

## An initial assessment of zooarchaeological assemblage sizes from South Africa

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### Abstract

Large faunal assemblages remain a concern in zooarchaeology. Without sufficiently large assemblages, interpretations about the past are less secure. The number of potential taxa in an assemblage is related to various factors such as the number of species found in an ecological zone, economic activities (hunting vs. farming) and taphonomy. In South Africa, no attempt has been made to determine what constitutes a sufficiently representative assemblage size, yet animal remains are frequently utilised to infer aspects of human behaviour during the past. We use faunal assemblages analysed using a standardised method, and we plot the number of taxa against the number of identified specimens (NISP). This way, we are able to determine the asymptote point of a faunal assemblage. Our initial study suggest that for subsamples, specifically those containing only large mammal remains, the asymptote is reached nearing 1000 NISP, whereas for those assemblages containing a full range of vertebrates and invertebrates, the asymptote is reached when the NISP nears 2000. The assemblages used are from different ecological zones and vastly different time periods, and each has its own taphonomic history. As a result, these asymptote points should not be considered as adequate samples for every faunal assemblage in South Africa. Instead, we advocate that zooarchaeologists analyse the largest possible assemblage to ensure more reliable interpretations are made from faunal remains. In many instances, only smaller assemblages are available; this is often beyond the control of the zooarchaeologist. Nevertheless, our data suggest that often, assemblages are adequate in size for archaeological sites as a whole; however, when comparisons are attempted between layers, occupational phases or spaces at a site, assemblage sizes are often severely reduced, requiring caution when making inferences about the past.

### Keywords

Zooarchaeology, assemblage size, number of identified specimens, species accumulation curve.

## 1. INTRODUCTION

Large sample sizes have been a concern in many fields (e.g. Heck *et al.*, 1975; Magurran, 1988) including archaeology (e.g. Cochrane, 2003; Cowgill, 1964; Mueller, 1975; Neff, 1993) and zooarchaeology (e.g. Cannon, 2001; Driver, 1982; Faith & Gordon, 2007; Grayson, 1984; Lyman, 2008, Schmölcke, 2013). Typically, the size of an assemblage can be measured in two ways; either by the volume of material excavated, or as the Number of Identified Specimens (NISP) and its derivatives (Lyman, 2008). One way to determine if faunal assemblages are adequate by NISP, is to sample to redundancy. The redundancy point can be determined by plotting the size of the assemblage and the number of taxa against one another and to continue sampling until the asymptote [a line on a graph of a function representing a value toward which the function may approach, but

does not reach (with certain exceptions)] is reached (e.g. Leonard, 1987; Lyman, 2008; Lyman & Ames, 2004; Schmölcke, 2013; Tourigny, 2017). This has not done explicitly in zooarchaeological research in South Africa (Badenhorst, 2011). Moreover, it is often difficult to access an adequate size of a single assemblage during analyses without having the benefit of larger comparative studies in a region.

Zooarchaeology is the study of faunal remains from archaeological sites. Zooarchaeological information is used to gain insights into a variety of aspects such as environmental conditions, human diets, the social role of animals, prey selection and site formation (Thomas, 1996). Unless an entire site is excavated and all the bones and teeth retrieved, the assemblage that zooarchaeologists study is a sample of all the available skeletal remains at the site. Yet all the skeletal remains at a site is a sample of

some other, original population(s), such as those animals utilised by people in the past. Zooarchaeologists, then, always study samples (Grayson, 1984), or what Klein & Cruz-Urbe (1984) calls, the ‘sample assemblage’. Reitz & Wing (1999) refer to the excavated fauna from a site as an assemblage, and a sample, a portion of the assemblage. We follow this latter convention in this paper. Zooarchaeologists have often noted that as the size of an assemblage increase, so does the number of identified taxa (e.g. Lyman, 2008). To make inferences about the past, large faunal assemblages are usually required to reflect the animal populations being studied (Reitz & Wing, 1999) and to be representative of the original diversity they derive from (Lyman, 2008).

South Africa is one of the most intensely-studied regions in Africa in terms of zooarchaeology (e.g. overviews in Mitchell, 2002; Plug, 2001; Plug & Badenhorst, 2001; Wadley, 2015). However, there is still little understanding of what constitutes a large assemblage size; a situation probably not unique to the region alone (cf. Grayson, 1984). Nevertheless, zooarchaeologists conducting analyses in South Africa often consider an assemblage containing a NISP of less than 1000 as being on the smaller end (e.g. Badenhorst & Plug, 2001; Badenhorst *et al.*, 2011a) compared to the larger end (e.g. Plug & Badenhorst, 2006; Badenhorst & Boshoff, 2015) of the scale. Gaining an understanding about the size of assemblages can assist in determining if interpretations are reliable (e.g. Driver, 1982). Moreover, with the increase in contract archaeology, where time and financial constraints may often only permit analyses of subsamples of fauna, understanding the size of an assemblage is of great value. In this paper, we attempt to provide an initial assessment of faunal assemblage sizes from South Africa; an aspect that will require more study in future.

