SAMPLING TO REDUNDANCY IN ZOOARCHAEOLOGY: LESSONS FROM THE PORTLAND BASIN, NORTHWESTERN OREGON AND SOUTHWESTERN WASHINGTON

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ABSTRACT.—A method for determining whether a group of samples is adequate to address a research question is presented. As each sample is analyzed the average value of a variable is recalculated and a cumulative graph is produced. When the value of the average stabilizes, one has empirical evidence that analysis of additional samples is not necessary—one has sampled to redundancy—and the collection is adequate for its intended analytical purpose. Analysis of two zooarchaeological collections of mammalian remains recovered from the Portland Basin of northwestern Oregon and southwestern Washington illustrates this point. Despite the spatial and temporal propinquity of the two sites, one assemblage is adequate for estimating taxonomic richness and diversity whereas the other, larger collection, is adequate for estimating richness but not diversity. Combined, the two collections are adequate for estimating taxonomic richness but do not provide an accurate measure of taxonomic diversity. Graphing procedures for monitoring sample adequacy, if implemented in the field, could help preserve finite archaeological resources.

Key words: mammalian zooarchaeology, sample adequacy, sampling to redundancy, taxonomic diversity, taxonomic richness.

RESUMEN.—Se presenta un método para determinar si un grupo de muestras es adecuado para abordar una investigación concreta. Al analizar cada muestra se vuelve a calcular el valor medio de la variable y se produce un gráfico acumulativo. Cuando se estabiliza el valor de la media se concluye empíricamente que no es necesario analizar muestras adicionales pues se ha muestreado de manera redundante y la recogida de datos es suficiente para el pretendido análisis. Este hecho se ilustra con el análisis de dos colecciones de restos de mamíferos recogidos en la cuenca del río Portland en el noroeste de Oregón y en el suroeste de Washington. A pesar de la proximidad espacial y temporal de ambos yacimientos, una de las colecciones es adecuada para estimar la riqueza taxonómica y la diversidad, mientras que con la otra colección que es mayor, se puede estimar la riqueza, pero no la diversidad. La combinación de ambas colecciones es adecuada para estimar la riqueza taxonómica pero no proporciona una medida exacta de la diversidad taxonómica. La realización en el campo de métodos gráficos que representan la idoneidad de la muestra, podrían ayudar a conservar recursos arqueológicos escasos.

RÉSUMÉ.—Nous présentons une méthode permettant de déterminer si un ensemble d'échantillons est suffisant pour répondre à une problématique de recherche.

Pour chacun des échantillons analysés, la valeur moyenne d'une variable est re-
calculée et un graphique cumulatif est créé. Lorsque la valeur de la moyenne
devient stable, l'on obtient une donnée empirique indiquant que l'analyse des
autres échantillons n'est pas nécessaire—et que les échantillons deviennent redon-
dants; la récolte de données est alors jugée suffisante pour les besoins des anal-
yses prévues. Des analyses de deux collections zooarchéologiques de restes de
mammifères découverts dans le bassin de Portland, au nord-est de l'Oregon et au
sud-ouest de Washington mettent en lumière ce point. Malgré la proximité tem-
porelle et spatiale des deux sites, un seul assemblage est adéquat afin d'évaluer
la richesse et la diversité taxonomique alors que l'autre collection plus importante
est suffisante pour évaluer la richesse, mais non la diversité. Si l'on combine les
deux collections, on peut évaluer adéquatement la richesse taxonomique, mais on
ne peut obtenir une mesure précise de la diversité taxonomique. Les méthodes
graphiques qui assurent le suivi d'un échantillonnage précis peuvent aider à con-
server les ressources archéologiques limitées; il faut cependant les mettre en place
sur le terrain.

INTRODUCTION

One of the hallmarks of the so-called "new" or "processual" archaeology of
the 1960s and 1970s was a call to utilize probability sampling to guide the col-
lection of archaeological materials (Binford 1964; Redman 1974; Rootenberg 1964;
Vescelius 1960). This call was echoed in paleontology (Krumbein 1965) and eth-
nography (Honigmann 1970) at about the same time. In archaeology the call was
accompanied by a concern over how large samples had to be in order to be
"representative" (Cowgill 1964), and various researchers worked toward empiri-
cally deriving a universal sample size that was in some sense representative
(Mueller 1974; various chapters in Mueller 1975). Most soon realized that the more
diverse the population in terms of the variable of interest, the greater the sample
size necessary to be representative. It was also recognized that accurate estimates
of different population parameters sometimes require samples of different sizes
(Hole 1980). In other words, a sample of some size that is representative in terms
of estimating one parameter will not necessarily be adequate or representative in
terms of estimating other parameters. There is no sample size (ignoring that of
100%) that will allow all parameters of a diverse population to be accurately
estimated statistically. Assuming that a representative sample could be generated
and also be shown empirically to be representative, the pressing question thus
became: How is sample adequacy to be determined in any particular case?

