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Sampling Fish: A Case Study from the Čix^Wicən Site, Northwest
Washington

by

Laura Maye Syvertson

A thesis submitted in partial fulfillment of the
requirements for the degree of

Master of Science
in
Anthropology

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Portland State University
2017

Abstract

Researchers on the Northwest Coast (NWC) are often interested in complex questions regarding social organization, resource intensification, resource control, and impacts of environmental change on resources and in turn human groups. However, the excavation strategies used on the NWC often do not provide the spatial and chronological control within a site that is necessary to document their variability and answer these research questions. The Číx^wicən site has the potential to address some of the limitations of previous Northwest Coast village site excavations because of its unique and robust sampling strategy, the wide expanse of time that it was occupied, and the multiple house structures present. An on-going project is examining changing human ecodynamics over the breadth of site occupation, focusing on zooarchaeology and geoarchaeological records.

This site, located on the Strait of Juan de Fuca in Port Angeles, WA was excavated in 2004 as part of a Washington State Department of Transportation (WSDOT) undertaking to build parts for the Hood Canal Bridge Large scale excavation (261.4 m³ 528 m²) generated enormous quantities of faunal remains. Radiocarbon dates and historic records show occupation extends from 2750 cal. BP to the early 20th century.

Statistical sampling methods provide an empirical way to maximize the amount of information obtained with the least amount of effort. My thesis addressed the utility of Sampling to Redundancy (STR) as a statistical sampling method for sampling faunal remains from large village sites. My project has documented the variability of fish family representation across time and space in one part of the Číx^wicən village, while minimizing the time and effort required to do so. This thesis applies STR to “S” (> 1/4

in.) 10 Liter bucket samples from eight excavation units and a total of 26 separate unique temporal and spatial contexts. I focused on 1/ 4 in. samples for my study for a particular reason. Previous fish faunal studies have focused on effects of mesh size on fish representation; and emphasized the need to use fine mesh (e.g., 1/ 8 in. or finer) to document small-bodied fishes. This focus on fine mesh typically means that only limited volumes of matrix are studied, which in turn may mean that remains of rarer, large-bodied fishes are under- represented. The on-going research project has focused on buckets screened to 1/ 8 in. mesh (called “C” buckets). I used STR to sample additional volumes of matrix screened to 1/ 4 in. to examine whether expanding the volume studied would affect fish representation, which was a second goal of my project.

Overall, I studied remains from 269 “S” buckets out of a total of 419 buckets, or 47% of the buckets. STR was most helpful for six of the high bone abundance and density contexts, where I analyzed less than 50% of the total buckets, was moderately helpful for 14 contexts, and not at all helpful for the six contexts with low fishbone abundance, where I analyzed 100% of the buckets. This analysis took me a total of 154 hours, and based on the percentage of material analyzed, 174 hours were saved.

As to the second project goal, to assess whether adding fish remains documented from additional matrix volume affected fish representation, I found the differences were minimal. Both for my study units as a whole, and for each time period, adding the fish records from the “S” buckets did not alter the main trends in fish representation as documented by the larger study, using a smaller volume. To further examine whether the added volume from >1/ 4 in “S” buckets affected results, I explored specific research questions that are relevant to the larger project regarding environment-animal interactions

and fishbone deposition and bone condition inside and outside of a house structure.

Adding the “S” bucket samples did not affect fish representation or fishbone distribution and condition, which affirms that the sampling strategy used in the larger research project was sufficient in most cases to characterize the fish record at the site.

My approach to STR has focused on fish remains that were previously excavated from a Pacific coastal village site with dense archaeological deposits. STR could be employed in other types of archaeological settings in a range of environments (coast or interior) representing a range of cultural contexts (from hunting camps to urban centers) to establish sample redundancy after an excavation is complete. STR could be used during on-going excavation. Further research is required to explore the implications of STR in these settings, however it is likely that the success of STR in other contexts will be dependent on the density and overall abundance of remains, the diversity or material types being studied, as well of course in the range and specificity of questions in each case.

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Chapter 1. Introduction

Researchers on the Northwest Coast (NWC) are often interested in complex questions regarding social organization, resource intensification, resource control, and impacts of environmental change on resources and in turn human groups (Ames and Maschner 1999; Ames 2001, 2007, 2008; Butler and Campbell 2004; Campbell and Butler 2010; Coupland 1996; Grier 2001; Matson et al. 1999; Matson et al. 2003; Moss 1993; Moss 2011). Researchers often use village site excavations to explore these questions. One would ideally have large samples from multiple contexts within and between houses from village sites, but this is generally not the case (Gray 2008; Monks 2000). Gray (2008) has noted that the excavation strategies used often do not provide the spatial and chronological control within a site that is necessary to capture their variability. Moreover, the total volume of material sampled is often very small. It is imperative that archaeologists explore alternative approaches to sampling that address the concerns of both sample control and sample size.

The main goal of my thesis is to demonstrate how Sampling to Redundancy (STR) can address the concerns of increasing sample size to a level that adequately represents population characteristics. Besides providing a way to make the most efficient use of resources (time and cost), STR could be used to identify locales that would benefit from more intensive sampling. I will use STR to sample the extremely large faunal assemblage recovered from the Číx^wicən site, a ~2,800 year old village in Port Angeles, WA, and in so doing, demonstrate these values.

A large National Science Foundation (NSF)-funded zooarchaeological and geoarchaeological project began in 2012 to study changing human ecodynamics over the breadth of occupation at the Číx^wicən site (e.g. Mohlenhoff and Butler 2016) (Figure 1). Materials collected during the 2004 excavation were processed using nested screens, some ending at 1/4 in. mesh and some ending at 1/8 in. mesh (Reetz et al. 2006). To study animal use, the researchers focused attention on faunal remains collected from 10 L buckets screened to $\geq 1/8$ in. While the $\geq 1/8$ in. nested screen samples represent large quantities of fauna, they comprise a fraction of the total volume of matrix collected from the site. Moreover, remains of large-bodied vertebrates, like birds, mammals and even large fishes are rare in deposits, relative to small fishes. For this reason, mammal and bird faunal analysts have included additional 10 L bucket samples screened to 1/4 in. to increase their sample size. It would be useful to know if the 1/8 in samples mainly used by the NSF project were adequate for representing the rarer, larger fish. My thesis project addressed this need by using STR to study fish remains recovered from a sample of the $> 1/4$ in. bucket samples. The project thus will highlight the potential of using STR in faunal analysis, and at the same time allow me to assess whether the $> 1/8$ in. buckets were sufficient to characterize abundance of relatively large-bodied fishes.

Figure 1. Location of the Čixʷicən Site.

This thesis is organized into five chapters. Chapter 2 presents background information on sampling statistics, previous approaches to sampling Northwest Coast villages, and the Čixʷicən site. Chapter 3 describes the methods I used to analyze fish remains, focusing on how I used STR to establish redundancy in proportional representation for fish families present in the units included in my study. In Chapter 4, I summarize my results, including the time savings that STR provided for the analysis of fish remains collected using $>1/4$ in. mesh. I compare the results from my study with

those obtained from previous faunal analysis at Čix^wicən to see whether adding volume affects proportional representation of fish. To further examine whether the added volume from >1/ 4 in samples affects fish representation, I explore specific research questions that are relevant to the larger NSF project regarding environment-animal interactions and site use. The first question will address whether kelp-adapted fish taxa, such as greenling (Hexagrammidae) are adversely affected by earthquakes. I examine change in greenling abundance relative to a migratory fish less likely affected by earthquakes, dogfish (Squalidae), against the timing of a known earthquake. As the NSF project is also concerned with spatial patterning in animal remains and their link to site formation and social factors within and outside houses, I will compare-contrast fishbone distribution and density inside and outside a house structure, and in particular, whether increasing the sample size by adding the >1/ 4 in samples alters our understanding about cultural depositional practices and taphonomy. Chapter 5 considers the results in a larger context and discusses ways STR can be applied to sampling other Northwest Coast sites and in zooarchaeology generally.

Chapter 2. Background

2.1 Sampling

Sampling can be applied at multiple levels, including regional survey, site excavation, and lab analysis. The type of sampling method used in each of these stages affects how the spatial and stratigraphic contexts are selected for examination, and the overall amount of examined area and material. One must select a sampling methodology to assess how large a sample is needed to answer the archaeological questions at hand and to select samples representative of the population of interest (Leonard 1987; Lyman and Ames 2007; Lyman 2008; Orton 2000; Poteate and Fitzpatrick 2013; Van der Veen and Fieller 1982; Woo et al. 2015). These methods for sampling include decisions about sample size (e.g. how many samples to take), sample selection (e.g. which parts of a site to take samples from), and methods for collecting samples (e.g. what screen size to use, how many bulk samples to take).

2.1.1 Screen Size Effects

Zooarchaeologists have focused much attention on the effects of screen size on faunal recovery (Ascher 1959; Cannon 1999; Casteel 1972; Gobalet 1989; Gordon 1993; Greenwood 1961; Grayson 1984; James 1997; McKechnie 2005; Moss 2007; Nagaoka 2005b; Nagaoka 1994; Partlow 2006; Rootenberg 1964; Shaffer 1992; Shaffer and Sanchez 1994; Sparks 1961; Stahl 1996; Thomas 1969; Vale and Gargett 2002; Zohar and Belmaker 2005). Screen size affects the recovery of small-bodied taxa, and various skeletal elements (Butler 1993; Casteel 1976; Nagaoka 2005b; Payne 1972; Thomas 1969). Screen size has been proven to affect the recovery of small mammals (Shaffer and Sanchez 1994; Stahl 1996; Thomas 1969), birds (Kirch et al. 1992; Stahl 1996; Steadman

1995; Steadman and Rolett 1996), reptiles, and amphibians (Stahl 1996). This issue has been most intensively studied in regards to fish recovery (Butler 1993; Casteel 1976; Gordon 1993; James 1997; Nagaoka 1994; Partlow 2006; Vale and Gargett 2002; Zohar and Belmaker 2005).

The examination of fish representation in sites in coastal Alaska and British Columbia shows small mesh size of 1/8 in. or even smaller is essential for the recovery of small-bodied taxa, such as herring (*Clupea pallasii*), which are often not recovered at all in larger mesh screens (McKechnie 2007; McMillan and St. Claire 2005; McMillan et al. 2008; McMillan and St. Claire 2012; Moss 2007, 2012). The degree of recovery of other small-bodied fish taxa such as small suckers, minnows, and eulachon also increases with the use of finer mesh screens (Butler 1996; Butler 2004; Butler and Delacorte 2004; Casteel 1976; McKechnie and Moss 2016; Partlow 2006; Rosenberg 2015).

Fine mesh screens provide important information on relatively small objects, but because more matrix is retained when using smaller mesh, both excavation and times increase. Studies of screen size in archaeology show that using 1/8 in. mesh or finer can more than quadruple the number of bones recovered and in some cases can even increase counts 10-20 times (James 1997; Thomas 1969). For example, fish remains from 18 bulk samples at the Cathlapotle site increased from a count of 184 bones to 1645 bones with the addition of samples from the 1/8 in. fraction, an increase of almost 10 times what was provided by the 1/4 in. fraction alone (Table 1). Fish remains from Meier, Burton Acres, and Duwamish show similar patterns (Table 1). This increase in quantity causes an increase in time spent on identification when analyzing material from fine mesh screens (Gordon 1993; Nagaoka 2005b). Smaller specimens also tend to lack distinguishing

landmarks, which further increases time and energy spent on identification (Gordon 1993; Nagaoka 2005b). Because less matrix is retained and more identifiable landmarks are retained on larger boney specimens, large mesh samples take less time to study, so that one may sample a wider variety of contexts. However, the information about smaller objects is lost, as these objects fall through large mesh screens and are not retained for study. With a finite amount of time, focusing resources on fine mesh samples makes it difficult to study wide spatial or temporal contexts. One solution to the increased effort is to decrease the number or volume of samples analyzed. When volume is limited, as is often the chosen compromise, our understanding of spatial and temporal variation in fish also becomes limited (Moss 2007).

Table 1. NWC example projects highlighting fish remains recovered from column and bulk samples that illustrate the effect of mesh size on fishbone recovery. Number of identified specimens (NISP; number of identified specimens assigned to a taxon finer than class) from 1/ 4 in. and 1/8 in. screens.

Site Name	> 1/4" NISP	>1/8 in. NISP	Citation
Meier 35CO5	82	739	Frederick 2007
Cathlapotle 45CL1	184	1645	Rosenberg 2015
Burton Acres 45KI437	423	7798	Kopperl and Butler 2002
Duwamish 45KI23	403	3999	Butler 1986

As noted above, remains of small-bodied taxa, less than 100 to 200 mm in total length when living, dominate fine mesh samples. Conversely remains of large-bodied taxa, greater than 200 mm in total length when living, are typically rare and uncommon. This is clearly illustrated by comparing representation of small fish, such as herring and

large-bodied fish such as Pacific cod (*Gadus microcephalus*) and greenling (Hexagrammidae) from 10 liter buckets screened using 1/8 in. nested screens from the Číxwicən site (Table 2) (Butler, personal communication). For each of these buckets the quantity of herring vastly outnumbers that of Pacific cod and greenling combined (Table 2) (Butler, personal communication). This example shows that in order to acquire large quantities of remains from large-bodied taxa, large volumes of sediment may need to be sampled.

Table 2. Frequency (NISP) of select large and small-bodied taxa from four 10 liter buckets screened using 1/8 in. nested screens at the Číxwicən site (Butler, personal communication).

Family	Bag Number			
	8205	9448	9572	10706
herring	14	1268	60	208
Pacific cod	0	5	5	5
greenling	1	2	0	2
Total	15	1275	65	215

To acquire the benefits of both screen sizes, Frederick (2012) and McKechnie (2012) used a combination of 1/4 in. samples and column samples screened with 2 mm mesh from Huu7ii, southern Vancouver Island, to capture both spatial representation of fish and representation of smaller taxa (McMillan and St. Claire 2012). Including larger screen sizes allowed them to sample more contexts, while including finer mesh examples from column samples allowed examination of the full range of species preserved at the site (see also Rosenberg 2015).

2.1.2 Statistical Sampling

Statistical sampling methods do not solve the dilemma of screen size trade-offs but they do provide an empirical way to maximize the amount of information obtained,

no matter the screening method chosen, with the least amount of effort. This thesis focuses on probabilistic sampling methods, with the goal of understanding the relationship between samples and the target population of interest, using probability theory. All statistical methods for sampling assume some level of homogeneity within a sample population to reduce error (Cochran 1977a; Neyman 1934). This means that in order for statistical methods to be effective, larger samples that do not have a unifying characteristic are better divided into smaller, more homogenous groups or dealt with as stratified samples (Cochran 1977b; Krishnaiah and Rao 1988; Neyman 1934). Determining which type of statistical sampling to use depends on the researcher's questions and goals. Two probabilistic sampling methods often used during the laboratory phase of archaeological research on discrete objects (e.g. faunal remains or modified objects) are rarefaction and STR (Grayson 1984; Lyman 2008; Orton 2000).