Zooarchaeologists use several methods to analyse faunal remains from archaeological sites. The method used have an effect on the size of an assemblage. In South Africa, Brain (1974) suggested a method, later adapted by Voigt (1983) which have been widely used during the last few decades (e.g. summaries in Badenhorst, 2011, 2018; Fraser & Badenhorst, 2014; Plug, 2001; Plug & Voigt, 1985). Essentially, this method regards some elements such as fragmented skull remains, rib pieces, vertebrae and indeterminate enamel fragments as unidentifiable specimens, along with bone flakes and other miscellaneous bones. The remainder of the bones and teeth, where possible, are identified to species, genus or family level (Brain, 1974; Voigt, 1983).

Many zooarchaeologists have long considered aspects biasing faunal analyses, such as assumptions made during the identification process (e.g. Driver, 1982, 1991). As a result, some (e.g. Driver, 1991, 2005) have advocated

the use of a standardised method of faunal analyses in an effort to increase reliability when comparing faunal assemblages analysed by different zooarchaeologists. This method is particularly explicit as to what is considered to be an identifiable specimen. According to this method, only specimens that can be assigned to skeletal element (e.g. humeri, tibiae, etc.) are considered identifiable. The remaining specimens are considered unidentifiable remains. This approach was first introduced about a decade ago in South Africa (Brunton, 2011; Le Roux, 2011). A number of faunal studies in the region have subsequently used this method (Arthur *et al.*, 2018; Badenhorst *et al.*, 2014; Badenhorst & Boshoff, 2015; Badenhorst *et al.*, 2016a, b, 2019; Brunton *et al.*, 2013; Kohtamäki & Badenhorst, 2017; Le Roux *et al.*, 2013; Le Roux & Badenhorst, 2016; Magoma *et al.*, 2018; Reynard *et al.*, 2016; Reynard & Henshilwood, 2019; Van Zyl *et al.*, 2013, 2016). While numerous other assemblages have been studied and reported (e.g. Plug & Badenhorst, 2001; Mitchell, 2002; Wadley, 2015, for overviews), we only used those where the data is available to us electronically, and that have been identified using the same methodology (Driver, 2005). While not dismissing the value of other assemblages, a definite aim of using the same method is to minimise biases introduced when assemblages are analysed using different methods. Many zooarchaeologists present their identifications as lists (e.g. Clark, 2009), but the data are tabulated by taxa and element, and not sequential as recorded during analyses. This makes the data less suitable for our current purpose. Moreover, most data of other sites, especially those analysed several decades ago, are only available on hardcopies. Our current study will enable us to identify appropriately large assemblages for future studies.

The Number of Identified Specimens (NISP) and the Minimum Number Individuals (MNI) are common techniques used by zooarchaeologists to determine the relative abundance of taxa within an assemblage and to compare animal use through time and space. While there is no perfect quantification method, NISP is the most basic and most utilised method (Lyman, 2008; Marshall & Pilgram, 1993; Reitz & Wing, 1999). MNI is highly problematic (O’Connor, 2000; Plug & Plug, 1990), but its use may be justified in some instances. For this study, we only utilise NISPs.

When large faunal assemblages are analysed, there is a tendency for a species accumulation curve (or collector’s curve) to develop (Gotelli & Colwell, 2001). This means that there is a tendency as more animal remains are identified, that the number of taxa also increases. When plotted against one another, a curve forms, which initially rises sharply as the NISP increases. However, at some point, called the asymptote, the curve flattens out, meaning that new taxa are added at a decreasing frequency (Colwell & Coddington, 1994; Reitz & Wing,

1999). At this stage of the analyses, many more bones and teeth must be identified to add new taxa to the species-list of the faunal assemblage. The rate of increasing the number of species in an assemblage therefore slows down as the size of the assemblage increases. When this happens, the saturation point of the curve is reached (Moreno & Halffter, 2000). This is an indication of adequate sampling and analyses, resulting in few species left undetected in the assemblage as a whole, and in some instances, there are no new species to be detected. The assemblage size closest to the asymptote would be considered an adequate representation of the population from which the assemblage was drawn (Reitz & Wing, 1999; Schmölcke, 2013).

