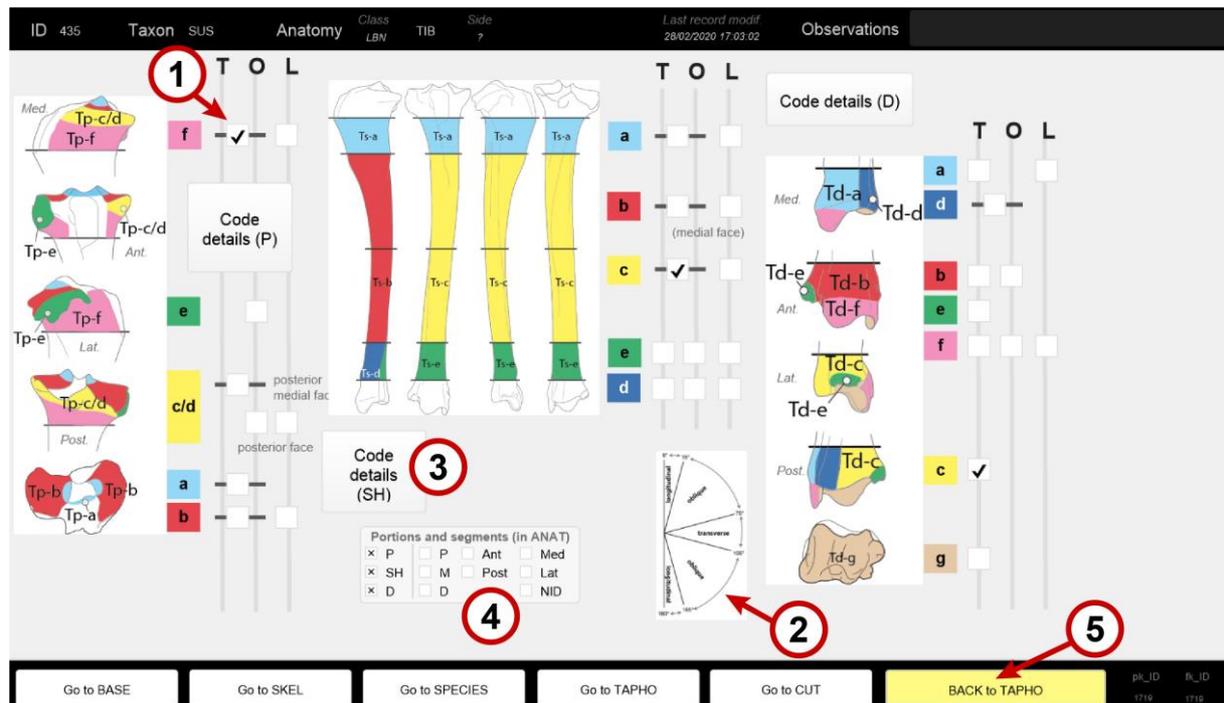
Microscopic	Carnivores?	C_pit	Carnivore pits	0 (absent) ? (uncertain) 1 (present)	Holes (length < 4*width) in compact bone. The abundant literature on these marks cannot be summarised up here.		Tooth
		C_punct	Carnivore punctures	0 (absent) ? (uncertain) 1 (present)	Holes in spongy bone. The abundant literature on these marks cannot be summarised up here.		Tooth
		C_scor	Carnivore scores	0 (absent) ? (uncertain) 1 (present)	Linear marks on compact bone. The abundant literature on these marks cannot be summarised up here.		Tooth
		C_furr	Carnivore furrows/grooves	0 (absent) ? (uncertain) 1 (present)	Linear marks on spongy bone. The abundant literature on these marks cannot be summarised up here.		Tooth

VI. Data entry for bone fragments: the CUT table

If a fragment has a cut-mark, you will have the possibility, by pressing a button in the TAPHO layout (named “> cut-mark code”), to record its position and orientation using the CUT table and layouts. Note that scrape marks should not be recorded using this system.