2.1.2.1 Rarefaction

Rarefaction is the process of establishing redundancy for the maximum number of taxa, also referred to as NTaxa or richness, represented in a population (Grayson 1984; Leonard 1987; Lyman 2008; Sanders 1968; Tipper 1979). This method has been used by ecologists (Colwell and Coddington 1994; Colwell et al. 2004; Gotelli and Colwell 2001; Wolda 1981) and paleobiologists (Alroy 2000; Barnosky et al. 2005; Bush et al. 2004; Miller and Foote 1996) as well as zooarchaeologists (Grayson 1989, 1991; Kirch et al. 1987; Leonard 1989a, 1989b; McKechnie 2013; Meltzer et al. 1992; Simek and Snyder 1988).

This type of statistical sampling is predominantly used by researchers *post-hoc* to examine the point at which one might have stopped in order to reach the greatest

taxonomic richness (Byrd 1997; Lyman and Ames 2004, 2007; McCartney and Glass 1990; Styles 1981). The greatest taxonomic richness found using rarefaction *post-hoc* has been used to verify whether differences in the NTaxa between multiple samples is a factor of sampling strategy, or a factor of true differences in the samples (Lyman 2008). Several statistical packages can be used to calculate rarefaction (Kintigh 1984; Holland 2005), but none are designed to be used as a predictive method that would specify when continuing to adding samples no longer adds taxa (Koch 1987; Lyman 2008). A number of researchers have argued against using rarefaction to predict when to stop adding samples, given the number of required assumptions (Grayson 1989; Lyman 2008), which include those about assemblage size, assemblage diversity, and the relationship between assemblage size and diversity.

Rarefaction used at the Meier site of the lower Columbia River determined whether enough mammalian fauna had been collected during excavations to represent the full range of mammalian taxa present. After four excavation seasons and 4080 specimens, additional taxa were not identified (Lyman and Ames 2004, 2007; Lyman 2008) (Figure 2). In addition, there were more taxa added between the first and second year, than between the third and fourth year where only two additional taxa were added (Figure 2). This example shows a search for rare taxa requires a large sampling effort (that would generate a large volume of matrix and a high NISP).

Figure 2. Cumulative richness of mammalian genera across cumulative annual samples (NISP) from the Meier site. Number adjacent to plotted points are cumulative NISP (Lyman and Ames 2007; Lyman 2008).

2.1.2.2 Sampling to Redundancy (STR)

Other research questions seek to establish redundancy for the proportional representation of taxa (Van der Veen and Fieller 1982). “Sampling to redundancy” (STR) estimates the changing proportions of taxa as subsamples are added to the sample of identified specimens. Redundancy is reached when taxonomic proportions stop changing with additional samples. These methods, as with binary redundancy for NTaxa, divide samples by context before identifying a subsample, but as stated above, the focus is on reaching a proportional representation rather than reaching the maximum richness of the population. STR as described by Van der Veen and Fieller (1982) and Cochran (1977a)

addresses the issues associated with capturing variability in spatial and temporal contexts and empirically defines the stopping point for sampling. STR provides the opportunity to understand population characteristics of the maximum number of stratigraphic and spatial contexts, with the minimum amount of material analyzed.

STR is used extensively by paleobotanists worldwide (Church et al. 2007; Hosch and Zibulski 2003; Jacomet and Brombacher 2004; Jones and Halstead 1995; Kohler-Schneider and Caneppele 2009; Neumann 1989). Archaeologists sampling plant remains from Holocene sites in Egypt and Sudan used STR to determine the number of charcoal specimens needed in order to reach redundancy for each site included in the study. This information was used to identify differing ecological zones in eastern Africa (Neumann 1989). For large samples consisting of 300 or more charcoal specimens, archaeologists examined 10-30% of the sample and for small samples with less than 300 charcoal specimens, 100% of the sample was examined. The reduced size of individual samples allowed researchers to examine a total of 320 samples from several sites in both ecological zones from Egypt and Sudan, covering a time span of almost 6,000 years (Neumann 1989). STR typically develops a stopping rule for an archaeological context such as a discrete entity (e.g., amphora, hearth, or other feature contents), an archaeological unit (e.g., excavation unit, level, or bulk sample), or an analytic unit (e.g., aggregate of archaeological samples such as time periods).

Despite its ubiquity in paleobotany, STR has rarely been used in zooarchaeology. Faced with extremely large numbers of fish remains from the Lower Columbia, Butler (2005) and Rosenberg (2015) have spearheaded the use of this method. Rosenberg (2015) analyzed 18 10 L bulk samples screened through 1 mm (3/64 in) mesh to estimate the

proportional representation of fish taxa in fine mesh samples from the Cathlapotle site. The number of subsamples analyzed for each bulk sample ranged from 50% - 100% of the total sample depending on the bulk sample, with an average identification of 85% of each bulk sample. While some time was saved using this method, this example shows how the fraction studied and overall sample size can vary depending on the complexity, variability, and absolute sample size of the population being characterized. In contrast, Butler's 2005 study at the St. Johns site identified an average of 51% of the estimated total fish specimens in each bulk sample. The total fish specimens analyzed in each bulk sample ranged from 38% - 63% analyzed at St. Johns.

There are at least two equations that can be used to determine redundancy: stratified STR (Equation 1) (stratification refers to subdivisions within a larger population) and simple random STR (Equation 2) (Cochran 1977b). These equations were developed by Cochran (1977b) to be used as deterministic sampling methods. I am adapting these equations for my thesis to be used as sequential sampling methods (Siegmund 2013). This will allow me to adjust the n in STR based on new information as I continue to sample more fish remains. All previous archaeological applications rely on Equation 2, which I also employ in my study. This method will allow me to treat each sample as an isolated entity, rather than as a sub sample of a larger entity. Doing so will allow me to collect slightly larger sample sizes than if each sample was treated as a sub sample.

When applying this methodology to samples that are stratified instead of homogenous, Cochran proposes the equation below:

Equation 1. Stratified Sampling to Redundancy

$$n_h \cong n \left[\frac{\frac{N_h}{N} \sqrt{P_h Q_h}}{\sum_{h=1}^L \frac{N_h}{N} \sqrt{P_h Q_h}} \right]$$

where:

n_h = the number of required specimens from the total target population (also known as the point of redundancy)

n = the total number of strata in the population

N = the total number of specimens in the entire target population (all strata) represented here as Number of Identified Specimens (NISP)

P_h = the proportion of a taxon in the target population

$Q_h = d/Z_{\alpha}^2$ Where:

d = the required accuracy

Z_{α} = the two-sided α percentage of the normal distribution

N_h = The total number of specimens in a single stratum within the target population represented here as NISP

Stratified STR develops a stopping rule but in this case the stopping rule is developed for all statistical strata together instead of treating each statistical stratum as a separate sample population (Cochran 1946). A statistical stratum is defined as a unified subgroup of a population. Stratified STR has yet to be used in an archaeological context. This method can be used to include samples from multiple contexts in a single calculation, and in so doing almost always results in a smaller variance for the estimated total than if the same calculation was done using a simple random sampling method. This type of STR

would be useful in future archaeological research for sampling large-scale complex sites where the research goal only requires a broad-scale comparison of materials. This method may not provide large enough sample sizes from individual spatial or temporal contexts within a site to analyze a specific spatial or temporal context's characteristics.

In cases where archaeological research questions require analysis of materials using finer contexts, Cochran's simple random method (1977b) may provide more statistically robust sample sizes. The simple random method for STR was first applied in archaeological contexts by Van der Veen and Fieller (1982) for the purposes of estimating proportional representation of seeds.

Equation 2. Simple Random Sampling to Redundancy

$$n = \frac{N}{1 + \frac{N - 1}{P(1 - P)^d / Z_{\alpha}^2}}$$

where :

n = the number of required specimens in the sample (also known as the point of redundancy)

N = the total number of specimens in the target population represented here as Number of Identified Specimens (NISP)

P = the proportion of a taxon in the target population

d = the required accuracy

Z α = the two-sided α percentage of the normal distribution

Researchers have applied various iterations of Equation 2, but the terms used in each iteration are analogous (Cochran 1977a; Cochran 1977b; Van der Veen and Fieller

1982) (Appendix A). STR (Equation 2) is designed to analyze homogenous samples of a multinomial nature using proportions. STR in this form analyzes proportions by dividing a sample into two groups where group one consists of a discrete category (e.g. fish family: Gadidae) and group two consists of all other categories (e.g. remaining fish families: Squalidae + Rajidae + Chimeridae + Embiotocidae + Cottidae + Pleuronectidae, etc.). The discrete category in this case is made up of whichever entity appears in the proportional majority (Cochran 1977b). This type of test is called a two classification test. Two classification tests are often used in statistics to deal with problems involving multinomial distributions, such as the distribution of taxa. These tests simplify multinomial problems by reducing them into binomials.

P in this equation sets the maximum value for group one. By setting P at 0.5, group one cannot exceed 50% of the total population for redundancy to be reached. Setting P at 0.5 creates the largest possible n value by minimizing the value in the denominator. Assuming a normal distribution, changing P to any other value would decrease the NISP required to reach redundancy, thereby creating a less conservative estimate of the proportional representation of group one. The law of large numbers states that $\hat{p}$ will approach P with a probability of 1 where $\hat{p}$ is the sample proportion and P is the population proportion. This law allows one to use P instead of $\hat{p}$ in this equation.

The margin of error is represented by d, set in this case at 0.05, which minimizes marginal error, while also minimizing the risk of a Type 2 error (α) where the actual error would be greater than d. The value of d in this equation is derived from $\frac{\partial}{Z_{\alpha}}$ where ∂ = the population standard deviation. Z_{α} (or t as it is expressed by Cochran) can be explained as

the parameter that sets the level of statistical confidence that our n value will be within the margin of error set by d . Setting Z_{α} at 1.96 sets the confidence at 95%. The function dZ_{α} sets the standard error. By setting d at .05 and Z_{α} at 1.96, the standard error is set at 0.1, which is one standard deviation from the mean P . The result of this is that our majority taxon (group 1) will lie at $50\% \pm 10\%$ or somewhere between 40 and 60% of the total population.

An estimate of N can be calculated using data collected from a randomly selected sample population within the target population. The same law of large numbers that was applied for P can also be applied to this situation. This means that as more samples are added to the estimate of N , the closer the estimate will be to actual N . In this situation one must make an assumption that when redundancy has been reached, the number of samples is large enough to estimate N . For this reason, N should be re-calculated as each additional sample of the target population is added.

2.2 Northwest Coast Villages

The study of complex hunter-gatherers on the Pacific Northwest Coast is important to archaeologists for understanding the lifeways of native people in North America, and understanding how the landscape has been used and modified in the past (Ames and Maschner 1999; Butler and Campbell 2004; Coupland et al. 2009; Matson and Coupland 1994; Matson et al. 1999, 2003; Moss 2011). Archaeologists often focus excavation on large villages to study social complexity (Ames and Maschner 1999; Ames 2006). Questions guiding studies of social complexity include: the role of sedentary villages as a fundamental economic unit, the importance of population growth, and the development of storage. Social complexity is often interpreted as an evolutionary process

where as houses get larger and settlements become more permanent over time, society and culture increases in complexity in other ways as well (Ames and Maschner 1999; Maschner 1991). This framework also leads to discussions about the durability of households over time (Ames and Maschner 1999) and the study of human-environment relationships (Butler and Campbell 2004; Campbell and Butler 2010).

Increases in house size in village sites world-wide are often associated with both an increase in population size, and an increase in degree of sedentism of the group (Ames and Maschner 1999; Boyd and Richerson 1985; Cosmides and Tooby 1987; Durham 1991; Mithen 1990). Both population size and sedentism are essential in the development labor organization on the Northwest Coast (Ames and Maschner 1999; Renouf 1991; Yesner 1981, 1987, 1998). Higher populations and increased resource use can cause resource depression (Butler and Campbell 2004; Broughton 1994, 2002a, Broughton et al. 2007, 2010, 2013; Campbell and Butler 2010; Grayson 2001).

On the Northwest Coast, changes in resource use (both faunal and floral), and increases in sedentism and population size are often associated with resource ownership. Systems of resource ownership create a more built environment where resources can be cultivated and traded (Ames 2006; Ames and Maschner 1999). Studies of developing cultural complexity, population growth, intra and inter-household dynamics use several measures: house size (Ames 1996), organization of sleeping quarters (Coupland et al. 2009), artifact and tool distribution (Ames 1995; Harris 2012; LaSalle 2008), and faunal distribution (Coupland 2006; Huelsbeck 1994; Frederick 2007; Matson et al. 1999, 2003; Moss 1993; Samuels 1994).

Given the importance of animals to models of Northwest coast cultural change, the zooarchaeology of Northwest Coast villages is an important area of study. Studies on Northwest Coast fauna have shown how increased social organization impacts resource use and availability through rules to control resource use, which contributes to long-term sustainable resource use (Butler and Campbell 2004; Campbell and Butler 2010). For example, the variation of faunal use across a household has been used to study resource control at the Cathlapotle site on the lower Columbia River (Rosenberg 2015). This study, and similar studies worldwide, show that faunal remains can be attributed to particular social groups and status, reinforcing social structures (Gumerman 1997; Singer 1987; VanDerwarker 1999).

The household has been an iconic measure for social organization, and resource control on the Northwest Coast (Ames and Maschner 1999). For that reason, it is important to understand the individual size, and estimated number of houses in Northwest Coast villages. Houses documented in the historic period on the Northwest Coast measure between 25 m² and 3,600 m² (Ames and Maschner 1999; 163). Based on their size, 30 to more than 100 individuals occupied houses in this region (Ames and Maschner 1999). Villages were composed of anywhere between 1 and 15 houses, sometimes more (Ames and Maschner 1999). To characterize the lifeways represented within and between these households, ideally researchers should sample multiple contexts within multiple houses.

Investigation into the sampling strategies used by previous researchers has shown that this is rarely the case (Dolan 2015; Gray 2008; Monks 2000). Gray's 2008 thesis focuses on problems with the location, and quantity of excavation units in village sites

and has noted that there are several issues with the comparability and robustness of traditional Northwest Coast village excavation sampling strategies. These issues include: differing sample sizes between sites, an overemphasis on excavation of the largest house in a village site, differing sampling strategies between houses in the same village site, and a lack of transparency when reporting how much material was excavated (such as volume excavated). Gray (2008) and Monks (2000) argue that NWC village sampling strategies often do not provide material that is representative of the range of contexts within and between house features.

Building on Gray's (2008) work and for the purpose of further documenting village site sampling and especially approaches to fish sampling, I synthesized excavation records from 16 village sites from coastal Oregon to Northern British Columbia (Table 3). I recorded information on number of houses sampled, the number of fish remains collected and identified, and the screen size used. Excavated volume was not generally provided. In some cases, such as at Meier and Broken Tops, only one or two houses were identified, and in such cases the small number of houses excavated is justified (Table 3). As well, most of the documented houses (four to five) at Ozette and McNichol Creek were sampled (Table 3). However, as shown in Table 3, most projects tested only one or two houses, while as many as 15 or 20 houses are present. Midden outside the house is often not sampled and when it is, the number of test units is limited. Limiting the number of houses sampled in this way reduces our information about household variation, and waste disposal practices.