## 2. MATERIALS, METHODS AND RESULTS

As indicated, a number of faunal assemblages from South Africa have been analysed using the method of Driver (2005). The advantage of these studies is that their data are available in electronic format (Excel), making it easy to calculate a species accumulation curve for the entire assemblage. This was done by only using the columns containing the taxa and respective elements (so the NISP), and incrementally calculating the Number of Taxa (nTaxa) and NISP on the electronic databases. Graphs were then created from the data. One of the disadvantages of the analysed assemblages is that most of them are relatively small in size, limiting the value of the comparisons. As a result, we selected four faunal assemblages from South Africa (Table 1, Fig. 1) which are relatively large in size, and with the data available electronically. They were all quantified using NISP, and they come from different time periods (overview in Mitchell 2002), including the Middle Stone Age (dating between 300 000 and 30 000 years ago), Later Stone Age (dating to the last 30 000 years) and Iron Age (dating to the last 1600 years).

Zooarchaeologists can start analysing an assemblage at different points, such as the top layers going down per

square, or analysing the lowermost material first working upwards in the deposits. Different areas of excavation are often analysed separately, although there are no definite procedures as such. Nevertheless, it is well-known that the order in which samples are added can influence the results (Kerrich & Clarke, 1967; Lyman, 2008). In our assemblages, we just used the data as it was recorded on the Excel spreadsheets. In most cases, the analyses started with the topmost layers, analysing each bag of specimens from a layer and square at a time. As a result, we used the assemblages as they were sequentially recorded on the spreadsheets.

The number of taxa in an assemblage is a reflection, *inter alia*, of sample size (Grayson, 1984; Lyman,

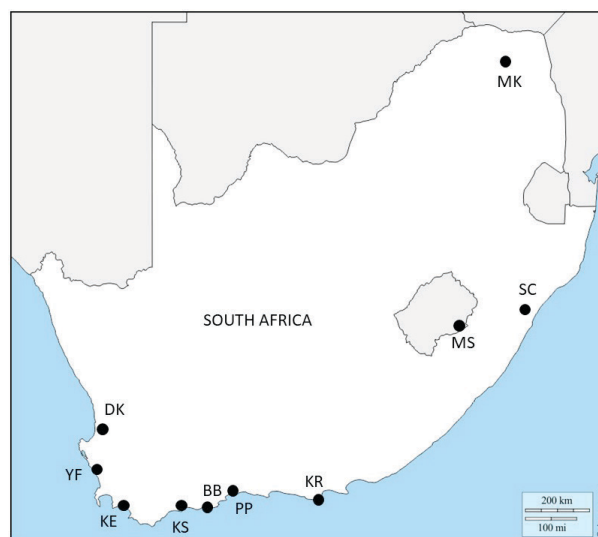


Fig. 1: Location of sites mentioned in the text (map adapted from: [https://d-maps.com/carte.php?num\\_car=768&lang=en](https://d-maps.com/carte.php?num_car=768&lang=en)). DK = Diepkloof, YF = Ysterfontein, KE = Die Kelders, KS = Klipdrift Shelter, BB = Blombos Cave, PP = Pinnacle Point, KR = Klasies River Mouth, MK = Mutokolwe, SS = Sibudu Cave (all located in South Africa), MS = Moshebi's Shelter (located in Lesotho).

Table 1: Data sets used in this study. nTaxa are the minimum number of species present in an assemblage, and were calculated using identifications made the species, genera, family and order levels as reported).

Sites	Period	NISP	nTaxa	Type	Reference
Blombos Cave	Middle Stone Age	5489	28	Mostly large mammals, with a few incidental non-mammals	Badenhorst <i>et al.</i> , 2016a
Moshebi's Shelter	Late Stone Age	655	26	Complete range of animals	Badenhorst <i>et al.</i> , 2019
Sibudu Cave	Middle Iron Age	3065	49	Complete range of animals	Le Roux, 2014; Le Roux & Badenhorst, 2016
Mutokolwe B	Late Iron Age	1338	9	Large mammals (likely handpicked during excavations)	Magoma, 2014; Magoma <i>et al.</i> , 2018

2008). Following previous studies (Faith, 2013; Reynard & Henshilwood, 2019), we use two calculations to control for this aspect (Table 2). First, we use residuals; assemblages that show a positive residual have a greater number of taxa predicted by sample size, and a negative residual have fewer taxa than expected (Faith, 2013; Grayson, 1984). Second, we used a Fisher's alpha ( $\alpha$ ) metric that measures the diversity of taxa that is relatively insensitive to the effects of sample size (Magurran, 1988).

Table 2: Residuals and Fisher's alpha calculations.

