

# 30 Diversity Indices and Archaeology

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## Abstract

Diversity indices were developed in population ecology as concise ways of summarising the structures of biological communities, and recently they have been applied by archaeologists to both biological and artifactual data. The underlying concept of diversity is described, paying particular attention to the important distinction between populations and samples and to the "intrinsic diversity profile". The various indices of diversity are set out, and it is concluded that the "expected species index" is by far the best choice, possessing various good characteristics as well as an unbiased estimator, thus avoiding the so-called "sample size-effect". Some recent archaeological publications in this area are critically reviewed, and it is pointed out that, in view of the above, the proposed solutions to the sample size-effect are both inaccurate and unnecessary.

## 30.1 INTRODUCTION

Diversity indices were developed in population ecology and have been used in several recent archaeological publications, most noticeably Leonard & Jones (1989), and the following is intended as a brief review of the notion of diversity and its quantification and a critical assessment of some archaeological applications. Magurran (1988) is a recent, and statistically unsophisticated, review of biological applications.

The setup in which diversity appears is that of a population of individuals, each belonging to exactly one of a number of classes. These are often individual animals and species, respectively, and here "class" and "species" will be taken to be synonymous. Pielou (1975) stated that diversity is the "variability in class identity" within a population — the equivalent of variance for qualitative observations. However, it is unclear how exactly to measure diversity as it has not been clearly de-

finied, so that "diversity" in fact corresponds more closely to "measures of dispersion", while a specific quantification of diversity is equivalent to a specific measure of dispersion, such as variance or range. Two main ways of quantifying diversity have been proposed, diversity indices, which are direct functions of the abundances of the different species, and abundance models, where a distribution is fit to the pattern of species abundances and the parameter(s) interpreted in terms of diversity. However, in abundance models the number of species plays the role normally taken in distribution-fitting by the sample size, so that they are usually only meaningful where this is large. Abundance models were largely developed for insect populations, where this is indeed the case, but in most other application areas, archaeological in particular, this is rarely so, so that diversity indices are preferable. The rest of this paper will deal solely with diversity indices.

When considering whether diversity is an appropriate concept to use in a particular application, it should be borne in mind that diversity is independent of species identity. For example, three populations, one of 3 hamsters and 5 lemmings, one of 3 lemmings and 5 hamsters and one of 3 alpacas and 5 llamas, all have the same diversity.

Some notation will now be defined. Assume that we are looking at a population, however this has been defined or delimited, and we have taken a sample of individuals from it, noting their species identity. Then define:

- $S$  = the number of species in the population (unknown)
- $p_i$  = the proportion of the number of individuals in the population that belong to the  $i$ -th species (unknown)
- $s$  = the number of species represented in the sample ( $s \leq S$ )
- $n_i$  = the number of individuals in the sample belonging to the  $i$ -th species

- $n$  = the total number of individuals in the sample

Diversity consists of two elements, species richness and evenness of species abundances (“equitability”). The fundamental definition here is that if all species in a population have the same abundance then this population is more diverse than any other with the same number of species, while if two populations each have this property then the population with more species is more diverse. However, it is not clear how to combine these two elements. It should be noted at this point that the diversity referred to here is the so-called “alpha” (within population) diversity. Beta (between population) and gamma (between and within population) diversities have also been defined — see Pielou (1975) for details.

### 30.2 POPULATIONS AND SAMPLES

Before discussing diversity itself and diversity indices in more detail it is necessary to clarify the distinction between populations and samples.

In most cases we have a sample from an underlying population and wish to estimate the diversity of the latter using the former. Most of the problems in estimating diversity come from the fact that  $S$  is unknown. When sampling,  $s$  will increase with  $n$ , but at a slower rate, as the rarer species are eventually found. Since diversity includes a species–richness element this means that our estimate of population diversity might increase solely due to increased sample size. Hence it is vital that our diversity estimator should not be sample size–dependent in this way, it should be, in a statistical sense, unbiased. This “sample size–effect” has been noted by archaeologists, and their attempts to allow for it are discussed in section 30.5.

Occasionally it may be appropriate to regard our sample as the full census of a population; Dunnell (1989) claims that if a set of artifacts has been recovered in its entirety then it should be regarded as such. However, Cowgill (1989) in the same volume rightly contradicts this, as does Rhode (1988:709). If we do regard our finds as the population then we will just get a “population size–effect”, which of course cannot be avoided by unbiased estimation. Hence, the artifacts that were found might be viewed as a sample of the population of all relevant artifacts made, or, alternatively, and perhaps preferably, the population might be regarded, at another step up, as including all artifacts that could possibly have been made.

