TITLE:

Statistically Robust Representation and Comparison of Mortality Profiles in Archaeozoology

AUTHORS:

GERBAULT Pascale[1, 2], GILLIS Rosalind[3], VIGNE Jean-Denis[3], TRESSET Anne[3], BREHARD Stéphanie[3], THOMAS Mark G.[1]

CORRESPONDING AUTHOR:

Gerbault Pascale <p.gerbault@ucl.ac.uk>

ADDRESSES:

[1] UCL Research Department of Genetics, Evolution and Environment, Darwin building, Gower Street, London WC1E 6BT, UK

[2] UCL Department of Anthropology, 14 Taviton Street, London WC1H 0BW, UK

[3] CNRS – Muséum National d'Histoire Naturelle – Sorbonne Universités, Archéozoologie, Archéobotanique: Sociétés, Pratiques et Environnement, (UMR 7209), CP56, 55 rue Buffon, F-75005 PARIS, France

ABSTRACT:

Archaeozoological mortality profiles have been used to infer site-specific subsistence strategies. There is however no common agreement on the best way to present these profiles and confidence intervals around age class proportions. In order to deal with these issues, we propose the use of the Dirichlet distribution and present a new approach to perform age-at-death multivariate graphical comparisons. We demonstrate the efficiency of this approach using domestic sheep/goat dental remains from 10 Cardial sites (Early Neolithic) located in South France and the Iberian Peninsula. We show that the Dirichlet distribution in age-at-death analysis can be used: (i) to generate Bayesian credible intervals around each age class of a mortality profile, even when not all age classes are observed; and (ii) to create 95% kernel density contours around each age-at-death frequency distribution when multiple sites are compared using correspondence analysis. The statistical procedure we present is applicable to the analysis of any categorical count data and particularly well-suited to archaeological data (e.g. potsherds, arrow heads) where sample sizes are typically small.

KEY WORDS: archaeozoology, mortality profiles, sheep/goat, dental wear, Dirichlet distribution, Cardial Neolithic

1. INTRODUCTION:

There is a high correlation between the known-age of an animal and its stage of tooth eruption and wear (e.g. for domesticate animals Ducos 1968; Payne 1973; Zeder 2006). Dental eruption and development have been employed to estimate age-at-death distributions for animals for several centuries (Cornevin and Lesbre 1894). Archaeozoologists typically use the eruption through the mandible or maxilla bone, development and replacement of teeth, which can be arranged into fixed age classes (e.g. Payne 1973; Klein and Cruz-Uribe 1984; Stiner 1990; Helmer 1995; Lubinski 2000; Zeder 2006). Although the recovery of dental remains is influenced by depositional practices of cranial material in the past (and may be biased towards certain age groups, and possibly sexes) and excavation protocols, teeth often have a greater survival rate compared to cranial and post-cranial elements (Lyman 1994a). In addition, the accuracy of caprine (Caprini Simpson 1945) age determination using teeth has been assessed (Hambleton 1999; Jones 2005; Greenfield and Arnold 2008) and reproduced (Helmer 1995; Vila 1998). Teeth eruption and wear patterns are generally regarded as the best proxy for age-at-death, and for inferring slaughter management practices (Vigne and Helmer 2007).

The frequency distribution of age-at-death classes inferred from dental remains – either as minimum number of individuals (MNI) or number of teeth (N) (Vigne 1988) – can be visualised using (i) ternary diagrams (Greenfield 1988; Stiner

1990; Steele and Weaver 2002; Steele 2005; Weaver, Boyko, and Steele 2011), (ii) survivorship curves (Payne 1973), (iii) frequency polygones (Ducos 1968; Vigne 1988; Vigne 2000) and (iv) histograms; also called mortality profiles (Brochier 2013). Interpretation of survival profiles is necessarily made assuming that all animals at an archaeological site have been killed by humans and that no animals or age classes have been preferentially removed from the site. Testing these assumptions can be very challenging. This is why in this study we favour mortality profiles, which are direct representations of what is observed in an archaeological site/context. We also favour histograms as an intuitive means of visualizing frequency distributions; such graphical representation has become very popular in the last few decades among archaeozoologists (Tresset 1997; Tresset and Vigne 2000; Steele 2005; Helmer, Gourichon, and Vila 2007; Vigne and Helmer 2007; Atıcı 2009; Makarewicz 2009).

The frequency distribution of domesticate animals within age classes varies depending on the slaughter management and the goals of the husbandry strategy (Higham 1967; Payne 1973; Helmer et al. 2005; Vigne and Helmer 2007), as well as on sampling variation (Millard 2006). Consequently, if we assume that the teeth or individuals determined from dental remains can be used as a proxy for past slaughter management, assessing how this frequency distribution changes through time can help to understand the evolution of husbandry practices (Ducos 1968; Payne 1973; Vigne 1988; Helmer 1992; Halstead 1998; Helmer et al. 2005).

However, various factors can affect the recovery of dental remains. The non-observation within a given age class may be due to specific herd management practices, or to under-sampling, or to taphonomic biases that are independent of the management practices (Halstead 1998; Munson 2000). In addition, the different durations of the age class categories may bias the frequency of dental remains recorded. The number of teeth in the mandible varies with age, which should favour the frequency of the age classes in which the number of teeth is the higher (Masset 1973).

These biases have two opposing effects on interpretation and comparison of age-at-death profiles: (i) a lack of confidence in relative frequencies due to the likely misrepresentation of certain age classes (Greenfield 2005) and (ii) over-interpretation of mortality profiles comparisons (Halstead 1998; Marom and Bar-Oz 2009). While a robust Bayesian approach to aging individual sheep/goats from toothwear exists (Millard 2006), there is no appropriate statistical means of accounting for sampling uncertainty around a single, or over comparisons of multiple, observed age-at-death frequency distribution(s).