Dunnell (1984:72) suggested that "it should be possible to determine sample
adequacy empirically by following an incremental program in which the signifi-
cance of the effect of adding additional sampling units is measured directly."
Leonard (1987) expanded on this suggestion and argued that one should sample
incrementally "to redundancy." He indicated that the way to do this was to "plot
the information gained against the number of samples taken and determine if the
curve is becoming asymptotic. It may then be reasonable to assume that the sam-
ple is sufficiently representative with regard to that particular information" (Leon-
ard 1987:499). This exact procedure had been used twelve years earlier by a pa-
leontologist who sought to determine if his collection of late Quaternary mam-

malian remains was representative in terms of genera identified (Wolff 1975). He plotted the cumulative number of genera on the vertical axis and the incremental samples on the horizontal axis; when the curve defined by the plotted points leveled off across multiple samples, he argued that he had sampled sufficiently to have collected remains of all genera. We emphasize that empirical demonstration of sample representativeness by the procedure of sampling to redundancy demands a total sample that is in fact larger than a merely representative sample.

To our knowledge, the sampling-to-redundancy procedure outlined by Dunnell (1984), described by Leonard (1987), and used by Wolff (1975) has seldom been used in archaeology and only once, so far as we know, in zooarchaeology (Butler 1990). Instead, many have followed Grayson's (1984) recommendation and determined if a correlation existed between the values taken by the variable of interest and sample size. Following this procedure, if the values of the variable covary significantly with sample size, then typically it is concluded that the value of the variable might be a function of the sample size rather than a function of the character of the population. Others have attempted to develop procedures much like a paleontologist's rarefaction technique (Tipper 1979) to circumvent sample-size effects on various analyses (Kintigh 1984). Archaeologists have used this procedure (e.g., McCartney and Glass 1990; selected chapters in Leonard and Jones 1989), though it has also been noted that this approach presumes much is already known about the structure of the archaeological record (Rhode 1988). In this paper we illustrate the incremental sampling-to-redundancy procedure. We use zooarchaeological materials from sites we have studied, plus zooarchaeological data generated by others, to explore the utility of the procedure. To be successful, explicit definition of variables is critical.

METHODS AND MATERIALS

The terms of probabilistic sampling and studies of diversity, particularly the latter, are not always consistently defined. It is thus critical to provide explicit definitions of the terms that we use in our discussion. A *population* is some set of phenomena about which we wish to know one or more characteristics. A *sample* is some subset of the phenomena making up a population. A *parameter* is a measurable property of a population; parameters are estimated by characteristics of samples. The *richness* of a population concerns the number of kinds or classes of phenomena comprising that population. The *evenness* of a population concerns the distribution of individual phenomena across classes of phenomena; high evenness occurs when each class has the same number of individuals as every other class. In both the ecological (Spellerberg and Fedor 2003) and zooarchaeological (Byrd 1997) literature, "diversity" sometimes refers to richness and sometimes to how we have defined the term. For us, *diversity* refers to a combined measure of richness and evenness; if richness, evenness, or both increase, then so too will diversity. A simple way to conceive of diversity is this: the lower the probability that the taxonomic identity of an individual randomly chosen from a population can be predicted, the more taxonomically diverse the population. Diversity may appear to stabilize when the effect of increased richness on the diversity index is offset by change in evenness. In the following, we presume that one is interested
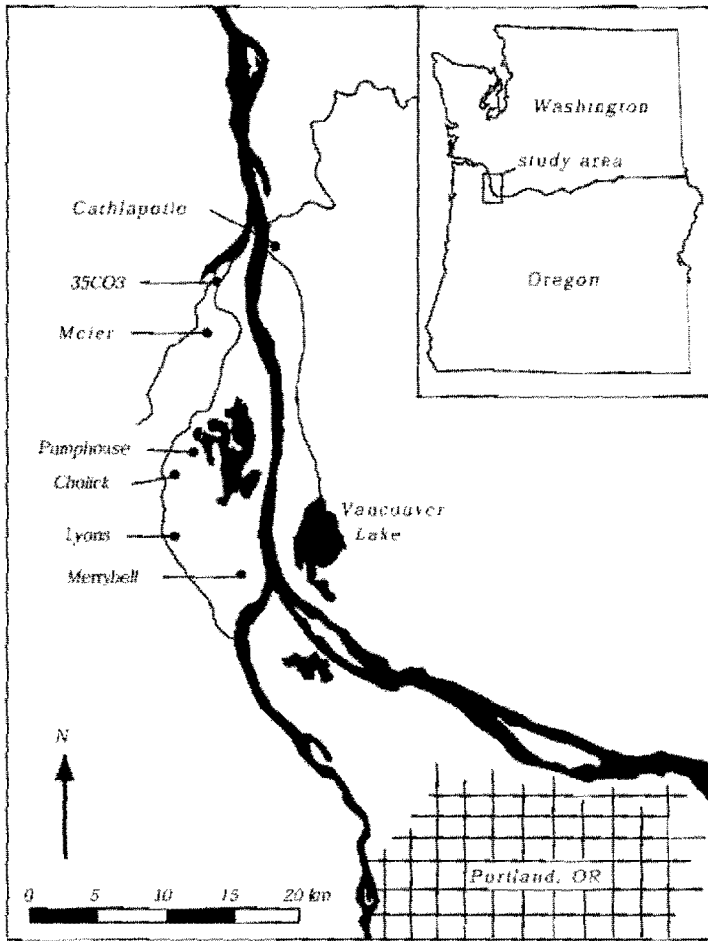
FIGURE 1.—Map of Portland Basin showing locations of sites mentioned in text.

in the quantitative property of diversity rather than the separate influences of richness and evenness on it.

