

ON RELATIVE QUANTIFICATION OF FAUNAL REMAINS FROM ARCHAEOLOGICAL SITES

E. DURING

Osteological Research Laboratory, University of Stockholm,
S-17171 Solna

Abstract

In analysing a bone material from a site there are often fragments which just can be identified as belonging to a group of species, or higher taxa, such as sheep/goat, bovids/cervids, without possibility to identify the actual species. Such fragments may in some connections be numerous and are generally disregarded in connection with the interpretation of the material, or more inconclusively with respect to the different species involved, treated as a unit. In connection with analysing a bone material from the Middle Neolithic Age in Sweden, the author has shown that a simple statistical argument may be applied in order to allocate the main part of fragments identified to groups of species as belonging to specified species. The application and the limitations of this principle is discussed.

Introduction

Excavations of archaeological sites often provide large materials of animal bones. The abundance of different species of animals which these materials represent provide us, modern people, important information on various economic and ecological elements that had great importance to people of previous times.

To make it possible to interpret these elements an osteological analysis is carried out. The starting point of such an analysis is to identify the bones with respect to specified bone elements and species. To be able to identify a bone fragment to a specified species one must have certain criteria which are characteristic for that particular species and not for any other.

If the material provides several different species, and the skeleton of one differs from the others especially in size, thickness and structure or in both, even rather small fragments of this specific species can be identified to a large extent. Let us assume that a material contains both cattle, pigs and small bovids (sheep and goat). In this case it is in general possible to identify almost all fragments belonging to cattle, even if it is not always possible to identify every single fragment to specified bone element.

If, on the other hand, in analysing a bone material, two or more species which are skeletally similar to one another are identified, there are often fragments which can only be identified as belonging to the group of these closely related species without possibility to be identified as belonging to one of them in particular.

Let us assume, in a hypothetical sample, that some bone fragments can be identified as belonging to sheep and some to goat, while a great number of fragments can be identified only to sheep or goat because the skeleton of these two species is, from a

general point of view, very much alike. Such fragments, identified to a group of closely related animals, can sometimes be numerous and are generally disregarded in connection with the interpretation of the material. This signifies a quantitative underestimation of the represented species and is a constantly recurring problem in archaeozoology. Furthermore one of the animals involved in the group is often more frequent than the other(s) in the part of material identified to specified species.

In animal osteology there are, very generally speaking, three different principles to quantify animal bone material (e.g. Chaplin, 1971): 1) The minimum number of individuals per species (the MNI method), 2) the number of identified fragments per species and 3) the weight of fragments identified to species. In order to provide a correct estimate of the real number of different animals occurring in the material the MNI method requires that exactly the same bone element or part of bone element is found from each single individual and that it can be identified. It is easy to demonstrate the larger the material, the greater the probability that this bone element or part of bone element is missing from one or several individuals. Because of this the MNI method is bound to a greater and greater extent to underestimate the real number of individuals per species the larger the material is.

The other two methods have not got just this disadvantage because the number of identified fragments and their weight include all animals of the species in question represented in the material. Thus the loss of fragments can be regarded as being of a stochastic nature. However, there is one great disadvantage with these two methods, a disadvantage in fact referred to above. Many fragments cannot be identified exactly to species but at the best to a group of closely related animals within the same higher taxon.

In the following statistical methods will be developed which sometimes will make it possible to use even the fragments which have been identified only to a group of species.

Statistical method for large samples

Assume that two skeletally similar species exist in the material from a site, and that the number of fragments identified to one species a is x . Assume, furthermore, that the total number of fragments identified to specified species is n . The proportion of a can then be denoted by $p = x/n$, whereas the proportion of the other is $1 - p$. In addition, there is another number of fragments m which can be identified as belonging to the two species, without possibility to decide to which one, because of the skeletal similarities. In the following the fragments identified to specified species and to a group of closely related animals will be referred to as the 'specified material' and the 'grouped material'.

Two important prerequisites are that the observed sample of identified fragments is random and that the conditions of identification are the same for all species involved, with respect to taphonomical aspects such as fragmentation due to different mechanical, chemical and physical processes. Furthermore it is to be assumed that it is not easier to identify skeletal remains from one of the species in question more than from the other. It is assumed that all species involved have an equal chance of being represented in the sample i.e. of being preserved, found and identified.

It can then be argued that the proportions of the 'specified material' give a good indication of the proportions of the fragments which have been identified only to the 'grouped material'. This provides a possibility to make an approximation of the

proportions within the 'grouped material' and also in the total material based on these two identified materials.

Thus by using the proportions of the 'specified material' as a measure for the corresponding proportions of the 'grouped material' and by regarding them both as random samples of the original bone material and independent of one another, the binomial probability distribution can be used to estimate the distribution of species within the 'grouped material'. We then assume that the original material is large compared to n and m . We use the normal distribution as an approximation, assuming that n and m are also large.