More specifically, statistical challenges remain in the way different profiles are compared among sites. While rank comparisons (Helmer 1992), confidence intervals (Tresset 1997; Valenzuela-Lamas et al. 2009), or statistical tests (Chi^2: (Klein and Cruz-Uribe 1984; Haber, Dayan, and Getzo 2005); Spearman r test: (Vigne 2000); Kolmogorov-Smirnov: (Marom and Bar-Oz 2009); Fisher exact test: (Brochier 2013)); bootstrapping: (Steele 2005; Price, Wolfhagen, and Otárola-Castillo 2016) have been applied, none of these techniques adequately assesses the high level of sampling uncertainty in age-at-death data (see discussion). For example, a Chi^2 test requires the data to meet the following assumptions: (i) independence of each observation, (ii) no outliers, (iii) no structural zeroes (Yates, Moore, and McCabe 1999). These assumptions are however not met in the case of age-at-death data since (i) age classes are not independent, (ii) archaeological data is by nature scarce, and outliers are not rare in this context, and (iii) zeroes may exist for some age classes.

Several scholars have proposed the use of multivariate correspondence analysis to visualise and compare a set of age-at-death profiles, rather than testing them with reference to statistical thresholds (Tresset 1996; Vigne 2000; Helmer, Gourichon, and Vila 2007; Vigne 2011; Gillis 2012). However, while well suited for visualizing the similarities and differences between profiles, correspondence analysis does not in itself provide any means of assessing statistical confidence of groupings or clusters, or of quantifying differences between observed profiles.

To account for sampling uncertainties in the downstream analysis and interpretation of age-at-death profiles, we propose the use of the Dirichlet distribution to generate random deviates of the population age-at-death profile given an observed sample or samples. The Dirichlet distribution is the conjugate prior of the multinomial distribution and can be used in a Bayesian framework to provide probability densities for the relative frequencies of age classes given observed counts in those classes and an appropriate prior. This distribution has been widely used as a model of how proportions vary (e.g. Rannala and Mountain 1997; Wong 1998; Chikhi, Bruford, and Beaumont 2001; Balding 2003; Madsen, Kauchak, and Elkan 2005), where the sum of these proportions equals 1, as is the case for age-at-death profiles (Millard 2006).

In this study, we first show how the Dirichlet distribution can be used to generate credible intervals around the age classes of an observed mortality profile. We then illustrate how this can be used to estimate confidence intervals on correspondence analysis plots comparing age-at-death frequency distributions from multiple sites. Here we apply this method to age-at-death data based on tooth eruption, replacement and wear patterns. However, we note that it can be used to analyse any categorical count data (e.g. potsherds, arrow heads).

2. DATASET and METHODOLOGY:

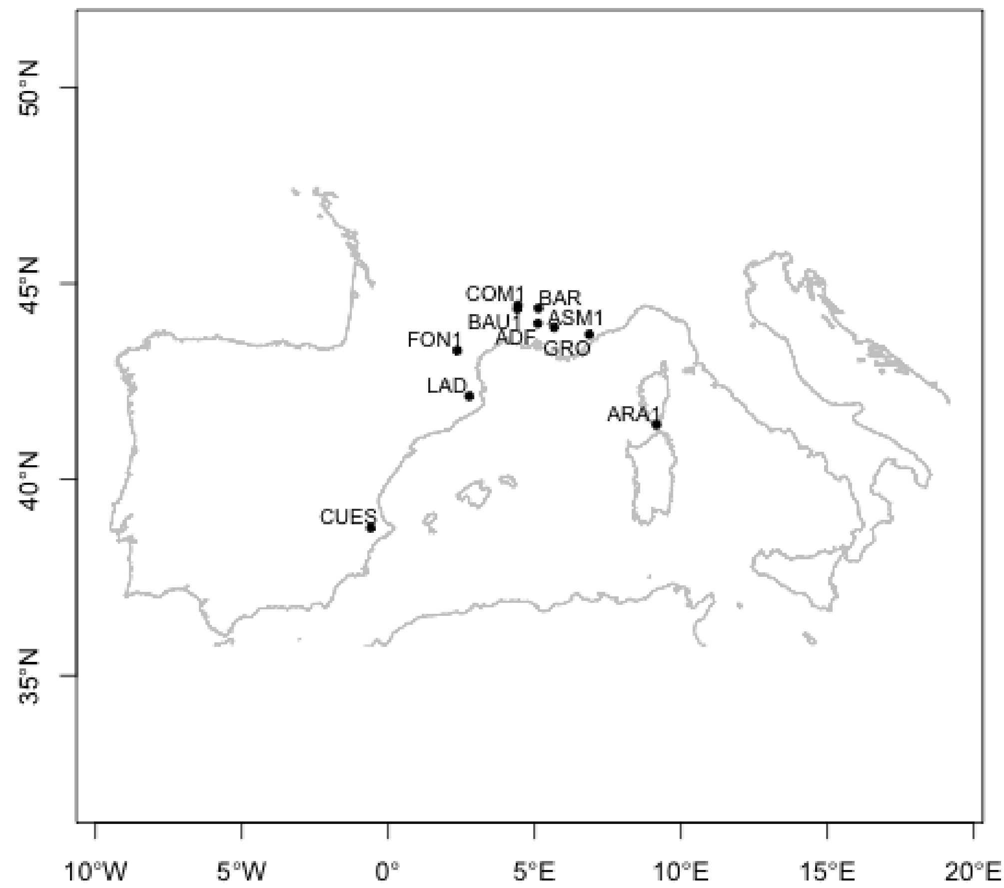
2.1. Dataset

In order to illustrate the robustness of our approach and to assess its sensitivity to clustering of sites with relatively homogeneous cultural backgrounds, we considered ten sites (Table 1 and Figure 1) from France and the Iberian Peninsula belonging to the Cardial, Epicardial or assimilated cultures of the North-West Mediterranean Early Neolithic and dated between 5500 and 4500 cal BC. These data are a part of a larger dataset collated for a PhD project (Gillis 2012); data for all sites were recovered from published sources (Boessneck and Von den Driesch 1980; Vigne 1988; Helmer, Gourichon, and Vila 2007), except for Font Juvenal and La Draga (see Table 1). We followed Payne (1973) and Ducos (1968) methodologies of study for all sites, except for Cueva de Sarsa, for which we used Habermehl (1975).