Zooarchaeological collections of mammal remains recovered from two late prehistoric sites within 10 km of one another provide the data. Both are found in what is locally known as the Portland Basin or the Wapato Valley of northwestern Oregon and southwestern Washington (Figure 1). All mammalian remains from both sites discussed here were recovered from one-quarter inch mesh screens in the field. The Meier site (35CO5) is located downstream (north) of modern Portland, Oregon, on the floodplain of the Columbia River, on the Oregon side. The Meier site comprises a single large cedar-plank house, which was occupied more or less continuously between approximately A.D. 1400 and A.D. 1800, and associated midden deposits (Ames 1996; Ames et al. 1992). The site was tested in 1973 (Pettigrew 1981) and 1984 (Ellis n.d.). It underwent extensive excavations every year from 1987 through 1991. The 1973 collection was made by Pettigrew (1981) and studied by Saleeby (1983). The 1984 tests were directed by Ellis (n.d.); any

recovered fauna remains from those tests have not been analyzed. Lyman studied all mammalian remains collected by Ames in later years. The six assemblages resulting from the annual field seasons are each treated as one incremental sample.

The other site, Cathlapotle (45CL1), is located northeast of Meier, on the Washington side of the Columbia River, on a series of levee-like scroll bars next to a distributary of the river (see the map in Ames and Maschner 1999:110). The site was visited by Lewis and Clark in March of 1806, at which time it comprised several large cedar-plank houses and associated midden deposits (Ames et al. 1999). Radiocarbon dates indicate the main occupation began about A.D. 1450. Seriation of ceramic trade goods indicates abandonment circa A.D. 1834 (Kaehler 2002). Auger sampling of the Cathlapotle sediments took place in 1992–93, and excavations took place each year from 1993 through 1996; both augering and excavation were under the direction of Ames. Faunal remains from the augering are here treated analytically as one incremental sample, and each assemblage resulting from an annual excavation season is treated as a distinct annual sample, for a total of five incremental samples. Lyman identified all mammalian remains recovered from this site.

With the probable exception of the auger samples from Cathlapotle, the assemblages of mammalian remains from the two sites were recovered from similar contexts. At both sites, the deposits are classified into analytical units (AU) defined on the basis of their age, their depositional origin, and their position in relation to the house structures that dominate the deposits. Deposits are first designated as exterior or interior deposits (outside or inside of a house, respectively). Exterior deposits are designated as "midden" deposits and "yard" deposits. The former have very high organic contact, lenses of freshwater mussel shells, and other indications that they formed as primary or secondary dumps (Ames et al. 1999). Yard deposits are generally broad sheet-like deposits that contain intact hearths, activity areas, pits, evidence of small structures, and so forth. They usually lack the very high organic content of middens though they can have some organic remains. Interior deposits are separated according to the structure facility in which they occur. We assign these deposits to walls, benches (deposits below the 2-m wide sleeping platforms that ran along the interior side of the house walls), storage pits, and hearth areas.

The houses at Meier and Cathlapotle had extensive subfloor storage features that, at Meier at least, formed a cellar almost 2 m deep that extended under the house floor between the sleeping platforms and the row of hearths in the house's center. The Cathlapotle features are less extensive, but are about 2 m wide by 2 m deep. They are below the sleeping platforms rather than next to them as at Meier. The mammalian remains from both sites were derived primarily from these storage pits and exterior areas.

All frequencies of mammalian taxa are given as number of identified specimens (NISP). Because taxonomic abundance data based on NISP values are typically at best ordinal scale (Grayson 1984), we use ordinal scale statistics in our analyses. We examine the influence of sample size on two parameters typically estimated in zooarchaeology—taxonomic richness and taxonomic diversity. We use the taxonomic level of genus when considering these parameters because some

genera in the collections are polytypic but the species represented by zooarchaeo-
logical specimens could not always be determined. We include what are likely to
be remains of intrusive rodents (*Scapanus, Sorex, Peromyscus, Microtus, Eutamias,
Tamiasciurus, Thomomys*) that lived in the area at the time of site occupation, but
we exclude the few remains of historically introduced domestic taxa in the col-
lections from our analyses (NISP < 10 at both sites). Richness is here measured
as the number of identified genera. To measure diversity we follow zooarchaeo-
logical tradition and use the Shannon index, $-\Sigma\ p_i \ln p_i$ in which p is the pro-
portion of the total NISP in a sample identified as taxon i, and ln is the natural
log. Evenness is generally measured as the Shannon index divided by the ln of
richness. We do not include evenness in our analyses here except to note how it
influences values of diversity.