I also found that faunal remains are collected using variable recovery methods, from hand picking, to screening using varying mesh sizes (Table 3) reducing

comparability. Many researchers exclusively used 1/4 in. samples, such as at Broken Tops, Kiusta, Ozette, and Paul Mason. Projects which incorporated fine mesh samples, such as Shingle Point, Psacelay, and Dionisio Point, tended to sample fewer contexts. Exceptions to this include Ts'ishaa and Huu7ii where the majority of the site was excavated using 1/4 in. mesh (or metric equivalent) and 1/8 in. and finer samples were collected from carefully selected column samples (Table 3). 1/16 in sampling is rarely included, and when integrated it is generally from column samples or other small volume samples. The ubiquity of 1/4 in. samples across contexts at village sites makes analysis of large-bodied fish easy to characterize. This is not the case for the small-bodied fish which, as noted above, are primarily encountered in finer mesh screens (1/8 in. or finer), and routine collection of fine mesh samples has only occurred in the past twenty years (Butler 2005; McKechnie 2005, 2007, 2012; McKechnie and Moss 2016; Rosenberg 2015).

Relatively limited sampling of large complex Northwest coast village sites is understandable. Excavation is expensive and time consuming. Exploring new and innovative methods for time savings is essential to maximizing the information retrieved from the data rich contexts of Northwest Coast village sites during future excavations.

STR would provide an innovative alternate approach to sampling that would allow material to be sampled from a wider variety of contexts. This statistical method allows researchers to sample large contexts without limiting the volume of material available to something as small as a column sample. Using STR allows the researcher to increase the volume of material represented without examining every specimen present in the samples included.

Table 3. Northwest Coast village sites, corresponding excavation strategies and mesh size used.

Site Name	Fish NISP	Number of Houses Sampled ¹	Number of Houses Identified	Outside Midden Excavated	Screen Size Used	Citation
Meier 35CO5	11,251	1	1	yes	4mm and 2mm mesh	Ames et al 1992; Smith 2006; Smith 2004; Frederick 2007
Ozette 45CA24	24,153	4	5	no	1/2 of units were hand collected ; other 1/2 of units wet-screened through 1/4 in. mesh	Samuels 1994; Huelsbeck 1994
Huu7ii DfSh-7	12,426	1	10	yes	Season 1, 1/8 in. + bulk samples taken from all hearth features. Season 2, 1/4 in. plus one column sample from each unit.	McMillan and St. Claire 2012; Gay Frederick 2012
Scowlitz	present	2	15	yes	1 liter samples saved from house floors for flotation; construction fill screened 100%-25%	Lepofsky et al 2000
Mauer/ Maurer DhRk-8	None noted	1	1	yes	screen size not discussed	LeClaire 1973; Schaepe 2003
Shingle Point DgRv-2	2,933	1	6	no	presence of green urchin and herring suggests 1/8 in. screening, but screening methods not described	Matson et al 1999, Matson 2003

¹ volume excavated provided for Meier, Cathlapotle, Huu7ii, Scowlitz, McNichol Creek, and Richardson Ranch

Dionisio Point DgRv-3	14,382	1	5	no	Screens variably used (Mitchell 1964); 1/8 in. (Grier 2001; Ewonus 2006)	Mitchell 1964; Grier 2001; Ewonus 2006
Paul Mason GdTc-16	230	2	12	yes	6 mm (approximately 1/4 in.)	Coupland 1988
McNichol Creek GcTo-6	9,900	5	15	yes	75% of all material from each layer was dry-screened through 6 mm mesh (approximately 1/4 in.), while the other 25% was water-screened through 3 mm mesh (approximately 1/8 in.)	Coupland 2006; Coupland et al 2010
Psacelay GbTh-4	57	1+	2	yes	75% of all cultural layers was screened through 4 mm (approximately 1/8 in.) mesh and 25% through 2 mm (approximately 1/16 in) mesh. In addition, 100% of material from features was screened through 2 mm mesh.	Martindale 2006, 1997, and 1999
Kiusta Richardson Ranch FjTx-1	1 105	1+ 1	15 3	yes no	5 mm screens (close to 1/4 in.) "screens employed infrequently"	Gessler 1975 Fladmark 1972
Broken Tops 35MU57	606	2	2	no	Flotation and standard excavation and screening methods	Ellis and Fagan 1993; Ellis 2006; Olson 1993

Ginakangeek GbTh-2	10	2	5	no	Layers A and B 25% screened through 1/4 in. mesh, Layer C 50% screened through 1/4 in. mesh, Layer D 25% screened through 1/4 in. mesh, and 25% screened through 1/8 in. mesh; houses were selectively sampled	Martindale 2005
Cathlapotle 45CL1	9,157	2+	6	no	4 mm (approximately 1/8 in.) and some 3 mm mesh (slightly less than 1/8 in.)	Ames et al 1999; Rosenberg 2015
Ts'ishaa DfSi-16 and DfSi-17	45,333	2	unknown	yes	bulk samples screened through 2 mm (approximately 1/16 in) and 1 mm mesh (slightly less than 1/16 in) 1/4 in. mesh except for 2 50x50 cm blocks where 1/8 in. screening was used, and 2 column samples water-screened through 1/16 in mesh; 2 column samples taken from back terrace for fine mesh analysis	McMillan and St. Claire 2005 ²

² All sites listed in Table were excavated using a judgmental sampling methodology except for Kiusta, which was excavated using a stratified random sampling strategy.

2.3 The Číx^wicən Site

The Číx^wicən site has the potential to address the limitations of previous Northwest Coast village site excavations because of its unique and robust sampling strategy, the wide expanse of time that it was occupied, and the multiple house structures present and available within the parameters of the NSF study. This site, located on the Strait of Juan de Fuca in Port Angeles, WA (Figure 1) was excavated in 2004 as part of a Washington State Department of Transportation (WSDOT) undertaking to build parts for the Hood Canal Bridge (Larson 2006; Mapes 2009). Číx^wicən is a traditional village affiliated with the Lower Elwha Klallam Tribe (LEKT). After over 300 human remains were recovered, the project was halted because of tribal concerns and mounting costs of the undertaking (Larson 2006; Mapes 2009). A report summarizing excavation methods and depositional contexts was produced (Larson 2006), but most of the recovered materials were not studied, including the faunal remains, which are currently curated at the Burke Museum, Seattle, Washington. Plans are underway to transfer these and other Číx^wicən collections to the LEKT for curation.

This excavation resulted in 261.4 m³ of material over an area of approximately 528 m² (Figure 3). Site excavations at the large village in 2004 focused on four large areas (Areas A, B, C, and D). Radiocarbon dates from the Číx^wicən site date its occupation starting at 2750 cal. BP (Sterling et al. 2017). Historic records suggest it was used by the Lower Elwha Klallam Tribe until the construction of a paper mill on the property in 1910.

Figure 3. Číx'icən (45CA523) showing location of Areas and excavation units from 2004 project.

Číx^wicən was excavated with exceptionally fine stratigraphic control using methods developed by Stein (1992) and popularized after the mid 1990's West Point excavations (Larson and Lewarch 1995). Units were excavated in natural strata; each stratum was subdivided into 10 cm arbitrary levels. Excavated material was collected using 10 L buckets, and wet-screened using nested mesh starting at 1 inch, moving down in size to 1/2 in with some ending at 1/4 in. mesh and some ending at 1/8 in. mesh. The majority of buckets from each level were screened to 1/4 in. mesh and labeled "S" buckets. From every level in each 1 x 1 m unit, every 20th 10 L bucket (labeled as a "C" bucket) was screened to 1/8 in. mesh. Where fewer than 20 buckets were recovered for a particular provenience, a minimum of one "C" bucket was collected.

During the 2004-2005 lab processing, faunal remains were sorted into broad animal types (bird, fish, mammal, and shell) and remains counted (Larson 2006). The preliminary counts of each animal type recorded during initial lab processing showed enormous quantities of animal remains, including fish. For example, from all areas combined (518.59 m²), 14,742 "S" buckets were retained which generated minimally 283,983 fish remains. A total of 3,302 "C" buckets provided an estimated number of 175,466 fish remains (counts from Larson 2006 catalog retained by the Burke Museum).

In 2012, Drs. Virginia Butler, Sarah Sterling, Sarah Campbell, Mike Etnier, and Kris Bovy obtained a grant from the NSF to analyze a sample of the faunal remains primarily from seven block excavations in Area A and two units from Area B (Figure 3; Figure 4). The NSF study focuses on seven block excavation areas within Area A (Figure 4). Researchers chose to focus on areas A1, A4, and A5 as geoarchaeological work had suggested these areas contained remains of houses. A23, A18, BX1, and BX4 were

selected to sample extramural areas. The study's goals are to examine community responses to seismic events and other environmental change through study of the subsistence strategies at the village site. In order to examine community responses to the environment, it is important to first identify the several types of environmental changes present at the site including both short term change such as seismic events and long term change such as climate and the stabilization of the Ediz Hook Spit (Mohlenhoff and Butler 2016). The knowledge gained from this NSF study will contribute to more general knowledge about coastal climate systems. In addition to the scientific values of this study, there are also values to the Lower Elwha Klallam people.

For various reasons the NSF project initially focused study on "C" buckets. Shell was retained only in the "C" buckets and since a key goal was to study all animal types from the same contexts, only "C" buckets provided such sample units. Also, including "C" buckets ensured recovery of small bones and shells, increasing representation of smaller fauna. The NSF project determined that about half the "C" buckets included in their study were in fact only screened to 1/4 in. Such buckets were labeled as "CX". As noted above, the mammal and bird bone researchers have included "S" buckets screened to 1/4 in. to increase the sample size of mammal and bird bone for study. My project will study the "S" buckets to consider whether adding more volume than the "C" and "CX" buckets affects fish representation.

Figure 4. Map of Čix'wicən showing areas included in NSF project.

As part of the NSF project, Sterling and Campbell created Chronological Zones (CZs) by combining field-defined strata using associated calibrated radiocarbon ages and stratigraphic superposition. CZs are a temporal aggregate of field-defined strata with a range of properties (e.g. variation in faunal abundance, position within a hearth or architectural feature). These CZs, representing units of time, are the basis for chronological comparisons of faunal remains, and subsequently subsistence strategies. The seven chronozones span a period between 1910 AD and 2150 cal BP (Table) (Sterling et al 2017).

Table 4. List of chronozones and date ranges for the Číx^wicən Site

Chronozone	Date Range (cal BP)
CZ 7	300 cal BP- 1910 AD*
CZ 6	550-300
CZ 5	1000-550
CZ 4	1300-1000
CZ 3	1550-1300
CZ 2	1750-1550
CZ 1	2150-1750

*End age based on an historic era papermill on the property.

Chapter 3. Methods and Materials

The Číx^wicən site's large excavated volume of matrix, quantity of faunal remains, and meticulously documented depositional history make it ideal for testing sampling methodologies. My thesis addresses the utility of STR particularly for sampling faunal remains from large village sites. Using STR, this project will try to document the variability of fish family representation across time and space in one part of the Číx^wicən village, while minimizing the time and effort required to do so. This thesis applies STR to "S" (> 1/4 in.) bucket samples from eight units in Area A4 (**Error! Reference source not found.**). Fish representation in the "S" bucket samples will then be compared to the fish remains recovered from the >1/4 in. mesh samples from the "C/CX" buckets, which has already been documented as part of the NSF project.

Because the "C/CX" buckets represent only a fraction of the total zooarchaeological materials sampled from the site, it is possible that the "C/CX" buckets alone may not be adequate for representing large-bodied fish. As previously stated in the background section, the NSF project focused its analysis efforts on the "C/CX" (>1/8 in.) buckets. These buckets represent 18% of the 18,044 buckets of material collected just from Area A at the site. As noted above (Table 2), remains of large-bodied taxa occur in much smaller quantities per "C/CX" bucket.

I chose to use "S" bucket samples for my study to compare representation of fish taxa in the "S" buckets to the representation of fish taxa in "C/CX" bucket samples to test whether fish representation remains consistent with the addition of the "S" bucket fish remains. If the volume studied from the "C/CX" buckets is sufficient to accurately represent large-bodied fish in site matrix, fish representation should not significantly

change with the addition of the “S” bucket fish remains. I anticipate, however, that adding “S” bucket samples may change proportional representation of taxa as it increases the volume of material analyzed. I predict that these effects will be most dramatic in chronozones with low densities and small matrix volume.

I chose Area A4 because this block of units has a long time span, encompasses a house, and has received the most attention in the larger NSF project. Given a key goal of my project is to show the usefulness of STR for sampling NWC house sites, it is important to establish the feasibility of applying the method to a house. I selected “S” buckets from a total of eight 1x1 m excavations units (Figure 5). I reasoned these eight units would provide sufficient faunal remains to meet the two major goals of this project: to illustrate the value of STR and to assess whether the $>1/8$ in mesh samples adequately represented large-bodied fish. I chose “S” buckets explicitly from four units because preliminary catalog counts suggested relatively large sample sizes were present; the units included house floor and outside midden. These units also encompassed occupations from several time periods (Table 5). Four additional units (17-20) were chosen for practical reasons as the faunal remains from those units were already on loan from the Burke Museum. These eight units provide a quantity of material that is feasible for a Master’s thesis project, and provide sufficient material to test the utility of my sampling method. By using fish from A4, which encompasses a house structure, my research may also contribute to understanding of variation in fish deposition and taphonomy within a household (Ewonus 2006; Frederick 2007; Huelsbeck 1994; Rosenberg 2015).

Figure 5. Map of Area A4 showing excavation units chosen for STR study. Dotted line indicates approximate boundary of structure.

Table 5. Characteristics of units selected for analysis

Unit	Characteristics
17	CZ 4, 5 and 6; during house occupation
18	CZ 4, 5 and 6; during house occupation
19	CZ 4, 5 and 6; during house occupation
20	CZ 4, 5 and 6; during house occupation
2	CZ 2, 4, and 7; oldest and youngest deposits in A4
8	CZ 2, 3, 4, and 7; oldest and youngest deposits in A4
25	CZ 3, 4, 5, and 6; large estimated sample size and broad occupation range
31	CZ 3, 4, 5, and 6; large estimated sample size and broad occupation range

Since I would like to characterize fish representation in each CZ and examine variation within and outside an identified house, I established redundancy as proportional representation of fish families for each CZ within an excavation unit. A total of 26 such unit/CZ contexts exist in the eight units in my study (Table 6). My subsamples are the buckets within a given chronological zone and unit, which allows me to study variation in fish representation across space and through time. An alternative sampling strategy could take subsamples from a single bucket to establish redundancy for that bucket. However, fishbone quantities from 1/4 in mesh in a given bucket were insufficient for this.