Let y represent the number of fragments from the 'grouped material' that will be allocated to a . We assume that x and y are binomially and independently distributed. We will now construct an interval for y . As y is a random variable, this interval is called a prediction interval. We search y such that the hypothesis that the probabilities of the two binomial distributions are equal is not rejected. A normal approximation leads to the following formula (Cox and Hinkley, 1974, 1978):

$$\frac{\left(y - \frac{m(x+y)}{m+n}\right)^2}{\frac{mn(x+y)(m+n-x-y)}{(m+n)^3}} \leq k^2 \quad (1)$$

where the constant k (1.96 for a 95 % prediction interval) is determined by the normal distribution. The interval determined by (1) is found by solving an equation of the second degree. By neglecting a few terms (e.g. k^2m is small in comparison with $n(m+n)$), we arrive at the following simple prediction interval for y :

$$y = mp \pm 1.96 \sqrt{\frac{m(m+n)}{n} p(1-p)} \quad (2)$$

The rest of the 'grouped material', i.e. $m - y$, will be allocated to the remaining species. Accordingly, the total number of fragments s allocated to a will be $s = x + y$.

If one species is much more frequent than the other the prediction interval is shorter than if the species occur with the same frequency ($p = 0.5$). If p is near 0 or 1, however, the normal approximation cannot be used. We will return to this case later on.

This method is based on a dichotomy, a contrasting relationship. It can be arranged so that e.g. two different species or two groups of families, within the same higher taxon, are used. If there are more than two species, the same method can be used by considering one species versus the others.

The practical consequences of the statistical method for large samples will be demonstrated on animal bone material from the Middle Neolithic period in Sweden. In this case the above mentioned conditions for applying the method are judged to be fulfilled.

An Application

In the bone material from the Middle Neolithic period three skeletally similar herbivores, cattle, elk and red deer, are represented. It is the fragments, more than 2500, identified to one or more of these animals that will serve to demonstrate the statistical method in the following. One of the species, cattle, is a bovid, the other two are

Table 1. Allocation of 'grouped material' among specified species. The example taken from a Middle Neolithic site

SPECIES	SPECIFIED MATERIAL	GROUPED MATERIAL	TOTAL
CATTLE	1260	857—916	2117—2176
ELK AND RED DEER	214	121—180	335—394
TOTAL	1474	1037	2511

cervids. According to this a dichotomy can be arranged between two closely related families within the same higher taxon. The species *a*, cattle, provides more than 1200 fragments. The others, elk and red deer, provide only a little more than 200 fragments together. Thus the total number of fragments identified to specified species *n* is large, more than 1400. The 'grouped material' *m* identified to the group of these three species is also large, more than a thousand fragments.

When applying the statistical method, let us see how the 'grouped material' can be allocated to *a*, the bovid family, and to the remaining cervid family. The results are shown in Table 1.

As can be seen in Table 1 the length of the prediction interval is 59. Hence 83—88 % from the 'grouped material' is allocated to the species *a*, in this case cattle.

Statistical method for small samples and skewed distributions

In this context a special case can be considered in connection with the identification of sheep and goat. As already has been mentioned in the introduction the skeleton of these two species is, from a general point of view, very much alike. Sometimes only one of them can be identified to species in a bone material. Very often there are many fragments left, which can only be identified to either sheep or goat. These fragments constitute, in archaeozoological connection, the wellknown group sheep/goat.

In the bone material from the Middle Neolithic period there are 62 fragments identified to sheep, none to goat and 59 to the group sheep or goat.

According to this $x = 0$, $n = 62$ and $m = 59$. The question is how many possible fragments of goat are there in the 'grouped material'?

Here we cannot use the normal approximation. From the theoretical argumentation to try to find those *y* for which the hypothesis that the probabilities of the two binomial distributions are equal is not rejected, we arrive at the hypergeometric distribution. In this case it is suitable to have a one-sided prediction interval for *y* with only an upper prediction bound for *y*. Since $x = 0$ we simply need the *y* values for which

$$Q = \frac{\binom{n}{0} \cdot \binom{m}{y}}{\binom{n+m}{y}} \quad (3)$$

is at least 5 % to get the 95 % prediction interval. If we calculate *Q* for *y* = 0, 1, 2 etc, we find that *y* = 4 gives *Q* = 0.054. Hence a one-sided prediction interval with an approximative 95 % level is $y \leq 4$.

In the bone material the practical consequences are that at most 4 fragments are allocated to goat from the 'grouped material', while the remaining 55—59 fragments, i.e. 93—100 % can be allocated to the rest of the 'grouped material', sheep.

In this case the calculations are simple — for an x greater than 0 we have to sum several expressions of the type Q , or possibly make some approximation.

Concluding remarks

The position taken in this study has been to apply simple statistical methods in order to make it possible to use 'grouped materials' in connection with the quantification of different animals occurring in bone materials from archaeological sites.

The methods can make it possible to allocate a larger amount than before of specified bone elements to some of the species involved.

This may lead to that more fragments of certain bone elements e.g. vertebrae, ribs and skulls can be allocated to the different species in question. Smaller fragments of these bone elements are often difficult to identify to specified species and can therefore be quantitatively underestimated in the interpretation of the material.

Including more of these bone elements and allocating them to specified species can clearly affect the relationship between different skeletal elements e.g. the frequency distribution of meaty and less meaty identified parts from the animal bodies.

Acknowledgements

The author wishes to thank Professor Torstein Sjøvold for unfailing support and stimulating discussions and Dr. Eva Elvers for valuable statistical help.

REFERENCES

- Chaplin, R. E., 1971. *The Study of Animal Bones from Archaeological Sites*. Seminar Press, London and New York.
- Cox, D. R. and Hinkley, D. V., 1974. *Theoretical Statistics*. Chapman and Hall, London.
- Cox, D. R. and Hinkley, D. V., 1978. *Problems and Solutions in Theoretical Statistics*. Chapman and Hall, London.