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LETTER TO THE EDITOR

Entheseal changes and estimation of adult age-at-death

In identified skeletal collections, age-at-death is the main variable explaining the distribution of entheseal changes (ECs) in adults: older individuals tend to display more ECs and more exuberant changes than younger ones (e.g., Mariotti et al., 2004; Milella et al., 2012; Shaibani et al., 1993; Villotte, 2009). This has led to an attempt, published recently in AJPA (now AJBA), to estimate adult age-at-death from EC stages (Milella et al., 2020). In their article, Milella and colleagues used scores of "robusticity" (one type of EC) as predictors in multiple regression analyses with age as the dependent variable. The results are relatively disappointing: even with an age prediction interval of ±20 years, the percentage of correctly classified individuals barely reaches 80% in their study. This poor performance is likely related to the expectation of an implicit linear relation between ECs and chronological age, whereas too many factors (e.g., genetic background, hormonal levels, physical activity levels) interact in EC development. As a result, the correlation between chronological age and ECs, although statistically significant, remains too low in our opinion to reliably and accurately estimate age-at-death using statistical approaches such as the one developed by Milella and collaborators. As we highly esteem the numerous and excellent studies carried on by our colleagues on various aspects of ECs (e.g., Bertsatos et al., 2021; Mariotti et al., 2004; Milella et al., 2012), and as their recent article in your journal motivated us to think about this issue, we would like to submit to them, and more broadly to the readers of the AJBA, a very simple idea that may create new avenues in the estimation of adult age-at-death using ECs.

If this correlation between age and ECs is well known, the underlying physio(patho)logical processes involved are not (Villotte & Knüsel, 2013). However, we do know that these processes likely differ, at least in part, for fibrocartilaginous and fibrous entheses (for this specific point, and for a presentation these two types of entheses in biological anthropology, see Villotte & Knüsel, 2013). Milella et al. (2020) noted that "When fibrous and fibrocartilaginous entheses are treated separately, the former outperforms the latter (in age-at-death estimation)". This is in agreement with a previous work that has shown a stronger correlation between chronological age-at-death and ECs at fibrous sites, compared to fibrocartilaginous ones (Villotte, 2009). However, careful data analyses indicate that (a) for both types of entheses this correlation remains too low for reliable age-at-death estimation (Henderson et al., 2017; Villotte, 2009) and (b) for some fibrocartilaginous entheses, major ECs appear almost exclusively after the fourth decade of life and are usually seen in 50+ year-old individuals (Villotte, 2009). By "Major ECs" we mean exuberant changes (usually mineralized tissue formation associated with surface discontinuity) that affect the entire attachment site. Thus, even if the correlation of EC stages and chronological age-at-death is weaker for fibrocartilaginous entheses, major ECs for these attachment sites seem potentially good indicators of older individuals (a similar idea has been recently formulated [though not tested] by Bertsatos et al., (2021)).

Major ECs could thus be relevant in the age-at-death estimation of adults, as they are likely "specific" to an age group. However, the contrary may be not true: healthy entheses and minor ECs can be seen in individuals of all ages (including older individuals), and we thus consider them as likely irrelevant for age estimation (Figure 1). This type of reasoning may look surprising, but it is actually applied quasi systematically in bioarcheology and forensic anthropology for another indicator of age-at-death for adult skeletons, namely the fusion stage of the

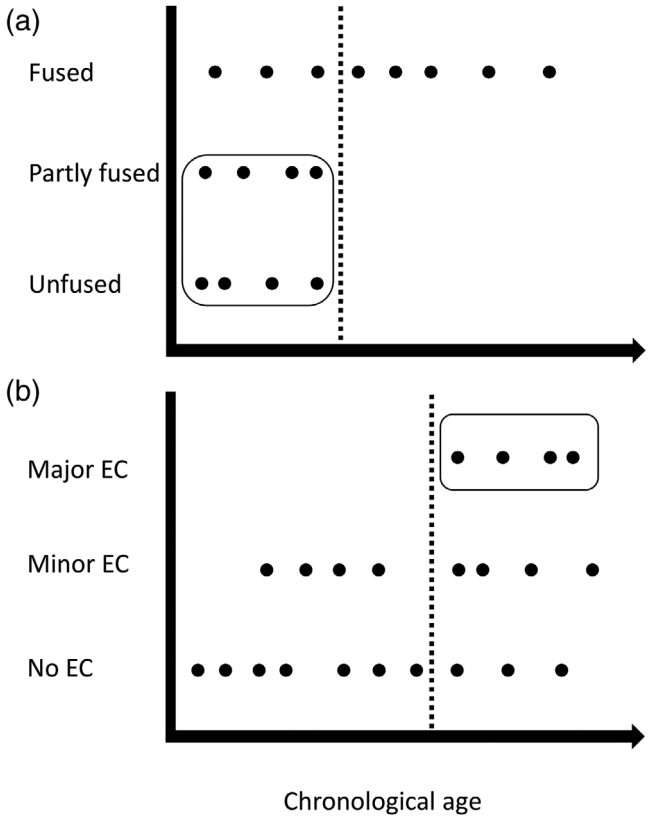

FIGURE 1 Schematic representations of approach of estimation of adult age-at-death using fusion stage of the sternal extremity of the clavicle (a), and major EC (b). Black dots: Theoretical adult individuals. Dashed lines: Maximum (a) or minimum (b) ages determined using these approaches. The rectangles indicate the individuals actually assessed for age using these approaches