Table 6. Number of “C/CX” and “S” Buckets by unit/CZ

Unit	Chronozone	Total Number of “C/CX” Buckets	Number of “S” Buckets Analyzed	Total Number of “S” Buckets*
2	CZ 7	5	15	21
	CZ 4	15	15	61
	CZ 2	3	7	9
8	CZ 7	3	17	20
	CZ 4	7	14	33
	CZ 3	1	4	5
	CZ 2	4	14	18
17	CZ 6	4	12	29
	CZ 5	4	7	13
	CZ 4	3	8	8
18	CZ 6	8	14	27
	CZ 5	4	7	7
	CZ 4	2	3	3
19	CZ 6	3	9	23
	CZ 5	2	8	18
	CZ 4	5	10	11
20	CZ 6	5	9	23
	CZ 5	3	7	13
	CZ 4	5	6	10
25	CZ 6	10	6	8
	CZ 5	3	7	13
	CZ 4	3	2	2
31	CZ 6	5	7	9
	CZ 5	5	14	18
	CZ 4	1	1	1
	CZ 3	5	9	14
Grand Total		118	232	419

*The NSF project determined that the mesh size listed for a given faunal sample was sometimes incorrect. For example, fish remains that were supposed to be from 1/4 in. mesh contained much larger specimens that should have been captured in the 1/2 in. mesh, as well as much smaller specimens that should have fallen through to 1/8 in. mesh. I addressed this problem for the “S” buckets fish remains by passing all the remains from a given bucket through nested screens (1/2 in., 1/4 in., 1/8 in.) and re-bagging and labelling the mesh size. For my STR project, I re-screened and analyzed remains from a sample of buckets from each unit/CZ, stopping when I had reached redundancy as described in the text. After this process of re-screening buckets from all the unit/CZs, 19 buckets no longer contained identifiable fish remains in the >1/4 in. mesh; and therefore such buckets could not be included in my study. The bucket counts listed above are

based on the original “S” bucket counts, that were listed as $> 1/4$ in. fish remains before rescreening (Appendix B).

Another decision influencing the rate at which I achieved redundancy is the taxonomic level chosen to calculate proportional representation. The intensity of sampling to reach proportional representation at the species level is much higher than it would be for the family level, simply because there are more categories as Linnaean classification becomes more specific. For example, the order Scorpaeniformes is represented by four families in Číx^wicən deposits (Table 7). Each family is represented by between one and five species. Achieving redundancy at the species level would require considerably higher sampling intensity because faunal counts would be distributed across a larger number of categories (Table 7). I have chosen to use the family taxonomic level because family level identification should provide enough detail to show taxonomic differences across CZs without requiring an excessive sampling effort, in line with my thesis goal. [Note: remains of flatfish represented by two families in the north Pacific, Pleuronectidae and Paralichthyidae, are difficult to distinguish, but can easily be assigned to the order Pleuronectiformes. Thus for flatfish, the taxonomic level applied was actually order, not family.

Table 7. List of taxa represented at Číx^wicən within the order Scorpaeniformes

Order	Family	Species
Scorpaeniformes	Cottidae	<i>Leptocottus armatus</i>
		<i>Myoxocephalus polyacathocephalus</i>
		<i>Enophrys bison</i>
		<i>Hemilepidotus sp.</i>
		<i>Scorpaenichthys marmoratus</i>
	Hexagrammidae	<i>Ophiodon elongatus</i>
		<i>Hexagrammos sp.</i>
	Anoplopomidae	<i>Anoplopoma fimbria</i>
	Scorpaenidae	<i>Sebastes sp.</i>

While family level identifications were used to calculate proportional representation, all specimens were also identified to finest taxon and element following the protocol established for the Číx^wicən project (Butler et al. in preparation). Thus genus and species identifications provide nominal records of fish representation, which can be compared with other fish records from the Číx^wicən site.

Another consideration is specimen quantification. Commonly used quantification methods include: Minimum Number of Individuals (MNI), Minimum Number of Elements (MNE), Minimum Animal Units (MAU) and Number of Identified Specimens (NISP) (Grayson 1984; Lyman 1994). MNI, MNE, and MAU are all derived counts, meaning that there is always some researcher interpretation involved in arriving at the final quantification (Lyman 1994).

My chosen quantification method is NISP, which has been shown to correlate with MNI and MAU (Grayson 1979, 1984). Because I also recorded whether specimens had unique landmarks, it will be possible to calculate MNE for future research if needed. One other quantification method I will use is Number of Specimens (NSP), which includes all remains that can be assigned to fish, including those identified to family, and simply can be assigned to “fish”.

A total of 419 “S” bucket samples (4190 L) with fish remains were collected from the eight units in my study (Table 6). A total of 118 “C/CX” buckets (1180 L) were retained from the same units (Table 6). Thus adding “S” bucket samples will increase the volume of material sampled by a factor of nearly four. Some CZs in units are represented by extremely small numbers of buckets (e.g. Units 18/CZ 3 with three buckets), while others contain much larger numbers of buckets (e.g. Unit 2/CZ 7 with 15 buckets).

The protocol I used to identify specimens is the same as that established by Butler for the larger Číx'wícən project (Butler et al. in preparation). Specimens were identified using the collections housed in the Department of Anthropology at Portland State University with additional comparative specimens from the personal collections of Robert Kopperl (Willamette Cultural Resources Associates) and Ross Smith (University of Oregon). A list of all elements identified for each taxon is listed in Butler et al. (in preparation) (Appendix C). For remains from each bucket selected in my STR study, I initially identified each specimen to family and finest taxon and element, which were then checked and adjusted by Butler. I recorded all my hours spent analyzing fish remains for this project. By calculating the number of hours spent on identification, and comparing that to the percentage of samples analyzed, I have estimated the amount of time saved by using STR when compared with the amount of time spent, had all “S” bucket samples from my project area been analyzed.

To implement STR I followed a series of steps, which began by selecting one of the 26 unit/CZ contexts to sample (Figure 6). The buckets in the selected unit/CZ were then randomly ordered for selection using an online random number generator (Figure 6). I then analyzed the first three buckets listed in the random order sequence (Figure 6).

The counts of specimens which could be identified to at least family level were then used to calculate N (Equation 2) (Figure 6), which represents an estimate of the total NISP if all fish remains were identified. In an iterative process, I began by taking the total NISP of the first three buckets, then dividing that NISP by the number of buckets analyzed, and then multiplying that number by the total number of buckets in a unit/CZ being analyzed (Figure 6).

The estimated N was then inserted into the Van der Veen and Fieller (1982) equation with the constants d, P, and $Z\alpha$ to find out what NISP must be studied to achieve redundancy (Equation 2). For my study I analyzed a minimum of three buckets, which was possible for all but two unit/CZs where only one or two buckets were collected (Table 6). In cases where my initial study of three buckets showed the NISP was insufficient, additional buckets were sorted and analyzed. These additional identifications were then used to recalculate N and re-run STR (Equation 2) (Figure 6) Redundancy was reached when the selected unit/CZs total NISP was greater than or equal to n, also known as the point of redundancy. This process was repeated for each unit/CZ.

Once the analysis was complete, I developed several additional measures to explore how bone distribution and abundance affected STR (the number of samples I needed to study to reach redundancy). I calculated bone density for each unit/CZ by taking the total NSP from a unit/CZ, and dividing it by the total volume in that same unit/CZ. Since each bucket is approximately 10 liters, the volume sampled in a given unit/CZ was easily calculated. For example, in unit 2/CZ 4 the fish NSP is 1543, and the total number of “S” buckets is 15, thus providing a density of $\frac{1543}{150}$ or 10.3. I also calculated an adjusted NISP, which will allow me to directly compare counts for each taxon from the “S” buckets to counts from the “C/CX” buckets from a given unit/CZ or for larger aggregates such as CZ. Such a comparison is important to one my research questions, which is to see if increased sample size from the “S” buckets changed our understanding of fish representation. I calculated the adjusted NISP for each family within each unit/CZ by dividing the observed NISP for a family by the number of buckets analyzed in a unit/CZ, and then multiplying that number by the total number of buckets in

the same unit/CZ. For example, in unit 17/CZ 6, sampling ceased at 12 buckets out of a total 29 buckets available. To find the “adjusted” family NISP, I multiplied each observed family NISP by $\frac{29}{12}$ or 2.41 (Table 8). The observed NISP for ratfish (Chimaeridae) in unit 17/CZ 6 was eight, and, after multiplying that observed count by 2.41, the adjusted NISP for Chimaeridae in unit 17/CZ 6 is 19 (Table 8). Such a process was carried out for each of the 26 unit/CZs.

Table 8. Comparison of NISP between “Observed” vs. “Adjusted” values from unit 17/CZ 6, to illustrate how adjusted values were obtained for all unit/CZs. Sampling ceased at 12 out of 29 buckets, thus the multiplier required to “adjust” for family NISP is 2.41.

Family	Observed NISP	Adjusted NISP
Chimaeridae	8	19
Rajidae	5	12
Squalidae	15	36
Embiotocidae	4	10
Salmonidae	28	68
Gadidae	109	263
Cottidae	57	138
Hexagrammidae	8	19
Pleuronectiformes	25	60
Scorpaenidae	3	7
Total	262	632

Figure 6. Flow chart showing the process for selecting "S" bucket samples and analysis to reach redundancy of proportional representation of fish family, outlined for unit 17, CZ 5

Chapter 4. Results

4.1 Summary of Fish Remains and STR Sampling

A total of 3,646 fish remains were identified to some taxon below “fish” from the “S” buckets (Table 9). A total of 29 taxa, including thirteen families and 22 species are represented (Table 9). The families with the highest abundance are: dogfish (Squalidae), salmon and trout (Salmonidae), cod (Gadidae), and sculpin (Cottidae), which represent 80% of the total NISP. As expected from 1/4 in. mesh, the fish fauna is dominated by large-bodied fish, which is seen in the finest taxa present. Large bodied Pacific cod (*Gadus macrocephalus*) and great sculpin (*Myoxocephalus polyacanthocephalus*) dominate the cod (Gadidae) and sculpin (Cottidae) families respectively. Small-bodied taxa such as Pacific tomcod (*Microgadus proximus*), and staghorn sculpin (*Leptocottus armatus*) are either absent or present in much smaller quantities than large-bodied fishes (Table 9). Unidentifiable fish make up 51% of the total 7,307 Number of Specimens (NSP). The “S” bucket fish remains were identifiable to a taxon below fish at a rate of 49%.

I studied remains from 269 “S” buckets out of a total of 419 buckets, or 47% of the buckets (Table 10). For some unit/CZs only a fraction of the buckets needed to be studied, while for others all the buckets needed to be studied. Translating this to volume, my STR study estimated fish representation for 4190 liters of matrix in A4, though I studied remains from only 2690 liters. The percentage of buckets I analyzed out of the total number of available buckets for each unit/CZ ranged from 22% - 100% (Table 10; Figure 7). 100% of the specimens were analyzed for six of the unit/CZs. STR was most helpful for six other unit/CZs where I analyzed less than 50% of the total buckets and was

moderately helpful for the remaining 14 unit/CZs. This analysis took me a total of 154 hours, and based on the percentage of material analyzed, 174 hours were saved.

Table 9. Frequency (NISP) of fish taxa from “S” buckets

Family	Finest Taxon	NISP
	Elasmobranchii	5
Rajidae	<i>Raja sp.</i>	69
Squalidae	<i>Squalus acanthias</i>	329
Chimaeridae	<i>Hydrolagus colliei</i>	81
Clupeidae	<i>Clupea pallasii</i>	12
Salmonidae	<i>Oncorhynchus sp.</i>	600
Gadidae	Gadidae	873
	<i>Gadus macrocephalus</i>	205
Embiotocidae	Embiotocidae	54
	<i>Damalichthys vacca</i>	1
Anoplopomatidae	<i>Anoplopoma fimbria</i>	1
Scorpaenidae	<i>Sebastes sp.</i>	19
Hexagrammidae	Hexagrammidae	3
	<i>Hexagrammos sp.</i>	59
	<i>Ophiodon elongatus</i>	76
Cottidae	Cottidae	38
	<i>Enophrys bison</i>	182
	<i>Hemilepidotus sp.</i>	146
	<i>Hemilepidotus/Scorpaenichthys</i>	168
	<i>Leptocottus armatus</i>	147
	<i>Myoxocephalus</i>	229
	<i>polyacanthocephalus</i>	
Pleuronectiformes		300
	<i>Citharichthys sp.</i>	8
	Pleuronectidae	32
	<i>Atheresthes stomias</i>	1
	<i>Eopsetta jordani</i>	2
	<i>Hippoglossus stenolepis</i>	4
	<i>Lepidopsetta bilineata</i>	1
	<i>Platichthys stellatus</i>	1
Total NISP		3,646
Unidentified Fish		3,661
Grand Total		7,307

Table 10. Summary information about fish remains and “S” buckets from each unit/CZ

Unit	CZ	Observed NISP Analyzed	Estimated Total NISP (N)	NISP Required to reach Redundancy (n)*	# of Buckets Analyzed **	Total # of Buckets ***	Percent Buckets Analyzed
2	7	83	109	85	16	21	76
	4	336	1206	292	17	61	28
	2	2	2	2	9	9	100
8	7	142	312	173	15	33	45
	4	352	414	200	17	20	85
	3	9	9	9	5	5	100
	2	16	17	16	17	18	94
17	6	234	424	202	16	29	55
	5	224	364	187	8	13	62
	4	39	39	35	8	8	100
18	6	302	582	232	14	27	52
	5	60	60	52	7	7	100
	4	7	7	7	3	3	100
19	6	289	739	253	9	23	39
	5	359	808	261	8	18	44
	4	35	39	35	10	11	91
20	6	288	662	243	10	23	43
	5	258	373	189	9	13	69
	4	17	15	15	11	10	100
25	6	55	55	48	8	8	100
	5	99	117	90	11	13	85
	4	6	6	6	4	4	100
31	6	124	159	113	7	9	78
	5	98	118	90	15	18	83
	4	2	2	2	1	1	100
	3	50	50	44	14	14	100
Total	26	3,646	6,688		269	419	

* calculated from Cochran (1977b)

**These bucket counts reflect the number of buckets with fish remains from >1/4 in. screens before re-screening. This means that even those buckets that did not retain > 1/4 in. fish remains are included. (Appendix B)

***These bucket counts reflect the original number of “S” buckets as listed in the Burke catalog, prior to re-screening. See Table 6 and Appendix B for further information.

Figure 7. Percent NISP analyzed by unit/CZ, “S” buckets.

Fishbone density in the “S” buckets varies greatly across unit/CZs, from a low of 0.2 to a high of 10.3 (Table 11). The average unit/CZ density of fish remains for the “S” buckets is 3.04. Densities tend to be lowest in CZ 2, and 3, under 1.0, much lower than the average (Figure 8). CZ 4 is the most variable with densities ranging from 0.2 to 10.3. Densities in CZs 5, 6, and 7 range from 1.4 to 9.6 (Figure 8).

CZs with limited representation across the eight excavation units tended to have low bone frequency (Figure 8). For example, CZ 2, 3, and 7 were only present in two or three excavation units and in all cases density is 3.0 or lower. On the other hand, CZs 4, 5, and 6 were distributed across all eight units, and bone density showed high and low values.

There is a strong inverse relationship between the percentage of buckets analyzed and bone density (NSP/liter) across unit/CZs: the lower a unit/CZ’s density, the more

buckets were analyzed (Figure 9; $R = 0.812$ $p\text{-value} = < 0.0001$). For example, unit 17/CZ 5 has a mid-range density of 4.8 and 62% of the buckets were sampled, while unit 25/CZ 4 had a low density of 0.2 and 100% of the sample was analyzed (Figure 9). One major exception to this pattern is unit 20/CZ 5, where 69% of the buckets were studied despite having a bone density of 6.8.

