Sampling Methods in Northwest Coast Household Archaeology:

A Simulation Approach Using Faunal Data from the Ozette Site

by

Brendan Gray
B.A., Simon Fraser University, 2004

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Supervisory Committee

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Abstract

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The methodological and theoretical considerations that must be addressed when excavating the traditional longhouses of the First Nation peoples who lived in the Pacific Northwest region are the foci of this thesis. The large amount of faunal data contained within the remains of houses require the use of explicit, justifiable sampling strategies; however, the methods used to sample these dwellings are not generally a central research focus. A sampling simulation of faunal data recovered from the excavation of numerous houses from the village site of Ozette is the empirical basis of this research, and provides a method for examining the efficacy of different sample strategies. Specifically, the effects of sample size and sample method on richness, relative abundance and the interpretation of status using faunal data are investigated. The results are of heuristic value for future household archaeology on the Northwest Coast and suggest alternative sampling methods which attempt to cope with the labour-intensive research generally required for shell-midden archaeology.

Table of Contents

List of Tables

List of Figures

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This thesis is dedicated to

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Chapter 1: Introduction

The longhouse, the traditional dwelling of many Northwest Coast (NWC) First Nations, is a central research focus for many archaeologists studying this region. This is due, in large part, to the fact that these dwellings were fundamental to the overlapping economic, social, political, and cosmological spheres of NWC inhabitants (Ames and Maschner 1999). Excavations of these dwellings – locations where relationships between individuals and groups are visible in the material record – can provide important information about daily and ritual practices of household members. Faunal data is one particularly important source of evidence which can be used to understand many aspects of past life on the NWC. Research into archaeological examples of these dwellings has occurred for over forty years, yet despite the abundance of ethnohistoric accounts which reference these dwellings and their inhabitants, there is still relatively little known about how households functioned during the pre-contact period (Ames 2006).

There appear to be two primary yet related reasons why large gaps in our knowledge of these dwellings still exist. Firstly, the size of the longhouse, in combination with the data-rich nature of these house floors, requires more time, labour, and money than is usually available to excavate the entire spatial extent of a house floor and therefore understand the range of behaviours associated with a particular household. Shell-midden house floors are particularly problematic in this respect, as the quantity of fauna contained within them requires significant time to excavate and analyze, and yet is an important source of evidence that can indicate the activities of household members. Secondly, and presumably because of the reason above, only a few houses, numbering under 20, have actually been extensively excavated with inter- and intra-household

dynamics in mind. This represents a very small excavated sample for such a large and culturally diverse region. As a first step to addressing these issues, this thesis will articulate and critique exactly how these problems have been approached in the past.

Simply identifying issues does not solve them, and in order to consider potential solutions to the issues mentioned above, a sampling simulation of faunal data from three houses from the Ozette site was undertaken. Ozette, located on what is now the west coast of the Olympic Peninsula in Washington State, is critical to archaeologists' understanding of houses on the NWC because it has been extensively researched. The entire spatial extent of three houses was excavated, and fauna, artifacts and perishable material from each of these houses analyzed. It is a much larger sample when compared to other excavated house deposits on the NWC, and a sampling simulation of the faunal data essentially allows one to ask: "How much less than the entire extent of a house floor has to be excavated in order to accurately understand specific parameters of the faunal assemblage from each house at Ozette?" Testing sample strategies on three houses that have different occupational histories, as is the case at Ozette, allows for the evaluation of different sample strategies and how these may be more or less optimal at each house. Although it is unlikely that other houses on the NWC share precisely the same spatial distribution of faunal elements as any of the Ozette houses, it *is* likely that the heterogeneity and complexity of faunal distributions at Ozette are of a similar scale to houses at other sites in this region. As such, a sampling simulation has heuristic value for future excavations throughout this region, particularly for shell-midden house floor excavations.

Sampling simulations using the Ozette data will allow for the investigation of two related effects: the effect of sample size and the effect of sample method. Sample sizes evaluated in this thesis range from approximately 0.1% of a house floor to approximately 40% of a house floor; the sample methods evaluated include simple random sampling, systematic sampling and judgmental sampling. The effects of sample size and method will be investigated with respect to three research foci:

1. How do sample size and sample method affect the richness (the number of different taxa identified) of a sample when compared to an entire house floor?

2. How do sample size and sample method affect the relative abundance of taxa when compared to the data from an entire house floor?

3. How do sample size and sample method affect the interpretation of household dynamics? Specifically, how do the sample size and sample method affect the interpretation of inter- and intra-house status?

Whether or not a specific sample strategy performs in the same manner or in a different manner at each of the houses at Ozette will also be considered during each of the above analyses.

1.1 Thesis Organization

In Chapter 2, I summarize some of the major research into the NWC longhouse, beginning with ethnohistoric accounts of these dwellings. The major archaeological research into house remains is then presented, and the various frameworks used to interpret these structures are discussed. This chapter concludes with an in-depth investigation into the methodological issues inherent in excavating houses on the NWC.

In the following chapter – Chapter 3 – sampling method and theory are discussed. A general overview of sampling, including definitions and methods, serves as an introduction to this topic. I then discuss different methods used to indicate whether or not

sample size is influencing the composition of an assemblage. These methods include the sampling to redundancy approach, the rarefaction approach, and the regression approach. The effects of sample configurations (i.e., sample strategies) are also discussed in this chapter, using the Modifiable Areal Unit Problem, or MAUP. This conceptual framework is applied in order to consider how the aggregation of excavation units may affect the interpretation of spatial data. The MAUP arises when arbitrary boundaries, rather than meaningful boundaries, are imposed upon spatial data which are not point-provenienced. The MAUP must therefore be addressed before sampling simulations can be executed, as explained in Chapter 5.

In Chapter 4 I summarize the limited research undertaken which has explicitly focused on sampling issues on the NWC. Subsequently, the sample strategies used to excavate houses and the rationale for such strategies are presented. It is argued in this chapter that ethnohistoric observations of inequality within and between houses in a village have been used as a central guiding principle through which many sampling strategies have been designed.

Chapter 5 describes the methods used to execute sampling simulations on the Ozette faunal data. Initially, the faunal database from Ozette had to be manipulated in order to address differential excavation strategies, missing data, and the MAUP. The resultant database was given spatial reference using GIS software. Finally, specific sample strategies, both probabilistic and judgmental, were selected for evaluation.

In Chapter 6 I present the results of a comparison of the richness of samples to the richness of an entire house. The differences and similarities between various judgmental and probabilistic samples with respect to their ability to detect the number of taxa within

a given house are presented and discussed. The relationship between sample size and the number of different taxa identified is also analyzed.

Chapter 7 presents the results of a comparison between the relative abundance of a taxon in a sample and its actual relative abundance in each house. Rather than examine each sample in its entirety, the sample is divided into three classes of fauna (mammals, fish and shellfish), as this is a common analytical procedure when studying zooarchaeological remains. The effectiveness of several sample strategies are evaluated based on these classes in order to observe whether or not there is congruence among all classes of data. As with Chapter 6, the effect of sample size and sample method on the data will be discussed.

Chapter 8 considers whether sample strategies can accurately detect the quantity and abundance of fauna which are thought to be indicative of status. Decorative, ceremonial, and symbolic (D/C/S) shellfish, whale, and the relative abundance of salmon and halibut remains have all been used as proxy evidence for status differences between and within houses at Ozette (Samuels 1994). These variables are scrutinized in each sample to observe whether or not they accurately identify inter- and intra-house differences in status.

In Chapter 9, I begin with a synthesis and discussion of the results, commenting on critical sample sizes needed to investigate each of the research questions delineated above. Similarities and differences between probabilistic and judgmental sampling methods and differences between houses will also be considered. Finally, the implications of this research, its limitations and avenues of future research will be discussed.

Chapter 2: The Northwest Coast Longhouse

In this chapter I outline the importance of the house and the household and how these have previously been studied on the Northwest Coast (NWC), both by archaeologists and ethnographers. I begin with ethnohistoric descriptions of the house, as these are less obscure than most archaeological examples. I then summarize some of the major archaeological investigations into houses, prefacing this discussion with an introduction to household archaeology. Finally, I consider the theoretical frameworks that are used to interpret the remains of houses, as well as the methodological issues inherent in "doing" household archaeology on the NWC.

2.1 Ethnographic Context

The longhouse, also known as the "big house" or "plank house", has been described in detail in many ethnohistoric accounts (e.g., Barett 1938; Boas 1888, 1966; Drucker 1951, 1955); these accounts and others are also synthesized in more recent publications (e.g., Gahr 2006; Mauger 1991:127-173, and references within; Suttles 1991). The longhouse had many functions including a "food-processing and storage plant … a workshop, recreation center, temple, theatre, and fortress" (Suttles 1991:214) and as such was central to almost all aspects of daily life on the NWC. These dwellings were often found grouped together as part of a village, and were generally aligned in one or two rows facing the water. They were rectangular or square in shape, and varied in size from eight by ten meters to as large as 200 meters in length (Gahr 2006).

The internal architecture of these houses was variable and may have included small, hip-level walls, as well as boxes or benches, all of which served to delineate different nuclear family living areas (Figure 1). Typically, a bench or sleeping zone

would be found around the interior perimeter of the house. The floor of the house varied

within and between houses, and may have consisted of planks, or a raised platform; some

houses even had a sub-floor storage facility dug into the central area of the house

(Drucker 1955). The separation of the house into nuclear family living areas, was
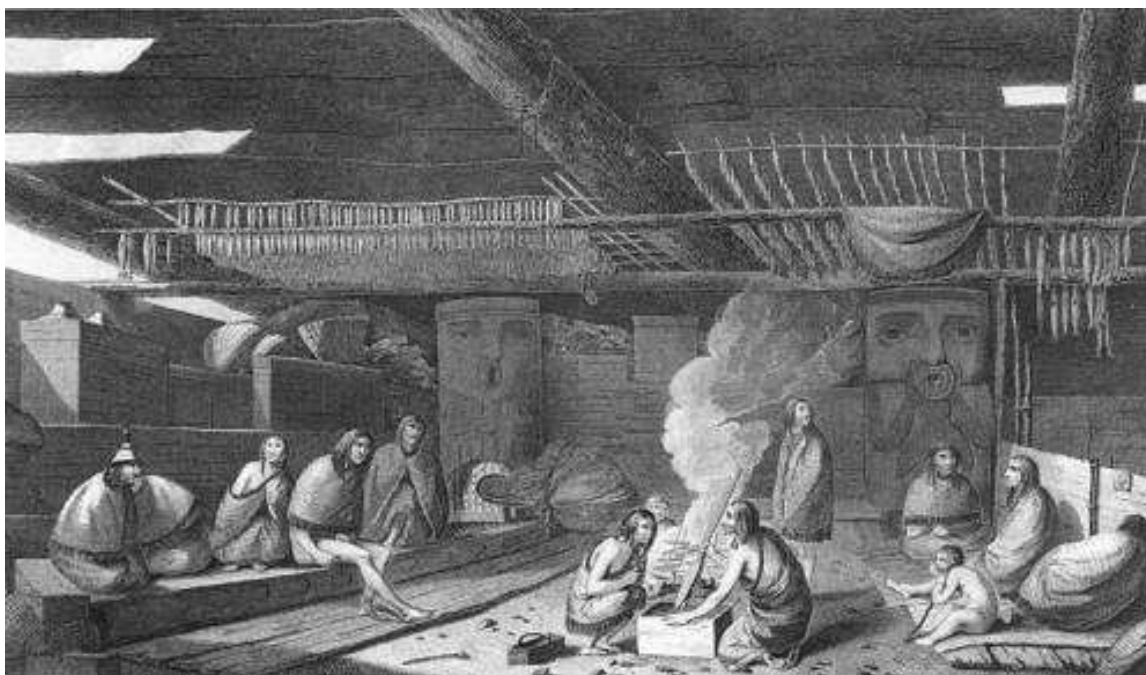
Figure 1. Interior of a Nootkan longhouse. Courtesy University of Washington Libraries, Special Collections, NA3918.

conceptualized with strict boundaries in mind, although these separations did not

necessarily translate into codified architectural divisions. These strict conceptual

boundaries were often related to status, as the house was one of the primary locations

where the communication and reinforcement of the hierarchical nature of NWC society

occurred. The several families that inhabited the longhouse were generally allocated

space based on their social status within the household:

> The principal family spaces were allotted according to an invariable system. The
> nominal owner of the house, that is, the chief of the lineage, occupied the right rear
> corner ("right" being used according to the native concept of the speaker standing
> inside the house facing the door)…The chief next in rank, usually a brother or other
> close kinsman occupied the opposite corner. The corners to the right and left of the

door were similarly places of honor, and occupied by other important branches of the lineage, and if the group was a large one, the two central places along each side, simply called "middle spaces"…were assigned to other branches of the family. [Drucker 1951:71].[1]

The spaces of the higher social status occupants were in much closer proximity to the fundamental structural components of the house: "[l]acking physical partitions, portions of the houses structures [i.e. corner posts and rafter support posts] served as reference points for the conceptual territories within the dwelling. Among the Katzie (Jenness 1955:7), Songish (Boas 1890:564) and Lummi (Stern 1934:31), for example, rafter support posts marked social subunits" (Mauger 1991:164-165). The low status spaces lacked these architectural cues because they were in the middle of the house, and as such were almost certainly liminal spaces whose boundary and ownership were more difficult to define.

There existed variability in house construction style within the region. Drucker (1955:67-71), for example, identified five house types defined by their approximate geographic distribution within the NWC region that included the Northern, Wakashan, shed-roof, Chinook-Oregon and Lower Klamath house types. The differences between these types resided mainly with the differences in the placement and configuration of posts, roof style, and organization of internal space. Mackie and Williamson (2003) illustrate that defining house types based on geographic sub-regions may be problematic, given that several construction methods were used within one village (Kiix?in) in Barkley Sound on the west coast of Vancouver Island. The variability of house types, and more generally between different NWC cultures, is often obscured because the most detailed

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[1] In this quote, Drucker is referring specifically to Nootkan social organization.

ethnohistoric accounts (e.g., Drucker 1951) are erroneously assumed to be describing pan-Northwest Coast phenomena (Ames 2005).

Both ethnohistoric and archaeological evidence indicate that house location, house form and the household itself were in many cases stable over long periods of time (Ames 2006; Grier 2006; Suttles 1991). Households generally consisted of individuals who resided within the same house (Wike 1958). This ethnographically-observed correlation between household membership and co-residence within a single house is important, as the house becomes the location where the economic and social relationships of individuals who comprised a household were manifested (Ames 1994; Wike 1958). This is especially useful for archaeologists, who can (and do) infer that the remains of a single house represent the activities of a single household or co-operative group.[2] The individuals cohabiting a single dwelling were therefore part of a group which "form[ed] the next bigger thing on the social map after an individual" (Hendon 1996:47). Interpreting the archaeological record in contexts where household membership may not have been commensurate with cohabitation may be problematic; however, this is unlikely to be the case on the NWC.

2.2 Household Archaeology

In archaeology, the domestic dwelling is often investigated under the rubric of household archaeology. Household archaeology is a relatively recent development[3], formally introduced by Wilk and Rathje (1982), who attempted to bridge the gap between the broad theories of cultural change and specific archaeological assemblages (Robin

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[2] This is not to suggest that different households of the same lineage, or entire village cooperation did not also occur.

[3] While the "household" as a unit of analysis is relatively new in archaeology, anthropologists and archaeologists have been investigating the relationship between dwelling form, the environment, and culture since the 1880s (e.g., Morgan 1965 [1881]).

2003; Wilk and Rathje 1982). These early analyses interpreted the household as a "unit of social and economic cooperation" (Wilk and Rathje 1982:621), a functional approach that has been a popular framework used to interpret houses on the NWC. Because household archaeology was developed for agricultural societies, the applicability of such theories to the hunter-gatherer-fisher societies on the NWC has recently been called into question (Ames 2006).

Current interests in household archaeology have moved beyond essentialist functional interpretations, and now address diverse theoretical interests in a variety of geographical locales including the NWC and elsewhere (e.g., Allison 1999; Coupland and Banning 1996; Gillespie 2000; Robin 2003; Hardin 2004). The theoretical perspectives have also diversified to include themes such as the archaeological correlates of houses and households, the evolution of dwelling form (Lawrence and Low 1990), the social (re)production of households (Grier 2006; van Gijseghem 2001), household demographics (Ames 2006; Frankel and Webb 2001), gendered analyses of households (Hendon 1996), and intrahousehold variability.