TABLE 1 Summary statistics for the samples

	Sex		Age			Number of missing EC data per individual	
Collections	*N* males	*N* females	Mean	*SD*	Min-max	Median	Min-max
Bologna	84	0	45.1	17.1	20–91	3	0–15
Coimbra	173	153	42.2	15.7	20–89	1	0–17
Spitalfields	83	95	53.4	15.7	21–87	5	0–17
Sassari	133	0	40.2	15.7	20–84	1	0–11
Schoten	25	20	61.2	21.7	19–94	7	1–15

Note: For a presentation of the individual collections, see Milella et al., 2020; Orban et al., 2011; Villotte, 2009. Ages are in years.

sternal extremity of the clavicle (Figure 1). An unfused or partly fused epiphysis is extremely valuable to identify young adults. Conversely, a fused sternal extremity is near totally irrelevant for adult skeletons, as it indicates an individual older than 20 years (Schaefer et al., 2009).

In order to test this hypothesis, we used five identified skeletal collections (Table 1) for which ECs were recorded for 18 appendicular entheses (group 1 in Villotte, 2006). The method identifies three stages for each enthesis (Villotte, 2006): A (no change), B (minor EC), and C (major EC). All individuals with at least one stage recorded were included. Individuals with systemic diseases, such as diffuse idiopathic skeletal hyperostosis or spondyloarthropathies were excluded. Stages for bones displaying macrotrauma were not taken into account. Three of the collections (Bologna, Coimbra, and Spitalfields) were used as a learning metapopulation sample and the last two collections were used as target samples. These later collections (Schoten and Sassari) were chosen as they differ dramatically from each other in terms of age-at-death distribution as well as in extent of preservation: older individuals and missing data are much more frequent in the Schoten collection than in the Sassari one (Table 1).

All the analytical process was carried out using R 4.0.5 (R Core Team, 2021); the whole R script along with complementary results being provided as Supporting Information S1. The first step was to provide some kind of reliable and generalizable estimate for the minimum age of individuals exhibiting stage(s) C, which allows us to distinguish between younger and older individuals (see Figure 1). In order to do so, we represented the age distribution of the individuals from the learning metapopulation sample exhibiting at least one, two, and three stage(s) C, and computed in each case the associated 5% empirical quantiles (Figure 2), that is, the age threshold *t* such that 95% of individuals are older than *t* year-old. These quantiles were approximately equal to 41, 47, and 50 years old respectively. In a second step, we tested on the individuals of the Sassari and Schoten collections the decision rules empirically defined on the learning sample; that is, that any individual with at least one stage C should be at least 41 year-old, and similarly for two stages C (47-year-old) and three stages C (50-year-old). Confusion matrices were computed to evaluate the accuracy of these decision rules (Table 2). In a final step, we computed the percentage of misclassified observations: the number of individuals exhibiting stage(s) C with an age-at-death below the defined minimum age divided by the number of all individuals exhibiting stage(s) C.