The relationship between the estimated total NISP and the percent of buckets analyzed in a unit/CZ (Figure 10) mirrors that of density (NISP/liter) and percent of buckets analyzed (Figure 9). As NISP in a unit/CZ increases, the percent of buckets in the same unit/CZ decreases (**Error! Reference source not found.**; $R = 0.915$, $p\text{-value} = < 0.0001$). For example, in unit 19/CZ 5 there is an estimated total NISP of 898 and I analyzed 44% of the buckets. Conversely, in unit 18/CZ 4 there is an estimated total NISP of 7 and I analyzed 100% of the buckets. One outlier to the trend is unit 4/CZ 4. With an estimated total NISP of 868, I should have had to study less than 50% of buckets, whereas I actually studied 85% of the total buckets.

The relationships between density or NISP and percentage of buckets analyzed do not follow a perfect linear trend because of heterogeneity in the CZs, which are aggregates of various deposit types, such as those dominated by shell, sand, or architectural components such as posts. Bone distribution and abundance is not uniform across such deposits. Therefore, one should not expect STR to conform directly to bone density, or absolute bone frequencies.

Table 11. Comparison of fishbone density (NSP/liter) between “S” and “C/CX” buckets. Values listed for “S” buckets represent those remains directly “observed” and tallied rather than those whose values were adjusted to account for variable volume of matrix studied in a given unit/CZ (see Table 8).

Unit	CZ	“S” Buckets (only analyzed buckets)			“C/CX” Buckets (> 1/4 in. only)		
		NSP	N of Buckets	NSP/Liter	NSP	N of Buckets	NSP/Liter
2	CZ 7	193	16	2.7	31	5	0.6
	CZ 4	854	17	10.3	371	15	2.0
	CZ 2	39	9	1.0	3	3	0.1
8	CZ 7	356	15	2.1	53	3	1.8
	CZ 4	721	17	5.2	240	7	3.3
	CZ 3	13	5	0.3	0	1	0.0
	CZ 2	48	17	0.3	4	4	0.1
17	CZ 6	474	16	4.0	192	4	4.8
	CZ 5	387	8	5.5	170	4	4.3
	CZ 4	73	8	0.9	14	3	0.5
18	CZ 6	586	14	4.2	266	8	3.3
	CZ 5	110	7	1.6	134	4	2.9
	CZ 4	8	3	0.3	1	2	0.1
19	CZ 6	512	9	5.7	158	3	5.3
	CZ 5	767	8	9.6	102	2	5.0
	CZ 4	83	10	0.8	44	5	0.9
20	CZ 6	589	10	6.5	119	5	2.4
	CZ 5	614	9	8.8	138	3	4.6
	CZ 4	14	10	0.2	24	5	0.5
25	CZ 6	93	8	1.6	205	10	2.1
	CZ 5	253	11	3.6	93	3	3.1
	CZ 4	8	4	0.4	1	3	0.0
31	CZ 6	245	7	3.5	133	5	2.7
	CZ 5	193	15	1.4	42	5	0.8
	CZ 4	2	1	0.2	0	1	0.0
	CZ 3	104	14	1.2	20	5	0.4
Total		7295	269		2480	121

Figure 8. Scatterplot showing relationship between "S" bucket Density (NSP/liter) and chronozone for unit/CZs.

Figure 9. Scatterplot showing the relationship between density (NSP/Liter) and percentage of buckets analyzed for each unit/CZ.

Figure 10. Scatterplot showing the relationship between the estimated total NISP of fish remains and the percent of buckets analyzed in a given unit/CZ.

4.2: “C/CX” vs. “S” Bucket Comparison

As previously stated, the “C/CX” buckets make up a small portion of the available material from the site as a whole. This is also true for my study samples. In the 26 unit/CZs that I included, I analyzed 269 buckets (2690 liters) of “S” (>1/4 in.) buckets, which represent 419 buckets (4190 liters) of matrix (Table 10). The “C/CX” buckets from the same unit/CZs make up 121 buckets (1210 liters), or 22% of the combined “C/CX” + “S” buckets from the 26 unit/CZs (Table 11).

Because large-bodied fish make up a small proportion of the fish remains collected from the “C/CX” buckets in particular, the 22% sample the “C/CX” buckets represent may not be adequate to represent large-bodied fish. To test whether the “C/CX” buckets are adequate for representing large-bodied fish, I have compared the NISP for fishes from “C/CX” buckets to fish representation with “S” bucket fish remains added. If “C/CX” buckets have adequately represented fish families, then fish family representation for “C/CX” vs. “C/CX” + “S” buckets should be similar. For this comparison, I used the adjusted NISP values for “S” buckets, which were calculated for each unit/CZ (see Table 8). The adjusted “S” bucket NISP (8062) make up 83% percent of the combined total (9815) (Table 12). This is largely because the “S” buckets represent a much larger volume of material.

Table 12. Comparison of fish representation (%NISP) between “S”, “C/CX”, and “C/CX” + “S” buckets from study units.

Family	“S” Buckets		“C/CX” Buckets		“C/CX” + “S” Buckets	
	Adjusted NISP	%	NISP	%	NISP	%
Rajidae	147	2.02	144	2.07	291	2.05
Squalidae	666	8.17	722	10.40	1388	9.78
Chimaeridae	166	2.29	165	2.38	331	2.33
Clupeidae	22	0.30	95	1.37	117	0.82
Salmonidae	1356	16.68	958	13.80	2314	16.30
Gadidae	2471	31.03	2323	33.47	4794	33.76
Merluccidae	0	0.00	2	0.03	2	0.01
Embiotocidae	95	1.31	78	1.12	173	1.22
Anoplopomatidae	3	0.03	9	0.13	12	0.08
Scorpaenidae	42	0.57	90	0.01	132	0.93
Hexagrammidae	349	3.80	406	5.85	755	5.31
Cottidae	1836	24.29	1793	25.84	3629	25.56
Pleuronectiformes	780	9.51	847	11.10	1591	11.21
Total	8062	100	1753	100	9815	100

As shown in Figure, for the unit/CZs as a whole, adding the “S” buckets does not affect the proportional representation of fish families. The Spearman’s rank order correlation for this relationship is high and significant ($R_s = .990$, $P\text{-value} = <0.001$), which suggests that for the study as a whole, the “C/CX” buckets were sufficient to characterize fish family representation.

Figure 11. Proportional representation of fish families (% NISP) from “C/CX” buckets (> 1/ 4 in only) as compared with proportional representation of fish families from “C/CX” + “S” buckets.

A closer look at family representation within each CZ shows that the rank order correlation between “C/CX” and “C/CX” + “S” buckets are significant, but the strength of the relationship varies between $R_s = 0.982$ (CZ 4) and $R_s = 0.728$ (CZ 3) (Table 13). The shifts in CZ 3 rank order are greatest, where Salmonidae is ranked 6th when the “S” buckets are added, but the same family is ranked 2nd for the “C/CX” buckets alone. Overall, however, the “C/CX” bucket samples provided good estimates of fish family rank order abundance.

Moving beyond rank order representation, fish family richness in two CZs is affected by adding the “S” buckets. As discussed in Chapter 2, richness is simply the number of taxa, in this case families, present. The “S” buckets added three families in CZ 7 and four families in CZ 2 (Table 14). These patterns are related to small sample size, as

CZ 2 and CZ 7 have the smallest samples among the CZs; much previous zooarchaeological research shows a high correlation between richness and sample size (Lyman 2008). While the taxa added from the “S” buckets in these few instances illustrate that CZs with small sample sizes are insufficient for characterizing fish family richness, the eight units included in my study represent only 20% of the units in A4, in which the “C/CX” bucket fish remains were studied. This additional volume from the remaining units in A4 and elsewhere in the site will document richness for those CZs. It is also important to note that the purpose of STR as used in my study was not to cease sampling when all taxa were added, but rather when proportional representation of families stabilized.

Table 13. Comparison of fish family rank order between “C/CX” and “C/CX”+”S” Buckets by CZ using Spearman’s Rho Correlation

CZ	P- Value	Rs	Family	“C/CX” + “S” NISP	“C/CX”+ “S” Rank	“C/CX” NISP	“C/CX” Rank
CZ 7	<.001	0.909	Gadidae	228	1	13	1
			Cottidae	100	2	8	2
			Squalidae	85	3	4	4
			Salmonidae	65	4	5	3
			Pleuronectiformes	38	5.5	3	7
			Hexagrammidae	35	5.5	3	7
			Chimaeridae	24	7	4	5
			Scorpaenidae	14	8	0	10
			Embiotocidae	9	9.5	3	7
			Rajidae	9	9.5	0	10
			Clupeidae	1	11	0	10
CZ 6	<.001	0.954	Cottidae	985	1	196	1
			Gadidae	899	2	152	2
			Salmonidae	378	3	55	4
			Pleuronectiformes	356	4	81	3

			Squalidae	222	5	28	5
			Chimaeridae	109	6.5	18	6.5
			Hexagrammidae	96	6.5	18	6.5
			Embiotocidae	51	8.5	5	10
			Rajidae	49	8.5	8	10
			Clupeidae	27	10.5	14	8
			Scorpaenidae	21	10.5	3	10
			Anoplopomatidae	1	12	1	12
CZ 5	<.001	0.948	Cottidae	678	1	101	2
			Gadidae	633	2	164	1
			Salmonidae	418	3	64	3.5
			Squalidae	275	4.5	45	5
			Pleuronectiformes	267	4.5	62	3.5
			Chimaeridae	34	7.5	6	7
			Embiotocidae	34	7.5	3	7
			Hexagrammidae	30	7.5	6	7
			Rajidae	19	7.5	1	10.5
			Clupeidae	9	11	1	10.5
			Anoplopomatidae	4	11	1	10.5
			Scorpaenidae	3	11	2	10.5
CZ 4	<.001	0.982	Gadidae	1140	1	117	1
			Salmonidae	636	2	47	3
			Cottidae	422	3	59	2
			Pleuronectiformes	257	4	39	4
			Hexagrammidae	224	5	25	5
			Squalidae	158	6	11	6
			Rajidae	81	7	6	7.5
			Chimaeridae	31	8	7	7.5
			Embiotocidae	13	10	1	11
			Scorpaenidae	11	10	3	9.5
			Clupeidae	2	10	2	9.5
CZ 3	0.04	0.728	Gadidae	43	1	34	1
			Hexagrammidae	19	2	11	3
			Squalidae	11	3	7	4.5
			Rajidae	10	4	7	4.5

			Pleuronectiformes	9	6	4	6
			Cottidae	9	6	1	7.5
			Salmonidae	37	6	14	2
			Clupeidae	1	8	1	7.5
CZ 2	0.006	0.863	Gadidae	9	2	1	3
			Cottidae	9	2	1	3
			Pleuronectiformes	8	2	2	1
			Salmonidae	5	4.5	1	3
			Hexagrammidae	5	4.5	0	6.5
			Chimaeridae	2	7	0	6.5
			Squalidae	2	7	0	6.5
			Rajidae	1	7	0	6.5

Table 14. Comparison of family richness in "C/CX" vs. "C/CX" + "S" Buckets

CZ	“C/CX” Buckets		“C/CX” + “S” Buckets	
	NISP	N of Families	NISP	N of Families
CZ 7	43	8	609	11
CZ 6	579	12	3194	12
CZ 5	456	12	2404	12
CZ 4	317	11	2976	11
CZ 3	79	8	139	8
CZ 2	5	4	42	8

4.2.1 How does adding the “S” buckets affect interpretation of earthquake impacts?

One of the major goals of the NSF project is to examine ways environmental change affected animals and in turn humans. To do this, researchers will be examining faunal representation before and after several major earthquake events. One of these events is Event “U”, dated to between 1260 and 1230 cal BP (Atwater et al 2004), which falls approximately at the beginning of CZ 4. Earthquake events often result in subsidence and liquefaction, directly impacting sea floors and intertidal landscapes. As a result, kelp beds are likely to be negatively affected by the earthquake events at Číx^wicən, such as event U, also documented in the sedimentation at the site. It is likely that kelp dependent taxa, such as Hexagrammidae (greenling), will also be negatively affected by earthquake events at Číx^wicən, and their representation should decrease after the event. On the other hand, migratory fishes, such as fish in the family Squalidae (dogfish), are less likely to be affected by environmental shifts that negatively affect kelp.

To examine whether adding the “S” buckets affect interpretations of fish use and representation at Číx^wicən, I examined the impact earthquake event U might have on

hexagrammid use at the site. I created the Hexagrammid Index

$$\left(\frac{\text{Hexagrammidae NISP}}{\text{Hexagrammidae NISP} + \text{Squalidae NISP}} \right)$$
 for each CZ based on fish records from the “C/CX”

buckets and the “S” buckets from the eight study units. As the index approaches 1.0, NISP of hexagrammid increases, which would suggest kelp beds are not affected. While several researchers have created such indices (Broughton 2002b; Butler 2000; Hildebrandt and Jones 1991), as a ratio, changes in the value could reflect change in the target taxon (in this case greenling), or change in the secondary taxa (here, dogfish). For example, an increase in value could indicate that dogfish are declining, rather than that greenling are increasing. The inverse is also true. Given the relative nature of this measure, one should seek independent evidence for environmental impacts. I use the Hexagrammid Index here more to evaluate sampling issues, and only secondarily to evaluate earthquake impacts.

For CZs 4, 5, 6, and 7, the indices created for the two samples are extremely similar (Figure 12). In both cases the index declines after CZ 4 and increases continually after CZ 5 (Figure 12). On the other hand, the index for CZ 2 and to a lesser extent for CZ 3 diverge, which is likely due to extremely small sample sizes (Figure 12).

Importantly, the Hexagrammid Index declines after event U, which is consistent with my predictions of the earthquake impact (Figure 12). This is true both for the “C/CX” buckets alone, and when the “S” buckets are added. As noted, given the limitations with the index, more work is needed to confirm this finding.

Figure 12. Hexagrammid Index for "C/CX" buckets and "C/CX" + "S" buckets.

4.2.2 How does adding "S" buckets affect interpretation of fishbone densities and deposition in and outside the house?

Researchers studying NWC archaeology have long noted differences in the way fauna are distributed across village contexts (Frederick 2007; Matson 2003; McMillan and St. Claire 2005, 2012; Samuels 1994; Rosenberg 2015). These differences represent differential resource access, and disposal patterns. Here, I focus on disposal patterns by examining changes in faunal frequency and taphonomy.

I included excavation units both inside and outside the house structure in A4, allowing me to explore the spatial patterns in fish representation. This will also allow me to assess whether adding the "S" buckets to the "C/CX" buckets affected fish representation across space. The Číx'wícən house occupation in Area A4 spans CZs 4, 5,

and 6. For my study, I focus on fish remains from the earliest period of house occupation, CZ 4, which represents an occupation from 1300-1000 cal BP. I split the fish remains into excavation units inside the house (units 17, 18, 19, 20, 25, and 31) and excavation units outside the house (units 2 and 8) in CZ 4. To assess whether fish remains are treated differently inside versus outside the house, I will measure both fragmentation and density of fish remains.