The following is an example to illustrate an important difference between how we should treat sample and population figures. Let  $N_i$  and  $N$  be the population equivalents of  $n_i$  and  $n$  respectively, and suppose we have population 1, with

$$N = 4, S = 2, N_1 = 2, N_2 = 2$$

and population 2, with

$$N = 8, S = 2, N_1 = 4, N_2 = 4$$

Then clearly the diversities of the two populations should be the same, that is only relative abundances should be taken into account. However, suppose we had the above as two samples from different populations (i.e. substitute lower-case for capital letters in the above). If we do not know  $S$ , but suspect that it is greater than 2, then it seems reasonable that we would want our estimate of the diversity of population 2 to be lower than that of population 1, since we have collected twice as many individuals but still only found the same number of species, giving more evidence of the dominance of these two species, and hence the unevenness or species–paucity of the population, than we have in the other case. This illustrates that we do not necessarily want diversity indices to behave in the same way with respect to sample as to population abundances, and that, as will be seen in section 30.4, estimates based on sample proportional abundances are likely to be unsatisfactory. As an aside, if in the second case above it was known that  $S = 2$  then we *would* want the diversity estimates to be equal, while if it were known and greater than two we would want the estimates to differ as before.

### 30.3 INTRINSIC DIVERSITY

The intrinsic diversity ordering has been suggested as a more rigorous definition of the concept of diversity, to replace the rather vague descriptions given above. It was originally proposed by Solomon (1975) and has been described by Solomon (1979), Kempton (1979) and Patil & Taillie (1979, 1982). Let two communities,  $C_p$  and  $C_q$  say, have relative abundances given by  $p_i$ 's and  $q_i$ 's respectively. These are ordered so that  $p_1 \geq p_2 \geq \dots$  and similarly for the  $q_i$ 's. Then  $C_q$  can be said to be “intrinsically more diverse” than  $C_p$  if the  $q_i$ 's can be derived from the  $p_i$ 's by a finite sequence of the following steps:

- add a new species, assigning to it some of the abundance of one already included;

- transfer abundance from one species to another less abundant one so that their abundances are closer.

The first operation represents an increase in species–richness, the second an increase in evenness. Under this definition, two communities may be such that one is intrinsically more diverse than the other, or such that they are not comparable. For example, a community cannot be intrinsically more diverse than another containing more species, or one which has its most abundant species less abundant than the community's own most abundant species, so that if  $C_q$  has more species than  $C_p$  but  $q_1 > p_1$  then the two communities cannot be ordered in this way. In fact this definition of  $C_q$  being intrinsically more diverse than  $C_p$  is equivalent to

$$\sum_{i>j} p_i \leq \sum_{i>j} q_i \quad \text{for all } j = 1, 2, \dots$$

Clearly the inequalities must be strict in at least one case. The relationship between two populations can easily be assessed using the second property by plotting the cumulative proportion of individuals (Y–axis) versus the cumulative number of species (X–axis), in increasing order of abundance of species, so that community  $C_q$  is intrinsically more diverse than community  $C_p$  if and only if it plots at least as high on this graph at each point. Note that we could also do this for samples, but sample profiles clearly cannot be regarded as unbiased estimates of the population ones, so that it is obviously not valid to compare them for substantially different sample sizes.

The intrinsic diversity ordering appears to offer a sound and intuitively reasonable basis for the concept of diversity, but we still need diversity indices to allow unbiased estimation of population diversities from samples and to impose a full ordering. Clearly it is desirable that a diversity index respects the intrinsic diversity ordering, and in fact all of the ones in common use (section 30.4) do.

### 30.4 DIVERSITY INDICES

Numerous indices have been defined and the following is a brief description of the most important. Note that it is very important to distinguish between the index itself and the way it is estimated from a sample, and this has been done as explicitly as possible.

The simplest measure of diversity is of course just  $S$ , the number of species in the population. However, clearly it has no unbiased estimator and takes no account of evenness.