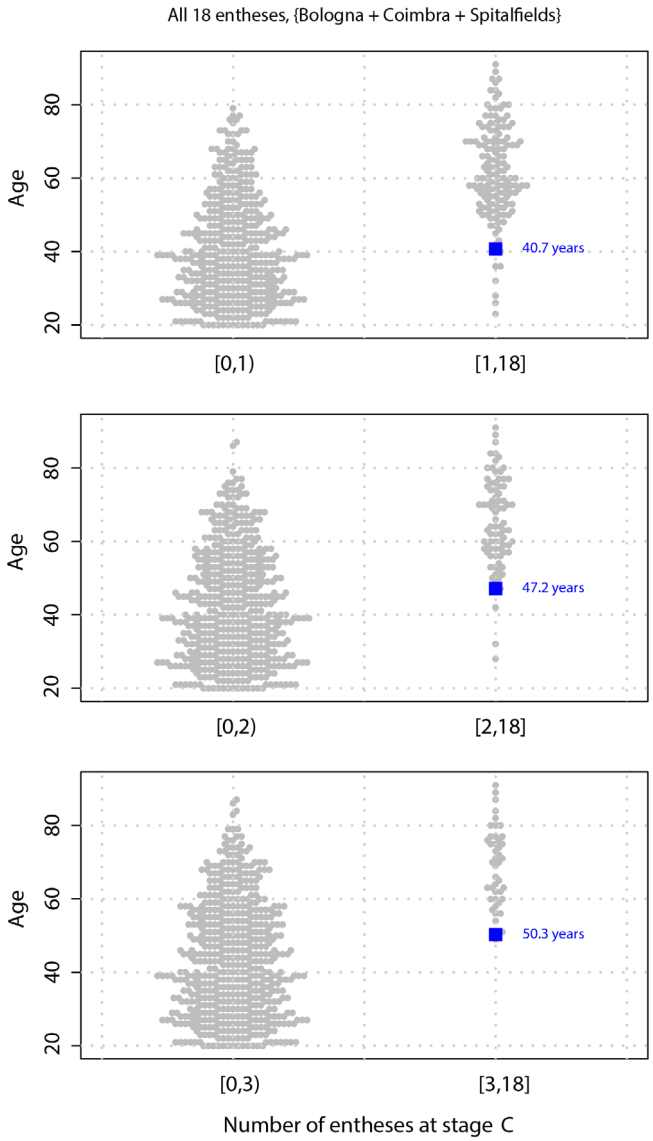

FIGURE 2 Age distributions of individuals from the learning metapopulation sample. (a) Individuals with no stage C, and individuals with at least 1 stage C. (b) Individuals with 0 or 1 stage C, and individuals with at least 2 stages C. (c) Individuals with 0, 1, or 2 stage(s) C, and individuals with at least 3 stages C. The blue squares indicate the empirical quantiles of order 5% (i.e., 95% of individuals are older than this threshold)

TABLE 2 Confusion matrices for age classes

	Sassari		Schoten		Both collections	
	(20,41)	(41,99)	(19,41)	(41,99)	(19,41)	(41,99)
<1	69	44	9	7	78	51
≥1	1	19	1	28	2	47
	(20,47)	(47,99)	(19,47)	(47,99)	(19,47)	(47,99)
<2	90	33	14	5	104	38
≥2	0	10	1	25	1	35
	(20,50)	(50,99)	(19,50)	(50,99)	(19,50)	(50,99)
<3	95	32	17	8	112	40
≥3	0	6	1	19	1	25

Note: Defined from Figure 2, and number of entheses having reached stage "C" in target samples. "<1", "<2", "<3": Individuals with less than, respectively, 1, 2, or 3 stage(s) C. "≥1", "≥2", "≥3": Individuals with, respectively, at least 1, 2, or 3 stage(s) C.

TABLE 3 Percentage of misclassified individuals for each collection

	Sassari	Schoten	Both collections
≥1 stage C	5.0%	3.6%	4.1%
≥2 stages C	0.0%	3.8%	2.8%
≥3 stages C	0.0%	5.0%	3.8%

Our approach seems promising, as it reliably identifies individuals over 40+ and/or 50+ year-old in the target skeletal samples with very few misclassified individuals (≤5.0% [Table 3], which was the expected error rate for these decision rules). This approach may thus be useful in forensic context, as reliable age-at-death estimation is crucial for identification. These broad, not clearly defined, age "categories" may not look particularly useful, but one has to remember that the age-at-death of individuals from this age "group" is systematically underestimated by almost all methods (see for instance references in Milella et al., 2020). Another important point that needs to be stressed is that this approach deals very easily with missing data. For instance, age-at-death can be estimated for an individual with only three entheses scored (out of 18) but who displays a stage C. This approach may thus have bioarcheological and forensic applications, as it may be used on poorly preserved skeletons or on isolated bones. One of the limitations, though, is that this approach relies on one or very few major ECs that can also be produced by a traumatic event or a systemic condition. Such cases need to be carefully excluded as a consequence.

In our opinion, this approach is promising because there is great scope for improvement. For instance, one way to increase the minimum ages would be to compute them from a lower percentage of individuals with stage(s) C from the learning metapopulation sample. Reducing this threshold to 90% of individuals with at least one stage C leads to a minimum age of 48 years (but significantly increases the percentage of misclassified individuals, see S1). It seems also possible to exclude some entheses in the analyses in order to reduce the percentage of misclassified individuals and/or to increase the minimum age. Other ways to improve this approach may be to focus on one specific feature (such as major enthesophytes), or to use the extremes of a multi-stage method that distinguish a greater number of gradations than the one used here (e.g., five stages instead of three). In any case, this approach seems promising, and we hope to see more articles, from Milella and colleagues and from other scholars, challenging and possibly improving it.

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CONFLICT OF INTEREST

The authors declare no conflicts of interest.

AUTHOR CONTRIBUTIONS

Sébastien Villotte: Conceptualization, data curation, funding acquisition, investigation, supervision, writing – original draft. Caroline Polet: Funding acquisition, supervision, writing – original draft. Chloé Colard: Investigation, writing – original draft. Frédéric Santos: Investigation, software, writing – original draft.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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SUPPORTING INFORMATION

Additional supporting information may be found in the online version of the article at the publisher's website.