These layouts are intended as a graphical aid to use the recording system of cut-marks defined by Soulier and Costamagno (Soulier and Costamagno, 2017; Costamagno and Soulier, 2019). These authors defined a coding system that allows one to link a cut-mark to a specific butchering activity depending on its orientation and position. Their coding system is however complex and hard to use (in total, there is more than 400 different codes!).

Pressing the “> cut-mark code” button will bring you to the appropriate layout (depending on the skeletal element):



Example of a record in the TIPZOO CUT layout for tibia fragments.

In the following paragraphs, numbers in brackets - as (1) or (2) - pertain to the image above.

(1) Once you have identified the anatomical region where a cut-mark is present using the colour codes of the images, you should click the correct box according to its orientation, with “T” for transverse, “O” for oblique, and “L” for longitudinal. In this example, the checked box records a cut-mark present in the Tp-f region that is transverse or oblique. The (2) image recalls how orientation classes are defined. Note that codes for the proximal extremity are often presented on the left of the layout, codes for the shaft in the middle, and codes for the distal extremity on the right.

(3) Pressing the “code details” buttons while bring a sub-menu with more information on the definition of cut-mark codes to ensure appropriate recording. Reading the *princeps* literature by Soulier and Costamagno (*ibid*) is obviously highly recommended.

(4) is a quick representation of which portions and segments were previously entered in TIPZOO to facilitate cut-mark recording.

(5) Once you are done, you should click this button to go back to the TAPHO layout.

The codes used in TIPZOO follow Soulier and Costamagno work, with only two exceptions: for the mandible, codes Man_c' (longitudinal cut-marks, vestibular side) and Man_g (oblique cut-marks, lingual side) were added.

VII. Data entry for MNE (minimal number of elements)

This layout is still in development, but accessible for test purposes. Hence, the description provided below is limited.

From the TIPZOO main menu, you can access the MNE recording layout by pressing the "RECORDING LAYOUT FOR MNE VALUES" button. In this layout, once you have selected the taxon and assemblage (one value from USfield, Group1, Group2 or Group3), you can create blank MNE records (either all records - one per anatomical element -, or one record only).

The main feature of this layout is that it gives you, in the bottom part, a list of all the fragments that are corresponding a given combination of species+skeletal element+assemblage (i.e. layer), and thus facilitates the consideration of these fragments for MNE calculation.

VIII. Appendixes

!/\ THE USER DOES NOT NEED TO LEARN THESE ABBREVIATIONS TO USE TIPZOO-FMP !/\

1. Codes used in the SKEL table for the Anat_Class field

Anat_Class	Element class
FBN	Flat bones
LBN	Long bones
SBN	Small bones
Skull	Skull fragments
NID	Unidentified
NMB	Non-mammal bones (added in version 1.1)

2. Codes used in the SKEL table for the Anat field

Anat_Class	Anat	Element
LBN	HUM	Humerus
	RAU	Radius et ulna
	FEM	Femur
	TIB	Tibia
	PHA	Phalange
	MC	Metacarpal
	MT	Metatarsal
	MP	Unidentified metapodial
	LBN	Unidentified long bone
	MPV	Vestigial metapodial
Skull	CRA	Cranium, including maxillary (can have antler and/or horn core)
	CRAT	Cranium with teeth (can have antler and/or horn core)
	MAN	Mandible
	MANT	Mandible with teeth
	ANT	Antler (only)
	HCO	Horn core (only)
	TTH	Isolated tooth
	SKU	Unidentified skull bone (maxillary or mandible)
	SKUT	Teeth with unidentified skull bone (maxillary or mandible)
FBN	FBN	Unidentified flat bone
	VRT	Vertebras
	RIB	Ribs and costal cartilage
	STE	Sternum
	SCP	Scapula
	COX	Coxal (pelvis)

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	HYO	Hyoid
SBN	SBN	Unidentified small bone
	CAR	Carpals
	TAR	Tarsals
	PAT	Patella
	MAL	Malleol
	SES	Sesamoids

Non-mammal bones are not listed here.