Throughout the discussion the terms cumulative graph and cumulative curve
are used as convenient shorthand for illustrations and descriptions of the rela-
tionship between the variable of interest and how it changes relative to cumulative
incremental samples. Given how richness and diversity are calculated, it is im-
portant to make clear what the curves on cumulative graphs will look like. In a
graph in which incremental samples are added on the X-axis and cumulative
taxonomic richness is plotted on the Y-axis, the curve will become progressively
less steep as fewer new taxa are added with new samples and will level off once
all taxa have been encountered. The curve on a graph with incremental samples
added on the X-axis and diversity on the Y-axis will increase as taxa are added,
as evenness increases, or both. Unlike a cumulative richness curve, a cumulative
diversity curve can decrease or have a negative slope. This is so because evenness
can decrease as samples are added (there is no reason to expect every sample to
have the same evenness). Thus cumulative curves, especially for diversity, may
tell us something about the underlying structure of the cumulative samples with
respect to richness and evenness that is not otherwise apparent in long tables of
NISP values.

Cumulative graphs are used here to illustrate how measures of richness and
diversity change with the addition of each incremental sample. The graphs grant
insight to the influences of sample size on the taxonomic richness and diversity
at each site. At neither site were excavation units chosen probabilistically. Rather,
both were excavated with similar research goals in mind and using similar clues
based on surface features and previous testing and excavation. If the mammalian
populations differ between the two sites, then cumulative curves should level off
at different positions in terms of incremental samples and perhaps at different
total NISP values. As Meltzer et al. (1992) indicate, the slope and shape of the
curve describing the relationship between cumulative sample size and cumulative
richness depend on the underlying structure of the population—its richness, even-
ness, and diversity (see also Byrd 1997). Assemblages with low richness and high
evenness will produce curves with short, steep slopes that level off quickly. If
richness is high, evenness is low, or both, the curve will level off more gradually.

Meltzer et al. (1992) follow Grayson (1984) and state that if a correlation is
found between sample size and richness or between sample size and diversity,
then the latter values are likely reflecting sampling and collection activities of the
archaeologist rather than the parameter of the population. We agree, and note that

the editors of *Science* recently saw fit to publish a case study from paleontology exemplifying the relationship between sample size and sampling intensity, and taxonomic richness and diversity (Crampton et al. 2003). They did so because many paleontologists assume that their samples are representative of the variable(s) of interest, rather than test the assumption (Smith 2003). It seems to us that many zooarchaeologists behave similarly (as do archaeologists studying lithics, ceramics, and virtually all other kinds of archaeological materials). The graphic technique described here is simple conceptually and quickly used as a test of sample adequacy. Although we focus on just this test here, we attempt to go a bit beyond exemplification of it by considering a little-used method that could have some analytical utility beyond its efficiency as a method to test for sample-size effects.

We refer to the entire set of identified remains from a site as a *collection* because entire sites were not excavated but rather only a portion of each site was excavated. Each collection is, then, actually a sample of what is present in site deposits. We refer to each annually recovered set of remains as a *sample*. Basic descriptive data for all 11 samples and both collections are presented in Tables 1 and 2. To illustrate how the definition of a population can influence whether a sample is representative or not, we identify two kinds of populations. The first is the typical site-specific population. That is, we are concerned with estimating taxonomic richness and diversity of the population of mammalian remains at each individual site. The second population we define is the suite of mammalian genera represented in archaeological deposits of the Portland Basin. The population characteristics of interest at this more inclusive geographic scale are again taxonomic richness and diversity.

RESULTS

The Individual Sites.—The Cathlapotle collection (NISP = 6920) is a bit larger than the Meier collection (NISP = 6420), yet the former site has only 22 genera whereas the latter has 25 genera represented. Plotting cumulative taxonomic richness against the cumulative incremental samples indicates that richness levels off subsequent to addition of the fourth sample (cumulative NISP = 4079) from Meier whereas the number of genera increases with the addition of each sample, including the fifth and final sample (cumulative NISP = 6920), from Cathlapotle (Figure 2). This indicates that despite the larger sample size measured as total NISP at Cathlapotle, we have not yet sampled to redundancy in terms of taxonomic richness—in this case, in terms of mammalian genera—at this site. The fact that nearly 2400 NISP are added by the last two incremental samples at Meier—a 59% increase to the cumulative NISP of 4079 after the first four annual samples—yet no additional mammalian genera were identified suggests that we have sampled to redundancy in terms of taxonomic richness at this site.

For each site, the NISP of each individual incremental sample is not correlated with the number of genera represented in the sample. At Meier, Spearman's rho = 0.77 (P = 0.1); at Cathlapotle, rho = 0.9 (P > 0.08). In other words, if one were to calculate this statistic to determine if taxonomic richness was a function of sample size at either of these sites, the site-specific coefficient would not reveal

TABLE 1.—Number of identified specimens (NISP) of mammalian taxa from each field season at the Meier site (35CO5).