Entheseal changes and estimation of adult age-at-death

Supporting Information: R code

Sébastien Villotte, Caroline Polet, Chloé Colard, Frédéric Santos*

May 19, 2021

Contents

This document provides the original R code used for all the results presented in our article, and adds several new figures and results.

All the analyses were performed with R 4.0.5 (R Core Team, 2021), and this document has been built with Org mode 9.4.5 for Emacs 27.2 (Schulte, Davison, Dye, & Dominik, 2012).

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1. R configuration

We provide here some details about our configuration and the R packages used:

```
### Use groundhog to control package versions:
library(groundhog)
today <- "2021-04-20"
### Load the following R packages:
groundhog.library(beeswarm, date = today)
groundhog.library(dplyr, date = today)
groundhog.library(RcmdrMisc, date = today)
```

```
### More information about our R session:
print(sessionInfo(), locale = FALSE)
```

```
R version 4.0.5 (2021-03-31)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Manjaro Linux

Matrix products: default
BLAS:   /usr/lib/libopenblasp-r0.3.13.so
LAPACK: /usr/lib/liblapack.so.3.9.1

attached base packages:
[1] stats     graphics  grDevices utils     datasets
[6] methods   base

other attached packages:
 [1] RcmdrMisc_2.7-1   car_3.0-10        ggplot2_3.3.3
 [4] lme4_1.1-26       survival_3.2-10   sandwich_3.0-0
 [7] sp_1.4-5          Matrix_1.3-2      nlme_3.1-152
[10] SparseM_1.81      viridisLite_0.4.0 carData_3.0-4
[13] Formula_1.2-4     lattice_0.20-41   dplyr_1.0.5
[16] beeswarm_0.3.1    groundhog_1.3.2
```

Those versions correspond to the 2021-04-20 snapshot from the MRAN repository (`https://cran.microsoft.com/snapshot/2021-04-20/`).

2. Load data into R

The original CSV file is not made publicly available, but is available upon reasonable request to Sébastien Villotte.

```
#####################
### Load CSV file ###
#####################
dat <- read.csv("./data/data_ajpa.csv",
                header = TRUE, row.names = 1,
                sep = ";", dec = ",",
                stringsAsFactors = TRUE,
                na.strings = "", fileEncoding = "utf-8")
```

Here is an overview of the first 6 rows and 8 columns of the data:

```
## Overview of the dataframe:
dat[1:6, 1:8]
```

	Population	Sex	Age	HSC_D	HSI_D	HEL_D	HEM_D	RBB_D
COIMM097	Coimbra	M	20	A	B	A	A	A
SARDM199	Sardaigne	M	20	A	A	A	A	A
BOLOM070	Bologne	M	20	A	A	A	A	A
SARDM136	Sardaigne	M	20	A	A	A	nil	B
COIMF189	Coimbra	F	20	A	A	A	A	A
COIMM422	Coimbra	M	20	nil	nil	nil	nil	B

Table 1: Overview of the original data.

The dataframe thus consists in individual metadata (Population, Age, Sex) and entheseal stages (either "A", "B" or "C") for all entheses under study, and for both right and left side.

The original data includes more than the 9 entheses studied here, so that we select only those columns in the dataframe for the subsequent analyses, correspond to the entheses from "System 1" in Villotte (2008):

```
## Select only some of the entheses:
entheses_sys1 <- c("HSC", "HSI", "HEL", "HEM", "RBB",
                   "CSB", "FPF", "FMF", "FIP")
sys1 <- select(dat, contains(c("Population", "Age", entheses_sys1)))
```

3. Define various R helpers

For the subsequent analyses, we will use some custom R functions.

The first function, `plot_nc()`, will help to display beeswarm plots comparing the age distribution of several groups of individuals, depending on their number of entheses having reached the stage C (argument `nmin` in the code below). Furthermore, an age threshold (argument `q`) will be added on the plot. With the default value `q = 0.9`, one can see the age reached by at least 90% of individuals in each group.

```
plot_nc <- function(data, nmin, q = 0.9, ...) {
### data: dataframe; must contain Pop, Age, *and* entheses values.
### nmin: minimal number of values "C" required
### q: required quantile value to add on the plot
### ...: further arguments passed to beeswarm()

    ## 0. First exclude those individual that are not well-preserved:
    nobs <- apply(data[, -c(1, 2)], MARGIN = 1,
                  FUN = function(x) sum(!is.na(x)))
    data <- data[nobs >= nmin, ]

    ## 1. Count number of entheses reaching a value of "C" for each individual:
    data$nsc <- apply(data[, -c(1, 2)], MARGIN = 1,
                      FUN = function(x) sum(x=="C", na.rm = TRUE))

    ## 2. Add "classes" of individuals depending on their number of C's:
    data$cl_nc <- cut(data$nsc, right = FALSE,
                      breaks = c(0, nmin, ncol(data) - 3))
    levels(data$cl_nc) <- gsub(x = levels(data$cl_nc), pattern = "\\)",
                               replacement = "\\[")

    ## 3. Plot age against those classes:
    par(cex = 1.1)
    beeswarm(Age ~ cl_nc, data = data, pch = 16,
             spacing = 0.69, xlab = "Number of entheses at stage C", ...)
    grid(lwd = 2)

    ## 4. Add quantile value:
    moy <- quantile(data[as.numeric(data$cl_nc) > 1, "Age"],
                    probs = 1-q)
    points(x = 2, y = moy, pch = 15, cex = 2, col = "blue")
    text(x = 2, y = moy, offset = 1.5, pos = 4, col = "blue",
         labels = paste(round(moy, 1), "years"))
}
```