The oldest, and unfortunately still the most commonly used, genuine diversity index is Shannon's index, given by

$$D_{SH} = \sum_{i=1}^s p_i \log p_i.$$

The usual estimator used is to substitute  $n_i/n$  for  $p_i$  in the original formula, but this is biased, and indeed there is no unbiased estimator. In addition the index value depends very heavily on the largest few  $p_i$ 's, that is if these are the same for two populations then they will have a very similar value of the index even if one has many more (low abundance) species than the other. In most cases this is an unwanted characteristic.

The next most frequently used is that which is usually referred to as Simpson's (or occasionally Gini's) index, and is defined as

$$D_{SI} = 1 - \sum_{i=1}^s p_i^2.$$

In fact, Simpson (1949) suggested just the summation part as a measure of dominance, and alternatives to the expression above are the reciprocal or minus the log of the summation. This has an unbiased estimator,

$$\hat{D}_{SI} = 1 - \sum_{i=1}^s \frac{n_i(n_i - 1)}{n(n - 1)}.$$

However, this index is also heavily dependent on the most abundant species.

Hill (1973) proposed a family of indices,

$$N_a = \left( \sum_{i=1}^s p_i^a \right)^{\frac{1}{1-a}}.$$

As  $a$  increases so does the effect of the more abundant species. However,  $N_1$  is (the exponent of) Shannon's index, which is very dependent on the most common species, while  $N_0$  is just  $S$ , which obviously isn't, so clearly the range  $0 < a < 1$  is most useful. However, these indices do not possess unbiased estimators, and investigations by Kempton (1979) suggested that the bias would be most severe for  $a < 2$ . Given all of the above, it seems that these indices are unlikely to be particularly useful.

Patil & Taillie (1979) proposed

$$\Delta_\beta = \frac{1}{\beta} \left( 1 - \sum_{i=1}^s p_i^{\beta+1} \right).$$

The standard indices can be expressed in terms of this family, with  $\Delta_{-1} = S - 1$ ,  $\Delta_0 = D_{SH}$ , and  $\Delta_1 = D_{ST}$ . This has an unbiased estimator for integer  $\beta = 1, 2, \dots, n$ , given by

$$\hat{\Delta}_\beta = \frac{1}{\beta} \left( 1 - \frac{\sum_{i=1}^s n_i(n_i - 1) \dots (n_i - \beta)}{n(n-1) \dots (n-\beta)} \right).$$

However, this suffers from the same drawbacks as Hill's family, in that when unbiased estimators exist, as above, the value of the index is dominated by the first few abundances.

Kempton & Taylor (1976) suggested the "Q statistic", based on the slope of the cumulative species vs log abundance curve in the inter-quartile range, which they claim should be robust to changes in the most and least abundant species. However, as in the case of abundance models, this was developed for use with insect populations and needs large numbers of species to be useful. Hence it is probably inappropriate in most archaeological situations and so is not given here.

Smith & Grassle (1977) proposed the "expected species" index of order  $m$ , defined as the expected number of species in a random sample of  $n$  individuals from a population.

$$s(m) = \sum_{i=1}^s [1 - (1 - p_i)^m].$$

Clearly  $s(2) = 1 + D_{ST}$  so that for small  $m$  the index value is dominated by the common species; for larger  $m$  the medium-abundance and rare species have more of an effect. This has an unbiased estimator for integer  $m = 1 \dots n$ , given by

$$\widehat{s(m)} = \sum_{i=1}^s \left[ 1 - \frac{C(n - n_i, m)}{C(n, m)} \right]$$

with  $C(a, b) = a! / (a - b)! b!$ , where  $k! = k(k - 1)(k - 2) \dots 1$ .

Probably the best way of using this family of indices, for comparing estimates of diversities of different populations, is to calculate  $s(m)$  for all integer  $m$  between 2 and the smallest of all the

sample sizes and plot it versus  $m$  for each sample. If one set of  $s(m)$  values ("profile") is completely above another then our estimates clearly suggest that this population is more diverse than the other, while if there are crossovers then we can use the knowledge that for low values of  $m$  the index is more sensitive to the more common species while for higher  $m$  it is more sensitive to the rarer species to help us interpret this. Note that if one sample is very small we may wish to use  $m$  up to the second or third smallest sample size, say, and accept that the smaller samples are not comparable in all cases. This suggestion may seem rather similar to that used for intrinsic diversity profiles in section 30.3, but it differs in that each profile is not a single measure of diversity but a set of similar measures with slightly different characteristics, while the sample quantities are now unbiased estimates of the population ones. Hence it is considerably more useful.