Table 1: Ten early Neolithic sites from southern France and the Iberian Peninsula were used in the present analysis (age classes following (Payne 1973; Helmer 1995); the data is the number of teeth in each age class (N_i) and come from (*) Gillis (2012), (#) Helmer et al. (2007) , ($) Boessneck and Von den Driesch (1980) and (§) Vigne (1988). Non-integer N_i values reflect that a tooth can be classified in to more than one age class and the number of teeth is therefore divided into as many age classes as it could be assigned to. The site locations are shown on Figure 1. Additional chronological information and references can be found in Vigne (2007) and Rowley-Conwy et al. (2013, Tab. 9.4 & 9.5).

		Age classes								
Site (reference)	Code	A	B	C	D	EF	G	HI	Total N	Site type
La Draga (*)	LAD	0	5.7	15.7	56.1	48.6	18.6	0	145	open
Grotte Lombard (#)	GRO	1	3	3	4	9	7	1	28	cave/rockshelter
Font Juvenal I (*)	FON1	7.5	2.66	9.66	12.16	5.66	4.66	1.66	44	cave/rockshelter
Cueva de la Sarsa ($)	CUES	1	9	9	6	13	2	1	41	cave/rockshelter
Combe Obscure I (#)	COM1	2	5	10	4	4	3	7	35	cave/rockshelter
Baume d'Oulen I (#)	BAU1	6	6	9.5	7.5	5.75	2.25	1	38	cave/rockshelter
Barret de Lioure (#)	BAR	0	2	9	4	8	5	1	29	cave/rockshelter
Abri de Saint-Mitre I (#)	ASM1	0	1	6	2	2	3	0	14	cave/rockshelter
Araguina-Sennola I (§)	ARA1	3	6.5	6.5	14	7	0	0	37	cave/rockshelter
Abri II du Fraischamp (#)	ADF	0	3	5	6	5	2	0	21	cave/rockshelter

Figure 1: Geographic locations of the 10 Early Neolithic sites analysed here. The site codes are given in Table 1.



2.2. Graphical and statistical methodology

All statistical analysis and generation of graphical representations were performed using the statistical analysis scripting language R, version 2.15.1 (R Development Core Team 2012). Plots were generated using the R library "ggplot2" (Wickham 2009). The R code developed and example input files are available at < http://www.ucl.ac.uk/mace-lab/resources/software>.

2.3. Histograms

We displayed age-at-death frequency distributions amongst the seven age classes using histograms where the unit of the x-axis is in years. Since distinct age classes have different time lengths (Table 2, age class width W_i column), and to respect the continuous x-axis unit, the 7 bin widths are unequal. This is one of the major differences to the recently published R package "zooaRch" (Price, Wolfhagen, and Otárola-Castillo 2016), where the age classes have equal bin width on the x-axis. In "zooaRch" the relationship between area under the curve and mean survival age (e.g. Fries 1980) is lost (Price, Wolfhagen, and Otárola-Castillo 2016), while it is conserved in the current approach. The frequency density in counts per unit of time (histogram y-axis, example on Table 2) is obtained by dividing the frequency by the bin width W_i. The y-axis of the histograms is consequently in units of corrected number of teeth observed in a given age class, i.e. N_i/W_i (see column "Corrected N_i" in Table 2). Please note that the scope of this study was to address statistical challenges faced by existing mortality profile techniques, i.e. histogram representation with x-axis unit in years. Since alternative representations would also involve debates concerning the counting protocol, we did not explore alternatives, such as representation accounting for the different number of cheek teeth per age class ((Masset 1973); Table 2, last column), but this aspect of the analysis of age-at-death data should be investigated in the future.

Table 2: Description of the 7 age classes used for sheep and goat (Payne 1973; Helmer et al. 2005), and data from the archaeological site of Font Juvenal I (Gillis 2012). The age class width vector W_i is obtained by dividing the estimated age in

months by 12 for drawing the continuous x-axis scale unit of the histogram (in years). The frequency density on the y-axis of the mortality profile (Figure 1 and S1) is the time-corrected N_i, i.e. (N_i/W_i). The last column shows the maximum number of cheek teeth (except the second premolar) that are actually present in a half lower jaw of a sheep/goat during this age class, including the tooth buds.

Age class i	Estimated age (months)	Age class width W_i (years)	Number of teeth N_i	Frequency density (N_i/W_i)	Maximum no. of cheek teeth in a lower hemimandible (except the second premolar)
A	0-2	0.17	7.50	44.12	2
B	2-6	0.33	2.66	8.06	3
C	6-12	0.5	9.66	19.32	4
D	12-24	1	12.16	12.16	7
EF	24-48	2	5.66	2.83	6
G	48-72	2	4.66	1.17	5
HI	72+ (up to 120)	4	1.66	0.42	5

2.4. Dirichlet distribution and Bayesian credible intervals

Relative frequencies (p_i) of an age-at-death count distribution can be obtained from the absolute frequencies (N_i), where *i* represent the age classes (i.e. age classes A, B, C, D, EF, G and HI). As $\Sigma p_i = 1$, the individual p_i values are not independent, and estimating confidence intervals can be challenging. However, credible intervals can be computed from the probability density function of the Dirichlet distribution, with 7 parameters Dir(N_A+0.5, N_B+0.5, N_C+0.5, N_D+0.5, N_{EF}+0.5, N_G+0.5, N_{HI}+0.5) to obtain the true population frequency distribution of age-at-death. The addition of 0.5 to each count for each age class corresponds to the uninformative Jeffreys' prior (Jeffreys 1946; Jeffreys 1961). Because we perform downstream analyses on these population age-at-death frequency estimates (see section 2.5, below), we first generated 10,000 Dirichlet deviates of the population age-at-death frequency distribution.