On the NWC, there are many excavations in which house deposits have been uncovered; however, there are few excavations at which houses or households were the specific research focus. The earliest excavations to focus on the house/household include the excavations at the Ozette site in Washington State (Samuels 2006, 1994, 1991), the Richardson Ranch site in Haida Gwaii (Fladmark 1972), and the site FbSx-9, a protohistoric house near Bella Bella (Carlson 1984). More recent excavations focused on the household include the Paul Mason site (Coupland 1988), the Shingle Point site (Matson 2003), the Meier site (Ames et al. 1992), the McNichol Creek site (Coupland et

al 2003; Coupland 2006), the Huu7ii site (Frederick et al. 2006), the Dionisio Point site (Ewonus 2006; Grier 2006), the Scowlitz site (Lepofsky et al. 2000), the Psacelay site (Martindale 2006), the Cathlapotle site (Sobel 2006), the Sbabadid site (Chatters 1989), the Tualdad Altu site (Chatters 1989) and, in the interior Plateau, the Keatley Creek site (Hayden 1997). The locations of these sites and additional information can be found in Table 1 and Figure 2. With the exception of the Keatley Creek site, which contained circular, semi-subterranean pithouse dwellings, all were rectangular or square dwellings.

Investigating the internal organization of one or more of these dwellings has generally involved the excavation of large areas of a house; however, this is not to suggest that productive research into these dwellings in all cases requires large-scale excavation. Midden ridges behind, in front and between houses often indicate the approximate boundaries of house platforms (which may themselves be visible as well) and can be used to comprehend the spatial organization of houses within a village. The mapping of villages in Barkley Sound, as well as dendrochronological samples taken from architectural features of abandoned houses, has elucidated information about variability in house style within this localized region (Mackie and Williamson 2003; Smith et al. 2005). Archer (2001) performed a regional survey of sites in the Prince Rupert area (northern NWC), recording the house platform area, and using this measure as proxy evidence to determine whether a village was considered to be egalitarian or ranked. Matson (2003) utilized ground-penetrating radar at the Shingle Point site in the Gulf of Georgia region to identify subsurface archaeological features prior to excavating a house floor. Other subsurface methods such as coring (e.g., Chatters 1989;

Site Names

A = Broken Tops
B = Meier
C = Cathlapotle
D = Sbabadid
E = Tualdad Altu
F = Ozette
G = Huu7ii
H = Dionisio Point
I = Shingle Point
J = Scowlitz
K = Mauer
L = Keatley Creek
M = FbSx-9
N = Richardson Ranch
O = McNichol Creek
P = Psacelay
Q = Paul Mason
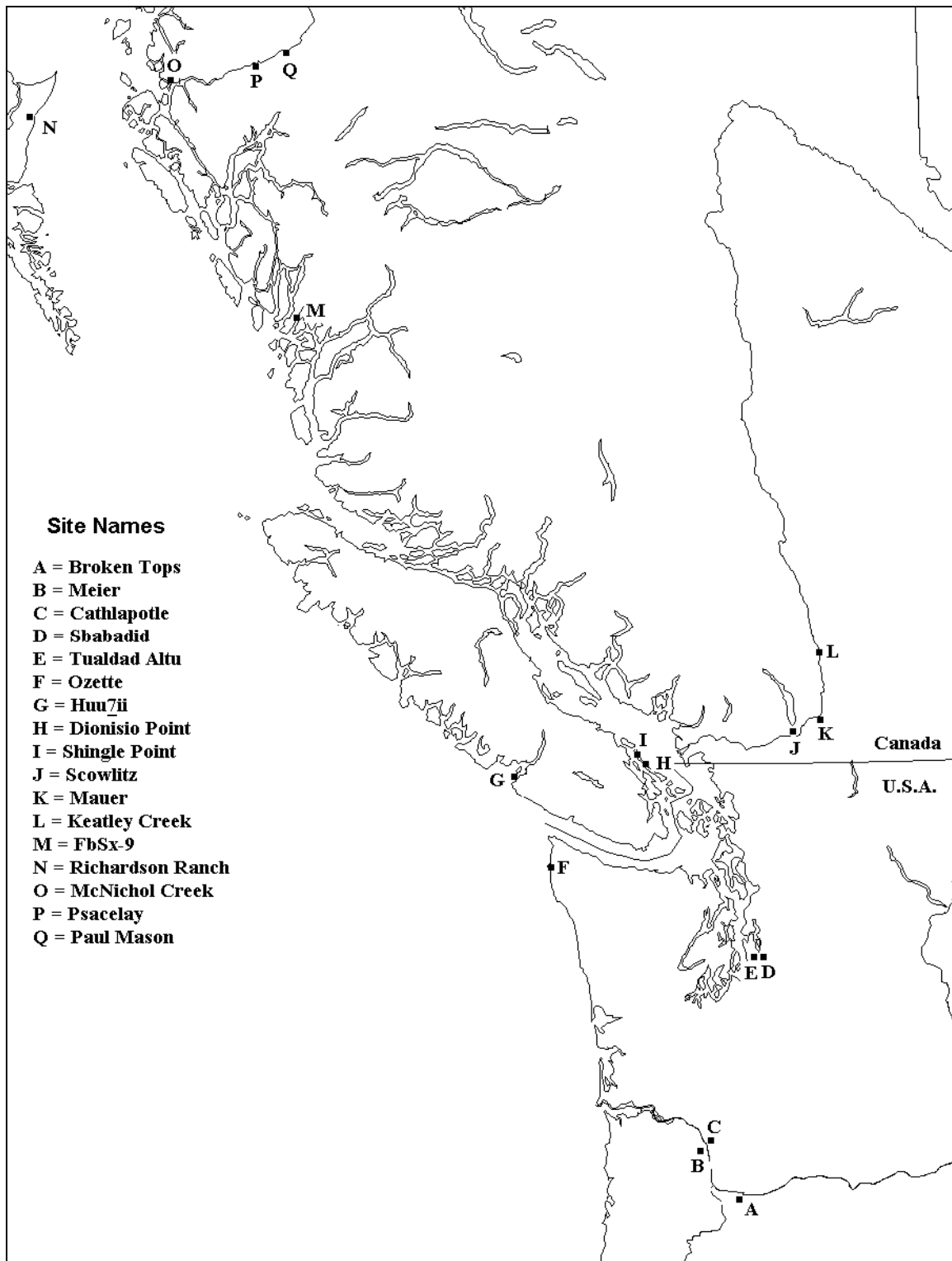
Figure 2. Locations of major house excavations on the Northwest Coast.

Map #	Site name	Approximate dates of house occupation[a]	Major excavation focus	Approx. size of excavated house (m^2)	Approx. % of house excavated	Faunal- rich housefloor deposits?	Reference
A	Broken Tops	14th – 16th century A.D.	2 small houses	72; 72	~40-50%; ~70-80%	No	Ellis (2006)
B	Meier	14th - 18th century A.D.	Single house (not a village)	490	35%	No	Ames et al. (1992)
C	Cathlapotle	16th – 19th century A.D.	Largest house (House 1) and small house (House 4); others sampled to a lesser extent	Unknown	Unknown	No	Sobel (2006)
D	Sbabadid	Late 18th - early 19th century A.D.	Largest house	243	~90%	No	Chatters (1989)
E	Tualdad Altu	4th century A.D.	Largest house	119	~68%	Yes	Chatters (1989)
F	Ozette	300-450 years B.P.	Largest house (House 1); 2 smaller houses (House 2 and House 5)	197; 160; 168	100%	Yes	Samuels (1994)
G	Huu7ii	1600-300 years B.P.	Largest house (House 1)	613	15%	Yes	Frederick et al. (2006)
H	Dionisio Point	1700-1500 years b.p.	House 2; others sampled to lesser extent	200	44%	Yes	Grier (2006)
I	Shingle Point	1000 years B.P.	2 compartments of a shed-roof house	Unknown; historic disturbance	1 compartment fully excavated	Yes	Matson (2003)

Map #	Site name	Approximate dates of house occupation[a]	Major excavation focus	Approx. size of excavated house (m^2)	Approx. % of house excavated	Faunal-rich housefloor deposits?	Reference
J	Scowlitz	2200-2400 b.p.	Structure 3	187	~50%	No	Lepofsky et al. (2000)
K	Mauer	~4000 years B.P.	Single house (not a village)	~96	100%	No	LeClaire (1976)
L	Keatley Creek	~3000-1100 years B.P.	Many houses	Variable	Some fully excavated; others variable	No	Hayden (1997)
M	FbSx-9 (near Bella Bella)	Late historic	Largest house	212	100%	No	Carlson (1984)
N	Richardson Ranch	Early 18th century	Largest house	308	12%	No	Fladmark (1972)
O	McNichol Creek	1800-1500 years b.p.	Largest house (House O)	99	36%	Yes	Coupland (2006)
P	Psacelay	Late pre-contact to early contact period	House 2	169	47%	No	Martindale (2006)
Q	Paul Mason	~3200-2800 years b.p.	2 small houses	~50; ~60	~40%; 25%	No	Coupland (1988)

Table 1. Summary of information relating to major house excavations on the Northwest Coast. Values listed without "~" indicate that a higher degree of precision is known. When the "~" is used, sample sizes, house floor areas or dates have been estimated by the author, as an approximation based on published literature, rather than on specific reported values.

[a]Note: "B.P." refers to calibrated dates, while "b.p." refers to uncalibrated radiocarbon dates.

Ruggles 2007) and bucket-augering are also gaining currency as approaches to

investigate houses (or at the very least to identify potential house features) that do not

require large scale excavation.

2.3 The Ozette Site

The Ozette site (45CA24) deserves particular attention for a number of reasons: it

has an abnormally large sample of recovered material when compared with other house

excavations, it has comparable data from both high-status and low-status houses, it is

central to our understanding of houses on the NWC in general (see Ames 2005 for a full

discussion of the importance of this site to NWC archaeology), and it is a central

component of this thesis. Much of the information about the site has been published in

two edited volumes[4] (Samuels 1991, 1994) and is summarized below. The Ozette

archaeological site is located at Cape Alva near the northwestern tip of the Olympic

Peninsula, in Washington State (see Figure 2). This site is located within the traditional

territory of the Makah Tribe.

During the protohistoric period[5], the site was suddenly and catastrophically

inundated by a mudslide. This disaster has provided a significant opportunity for

archaeologists, albeit to the detriment of the inhabitants. The houses and their contents

were sealed underneath the mud in an anaerobic environment, resulting in the excellent

preservation of many different organic materials including fauna, wooden structural

remains and woven baskets. The effects of bioturbation, root disturbance and other

natural site formation processes, which have been observed at many NWC longhouse

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[4] These two edited volumes are primarily synopses of PhD research about Ozette conducted by David Huelsbeck, Gary Wessen, Stephan Samuels, Jeff Mauger and Raymond DePuydt.
[5] The absolute dates for the house occupations at Ozette remains somewhat unknown. Researchers' best estimate is that the village was initial constructed 450 years ago and occupied for about 100 years, at which point the massive clay slide destroyed a large portion of the village (Mauger 1991:181).
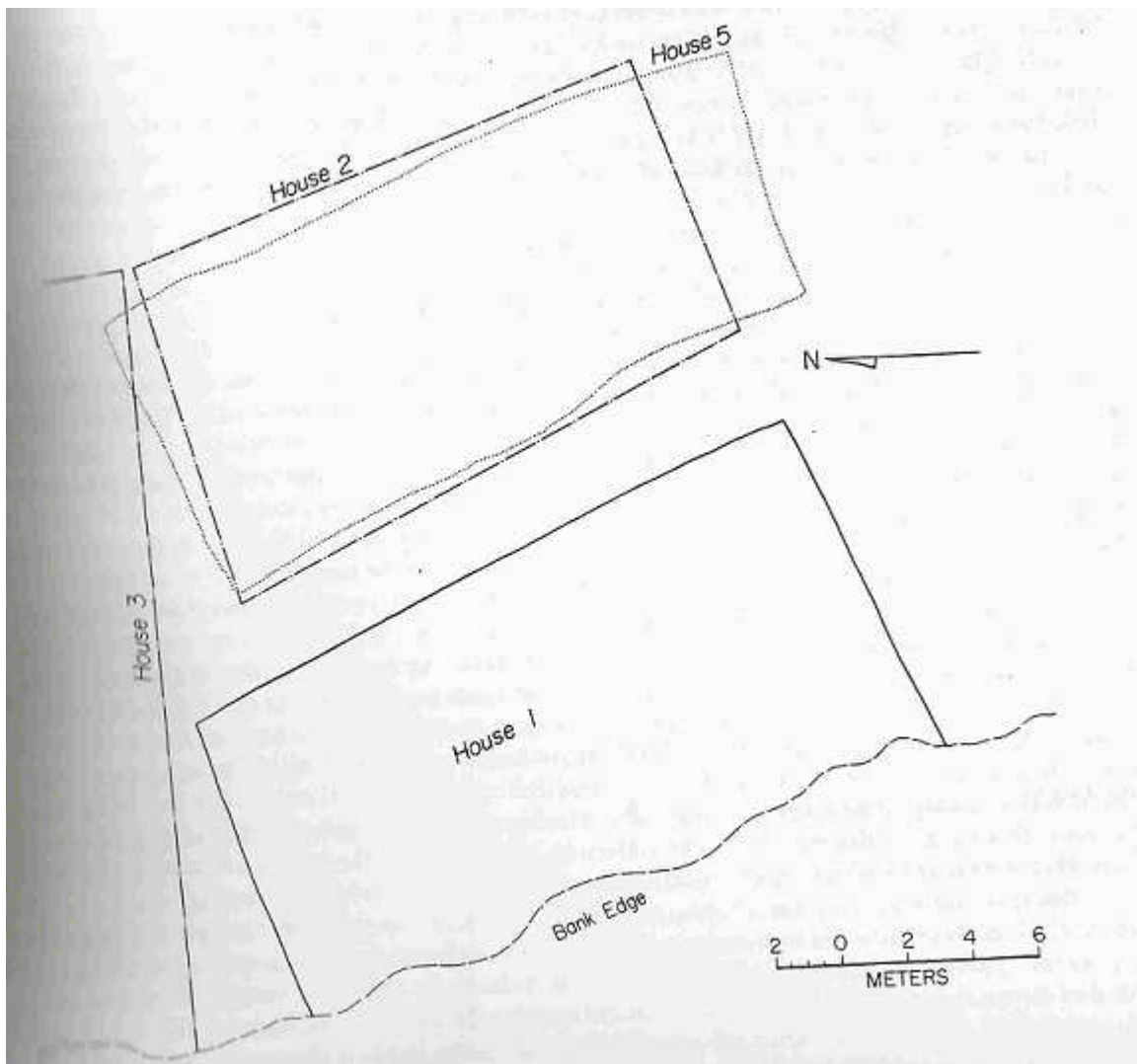
Figure 3. Spatial relationships of three excavated houses at Ozette (Courtesy Ozette Archaeological Project).

excavations, were not as great an issue at Ozette, although the mudslide itself did create

some post-depositional disturbance. The mudslide created a Pompeii effect: domestic

activities were abandoned in order to escape the mudslide and as such, one can assume

that the excavated material represents a fairly accurate picture of past daily life in the

village of Ozette, although the fauna within each house represents several distinct

activities. For example, House 1 was likely subjected to routine house-cleaning, whereas

House 2 was not, resulting in much more fauna being uncovered at the latter. House 5

was abandoned prior to the large mudslide that destroyed the other two houses, and

House 2 subsequently built on top of House 5. However, House 5 deposits can be distinguished from House 2 deposits, as clay slurries were deposited after the abandonment of House 5 and prior to the construction of House 2 (Mauger 1991). At other sites, the intentional abandonment and reoccupation of houses did not usually result in such discrete housefloor layers because they were not sealed by mudslides and/or clay slurries.