This index is in fact equivalent to the technique of "rarefaction". This was introduced by Sanders (1968), and corrected by Hurlbert (1971), in order to find how many species he would expect to have found if a sample of size  $n$  had in fact been of size  $m$  ("rarefying" the sample), so that he could compare the species-richness of different-sized samples. This method has been widely used in both ecology and palaeoecology although, in keeping with its origin, it usually seems to be regarded as a species-richness measure rather than a diversity index *per se*. In addition Tipper (1979) is critical of the use of rarefaction in palaeoecology. However, he mainly discusses using the method for assessing the (dis)similarity of biological communities, rather than viewing it as a diversity index, and this is not really a valid application anyway, so that his objections can be largely discounted.

Thus, the expected species index is an intuitive measure of diversity, is not dominated by the most abundant species (if  $m$  is large) and has an unbiased estimator (in fact Smith, Grassle & Kravitz, 1979, show that only polynomial functions of  $p_i$ , of degree  $m < n$ , can have unbiased estimators). Hence it clearly seems to be the best choice of all the indices proposed so far.

Finally, if it is appropriate to regard one's sample as a fully censused population (and, as noted above, in archaeology it is very difficult to think of a case where this might be so) then we do not use the above formulae for unbiased estimators, we simply use the fact that, by definition,  $n_i/n$  is  $p_i$  in the original definition of each index. However, the expected species index still seems to be the most appropriate even in this situation.

### 30.5 ARCHAEOLOGICAL APPLICATIONS

This section aims to provide a short summary and critique of recent archaeological applications of diversity indices.

Applications in vertebrate faunal archaeology include Cruz-Urbe (1988) and Avery (1982, 1987), both of whom used simple indices, mainly Shannon's. Faunal data are extremely vulnerable to taphonomically-caused bias, so that, even when using diversity indices in an exploratory way, it is rather dangerous to use them for inter-sites comparisons if there is evidence of differences in taphonomy.

Numerous works deal with the diversity of artifact assemblages. These have usually just viewed diversity as the number of artifact classes in an assemblage ("species-richness",  $s$ ) but have rightly noted that more would be expected in larger assemblages (samples) — the "sample-size effect". Two approaches to this problem have been suggested in the archaeological literature, and Rhode (1988) has commented critically upon them, although unfortunately his criticisms seem to have been ignored so far.

What Rhode (1988) called the "sampling approach" was proposed by Kintigh (1984), who suggested repeated sampling, by simulation, from a parent population  $p$  to obtain a mean and variance of  $s$  (the class richness) for any given sample size  $n$ . Comparing actual to predicted class-richness for the appropriate sample sizes could then be used to conclude whether particular sites were unusually rich or poor in numbers of types of artifact. Rhode (1988) correctly noted that such a procedure is heavily dependent on the chosen distribution  $p$  and that Kintigh's (1984) proposal, to use the pooled collection from all assemblages being studied to define this, is inappropriate. However, his argument, that if we pool then any differences not due to sample size invalidate the pooling, is not the whole story. An even more serious problem is that the pooled data set may not look anything like any of the individual samples. Firstly, it will always contain at least as many classes as any of the individual samples, never fewer, and secondly it is easy to think of situations where it has either a much more or a much less even distribution than any of the individual samples. For example, sample 1 contains 5 llamas, 3 alpacas and 1 vicuna, while sample 2 contains 5 vicunas, 3 alpacas and 1 llama, so that the pooled sample contains 6 vicunas, 6 alpacas and 6 llamas. Thus, two uneven individual samples lead to a perfectly even pooled sample. It is clear, then, that any kind of compari-

son between individual and pooled samples could be grossly misleading. Rhode (1988) concludes that this method is only useful if the parent population is well known already. This seems unlikely in archaeology. He also notes that simulation is unnecessary as the results can be computed exactly from the formulae in Smith & Grassle (1977); in the notation used above, the mean is given by  $s(m)$  when  $m$  is the sample size and  $n$  and the  $n_i$ 's are the total and class abundances from the  $p$ . However, he does not seem to consider the possibility of using  $s(m)$  itself as a diversity index, even though he notes that this is how Smith & Grassle (1977) treat it. The problem here is, of course, exactly the same as that which prompted Sanders (1968) to define "rarefaction". However, Sanders' solution was, as mentioned previously, to look at how many species a sample would have contained had it been smaller, and did not involve pooling.