Taxon	1973	1987	1988	1989	1990	1991	Total
Scapanus	4	4	3	4	1	2	18
Sylvilagus	2	3	1	1	10	1	18
Aplodontia	2	1	—	1	—	3	7
Eutamias	—	—	—	1	—	—	1
Tamiasciurus	—	—	2	—	—	—	2
Thomomys	—	2	—	1	5	1	9
Castor	13	100	65	52	41	71	342
Peromyscus	—	4	12	12	4	3	35
Neotoma	—	—	1	—	—	—	1
Microtus	—	15	25	34	15	11	100
Ondatra	37	97	55	59	74	52	374
Erethizon	—	—	—	1	—	—	1
Canis	21	25	13	16	11	25	111
Vulpes	3	1	1	—	—	—	5
Ursus	20	16	20	7	13	26	102
Procyon	15	79	51	35	43	64	287
Martes	1	6	1	—	1	11	20
Mustela	4	35	17	19	38	21	134
Mephitis	—	1	1	—	—	2	4
Lutra	6	12	6	2	11	14	51
Felis	—	4	1	—	3	1	9
Lynx	9	5	4	1	4	8	31
Phoca	3	6	5	10	6	13	43
Cervus	103	165	191	152	106	218	935
Odocoileus	276	788	756	562	570	838	3780
Annual sample totals							
NISP	519	1359	1231	970	956	1385	6420
Richness	16	21	21	19	18	20	25
Diversity	1.606	1.618	1.440	1.547	1.593	1.489	1.555
Cumulative totals							
NISP	519	1878	3109	4079	5035	6420	
Richness	16	21	23	25	25	25	
Diversity	1.606	1.623	1.558	1.559	1.568	1.555	

TABLE 2.—Number of identified specimens (NISP) of mammalian taxa from each field season at Cathlapotle (45CL1).

Taxon	Augering	1993	1994	1995	1996	Total
Scapanus	—	—	—	—	3	3
Sorex	—	—	4	—	—	4
Lepus	—	—	12	20	18	50
Aplodontia	2	18	41	42	33	136
Castor	1	32	123	185	51	392
Peromyscus	—	—	4	1	—	5
Microtus	1	—	12	16	39	68
Ondatra	—	19	34	32	21	106
Canis	—	4	27	5	3	39
Vulpes	—	1	3	1	—	5
Ursus	1	23	29	31	18	102
Procyon	1	57	59	70	20	207
Martes	—	—	—	2	—	2
Mustela	—	3	14	7	5	29
Mephitis	—	—	—	—	3	3
Lutra	—	14	19	13	19	65
Felis	—	5	3	3	1	12
Lynx	—	2	6	12	6	26
Phoca	—	1	19	41	4	65
Ovis	—	—	1	—	—	1
Cervus	16	462	879	1184	683	3224
Odocoileus	18	332	797	821	408	2376
Annual sample totals						
NISP	40	973	2086	2486	1335	6920
Richness	7	14	19	18	17	22
Diversity	1.244	1.395	1.503	1.434	1.438	1.472
Cumulative totals						
NISP	40	1013	3099	5585	6920	
Richness	7	15	19	20	22	
Diversity	1.244	1.395	1.479	1.469	1.472	

any such correlation. One could, of course, argue that with only five samples from Cathlapotle and six from Meier, we would be hard pressed to find a statistically significant correlation. Cumulative incremental samples can not be used in such correlations because of the interdependence of the cumulative samples. The graph in Figure 2 reveals the relationship between sample size and taxonomic richness in clear, unambiguous, and readily interpreted form, given the size and scale of the Y-axis and knowing the richness values.

Taxonomic diversity at both sites stabilizes after the addition of the third incremental sample (Figure 3; Meier cumulative NISP = 3109; Cathlapotle cumulative NISP = 3099). This suggests that both collections are statistically representative in terms of the diversity of mammalian genera, at least as measured by the Shannon index. It may be significant for assessing mammalian exploitation patterns in the Wapato Valley in general that diversity is accurately estimated at both sites when NISP is about 3100. We cannot as yet test this observation with other collections because none in the area have sufficiently large NISP values. Interestingly, there is no significant correlation for either site between the annual
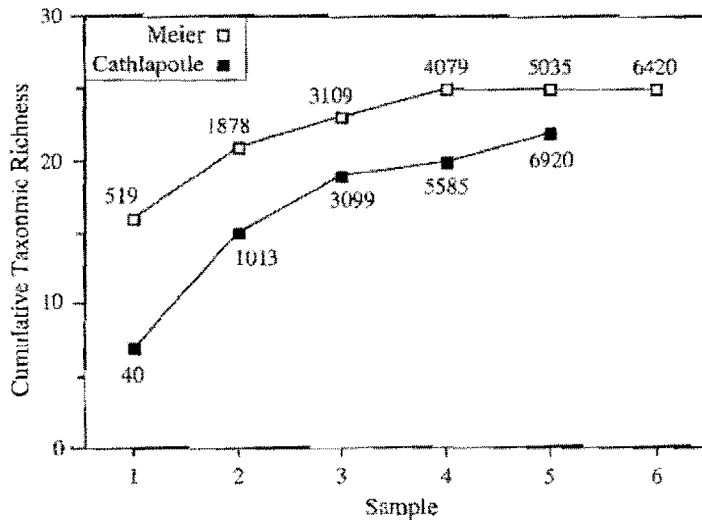
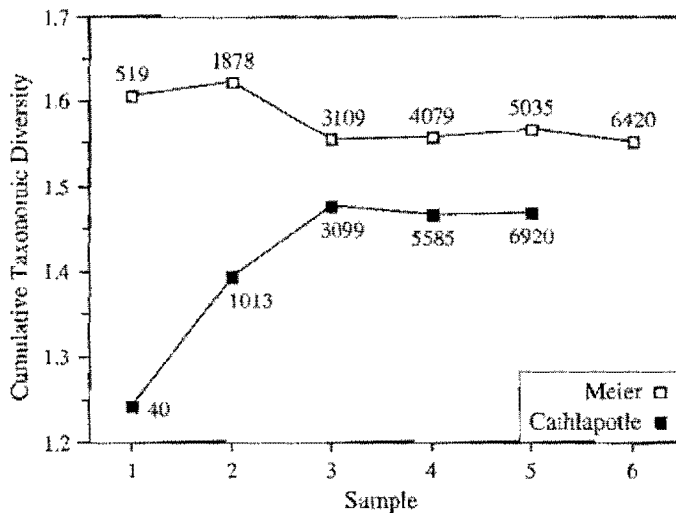FIGURE 2.—Cumulative richness of mammalian genera across cumulative incremental samples from the Meier site and Cathlapotle. Numbers adjacent to plotted points are cumulative NISP.