Richard R. Daugherty, during a survey of the west coast of Washington State, was the first archaeologist to record information about Ozette, noting its large size and exposed shell midden. Excavation at Ozette did not begin in earnest until 1966, during which Daugherty supervised test excavation of this site and of surrounding islands just offshore. During the summer of 1967, further test excavation uncovered the corner of a domestic structure. Throughout these field seasons, an abundance of perishable material was excavated from a water-saturated clay matrix, indicating the possibility of excellent preservation due to anaerobic conditions. A storm in 1970 eroded the sea bank and exposed the front edge of another house platform, later defined as House 1 (see Figure 3). Because of the excellent preservation of perishable material within the site, funding was secured which allowed excavation to continue at this location (Area B70) for the next 11 years. Funding was also provided in order to analyze the massive amount of data recovered from the site.

The excavations from 1970 until 1981 focused on Area B70, during which four house platforms were uncovered (Figure 3). House 1 was the house that initially caught researchers' attention because it was eroding out of the cut bank due to wave action. As such, material from the front of House 1 was not entirely recoverable, although the

majority of the house remains were found *in situ*. House 5 and House 2 were completely excavated. A three meter wide area which included the south end of House 3 was also excavated, although this sample represents a significantly smaller sample than the samples obtained from Houses 1, 2 or 5. Other houses (Houses 4, 6, 7 and 8) were also tested; however, the volume of data obtained from these houses in comparison to Houses 1, 2, and 5 is minor.

The occupation of these houses is estimated to have begun around 450 years ago and cultural materials from these occupations have been designated early, middle and late Unit V[6] (Samuels 1991:181). During the Early Unit V, House 1 and House 5 were constructed. House 5 was occupied for a short time, and was intentionally abandoned soon after, probably because this area was poorly drained and affected by several small clay slides. During the Middle Unit V, House 3 was constructed on top of the midden of House 1 and House 5. During the late Unit V, House 2 was constructed in the same location as House 5, and House 3 was probably abandoned during this period. Stratigraphic layer Unit IV was a massive clay slide, up to three meters in height, which covered the entire B70 area. Units III through I relate to the historic occupation of the village and are not reported in great detail by the Ozette researchers. Based on midden accumulation rates derived by comparing the quantity of features, stratigraphic evidence and house floor midden thickness, Samuels (2006:208) proposes that House 1 stood for approximately 50 years, House 2 for 20-25 years and House 5 for 10-12 years, although absolute dates for the occupation of houses have been difficult to determine.

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[6] The "Unit" designation refers to different cultural layers. Units VIII, VII and VI are all prehistoric cultural layers from an earlier occupation, however areal excavation has focused on the excavation of Units VI and V.

2.4 Interpretive Issues and Frameworks

Interpreting the archaeological remains of longhouses has primarily been

accomplished through the direct historical approach, in which ethnographic accounts are

used as analogues for prehistoric houses. As Ken Ames notes, the use of ethnography in

the interpretation of archaeological remains on the NWC is at times problematic:

> Ethnographic patterns (of inequality for example) are explained based on the
> presence or absence of the relevant ethnographic objects (e.g. ethnographic status
> markers e.g. labrets). The argument can become [']we know they had ranking
> because ethnographic form of ranking is present[']. The only escape from this
> circularity is to test…the links we make between the ethnographies and the
> archaeology. Despite these problems, the direct historical approach is virtually
> forced upon NWC archaeology...If the archaeological record does not fit the
> ethnographic record, then the flaw rests with archaeology. [Ames 2005:13-14].

Using ethnography is not necessarily a problem; however, when it is used in an

illustrative fashion as indicated above, rather than in a comparative one, it can be a

problematic method of interpreting the past (cf. Stahl 1993). The applicability of

ethnography to archaeological examples is only half of the problem: the other is whether

in fact the ethnography is itself accurate. As Stahl (1993:243) notes, ethnohistoric

accounts in North America "were highly selective in their reporting of contemporary

cultures due to the emphasis placed on "traditional" practice, stripped of the veneer of

modernity" and were often accepted as "unproblematic representations" of indigenous

cultures.

Despite these issues, ethnographic and ethnohistoric accounts are used to interpret

the archaeological evidence of houses. As a result, houses are frequently interpreted

within an evolutionary framework as the apogee of social complexity and a reflection of

the hierarchical nature of NWC society (e.g., Ames 1981, 2001, 2003; Ames and

Maschner 1999; Archer 2001; Coupland 2006; Maschner 1991; Matson 1985). Social

inequality, its importance in day-to-day practices, its representation archaeologically, and the causes of its development were seen and are still seen as intricately linked to these dwellings. The direct historical approach may be legitimate when excavating protohistoric houses such as the ones at Ozette (Samuels 1994) or Richardson Ranch (Fladmark 1972) or FbSx-9 at Bella Bella (Carlson 1984), although as noted above the accuracy of ethnographic accounts should perhaps be scrutinized rather than accepted at face-value. Regardless, this approach becomes much more tenuous when applied to houses that were occupied well before the contact period.

Another issue that household archaeologists have recently addressed is the functional approach. Because they have emphasized the materiality of the house and household as a unit of economic cooperation which simultaneously communicates the power of the elite through their accumulation of resources derived from this cooperation, these interpretations neglect to consider other ways in which social structure may be maintained or contested.

The recently published volume entitled *Household Archaeology on the Northwest Coast* (Sobel et al. 2006) provides proof that we are beginning to move beyond functional, materialistic, economic and technology-driven interpretations, although some important topics, such as the archaeology of gender and the archaeology of children, have yet to be explored in-depth. Grier (2006) uses Bourdieu's theories, in particular his notion of *habitus*[7], to analyze NWC houses from a new perspective; one that considers the transfer of ideational structures of a household from generation to generation (and how

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[7] The notion of habitus (Bourdieu 1977:72) rests on the idea of routinized behaviour, or "dispositions" which are inculcated through one's interaction with the material and social world. In his ethnographic exposition of habitus, Bourdieu argues that the house is often an important location where the habitus is inculcated, which dovetails nicely with the importance of the house on the NWC.

these may be represented archaeologically) rather than focusing only on the material reproduction of the house by household members.

Coupland (2006) incorporates Blanton's ideas about canonical and indexical communication within the built environment into his analysis of a prehistoric house at the McNichol Creek Site. Blanton (1994, 1995) argues that the built environment communicates non-verbal symbolic messages and meanings. Canonical communication is closely related to Bourdieu's notion of habitus[8]: "typically, symbolic communication through the medium of the dwelling involves the creation of a built environment that manifests social divisions based on gender, generation and rank, [and] links cosmological schemes that express categorical oppositions" (Blanton 1994:10-11). Indexical communication refers to non-verbal messages which are communicated to individuals who are not part of the household. Coupland (2006) successfully applies these two theories of communication via the built environment, demonstrating that the largest house at the McNichol Creek site was very likely an expression of the chief's power to both members of his own household and to other households.

Another theoretical framework that may be applied to the NWC is Foucault's (1977:197-228) theory of panopticonism. The Panopticon was originally developed as an architectural layout for a prison. Foucault (1977:205) extends this concept beyond the setting of the prison, arguing that the Panopticon must be "understood as a generalizable model of functioning; a way of defining power relations in everyday life". The functioning of the Panopticon is accomplished by an architectural form that is highly

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[8] Blanton explicitly acknowledges this similarity and actively utilizes Bourdieu's theory in explaining canonical communication.

structured and allows a few individuals to observe many. The spatial organization of the

Panopticon consists of an

> enclosed, segmented space, observed at every point, in which individuals are
> inserted in a fixed place, in which the slightest movements are supervised, in which
> power is exercised without division, according to a continuous hierarchical figure,
> in which each individual is constantly located, examined and distributed among the
> living beings… – all this constitutes a compact model of the disciplinary
> mechanism. [Foucault 1977:197]

This model has distinct features that parallel the spatial organization of the

interior architecture of Northwest Coast longhouses. As noted above, family living areas

in a longhouse were spatially distinct, and therefore the elite could easily have monitored

each family whose location was clearly "fixed in space". The ability to monitor extends

beyond locating individuals in space to include the activities that were occurring within a

space, as well as individuals' interactions and communications with others. In essence, all

activities, including interactions between individuals could easily be monitored by the

elite.

The Panopticon, however, allows for an even more insidious form of power to be

established than that accomplished by direct surveillance. Individuals who recognize that

they are under surveillance begin to discipline themselves:

> He who is subjected to a field of visibility, and who knows it, assumes
> responsibility for the constraints of power, he makes them play spontaneously upon
> himself; he inscribes in himself the power relation in which he simultaneously
> plays both roles; he becomes the principle of his own subjection. [Foucault
> 1977:202-203]

Commoners and slaves on the Northwest Coast would have monitored their own

activities, induced by multiple sources of observation. The high status individuals would

have had their backs against a wall in the corners of the dwelling, thereby negating the

possibility that someone else could observe them without their knowledge. This provides

an explanation for why the elite chose to occupy the corners of the house: it allowed them to monitor others, without inducing a feeling of surveillance and therefore of self-discipline.

From an entirely different perspective, Marshall (2006) argues that we need to see NWC settlements in terms of "continuity and change" rather than in linear, stage-like (evolutionary) progressions which are usually considered to be the result of environmental factors. She proposes that we shift our analyses from the study of the temporal sequences (typically defined by tool typologies) to an examination of "place". In order to do so, she combines Levi-Strauss's concept of *House societies* with Peter Wilson's concept of *Domesticated societies*. In House societies, the house is the material expression of a household's ability to socially reproduce itself over time: "[h]ouses link social groups with architectural units that facilitate their physical delimitation and position in society, thereby integrating the social with the material life in its pragmatic and semiotic aspects" (Gillespie 2000:2). This perspective is useful because it integrates non-material aspects of daily life (signification, meaning, and social reproduction) with the material aspects of life (the house).

Domesticated societies are those which form some sort of permanent connection between places and people, thus bounding a specific area as living space (e.g., the village) and differentiating it from the outside world. Marshall (2006) demonstrates that the earliest indigenous NWC inhabitants – those without houses – would have imbued spaces with a variety of cultural meanings just like the later inhabitants who built houses did. From this perspective she therefore emphasizes cultural continuity rather than change and evolution.

2.5 Methodological Issues

In addition to interpretive issues there are several methodological issues inherent in excavating houses on the NWC. The latter of these, while separated from interpretive issues in order to present the ideas clearly, are to a certain extent mutable with the interpretive issues described above. For example, a large part of the focus of past research was aimed at developing the culture history of a region (a theoretical/interpretive orientation) which necessitated excavation units to reach basal (non-cultural) deposits which spanned the entire temporal occupation of the site (a methodological consideration). These deposits can be represented by several vertical meters of cultural deposits. While current research has moved beyond culture-history, excavation sampling strategies have evolved little. One suspects that this may be the case because new strategies have not been developed, rather than the alternative conclusion that the current strategy is the most optimal.

Another methodological issue is the lack of direct comparability between samples. Different excavation strategies used at different houses force one to confront the possibility that the data are not directly comparable because different sample sizes are often utilized. This is less of an issue if the differences in sample sizes are acknowledged, but this is rarely done explicitly. Archaeologists have often compared the data from their own excavations with data from Ozette because of its importance on the NWC (e.g., Ames et al. 1992; Coupland 2006; Grier 2006). Having discovered spatial patterning within a house that correlates closely to the data at Ozette, as well as ethnohistoric records, these researchers have posited conclusions similar to those of the researchers at Ozette. If large sections of the house are not sampled at all, it is difficult to say whether

or not the patterns discovered truly reflect the same spatial patterning as at Ozette, since the unexcavated areas may contain data which are incongruent with the Ozette data.

Deciding which feature(s) in a village one wishes to excavate is another methodological issue that researchers are forced to confront, since an entire site cannot be excavated. On the NWC, it is generally the larger houses at a site that have been excavated (Ellis 2006; see also Table 1). When other smaller houses are in fact excavated, the sample size is usually smaller, and the spatial configuration of excavation units is not the same as that used for the largest house, making it hard to compare different houses within a single site as well as to carry out inter-site comparisons. This is not to suggest that all house excavations should follow the same template so as to facilitate comparison; this notion is unreasonable given the idiosyncrasies of different research goals. Rather, if comparison between different houses and households is one of the expressed goals of a given research design, then questions of comparability should be considered prior to implementing the sampling designs. This issue has not been directly addressed in the published literature.

Finally, excavation is complicated by site formation processes (e.g., Smith 2006). The single most challenging, albeit beneficial, factor to address is the quantity of data that exists due to the excellent preservation of faunal remains within shell middens.[9] Other natural site formation processes may also complicate the excavation of houses. For example, the presence of large trees, which sometimes grow on the remains of house platforms, make it difficult to sample those areas of the house beneath the tree (e.g., Coupland 1999:11). Furthermore, bioturbation, root disturbances and the deposition and

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[9] This is of less concern in situations where shell middens do not form a significant part of the house floor assemblage, as is the case for some sites (see Table 1).

subsequent decomposition of organic matter are all significant factors in the formation of archaeological deposits on the NWC. Grier (1999:18) explicitly states that some of these factors influenced his choice of houses to sample at Dionisio Point, choosing to excavate House 2 and House 5 in part because "they appeared to be well preserved (based on surface expression)".

Cultural site formation processes may be equally complex: multiple and/or long-term occupation, abandonment and reoccupation of house locations are documented ethnographically (Suttles 1991) and archaeologically (Grier 2006; Samuels 1991). In the case of abandonment, the planks used for the sides and roof were often removed, leaving only the house posts intact. Upon return to the village, the house was rebuilt. Whether the new house was exactly the same size and shape as the original is often unknown; the fluctuating population of households may have prompted remodeling of the longhouse in order to accommodate newcomers (Suttles 1991). In addition to the above disturbances, specific behaviours within localized areas of the house (i.e. "activity areas") can create intricate and discontinuous stratigraphy. Some remains may be the result of a single behavioural episode (e.g. lithic debitage related to the manufacture of a single tool), while other evidence may represent repeated behaviour over years (e.g. use of a hearth). Because of the range of activities that occurred within these dwellings, the spatial distribution of artifacts, ecofacts, and features is often complex and heterogeneous. In short, a NWC house floor is a palimpsest created by behaviours which occurred on a variety of spatial and temporal scales.

In summary, the house was a key locale, materially and socially, for Northwest Coast societies. In part because the ethnographies of the region are replete with descriptions of the centrality of houses in daily life, and in part because methodological issues prevent the excavation of a large number of these dwellings, the direct historical approach is almost always utilized as an interpretive tool to understand archaeological examples of houses, which, as noted above, may be problematic. A careful consideration of sampling methods has the potential to address these issues and is the focus of Chapters 3 and 4.

Chapter 3: Sampling Method and Theory

In this chapter I review several key aspects of sampling theory and how sampling methods are applied by archaeologists. Initially, I provide a general overview of sampling and explain some of the sampling methods used by archaeologists. Secondly, I review various methods of estimating the effects of sample size as discussed in zooarchaeological literature. Finally, I consider how sample location affects the interpretation of human behaviour within the context of the modifiable areal unit problem (MAUP).

3.1 Sampling Overview

Sampling is a key element of archaeological practice and, due to the variety of sampling strategies available, selecting a specific sampling strategy requires a focus on the major methodological and/or theoretical components of the research objectives. The choice of sampling strategy eventually selected influences the range and the variety of data that is gathered, which, in turn, will affect the types of questions that can be answered. Furthermore, though these strategies are pivotal to establishing validity and/or statistical confidence in one's interpretations of the data, they are often only partially understood (Aldenderfer 1987; Orton 2000). Archaeologists have always recognized that site formation processes alter the constituents of a population (i.e., change the sample) as it is transformed from a living assemblage to a deposited assemblage to an archaeological assemblage (Orton 2000; O'Connor 2000; Reitz and Wing 1999; Schiffer 1976). However, an explicit interest in how to sample an archaeological assemblage did not occur until the 1960s (e.g., Binford 1964; Vescelius 1960). The subsequent interest in sampling generally focused on the feasibility of implementing probabilistic rather than

non-probabilistic sampling, as the former method dovetailed well with the hypothetico-deductive methods that were popular during the 1960s and 1970s (Hole 1980; Mueller 1975; Plog 1978). Currently, sampling literature has become much more statistically rigorous, although the volume of literature devoted specifically towards sampling issues has lessened since that time (Orton 2000).

