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Does the choice of a reference matter for log size index analysis? A case study from roman times in southern France

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ABSTRACT

Log Size Index (LSI) has been developed and used in archaeozoology to perform biometric studies of often small datasets, a recurrent limitation of archaeological faunal assemblages. This approach consists of aggregating measurements taken on different anatomical parts by standardisation, using a reference to which the studied measurements are scaled. No consensus exists in the choice of the reference to be used for LSI analyses and several datasets are now available, differing in their specimens and variables composition, and geographic and temporal origin. Using a biometric dataset of 5533 measurements of cattle, suids, sheep and goat from southern France and dated from the Roman times we compared the use of several references, provided by the R package zoolog, with a 'mean' reference specifically built for our studied sample and that corresponds to an averaged specimen. We demonstrated that references differ both in their raw measurements and their allometries, and that the choice of the reference influences the number of variables and measurements that can be analysed, but also diachronic LSI analyses and potentially their interpretations. While the main patterns are similar among references, local variation exist and it could not be excluded that the choice of the reference will more strongly influence other studies. We advocate to use the mean of the studied archaeological assemblage as reference, with the double benefit of exploiting to the maximum the number of available measurements, and of minimising, on average, the possible allometric differences between the studied population and the reference.

Keywords: Biometry, Archaeozoology, Allometry, Standard

1. Introduction

Archaeological bones are often found fragmented, notably those of domesticated species that especially suffer from human actions before burial. Biometric analyses exploring the spatial or temporal variation of populations based on these often-incomplete bones involve both disparate sets of measurements, *i.e.* not all variables can be measured on all bones, and often a small number of measurements are available per variable. To cope with these small datasets, it has been proposed to use the technic of the «Log Size Index» (LSI) (Simpson, 1941; Simpson et al., 1960; Meadow, 1981; Meadow et al., 1999) that certainly became one of the most commonly used morphometric method in archaeozoology. The LSI approach consists of aggregating measurements taken on different anatomical parts by standardisation. Each studied archaeological measurement is compared and standardised to the corresponding measurement of a reference. This scaling procedure permits to combine measurements (*i.e.* distances in mm) of different variables (*e.g.* distal breadth (Bd), greatest length (GL)) and bones in the same analysis by computing a new variable, the LSI, which variation can be studied similarly as any univariate variable. The LSI approach is therefore a biometric tool for (artificial) data augmentation that allows to statistically compare assemblages that could not, or only partially, be studied otherwise. LSI is traditionally restricted to studies dealing with small number of measurable skeletal parts (Meadow et al., 1999), or to study overall size variation (*e.g.* (Uerpmann and Uerpmann, 1994; Davis, 1996; Meadow et al., 1999; Baudry, 2012; Arbuckle et al., 2014, 2016; Duval, 2015; Fr´emondeau et al., 2017; Robin and Clavel, 2018)). There is no general rule in the choice of which reference to use for standardisation and several references are now available publicly ((Pozo et al., 2022) and references there in https://cran.r-project.org/web/ packages/zoolog/index.html)). In addition, there is currently a desire to homogenise practices in LSI analyses in order to make the results more easily comparable (Pozo et al., 2022). Used references are either the measurements of a single specimen of known breed, wild population, or ancient context (*e.g.* Zeder, 2008; Duval et al., 2012; Arbuckle et al., 2014; Zeder and Lemoine, 2020a, 2020b), or mean measurements of a group of individuals (*e.g.* Meadow et al., 1999; Sykes et al., 2011; Manin et al., 2016). Some others, like us (*e.g.* (Jeanjean et al., 2022)), chose to use as a reference dataset the average measurements of their own assemblage. To which extent the references differ from each other, and if and how the choice of the reference influences LSI analyses and interpretations, is not yet well known.

The main assumption behind the LSI is the principle of isometry, according to which the body proportions of all animals are the same and evolve similarly, *i.e.* the differences between the reference and the studied population are constant, regardless of the studied variable or bone. However, the relative dimensions of the different parts of an organism may differ from one individual to another, correlated to its overall size. This tendency is called allometry (Huxley and Teissier, 1936; Gould, 1966; Levinton, 1988; Gayon, 2000). Three types of allometry can be described: static, *i.e.* within a population among individuals of similar age, ontogenetic, *i.e.* during growth (Huxley and Teissier, 1936), and evolutionary allometry, *i.e.* among individuals from distinct evolutionary lineages (Klingenberg and Zimmermann, 1992). In the context of the LSI approach, differences between references correspond to static allometry and ontogenetic allometry is implicitly assumed to be limited since bones of juveniles are discarded, with the variation that bones of unknown fusing status are or are not included (Forest, 1997).

In this context, this paper examines the importance of the choice of the reference used to standardise the archaeological data during LSI analyses. First, differences between a series of available references and our own 'mean' reference were explored using their raw measurements.