incremental sample NISP and the annual Shannon index (P > 0.2). This result corroborates our interpretation of Figure 3, but again one might argue that it is difficult to find a correlation when N = 5 or 6. As with sample size and richness (Figure 2), the graph in Figure 3 reveals the relation between cumulative sample size and cumulative taxonomic diversity in clear, unambiguous, and readily interpreted form, again allowing for the size and scale of the Y-axis or knowing the

FIGURE 3.—Cumulative diversity of mammalian genera across cumulative incremental samples from the Meier site and Cathlapotle. Numbers adjacent to plotted points are cumulative NISP.

diversity values. We see in that graph when we have reached a representative sample and when we have not.

The Portland Basin.—Given growing interests in regional-scale questions such as those involving land use, settlement patterns, and subsistence systems, it might be the case that researchers have cause to somehow lump zooarchaeological data from multiple sites (Lyman 2003 and references therein). In such cases the geographic scale shifts from a site to an area containing multiple sites. It is a well-known principle of biogeography that an increase in the size of the geographic area sampled will typically concomitantly increase the number of taxa included in the area (Brown and Lomolino 1998). This is precisely what happens when the lists of mammalian genera represented at the Meier and Cathlapotle sites are examined. Note, for example, that *Sylvilagus* is the genus of leporid represented at Meier whereas *Lepus* is the genus of leporid represented at Cathlapotle. This is a reflection of the biogeography of local mammals (Johnson and Cassidy 1997; Verts and Carraway 1998). We believe a similar explanation accounts for the single *Ovis* specimen recovered from Cathlapotle (Johnson 1983). The Meier site collection includes four genera (excluding *Lepus*) not found in the Cathlapotle collection, and the Cathlapotle collection includes two genera (excluding *Sylvilagus*) not found in the Meier collection. Several hundred bulk samples were collected from each site, and these are still being processed. We think it likely that once the faunal remains from these samples are analyzed, the genera unique to each site will be added to the other site's list. But do these two sites represent the full suite of mammalian genera in Portland Basin archaeological sites?

Additional late Holocene sites in the Portland Basin were sampled in the 1970s (Pettigrew 1981; Saleeby 1983). Each collection of mammalian faunal remains from these additional sites are summarized in Table 3, along with the collections from Meier and Cathlapotle. The additional collections add two new genera (*Enhydra* and *Spermophilus*) to the Portland Basin mammalian zooarchaeological record. Superficially, this is not surprising given that these collections also increase the total NISP for the areal record. The summed collections from the two sites that produced these two new genera (NISP = 1 for each) comprise 171 NISP, a mere 1.2% of the total 13,887 mammalian NISP from the Portland Basin. There are four variables that could account for the fact that an increase in the all-sites-summed sample size by 1.2% also increases the all-sites-summed taxonomic richness from 27 to 29, or by 7.4%. First and most obvious is the fact that the two new taxa are exceptionally rare locally and thus it is not unusual at all that they would appear only when sample sizes are exceptionally large. This readily accounts for *Enhydra* (monotypic species *lutris*)—the sea otter—which is a saltwater obligate virtually never found in rivers (Kenyon 1969), even those influenced by oceanic tides, such as the Columbia River in the Portland Basin (Richardson and Allen 2000). Perhaps the single specimen identified as this species was procured on the coast and transported by prehistoric people inland to the Portland Basin.

