CO-MOVE - Structure of the database (project)

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**Each ancient individual should occupy a separate line of the database:**

* **Own\_ID**
* **Skeleton\_ID** (usually the burial number, as given in the archaeology literature, NB: if multiple individuals are buried within the same burial, separate data entries should be created for each individual, e.g. “54b”, “54e”; the recording system for individual skeletons may vary a great deal from excavations to excavations – e.g. “ZHP”, “10986.X29”, “89D-17.1-07”)
* **Mound\_ID** (if relevant, e.g. “Barrow 5”, “Tumulus 1”)

Mound

width

height

* **Geography**
  + **Locality** (usually nearby village/town, e.g. “Altwies”, “Mogila”)
  + **Site\_Name** (may be same as above or different, e.g. Altwies-“Op dem Boesch“; can also refer to one part of the general site e.g. “Çatalhöyük East”, “Çatalhöyük West”)
  + Site\_code (I would suggest a three-letter code, e.g. “ALW” for Altwies, “LV\_” for Lepenski Vir; can be harmonized later on)
  + **Country\_code** (ISO2 should be fine, e.g. “FR” – France, “DE” – Germany)
  + **Latitude** (in decimal degrees with five decimal places, e.g. “48,58187”)
  + **Longitude** (same as above, e.g. “7,62651”)
* **Chronology** (referring here to the chronology of the specific skeleton, not the overall tumulus/site)
  + **Period** (if available, as ascribed in the literature, e.g. “LN” – Late Neolithic, “EBA” – Early Bronze Age; can be harmonized later on)
  + **Phase** (if available, as ascribed in the literature, e.g. “A2”) – not necessary, combined with period, complex to validate dependent columns
  + **Context\_Date** (if no 14C date is available, but a chronological assessment has been made based on material recovered inside the grave etc., an approximate date or range should be reported here in years BC, e.g. “2500-1700”; if a 14C date is available, leave blank?) **-** context\_from and context\_to, for single date, leave context\_to empty
  + **14C\_Date** (if available, “Y” – yes, “N” – no, “..” – no data) – not necessary, oxcal\_mu will be null or not
  + **C14\_Date** (the weighted mean / μ value of the calibrated radiocarbon interval in years BC, as provided by OxCal, e.g. “5888”; if several 14C dates are given, the μ value should be obtained using the Combine\_ function in OxCal)
    - **A\_Date**
      * **14C\_type** (if direct date from the skeleton, report as “direct”; if taken from material recovered in the grave, report as “indirect”)
      * **Lab\_ID** (the lab code, as reported, e.g. “OxA-25207”, “BRAMS-2564”)
      * **Age\_BP** (the uncalibrated BP age, as reported, e.g. “7757”)
      * **Interval** (the interval of the uncalibrated BP date, e.g. “24”)
      * **Material** (if the sample dated was taken directly from the human skeleton, this should be reported as “human bone” or actual body part e.g. “LPP” – left pars petrosa; if material from the grave fill, this should be reported as e.g. “charcoal”, “grain”, “animal bone”)
      * calBC\_1sigma\_Max
      * calBC\_1sigma\_Min
      * calBC\_2sigma\_Max
      * calBC\_2sigma\_Min
      * date\_note
      * cal\_method
      * ref\_14c
    - **B\_Date**
    - **C\_Date**
    - **…**
  + **Ref\_14C** (usually the publication in which the 14C date was first reported; if multiple dates are reported, a list of those should be provided separated by a semi-colon, e.g. “Borić 2011; Borić and Price 2013; Bonsall et al. 2015”) **– should also be in C14\_Date**
  + **Cal\_method** (eventually should be the same for all samples, e.g. OxCal 4.4.2 / IntCal20) **- should be contained in C14\_Date**
  + **Date\_Note** (an open field for important additional chronological information, e.g. “needs correction for freshwater reservoir effect”) **- should be contained in C14\_Date**
* **Taxonomy**
  + **Culture** (first-level cultural attribution, as given in the literature, e.g. “LBK” – Linearbandkeramik, “Rössen”, “CW” – Corded Ware, “BB” – Bell Beaker, “GA” – Globular Amphora, “YA” – Yamnaya, “Proto-YA” – Proto-Yamnaya)
  + **Culture\_Note** (an open field to record second- or third-level cultural attribution or regional variant, e.g. “Eastern Baltic Corded Ware”, “Złota Group”)
  + **Culture\_reference** (in effect the reference in which the cultural attribution was given, e.g. “Limbursky 2012”)

* **Anthropology**
  + **Sex\_Morph** (morphological sex, as reported, in the format “f” – female, “m” – male, “u” – unclear, “..” – no data)
  + **Sex\_Gen** (genetic sex, as reported, in the format “XX” – female, “XY” – male, “U” – unclear, “..” – no data)
  + Sex\_Consensus(a consensus determination for the sex of the individual, based on the quality of the data, with genetic sex as major e.g. a ‘f’, ‘U’ burial would be a “f”; but a ‘f’, ‘XY’ would be a “XY”)
  + **Age\_as\_reported** (e.g. “35-45”, “mid-adult”, “maturus II”)
  + Age\_Class (ideally should be harmonized, e.g. “neonate”, “child”, “young adult”; the estimated age could be given in brackets, e.g. “child (2-5)”)
  + **Height** (if available, in cm, e.g. “164,22”)
  + **Pathologies** (if available, “Y” – yes, “N” – no, “..” – no data)
  + **Pathologies\_type** (an open field, describing any relevant pathology observed on the skeleton, e.g. “Caries, osteoarthritis”)
  + disturbed (contemporary, later, no, unclear)
  + Species (Human, Cattle, Horse etc)