An "uninformative prior" is a function that maximizes some measure of distance or divergence between the posterior and prior, as data observations are made. By maximizing the divergence, we allow the data to have the maximum effect on the posterior estimates. The Jeffreys' prior satisfies the local uniformity property: a prior that does not change much over the region in which the likelihood of the data is significant and does not assume large values outside that range. We note that for other archaeological dataset a different prior may be more appropriate.

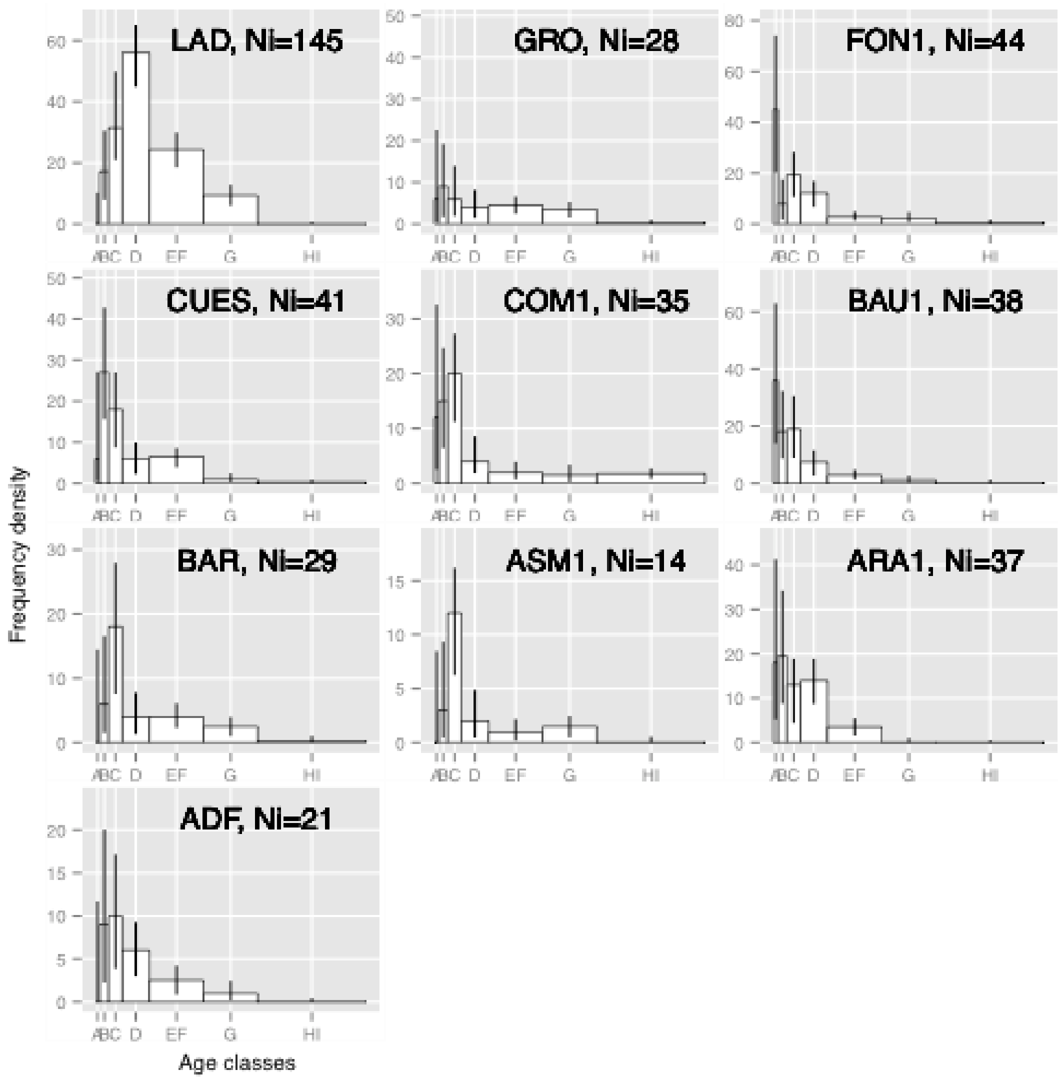
Random deviates of the population age-at-death frequency distribution were generated using the 'rdirichlet' function (Bolker 2000) from the R library "gtools" (CRAN repository, http://cran.r-project.org/web/packages/gtools/). The 'rdirichlet' function considers absolute counts from the sample and returns random deviates of the population relative frequencies, given the observed data. We subsequently multiply each Dirichlet deviate by the number of teeth observed at the corresponding archaeological site in order to obtain comparable simulated datasets. The Dirichlet deviates were then divided by the bin width (W_i) to obtain the corresponding frequency density distribution per unit time. These Dirichlet deviates were finally used to obtain the 95% credible interval of each age class using the 'p.interval' function (Bernardo 2005) from the R package "LaplacesDemon" (Byron Hall <laplacesdemon@statistcat.com> 2012) and plotted on the histograms.

2.5. Correspondence Analysis and kernel density estimation

Correspondence analysis is a useful multivariate descriptive statistical technique for summarizing multiple rows and columns of categorical data in two or more dimensions (Benzécri 1973). Correspondence analysis was performed on an array made of the 10 observed age-at-death profiles and each of their 10,000 Dirichlet random deviates using the 'ca' function (Nenadic and Greenacre 2007) from the R library "ca" (CRAN repository, http://cran.r-project.org/web/packages/ca/). Kernel density estimation is a non-parametric approach to estimate the probability density of a random variable, (Parzen 1962). We used these 10,000 Dirichlet deviates to estimate the two-dimensional kernel density for each mortality profile. The density was estimated using the 'kde2d' function (Venables and Ripley 2002) from the R library "MASS" (CRAN repository, http://cran.r-project.org/web/packages/MASS/). We then obtained the fifth quantile density value, above which 95% of the values lie. This was performed using the R function 'quantile'. We then plotted the contour lines around this fifth quantile, showing the region in which 95% of the deviates fall, thereby representing the 95% confidence interval of each mortality profile on the correspondence analysis plot. The 95% confidence intervals were drawn using the R function 'contour' (Becker, Chambers, and Wilks 1988).