We then explored the morphometric proximity between these various references. Finally, we assessed the impact of the choice of the reference on a diachronic LSI analysis using here a dataset of measurements dated from 200BC to 400AD and originating from southern France.

1. Material

The data correspond to those analysed in Jeanjean et al. (2022) and include 5533 measurements, from which 1950 correspond to cattle, 2197 to suids (wild boar and domestic pigs undistinguished), 273 to goat, and 1113 to sheep. The measurements come from almost 30 years of preventive archaeology and were all acquired by one of us (VF) during the faunal analysis of 64 archaeological sites. These sites are located in the South of France and cover the period of time ranging from 200 BC to 400 AD (Jeanjean

et al., 2022). The measurements were acquired following the Von Den Driesch guideline (von den Driesch, 1976) to which were added few extra measurements (see Jeanjean et al. (2022)). To each measurement was assigned a dating corresponding to the mean of the *terminus post quem* (TPQ) and *terminus ante quem* (TAQ) of the stratigraphic unit where the bone was recovered (similarly as in Jeanjean et al. (2022)). The formulation used for LSI computation was: LSI = Log (x/y) = Log (x) - Log (y), with x the measure of the studied specimen, y that of the reference, and Log being the natural logarithm. For each species, an average specimen was calculated whose measurements correspond to the mean, per variables, of all available measurements in our archaeological dataset based only on a selection of post-cranial bones (see Jeanjean et al. (2022)). This 'mean' specimen was used as a reference dataset specifically designed for our study. The measurements of this chimeric specimen are available in Jeanjean et al. (2022). The other references used are those provided in the R package *zoolog* (Pozo et al., 2022). A total of 19 references were used: 5 for bovids (cattle and aurochs), 5 for suids (wild and domestic), 5 for sheep (domestic, *Ovis orientalis* and *Ovis musimon*) and 4 for goat (wild and domestic) (Table 1). Only the measurements of the bones already retained in the study by Jeanjean et al. (2022) were analysed. Thus, in order to have a direct comparison, the variables acquired on teeth, vertebrae, pelvic bones and phalanges present in the references of the *zoolog* package were not included in the number of available variables (Table 1). The references are called in quotes and named following the first author of the original publication (*e.g.* 'Nieto' for Nieto-Espinet, 2017) or following the *zoolog* nomenclature (*e.g.* 'Basel', Table 1).

Table 1 *Description of the references used for the LSI analyses with number (Nbr.) of available variables and measurements. Number of variables excludes those acquired on teeth, vertebrae, pelvic bones and phalanges that are absent in the 'mean' reference. F: female, M: male, ? unknown.*

	Taxa	**Name of the reference**	**Geographic Origin/Breed**	**Temporal Origin**	**Sex**	**Single specimen/mean**	**Nbr. measures**	**Nbr. variables**	**Reference**
Cattle	*Bos taurus*	'Mean'	South of France	Antiquity	?	Pop.	1950	50	Jeanjean, et al. (2022)
	Bos taurus	'Nieto'	Catalonia, Spain	Early Bronze Age (site of Minferri)	F	Single	1315	44	(Nieto-Espinet, 2018)
	Bos taurus	'Basel'	Hinterwälder breed	Modern	F	Single	1609	33	(Stopp and Deschler-Erb (2018)
	Bos primigenius	'Degerbol'	Denmark	Early Holocene (Boreal)	F	Single	1513	34	(Degerbøl and Fredskild, 1970)
	Bos taurus	'Johnstone'	Elms Farm, (England)	Late Iron Age to Romano-British transition	?	Pop.	706	22	(Johnstone and Albarella 2002)
Suids	*Sus sp.*	'Mean'	South of France	Antiquity	?	Pop.	2197	48	Jeanjean, et al. (2022)
	Sus domesticus	'Albarella'	England	Late Neolithic (site of Durrington Walls)	?	Pop.	1016	17	(Albarella and Payne, 2005)
	Sus scrofa	'Basel'	?	?	M	Single	1798	37	(Stopp and Deschler-Erb (2018)
	Sus scrofa	'Hongo'	Turkey	Modern	F	Single	1902	96	(Hongo & Meadow 2000)
	Sus scrofa	'Payne'	Kizilcahamam, Turkey	Modern	Mix	Pop.	767	12	(Payne and Bull , 1988)
Sheep	*Ovis aries*	'Mean'	South of France	Antiquity	?	Pop.	1113	40	Jeanjean, et al. (2022)
	Ovis aries	'Davis'	Shetland breed, island of Hoy, Orkney, Scotland	Modern	F	Pop.	742	23	(Davis, 1996)
	Ovis aries	'Clutton'	Soay sheep, island of Hirta, St Kilda, Scotland	Modern	M	Pop.	995	50	(Clutton-Brock et al., 1990)
	Ovis orientalis	'Basel'	?	?	M	Single	1041	34	(Stopp and Deschler-Erb (2018)
	Ovis orientalis	'Uerpmann'	Iran	Modern?	F	Single	1051	42	(Uerpmann and Uerpmann, 1994)
Goat	*Capra hircus*	'Mean'	South of France	Antiquity	?	Pop.	273	25	Jeanjean, et al. (2022)
	Capra hircus	'Basel'	?	?	M	Single	258	33	(Stopp and Deschler-Erb (2018)
	Capra hircus	'Clutton'	Holy island, Arran, Scotland	Modern	?	Pop.	214	47	(Clutton-Brock et al., 1990)
	Capra aegagrus	'Uerpmann'	Turkey	?	Mix	Pop.	243	42	(Uerpmann and Uerpmann, 1994)