Injuries

* + - origin - inter human violence, accidents, sickness etc
    - position of the injury
* **Stable Isotopes**
  + **Delta\_C\_13** (*δ*13C value ‰, if multiple values are given for the same individual, each value should be recorded separately)
    - **A\_Delta\_C\_13** 
      * **Iso\_ID** (if available, the lab code of the stable isotope value, e.g. “AJ.13.b”)
      * **Iso\_bone** (the tooth/bone sampled, e.g. “PM2 right”)
      * **Iso\_value** (*δ*13C value ‰, e.g. “-19,80”)
      * **Ref\_Iso** (usually the publication in which the stable isotope value was first reported, e.g. “Borić and Price 2013”)
    - **B\_Delta\_C\_13**
    - **C\_Delta\_C\_13**
    - **…**
  + **Delta\_15\_N** (*δ*15N value ‰, if multiple values are given for the same individual, each value should be recorded separately)
    - **A\_Delta\_15\_N** 
      * **Iso\_ID** (if available, the lab code of the stable isotope value, e.g. “AJ.13.b”)
      * **Iso\_bone** (the tooth/bone sampled, e.g. “PM2 right”)
      * **Iso\_value** (*δ*15N value ‰, e.g. “8,71”)
      * **Ref\_Iso** (usually the publication in which the stable isotope value was first reported, e.g. “Borić and Price 2013”)
    - **B\_Delta\_15\_N**
    - **C\_Delta\_15\_N**
    - **…**
  + **87Sr\_86Sr** (87 Sr/86 Sr ratio, if multiple values are given for the same individual, each value should be recorded separately
    - **A\_87Sr\_86Sr** 
      * **Iso\_ID** (if available, the lab code of the stable isotope value, e.g. “AJ.13.b”)
      * **Iso\_bone** (the tooth/bone sampled, e.g. “PM2 right”)
      * **Iso\_value** (87 Sr/86 Sr ratio, as reported, e.g. “0,710942”)
      * **Sr\_baseline** (assessment based on the local baseline, either “local” or “non-local”)
      * **Ref\_Iso** (usually the publication in which the stable isotope value was first reported, e.g. “Borić and Price 2013”)
    - **B\_87Sr\_86Sr**
    - **C\_87Sr\_86Sr**
    - **…**
  + **Delta\_34\_S** (*δ*34S value ‰, if available, same as above)
  + **…**
* **Genetics**
  + **Genetic\_ID** (The lab code, e.g. “I4688”; if the individual has been sampled multiple times for DNA analysis, each sample should be recorded separately)
    - **A\_Gen\_ID** 
      * **Data\_type** (the quality of the DNA data, Reich data are typically “1240K.capture”; if a mitochondrial capture method was used, record as “mt.capture”; if the data has been shotgun sequenced, record as “shotgun”; if only screened for endogenous content, record as “screened”)
      * **Endo\_content** (endogenous DNA content, as reported in %, e.g. “42,80”)
      * **Gen\_bone** (the bone sampled for DNA, e.g. “PP” – pars petrosa, “L femur” – left femur)
      * **mtDNA\_haplo** (the mitochondrial haplogroup, e.g. “T2a1b2b”)
      * **Y\_haplo** (the Y haplogroup, e.g. “G2a2b2a3”; if female, record as “n/a (female)”, if no data, record as “..”)
      * **Ref\_Gen** (usually the publication in which the genome was first reported, e.g. “Patterson et al. 2021”)
    - **B\_Gen\_ID**
    - **C\_Gen\_ID**
    - **…**
* **Archaeology**
  + **Research\_year** (the year(s) in which the site was excavated)
  + **Research\_type** (typically “systematic excavation” if the site was systematically excavated for research purposes; “restricted excavation” if only a section of the site was excavated; “rescue excavations”; “accidental find”; “..” if no data available)
  + **Barrow\_info**
    - **Position\_in\_mound** (typically “central/close to centre”, “periphery”, “..”)
    - **Burial\_type**
    - **No\_inhumations**
    - **Pit\_length**
    - **Pit\_width**
    - **Pit\_depth**
    - **Pit\_shape**
    - **Pit\_type**
    - **Pit\_construction**
  + **Body\_info**
    - **Funerary\_practice** (typically “inhumation”, “cremation”)
    - **Inhumation\_type** (typically “primary” for an articulated skeleton, or “secondary” if disarticulated)
    - **Anatomical\_connection**
    - **Body\_position** (typically “crouched on the left”, “crouched on the right”, “extended supine” if the entire skeleton lays on its back, or “supine” if only the upper body lay on its back; “prone” if buried face down; “scattered bones” if bones are disarticulated or only lie in partial anatomical connection, without the possibility to infer burial type; “..” – no data)
    - **Crouching\_type** (“contracted” when the legs are drawn up to the chin and have an angle of 90° or less with the spinal column, “flexed” if the angle is more than right angle [Heise 2016, 96; after Childe 1947, 346])
    - **Arms\_position**
    - **Legs\_position**
    - **Head\_orientation**
    - **Head\_facing**
    - **Ochre** (if available, “Y” – yes, “N” – no, “..” – no data)
    - **Ochre\_position** (in relation to the body)
    - **Other** (an open field, to record any other important attribute, e.g. “phytolith layer” suggesting the presence of a mat or rug)

**Grave\_goods**

**grave**

**skeleton**

**type** - shaft axe, amber, pot, etc

closest\_bone (when skeleton)

bounding box (x1, y1, x2, y2)

Grave

general type (kurgan, megalithic, stone cyst, pit, etc)

area

arc\_length

depth