Another, perhaps less obvious reason the new taxa may have been added is that a different person made the identifications. Contrary to what some might think, making taxonomic identifications of faunal remains comprising broken bones and tooth fragments is neither simple nor straightforward (Lyman 2002

TABLE 3.—Number of identified specimens (NISP) of mammalian taxa from Portland Basin archaeological sites.

| Taxon	Meier	Cathlapotle	Cholick	Pumphouse	35CO3	Lyons	Merrybell
Scapanus	18	3	—	—	1	—	—
Sorex	—	4	—	—	—	—	—
Sylvilagus / Lepus	18	50	—	—	—	—	1
Aplodontia	7	136	—	—	—	—	—
Eutamias	1	—	2	—	—	—	—
Tamiasciurus	2	—	—	—	—	—	—
Spermophilus	—	—	—	1	—	—	—
Thomomys	9	—	—	—	—	—	—
Castor	342	392	10	8	4	—	—
Peromyscus	35	5	7	—	—	—	—
Neotoma	1	—	—	—	—	—	—
Microtus	100	68	30	3	—	—	—
Ondatra	374	106	5	2	—	—	1
Erethizon	1	—	—	1	—	—	—
Canis	111	39	36	3	4	—	1
Vulpes	5	5	—	—	—	—	—
Ursus	102	102	3	3	1	—	1
Procyon	287	207	32	6	6	1	—
Martes	20	2	—	—	—	—	—
Mustela	134	29	3	—	—	—	—
Mephitis	4	3	—	—	—	—	—
Lutra	51	65	—	—	—	—	—
Enhydra	—	—	—	—	1	—	—
Felis	9	12	—	—	—	—	—
Lynx	31	26	2	1	—	—	—
Phoca	43	65	—	—	—	—	—
Ovis	—	1	—	—	—	—	—
Cervus	935	3224	40	7	10	17	—
Odocoileus	3780	2376	160	74	35	22	2
Site-specific totals							
Total NISP	6420	6920	330	109	62	40	6
Richness	25	22	12	11	8	3	5
Diversity	1.570	1.472	1.692	1.290	1.398	0.785	1.562
Cumulative totals							
Richness	25	27	27	28	29	29	29
Diversity	1.570	1.593	1.604	1.606	1.604	1.604	1.605
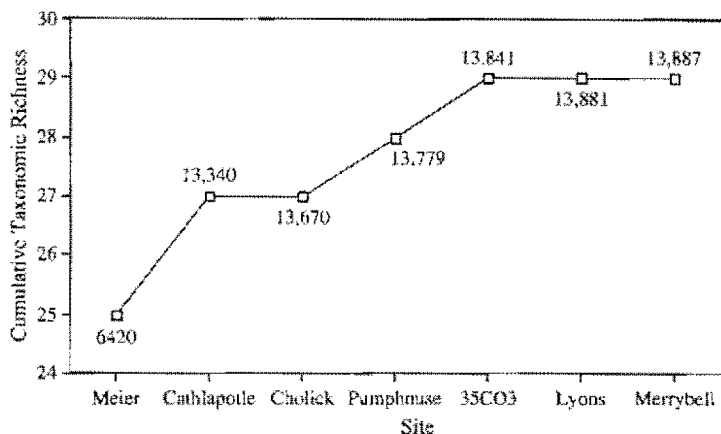
FIGURE 4.—Cumulative richness of mammalian genera across cumulative site collections from the Portland Basin. Numbers adjacent to plotted points are cumulative NISP.

and references therein). Another reason the additional taxa may have been added was mentioned earlier and comprises the fact that new geographic areas were sampled by the new sites. Human occupants of each site likely exploited different catchment areas, which could mean different habitats and thus different animal taxa. The fourth and final possible cause of an addition to taxonomic richness resides in the fact that the time and duration of site occupation varies. Even given the limited resolution of archaeological dating techniques it is clear that these seven sites were not all occupied simultaneously or for similar spans of time. For example, the Lyons site was occupied very late in time for about 100 years whereas the Merrybell site was occupied about 2000 years ago for about 800 years (Petti-grew 1981; Saleeby 1983). If local faunas changed over time for any of myriad reasons, then different taxa are to be expected in the zooarchaeological record. Even if there was no local faunal turnover during the late Holocene, we suspect a site occupied for a longer period of time would produce remains of more taxa than a site occupied for a shorter period of time (all else being equal, of course).

It is at present unclear which of the four variables, or combination of them, accounts for the two additional taxa that appear when the sites excavated in the 1970s are included. But knowing which of those variables is responsible is less important than our main point. Adding the collection from each site in a cumu-lative fashion indicates that the total collection from the Portland Basin is repre-sentative of the areal mammalian fauna. This is so because, as Figure 4 makes clear, the addition of the site samples to the two largest and richest—Meier and Cathlapotle—in descending order of size produces a cumulative richness graph that levels off after the addition of the fifth sample. The two smallest samples provide a mere 46 NISP, and thus perhaps not surprisingly do not provide ad-ditional taxa. Also not surprising is the fact that taxonomic richness per site is correlated with site collection NISP (rho = 0.93, P = 0.007). What is disconcerting is that for a relatively small physiographic area, nearly 14,000 specimens had to be identified in order to have evidence of the 29 mammalian genera that comprise the archaeofauna.
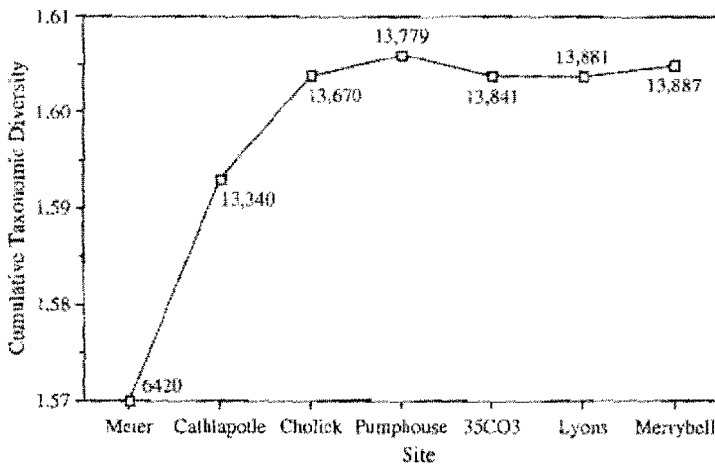
FIGURE 5.—Cumulative diversity of mammalian genera across cumulative site collections from the Portland Basin. Numbers adjacent to plotted points are cumulative NISP.