2. Methods

All analyses were performed in R, the language and environment for statistical computing (R Core Team, 2021). The LSI analyses were carried out using the *zoolog* package (Pozo et al., 2022). Because the number of measurements that can be included in the LSI analysis depends on the variables included in the reference, the number of variables included in each reference and the number of archaeological

measurements that can be analysed per reference were recorded. The relationship between the number of available measurements and variables was assessed by regression. In order to assess the similarity between references and to explore allometry, the raw measurements of all studied references were compared to each other and to our 'mean' reference. Only the variables common to the different studied references have been visualised. In such analysis, references with similar body proportions (*i.e.* isometry) will show similar amount of differences for all variables. Conversely, in case of allometry, the variables between two references would not have the same deviations, depending on the anatomical element analysed. The 'mean' reference was then used to standardise all the other references. This allows exploring specifically the amount of variation between our dedicated 'mean' reference, that will be used as a baseline (*i.e.* LSI = 0) and all other available references. In addition, to visualize the differences between the references, LSI values computed for each reference and the 'mean' were passed into a scaled principal component analysis (R function *prcomp* package *stats*). The PCA coordinates were then used to compute distance matrices (function *dist* from the package *stats*) (Paradis and Schliep, 2019). Because in the companion paper of the present work (Jeanjean et al., 2022) we demonstrated that the LSI values obtained from the length, breadth, and depth dimensions of the bones provided similar diachronic evolution patterns they were not separated in the present analyses. It should be noted that this trend should not be considered as a generality since the variation between dimensions may vary depending on the sample, archaeological context and research question, that a formal comparison of dimensions is still lacking, and that available studies does not necessary provide similar results (*e.g.* (Davis, 1996; Guintard and Lallemand, 2003)). In addition, it has been proposed to use only one measurement per bone and one bone per articulating group of bones to avoid including multiple measurements from a single specimen (Trentacoste et al., 2018, 2021; Pozo et al., 2022). However, because in archaeozoology it is often impossible to identify all the bones that belong to single animals, and because we have demonstrated that LSI values obtained from measurements of a single articulated skeleton can greatly vary (Jeanjean et al., 2022), and that no rationale exists (to our knowledge) for selecting the measurement to retain and its influence on the LSI analyses, our analyses are based on all available measurements. All references were then used to assess the diachronic evolution of the domestic triad in Southern France (similarly to the analyses performed in Jeanjean et al. (2022)). Changes in size through time were visualised, and studied with the 90% confidence interval of each curve, using regression fitting (function loess of the R package 'stats' (Cleveland et al., 1992)). Two trends differ when their confidence intervals do not overlap. Two series of curves have been constructed. The first one includes only the set of variables common to the different references, in order to check whether the allometry between references can influence their trends. In the case of isometry, the curves are expected to have exactly the same profile, whereas in the case of allometry they are expected to differ. The second series of diachronic graphs aggregates all available LSI values per reference.

4. Results

4.1. Analysable sample size per reference dataset

The number of variables and the resulting number of measurements that can be included in a LSI analysis greatly differ between references (Table 1). For all species, the reference that allows analysing the maximum number of measurements is the 'mean'. The most extreme case concerns suids for which the 'mean' reference allows analysing 2197 measurements *contra* 767 with the 'Payne' reference (Table 1). Altogether, the number of analysable measurements is not related to the number of variables included in the references ($p = 0.06$, adjusted $R2 = 0.15$, Table 1, all species combined).

4.2. Differences between references

The comparison of the raw measurements of the references reveals a relatively homogeneous trend, regardless of their respective overall sizes (Fig. 1, SI Fig. 1). This is true both when all variables are analysed (SI Fig. 1) and even clearer when only the variables in common between all references are compared (Fig. 1). However, the distance between references vary across variables and the lines joining the measurements are not parallel and even crossing (Fig. 1). The relationship between variables is not isometric.