The second R function is used to test on new population samples the decision rules empirically determined using the learning metapopulation sample. It returns the confusion matrix between age classes (dichotomously defined thanks to an age `threshold`), and entheseal classes (dichotomously thanks to a threshold in the number of observed entheses in stage 2, `n2`).

```
test_rule <- function(data, nc, threshold) {
### data: dataframe with Population, Age, and entheses values
### nc: required number of entheses at stage "C"
### threshold: age threshold
    data$nsc <- apply(data[, -c(1:2)], MARGIN = 1,
                      FUN = function(x) sum(x == "C", na.rm = TRUE))
    data$ClEnt <- factor(ifelse(data$nsc >= nc,
                                yes = paste(">= ", nc),
                                no = paste("< ", nc)))
    data$ClAge <- cut(data$Age, breaks = c(0, threshold, 99), right = FALSE)
    levels(data$ClAge) <- gsub(x = levels(data$ClAge), pattern = "\\)",
                               replacement = "\\[")
    table(data$ClEnt, data$ClAge)
}
```

4. Main results for age estimation

In what follows, we first observe age distribution on a learning subset composed of the populations from Bologna, Coimbra and Spitalfields; we derive a possible decision rule for age estimation from these populations; and finally test this decision rule on two other population samples (Sassari and Schoten).

```
### Define learning and test datasets:
learndtf <- subset(sys1, Population %in% c("Coimbra", "Spitalfields", "Bologne"))
sard <- subset(sys1, Population == "Sardaigne")
schoten <- subset(sys1, Population == "Schoten")
```

4.1. Inspection of the learning metapopulation sample

We first find, on figure 1, that 95% of the individuals exhibiting at least one stage C among all entheses, are at least 40 years old.

```
plot_nc(data = learndtf, nmin = 1, col = "gray", q = 0.95,
        main = "All 18 entheses, {Bologna + Coimbra + Spitalfields}")
```

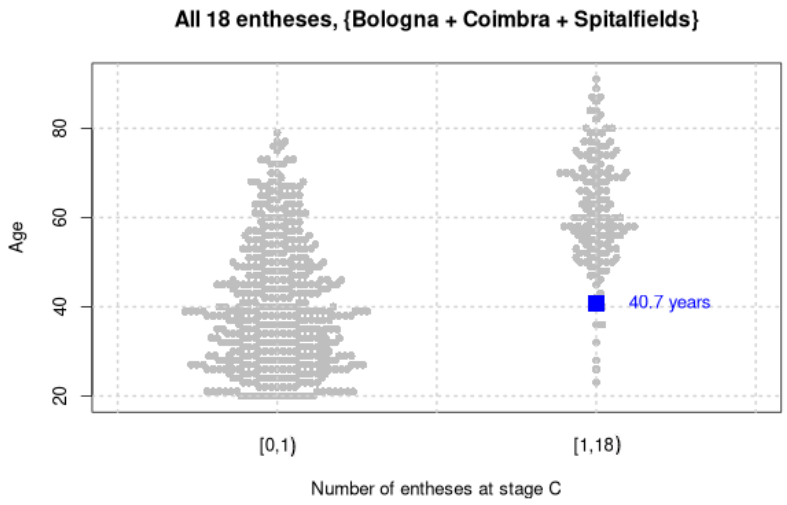

Figure 1: Age distributions of individuals with 0 enthesis at stage C, and individuals with at least one stage C. Blue squares indicate quantiles of order 5%.