Archaeologists' attitudes towards sampling are diverse. Orton (2000:4-5) lists seven caricaturized attitudes towards sampling, although he admits that there is mutability between the various caricatures. Many archaeologists continue to treat sampling with trepidation, annoyance or inevitable resignation, and this attitude is somewhat understandable, as the logistical constraints involved in the implementation of a probabilistic sampling technique and the mathematics required to describe the reliability of such a sample can be frustrating (Hole 1980). Others address sampling in order to evaluate the effect of sample size, or to critique the work of others (e.g., Lepofsky and Lertzman 2005; Lyman and Ames 2004; Lyman 2008). Another attitude towards sampling, the one I favour, is to investigate sampling to observe whether it is possible to "do more with less" (e.g., Monks 2000; O'Neil 1993), either because the funding/resources are not available for larger projects, or because limited excavation limits the destruction of the archaeological record.

Sampling occurs at a variety of scales. At the regional scale, archaeologists have evaluated the efficacy and biases of different sampling methods to detect, and subsequently predict, the presence and density of archaeological sites on landscapes (e.g., Alexander 1983; Plog 1978; Read 1986). When the focus of investigation is a single archaeological site, the sample should be designed to be representative of specific areas

of the site, or in some cases the entire site (e.g., Nance 1981; Orton 2000; Shott 1987).

The selective recording and collection of features, artifacts and ecofacts during

excavation are other critical components of the sampling process which includes certain

components of the archaeological record for study while excluding others. The mesh size

used while screening excavated material is another prime example of how sampling

procedures will influence the quantity and diversity of artifacts or ecofacts (Peacock

2000; Zohar and Belmaker 2005) and is well-documented on the NWC (e.g., Casteel

1972; McKechnie 2005; Stewart et al. 2004). Additionally, material that is collected but

not identified, because the resources (be they monetary, lack of adequate reference

collection, etc.) are not available further reduce the size of a sample (Orton 2000). The

resultant data are then selectively used to develop theories and make generalizations

about the entire assemblage and/or cultural behaviours.

3.2 Sampling Terminology and Methods

The terms used to describe different components of the sampling process are

explained below in order to maintain clarity throughout this thesis. The *population* refers

to all of the constituents of interest, e.g., all of the faunal remains from a single house.

The *sample fraction* or *sample size* refers to the amount of material that is included in the

sample. This can be quantified in a number of ways, but generally includes the number of

objects found (e.g., for zooarchaeologists the number of identified specimens (NISP)),

and/or the area or volume of excavated material. The *sample method* refers to the

procedure used to draw samples from the population. Sample methods fall into three

categories: non-probability sampling, probability sampling, and systematic sampling

methods, and are explained in detail below. In this thesis, then, *sample strategy* refers to

both the size of the sample (the sample fraction), as well as the way in which the sample was selected (the sample method).

The non-probability method of selecting excavation units is synonymous with judgmental, grab, or haphazard sampling, and requires intentional selection (Orton 2000:21). Archaeologists often use this type of sampling when they have knowledge of or have made assumptions about the archaeological deposits prior to excavation, or because logistical issues make other types of sampling difficult. Using this method of sampling to the exclusion of all others receives little endorsement from statisticians or archaeologists specializing in sampling techniques (Orton 2000:21), and may result in significant constraints on the interpretation of the data generated, (although this is not always the case).[10] Selecting features judgmentally prior to laborious excavation is a useful strategy, as long as researchers recognize that they may be overlooking features that have no surface expression, or which are not detected through the use of survey instruments such as ground-penetrating radar, aerial photography, etc. On the NWC, the visibility of house platforms and/or structural remains in some cases allows archaeologists to sample the interior of these dwellings without requiring extensive excavation to determine the boundaries of the houses. However, features and/or sites that have no identifiable surface expression will not be identified unless other sampling methods are used.

Probabilistic sampling, also known as random sampling, requires that the units to be tested be chosen from a set of randomly generated numbers. Within the rubric of probabilistic sampling, there are a variety of different methods that may be employed, depending on the purpose of the investigation: these include simple random sampling,

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[10] As noted in Chapter 2, samples of different sizes and shapes are compared directly in NWC archaeology; an instance when sample size should have been considered when interpretation was undertaken.

stratified random sampling, cluster sampling and sampling with probability proportional to size. The advantage of this type of sampling is that it allows archaeologists to generate estimates of reliability for the sample in question, but it does not necessarily result in a more representative sample than a judgmental sample (Orton 2000:8).

In contrast to the methods described above, systematic sampling requires that samples be selected at equal intervals within the sample area. This type of sampling may be problematic if a specific element within the population is located at intervals that are the same as the sample interval. In this case, the elements in question will be present in all or none of the samples. In order to minimize the possibility of this situation occurring, a stratified systematic sample method can be used, in which the sample area is gridded and an excavation unit placed randomly within each section of the grid such that even yet unaligned sampling of the sample area occurs.

3.3 Identifying Sample Size Effects

Identifying the effects of sample size is addressed in-depth in zooarchaeological literature[11] (e.g. Grayson 1984; Lyman 2008; Plog and Hegmon 1993). Three main approaches are utilized to investigate different facets of the sample size effect: the sampling to redundancy approach (Lyman and Ames 2004, 2007), the rarefaction approach (Gotelli and Colwell 2001; Lepofsky and Lertzman 2005; Tipper 1979), and the regression approach (Grayson 1984). The goal of all of these methods, often represented graphically as "species-area curves" (SAC), is to analyze the relationship between sample size (defined in terms of volume excavated, area excavated or NISP) and the number of

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[11] I focus on this literature as it is faunal remains that I analyze in Chapters 6, 7 and 8. The theory explained in this section can be applied to other classes of archaeological data such as lithics.

different taxa identified (i.e., richness or NTAXA; (see Lyman and Ames 2007; Lyman

2008:164-167 for a discussion of SAC curves).

3.3.1 Sampling to Redundancy

The sampling to redundancy approach (Lyman 2008; Lyman and Ames 2004) is

used to determine at what point the addition of new samples is unlikely to produce new

information for a given assemblage; it should not be used to compare richness between

two or more populations (Lepofsky and Lertzman 2005). Following Lyman and Ames

(2004, 2007), NTAXA from a given subsample (e.g., from a single excavation unit or

from a single field season) is plotted versus sample size; information derived from

subsequent units or field seasons are added cumulatively until the entire sample has been

plotted. Once all subsamples are graphed, if the curve of the line is asymptotic (Figure

4a.), redundancy has been reached and it is argued that new samples are unlikely to

increase taxonomic richness. Alternatively, if the curve of the line continues to rise

(Figure 4b.) then sample redundancy has not been reached and new samples are likely to

produce new taxa. There are several issues inherent to this method (see Lepofsky and

Lertzman (2005) for a full critique). The most significant of these is that the sequence in

which subsamples are added to the graph will affect the curve of the line and can result in

the redundancy criterion being reached when in fact some taxa have not yet been found,

i.e., "false plateaus" (Lepofsky and Lertzman 2005:189). This is most likely to occur for

populations that consist of a few ubiquitous taxa and many rare taxa, a commonly

observed pattern for many archaeofaunal assemblages (e.g., Grayson 1984). One possible

solution for this problem is to select samples randomly, although this does not necessarily

eliminate the problem. Nevertheless, the simplicity and ease of interpretation with this

method make it an attractive method of indicating adequate sample size for a single

population.
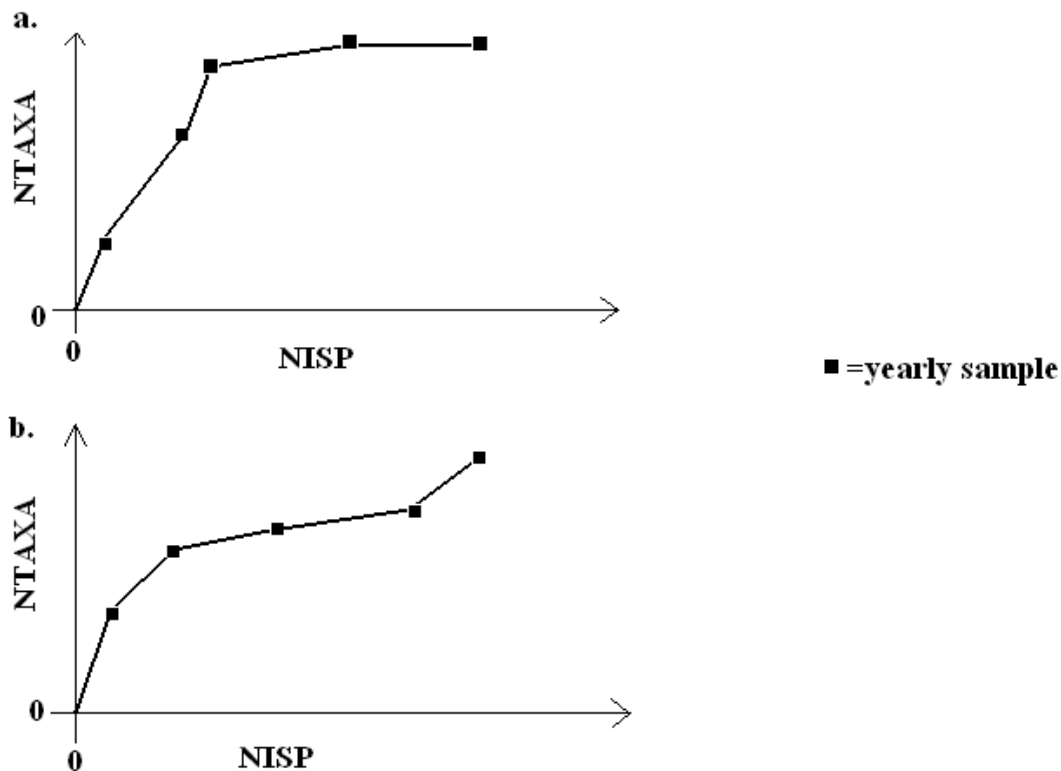
Figure 4. Example of sampling to redundancy showing hypothetical data from two separate sites, Site a. and Site b. When data from the samples from each of five field seasons at Site a. are successively added to the data from the previous field season, the final field season produced no new taxa and therefore the redundancy criteria has been reached. When the same procedure is performed at Site b., new taxa are uncovered in the final sample, indicating redundancy has not been reached.

3.3.2 Rarefaction

The rarefaction method can be utilized to compare different assemblages because

it reduces the NTAXA of larger samples to make them comparable with smaller samples,

and therefore rarefaction curves from different populations of different sample sizes can

be compared (Baxter 2001; Tipper 1979). Briefly, one variation of this method requires

that subsamples are randomly and repeatedly drawn from an assemblage, and the mean

NTAXA value for each sample size is used to create a smoothed rarefaction curve with

confidence intervals for a given assemblage (Gotelli and Colwell 2001:380; Lepofsky and Lertzman 2005:185). Kintigh (1984) proposed a variation of the rarefaction method in which assemblages are combined and constituents are drawn randomly from the new cumulative assemblage. Mean NTAXA values for each sample size are generated by the simulation and are defined as the expected richness. Actual samples can then be compared to this expectation (e.g., McCartney and Glass 1990). Kintigh's (1984) simulation approach has been heavily criticized on the basis that, by combining several different assemblages, one is assuming that the parameters of the population from which the sample has been taken are known, even though this is rarely the case in archaeology (Rhode 1988). Despite this fact, rarefaction curves are considered to be the most reliable method of comparing the richness of samples of different sizes (Lepofsky and Lertzman 2005; Orton 2000).

3.3.3 Regression

The regression approach is used to identify whether sample effect exists for a given target variable between samples of different size (Lyman 2008; Rhode 1988). This approach involves creating a bivariate plot of the target variable of interest (e.g. NTAXA) versus sample size and then determining the best-fit regression line for these samples. As Grayson (1984:138-148) notes, if there is a significant correlation between the variable of interest and sample size, then comparison between two samples should be undertaken very carefully. Comparing the slope of regression lines for different samples or considering why certain samples are statistical outliers are other avenues of research which can elucidate sample effects using the regression approach (Lyman 2008).

3.4 Identifying the Effects of Sample Configurations: the MAUP

The effects of sample location are not a central methodological issue in sampling literature, probably because the same phenomena cannot simultaneously be investigated using two different sample methods. Since the target population which is sampled during archaeological inquiry is rarely able to be completely excavated, collected and identified, even if it were possible to excavate the same assemblage using two strategies, evaluating which was more optimal would still be no simple matter. While there is no panacea for this problem, the MAUP, or modifiable areal unit problem, is a useful framework which can be used to articulate some of the problems of sample location. Below, I discuss ecological fallacy, explain what the MAUP is, and why it is an important issue to consider with respect to analyses of spatial data in archaeology. I will then demonstrate how the MAUP can be applied as a conceptual framework to help understand issues associated with archaeological sampling methods and the interpretations of house remains on the NWC.

3.4.1 Ecological Fallacy and Issues of Scale

At the root of the concept of ecological fallacy are the inferences or assumptions that are made about a specific population. These inferences are the result of gathering data at a specific scale or resolution, and then attempting to apply the results of this analysis to another scale or at a different resolution (Harris 2006; King 1997; Marceau 1999). For example, an archaeologist studying lithic remains from two hypothetical sites, Site A and Site B, discovers that, at Site A, 90% of the lithic assemblage consists of bifaces, while at Site B, only 15% of the lithic assemblage consists of bifaces. However, when the archaeologist randomly (without looking or touching) selects a single stone artifact from each assemblage, he or she is surprised to discover that the artifact from Site

A is not a biface, while the artifact from Site B is a biface. This surprise is the result of the principle of ecological fallacy: the characteristics of the assemblage, which have been analyzed using one particular scale, do not necessarily apply to individual artifacts, which are analyzed at a scale that is different than that used for the entire assemblage. In the context of archaeological excavation, ecological fallacy is sometimes unavoidable. For example, when fauna is collected, the density of faunal remains may differ significantly if it is calculated based on 50cm X 50cm (50 centimeter by 50 centimeter) units rather than on 2m X 2m (2 meter by 2 meter) units, especially if faunal distribution is "patchy". This example of ecological fallacy also provides an example of the MAUP.

The MAUP is associated with analyzing areal data; in other words, analyzing a set of aggregated data that are derived from a specific geographical location or region (Figure 5). Because the data are only available in aggregated form, one is forced to assume that the data discovered within each unit were distributed homogeneously within the unit, even though this is an ecological fallacy. The issues associated with the MAUP have been known to geographers for a long time; however, they have received little mainstream attention in the discipline of geography (Openshaw 1984; Setton 1996). In archaeological literature few researchers have explicitly acknowledged the problems caused by the MAUP or investigated its effects (Harris 2006).

When considering the specific geographic area one is studying, the MAUP occurs when it is possible to subdivide the space within the study area in a number of different ways, and thus create new areas or areal units within the initial study area, hence the designation of "modifiable" in the acronym MAUP. By changing the size and/or shape of an areal unit, often a subjective or arbitrary process, one may also discover that one has

changed the values of the data associated with these units (Amrhein 1995; Openshaw 1984; Svancara et al. 2002). Setton (1996:9-13) provides an excellent overview of studies which have empirically examined the effects of the MAUP. For those studying the social sciences, the MAUP is a particularly complex issue because, in many cases, the size of a particular areal unit has no logical correlation with the cultural/behavioural processes being studied (Harris 2006). If several different phenomena are being studied at once, the ideal scale of analysis for a particular phenomenon rarely coincides with the ideal scale of analysis for every other phenomenon one wishes to analyze (Marceau 1999).