Cumulative diversity across these seven sites, if added in the same order as for richness, stabilizes with the addition of the third sample and hardly fluctuates with the subsequent addition of site samples (Figure 5). Interestingly, the addition of the several small site collections to the summed Meier and Cathlapotle collections causes the Shannon index to increase slightly, no doubt in part because of the addition of new taxa. Taxonomic diversity per site is not correlated with site collection NISP (rho = 0.39, P = 0.39).

CONCLUSION

Anyone who has done any amount of archaeological research knows that archaeologists seldom have sufficient time and money to accomplish all of the goals set by a project. For this reason alone one might adopt a sample-to-redundancy protocol during field work such that it will be known when a sample is sufficient to estimate some parameter of interest. It seems to us that the most difficult aspect of implementing this sort of protocol will involve the rate of identification of materials keeping pace with the rate at which they come out of the field. If it could be done, say, on a year-to-year basis, it could result in the *in situ* preservation of scarce archaeological resources, because it could be demonstrated that additional excavation was unnecessary with respect to the variable(s) of interest. For example, it is clear that the first annual incremental sample from Meier correctly indicated that deer remains outnumber those of elk at this site. Similarly, one would know by the time the third incremental sample from Cathlapotle had been analyzed that elk outnumber deer at this site. If the parameter of interest was merely the relative abundance of deer and elk, then we could have stopped excavating at both sites after a few years. This would not only have saved archaeological resources, but it would have saved the cost of collecting and curating the recovered materials as well. Yet another example concerns the relatively rare remains of *Phoca*, the harbor seal. We were able to demonstrate this taxon was

found prehistorically in the Columbia River (Lyman et al. 2002), and we could have done so without the last year or two of samples from both sites. In contrast, we needed all annual samples from both sites in order to have sufficient specimens to demonstrate statistically that mountain beaver (*Aplodontia*) mandibles were used as tools by the occupants of Cathlapotle but apparently not by those who lived at Meier (Lyman and Zehr 2003). The point, then, is that a sample is (or is not) representative relative to the question asked and the variables pertinent to that question.

In this paper we focus our attention on the mammalian remains from the two sites where we have worked. Our intention is to perform similar analyses with the fish remains, the bird remains, and the artifact and feature classes at these sites. In doing so, we can assess the adequacy of these samples in terms of numerous variables that are central to the research questions we have. Further, the graphic technique may reveal similarities and differences between the two sites in terms of richness, evenness, and diversity that would not otherwise be apparent in columns of numbers.

We perceive several other lessons from the results presented above. First, what comprises a representative sample at one site need not comprise a representative sample at a nearby site of approximately the same age. The collection from Meier is smaller than that from Cathlapotle, but the Meier collection seems to be sufficient to give a good estimate of taxonomic richness and also of taxonomic diversity. Collection uniqueness is no doubt a result of the historical contingencies of its formation. Thus even though the Meier and Cathlapotle sites are within 10 km of each other and overlap considerably in terms of age and apparent site function, the size of the sample that must be analyzed to provide a fair representation of the assemblage at one site does not necessarily provide a good indication of a representative sample size at the other site. This adds empirical support to Rhode's (1988) contention that to use rarefaction techniques based on summed collections from multiple sites such as are suggested by Kintigh (1984) is ill advised because it presumes that we know much more about the quantitative properties of the record than we perhaps actually do.

A second lesson is that we must be explicitly clear about the scale of the parameter we seek to measure. Although it seems that we have a representative sample in terms of taxonomic richness at Meier, the collection from that site does not comprise a representative sample in terms of taxonomic richness for the Portland Basin. Even more than doubling the size of the total collection by adding the Cathlapotle collection to the Meier collection does not produce a complete list of all mammalian genera represented in the areal zooarchaeological record. And third, some of these lessons and some of our insights to the structure of the Portland Basin mammalian faunal collections we describe here would not be evident if all we had done was to correlate taxonomic richness or diversity with sample size. The sampling-to-redundancy procedure is simple and straightforward, and the graphs produced are readily interpreted. In terms of the Meier and Cathlapotle collections, we now know that we should not compare the two in terms of taxonomic richness (the latter is not a representative sample), though we might compare their respective diversities.

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