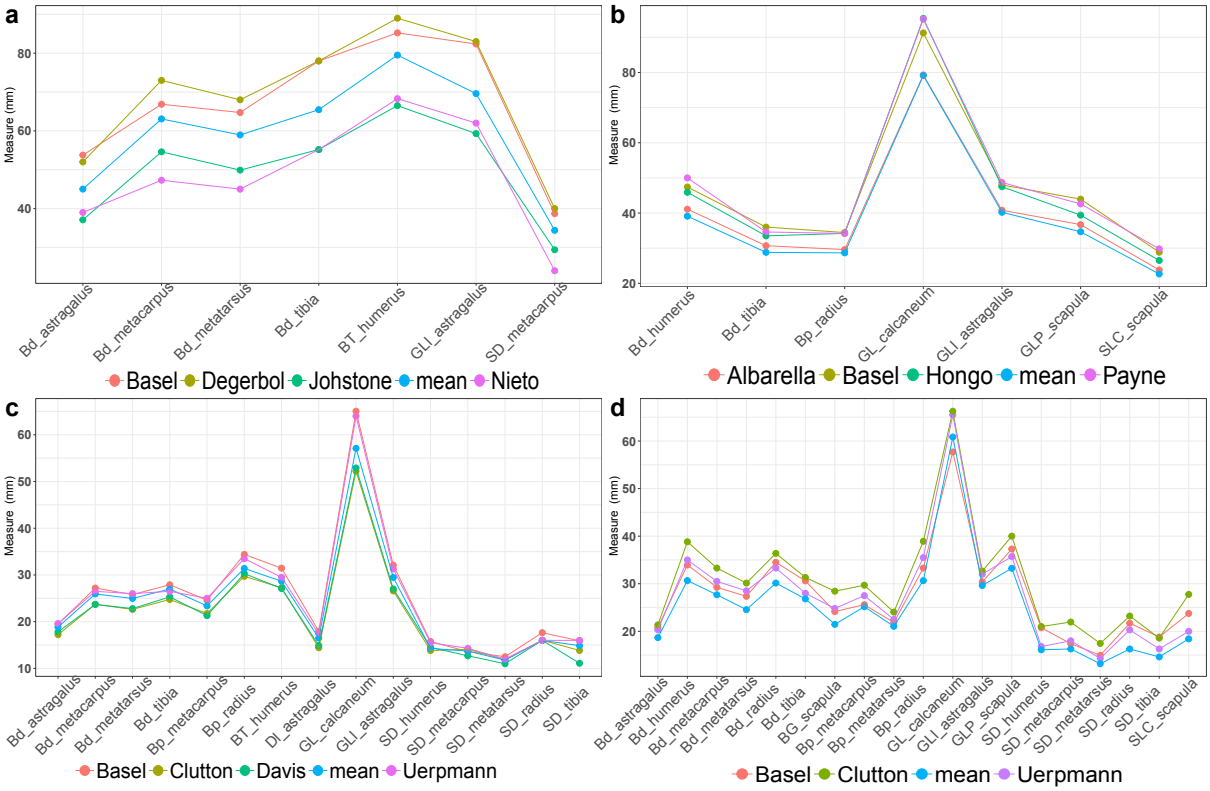

Fig. 1. *Comparison of the references based on their common raw measurements (in mm). The analyses are done separately for cattle (a), suids (b), sheep (c) and goat (d). An extended version including all variables present in the 'mean' reference can be found in SI-fig1.*

Differences between references were further explored first by standardising the references with our 'mean' reference (Fig. 2), then by exploring the overall proximities between all references (Fig. 3). As for raw measurements, unparalleled curves between references highlight allometries (Fig. 2).