It is possible to more rigorously examine the issues described above by considering two problems which form the basis of the MAUP: the aggregation problem and the configuration problem. The first of these two, the aggregation problem, occurs when two or more contiguous areal units are combined to form fewer, larger areal units (Figure 5B and 5C). In the example given in Figure 5, the mean value of each unit changes once the smaller units have been aggregated. Furthermore, the variability that is obvious in each smaller areal unit (Figure 5A) is no longer apparent in the larger, aggregated units (Figure 5B and 5C), a trend observed in many analyses of aggregated data (Setton 1996). The second problem, the configuration problem, is the result of dividing up the area under study using a number of different configurations, but without changing the total number of areal units. The effects of different configurations are illustrated in Figure 5D and 5E.
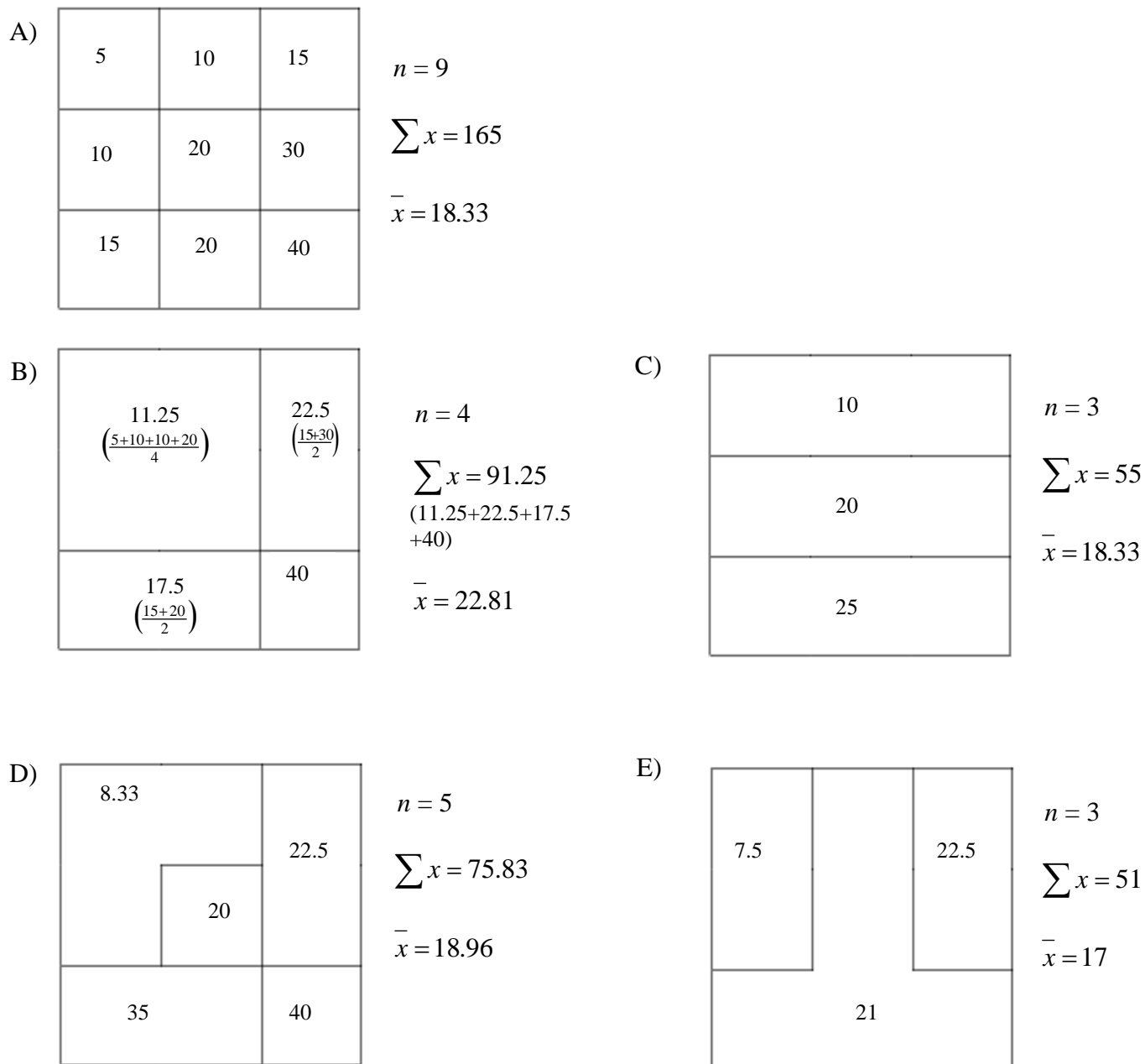
Figure 5. This figure illustrates the effects of MAUP as a result of different aggregations and configuration on areal data. Figure 5B illustrates how values for aggregated areal units are calculated. Modified from Amrhein (1995:106).

Numerous studies have attempted to determine a systematic way to manipulate data in order to correct for the effects of the MAUP. The results of these studies conclude that no systematic method to correct the problem caused by this effect exists (Amrhein 1995; Openshaw 1984). Several solutions have been proposed, but these are impractical

as "real-world" solutions (see Setton 1996:21-28). Given the non-systematic effects of the MAUP, many researchers have chosen to avoid the issue altogether (Openshaw 1984). However, recognizing and articulating how the MAUP affects areal data is a preferable alternative to accepting the results as unproblematic and unbiased.

3.4.2 The MAUP and Archaeology

Given that the MAUP is a problem related to the analysis of spatial data, and as all archaeological data are inherently spatial, archaeologists should have an interest in the effects of the MAUP. However, this term is relatively unknown in archaeological literature, and there are only a handful of archaeologists who consider its effect. A first step in clarifying the MAUP issue is to consider when it is *not* an issue. The MAUP does not apply when point distributions, rather than spatially aggregated data, are analyzed. While point-provenience data are preferable from the perspective of eliminating the effects of the MAUP, this form of data collection is often an impractical means of recording information during an archaeological investigation. In some cases, point data may need to be aggregated and thus the data is transformed into areal data, or, the quantity of data that is excavated may be too great to allow for the recording of the 3-dimensional provenience of every artifact and ecofact. Any remains collected via screening, often a significant component of archaeological investigations, become part of the areal data set for a given site. When spatial analysis is performed on archaeological remains that have not been point-provenienced, the effects of the MAUP should be addressed.

The effects of the MAUP apply in a number of different cases with respect to archaeology. A prime example of all three types of aggregation occurs when

archaeologists attempt to quantify faunal remains using the minimum number of individuals (MNI) statistic (e.g. Grayson 1984; Lyman 2008). While the effects of aggregation for faunal quantification may be problematic, using alternative lines of evidence (such as stratigraphy) make it much easier to decide whether or not aggregation is meaningful in some way and therefore warranted.

The basic areal unit used to excavate archaeological remains is often a 1m X 1m (1 meter X 1 meter) square, an arbitrary unit of analysis. The cultural and natural processes which create spatial distributions rarely coincide with 1m X 1m (Harris 2006). Even if by some coincidence there was a behaviour that produced spatial data that coincided exactly with a 1m X 1m square (i.e. excavation unit), archaeologists would have to place this unit in the exact location of the spatial distribution of data without knowing it existed beforehand, in order to record the spatial distribution in its entirety. This is clearly an implausible scenario. Excavation units, be they trenches, square units, test pits, etc., are therefore de facto areal units that are subject to the effects of the MAUP in which "the imposition of artificial units of spatial reporting on continuous geographic phenomena [result] in the generation of artificial spatial patterns" (Heywood et al. 2002:8).

In order to address this issue more concretely, Ozette is presented to examine the aggregation of areal excavation units at that site. Consider Figure 6, which shows two different conceptual schemas (or configurations) of dividing up the space within House 1 at Ozette (Samuels 1994:109-111). In schematic "A", 12 areal units are delineated. In
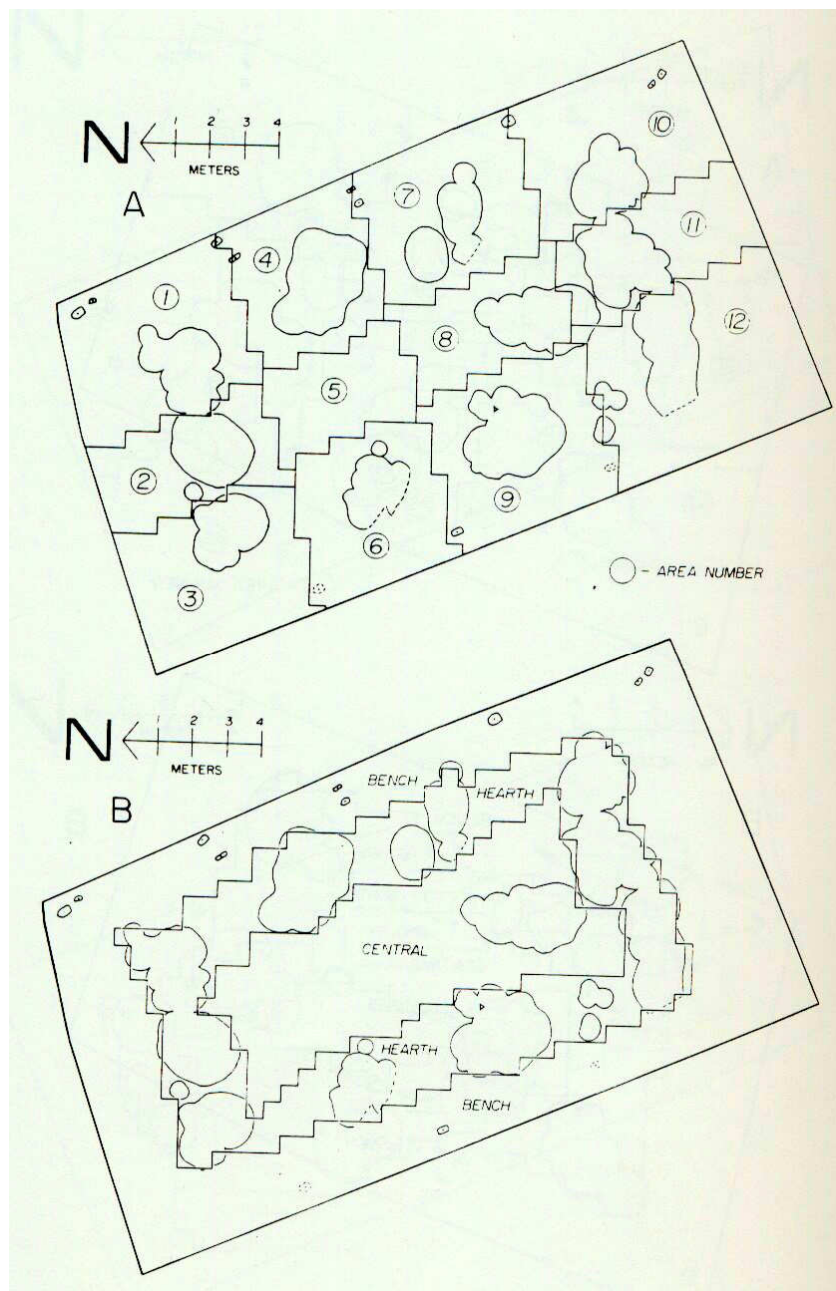
Figure 6. Different conceptual schemes that could be used to organize space and delineate areal units within a NWC longhouse (Ozette House 1 shown above). Note how hearth features (the twelve irregularly drawn objects within the house) are used in each case to define the different units within the house.

schematic "B", three areal units are delineated for each house. These areal units are the

result of aggregating a number of 2m X 2m excavation units, which are also areal units.

Aggregations "A" and "B" are meant to infer different facets of everyday life: the former

delineate nuclear family living areas and associated social status, while the latter

delineate functional areas within the house. The aggregated faunal data for each areal unit

helps in the interpretation of the function of each unit (Samuels 1994). Similar

discussions of the different functional uses of space for other longhouses also exist (e.g.,

Coupland 2006; Matson 2003; Smith 2006).

One could consider what the result would be if only one out of the two

configurations was analyzed, or if a different configuration altogether was utilized. It is

likely that the interpretation of the faunal data would be significantly different. Because

of the extensive excavation and multiple lines of evidence utilized at Ozette (architectural

remains, features, and ethnographic evidence), archaeologists have been able to make a

convincing argument that the areal units they used represent meaningful social

boundaries rather than arbitrary boundaries. However, when other lines of evidence are

not available the MAUP may become a much more difficult problem to resolve. This can

occur when the time-depth is too great to use the direct historical approach, or if the

entire house is not excavated and therefore the spatial relationships between features such

as hearths are difficult to interpret. In these cases, archaeologists must aggregate areal

data in an arbitrary manner, and then justify the specific aggregation and configuration

that was used. The analysis of spatially aggregated data is perceived by the archaeologist

to represent past human behaviour, when in fact specific aggregation of contiguous

excavation units may be confounding the interpretation of these behaviours.

This chapter has summarized the main types of sampling strategies that are

currently employed by archaeologists, and has discussed methods used by

zooarchaeologists to investigate the issues and problems related to sample size. Sampling

issues related to sample location and configuration have received much less attention, and I have proposed that the MAUP provides a useful framework to consider the location of sample units and the effects of spatial configuration on archaeologists' interpretation of assemblages which are not point-provenienced. In Chapter 2 (Section 2.5) I noted that house excavations on the Northwest Coast are complicated by a variety of issues idiosyncratic to this region, and that sampling may be able to address them. In the following chapter (Chapter 4) I investigate NWC sample methods within the context of the sampling issues described above.

Chapter 4: Sampling on the Northwest Coast

4.1 Sampling Studies

Given the logistical difficulty of excavating the entire spatial extent of plankhouse floors on the NWC, one would expect sampling methods to be of central concern for archaeologists working in this region. The biases associated with particular sampling strategies have been investigated with respect to shell middens on the Northwest Coast; however, this body of research generally refers to exterior midden contexts rather than to interior house floor midden (e.g., Cannon 2000; Casteel 1972; Greenwood 1961; Monks 2000; O'Neil 1993; Stewart et al. 2004; Treganza and Cook 1948). Furthermore, these studies generally focus on the biases related to different recovery techniques (e.g., Casteel 1972; McKechnie 2005; Stewart et al. 2004) or on changes in relative abundance of taxa over time (e.g., Cannon 2000), rather than addressing how the spatial location of a sample unit within a site may bias its contents, although McKechnie (2005) does address this facet of sampling. Studies by Lyman and Ames (2004, 2007) and Lyman (1991, 2008) have examined sampling issues from a broad theoretical perspective using faunal assemblages from sites in Washington and Oregon as examples; however, these studies are not primarily concerned with the methodological issues of data-rich shell middens on the NWC in conjunction with the sampling procedures utilized by NWC household archaeologists.

There is relatively little previous sampling research in the region which is directly relevant to the research in this thesis. Monks (2000) provides a useful discussion on sampling in his analysis of the faunal data from the Nuu-chal-nulth site of Ma'acoah, located in Barkley Sound. As a heuristic exercise, he randomly selected 100 faunal

records for all ichthyofauna (each record grouped by unit, stratigraphic level and taxon) to observe the effects of sample size on the richness and diversity of a subsample when compared to the complete assemblage.[12] His analysis suggested that as little as 25-30% of the entire assemblage (quantified in terms of NISP and drawn randomly), was required in order to accurately characterize the diversity and richness of the entire ichthyofaunal assemblage. Since all fauna from the site are grouped together to form one assemblage, the effects of sample method are not investigated. In another study, O'Neil (1993) excavated a shell midden in California, arguing that significant[13] components of the midden were not detected until approximately 50% of the spatial extent of the midden was excavated. The above studies highlight the fact that no one sample fraction will be ideal in all situations and that the sample strategy employed will depend heavily on the research goals.

Spurling (1976), while not explicitly working with domestic house deposits, compared the efficacy of simple random sampling with that of judgmental sampling to detect artifacts within a shell midden in Esquimalt Lagoon (situated near Victoria, British Columbia). Statistical comparison between the two samples revealed that they could both have been derived from the same population and he concluded that neither strategy was more optimal than the other (from a statistical point of view) (Spurling 1976:64). Only one article exists that explicitly examines spatial sampling issues within a domestic structure on the NWC (Blake 1974). Blake (1974) utilized data from a previously excavated pithouse from the Lillooet area and subsampled the artifacts and ecofacts from the excavation in order to investigate the benefits of different types of probabilistic

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[12] The completed assemblage had a NISP of 5553, which Monks (2000) recognizes is a sample as well.
[13] In this specific study, the significant discovery was the detection of a historic component to the site.

sampling. He concluded that stratified random sampling was the most beneficial method to use (1974:15). Using this method, the house floor was divided into different areas to be sampled based on the functional use of space within the house, which included (1) the central and peripheral floor of the pithouse, and (2) the bench and wall area of the house.