Sites	NISP	nTaxa	Residuals	Fisher's Alpha
Blombos Cave	5489	28	-7.074	3.86
Moshebi's Shelter	655	26	3.353	5.41
Sibudu Cave	3065	49	19.843	8.28
Mutokolwe B	1338	9	-15.492	1.30

The faunal assemblages vary in terms of parameters. For Blombos Cave, the assemblage contain mostly large mammals (animals exceeding the rock hyrax *Procavia capensis* in size) (Badenhorst *et al.*, 2016a). Moshebi's

Shelter and Sibudu Cave on the other hand, contain the full range of vertebrates and invertebrates (Badenhorst *et al.*, 2019; Le Roux & Badenhorst, 2016). At Mutokolwe B, 99% of the assemblage was identified. Such a high rate of identified specimens in a faunal assemblage from South Africa is exceptionally rare (Badenhorst & Plug, 2011), and it is very likely that during excavations, large bones were selected for analyses (Magoma *et al.*, 2018, also Badenhorst *et al.*, 2011b). Each site has its own taphonomic history, geological and environmental setting and range of available animal taxa.

First, as expected, the data show that there is a (moderate) correlation between the total size of the assemblages and the number of taxa identified (Fig. 2). Second, the species accumulation curves of the assemblage show that as NISPs increase, the number of taxa also increases (Fig. 3). For the two subsamples, Blombos Cave and Mutokolwe, the asymptote is reached when the NISP nears 1000 specimens. For the larger assemblage from Sibudu Cave, which contains both vertebrates and invertebrates, a NISP closer to 2000 specimens reach the asymptote. The assemblage from Moshebi's Shelter is smaller than that of Sibudu Cave, but also contains both vertebrates and invertebrates. For Moshebi's Shelter, the asymptote is not reached yet, but it is conceivable that it would be reached with a NISP closer to 2000 specimens. However, in all cases, continual adding of taxa as more