The extent to which waste from fish processing or consumption is disposed of inside versus outside houses has been little studied. Researchers have studied within house patterning of faunal remains to explore questions of prestige or resource control (Ewonus 2006; Frederick 2012; Rosenberg 2015), but whether more or less disposal takes place inside or outside a house is not known. Therefore, my comparison is exploratory. My goal is simply to assess whether the abundance estimates of fish remains inside and outside the house varies between the two samples, “S” vs. “C/CX” + “S”.

As seen in Table 15, units outside the house have orders of magnitude more fishbone than interim units. Some of this difference is related to volume excavated (Table 15). Density (NSP/liter) is also higher outside the house than inside (Table 15, Figure 13). Densities in units 2 and 8, outside the house, are above 1.5 fish remains per liter (Figure 13). For example, densities in units 2 and 8, outside the house, are above 1.5 fish remains per liter (Figure 13). Both the “C/CX” buckets alone and the “C/CX” + “S” buckets show this trend, suggesting that added volume did not change interpretations of fish distribution. However, the difference in density for outside units after “S” buckets were added is considerable. This pattern will be further studied in the larger fishbone project.

Table 15. Frequency and Density (NSP/liter) of fishbones in CZ 4, within and outside the house boundary

	Unit	"C/CX" Buckets				"C/CX" + "S" Buckets			
		NISP	NSP	Volume (liters)	Density (NSP/ liter)	NISP	NSP	Volume (liters)	Density (NSP/ liter)
Outside the House	2	128	305	170	1.79	1503	3369	760	4.43
	8	110	233	170	1.37	1100	1081	270	4.0
Total		238	538	340	1.58	2603	4450	1030	4.32
Inside the House	17	8	14	80	0.47	47	87	110	0.15
	18	1	1	30	0.05	8	9	50	0.05
	19	12	44	100	0.88	51	135	160	0.15
	20	13	24	100	0.48	20	37	150	0.06
	25	0	1	40	0.03	4	6	70	0.02
	31	0	0	10	0.00	2	2	20	0.10
Total		34	84	360	0.23	132	276	560	0.49

Figure 13. Comparison of fishbone density (NSP/liter) inside and outside the house from CZ 4, based on "C/CX" buckets vs. "C/CX+S" buckets.

I anticipate that fragmentation will be higher inside the house than outside the house, as fish remains are more likely to be trampled where there is more foot traffic. To measure fragmentation, I am using a ratio of NISP/NSP, which has been used for such purpose previously (Grayson 1991; Mohlenhoff and Butler 2016; Nagaoka 2005a). This measure is based on the reasoning that specimens which can be assigned to family and element are less fragmented than specimens which cannot be assigned to family and element. In this way, the higher the ratio, the lower the fragmentation. As Figure 14 shows, fragmentation is slightly lower inside the house vs. outside, which is contrary to my expectation. One possible explanation for this is that most of the remains are being disposed of outside the house where they cannot be trampled. This hypothesis is supported by the higher densities of fish remains, higher NISPs, and higher volumes of

material from units outside the house (Table 16). These conclusions do not change with the addition of the “S” buckets, thus the “C/CX” buckets were sufficient to document this patterning (Figure 14).

Figure 14. Fragmentation (NISP/NSP) of fish remains inside and outside the household in A4 CZ 4 comparing “C/CX” vs. “C/CX”+ “S” Buckets.

Chapter 5. Discussion

Most previous research on the sampling of archaeological fish remains has emphasized the use of fine mesh screens to adequately document small-bodied fish. This focus often means that less matrix is actually studied, limiting the spatial and temporal contexts examined. This has two main consequences: less matrix studied means that we may not be characterizing abundance of larger-bodied fish adequately, given their remains are relatively rare in fine mesh samples. As well, we may not be sampling the range of deposits critical to questions of resource use in Northwest Coast households. STR provides a general way to study larger volumes of matrix to the point at which any additional analysis would be redundant.

My project had several goals. My first goal was to show the value of STR, through the analysis of fish remains from Číx^wicən. I anticipated that STR would provide substantial time savings, and it did. I saved more than 100 hours of time on analysis over the course of this study by using STR, there was a substantial increase to the overall NISP for the unit/CZs included, and all of this was achieved without sacrificing accuracy of fish family proportional representation for each unit/CZ. Not surprisingly, the greatest time savings came from unit/CZs with higher densities and NISPs where I was able to analyze a lower percentage of buckets. Other unit/CZs with lower densities and NISPs provided less time savings, as I was required to analyze a larger percentage of buckets.

My second goal was determining whether adding additional volume, the “S” buckets, changed our understanding of fish representation based on “C/CX” buckets alone. Analyzing the “S” buckets allowed me to investigate whether the “C/CX” buckets were adequate for representing large-bodied, but rarer fish families. By focusing on the

“C/CX” buckets, the NSF researchers analyzing the Číx^wicən site have chosen to limit the volume of matrix studied, much like many others with a few notable differences, in order to document small-bodied fish, such as herring. As the “S” bucket fish remains I analyzed using STR represented over four times the volume of the “C/CX” buckets, I anticipated that this addition might alter our picture of large-bodied fish representation. I have shown that, with the exception of low density, low NISP unit/CZs (especially in the oldest CZ 2 and CZ 3) the “C/CX” buckets are sufficient to represent fish at the site. The oldest CZs 2 and 3 had fewer bones and less matrix, however a test of the Spearman’s rank order was still relatively high. I have demonstrated that the “C/CX” buckets are sufficient both for my sample overall, but also for CZs 4, 5, 6, and 7.

This case study demonstrates how STR can be used at the beginning of analysis to minimize effort towards characterizing an assemblage (in this case “S” bucket fish remains, recovered from 1/ 4 in.) and to identify locales (in this case CZs) that could benefit from increased sampling. In the case of the Číx^wicən site, the larger NSF project has already analyzed material from all of the “C/CX” buckets available in A4, and in several other locales at the site.

I found the “C/CX” buckets to be adequate for addressing more specific research questions as well. To tie my research in with the NSF research and examine fish representation over time, I examined the representation of an individual taxon, in this case Hexagrammidae relative to dogfish, in response to an environmental event (Event U earthquake). My interpretations of the hexagrammid’s response to the Event U earthquake, did not change with the addition of the “S” buckets. My interpretations held despite some minor differences in the Hexagrammid Index between the “C/CX” buckets

alone and the “C/CX” and “S” buckets combined. In addition to demonstrating that the “C/CX” buckets are sufficient for assessing a particular taxon’s trends over time, I also affirmed my hypothesis on the effect of the earthquake event U on the Hexagrammid Index. The index declined after event U, consistent with the prediction that event U negatively affect Hexagrammidae at Čix^wicən. This trend will be further studied using additional samples from Čix^wicən, based on fish as well as other faunal resources.

An examination of trends in fishbone representation and fragmentation within and outside a house, also shows that the “C/CX” buckets were adequate, that adding additional volume from the “S” buckets did not affect trends. I measured density (NSP/liter) and fragmentation (NISP/NSP) of fishbone during the CZ 4 house occupation in A4, between 1300 and 1000 cal BP. Density and absolutely abundance of fishbone is higher outside the house than inside, suggesting differences in disposal patterns. While I expected that bone fragmentation would be higher inside the house than outside, the differences were minor. More important than specific spatial patterns in density and fragmentation is whether the addition of “S” buckets affected my interpretation. Overall, adding the “S” buckets did not affect the main trends.

5.2 The Influence of Sample Selection on STR

There are more ways to use STR than I have explored here. The rate at which one reaches redundancy using STR is influenced by the methods one chooses to select what is included in a sample. If one chooses to seek redundancy for the site as a whole, a stable proportional representation will be reached much faster, but the nuance of differences between contexts will be lost, as the sample sizes will be much smaller than if one seeks redundancy for a smaller sample group, such as unit/CZ, a unique strata, or an individual

bucket. By choosing to sample at unit/CZ I have lost some of the nuance of variability between strata that represent a variety of contexts, however the units of time that each CZ represents provide enough resolution to track large- scale temporal changes and meet the research goals of the NSF project.

5.3 Applying this Method to the Northwest Coast and Beyond

On the NWC many researchers have reached various conclusions about households, often using small sample sizes and limited contexts, as Gray (2008), and Monks (2000) have both noted. The dense deposits from villages make large-scale analyses somewhere between difficult and impossible to complete. This has led researchers to focus excavations on one or two houses out of a village consisting of as many as 15 or more houses. The density of village deposits has also led to variable quantities of excavation of midden outside house boundaries, and a variety of screening methods. In cases where the analysis of fish remains is further limited by column samples or selective sampling, sampling issues are only compounded.

By analyzing fish remains from one large NWC village site, I have demonstrated that STR can provide the means to better answer the big questions being asked about social and ecodynamics in this region. The Číx'wícən site has many characteristics in common with other NWC village sites that make it an excellent candidate for the application of STR including excellent faunal preservation, dense faunal deposits, and identifiable boundaries from multiple houses. Despite including samples from only eight excavation units, I have shown that STR can expand the spatial and temporal breadth of analyses without significantly increasing the data burden of innumerable quantities of data.

Using STR at NWC village sites, as I have done, to highlight locales that require larger sample sizes can serve as a model for future researchers that would allow them to direct their sampling efforts more efficiently. STR does so by highlighting low frequency locations that would benefit from increasing sample sizes, while still adequately sampling higher frequency locations. Those samples with higher densities and NISPs will likely reach redundancy faster, saving time that can be focused on the lower density, lower NISP samples that require more intensive sampling to reach redundancy. This would provide future researchers with the ability to minimize effort towards characterizing an assemblage as a whole, while also increasing sample sizes in necessary targeted locations.

5.4 Future Work

My approach to STR has focused on fish remains that were previously excavated from a Pacific coastal village site with dense archaeological deposits. STR could be employed in other types of archaeological settings in a range of environments (coast or interior) representing a range of cultural contexts (from hunting camps to urban centers) to establish sample redundancy after an excavation is complete. STR could also be used during on-going excavation (Leonard 1987). Further research is required to explore the implications of STR in these settings, however it is likely that the success of STR in other contexts will be dependent on the density and overall abundance of remains, the diversity or material types being studied, as well of course in the range and specificity of questions in each case.

5.3 Conclusions

Researchers on the Northwest Coast (NWC) are often interested in complex questions regarding social organization, resource intensification, resource control, and impacts of environmental change on resources and in turn human groups. Gray (2008) has noted that the excavation strategies used on the NWC often do not provide the spatial and chronological control within a site that is necessary to document their variability and answer these research questions. The Číx^wicən site allowed me to address some of the limitations of previous Northwest Coast village site excavations because of its unique and robust sampling strategy, the wide expanse of time that it was occupied, and the multiple house structures present.

This site, located on the Strait of Juan de Fuca in Port Angeles, WA was excavated in 2004 as part of a Washington State Department of Transportation (WSDOT) undertaking to build parts for the Hood Canal Bridge Large scale excavation of (261.4 m³ 528 m²) generated enormous quantities of faunal remains. Radiocarbon dates and historic records show occupation extents from 2750 cal. BP to the early 20th century. An ongoing NSF project is using these records to examine changing human ecodynamics over the breadth of site occupation, focusing on zooarchaeology and geoarchaeological records.

Statistical sampling methods provide an empirical way to maximize the amount of information obtained with the least amount of effort. My thesis addressed the utility of Sampling to Redundancy (STR) as a statistical sampling method for sampling faunal remains from large village sites. My project has documented the variability of fish family representation across time and space in one part of the Číx^wicən village, while minimizing the time and effort required to do so. This thesis applies STR to “S” (> 1/4

in.) 10 Liter bucket samples from eight excavation units and a total of 26 separate unique temporal and spatial contexts. I focused on 1/ 4 in. samples for my study for a particular reason. Previous fish faunal studies have focused on effects of mesh size on fish representation; and emphasized the need to use fine mesh (e.g., 1/ 8 in. or finer) to document small-bodied fishes. This focus on fine mesh typically means that only limited volumes of matrix are studied, which in turn may mean that remains of rarer, large-bodied fishes are under- represented. The on-going NSF research project has focused on buckets screened to 1/ 8 in. mesh (called “C” buckets). I used STR to sample additional volumes of matrix screened to 1/ 4 in. to examine whether expanding the volume studied would affect fish representation, which was a second goal of my project.

Overall, I studied remains from 269 “S” buckets out of a total of 419 buckets, or 47% of the buckets. STR was most helpful for six of the high bone abundance and density contexts, where I analyzed less than 50% of the total buckets, was moderately helpful for 14 contexts, and not at all helpful for the six contexts with low fishbone abundance, where I analyzed 100% of the buckets. This analysis took me a total of 154 hours, and based on the percentage of material analyzed, 174 hours were saved.

As to the second project goal, to assess whether adding fish remains documented from additional matrix volume affected fish representation, I found the differences were minimal. Both for my study units as a whole, and for each time period, adding the fish records from the “S” buckets did not alter the main trends in fish representation as documented by the larger study, using a smaller volume. To further examine whether the added volume from >1/ 4 in “S” buckets affected results, I explored specific research questions that are relevant to the larger project regarding environment-animal interactions

and fishbone deposition and bone condition inside and outside of a house structure.

Adding the “S” bucket samples did not affect fish representation or fishbone distribution and condition, which affirms that the sampling strategy used in the larger research project was sufficient in most cases to characterize the fish record at the site.

My approach to STR has focused on fish remains that were previously excavated from a Pacific coastal village site with dense archaeological deposits. STR could be employed in other types of archaeological settings in a range of environments (coast or interior) representing a range of cultural contexts (from hunting camps to urban centers) to establish sample redundancy after an excavation is complete. STR could be used during on-going excavation (Leonard 1987). Further research is required to explore the implications of STR in these settings, however it is likely that the success of STR in other contexts will be dependent on the density and overall abundance of remains, the diversity or material types being studied, as well of course in the range and specificity of questions in each case.

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Appendices

Appendix A. On the Determination of Sample Sizes in Stratified Data

Preface:

This Appendix breaks down the mathematical reasoning developed by Cochran 1977 for both Equation 1 and Equation 2 of STR. This appendix also illustrates the mathematical factoring required to link Equation 1 in Cochran 1977 to Equation 1 as illustrated in Van der Veen and Fieller 1982.