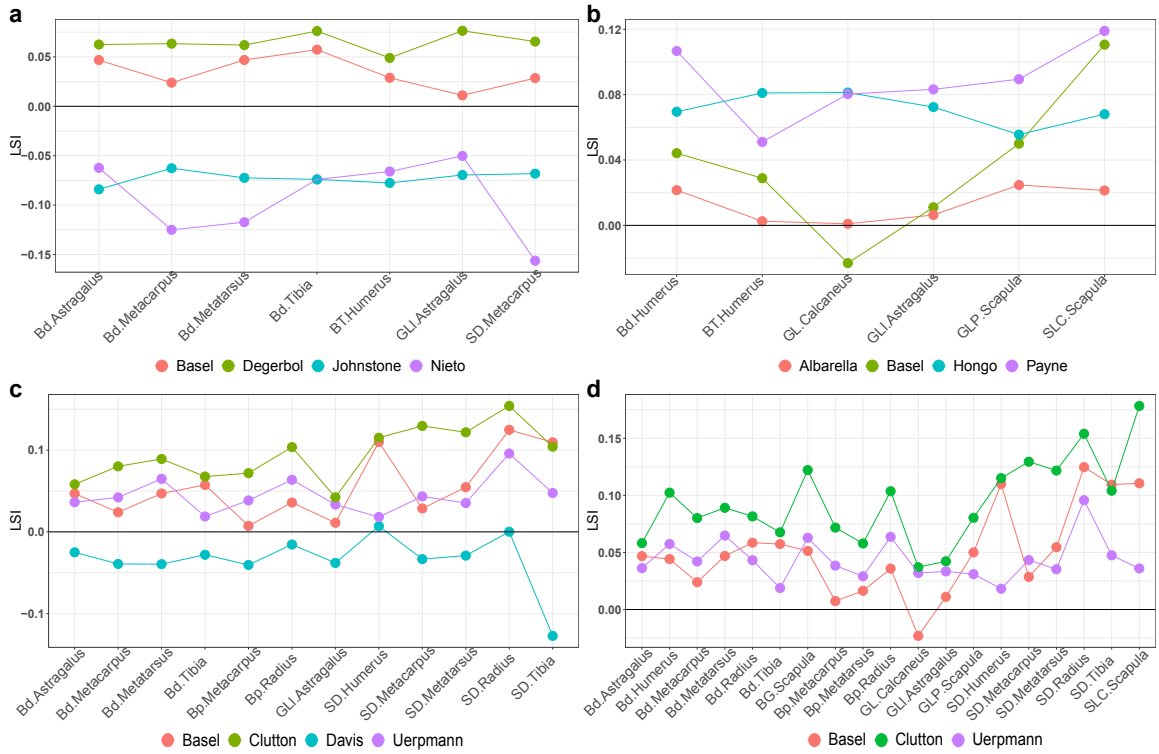

Fig. 2. *Variation between references in LSI values obtained by standardisation with the 'mean' reference. The analyses are done separately for cattle (a), suids (b), sheep (c) and goat (d).*

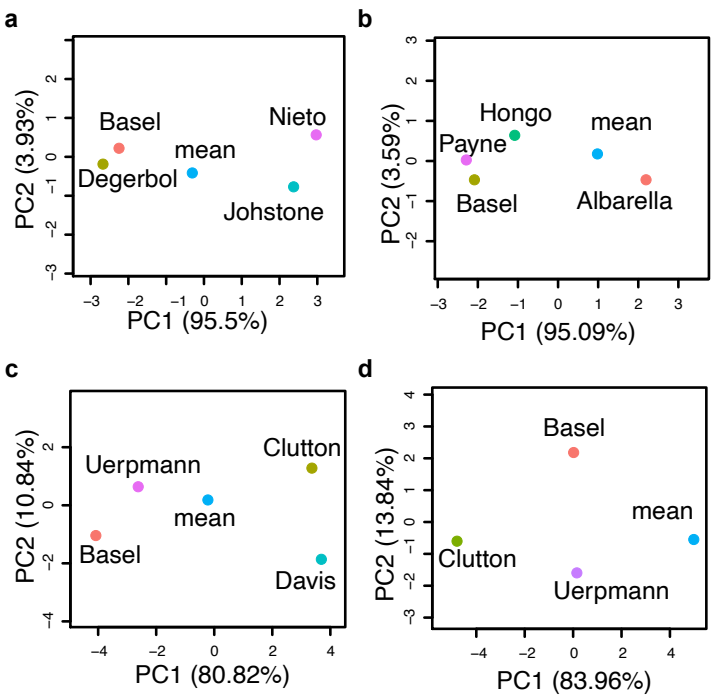

Fig. 3. *Proximity between references for cattle (a), suids (b), sheep (c) and goat (d). Visualisation of the two first axes of a PCA.*

For cattle (Fig. 2a), the 'mean' reference is larger than the archaeological references of 'Nieto' and 'Jonhstone', but smaller than the aurochs ('Degerbol') and modern cattle ('Basel') references. The variable differing the most between references is the SD of the metacarpus with a variation exceeding 0.2 in LSI value (Fig. 2a). This pattern is confirmed by the PCA showing the 'mean' not being specifically close to any of the other references (Fig. 3a).

For suids (Fig. 2b), the 'mean' has smaller measurements than all other references, except for the calcaneus greatest length (GL) of the 'Basel' reference. The scapula SLC is the variable differing the most between references with a maximum of 0.12 LSI value observed for the modern 'Payne' reference. The closest reference to the 'mean' is that from the Late Neolithic domestic pig population of 'Albarella' (Fig. 3b).

For sheep (Fig. 2c), the 'mean' appears only larger than 'Davis' and the maximum difference between references is observed for the tibia SD with a variation of ~0.25 in LSI value. Overall, the 'mean' appears morphometrically in between 'Uerpmann' and 'Basel' of unclear origin (Table 1) in one side and the modern references of 'Davis' and 'Clutton' in the other side of the PCA (Fig. 3c).

For goat (Fig. 2d), the three references show higher measurements than the 'mean' except the 'Basel' reference for the greatest length (GL) of the calcaneus. The most distant reference to the 'mean' appears to be that of modern 'Clutton' reference with a maximum variation of ~0.2 in LSI value observed for the scapula SLC. This reference also shows the greatest amount of LSI variation. This trend is confirmed by the PCA (Fig. 3d) showing an opposition between the 'mean' and 'Clutton' references, the two other references falling in between.