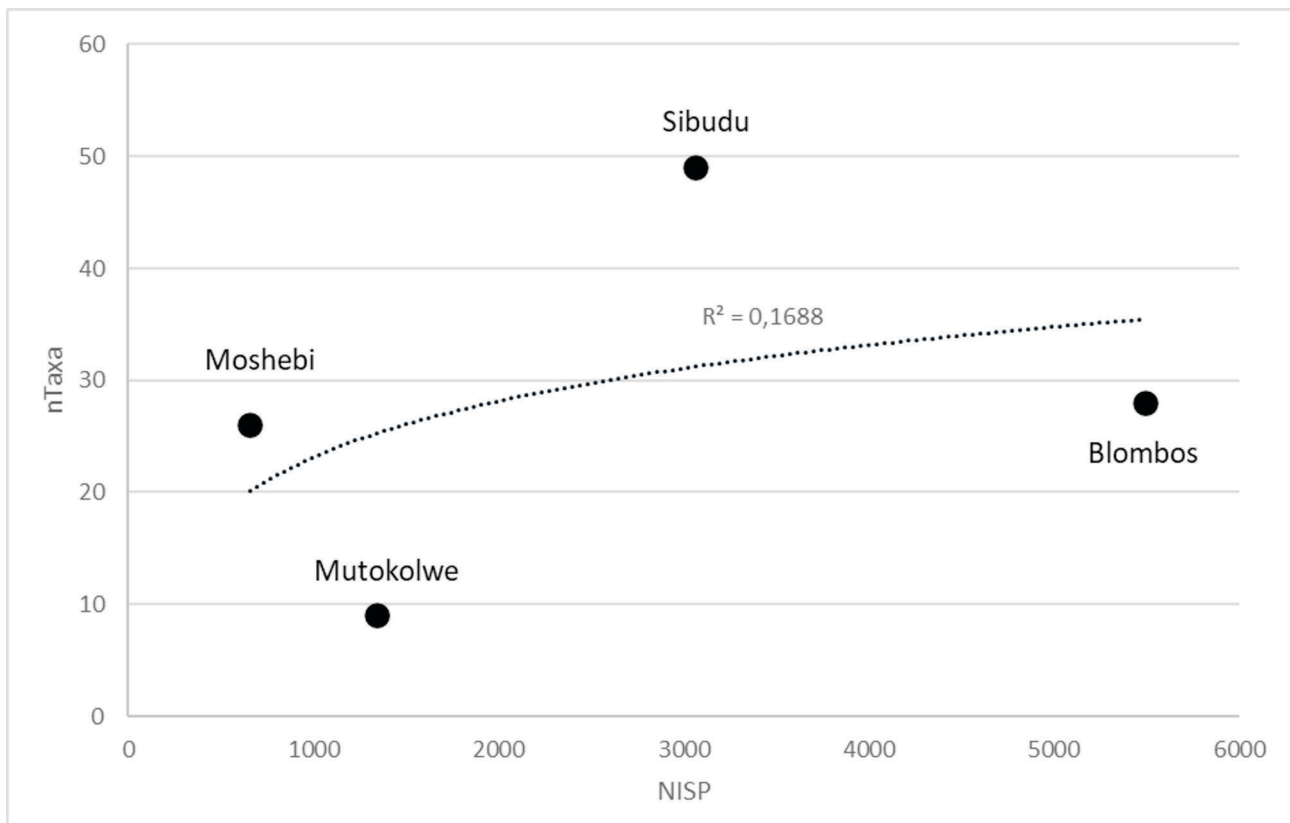


Fig. 2: Assemblage size and the number of taxa are correlated for the faunal assemblages used in the study.

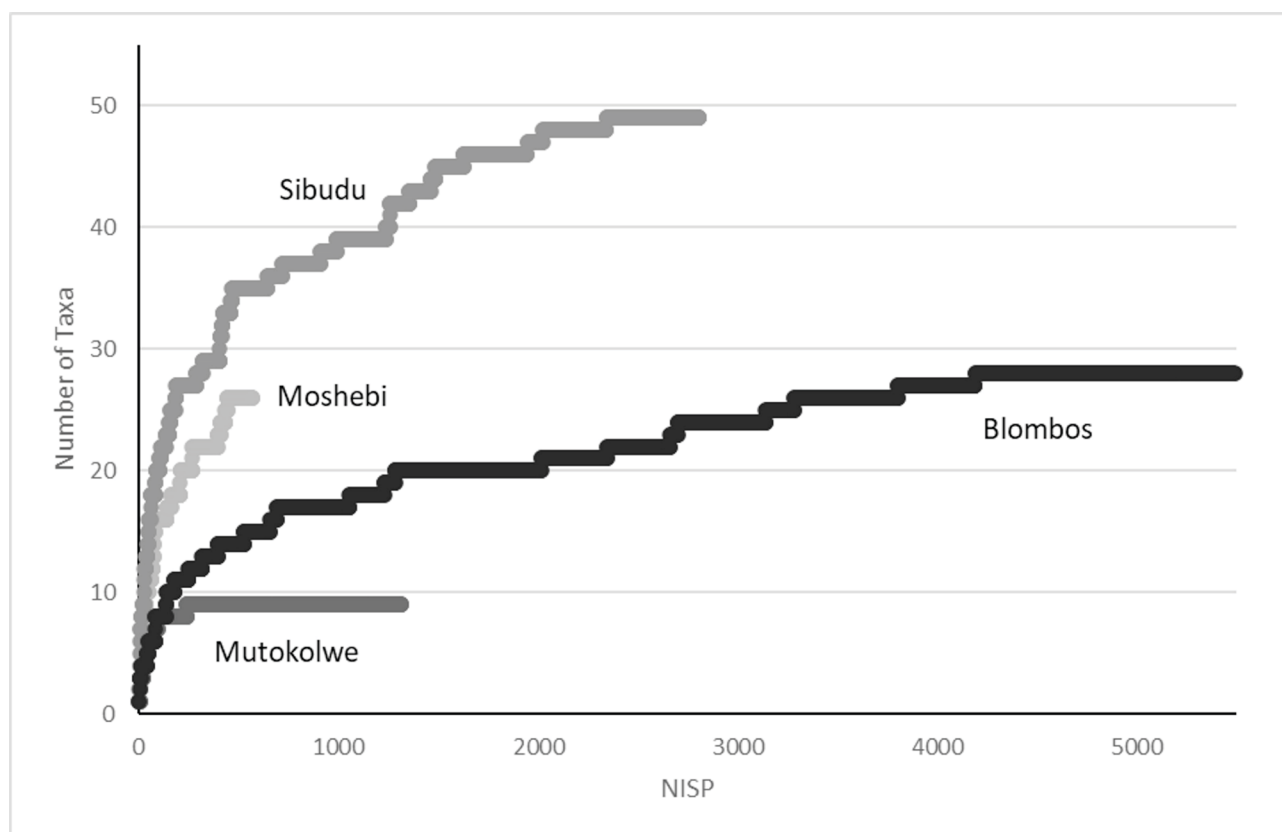


Fig. 3: Species Accumulation Curves for the four assemblages used in this study.

specimens are identified lets the curve grow, suggesting that larger assemblages are optimal and desirable. Third, the residuals and Fisher's alpha confirms that for Mutokolwe B, the diversity of taxa is very low, and very high for Sibudu Cave.