By Cameron Yee, Portland State University

Assume a random sample $X_1, \dots, X_n$ from a population of size N . Let $X_i = 1 \forall i =$

$1, \dots, n$ if a set of remains belongs to a particular species. $X_i = 0$ if a set of remains does not. Let

$N_1 = \text{total number of positive identifications}$

$N - N_1 = \text{total number of negative identifications}$

Thus, we have the following definitions:

$$P(\text{positive ID}) = P = \frac{N_1}{N},$$

$$P(\text{negative ID}) = 1 - P = \frac{N - N_1}{N}$$

If we let $Y = \sum_{i=1}^n X_i$, then Y is the total number of successes in the sample, where successes are those cases with a positive identification. This implies that

$$P^* = \frac{1}{n} \sum_{i=1}^n X_i$$

which is the proportion of positive identifications within the given sample. This also implies that

$$Y = \sum_{i=1}^n X_i \sim \text{Hypergeometric}$$

We are able to fix the variance in our sample to a desired level, but first we need to determine an equation for the variance.

$$V[Y] = n \left(\frac{N_1}{N} \right) \left(\frac{N - N_1}{N} \right) \left(\frac{N - n}{N - 1} \right)$$

$$\begin{aligned} V[p^*] &= V \left[\frac{Y}{n} \right] = \frac{1}{n^2} V[Y] = \frac{1}{n^2} n \left(\frac{N_1}{N} \right) \left(\frac{N - N_1}{N} \right) \left(\frac{N - n}{N - 1} \right) \\ &= \frac{1}{n} P(1 - P) \left(\frac{N - n}{N - 1} \right) \end{aligned}$$

Fixing $V[p^*] = \sigma^2 = \left(\frac{d}{Z_{\frac{\alpha}{2}}} \right)^2$ where d is some desired level of precision (rule of thumb is 5%, but is determined somewhat arbitrarily by the sampler) and $Z_{\frac{\alpha}{2}}$ is the abscissa of the normal distribution at a desired significance level α . Plugging in this fixed quantity for variance, we have

$$\left(\frac{d}{Z_{\frac{\alpha}{2}}} \right)^2 = \left(\frac{PQ}{n} \right) \left(\frac{N - n}{N - 1} \right)$$

In Cochran's *Sampling Techniques* (1977), he solves for n where

$$n = \frac{\left(\frac{Z_{\frac{\alpha}{2}}^2 PQ}{d^2} \right)}{1 + \left(\frac{1}{N} \right) \left(\frac{Z_{\frac{\alpha}{2}}^2 PQ}{d^2} - 1 \right)}$$

Reworking this through some algebra manipulation, we get

$$n = \frac{\left(\frac{Z_{\alpha}^2 PQ}{\frac{d^2}{2}} \right)}{1 + \left(\frac{Z_{\alpha}^2 PQ}{\frac{d^2}{2}N} - \frac{1}{N} \right)}$$

$$n = \frac{\left(\frac{Z_{\alpha}^2 PQ}{\frac{d^2}{2}} \right)}{\left(\frac{d^2 N + Z_{\alpha}^2 PQ + d^2}{\frac{d^2}{2}N} \right)}$$

$$n = \frac{\frac{Z_{\alpha}^2 PQ N}{\frac{d^2}{2}}}{d^2 N + \frac{Z_{\alpha}^2 PQ}{\frac{d^2}{2}} + d^2}$$

$$n = \frac{N}{\frac{d^2 N}{\frac{Z_{\alpha}^2 PQ}{\frac{d^2}{2}}} + 1 - \frac{d^2}{\frac{Z_{\alpha}^2 PQ}{\frac{d^2}{2}}}}$$

$$n = \frac{N}{1 + \left(\frac{d}{\frac{Z_{\alpha}}{2}} \right)^2 \left(\frac{N}{PQ} - \frac{1}{PQ} \right)}$$

$$n = \frac{N}{1 + \left(\frac{N-1}{PQ} \right) \left(\frac{d}{\frac{Z_{\alpha}}{2}} \right)^2}$$

which matches the formula from van der Veen & Fieller 1982.

This is maximized when we take $P = 0.5$, thus we can get an upper bound on total sample size. In this particular situation, we have stratification within our data. Cochran again has a theorem which states

$$V[\bar{y}_{st}] = \sum_{h=1}^L W_h^2 V[\bar{y}_h]$$

$\bar{y}_{st}$: unbiased estimate of $\bar{Y}_h$, the population mean

$\bar{y}_h$: sample mean of the h^{th} strata

$$W_h = \frac{N_h}{N}, h^{th} \text{ stratum weight}$$

$$V[\bar{y}_{st}] = \sum_{h=1}^L \left(\frac{N_h}{N} \right)^2 V[\bar{y}_h], \quad V[\bar{y}_h] = \frac{S_h^2 (N_h - n_h)}{n_h N_h}$$

$$V[\bar{y}_{st}] = \frac{1}{N^2} \sum_{h=1}^L \left(\frac{N_h}{n_h} \right) (N_h - n_h) S_h^2$$

If n_h/N_h is negligible for all strata h , then we can ignore the finite population correction.

$$\rightarrow V[\bar{y}_{st}] = \frac{1}{N^2} \sum_{h=1}^L \frac{N_h^2 S_h^2}{n_h}$$

Given that we have stratification for every level, $n_1 + \dots + n_L = n$, we can minimize the variance by using a Lagrange multiplier. We will now use the notion that we are able to in fact neglect the finite population correction, we introduce the multiplier such that

$$L(n_1, \dots, n_L, \lambda) = \sum_{h=1}^L \left(\frac{N_h}{N} \right)^2 \left(\frac{S_h^2}{n_h} \right) + \lambda \left(\sum_{h=1}^L n_h - n \right)$$

For every $h = 1, \dots, L$

$$\frac{\partial L}{\partial n_h} = - \left(\frac{N_h^2}{N^2} S_h^2 \right) \left(\frac{1}{n_h^2} \right) + \lambda \stackrel{\text{def}}{=} 0$$

$$n_h = \frac{\frac{N_h}{N} S_h}{\sqrt{\lambda}}, h = 1, \dots, L$$

To determine λ , we need to sum over h such that

$$n = \frac{1}{\sqrt{\lambda}} \sum_{h=1}^L \frac{N_h}{N} S_h$$

$$\frac{1}{\sqrt{\lambda}} = \frac{n}{\sum_{h=1}^L \frac{N_h}{N} S_h}$$

Taking the result for $1/\sqrt{\lambda}$ and plugging it back into the equation for n_h , we get

$$n_h = n \left[\frac{\frac{N_h}{N} S_h}{\sum_{h=1}^L \frac{N_h}{N} S_h} \right]$$

Cochran showed that for this case (a Bernoulli Covariate), and given the following:

$$\bar{Y} = \frac{\sum_{i=1}^N y_i}{N} = P, \quad \sum_{i=1}^N y_i^2 = NP$$

$$S^2 = \frac{\sum_{i=1}^N (y_i - \bar{Y})^2}{N - 1}$$

$$S^2 = \frac{\sum_{i=1}^N y_i^2 - N\bar{Y}^2}{N - 1}$$

$$S^2 = \frac{1}{N - 1} (NP - NP^2)$$

$$S^2 = \frac{N}{N - 1} PQ$$

Hence if we apply this to our situation, each stratum will have sample variance

$$S_h^2 = \frac{N_h}{N_h - 1} P_h Q_h$$

Taking this result and using it in our result for n_h :

$$n_h = n \left[\frac{\frac{N_h}{N} \sqrt{\frac{N_h}{N_h - 1}} \sqrt{P_h Q_h}}{\sum_{h=1}^L \frac{N_h}{N} \sqrt{\frac{N_h}{N_h - 1}} \sqrt{P_h Q_h}} \right]$$

For sufficiently large N_h , this can be approximated by:

$$n_h \cong n \left[\frac{\frac{N_h}{N} \sqrt{P_h Q_h}}{\sum_{h=1}^L \frac{N_h}{N} \sqrt{P_h Q_h}} \right]$$

Appendix B. Description and overview of Re-screening Process

Working in consultation with Laura Phillips, NSF project PIs have assigned new catalog numbers to all the “C” and “S” buckets of remains that were analyzed.

The main reason for this is that project PIs realized in Summer 2012 that remains within each bag were not sorted to the screen size recorded on the bag tag/in the Burke Catalog. For example, fish remains that were supposed to be from 1/4 in. mesh contained much larger specimens that should have been captured in the 1/2 in mesh, as well as much smaller specimens that should have fallen through to 1/4 in. mesh. To mitigate this second problem, and ensure comparability with other Northwest Coast faunal assemblages, as well as the other faunal classes within this site (bird, invertebrate, mammal), I rescreened all remains that were part of the STR analysis. Only “S” bucket fish that were analyzed to redundancy were re-screened.

The process for doing this: “S” bucket fish remains from a single bucket number (one 10-liter bucket sample) divided into separate bags based on screen-size were removed from their bags and screened through nested mesh screens (1 in., 1/2 in., 1/4 in.). I then re-bagged the newly screened material into 1/2 in., 1/4 in. and < 1/4 in. screen size bags, and assigned new catalog numbers. Please note too: according to LAAS records, 1/4 in. mesh was the finest screen used for “S” buckets, but in almost all cases for fish, some remains slipped through this mesh, were retained and bags labelled <1/4 in.. After re-screening, 19 buckets no longer had remains from greater than 1/4 in. mesh and these less than 1/4 in. remains were not included in STR analysis.

As part of this rescreening, I created a new catalog numbering system, for the “sub numbers”, that was more logical than was previously in place. The original cataloging

system contained a bag # (e.g. 7689), followed by 2 sub numbers (e.g. “.02.04”) for specific screen sizes and material types. However, these sub numbers were arbitrarily assigned for each bag, so it was impossible to tell the screen size from the catalog # without consulting the catalog database. Given these issues, project PIs developed a plan, in collaboration with Burke Museum staff, to standardize the labelling and cataloging making it much more “user-friendly” and less susceptible to coding errors.

Example: Old system: catalog number WS-9122.02.02

New System: WS-9122.99.04.23, where

WS (=water screen), 9122 (= Bag No same as before), **99** (=rescreened), 0.04 (=mesh size, in this case 1/4” mesh), and .23 (= animal type, in this case FISH).

Standard Sub-number values used across all Faunal Analysts

<u>screen size</u>	<u>Material type:</u>
.01 – 1 in.	.10 - shell (all marine inverts)
.02 – 1/2 in.	.20 – bone (when cannot determine vertebrate class, or whether shell)
.04 – 1/4 in.	.21 - mammal
.99 - < 1/4 in.	.22 - bird
.23 - fish	
.24 – herp	

For fish remains, in the process of rescreening and cataloging, we created an inventory for each new catalog number, which was entered into an Excel Spreadsheet, and have included that spreadsheet in each box of returned fish remains.

As previously stated, for each set of unit/CZs, I re-screened remains from a minimum of three buckets in the sequenced random order as part of STR with the exception of those unit/CZs where there were less than three total buckets (Chapter 3). As previously also stated, I only re-screened the buckets that were included in STR. In several cases, after re-screening, there were no longer fish remains in the > 1/4 in. screens. These < 1/4 in. remains were not analyzed. Because buckets were sequenced for the equation before being re-screened, there are several cases where buckets that did not retain any fish in the >1/4 in. mesh were still included in the bucket totals (Table B-1).

Table B-1. S buckets included in STR showing which buckets have analyzed > 1/4 in. fish remains

*These buckets did not retain material > 1/4 in. after rescreening

Bag Number	Unit	CZ	Order to Analyze	Rescreened to use for Analysis
15023		2 NLR ¹	Not Analyzed	No
15129		2 NLR ¹	Not Analyzed	No
15473		2 NLR ¹	Not Analyzed	No
1335	2	Chr07	1	Yes
1248	2	Chr07	2	Yes*
3032	2	Chr07	3	Yes
20630	2	Chr07	4	Yes
21166	2	Chr07	5	Yes
5750	2	Chr07	6	Yes
21957	2	Chr07	7	Yes
21500	2	Chr07	8	Yes
1458	2	Chr07	9	Yes
1072	2	Chr07	10	Yes
21779	2	Chr07	11	Yes
8309	2	Chr07	12	Yes
5302	2	Chr07	13	Yes
22327	2	Chr07	14	Yes
21230	2	Chr07	15	Yes
5657	2	Chr07	16	No
20260	2	Chr07	17	No
4023	2	Chr07	18	No

7715	2	Chr07	19	No
2370	2	Chr07	20	No
1325	2	Chr07	21	No
1016	2	Chr07	22	No
5299	2	Chr07	23	No
5166	2	Chr07	24	No
1053	2	Chr07	25	No
946	2	Chr07	26	No
1543	2	Chr07	27	No
22372	2	Chr07	28	No
21310	2	Chr07	29	No
20257	2	Chr07	30	No
20906	2	Chr07	31	No
20826	2	Chr07	32	No
10781	2	Chr07	33	No
1296	2	Chr07	34	No
21900	2	Chr07	35	No
22605	2	Chr07	36	No
20035	2	Chr07	37	No
5014	2	Chr07	38	No
1079	2	Chr07	39	No
19937	2	Chr07	40	No
21344	2	Chr07	41	No
1087	2	Chr07	42	No
5736	2	Chr07	43	No
20445	2	Chr07	44	No
1002	2	Chr07	45	No
4553	2	Chr07	46	No
2767	2	Chr07	47	No
20528	2	Chr07	48	No
8469	2	Chr07	49	No
21164	2	Chr07	50	No
21174	2	Chr07	51	No
6243	2	Chr07	52	No
836	2	Chr07	53	No
20546	2	Chr07	54	No
19936	2	Chr07	55	No
6169	2	Chr07	56	No
20388	2	Chr07	57	No
22373	2	Chr07	58	No
21375	2	Chr07	59	No
22268	2	Chr07	60	No

2637	2	Chr07	61	No
17805	2	Chr06	1	Yes*
845	2	Chr06	2	Yes
1690	2	Chr06	3	Yes
1544	2	Chr06	4	Yes
21382	2	Chr06	5	Yes
21595	2	Chr06	6	Yes
5101	2	Chr06	7	Yes
917	2	Chr06	8	Yes*
21423	2	Chr06	9	Yes
19673	2	Chr06	10	Yes
6896	2	Chr06	11	Yes
7482	2	Chr06	12	Yes
1042	2	Chr06	13	Yes
20449	2	Chr06	14	Yes
7614	2	Chr06	15	Yes
7592	2	Chr06	16	Yes
2136	2	Chr06	17	Yes
21647	2	Chr06	18	No
22267	2	Chr06	19	No
19245	2	Chr06	20	No
1126	2	Chr06	21	No
14005	2	Chr01	1	Yes
11866	2	Chr01	2	Yes
13653	2	Chr01	3	Yes
11840	2	Chr01	4	Yes
13346	2	Chr01	5	Yes*
13724	2	Chr01	6	Yes
8993	2	Chr01	7	Yes
7441	2	Chr01	8	Yes
14426	2	Chr01	9	Yes
769	8	NLR ¹	Not Analyzed	No
1114	8	NLR ¹	Not Analyzed	No
5938	8	NLR ¹	Not Analyzed	No
15373	8	NLR ¹	Not Analyzed	No
15381	8	NLR ¹	Not Analyzed	No
19170	8	NLR ¹	Not Analyzed	No
19881	8	NLR ¹	Not Analyzed	No
20564	8	NLR ¹	Not Analyzed	No
21176	8	NLR ¹	Not Analyzed	No
21569	8	NLR ¹	Not Analyzed	No
21931	8	NLR ¹	Not Analyzed	No