Other reports explaining the excavation of houses rarely devote more than a brief paragraph to explain the sampling rationale that has been employed. A further example of this lack of research interest in sampling can be found if one refers to the introduction of *Household Archaeology on the Northwest Coast*. The authors state that

> The studies in this volume address a variety of methodological concerns. Among these concerns, three seem especially important to the productive analysis and interpretation of the archaeological remains of households: 1) methods for studying the site formation processes that create household remains, 2) identifying useful archaeological correlates of the household, and 3) the integration of ethnographic, ethnohistoric, and archaeological household data. [Sobel et al. 2006:8]

To these considerations I suggest adding a fourth: namely, a concern with sampling methodology.

4.2 Sample Strategies Used to Excavate Houses

There exist fewer than 20 sites where large-scale excavation of longhouses has occurred (see Figure 2 and Table 1). Of all of the longhouses excavated on the Northwest Coast, few examples exist where the house floor has been excavated to its full spatial extent. "Corner Post House", located on the northwestern tip of Graham Island in Haida Gwaii (also known as the Queen Charlotte Islands), was entirely excavated by Gessler (1975). Data from this excavation were not published and as such do not contribute to our knowledge of the variability between this and other houses excavated on the Northwest Coast. Matson (2003) excavated the full spatial extent of a single compartment of a shed-roof house floor at Shingle Point, Valdes Island (part of the Gulf Island archipelago);

however, excavation of this house was complicated by historic-period disturbances (Matson 2003:102). LeClaire (1976) excavated a rectangular house depression in the Fraser Valley (the Mauer site), although no information on faunal data was reported from the site. In addition, a large house at the site of Sbabadid, located in Puget Sound, was almost completely excavated. Faunal data from this site, however, was not included in analyses as too small a sample of fauna was identified (Chatters 1989). These completely excavated house floors can be contrasted with the excavations at Ozette, where information about the faunal remains is extensive, readily available and used as a comparative sample with other house excavations (Samuels 1991, 1994, 2006). At Ozette, thousands of artifacts and millions of ecofacts were collected and documented during fieldwork and subsequently analyzed. The small number of houses excavated on the Northwest Coast, in contrast with other regions where many more houses have been excavated[14], is most likely the result of the extremely data-rich environment and the resulting labour-intensive excavation and analysis required.

Given the paucity of sampling research available from this region and the very specific constraints involved in excavating middens on the NWC, it is not surprising that similar strategies often appear to have been utilized by different researchers at different sites. Most notably, almost all researchers have utilized a judgmental sampling strategy, although Gessler (1975) and Chatters (1988) did incorporate some probability sampling

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[14] Investigations in other parts of the world reveal that much larger samples are typical. For example, investigations into the early Neolithic site of Zhaobaogou in northeastern China included the complete excavation of 20 structures, 17 of which were defined as domestic structures (Shelach 2006). This field research, totaling 2000m^2 of excavated area, was completed in a single field season (Shelach 2006). Research by Bamann et al. (1992) considers the archaeological correlates of 417 Iroquoian longhouses, while Kapches (1990) compared the internal spatial organization of over 80 different Iroquois longhouses. Similarly, significant numbers of pithouses have been thoroughly excavated in the American Southwest. From a brief review of existing publications, these excavations have investigated well over 100 pithouses (Cameron 1996; Diehl 1998).

into their sample strategies. Initially, a judgmental sampling strategy is often used to determine which house within a site to excavate. The investigations at McNichol Creek, Richardson Ranch, FsBx-9, Cathlapotle, Sbabadid and Huu7ii all focused on the excavation of the largest house within the village, although limited sampling of other houses did occur at some of these sites.

Once a house is selected for excavation, the researchers place units judgmentally within the house. Generally, samples consist of a number of contiguous excavation units in order to expose part of the house floor. Excavation unit size is typically $2m^2$, with $1m^2$ or $50cm^2$ subunits. In most cases, more than one area of the house floor is sampled (e.g. Meier site, Dionisio Point site, Huu7ii site, McNichol Creek site), and often the areal excavations are joined to one another by trenching. The trenches are often described as a means to help in the interpretation of complex stratigraphy (Coupland 1999:24; Grier 1999:24; Lepofsky 1999:6) and to elucidate the association between features, artifacts and ecofacts, both spatially and temporally. Additionally, by selecting sample locations judgmentally, one can also choose to avoid areas high in root disturbance.

How are judgmental samples selected? Does the rationale vary significantly depending on the researchers and the research goals? As noted above, the complexity of house floor deposits is no doubt one guiding factor; however, ethnohistoric evidence appears to play an even more significant role in determining which areas of the house are sampled, regardless of the specific research questions. The largest house is often selected because it is, ethnohistorically, the high-status house. As noted in Table 1, excavations at FbSx-9, Richardson Ranch, Cathlapotle, McNichol Creek, Huu7ii, and Tualdad Altu all focused on the largest house. Similarly, units within this house were often placed in one

or both rear corners of the house because ethnographically, the area of highest status was

generally considered to be at the rear corner (rear meaning furthest from the door) of this

house (Drucker 1951). For example, Martindale states of his excavations at the Psacelay

site (near Prince Rupert):

> The sampling of the horizontal excavation was largely a *judgmental process* in
> which areas of House 2 were selected as representative of the building in general.
> *Based on ethnographic descriptions* [primarily Garfield (1951)], it was assumed
> that the house had three significant types of spatial subunits: high status family
> areas at the back of the house (away from the river), low status family areas at the
> front of the house, and a common area in the centre. Each of these areas was
> excavated in 1997, which exposed more than 47% of the floor of House 2.
> [Martindale 1998:216, emphasis added].

Similarly, Grier (1999:18) notes that the location of excavation units within house floors

at Dionisio Point was "influenced by archaeological and ethnographic observations that

the use of space inside of large plank houses was highly structured and varied across the

house floors". Ames et al. (1992:280), when describing the excavation of the Meier

House, identified different areas of the house based on an ethnographic model for the

organization of interior house space, as well as on previous archaeological research (i.e.

data from Ozette). Whether this influenced the sampling design prior to its

implementation is not known; however, an examination of the sampling design utilized at

this house reveals that the rear corners of the house (the supposed high status areas) have

been thoroughly tested (see Figure 7). The sampling design utilized at Huu7ii also

focused on the rear half of the largest house. The McNichol Creek strategy tested the

centre of the house as well as one rear corner of the house. Although all samples differ in

the size, shape and orientation of excavation units, the emphasis on the back of the house
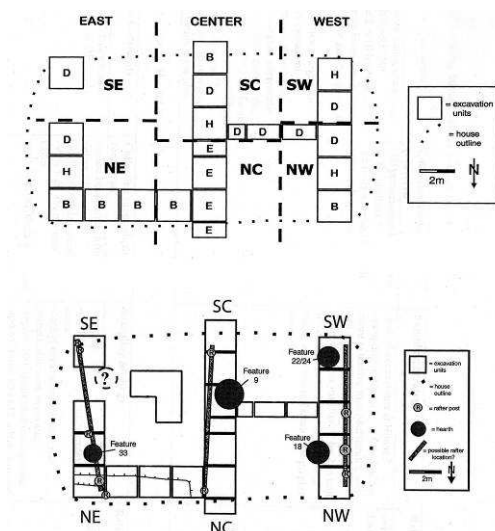
Dioniso Point sample strategy used at House 2 (Grier 2006:106).

McNichol Creek sample strategy used at House O (Coupland 2006:90)
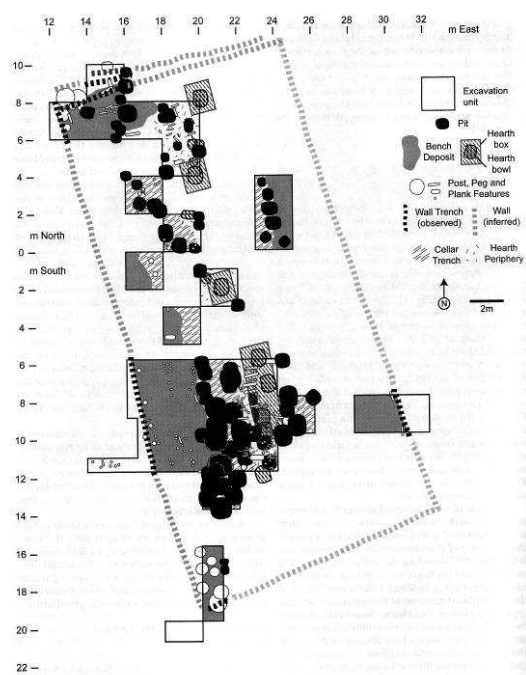
Meier House sample strategy (Smith 2006:236).
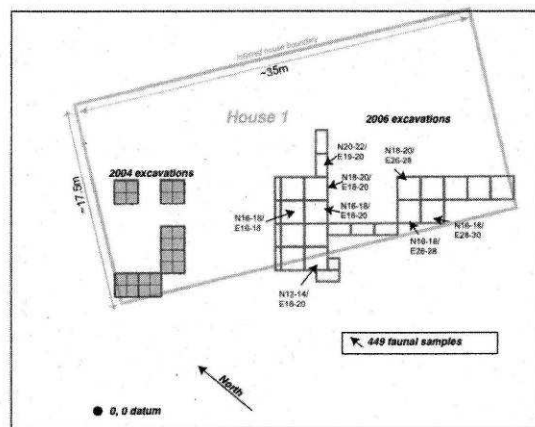
Huu7ii sample strategy used at House 1. Courtesy Alan MacMillan and Iain McKechnie.

Figure 7. Examples of sample strategies used at different sites to excavate houses on the Northwest Coast. The rear corners (i.e., furthest from the river/ocean) were tested in all houses (the SE/SW corners of House 2 at Dionisio Point, the NW/SW corners at the Meier House, the NW corner of the McNichol Creek House O, and the SW/SE corners of House 1 at Huu7ii). The use of trenches and larger areal excavation is evident at all houses.

is apparent in almost all major excavations (see Figure 7; in addition, a more complete list of sample strategy diagrams can be found in Appendix 1).

Because of the large quantity of fauna contained within many of these dwellings, it is not often possible to identify all of the faunal remains collected from the large, areal excavations of house floors. As a result, judgmental sampling is once again utilized to select the specific units for faunal analysis. Ewonus (2006:29) judgmentally selected units at the Dionisio Point site, choosing to analyze fauna from hearth contexts and those contexts immediately adjacent to hearths. Coupland et al. (2003) also judgmentally selected four 2m X 2m units from House O for faunal analysis at the McNichol Creek site.

In summary, the influence of ethnohistoric accounts on archaeologists' interpretations of houses also extends to the methodology used to excavate them. This is problematic, as it means one is – to a certain extent – assuming that the ethnographic record holds true for archaeological examples, rather than through the actual testing of this hypothesis. Using the Ozette faunal data, I will test different sample strategies on a relatively large and complete dataset to observe whether sample strategy affects the interpretation of the data. The results of this research may also address another major methodological issue on the NWC, that of data-rich shell midden house deposits. In Chapter 5, I describe in detail the Ozette faunal data and the methods used to evaluate different sampling strategies.

Chapter 5: Sampling Simulation Methods

This chapter explains the methods that were used to investigate the effects of sample size and sample location on faunal data from Ozette. Firstly, the database containing Ozette faunal records had to be modified in order to correct for differential recovery methods, to account for missing data, and to circumvent the MAUP. Secondly, the modified faunal database was projected using ARCMAP software in order to display the spatial distributions of different taxa in House 1, House 2 and House 5. Thirdly, the rationale for selecting specific sampling strategies is explained. Finally, I will discuss why I chose to compare samples with respect to the effect of richness, relative abundance and status.

5.1 Obtain and Modify Ozette Faunal Data

5.1.1 The Raw Faunal Database (RFD)

Permission was granted by the Makah Tribe to access the database containing the faunal data from the Ozette excavations. The database contained all the catalogued information for the fish, mammals and shellfish collected and identified from the Area B70 excavations; and will be referred to as the Raw Faunal Database (RFD). Not all of the material collected has been identified or catalogued; the fish remains from House 5 and the exterior midden, as well as a small portion of mammals and shellfish from the exterior midden have yet to be identified. In spite of this fact, the collection of identified specimens is still impressive, consisting of more than 306,000 shellfish specimens, 52,000 mammal bones and 24,000 fish[15] bones, making it the largest known collection of identified fauna from a single site on the Northwest Coast. Although reported in

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[15] This number is small in relation to the other two because it represents only fish from inside House 1 and 2 and not exterior midden contexts.

published literature (DePuydt 1994), the bird bone data were not available, and as such, are not included in this research.

The database had not been utilized or analyzed since its creation (Dr. Jeff Mauger, pers. comm. 2007), and on close examination there appeared to be several minor inconsistencies between the published reports about the fauna and the actual database of fauna. For example, a small number of shellfish species recorded in the published reports were not entered into the RFD. Similarly, the NISP of several mammalian taxa in the RFD were different than the published NISP values for these taxa. However, in all cases the differences in NISP, not only for mammals but also for fish and shellfish, were minimal (<2%). These differences are not unexpected given that the number of data entries in the RFD is in the hundreds of thousands.

The RFD contained significantly more information than was necessary for this project and thus, the unnecessary information first had to be removed. Since the research in this thesis is focused on household archaeology, only those bones found within house floor midden contexts have been included in this research. Bones excavated from cultural levels below (Levels VIII-VI) and above (Levels III-I) the house floors (Levels V-VII) are not included. Faunal data from House 3 were omitted because it was only partially excavated and therefore less amenable to sampling than Houses 1, 2, and 5.

Additionally, because the excavation grid of 2m X 2m units utilized at Ozette did not have the same orientation as the House platforms (see Figure 8), several units contained fauna from both the interior and exterior midden contexts. In these cases, the excavators recorded the context of a specimen as within a house, "exterior deposits" or "uncertain or indeterminate context" (Samuels 1994:310); any fauna of indeterminate or

exterior midden context has not been included in this thesis. Investigating sampling issues related to exterior midden contexts, comparing samples from the exterior midden with those of the interior midden, or comparing sampled fauna from different cultural layers would all be productive questions to research; however those questions are beyond the scope of this thesis.
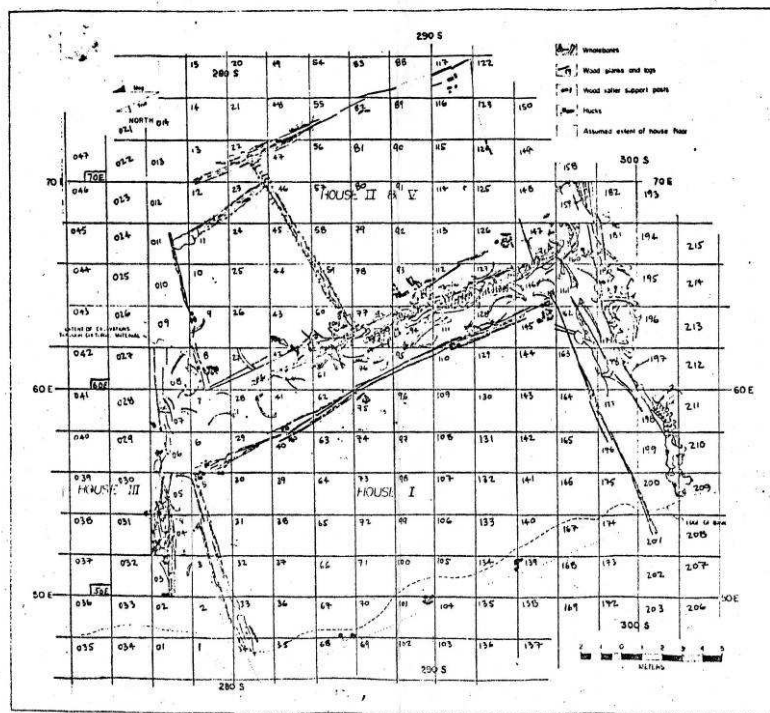
Figure 8. 2m X 2m excavation unit grid and approximate house locations for Area B70 excavations at Ozette (Courtesy Ozette Archaeological Project).