We also plot the NISPs and number of taxa (Fig. 4) for two assemblages, Sibudu Cave and Moshebi's Shelter using only the large mammal remains (taxa similar and larger in size than the rock hyrax). Both assemblages are more similar size. The results indicate that both assemblages seemed to have reached the asymptote before a NISP of 200. However, as the data from Sibudu Cave indicate, more taxa are added when the NISP approaches 1000. This confirms our results that for samples containing only large mammals, a NISP nearing 1000 are optimal.

### 3. DISCUSSION AND CONCLUSION

It is important to study large assemblages in zooarchaeology since it ensures that the taxa represent the entire range of obtained animals (or at least close to) as accurately as possible. Large assemblages decrease biases and they increase reliability of the interpretations (Lyman, 1996). Our study suggest that for subsamples

containing only large mammals, the asymptote is reached close to 1000 NISP, and for those assemblages containing a range of vertebrates and invertebrates, it is reached when the NISP is closer to 2000 specimens. However, these asymptote points should not be regarded as the minimum and adequate size of an assemblage in all cases; the four assemblages are from vastly different regions and time periods. Nevertheless, the results provide a baseline for further studies on the size of assemblages.

Zooarchaeologists often cannot determine the size of an assemblage before an analysis commences. The eventual size is determined by factors such as preservation, length of occupation, range of available animals in the area, site usage, the size and location of excavations, mesh size, the research agenda of the excavator, and that subsamples like fish and molluscs are often analysed by specialists (e.g. Lyman, 1994, 2008). In addition, the number of taxa in an assemblage is influenced by similar factors, as well as others such as the biodiversity in ecological zones, economic activities at sites (hunting vs. farming), social roles of animals, bone transportation decisions, preservation, excavation and retrieval methods, and taphonomy (e.g. Lyman, 1994). Moreover, deposits at older sites are often subjected to time-averaging with layers representing several thousands of years with

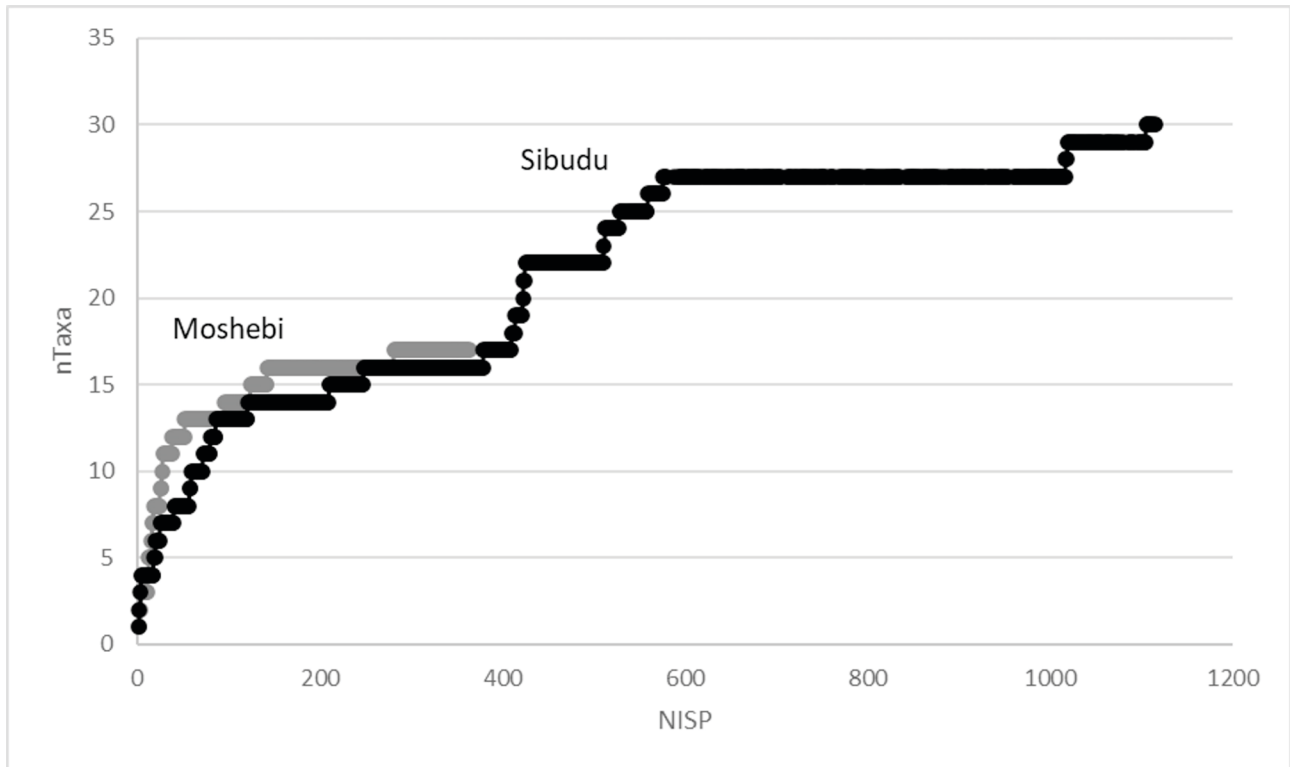


Fig. 4: Large mammal assemblage sizes (excluding the very large assemblage from Blombos Cave, which were excluded for clarity of the data below).