It should be noted that we compute credible intervals on the age-at-death profiles (i.e. the histograms) but confidence intervals on the correspondence analysis. The former are directly obtained from the Dirichlet deviates of the observed age-at-death data, used as a posterior probability distribution, and are consequently by definition credible region estimates. However, in the correspondence analysis, we used these Dirichlet deviates to define a range of values so that there is a specified probability (95%) that the value for the site lies within it. Hence we refer to these as confidence intervals and not credible intervals.

Figure 2: Mortality profile representations of the 10 observed age at death frequency distributions (observed number of teeth per age class) shown in Table 1. The x-axis (age classes) is on a continuous scale in years. The y-axis is the frequency per unit time density, where frequency per unit time density = frequency / bin width (N_i/W_i; see Table 2). The black vertical bars represent the 95% credible intervals of the frequency density through time computed from the 10,000 Dirichlet deviates generated on the (N_i+0.5) observed age at death frequency distribution (see above for further details).



3. RESULTS:

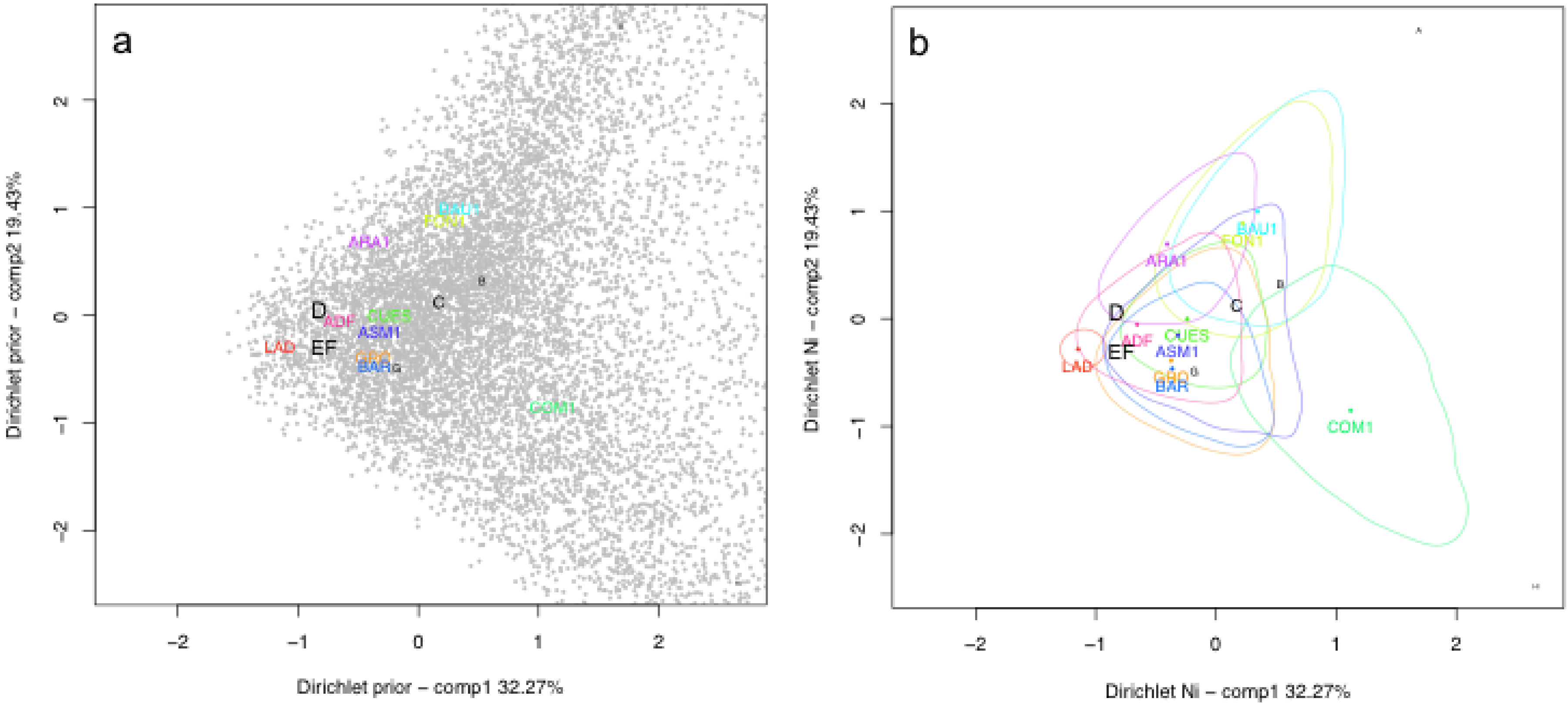
The properties of the Dirichlet distribution permit the generation of random deviates of the population frequencies given the observed sample data and a suitable prior. Figure 2 represents the 10 mortality profiles presented in Table 1, with 95% credible intervals of the frequency density through time, generated by 10,000 Dirichlet deviates.

All 7 age classes are represented on the age-at-death data from the archaeological site Font Juvenal I (FON1, Table 1 and Table 2, number of teeth $N_i > 0$). The youngest age class (A) has the largest credible interval, while the oldest age class (HI) has the smallest, which is directly related to their observed counts (Figure 2). There is no overlap between the credible intervals of class A and any of the other classes, except class C. This increases our ability to differentiate between age class representations in an archaeological sample. It should be noted that these are 95% credible intervals on the frequency density per unit time of each age class, and not on the frequency in each age class.