Also, 95% of the individuals exhibiting at least two stages C among all entheses, are at least 47 years old (Fig. 2). Finally, as shown on Figure 3, there was yet another small improvement when switching to the individuals exhibiting at least three entheses at stage C: 95% of them are at least 50 years old.

```
plot_nc(data = learndtf, nmin = 2, col = "gray", q = 0.95,
        main = "All 18 entheses, {Bologna + Coimbra + Spitalfields}")
```

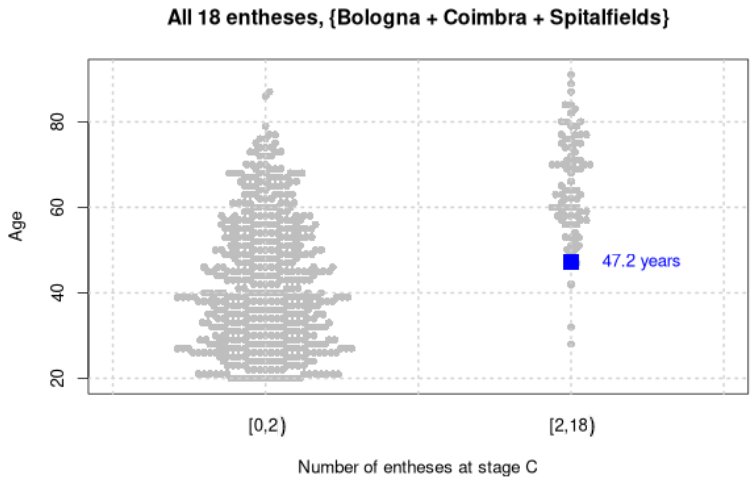

Figure 2: Age distributions of individuals with 0 or 1 enthesis at stage C, and individuals with at least two entheses at stage C. Blue squares indicate quantiles of order 5%.

```
plot_nc(data = learndtf, nmin = 3, col = "gray", q = 0.95,
        main = "All 18 entheses, {Bologna + Coimbra + Spitalfields}")
```

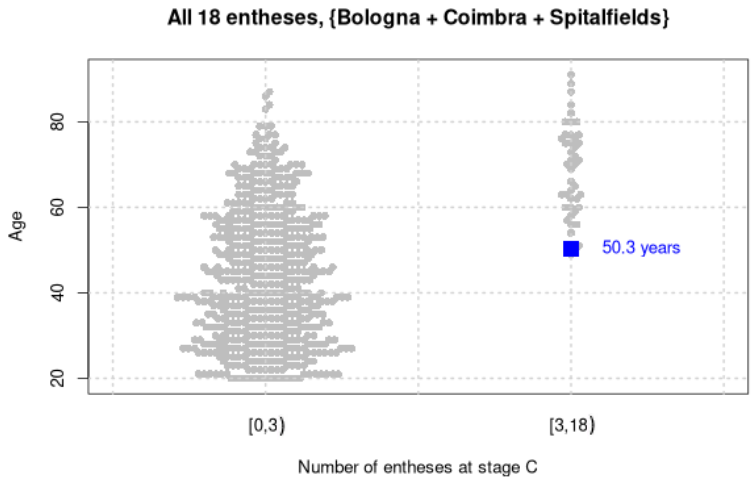

Figure 3: Age distributions of individuals with 0 to 2 entheses at stage C, and individuals with at least three entheses at stage C. Blue squares indicate quantiles of order 5%.

4.2. Application to target samples

We consider that we have defined three decision rules on the learning dataset:

- around 95% ofindividuals with at least one enthesis at stage C, are supposed to be over 41 years old;
- around 95% ofindividuals with at least two entheses at stage C, are supposed to be over 47 years old;
- around 95% ofindividuals with at least three entheses at stage C, are supposed to be over 50 years old.

We now test these rules on two target samples, Sassari and Schoten.

4.2.1. Sassari

As shown on Tables 2 to 4, these decision rules also work well on the Sassari sample:

- 95% (19 out of 20) ofindividuals with at least one enthesis at stage C, are indeed over 41 years old;
- 100% ofindividuals with at least two entheses at stage C, are indeed over 47 y.o.;
- 100% ofindividuals with at least three entheses at stage C, are indeed over 50 y.o.

```
### Test on Schoten population sample
test_rule (sard, nc = 1, threshold = 41)
```

	[0,41)	[41,99)
< 1	69	44
>= 1	1	19

Table 2: Confusion matrix for age class and number of entheses having reached stage C in Sassari population sample ("< 1": individual with no enthesis at stage C; ">= 1": individual with at least one enthesis at stage C).

```
test_rule (sard, nc = 2, threshold = 47)
```

	[0,47)	[47,99)
< 2	90	33
>= 2	0	10

Table 3: Confusion matrix for age class and number of entheses having reached stage C in Sassari population sample ("< 2": individual with zero or one enthesis at stage C; ">= 2": individual with at least two entheses at stage C).

```
test_rule (sard, nc = 3, threshold = 50)
```

	[0,50)	[50,99)
< 3	95	32
>= 3	0	6

Table 4: Confusion matrix for age class and number of entheses having reached stage C in Sassari population sample ("< 3": individual with zero to two entheses at stage C; ">= 3": individual with at least three entheses at stage C).