sporadic occupation, whereas younger farming sites had shorter, intense occupation spans of several decades or hundreds of years at best. The extant and extinct vertebrate fauna from South Africa is diverse (O'Connor, 2000). In the case of faunal assemblages from archaeological sites, it is often ambiguous to predetermine exactly the available taxa in an area. Not only is it impossible to separate some species from one another (due to factors such as incomplete comparative collections, the taxonomic uncertainty of some species, or whether or not they can actually be separated based on skeletal remains, etc.), but animals may be found outside their natural habitat (changing environments, trade in animal products, etc.). These factors no doubt have an influence on the number of taxa identified from assemblages.

Many of the faunal assemblages studied over the years in South Africa, is certainly small. For one, there is a tendency amongst archaeologists to excavate smaller areas as knowledge accumulates about the past in the region (overview in Mitchell, 2002). In some contexts, such as for those areas and time periods in South Africa where little or no information on animal usage may be available, small assemblages are often the only available material to study (e.g. Badenhorst *et al.*, 2011b, 2015). For example, fossil samples from Plio-Pleistocene

sites in South Africa are often small (Badenhorst *et al.*, 2011c; Van Zyl *et al.*, 2016). Moreover, patterns in smaller assemblages (e.g. Badenhorst *et al.*, 2011a) may sometimes mimic those found in larger ones (Badenhorst, 2011; Fraser & Badenhorst, 2014). Small assemblages can also contribute as building blocks to gain a perspective of regional patterns (e.g. Plug & Badenhorst, 2001). All these factors emphasise that a wider and ongoing study of the size of assemblages is important in South Africa, an aspect we are only now starting to understand.

Zooarchaeologists often attempt to investigate changes in faunal utilisation over time, either by comparing different layers or phases from the same site with one another (Badenhorst, 2015), or comparing faunas from different sites within a region with one another (e.g. Badenhorst, 2011, 2018; Fraser & Badenhorst, 2014). In this process, small assemblages often pose a problem (Badenhorst, 2011). As an example, the Middle Stone Age in South Africa is a critical time in the evolution of modern humans (Mitchell, 2002). During this time, active hunting became widespread (Badenhorst & Plug, 2012; Clark 2011). The success and ability of early humans in securing prey have long been debated (e.g. Klein, 2000). Most faunal assemblages from MSA sites in the Eastern and Western Cape of South Africa

are large in total (Table 3, Fig. 5). This area of South Africa is particularly well-studied. However, a problem arises when making comparisons between the layers of individual sites, as then sample sizes often decline to well below 1000 NISP as they become insufficient in size for proper comparisons. This is evident at many sites, including Blombos Cave (Table 4). This suggests that zooarchaeologists need to be cautious when making

intra-site comparisons between layers, phases and spaces using both small and large samples.

Plotting the NISPs against the number of taxa is easy if the data are available electronically, and can be done during analyses. It is then possible to determine the asymptote of an assemblage. We are by no means advocating halting an analysis when the asymptote point

Table 3: Middle Stone Age sites from the Western and Eastern Cape with their respective NISPs and nTaxa (nTaxa and NISPs exclude hominin and tortoise remains). Analyses consist of mammals only, and represent largely anthropogenic accumulations.

Site	NISP	nTaxa	Reference
Blombos Cave	9620	35	Henshilwood <i>et al.</i> , 2001; Badenhorst <i>et al.</i> , 2016a; Reynard & Henshilwood, 2019
Die Kelders Cave	174, 789	39	Klein & Cruz-Uribe, 2000
Diepkloof Cave	3244	30	Steele & Klein, 2013
Klasies River Cave	5346	30	Reynard & Wurz, 2020; Van Pletzen, 2000
Klipdrift Cave	1603	22	Reynard <i>et al.</i> , 2016
Pinnacle Point	156	17	Rector & Reed, 2010
Ysterfontein 1	3669	19	Avery <i>et al.</i> , 2008