4.3. Diachronic trends

Three visualisations of the diachronic trends have been carried out: first including only the variables in common to all references (all trends are computed on the exact same number of measurements, Fig. 4 left), second including all possible variables for each reference (the number of available measurements differ for each reference following Table 1, Fig. 4 middle), then third, shifting the references so they superimpose (Fig. 4 right).

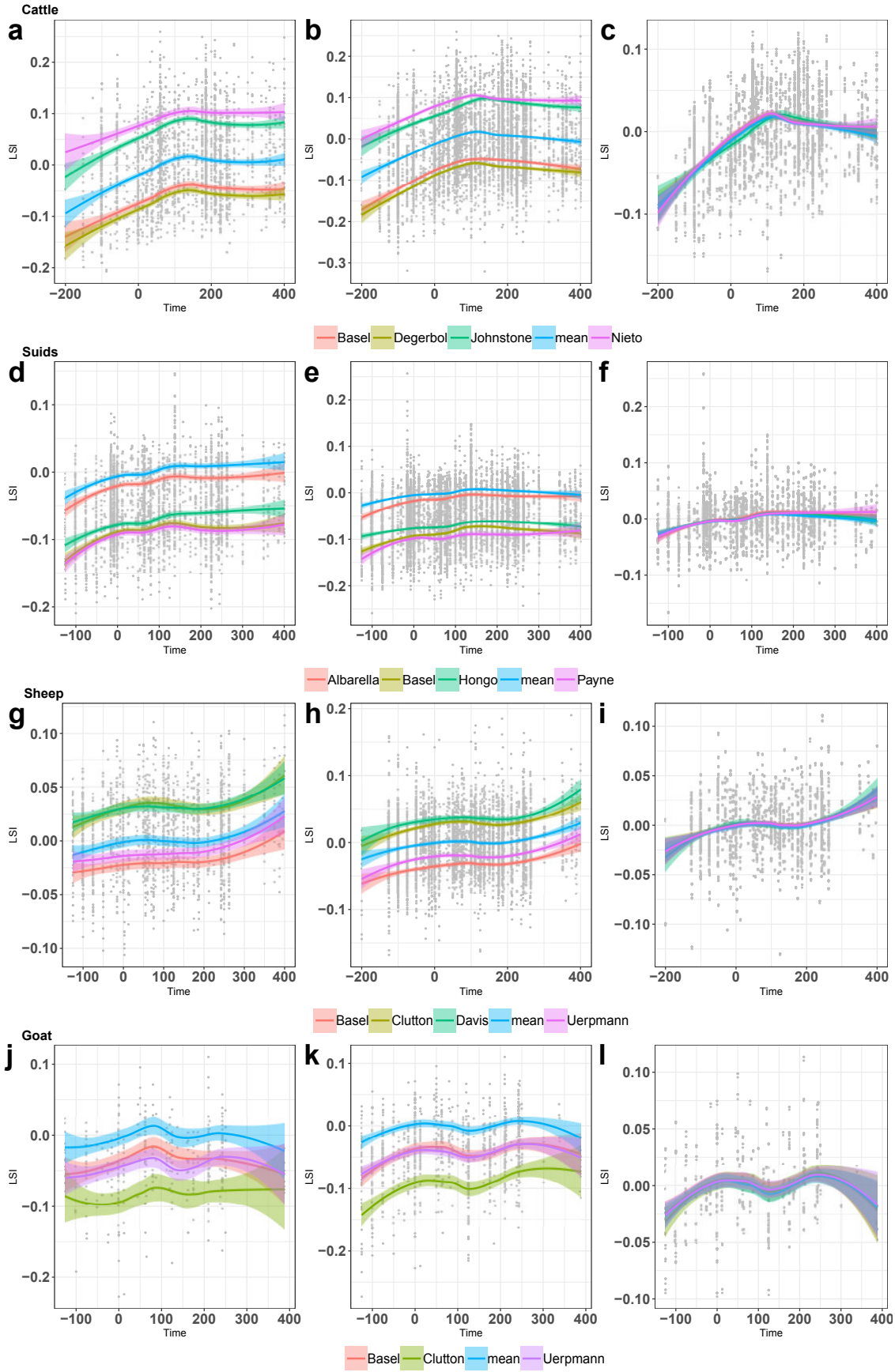

Fig. 4. *Visualisation of the diachronic trends using the various reference datasets (Table 1). The analyses are done separately for cattle (a, b, c), suids (d, e, f), sheep (g, h, i) and goat (j, k, l). Variables common to all references (left: a, d, g, j) and all variables (middle: b, c, e, f, h, i, k, l). The trends are not centred (left and middle) or centred around 0 (right: c, f, i, l). Each point represents LSI values compared to the 'mean'. The number of curves per species depend on the number of available references.*