Similarly, on the age-at-death frequency distribution of the archaeological site La Draga (LAD), there is no overlap between the credible intervals of class D and any of the other age classes, except with class C (Figure 2). Here again, our approach enables us to be more confident when interpreting the observed pattern. More specifically, while the youngest and the oldest age classes are not observed on this profile (Table 2, number of teeth $N_i = 0$), the properties of the Dirichlet distribution allow us to generate random deviates of the population age-at-death frequency distribution and estimate credible intervals for those unrepresented classes.

The credible intervals of the youngest age class (A) are generally the widest (Figure 2). The Cueva de Sarsa – CUES profile contrasts well against those from Font Juvenal – FON1 and La Draga – LAD. There is less visible contrast between the profiles from Combe Obscure 1 – COM1, Baume d'Oulen – BAU1, and Abri I de Saint Mître – ASM1. For Barret de Lioure – BAR, Abri II du Fraischamp – ADF, Araguina-Sennola – ARA1 and Grotte Lombard – GRO in general, nearly all the credible intervals overlap, suggesting low differentiation or poor resolution in the data.

Figure 3: Correspondence analysis performed on the ten Cardial, Epicardial and assimilated archaeological culture mortality profiles from France and the Iberian Peninsula, dated to between 5500 and 4500 cal BC (Table 2). The site and age class coordinates are those for the first two dimensions of the correspondence analysis (representations on dimensions 1 and 3 and 2 and 3 are shown on Figure S1a and S1b, respectively). The site codes (coloured names) are given in Table 1. The relative positions of the age classes are shown in black and their font size is proportional to their relative contribution to the analysis (Table S2). Age classes A (at the top right corner) and HI (at the bottom right corner) are in small font size because of their small contribution to the representation. Figure 3a (left): Grey dots are some of the 10,000 deviates of the population frequency given the observed data, using the Jeffreys' prior, i.e. 'rdirichlet (0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)'. Figure 3b (right): Correspondence analysis and kernel density estimates of the 10 mortality distributions. The two-dimensional kernel density estimates for an age-at-death frequency distribution (i.e. one site) were obtained from the x and y coordinates generated by the correspondence analysis for the 10,000 Dirichlet deviates of this site. The contour lines were drawn around the density value containing 95% of the deviates. Colour dots show the relative position of the observed age-at-death frequency distribution for the corresponding sites.


a
Dirichlet prior – comp2 19.43%
Dirichlet prior – comp1 32.27%
BAU1
FON1
ARA1
D
ADF
CUES
ASM1
C
LAD
EF
GRO
BAR
COM1
b
Dirichlet Ni – comp2 19.43%
Dirichlet Ni – comp1 32.27%
BAU1
FON1
ARA1
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ADF
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ASM1
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GRO
BAR
COM1

Correspondence analysis was performed on the observed number of teeth (N_i) per age class *i* to compare the ten age profiles (see Table S1 for the proportion of variations explained by the Correspondence Analysis components). Figure 3a and 3b represent the projections of the first two components, i.e. summarizing 52% of the total variation. Figure 3a shows that the age classes (black letters) are arranged according to the age gradient (A to HI class; the "Guttman effect"). The distribution of the age classes and sites (coloured names) for the observed data only, in two dimensions, overlaid with the 10,000 random deviates (grey dots) obtained from Jeffreys' prior, i.e. 'rdirichlet(0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5)'. The cloud of grey dots represents the correspondence analysis distribution of Dirichlet simulated mortality profile. It can be thought of as the Correspondence Analysis projection of a null distribution of age-at-death data, i.e. expected correspondence analysis plot, given only the prior. As expected, this cloud of random points covers the range of the 10 observed mortality profiles. This highlights that any interpretation of correspondence analysis plots, without statistical assessment, can be misled by the shape of the possible plot space, which is itself determined by the input data. Such factors should be considered when comparing age-at-death frequency distributions using such plots. Figure 3b shows the contour lines representing the confidence interval for an observed age-at-death frequency distribution within which 95% of the deviates lay.

The use of the kernel density estimation aids interpretation of similarity/dissimilarity of age-at-death profiles to the extent that it provides areas of possible overlap with statistical confidence. Figure 3b indicates that we can be confident at approximately the 0.05% level that two clusters of sites overlap: the first contains five sites (GRO, CUES, BAR, ASM1, ADF) and the second contains (BAU1 and FON1). The overlap of these sites within each cluster suggests that their slaughter profiles cannot be differentiated, and could be interpreted as indicating similar slaughtering strategy within each cluster, or poor resolution in the data. Figure 3b also indicates that three sites do not overlap with one another (LAD, ARA1, COM1). This suggests that these sites' mortality profiles differ significantly, which may represent specific slaughter strategies, differences in taphonomic loss or management of the carcasses occurring at these sites.

It should be noted that the correspondence analysis reported in this study necessarily only shows 2 dimensions of variation; further dimensions of variation may permit statistical differentiation of observed datasets. We recommend exploration of dimensions of variation beyond the first 2 before confidently stating that 2 datasets are not statistically differentiated (see, for example, Figures S1a and S1b).

4. DISCUSSION:

This study demonstrates how the Dirichlet distribution can be used to produce credible intervals for mortality profiles and confidence intervals on correspondence analysis, even when some age classes are not observed, as an aid to interpretation of clustering patterns. Below we discuss interpretation of age-at-death frequency distributions and comparisons of these distributions using correspondence analyses.

4.1. Methodological considerations

The accumulation of age-at-death data over the last few decades, and its use to make inferences on animal domestication and husbandry strategies, has highlighted a number of theoretical and methodological challenges (Brochier 2013). Some of these challenges are due to (i) the high sampling uncertainty associated with archaeological assemblages (ii) the discretization of age estimates into non-independent age categories. The latter generates categorization uncertainty that depends on the number and duration of the age classes, as well as on precision with which teeth can be attributed to one age class or another (Steele 2005).