The RFD also contained information pertaining to element, portion, pathologies, burning and other modifications for many of the specimens. This information was also removed as it could not easily be accounted for when creating a corrected faunal database (see Section 5.1.2). Only the species, genus, family, or order identification and the excavation unit associated with each bone were extracted from the RFD for this project. This did, however, create two minor limitations. Firstly, since descriptive information

about each bone (element, portion and side) was removed from the RFD, the minimum

number of individuals (MNI) statistic could not be calculated. NISP values, despite some

limitations, are nevertheless an appropriate method of quantifying fauna (Grayson 1984;

Lyman 2008). In order to limit the biases related to differential skeletal parts, data were

primarily compared within rather than between classes; the faunal data in this thesis were

separated into three classes comprising mammal, fish and shellfish. Secondly, because

additional information such as burning, articulation, pathologies, etc. was not utilized in

the analyses, interpretations that would be related to these characteristics of the bones

could not be made. For example, the Ozette researchers argued that the distribution of

mammal bones which had been gnawed was different from the overall distribution of

mammal bones, and therefore that the distribution of mammal bones was predominantly

the result of human behaviour rather than animal behaviour (Huelsbeck 1994). These

interpretations have not been considered in the research for this thesis because the

information about gnawing was not included. Nevertheless, by looking at the quantity

and distribution of different species within a single house floor or between house floors, it

is possible to discern extensive information about the practices and social structure of the

inhabitants of these houses.

5.1.2 The Corrected Faunal Database (CFD)

Once all the information extraneous to this research was removed from the RFD,

the data needed to be manipulated for reasons described below; the resulting database is

referred to as the Corrected Faunal Database (CFD). Different collection strategies will

result in different quantities and types of fauna material recovered. At Ozette, roughly

half of the excavation units within each house were hand-picked in order to obtain a

representative sample in terms of types and numbers of faunal elements, while in the

remainder of the units, material was collected by wet-screening the matrix through

6.4mm (6.4 millimeter) mesh (Huelsbeck 1994). Considerably less faunal material was

collected using the former strategy. For the fish and mammal collections, analysis of

variance (ANOVA) indicated a significant statistical (p<.05) difference in the number of

specimens recovered using the water-screened units versus the judgmentally-picked units

(Table 2; Huelsbeck 1994:56). Wessen (1994:134-139) conducted ANOVA on shellfish

data with more ambiguous results. He investigated the effects of collection strategy in

relation to various groups[16] and sizes, rather than considering the shellfish collection as a

whole, and discovered that while differences were significant for many groups, the

effects of differential recovery techniques were not the same for all taxa. Based on his

research, the statistical differences were significant for the groups of shellfish from the

exterior midden, Houses 1 and 2, but not from House 5. However, the number of

specimens recorded in the RFD clearly showed considerable differences in numbers

between the two sample strategies, and based on the spatial nature of this research, I

decided that corrective factors were warranted for House 5 as well. These were generated

by dividing the NISP of water-screened units by the NISP of the judgmentally picked

units. In the case of crabs (*Cancer productus*) and octopus (*Octopus dofleini*), no

specimens were recorded in the House 5 judgmentally picked samples, and therefore no

corrective factors could be generated. All the corrective factors utilized for shellfish can

be found in Table 3.

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[16] Not all shellfish were subjected to ANOVA; most notably, barnacles (Cirripedia) were not subjected to ANOVA analysis.

While the corrective factors aid in addressing the difference in numbers found in judgmental versus water-screened samples, these factors obviously do not provide a panacea for all issues related to differential collection strategies. Taxa that are very small and unlikely to be obvious to the excavator during hand-picking, especially molluscan remains, may be overlooked and omitted from a judgmental sample (Sparks 1961). This may result in a significant underestimate of the quantity of that species from that unit relative to other species which are more visible. Even when corrective factors are applied, the numbers of these less-visible species may still be under-represented, as Wessen (1994) argues may be the case for shellfish at Ozette. Similarly, McKechnie (2005) has shown that the relative abundance and richness of ichthyofaunal remains are highly dependent on the recovery method employed; even material screened through 6.4mm mesh will significantly under-represent small fish species such as herring, sardines, and eulachon. Additionally, if there are only a few specimens from a given species in an excavation unit to begin with, it is more likely that these specimens will be collected in a screened sample, but may be inadvertently overlooked during judgmental hand-selection. The data from these units are likely to exhibit lower richness than water-screened units; this cannot be rectified using corrective factors. Fortunately, the issue of species richness differences between screened and hand-selected units was minor for mammal and fish remains at Ozette (Huelsbeck 1994). The relatively large size of specimens, coupled with the ubiquity of many species, resulted in their recovery and identification using either sample strategy, although it is almost certain that many taxa were not identified at all as they were not retained in the 6.4mm screens. There were several shellfish species for which only a few specimens were identified in each house (i.e. rare species), and, not

surprisingly, Wessen (1994:135) observed that the abundance of 24 species of shellfish

showed a high degree of association with the water-screen excavation technique. In other

words, the richness of shellfish taxa from a given excavation unit (EU) was correlated

with the excavation strategy, rather than being influenced solely by the deposition of

different taxa in the given EU.

Despite the biases inherent in any recovery method, addressing differences in

quantities of fauna related to differential recovery techniques were particularly important

to address for this thesis because the spatial distribution of bones is of central interest. If

corrective factors had not been applied, spurious concentrations – occurring because of

differential collection strategies rather than because of cultural behaviours – would have

made the interpretation of spatial patterning very difficult. It would also have made

Corrective factors for mammals and fish[a]	
Data set	Corrective factors
House 1 complete mammal bones	1.64
House 1 mammal bone fragments	2.85
House 1 fish bones	5.50
House 2 mammal bones	1.31
House 2 mammal bone fragments	7.33
House 2 fish bones	13.75
House 5 mammal bones	2.22
House 5 mammal bone fragments	1.61

Table 2. Corrective factors applied to judgmentally-picked samples of mammal and fish.
[a] Based on data from Huelsbeck (1994:56).

Corrective factors for shellfish			
Dataset	Corrective factors[b]		
	House 1	House 2	House 5
Bivalves	3.46	4.37	4.44
Univalves	2.05	11.27	4.27
Chitons	6.38	26.47	14.33
Octopus	5.50	96.33	Not possible
Crabs	18.00	10.65	Not possible
Sea urchins (Strongylocentrotidae)	1.87	5.32	1.35

Table 3. Corrective factors applied to judgmentally-picked samples of various shellfish classes.
[b] All corrective factors, with the exception of House 5 corrective factors, have been obtained from Wessen (1994:138.)

the effects of sampling on these distributions very difficult to separate from the effects of

recovery methods, and therefore corrective factors were deemed appropriate and

necessary for this research. These corrective factors were applied only to the

judgmentally picked excavation units in the RFD. The resultant database, the CFD,

included the actual number of identified specimens from water-screened units, and a

corrected value for the number of specimens from judgmentally-picked units. Once all of

the corrected factors had been applied, the resulting CFD was displayed spatially. Up

until this point, the data were simply numerical counts of species associated with an

excavation unit (see Table 4 for a summary of faunal counts, or Appendix 2 for a list of

the entire faunal assemblage once corrective factors had been applied).

	House 1	**House 2**	**House 5**
NISP for fish	7,420	40,597	No analysis
NISP for mammal	7,410	13,866	2,286
NISP for shellfish	33,516	135,915	11,521
Total NISP	48,346	190,378	13,807

Table 4. NISP values for corrected data from House 1, House 2, and House 5.

5.2 Spatial Display of the CFD

Data from Houses 1, 2, and 5 were displayed using ESRI ARCMAP 9.2 software.

After drawing the outline of the three houses based on the site map provided by the

Ozette researchers, the 2m X 2m excavation units were then drawn as a separate layer.

Each excavation unit was then given the unit designation used for the original excavation

(Figure 8). The CFD, which included the unit designation for each bone, was then linked

to the excavation units that were drawn in ARCMAP. In this way, all the faunal data were

given a general spatial location, if only defined by their association with a specific

excavation unit (EU).

Technically, sampling could begin at this stage; however, the areal nature of the data had to be addressed. Ideally, numerous simulated excavation strategies including auger, judgmental and probabilistic sample methods should be tested; however, 2m X 2m excavation units lack the flexibility to allow one to test all of these strategies. Additionally, as discussed in Chapter 3, issues of the MAUP complicated the sampling at Ozette if the data had been left in areal form. In order to generate multiple configurations and aggregations of sample units (i.e. different sampling strategies) without generating results that were affected by the MAUP, the faunal data were converted from areal data to point-provenienced data. This was accomplished by randomly distributing the number of bones for each species within each excavation unit. For example, if Excavation Unit #45 (EU #45) hypothetically contained 312 lingcod (*Ophiodon elongatus*) bones, then 312 points would be placed randomly within EU #45, each point representing one lingcod bone. The actual distribution of all taxa is different than this randomization within each unit. In some cases, it is likely that the fauna is more evenly distributed throughout the unit, while in other cases, (e.g., articulated bones), the random distribution is less clustered than in reality.

A side effect that resulted from the display of all of the bones from each EU as individual points is that the boundaries of the EUs were in some cases visible because of the density of faunal remains found within these EUs (Figure 9). Because the data were only displayed in two dimensions, all of the fauna was displayed as if it were distributed within the unit at the same depth below the surface. In actuality, the fauna was continually deposited during the occupation of the house resulting in an average midden thickness of 23.2cm, 24.1cm, and 10.2cm for House 1, House 2 and House 5 respectively

(Samuels 2006:210). The layers of clay did create a discrete house floor midden separate

from the cultural layers above and below it, and it is therefore appropriate to group all the

fauna from a single house floor together. However, the visual display of this fauna should

not be interpreted as fauna lying on the surface of a house floor, but rather as the sum

total of all of the fauna incorporated into the living surface during the occupation of a

house.
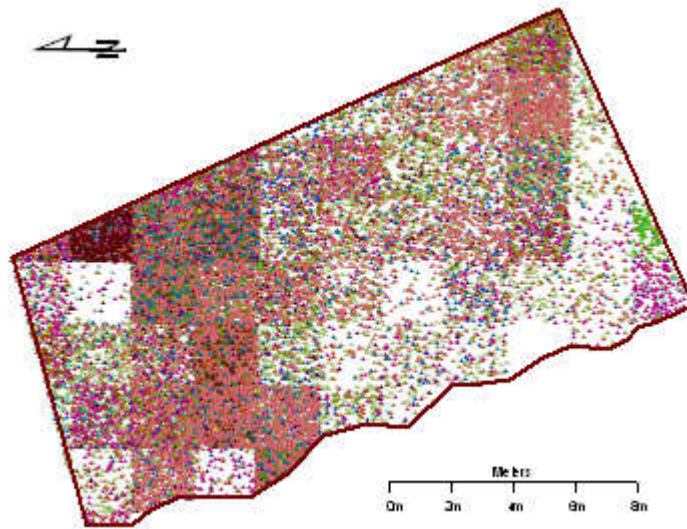
Figure 9. Spatial distribution of shellfish in House 1 is displayed above in order to demonstrate the density of faunal remains. Each point represents a bone for a given species that has been distributed randomly within the excavation unit from which it was excavated. Different shades represent different taxa.

In addition to the MAUP, another issue which had to be addressed was the lack of

data for several units. Once the data were imported from the database into ARCMAP, it

was observed that a few excavation units in House 1 lacked data for one or more classes

(i.e. the shellfish, and/or fish, and/or mammal data were completely absent). In most

cases, these units were near the edge of the house and in several cases these units were

near the front of the house where wave action had eroded part of the house and therefore

no intact interior midden remained. There were also three excavation squares in the

middle of House 1 for which data were missing. If data were missing, the NISP for each

species of the surrounding units were averaged to create data for the excavation unit lacking data.

The data displayed in ARCMAP, as documented in Section 5.1 and 5.2 above, have been manipulated and therefore do not represent exactly the original fauna excavated from Ozette. These manipulations (1) minimize differences between collection strategies (by using corrective factors), (2) account for missing data (by averaging data from surrounding units), and (3) address the MAUP (by using point distributions rather than areal data). Despite the manipulations, the spatially displayed data are a plausible archaeological assemblage from a NWC house, represented by a large number of different taxa with different patterns and degrees of spatial clustering for each taxon within each house. These are characteristics that have been observed at other excavations of shell-midden house floors to date. The results of different sample strategies applied to this dataset should prompt researchers to consider how they sample other houses at other village sites, as it is likely that the fauna from these houses exhibit a scale of complexity that is similar to the faunal distributions based on the Ozette data. As such, a sampling simulation of the dataset generated for this thesis has heuristic value for future excavations at other fauna-rich house floor deposits.

5.3 Selecting and Testing Sample Strategies

Once the faunal data were displayed for each house, sampling units could be placed within the house. This was a two-step process, which required excavation units to be gridded over the entire house, and then different units selected according to specific sample strategies. Units which were 50cm X 50cm in size were chosen as the basic unit for the sampling simulations, except for the auger samples. This size of unit was selected

for several reasons. Firstly, this is generally the smallest size of areal unit utilized in excavations on the Northwest Coast and therefore is a close approximation to reality. Secondly, this size is not too small to exclude the possibility that each one could serve as an evaluative unit on its own. Thirdly, in order to create judgmental excavation strategies, 50cm X 50cm units allow for flexibility in that trenches, non-symmetrical and unevenly-spaced sampling schematics are much easier to approximate with 50cm X 50cm units, which can then be aggregated if necessary to replicate these different sampling strategies.

There are almost limitless sampling designs that could be tested; however, the ones applied in this thesis were selected because of their heuristic value and the possibility that they would be used in future excavations. Both probabilistic and judgmental strategies were tested. The specific samples chosen for each group are discussed below. In order to demonstrate how these sample strategies were applied, schematics from House 1 are presented in Figure 10. To view all the sampling strategies for all three houses, see Appendix 3.

5.3.1 Probabilistic Samples

One of the probabilistic sample methods evaluated was simple random sampling. Three sample fractions were chosen: 1%, 5%, and 10%. There were several reasons why these sample fractions and this method were chosen. Initially, the small sample sizes were chosen to observe whether or not samples of this size still produced accurate results. Another reason random samples were tested was to compare them to judgmental sample strategies. As noted in Chapter 2, many house excavations sample nearly 50% of the
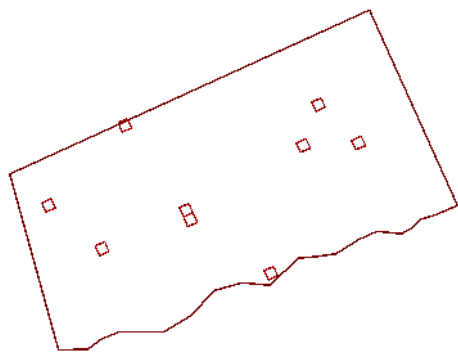
A) 1% random sample (trial 1)

B) 5% random sample (trial 1)

C) 10% random sample (trial 1)

D) 5% systematic sample (evaluative units)
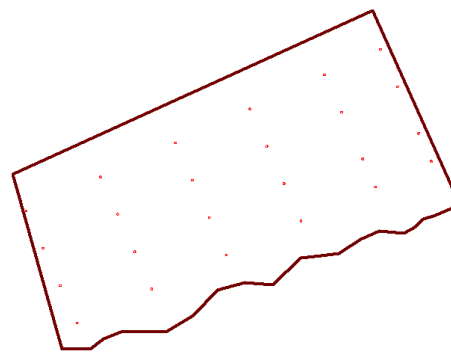
E) 0.1% systematic sample (auger)
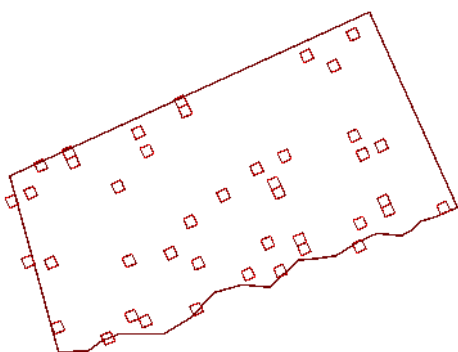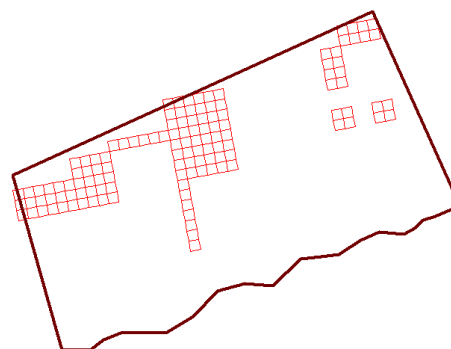
F) Huu7ii excavation strategy (15%)
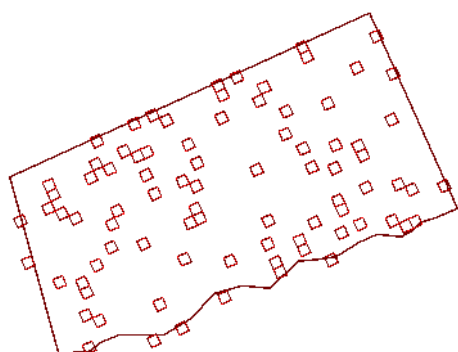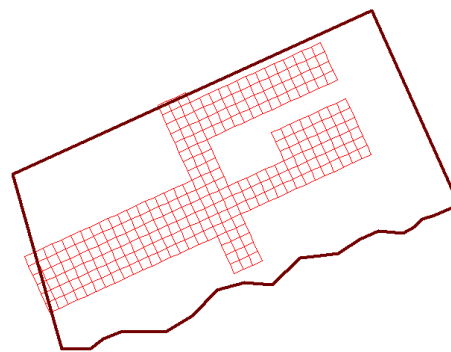
G) McNichol Creek excavation strategy (35%)
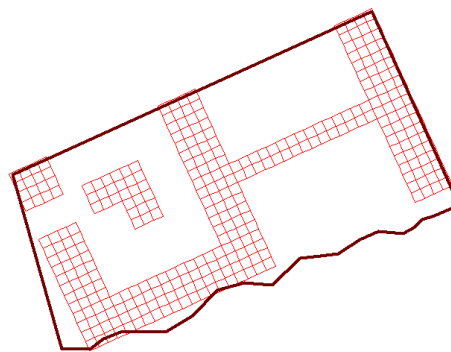
H) Dionisio Point excavation strategy (40%)

Figure 10. Sample strategies applied to House 1.

house, and if the small random samples appeared to be just as accurate as the larger judgmental samples, there is the possibility of "doing more with less".