!/\ THE USER DOES NOT NEED TO LEARN THESE ABBREVIATIONS TO USE TIPZOO-FMP !/

3. Codes used in the SKEL table for the Anat_Detail field

Anat	Anat_Detail	Element (detail)
PHA	PH1	First (proximal) phalange
	PH2	Second phalange
	PH3	Third (distal) phalange
	PH1v	First vestigial phalange
	PH2v	Second vestigial phalange
	PH3v	Third vestigial phalange
	PHA	Unidentified phalange
MC	MC1	First metacarpal
	MC2	Second metacarpal
	MC3	Third metacarpal
	MC4	Fourth metacarpal
	MC5	Fifth metacarpal
MT	MT1	First metatarsal
	MT2	Second metatarsal
	MT3	Third metatarsal
	MT4	Fourth metatarsal
	MT5	Fifth metatarsal
VRT	ATL	Atlas
	AXI	Axis
	CER	Other cervical
	THO	Thoracic
	LUM	Lumbar
	SAC	Sacrum
	CAU	Caudal
	VRT	Unidentified vertebra
CAR	CAR	Unidentified carpal
	SCA	Scaphoid
	LUN	Lunatum (semilunar)
	PYR	Pyramidal (triquetal)
	PIS	Pisiform

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	CAP	Capitatum
	HAM	Hamatum (unciform)
	CTT	Capitato-trapezoid
	TRZ	Trapezoid
	TRA	Trapeze
	SCL	Scapholunate
TAR	GCF	Greater cuneiform
	SCF	Smaller cuneiform
	CBN	Cubonavicular
	CAL	Calcaneus
	TAL	Talus (astragalus)
	CUB	Cuboid
	NAV	Navicular
ANT	Shed	Shed antler
	Massacred	Massacred antler (i.e. from an animal that was killed)

Non-mammal bones are not listed here.

!/\ THE USER DOES NOT NEED TO LEARN THESE ABBREVIATIONS TO USE TIPZOO-FMP !/

4. Codes used in the SKEL table for the Portion field

Anat	Portion	Portion (description)
COX	ILI	Ilium
	ISC	Ischium
	PUB	Pubis
	ACE	Acetabulum
CRA and CRAT	MAX	Maxillary
	NAS	Nasal
	FRO	Frontal
	ORB	Orbit
	TEM	Temporal / petrous
	PAR	Parietal
	OCC	Occipital
	ANT	Antler
SCP	HCO	Horn core
	GLEscp	Glenoid cavity
	BODscp	Body
VRT	SPIscp	Spine
	BOD	Body
	BODe	Body with unfused discs
	DISC	Fused disc
	DISCe	Unfused disc
	TRP	Transverse process
ARP	Articular process	

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	SPlvrt	Spine
LBN other than RAU	P	Proximal extremity
	SH	Shaft
	D	Proximal extremity
	E	Unidentified extremity
RAU	radP	Proximal extremity of the radius
	radSH	Shaft of the radius
	radD	Proximal extremity of the radius
	radE	Unidentified extremity of the radius
	ulnP	Proximal extremity of the ulna
	ulnSH	Shaft of the ulna
	ulnD	Proximal extremity of the ulna
	ulnE	Unidentified extremity of the ulna
MAN and MANT	COND	Condyle
	CORO	Coronoid process
	RAM	Ramus (branch)
	ALV	Alveolar process
	BODman	Body (horizontal)
	SYM	Symphysis
HCO and ANT	TIP	Tip
	BASE	Base
RIB	BOD	Body
	P	Proximal end
	D	Distal end
	COST	Costal cartilage

Non-mammal bones are not listed here.

!/\ THE USER DOES NOT NEED TO LEARN THESE ABBREVIATIONS TO USE TIPZOO-FMP !/

5. Codes used in the TEETH table

Type	Class	Dentition	Number	UW_Crown	UW_Root	UW_RootResorp
Anterior	Incisor	Permanent	1	0 (no use)	0 (closed, complete)	1 (if root resorption)
Cheek	Canine	Deciduous	2	1 (little use)	1 (open, >50% of the root formed)	
?	Premolar	?	3	2 (in use)	2 (open, <50% of the root formed)	
	Molar		4	3 (very used)		
	?		?			