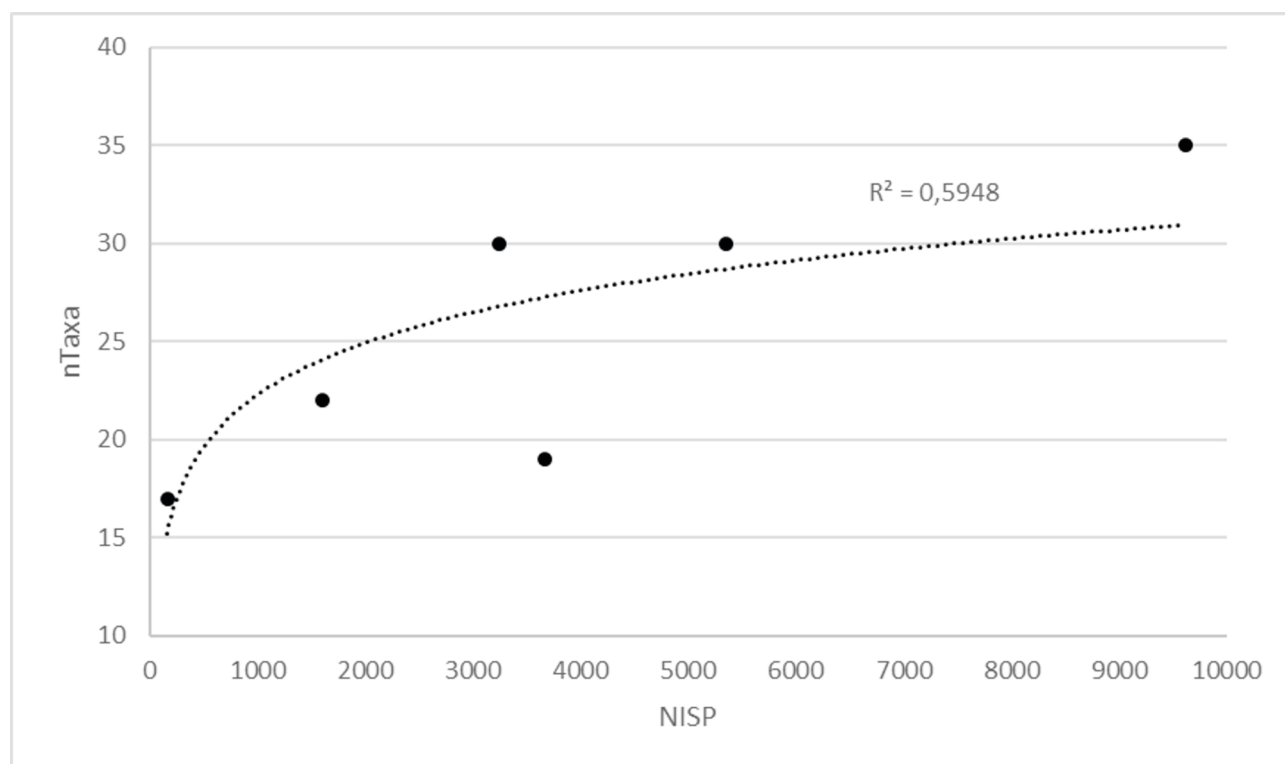


Fig. 5: Middle Stone Age sites NISPs and nTaxa (from Table 3, excluding the very large assemblage from Die Kelders)

Table 4: Blombos Cave NISPs for the layers of the M3 phase dating to between 94 000 and 101 000 years ago (Badenhorst *et al.*, 2016a).

Layer	NISP
CH-CI	2297
CJ	1202
CK	149
CL	135
<b>Total</b>	<b>3783</b>

is reached, or that subsampling should be practiced (Levitan, 1983 *pace* Turner, 1984). However, in some circumstances, such an approach may be warranted (e.g. for contract analyses, or when limited resources are available). Where feasible, zooarchaeologists should use the largest possible assemblage size when conducting any quantitative study and to minimise the margin of error and increase reliability of the comparisons (Payne, 1972). The presence or absence of species in assemblages, their diversity, skeletal part representation, taphonomy, aging and sexing are all directly linked to the size of the assemblage (Lyman, 2008).

Large assemblages are crucial for understanding the past. In this initial study, we suggest that NISPs nearing 1000 for those assemblages containing only large mammals, and NISPs nearing 2000 specimens for assemblages containing a full range of vertebrates and invertebrates are regarded as sufficient in size (also see Tourigny, 2017). However, the largest possible assemblage size must be studied when possible. This initial research must be expanded in future by investigating the nTaxa and NISPs from sites in the same region within the same biome and same relative ages using best-fit logarithmic trend-lines. Moreover, as more archaeofaunas are analysed using the same method in future, and having the data available in electronic format, would allow for a larger study incorporating more assemblages.

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