From a general point of view and for the four taxa, the LSI diachronic trends computed with the various references revealed a similar pattern with a similar shape but with a vertical shift of LSI values (*i.e.* variation in y axis) (Fig. 4 left and middle). Confidence intervals are smaller when more measurements are included (as expected) (Fig. 4 middle) than when only common variables were included (Fig. 4 left). When only the variables common to all references are used (Fig. 4 left), the diachronic trends for cattle (Fig. 4a) show similar overall shape for all references, with a slight decrease after ~200 AD then increase of the LSI values, expect for the 'Nieto' trend that appears constant throughout the end of the sequence. For suids, the trends of 'Payne' and 'Basel' show a drop-off in LSI values from ~125 AD not visible with the other references (Fig. 4d). For sheep, even if all trends look similar, the 'mean' appeared more distant (non-overlapping confidence intervals) from 'Uerpmann' between ~75 BC and 150 AD than during the rest of the period where the confidence intervals overlap (Fig. 4g). Finally for goat, for which the number of available measurements was much smaller than for the other species, it can be noted that the curves obtained for 'Basel' and 'Uerpmann' cross at ~225 AD, though the confidence intervals overlap (Fig. 4j). When the analyses are done using all possible measurements for each reference (Fig. 4 middle), some differences between references can also be noticed. For cattle, the 'Basel' trend appeared smoother and does not show the small drop-off between 100/150 AD observed with all other references (Fig. 3b). In addition, a slight LSI decrease at the end of the sequence is observed for all references except 'Nieto' that rather shows a stability (Fig. 4b). Finally, the two curves obtained with 'Nieto' and 'Johnstone' overlap around 100/150AD while they differ otherwise (Fig. 4b). For suids (Fig. 4e), the 'Basel' trend differs from the others with a slightly more marked increase in LSI values between 75/125 AD and a varying proximity through time with the two more adjacent trends ('Hongo' and 'Payne'). For sheep and goat, the differences between references appeared less marked (Fig. 4h, k). When the trends are superimposed (Fig. 4 right), all the curves largely overlap, but not with a perfect fit, especially at the beginning and end of the time sequence where the data are less numerous.

5. Discussion

From the outset of the method, the purpose of the Log Size Index approach was to increase the sample size of biometric measurements that can be analysed simultaneously, and to mitigate the problem of bone fragmentation, inherent to the study of archaeozoological material (Wolfhagen, 2020). The choice of reference to be used for LSI analyses does not mathematically change the results as long as the analyses are done on a single variable, or as long as a set of different variables are studied separately. This is not the case for most, if not all, of the LSI studies, that, by definition, wish to mix measurements of diverse variables. The idea of mixing measurements corresponding to different variables all the more acquired on multiple skeletal elements seems, *a priori*, a daring idea from a morphometric point of view. Here, we indeed have shown that both differences in relative size proportion of variables, *i.e.* allometry, and the choice of the reference used to carry the analyse impact LSI results and potentially their bioarchaeological interpretation. Even if the results appear relatively homogeneous regardless of the reference some differences have been noted. The impact of the choice of the reference will be all the more problematic as the assemblages studied show small differences. In our case, the time-related variation greatly outweighs allometry linked to the reference choice.

5.1. Allometries

The references differ in their raw bone measurements not only in overall size, but also in their between variables relationships. As a consequence, the LSI standardisation will differ depending of the chosen reference. The representativeness of bones and variables in the studied archaeological assemblage will therefore influence the distribution of LSI values and can be a confounding factor. On the exact same dataset it was demonstrated (Jeanjean et al., 2022) that variables of a same bone, in particular for the scapula, but especially the lengths, breadths and depths of bones, can follow distinct evolutions through time due to different factors as allometry, sexual dimorphism, or presence of both wild and domestic specimens.