Even though some archaeozoological studies have attempted to deal with these issues (Price, Wolfhagen, and Otárola-Castillo 2016), we believe the statistically tractable approach we propose here has 4 major advantages over other existing approaches. First, it infers the joint distribution of the population frequencies of the 7 age classes and provides a better resolution of the underlying herding strategy than ternary diagrams, which use only 3 age classes (Steele 2005; Weaver, Boyko, and Steele 2011). Second, analogous to Millard (Millard 2006)'s Bayesian approach, sampling uncertainty is estimated with a Dirichlet distribution instead of bootstrapping (Steele 2005; Price, Wolfhagen, and Otárola-Castillo 2016). While bootstrapping (i.e. sampling with replacement) can be useful, it (i) assumes the age classes are independent, which is not the case since a tooth can sometimes be assigned to more than one age class, while some age classes are exclusive of each other; (ii) when the sample size is small, as is typically the case in most archaeological assemblages, the bootstrap sample mean may not converge to the true sample mean (Athreya 1987), and (iii) when the sample size is small bootstrapping systematically under-represents variation. Third, in contrast to the approach introduced by Price et al. (Price, Wolfhagen, and Otárola-Castillo 2016), where the age class bin widths are equal, the Bayesian method we propose conserves the relationship between survival rate and the area under the survival curve since the age class bin widths depend on their time span (e.g. Fries 1980). Fourth, our approach allows more flexibility when comparing age-at-death frequency distribution, since multiple profiles can be compared against each other rather than the comparison of one observed profile against a reference profile (Price, Wolfhagen, and Otárola-Castillo 2016).

Alternatively, some archaeozoological studies have attempted to account for age uncertainty and small sample size error using confidence intervals or standard errors on age-at-death data (e.g. Tresset 1997; Valenzuela-Lamas et al. 2009). However, these approaches have limited applicability since the data is not normally distributed and age class frequencies are not independent. The Dirichlet distribution is well suited for statistical assessment of such age-at-death data as by definition it takes as parameters a vector of counts over categories (Millard 2006). Our approach has the major advantage of accounting for this sampling uncertainty, while accommodating all the information provided by the observed sample. This is evident by the large credible intervals seen for the infant/juvenile classes (Table 1 and Figure 2).

The age-at-death category divisions can lead to difficulties in interpreting profiles because of (i) variations in the number of teeth in a hemi-mandible according to the age of the animal (Masset 1973) and (ii) their unequal time duration. While the former has mostly been ignored (probably due to challenges raised by counting protocols issues), Helmer and Vigne (Helmer and Vigne 2004; Vigne and Helmer 2007) attempted to solve the latter by introducing an "*a priori* correction" of the relative frequencies, instead of the standard correction for constructing the density histograms. This led to some misunderstanding by scholars who did not account for the unequal probability of the age classes (Greenfield 2005; Brochier 2013). The "*a priori* correction" is however not appropriate, since it assumes that the age class frequencies are independent.

The final step in domesticate animal mortality analysis is the comparison of multiple profiles from archaeological sites that differ in time period and/or location of origin. The choice of statistical tests to compare age-at-death profiles (Vigne 2000; Brochier 2013) and assess how significantly any two profiles may differ (Marom and Bar-Oz 2009) have been debated intensively. For example, some archaeozoologists (Tresset 1996; Vigne 2000; Helmer, Gourichon, and Vila 2007; Vigne 2011; Gillis 2012) proposed the use of multivariate differentiation among age-at-death profiles based on correspondence analyses of the raw frequencies of each age class. However, because of the high level of sampling uncertainty in age-at-death data, we argue that none of the tests or distance estimates proposed thus far in the archaeological literature are appropriate.

Correspondence analysis permits visualization of differences among age-at-death profiles, and has the additional advantage of integrating the information content of all 7 age classes (in contrast to triangular diagrams which use only three age classes; (Greenfield 1988; Stiner 1990; Atıcı 2009)). None-the-less, visual interpretation of how close age-at-death frequency distributions are, based on a single point per age-at-death profile, is easily steered by subjective biases (Brochier 2013) and not amenable to statistical assessment of these differences. We have shown that generating a large set of random sample deviates using the Dirichlet distribution, in combination to multivariate kernel density estimation of these random deviates, permits robust comparison of age-at-death profiles on correspondence analysis plots (Figure 3 and S1). However, as noted above, it is important to consider all dimensions of variation in a correspondence analysis and the contributions of the different age classes to the analysis (Table S2).

We believe that the approach proposed here is novel in zooarchaeology and constitutes a valuable addition to the age-at-death data analysis toolkit. Indeed, we suspect that the approach proposed here will be useful in the analysis of other categorical count data from archaeological sites, especially when sample sizes are relatively small.

The approach proposed here does not solve all the challenges to analysing age-at-death data. Robust consensual standards for age-at-death estimates, using, for example, large modern reference collections for some domestic species, are still required. In the introduction, we briefly argued for the use of dental age – using the MNI or number of teeth as basic units of quantification – and of mortality profiles rather than survival profiles; here again, the lack of consensual standards has hampered development of age-at-death analysis techniques. Frequency MNI (sensu Poplin (1976)) is replicable, but is not linearly correlated with the absolute frequency. However, pairing MNI, used for elaborating age profiles based on teeth, is often based on pairing right and left mandibles; which may not be as replicable (Vigne 1988). Conversely, the number of teeth is a true representation of the archaeozoological evidence. It is none-the-less subject to the fragmentation-dissociation of teeth and to the initial number of teeth in the mandible (Poplin 1976; Vigne 1988; Lyman 1994b). MNI are better adapted for the less fragmented series of mandibles, whereas the number of teeth is much suitable for series with numerous isolated teeth. Either frequency MNI and number of teeth raw data are informative for addressing archaeozoological debates (Vigne 1988).