6. Codes used for mammal species in the SPECIES table

Code	Scientific name	Common name	Size class	Used in:				
				European wild macrofauna	Domestic taxa	African carnivores	African herbivores	Arctic mammals
ACYN	<i>Acynonix</i> sp.		LCARN		x			
AEPY	<i>Aepyceros</i> sp.		MAM2				x	
ALCE	<i>Alcelaphus</i> sp.		MAM3				x	
ANTID	<i>Antidorcas</i> sp.		MAM2				x	
BB	Bovinae	Auroch and bison	MAM4	x				
BOST	<i>Bos taurus</i>	Cattle	MAM4		x			
CAB	<i>Equus ferus</i>	Horse	MAM3	x	x			
CANF	<i>Canis familiaris</i>	Dog	-		x			x
CANI	<i>Canis</i> sp.		SCARN		x	x		
CAPRA	<i>Capra</i> sp.	Ibex	MAM2	x				
CAPREO	<i>Capreolus</i> sp.	Roe deer	MAM1	x				
CAPRH	<i>Capra hircus</i>	Domestic goat	MAM2		x			
CAPRI	Caprinae	Caprinae (goat, sheep...)	MAM2		x			
CARC	<i>Caracal</i> sp.		SCARN			x		
CAST	<i>Castor</i> sp.	Beaver	SVERT	x				
CC	<i>Cystophora cristata</i>	Hooded seal	LP					x
CEL	<i>Cervus elaphus</i>	Red deer	MAM23	x				
CEPH	<i>Cephalophus</i> sp.		MAM1				x	
CHASM	<i>Chasmaporthetes</i> sp.		LCARN			x		
CONNO	<i>Connochaetes</i> sp.		MAM3				x	
CROC	<i>Crocuta crocuta</i>	Spotted hyena	LCARN	x		x		
DAM	<i>Damaliscus</i> sp.		MAM23				x	
DAMA	<i>Dama dama</i>	Fallow deer	MAM2	x				
DINO	<i>Dinofelis</i> sp.		LCARN			x		
EB	<i>Erignathus barbatus</i>	Bearded seal	LP					x
EQUA	<i>Equus africanus</i>	African wild ass & donkey	MAM23		x			
EQUID	<i>Equus</i> sp.		MAM3	x	x		x	
FEL	<i>Felis</i> sp.		SCARN			x		
FELIC	<i>Felis catus</i>	Cat	SCARN		x			
FELIS	<i>Felis silvestris</i>	Wild cat	SCARN	x				
GIRAF	Giraffidae		MAM45				x	
HG	<i>Halichoerus grypus</i>	Grey seal	LP					x
HIPPOP	Hippopotamidae		MAM45				x	
HIPPOT	<i>Hippotragus</i> sp.		MAM3				x	