5.2. Choice of the reference

It has been stated before that the choice of reference does not affect the variation in LSI (*e.g.* Wolfhagen, 2020). This is true only when variables are studied separately, but when multiple variables are combined into a global LSI value, the choice of the reference does affect LSI variation, as demonstrated in this study. Not all references perform equally and this is not due to the fact that all references do not include the exact same list of variables. Allometric differences between the studied population and the references are responsible for the variation in diachronic trends we observed. However, this variation does not influence drastically the archaeological interpretation of our results that are more heavily influenced by diachronic variation. However, when the differences between the studied assemblages are small, allometry can have a stronger influence that should be systematically explored prior to LSI analyses, by computing the LSI analyses on various references as we did here. The choice of the reference dataset has also consequences on the number of measurements and variables that can be included in the analyses. For example, we excluded the phalanges that are often not distinguished latero-medially or antero-posteriorly contrary to other references (*e.g.* Duval and Clavel, 2018). Conversely we included variables not proposed by von den Driesch (1976) and that are absent from the other references. The purpose of LSI being to increase the sample size, this is an important argument to consider, and in that sense no available reference outnumber the mean of the studied population: using the mean of the population allows maximising the sample size since all available measurements can be used. Even if using as reference a specimen or a population that is distant geographically, chronologically or even taxonomically does not seem to affect drastically the trend in LSI change through time, at least as seen here, it remains questionable. It remains difficult to imagine a case study where a distant reference would be more appropriate than one specifically built for the current study. Here, we found that for cattle, sheep and goat, all the studied references appeared far from the averaged specimen used as a 'mean' reference specially built from the studied dataset. For cattle, studied references include both archaeological and modern references as well as both cattle and aurochs. The geographically closest reference is 'Nieto' from Early Bronze Age Catalonia (Spain), while the chronologically closest is 'Johnstone' from Late Iron Age to Romano-British transition (England). For sheep and goat, three references correspond to insular populations and especially for sheep they correspond to averaged populations of modern Soay and Shetland sheep, known for their peculiar small body size and for the extreme environmental conditions they live in. Only for suids, the 'mean' reference appears noticeably close to one reference, the 'Albarella' Late Neolithic domestic pigs from England (Table 1), but distant to the other references corresponding to modern wild boar from the Near East ('Payne' and 'Hongo') or from unknown precise origin ('Basel'). However, in theory, no perfect reference exists because allometry can differ between contemporaneous populations and evolve through time. As a consequence, in our case, the chimeric specimen used as reference is certainly suitable on average, but not equally suitable for each period of time, and in addition may have never existed. In our case, the mean was computed on relatively large series of measurements but it is not known how and to which extent similar analysis based on smaller datasets, more likely prone to *e.g.* composition differences, would differ. The use of the mean implies that the reference will vary according to the data set analysed, but on the other hand provides a reference better adapted to the local bioarchaeological question posed. It seems therefore difficult, if not impossible, to aim for a single, universal, reference system that is ideal for all studies. This is not necessary a problem as long as the raw measurements used for computing the LSI values are made available. It should however be noted that, compared to using the mean reference, the use of a modern known breed as a reference facilitates the visualisation of ancient specimens since it allows more direct comparison with a living organism. In addition, even if the choice of a standard is a convention, this choice is not trivial and has implications, and so far there is no formal agreement on which standard to use. The standardisation of biometric approaches proposed by von den Driesch (1976) has greatly improved the consistency between the measurements acquired by multiple operators. However, differences between measurers still exist and for example the variation we observed between raw measurements of the Tibia SD for sheep (Fig. 1), that appears particularly small for the 'Davis' reference, likely results from a methodological difference in the positioning of the calliper during the measure acquisition. As a matter of fact, and because the way the measurements were acquired was clearly stated, it appeared that the 'SD' corresponds to "*smallest diameter of the shaft taken antero-posteriorly*" (Davis, 1996) or to the medio-lateral width of the shaft in von den Driesch (1976). It is therefore of prime importance to pair

any LSI analyses not only to the publication of raw measurements, and measurements of the reference use (or the original publication containing them) (as stated earlier *e.g.* Meadow et al., 1999), but also an explanation about how the measurements were obtained. The R package *zoolog* offers tools to manipulate biometric data for log size index and incorporate a series of references, classically used in archaeozoology, directly available for computation and comparison. It is likely that this type of analytical tool will make LSI analysis more widespread and improve meta-analysis. However, it should not be forgotten than in addition to allometry and importance of the choice of the reference, a careful control of the origin of the data should be made before any large-scale biometric analysis. A number of biases can affect biometric analyses including inter-operator differences in the selection and measure of the bones, or even differences between callipers which all come in addition to archaeozoological bias (*e.g.* taphonomy, excavation, etc …).

6. Conclusion

The Log Size Index is one of the available biometric tools for studying the size of ancient animal through their archaeozoological remains. The choice of the reference dataset used as a standard for making comparable the measurements obtained on different skeletal elements can influence, at least in our case, the results and their bioarchaeological interpretations. Each reference has its own relationships between variables and allometric differences between the studied population and the reference can alter the obtained results. We presented the advantages and disadvantages of using as reference the mean of the studied assemblage with the double benefit of exploiting to the maximum the number of available measurements without being limited by the variables present in an external reference, and of minimising the possible allometric differences between the population studied and the reference. Other biometric tools, somehow less popular, such as the Log Shape Ratio (Mosimann, 1970) that better control the relationship between size and shape but require complete skeletal elements, can provide a useful, complementary method for finer scale analyses.

Author contributions

VF: data acquisition. AE, MJ, CM, SG: analyses. All authors: interpretations and writing. AE: conception and funding acquisition.

Data availability

All data used in this study are published in Jeanjean et al. (2022) and in the zoolog R package (Pozo et al., 2022).

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.quaint.2022.11.002.

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