Taphonomic loss is a direct outcome of site-specific depositional and post-depositional histories (Brain 1981; Lyman 1987; Lyman 1994a; Halstead 1998) and considerable challenges remain in assessing its effects. Taphonomic and sampling biases, such as higher attrition caused by scavengers (Payne and Munson 1985; Munson 2000) and differential survival or visibility of sub-adult teeth (Lyman 1994a) may lead to observed age class profiles not representing true age-at-death profiles at the time of deposition (Ducos 1988; Vigne 1988).

However, if these processes are similar at different sites then the approach we describe here still permits relative comparison of observed site profiles. None-the-less, the construction of credible intervals on mortality profiles improves our confidence in interpreting the underlying management strategy.

4.2. A tentative interpretation of Cardial stock-keeping practices

This study primarily aims at introducing a novel statistical method to assess mortality profiles from age-at-death data. This data is by nature scarce and sample sizes typically small; the dataset presented here is no exception. Indeed, while half of the sites are well dated and have good quality material (La Draga – LAD, Grotte Lombard – GRO, Font Juvenal I – FON1, Combe Obscure I – COM1, Baume d'Oulen I – BAU1), the others are either smaller samples from older excavations (Cueva de la Sarsa – CUES, Abri I de Saint Mitre I – ASM1, Araguina-Sennola – ARA1) with stronger taphonomic alterations (Abri II du Fraischamp – ADF) and/or less accurately dated (Barret de Lioure – BAR; (Vigne 2007)). These 10 sites are therefore best thought of as a toy-dataset that is typical of other age-at-death data generally used in archaeozoology. In order to explore the potential power of the approach we develop here, we limited our analysis to those 10 sites as they belong to a common Early Neolithic chrono-cultural entity (Cardial-Epicardial), while showing some heterogeneity. Even though the aim of this study is not to draw firm conclusions on Cardial herding strategies based on only 10 sites, some interesting observations can be made from the analyses presented.

In the correspondence analysis presented in Figure 3a, we see that the profiles are arranged according to a gradient (Guttman effect) following the succession of the age classes from A to HI. However, in contrast to traditional analyses where these two classes played an important role, they contribute little in the current analyses (Table S2).

Figure 3b shows large overlaps in the density contours of five sites: Grotte Lombard, Cueva de la Sarsa, Barret de Lioure, Abri de Saint Mître and Abri II de Fraischamp. They cluster between the high frequencies of the C class (6-12 months) and D and E-F classes (12-48 months: adults). On the age-at-death profiles (Figure 2) we see that three of these sites (Barret de Lioure, Abri de

Saint Mître and Abri II du Fraischamp), all located in Provence, display a similar profile, with a clear dominance of class C. This pattern may correspond to mixed milk and meat exploitation, with a dominance of tender meat production (Vigne and Helmer 2007). The overlap of the profile of Grotte Lombard may be due to a relatively even distribution of the frequencies between age classes (Figure 2); this profile shows wider credible intervals, which may be due to the sample size. Although Cueva de Sarsa overlaps with the other four sites (Figure 3b and S1), it displays a slightly different profile (Figure 2) characterized by a well-represented age class B, followed by age class C. This pattern indicates slightly different practices, where younger individuals are more common, suggesting lambs may have been removed early, and that an increase in milk production was sought (Blaise 2005).

Located in Cataluña, La Draga plots apart, very near D and E-F with little overlap except with Abri II of Fraischamp (Figure 3b). This site shows a narrow 95% confidence interval, in line with its large sample size (N_i=145). This profile (Figure 2) is dominated by age class D (12-24 months) with a secondary but important contribution from E-F class (24-48 months). This could be interpreted as indicating an overall meat exploitation (Vigne and Helmer 2007), with a selective slaughtering of retired females, possibly for increasing lamb production (and consequently milk?).

The three Languedoc cave sites plot at the other extremities of the gradient of the Correspondence Analysis (Figure 3b). Combe Obscure stretches from B-C (milk and tender meat) in the direction of HI, due to the relatively high proportion of old adults (Figure 2); this can be due to hunting of feral sheep (lower occurrence of flock leaders or old reproductive male). Baume d'Oulens and Font Juvénal plot together and apart from the other sites due to their high proportion of very young animals (class A), which may result from perinatal mortality in the cave as they were used as sheep pen or due to a specialized seasonal milk exploitation (Helmer et al. 2005; Vigne and Helmer 2007).

The only Corsican site (ARA1) plots in an intermediate position between the three Provence shelter sites with tender meat exploitation (ASM, ADF1, BAR) and the two Languedoc sites with specialized milk exploitation (FON1, BAU), probably because of successive distinct occupation practices (Vigne 1988).

It is not possible to deduce the general pattern of exploitation practices of caprines during the Early Neolithic from this small sample of heterogeneous profiles. However, it seems that collectively they indicate distinct types of mixed milk and meat exploitation. In addition, the inferred differences may represent distinct regional strategies with more meat exploitation in the Provence sites (ASM, ADF1, BAR), in contrast to a relatively higher tendency towards milk production in the Languedoc sites (FON1, BAU, COM1). The two sites from Catalunya and the one from Corsica show small differences with reference to these sites.

5. FINAL COMMENTS

We introduce here a Bayesian approach to aid statistical comparison of multivariate count data in archaeology. We exemplify this new approach on age-at-death analysis for domestic animals using caprine toothwear data from 10 sites from the North Western Mediterranean Early Neolithic. Although our dataset is small and disparate, some statistically robust patterns seem to emerge, permitting a sketching of interesting geographical differences in herding strategies. We suggest that the use of statistical approaches such as the Dirichlet distribution will herald a new era in animal age-at-death analysis and husbandry strategy reconstruction. Further large-scale analysis of sites from different time periods and geographic locations should be performed to fully assess the power of the approach suggested here in site comparisons.

While we have focused on data visualization using correspondence analysis, there is also a clear need for the development of multivariate distance measures to better assess relationships between age-at-death profiles at different sites; such distance measures should lend themselves well to the analysis of the Dirichlet population deviates generated as described here.

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