7931	8	Chr07	1	Yes
20589	8	Chr07	2	Yes
7688	8	Chr07	3	Yes
5490	8	Chr07	5	Yes
1106	8	Chr07	6	Yes
1519	8	Chr07	7	Yes
7814	8	Chr07	8	Yes
7690	8	Chr07	9	Yes
940	8	Chr07	10	Yes
20478	8	Chr07	11	Yes
18821	8	Chr07	12	Yes
19384	8	Chr07	13	Yes
14211	8	Chr07	14	Yes
21190	8	Chr07	15	Yes
1195	8	Chr07	16	No
1311	8	Chr07	17	No
21872	8	Chr07	18	No
19606	8	Chr07	19	No
20627	8	Chr07	21	No
21404	8	Chr07	22	No
1120	8	Chr07	23	No
20849	8	Chr07	24	No
19809	8	Chr07	25	No
9727	8	Chr07	26	No
18826	8	Chr07	27	No
19244	8	Chr07	28	No
7901	8	Chr07	29	No
4528	8	Chr07	30	No
1546	8	Chr07	31	No
1432	8	Chr07	32	No
22050	8	Chr07	33	No
1716	8	Chr07	34	No
21947	8	Chr07	36	No
7639	8	Chr06	1	Yes
7823	8	Chr06	2	Yes
20559	8	Chr06	3	Yes
1719	8	Chr06	4	Yes
21340	8	Chr06	5	Yes
7459	8	Chr06	6	Yes
21783	8	Chr06	8	Yes
1315	8	Chr06	9	Yes
22102	8	Chr06	10	Yes

8688	8	Chr06	11	Yes
21468	8	Chr06	12	Yes
19210	8	Chr06	13	Yes
7579	8	Chr06	14	Yes
20541	8	Chr06	15	Yes
22330	8	Chr06	16	Yes
20558	8	Chr06	17	Yes
4562	8	Chr06	19	No
1319	8	Chr06	20	No
22085	8	Chr06	21	No
1082	8	Chr06	22	No
1243	8	Chr02	1	Yes
19236	8	Chr02	2	Yes
7776	8	Chr02	3	Yes
8342	8	Chr02	4	Yes
1767	8	Chr02	5	Yes
21339	8	Chr01	1	Yes*
14885		8 Chr01	2	Yes
15354		8 Chr01	3	Yes
16320		8 Chr01	4	Yes
1884	8	Chr01	5	Yes
6095	8	Chr01	6	Yes
14272		8 Chr01	7	Yes
6589	8	Chr01	8	Yes
16007		8 Chr01	9	Yes
17338		8 Chr01	10	Yes
16271		8 Chr01	11	Yes*
14702		8 Chr01	12	Yes
14793		8 Chr01	13	Yes
15986		8 Chr01	15	Yes
13721		8 Chr01	17	Yes*
15284		8 Chr01	18	No
20041	8	Chr01	19	No
15463		8 Chr01	20	No
14477	17	NLR ¹	Not Analyzed	
7390	17	Chr05	1	Yes
13949	17	Chr05	2	Yes
17599	17	Chr05	4	Yes
8528	17	Chr05	5	Yes
15044	17	Chr05	6	Yes
10577	17	Chr05	7	Yes
9335	17	Chr05	8	Yes

7021	17	Chr05		9	Yes
12074	17	Chr05		10	Yes
19967	17	Chr05		11	Yes*
13981	17	Chr05		13	Yes
8996	17	Chr05		15	Yes*
14294	17	Chr05		16	Yes
10827	17	Chr05		18	Yes
10806	17	Chr05		20	Yes
7395	17	Chr05		22	Yes
7019	17	Chr05		23	Yes
7015	17	Chr05		24	No
6834	17	Chr05		26	No
11584	17	Chr05		27	No
6885	17	Chr05		30	No
10919	17	Chr05		32	No
11606	17	Chr05		33	No
7802	17	Chr05		34	No
8258	17	Chr05		35	No
11100	17	Chr05		36	No
6528	17	Chr05		40	No
9302	17	Chr05		41	No
8621	17	Chr05		42	No
9401	17	Chr04		3	Yes
14456	17	Chr04		12	Yes
13238	17	Chr04		14	Yes
12788	17	Chr04		17	Yes
15845	17	Chr04		19	Yes
9246	17	Chr04		21	Yes
13469	17	Chr04		25	Yes
15330	17	Chr04		28	Yes
16319	17	Chr04		29	No
9753	17	Chr04		31	No
13677	17	Chr04		37	No
18120	17	Chr04		38	No
9685	17	Chr04		39	No
9162	17	Chr03	1		Yes
13650	17	Chr03	2		Yes
8934	17	Chr03	3		Yes
10038	17	Chr03	4		Yes
14701	17	Chr03	5		Yes
15601	17	Chr03	6		Yes
14367	17	Chr03	7		Yes

14021	17	Chr03	8		Yes
8438	18	Chr05		1	Yes
14072	18	Chr05		2	Yes
11734	18	Chr05		3	Yes
10683	18	Chr05		4	Yes
8814	18	Chr05		6	Yes
7124	18	Chr05		7	Yes
10799	18	Chr05		9	Yes
11633	18	Chr05		11	Yes
14354	18	Chr05		13	Yes
8644	18	Chr05		14	Yes
8653	18	Chr05		15	Yes
14490	18	Chr05		16	Yes
12211	18	Chr05		19	Yes
7022	18	Chr05		20	No
6462	18	Chr05		21	No
8446	18	Chr05		22	No
8133	18	Chr05		23	No
18741	18	Chr05		24	No
11337	18	Chr05		26	No
12066	18	Chr05		27	No
14026	18	Chr05		28	No
6401	18	Chr05		29	No
20718	18	Chr05		30	No
7410	18	Chr05		31	No
8782	18	Chr05		32	No
9093	18	Chr05		33	No
18475	18	Chr05		34	No
16394	18	Chr04		5	Yes
15203	18	Chr04		8	Yes
15224	18	Chr04		10	Yes
13590	18	Chr04		12	Yes
15059	18	Chr04		17	Yes
9212	18	Chr04		18	Yes
9160	18	Chr04		25	Yes
8983	18	Chr03	1		Yes
16089	18	Chr03	2		Yes
11300	18	Chr03	3		Yes
10170	19	NLR ¹	2		No
8471	19	Chr05		3	Yes
8497	19	Chr05		5	Yes
7024	19	Chr05		6	Yes

13110	19	Chr05		8	Yes
11600	19	Chr05		10	Yes
12142	19	Chr05		11	Yes
12266	19	Chr05		12	Yes
8784	19	Chr05		13	Yes
9491	19	Chr05		14	Yes
10876	19	Chr05		15	No
8252	19	Chr05		17	No
8256	19	Chr05		18	No
6394	19	Chr05		19	No
8361	19	Chr05		20	No
12675	19	Chr05		23	No
14181	19	Chr05		24	No
12118	19	Chr05		25	No
8364	19	Chr05		26	No
11971	19	Chr05		27	No
8322	19	Chr05		31	No
11566	19	Chr05		33	No
10463	19	Chr05		36	No
11229	19	Chr05		37	No
13501	19	Chr04		1	Yes
10887	19	Chr04		2	Yes
13984	19	Chr04		4	Yes
14063	19	Chr04		7	Yes
16321	19	Chr04		9	Yes
10780	19	Chr04		16	Yes
13228	19	Chr04		21	Yes
12708	19	Chr04		22	Yes
9001	19	Chr04		28	No
9462	19	Chr04		29	No
11991	19	Chr04		30	No
9482	19	Chr04		32	No
18506	19	Chr04		34	No
8141	19	Chr04		35	No
15786	19	Chr04		38	No
11141	19	Chr04		39	No
14390	19	Chr04		40	No
15249	19	Chr04		41	No
8986	19	Chr03	1		Yes
13373	19	Chr03	2		Yes
10126	19	Chr03	3		Yes
15036	19	Chr03	4		Yes

11080	19	Chr03	5	Yes
9189	19	Chr03	6	Yes
11215	19	Chr03	7	Yes
14802	19	Chr03	8	Yes
15571	19	Chr03	9	Yes
13142	19	Chr03	10	Yes
10243	19	Chr03	11	No
9924	20	NLR ¹	Not Analyzed	No
10146	20	NLR ¹	Not Analyzed	No
10455	20	NLR ¹	Not Analyzed	No
16550	20	Chr05	2	Yes
10291	20	Chr05	4	Yes
15312	20	Chr05	5	Yes
13898	20	Chr05	10	Yes
8816	20	Chr05	11	Yes
6981	20	Chr05	14	Yes
8851	20	Chr05	15	Yes
7026	20	Chr05	16	Yes
16242	20	Chr05	17	Yes
12135	20	Chr05	19	Yes
10392	20	Chr05	21	No
9404	20	Chr05	22	No
8476	20	Chr05	23	No
11558	20	Chr05	25	No
8783	20	Chr05	27	No
10351	20	Chr05	28	No
10593	20	Chr05	29	No
9999	20	Chr05	30	No
9687	20	Chr05	31	No
22630	20	Chr05	32	No
12974	20	Chr05	33	No
14469	20	Chr05	34	No
8627	20	Chr05	36	No
14070	20	Chr04	1	Yes
10290	20	Chr04	3	Yes
16534	20	Chr04	6	Yes
13516	20	Chr04	7	Yes
14335	20	Chr04	8	Yes
18201	20	Chr04	9	Yes*
22609	20	Chr04	12	Yes
15890	20	Chr04	13	Yes
11495	20	Chr04	18	Yes

12816	20	Chr04		20	No
13170	20	Chr04		24	No
16156	20	Chr04		26	No
12442	20	Chr04		35	No
9868	20	Chr03	1		Yes*
9991	20	Chr03	3		Yes*
11863	20	Chr03	4		Yes
11704	20	Chr03	5		Yes
9628	20	Chr03	6		Yes*
11202	20	Chr03	7		Yes
9520	20	Chr03	8		Yes
12633	20	Chr03	9		Yes
12134	20	Chr03	10		Yes
10968	20	Chr03	11		No
8529	25	NLR ¹	Not Analyzed		No
8857	25	NLR ¹	Not Analyzed		No
9864	25	NLR ¹	Not Analyzed		No
9996	25	NLR ¹	Not Analyzed		No
13370	25	NLR ¹	Not Analyzed		No
14073	25	NLR ¹	Not Analyzed		No
15423	25	Chr05	1		Yes
13247	25	Chr05	2		Yes
8733	25	Chr05	3		Yes
8047	25	Chr05	4		Yes
9379	25	Chr05	6		Yes
9787	25	Chr05	7		Yes
13530	25	Chr05	8		Yes
11381	25	Chr05	9		No
15014	25	Chr04	1		Yes*
14483	25	Chr04	3		Yes*
10975	25	Chr04	4		Yes
8613	25	Chr04	5		Yes
8519	25	Chr04	6		Yes
8626	25	Chr04	7		Yes
14750	25	Chr04	8		Yes
15693	25	Chr04	9		Yes
20696	25	Chr04	10		Yes*
8754	25	Chr04	11		Yes
10349	25	Chr04	12		No
8633	25	Chr04	13		No
15780	25	Chr04	14		No
9820	25	Chr03	1		Yes

9188	25	Chr03	2	Yes*
9563	25	Chr03	3	Yes
22572	25	Chr03	4	Yes
13234	31	Chr05	1	Yes
9770	31	Chr05	2	Yes
14899	31	Chr05	3	Yes
10465	31	Chr05	4	Yes
10216	31	Chr05	6	Yes
17860	31	Chr05	7	Yes
13723	31	Chr05	8	No
11522	31	Chr05	9	No
16224	31	Chr05	10	No
9168	31	Chr04	1	Yes
15418	31	Chr04	2	Yes
11481	31	Chr04	3	Yes
14713	31	Chr04	4	Yes*
9818	31	Chr04	5	Yes
13904	31	Chr04	6	Yes
10015	31	Chr04	7	Yes
9798	31	Chr04	8	Yes
16194	31	Chr04	9	Yes
14727	31	Chr04	10	Yes
9679	31	Chr04	11	Yes
14974	31	Chr04	12	Yes
12304	31	Chr04	13	Yes
13944	31	Chr04	14	Yes
9559	31	Chr04	15	Yes
13787	31	Chr04	16	No
9565	31	Chr04	17	No
15965	31	Chr04	18	No
10754	31	Chr03	1	Yes
11442	31	Chr02	1	Yes
8552	31	Chr02	2	Yes
13232	31	Chr02	3	Yes*
14393	31	Chr02	4	Yes
9879	31	Chr02	5	Yes*
15527	31	Chr02	6	Yes
8931	31	Chr02	7	Yes
17136	31	Chr02	8	Yes
9666	31	Chr02	9	Yes
15745	31	Chr02	10	Yes
9241	31	Chr02	11	Yes

15486	31	Chr02	12	Yes
14612	31	Chr02	14	Yes
11738	31	Chr02	15	Yes

¹Some buckets were not given CZs either because an excavation record with their provenience could not be found. In such cases, buckets were instead given a designation of No Level Record (NLR).

Appendix C. List of cranial, paired fin, and vertebral elements included in fishbone analysis.

From Butler In Preparation

Table C-1. fish post-cranial, and paired fin skeletal elements

	All Bony Fishes	Salmonids Only	Surfperch only	Herring only (order, family, species)	Flatfish only	Ratfish only	Skate only	Dogfish only	Buttalo Sculpin/Starry Flounder only
Elements: Cranial									
angular/articular	2								
basioccipital	1								
ceratohyal	2								
dentary	2								
epihyal	2								
hyomandibula	2								
interhaemal spine					1				
maxilla	2								
opercle	2								
otics: prootic and pterotic				4					
otolith (sagitta only)	2								
palatine	2								
parasphenoid	1								
pharyngeal (lower & upper)			3						
premaxilla	2								
preopercle	2								
quadrate	2								
subopercle				2					
supraoccipital				1					
dental plates/teeth						6	xx	xx	
urohyal	1								

vomer	1									
Total cranial elements	28		3	7	1	6				
	All Bony Fishes	Salmonids Only	Surfperch only	Herring only (order, family, species)	Flatfish only	Ratfish only	Skate only	Dogfish only	Buttalo Sculptin/Starry Flounder only	
Elements: Paired Fin										
cleithrum	2									
coracoid		2								
mesocoracoid		2								
pectoral fin ray		2								
postcleithrum		6								
posttemporal	2									
scapula	2									
supracleithrum	2									
basipterygium	2									
dorsal spine						1		2		
Total fin elements	10	12				1		2		
Elements: Misc.										
dermal denticle/scales							xx		xx	
dorsal vertebra spine		xx								
Total cranial/paired fin elements	38	12	3	7	1	7		2		

*Elements listed "xx" recorded but not used in most quantitative analyses.

Table C-2. Number of vertebrae recorded by taxon

Taxon	N Vertebrae*
Anoplopomatidae	55.3
Clupeidae	48.3
Cottidae	24.7
<i>Enophrys bison</i>	21
<i>Hemilepidotus</i> sp.	21
<i>Hemilepidotus/Scorpaenichthys</i>	23.5
<i>Leptocottus armatus</i>	28
<i>Myoxocephalus polyacanthocephalus</i>	27
Embiotocidae	24.5
<i>Gadus macrocephalus</i>	42
<i>Microgadus proximus</i>	45.5
Hexagrammidae	43
<i>Hexagrammos</i> sp.	43
<i>Ophiodon elongatus</i>	43
<i>Oncorhynchus</i> sp.	66.3
Pleuronectiformes	26.6
<i>Sebastes</i> sp.	18.7
<i>Raja</i> sp.	86
<i>Squalus acanthias</i>	100

*Obtained from averaging multiple skeletons. Note the most posterior vertebrae on most bony fishes were not identified beyond fish, so N vertebrae is what was tallied and recorded for a given taxon, not the number of vertebrae on a given taxon.