4.2.2. Schoten

As shown on Tables 5 to 7, these decision rules work well on the Schoten population sample:

- 96.5% (28 out of 29) ofindividuals with at least one enthesis at stage C, are indeed over 41 years old;
- 96.1% (25 out of 26) ofindividuals with at least two entheses at stage C, are indeed over 47 years old;
- 95% (19 out of 20) ofindividuals with at least three entheses at stage C, are indeed over 50 years old.

```
### Test on Schoten population sample
test_rule (schoten, nc = 1, threshold = 41)
```

	[0,41)	[41,99)
< 1	9	7
>= 1	1	28

Table 5: Confusion matrix for age class and number of entheses having reached stage C in Schoten population sample ("< 1": individual with no enthesis at stage C; ">= 1": individual with at least one enthesis at stage C).

```
test_rule (schoten, nc = 2, threshold = 47)
```

	[0,47)	[47,99)
< 2	14	5
>= 2	1	25

Table 6: Confusion matrix for age class and number of entheses having reached stage C in Schoten population sample ("< 2": individual with zero or one enthesis at stage C; ">= 2": individual with at least two entheses at stage C).

```
test_rule (schoten, nc = 3, threshold = 50)
```

	[0,50)	[50,99)
< 3	17	8
>= 3	1	19

Table 7: Confusion matrix for age class and number of entheses having reached stage C in Schoten population sample ("< 3": individual with zero to two entheses at stage C; ">= 3": individual with at least three entheses at stage C).

5. Appendix: alternative results for a threshold of 90%

In what follows, we follow the previous procedure, just replacing the 95% threshold by a 90% threshold

5.1. Inspection of the learning metapopulation sample

We first find, on figure 4, that 90% of the individuals exhibiting at least one stage C among all entheses, are at least 48 years old.

```
plot_nc (data = learndtf, nmin = 1, col = "gray" , q = 0.90 ,
         main = "All 18 entheses, {Bologna + Coimbra + Spitalfields}" )
```

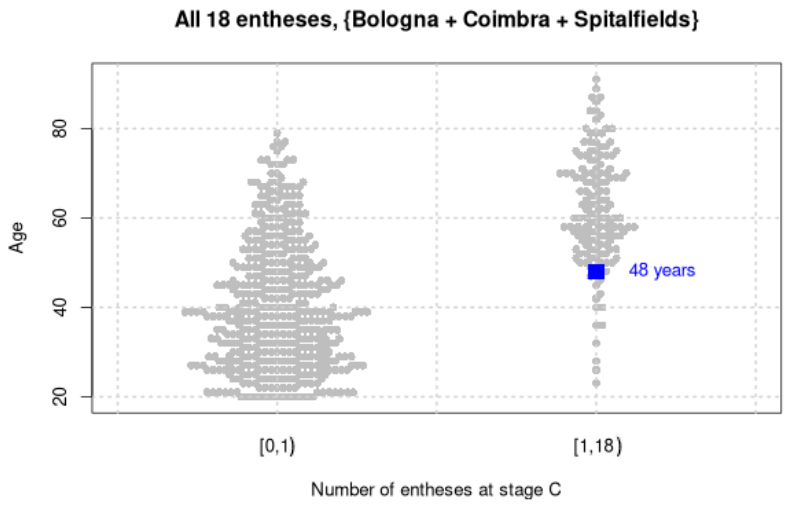

Figure 4: Age distributions ofindividuals with 0 enthesis at stage C, and individuals with at least one stage C. Blue squares indicate quantiles of order 10%.

Also, 90% of the individuals exhibiting at least two stages C among all entheses, are at least 50.3 years old (Fig. 5). Finally, as shown on Figure 6, when switching to the individuals exhibiting at least three entheses at stage C, 90% of them are at least 52.5 years old.

```
plot_nc(data = learndtf, nmin = 2, col = "gray", q = 0.9,
        main = "All 18 entheses, {Bologna + Coimbra + Spitalfields}")
```

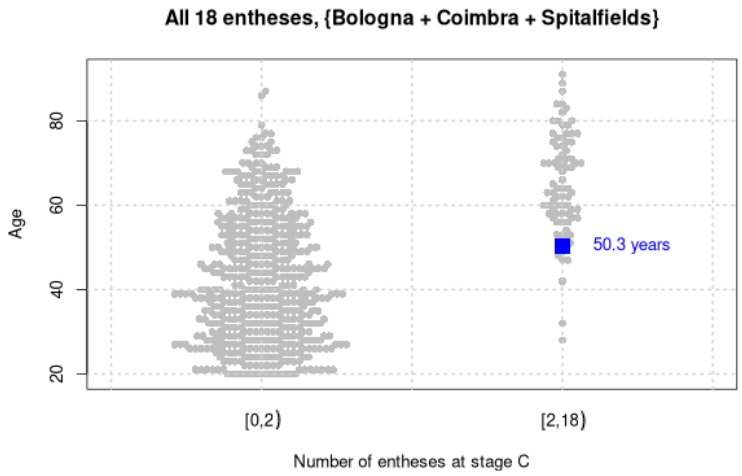

Figure 5: Age distributions of individuals with 0 or 1 enthesis at stage C, and individuals with at least two entheses at stage C. Blue squares indicate quantiles of order 10%.

```
plot_nc(data = learndtf, nmin = 3, col = "gray", q = 0.9,
        main = "All 18 entheses, {Bologna + Coimbra + Spitalfields}")
```