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HYDR	<i>Equus hydruntinus</i>	Wild ass	MAM23	x				
HYEN	<i>Hyaena hyaena</i>	Striped hyena	LCARN			x		
KOB	<i>Kobus sp.</i>		MAM23				x	
LAGO	Lagomorpha	Lagomorphs	SVERT	x				x
LBOV	-	Unidentified large bovid	MAM4				x	
LCARN	-	Unidentified large carnivore	LCARN	x	x	x		x
LEP	<i>Lepus sp.</i>	Hare	SVERT	x				
LEPA	<i>Lepus arcticus</i>	Arctic hare	SVERT					
LP	-	Unidentified large pinniped	LP					x
LUP	<i>Canis lupus</i>	Wolf	LCARN	x				x
LYC	<i>Lycaon sp.</i>		LCARN			x		
LYNX	<i>Lynx sp.</i>	Lynx	SCARN	x				
MAD	<i>Madoqua sp.</i>		MAM1				x	
MALC	-	Unidentified medium alcelaphine	MAM23				x	
MAM	-	Unidentified mammal	-					x
MAM1	-	Unidentified mammal, size 1	MAM1	x	x	x	x	
MAM12	-	Unidentified mammal, size 1/2	MAM12	x	x	x	x	
MAM2	-	Unidentified mammal, size 2	MAM2	x	x	x	x	
MAM23	-	Unidentified mammal, size 2/3	MAM23	x	x	x	x	
MAM3	-	Unidentified mammal, size 3	MAM3	x	x	x	x	
MAM34	-	Unidentified mammal, size 3/4	MAM34	x	x	x	x	
MAM4	-	Unidentified mammal, size 4	MAM4	x	x	x	x	
MAM45	-	Unidentified mammal, size 4/5	MAM45	x	x	x	x	
MAM5	-	Unidentified mammal, size 5	MAM5	x	x	x	x	
MARM	<i>Marmota sp.</i>	Marmot	SVERT	x				
MBOV	-	Unidentified medium bovid	MAM23				x	
MEG	<i>Megaloceros giganteus</i>	Irish elk	MAM4	x				
MEGAN	<i>Megantereon sp.</i>		LCARN			x		
MELES	<i>Meles meles</i>	Badger	SCARN	x				
MUST	Mustelidae	Mustelids	SCARN	x				
NEO	<i>Neotragus sp.</i>		MAM1				x	
OREO	<i>Oreotragus sp.</i>		MAM1				x	
ORY	<i>Oryctolagus sp.</i>	Rabbit	SVERT	x				
OURE	<i>Ourebia sp.</i>		MAM1				x	
OVIA	<i>Ovis aries</i>	Sheep	MAM2		x			
PARAH	<i>Parahyaena brunnea</i>	Brown hyena	LCARN			x		
PELE	<i>Pelea sp.</i>		MAM2				x	
PG	<i>Pagophilus groenlandicus</i>	Harp seal	SP					
PH	<i>Phoca hispida</i>	Ringed seal	SP					x
PLEO	<i>Panthera leo/spelaea</i>	Lion	LCARN	x		x		
PPAR	<i>Panthera pardus</i>	Leopard	LCARN	x		x		
PROBO	Proboscidea	Proboscideans	MAM5	x			x	
PROT	<i>Proteles sp.</i>		SCARN			x		
PSP	-	Unidentified seal	-					x
PV	<i>Phoca vitulina</i>	Harbor seal	SP					x
RANG	<i>Rangifer tarandus</i>	Reindeer/caribou	MAM2	x				

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RAPHI	<i>Raphicerus</i> sp.		MAM1					x	
REDUN	<i>Redunca</i> sp.		MAM2					x	
RHINO	Rhinocerotidae	Rhinoceros	MAM45	x				x	
RUPI	<i>Rupicapra</i> sp.	Chamois	MAM1	x					
SAIGA	<i>Saiga tatarica</i>	Saiga antelope	MAM2	x					
SBOV	-	Unidentified small bovid	MAM1					x	
SCARN	-	Unidentified small carnivore	SCARN	x	x	x			
SP	-	Unidentified small pinniped	SP						x
SUD	<i>Sus domesticus</i>	Domestic pig	MAM2		x				
SUI	<i>Sus</i> sp.	Wild boar or domestic pig	MAM2		x				
SUID	Suidae		MAM23					x	
SUS	<i>Sus scrofa</i>	Wild boar	MAM2	x					
SYLVI	<i>Sylvicapra</i> sp.		MAM1					x	
SYNC	<i>Syncerus</i> sp.		MAM4					x	
TAURO	<i>Taurotragus</i> sp.		MAM4					x	
TRAG	<i>Tragelaphus</i> sp.		MAM23					x	
UMM	-	Unidentified marine mammal	-						x
URSA	<i>Ursus arctos</i>	Brown bear	LCARN	x					x
URSAM	<i>Ursus americanus</i>	American black bear	LCARN						x
URSI	<i>Ursus</i> sp.	Bear	LCARN	x					x
URSM	<i>Ursus maritimus</i>	Polar bear	LCARN						x
URSS	<i>Ursus spelaeus</i>	Cave bear	LCARN	x					
UTM	-	Unidentified terrestrial mammal	-						x
VULPA	<i>Vulpes lagopus</i>	Polar fox	SCARN	x					x
VULPI	Vulpinae	Fox	SCARN	x		x			x
VULPV	<i>Vulpes vulpes</i>	Red fox	SCARN	x					
WAL	<i>Odobenus rosmarus</i>	Walrus	LP						x

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