The second method is the "regression approach" put forward by Jones, Grayson & Beck (1983), which entails regressing  $s$  on  $n$  (or more often using the logarithm of one or both of these) for the assemblages being studied and using the relative positions of points above and below the regression line to assess more or less class-rich sites. Rhode (1988) notes that this is good at locating a sample-size effect but that its utility for a detailed study of the differences between sites is minimal. He does not note that even if an effect does not appear in the regression (a slope of zero) this could mean that the smaller samples are in fact from more diverse populations.

Shott (1989) discusses the sample-size effect for Shannon's index, studying several ethnographic and archaeological assemblages, plotting the log of Shannon's index against  $\log n$  or  $n$  and calculating regression and correlation coefficients (as in Jones *et al.* 1983). His contention is that the existence of a clear relationship for a group of assemblages indicates that they all come from «the same population of tool-using and discard episodes» and that such samples can be assumed to be the same in terms of «substantive behaviour» by the people producing them. Absence of a relationship is said to imply «substantial behavioural diversity». This is all quite clearly untrue, and indeed Todd (1989), in a comment on the paper, quite rightly says that diversity indices have exploratory but not explanatory utility.

Leonard & Jones (1989) is a collection of papers dealing with diversity in archaeology, most of which follow the above approaches. Shannon's and Simpson's indices seem to be the only diversity measures (apart from simple class-richness)

considered. Bobrowsky & Ball (1989) mention numerous other indices, including  $s(m)$ , though none of the contributors use them, and refer to Grassle *et al.* (1979), but do not appear to have read most of the papers in this volume. An excellent example of the drawbacks of the "sampling approach" is that in Kintigh (1989, figs 4.11, 4.12, pp 34–35) the majority of the points are noticeably below the "expected" line, and much further from it than the small number of points above the line, while some of Rothschild's (1989) plots show all of her three sites to be of above-average diversity(!).

All of the above leads to the obvious point that the main reason for the existence of the sample-size effect is the use of quantities without unbiased estimators, i.e. the species count and the Shannon index. Both proposed solutions have little theoretical or practical appeal, and in fact there is no need for them. The use of the expected species index should allow studies to be both more informative and easier to perform without the need for either simulation or regression.

### 30.6 DISCUSSION

The search for a diversity measure with an unbiased estimator might be thought to be a case of allowing the tail to wag the dog, of subordinating biological (or archaeological) meaning to statistical convenience. However, the expected species index seems to fulfil both criteria so that there is no problem.

For most of the indices above there exists an expression for the variance of the estimate, in other words we can estimate how accurate our estimate of diversity is. However, in many cases these involve  $S$  and hence are useless. There is another, less obvious, problem, though, which affects variances even when  $S$  does not need to be known, for example in the case of the expected species index. This is that, as stated by Kempton (1979), in most situations these theoretical variances are likely to be underestimates of the true amount of variation possible under our sampling. This is because they assume strictly random sampling, which is almost impossible in practice, especially in archaeological cases. Hence the usefulness of these variances is open to question; they may be useful as lower bounds, but this may run the risk of producing spurious "accuracy". It is probably better in most situations to ignore the variances and just look at the patterns in the diversity values, and therefore they have not been presented here. As an aside, the British general election of 1992 is a classic example of

sample values (opinion polls) purporting to be far more accurate (via the "margins of error") than they in fact turned out to be.

Finally, it is reasonable to ask if the use of diversity indices in ecology has led to greater ecological understanding. I am in complete agreement with Pielou (1975:34), who stated that arguing back from statistical hypotheses to ecological hypotheses is the hardest part of any investigation, and that nobody has succeeded at it yet, and that the usefulness of the methods lies in economy of expression, aiding the search for patterns in natural systems. In other words they are tools for exploratory data analysis, as are most of the other statistical methods used in archaeology. Diversity indices (and the parameters of abundance models) are simply summary statistics or transforms of the sampled data which express aspects of the structure of the data in a particular way, focussing on the number of species included and the evenness of their relative abundances. Patterns in the values of these measures may not be immediately explicable, and care must be taken that measures are chosen so that patterns are not artifacts of sample size, but such patterns are generally more easily found in summaries than in the raw data, and understanding of the nature of the different measures may lead to greater understanding of the structure of the data (abundance distributions) themselves.

I have a PASCAL program which calculates most of the indices mentioned above as well as the intrinsic diversity profile, and will be happy to supply it to anyone who is interested.

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