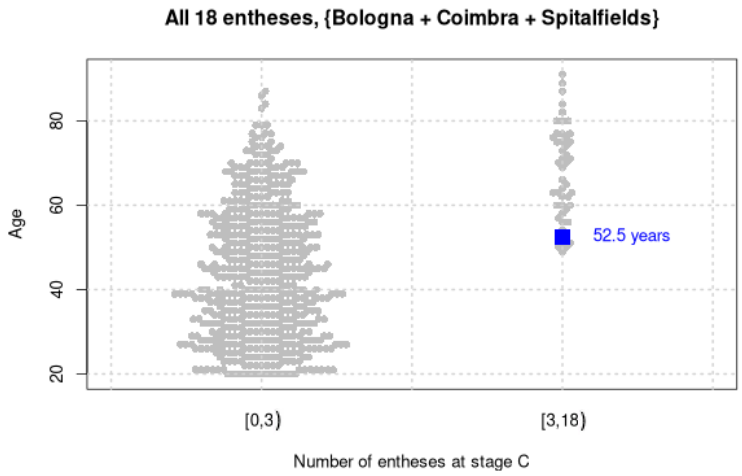

Figure 6: Age distributions of individuals with 0 to 2 entheses at stage C, and individuals with at least three entheses at stage C. Blue squares indicate quantiles of order 10%.

5.2. Application to target samples

We consider that we have defined three decision rules on the learning dataset:

- around 90% ofindividuals with at least one enthesis at stage C, are supposed to be over 48 years old;
- around 90% ofindividuals with at least two entheses at stage C, are supposed to be over 50 years old;
- around 90% ofindividuals with at least three entheses at stage C, are supposed to be over 52 years old.

5.2.1. Sassari

Tables 8 to 10 show the results of those classifications rules applied on the Sassari population sample:

- 75% (15 out of 20) ofindividuals with at least one enthesis at stage C, are indeed over 48 years old;
- 100% ofindividuals with at least two entheses at stage C, are indeed over 50 years old;
- 66.7% ofindividuals (4 out of 6) with at least three entheses at stage C, are indeed over 52 years old.

```
### Test on Schoten population sample
test_rule (sard, nc = 1, threshold = 48)
```

	[0,48)	[48,99)
< 1	87	26
>= 1	5	15

Table 8: Confusion matrix for age class and number of entheses having reached stage C in Sassari population sample ("< 1": individual with no enthesis at stage C; ">= 1": individual with at least one enthesis at stage C).

```
test_rule (sard, nc = 2, threshold = 50)
```

	[0,50)	[50,99)
< 2	95	28
>= 2	0	10

Table 9: Confusion matrix for age class and number of entheses having reached stage C in Sassari population sample ("< 2": individual with zero or one enthesis at stage C; ">= 2": individual with at least two entheses at stage C).

```
test_rule (sard, nc = 3, threshold = 52)
```

	[0,52)	[52,99)
< 3	102	25
>= 3	2	4

Table 10: Confusion matrix for age class and number of entheses having reached stage C in Sassari population sample ("< 3": individual with zero to two entheses at stage C; ">= 3": individual with at least three entheses at stage C).

5.2.2. Schoten

Tables 11 to 13 provide the results for those decision rules applied to the Schoten population sample:

- 89.7% (26 out of 29) ofindividuals with at least one enthesis at stage C, are indeed over 48 years old;
- 92.3% (24 out of 26) ofindividuals with at least two entheses at stage C, are indeed over 50 years old;
- 95% (19 out of 20) ofindividuals with at least three entheses at stage C, are indeed over 52 years old.

```
### Test on Schoten population sample
test_rule (schoten, nc = 1, threshold = 48)
```

	[0,48)	[48,99)
< 1	13	3
>= 1	3	26

Table 11: Confusion matrix for age class and number of entheses having reached stage C in Schoten population sample ("< 1": individual with no enthesis at stage C; ">= 1": individual with at least one enthesis at stage C).

```
test_rule (schoten, nc = 2, threshold = 50)
```

	[0,50)	[50,99)
< 2	16	3
>= 2	2	24

Table 12: Confusion matrix for age class and number of entheses having reached stage C in Schoten population sample ("< 2": individual with zero or one enthesis at stage C; ">= 2": individual with at least two entheses at stage C).

```
test_rule(schoten, nc = 3, threshold = 52)
```

	[0,52)	[52,99)
< 3	17	8
>= 3	1	19

Table 13: Confusion matrix for age class and number of entheses having reached stage C in Schoten population sample ("< 3": individual with zero to two entheses at stage C; ">= 3": individual with at least three entheses at stage C).

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