In order to generate random samples, a random number generator randomly selected[17] 50cm X 50cm excavation units; the total number of units selected was based on the number of units required for the sampling fraction in question (see Table 5).

	Sample Strategy	Number of 50cm X 50cm units	Area Excavated (m²)	Percent of House Excavated
House 1	Random	9	2.25	1.1%
		42	10.5	5.4%
		84	21.0	10.8%
	Systematic (auger)	n/a	0.19	0.10%
	Stratified Systematic[a]	n/a	12	6.14%
	Systematic (evaluative units)	40	10	5.1%
	Huu7ii	123	30.75	15.7%
	McNichol Creek	284	71	36.4%
	Dionisio Point	321	80.25	41.0%
House 2	Random	7	1.75	1.1%
		35	8.75	5.4%
		70	17.5	10.8%
	Systematic (evaluative units)	36	8.5	5.2%
	Systematic (auger)	n/a	0.157	0.10%
	Huu7ii	99	24.75	15.2%
	McNichol Creek	234	58.5	36.0%
	Dionisio Point	264	66	41.0%
House 5	Random	8	2	1.2%
		36	9	5.4%
		72	18	10.8%
	Systematic (evaluative units)	35	8.75	5.2%
	Systematic (auger)	n/a	0.18	0.10%
	Huu7ii	104	26	15.7%
	McNichol Creek	234	58.5	35.2%
	Dionisio Point	259	64.75	39.0%

Table 5. The sample fraction and corresponding area excavated for various sample strategies at Houses 1, 2 and 5 at Ozette.
[a]This sample strategy was only applied at House 1 to test for intra-house differences in status.

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[17] Units were selected without replacement: once a unit was selected it was not available to be selected again within the same sample. This type of random sampling requires more complex statistical theory than sampling with replacement; however, in practice, archaeologists would not select the same unit twice in a single sample (Orton 2000).

This operation was performed three times in order to produce three different sample results for each sample fraction. Multiple samples were generated because it is difficult to evaluate the efficacy of a given sampling fraction based on a single random sample.

There is the possibility that the chosen random sample might be particularly accurate and therefore might have performed exceptionally well when compared with other random samples of the same sampling fraction. The reverse may also be true: any given random sample may be inaccurate when compared to most others from the same sampling fraction. By testing three samples, it was hoped that if a particularly anomalous sample was drawn, it would become apparent when compared to the other two samples. Additionally, running a small number of samples allows the results of each sample to be analyzed individually. This is a close analogue for reality, in which only one sample would be excavated from a house. By investigating a small number of samples, the accuracy of shellfish remains from a sample can be compared to the accuracy of fish remains and to the accuracy of mammal remains from the same sample, in order to observe if all datasets are equally accurate for a given sample. It is possible that these different classes of fauna vary systematically in their distribution within a house, and it would not be unexpected if only one or two out of these three datasets were found to be accurately identified in a single sample. With a small number of simulations, individual taxa can also be examined in relation to others, in order to establish if any particular taxon is consistently over-represented or under-represented.

Using only three samples from each house allows each sample to be scrutinized individually, and in doing so approximate a "real-world" excavation scenario in which only a single sample would be excavated. However, the number of samples is too small

to develop statistical probabilities concerning the efficacy of a particular sample size compared to another sample size. In order to investigate these probabilities, Monte-Carlo simulation of random samples was undertaken for a limited number of research questions. Briefly, Monte-Carlo simulation involves repeatedly drawing random samples and observing the results for a target variable in order to ascertain the confidence limits and the probability of success at the given sample fraction (Cannon 2001). Monte-Carlo simulation was utilized on two specific target variables in this thesis. The first, richness, was developed to ascertain the probabilities of identifying a given number of taxa using a random sample strategy of specific size (see Chapter 6, Section 6.4). The second target variable was high-status symbolic shellfish and whale (see Chapter 8, Section 8.1). These taxa were investigated in order to develop probabilities that a random sample of specified size would indicate differences in status between houses based on this fauna. Hypothetically, if 490 out of 500 random samples drawn from House 1 showed considerable differences when compared to House 2 random samples, the probability of success (98% or 490/500) might provoke researchers to use such a strategy. Future research using this dataset may expand the use of Monte-Carlo simulation to provide confidence limits for entire classes of data, but this is beyond the scope of the present research.

While investigating random samples will indicate to what extent these samples may reduce the amount of faunal data being excavated without resulting in a significant loss of information, the random sampling method has one major drawback: it is difficult to implement in the field. Firstly, determining the placement of units is complicated because they follow no logical order. In order to accurately place the sample in relation to

other sample locations within the house, it may be necessary to create a grid on the surface of the entire house floor. Creating this grid is complicated and time consuming, and has the potential of being inefficient if only a small fraction of the grid is to be excavated. Secondly, in order to execute a random sample strategy, units may need to be placed in locations that are difficult to access. For example, units which are randomly placed where a tree is growing within the house platform will be difficult to access and may contain information of limited value given the disturbances to the archaeological deposit caused by the root structure of the tree. Finally, previous archaeological work at Ozette and other sites (e.g., Ames et al. 1992; Coupland 2006; Grier 2006; Samuels 1994) has shown that the interior of a longhouse is highly heterogeneous in its artifact and ecofact composition, and random samples may not be placed in all of these distinct activity areas, a scenario unpalatable to many researchers. Although larger judgmental samples may target these areas more directly, random samples do not require any *a priori* assumptions about the division of space within a house. As such, this latter sample method may sample areas of the house which are usually not tested, and in doing so may provide data that reinforce or call into question assumptions made about the internal organization of space within a longhouse.

With the preceding information in mind, systematic sampling offers an alternative probabilistic method which is much easier to operationalize than random sampling because excavation units are placed at equal intervals; therefore, once the location for the first unit has been defined, the location of all other units is easy to determine. Admittedly, there may still be difficulties if there are many trees growing on the house platform. The other issue with systematic samples revolves around the potential for elements within the

population to occur at the same interval as the sample unit. In these cases, samples will contain all or none of that element depending on whether their placement coincides or not.

Two systematic samples were tested at all three houses: a 5% systematic sample based on 50cm X 50cm evaluative units, and bucket-auger[18] samples which covered approximately 0.1% of the house floor at each house. Each of these strategies was chosen because it represents probabilistic sampling designs that could plausibly be implemented in the future. The use of auger samples to track changes in relative abundance of fish species has already been documented (Cannon 2000), and by testing this strategy at Ozette, its efficacy to identify spatial differences in a single house floor can be evaluated. Similarly, a 5% systematic sample of evaluative units significantly reduces the quantity of data excavated when compared with larger judgmental strategies. If this strategy works, there is an opportunity to investigate several houses rather than just one and obtain comparable data from each house investigated.

A stratified systematic sample strategy was also tested at House 1 in order to observe whether differences in status could be determined using fauna based on this sample method instead of using a much larger judgmental sample. House 1 was divided into nuclear family living areas of approximately the same size and then a single 1m X 1m excavation unit placed within each of these nuclear family living areas. Technically, this sampling design contained elements of both probabilistic and judgmental sampling strategies. On the one hand, each stratum (i.e. each nuclear family living area) had an equal probability of being tested, which is similar to probabilistic sampling where the sampling intensity for each stratum can be defined. On the other hand, each sample unit

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[18] The diameter of the bucket-auger used in this simulation was 10 centimeters.

was intentionally placed in approximately a systematic fashion within each stratum in an attempt to sample all areas of the house while sampling each individual family area. Since this strategy was created with a very specific purpose, it will only be examined in terms of its ability to indicate intra-house differences in status (see Chapter 8, Section 8.4).

5.3.2 Judgmental Samples

The other category of sample strategies tested was judgmental samples. It was decided that existing judgmental sample designs from other house excavations on the Northwest Coast would be utilized. Since the author had intimate knowledge of the spatial distribution of all fauna within each house, it would be impossible to create judgmental strategies without intuitively predicting the results, and therefore another source of judgmental sample strategies was required. Additionally, using existing excavation strategies allowed for a detailed analysis of household method and theory. The results of these samples methods could be used to evaluate their ability to accurately detect status differences on a dataset for which an ethnographic pattern is known to be reflected by the distribution of specific fauna, as is the case at Ozette (see Section 5.4.3 below).

The specific sampling designs chosen were based on the Huu7ii (Frederick et al. 2006), Dionisio Point (Grier 2006) and McNichol Creek (Coupland 2006) sampling designs. There were several reasons for selecting these particular sampling designs. The houses at these sites contained fauna-rich house floor midden, and therefore the researchers had to address the amount of fauna excavated in their samples, much like at Ozette. Secondly, the Huu7ii and Dionisio Point sites contained houses of the shed-roof

type which are of the same general form as the houses at Ozette, and therefore likely shared some of the same internal features with Ozette such as benches, hearths, and a central communal area. As a result, the house midden deposits at all of these houses may be structured in similar ways. Strategies used to excavate other shed-roof houses, such as the excavations at Shingle Spit, Tualdad Altu or Sbabadid, were not chosen because their sampling strategies were not articulated very clearly. However, a third judgmental strategy was desired, and the sample strategy from McNichol Creek excavation of House O was selected. This sample strategy was selected because it was clearly articulated and because a data-rich midden was uncovered at this house, despite the fact that it is a northern coast type rather than a shed-roof type like Ozette (Coupland 2006; Gahr 2006).

There is considerable variability between each of these sample designs with respect to their size and their spatial configuration (Figure 10). The Huu7ii sampling strategy is the smallest sample (15%), and focuses on the rear of the house. The McNichol Creek sampling strategy is significantly larger (35%) and focuses on the middle of the house as well as on one of the rear corners of the house. In contrast, the Dionisio Point sample is only slightly larger than the McNichol Creek strategy (40%), although a combination of trenches was employed to sample many distinct areas of the house. These samples also allow one to consider whether the interpretation of Ozette data would change if the researchers had not excavated the entire house, but had instead utilized a strategy similar to ones used at other sites on the NWC. The purpose was not to evaluate the efficacy of these sample methods in their original context.

5.4 Narrowing the Focus

Once the sample assemblages had been derived using the strategies described above, the questions that could be investigated are still very numerous. In order to maintain a focus, several avenues of research were pursued in favour of others; these foci have been divided into three phases of research. The first phase is an investigation of the relationship between richness (NTAXA), and sample strategy. The second phase is an examination of the effects of sampling on the relative abundance of fauna. These two phases were approached primarily with methodological concerns in mind. Subsequently, these methodological concerns were re-examined within the context of an interpretive issue: the relationship between sample strategy and the interpretation of status. In other words, the sample strategies that provided the most accurate prediction of the known differences in status between and within houses at Ozette are assessed. This final phase is of particular relevance to Northwest Coast archaeology, given the hypothesized relationship between the development of complexity, hierarchy, and sedentism and the role that houses played in these developments (Ames 2001; Ames and Maschner 1999). The three phases of investigation are elaborated below.

5.4.1 Phase 1: Taxonomic Richness

Faunal analysts are interested in the degree to which their samples accurately identify the range of species found within the site or feature they are excavating, as this measure is often used to infer different resource exploitation patterns. Large NTAXA values are often interpreted as indicative of a broader resource base, while small NTAXA values are interpreted as specialized resource exploitation (see Lyman 2008:179, and references within). At Ozette, for example, the taxonomic richness of mammals at House 1 was less than at House 2, which led to the theory that household members at House 1

were more specialized (i.e. narrower dietary breadth) in their subsistence practices than

were House 2 household members (Huelsbeck 1994). While interpretations based on

richness may seem straightforward, they are not. As noted in Chapter 3, NTAXA values

may have as much to do with the size of the sample as with the actual taxonomic richness

of the target population, making direct comparisons between assemblages difficult. The

effects of sampling on richness will be investigated with respect to several questions:

1. How does richness vary with sample size?

2. How does richness vary with sample method? Do certain sample methods perform more optimally than others, and if not, does this imply a lack of correlation between sample method and NTAXA values?

3. When taxa are not present in a sample, what kinds of taxa are omitted? Is it because they are rare and therefore less likely to be found? Alternatively, are there abundant taxa whose clustered distribution results in their absence from most samples?

4. Are there significant differences between any of the houses in terms of the effectiveness of different sample strategies? If there are differences, what are causes of these differences?

5.4.2 Phase 2: Taxonomic Abundance

Determining the effects of sampling on NTAXA is informative; however the

interpretive potential of the relative abundance of taxa is much greater. Relative

abundance may be used as the measure of the role of a specific taxon to diet (Jones

2004). This requires further interpretation and theorizing about the reasons why certain

foods were consumed in favour of others and includes reasons such as ease of capture,

caloric value, social significance, or some combination of all of these reasons (Reitz and

Wing 1999). The distribution of fauna is also used to infer behavioral patterns over time

and space through an examination of the changes in relative abundances. Given the

centrality of relative abundance data to the types of interpretations listed above, four

questions were considered for the samples taken from each house at Ozette:

1. How accurately do different sample sizes identify the relative abundance of all taxa?

2. How accurately do different sample methods identify the relative abundance of all taxa?

3. Do certain sample fractions work better for different classes of data? Do smaller samples work better for specific classes than they do for others?

4. Is there significant variation in the accuracy of a given judgmental sample strategy when it is applied to the different houses at Ozette?

5.4.3 Phase 3: Status

As noted in Chapter 2, differences in status are a central component of research

on the Northwest Coast. Differences in faunal assemblages are often seen as proxy

measures of status both between and within houses (e.g., Coupland 2006; Crabtree 1990;

Kirch and Jones O'Day 2003; Moss 1993). The indicators of status that will be tested are

summarized in Table 6. Specifically, the following questions will be investigated:

1. How does sample size affect the interpretation of status between houses?

2. How does sample method affect the interpretation of status? Does one sample strategy perform more optimally as an indicator of status between houses?

3. Is it possible to get an inaccurate interpretation of inter-house status using sample strategy?

4. Can sample strategies identify intra-house differences within House 1?

This chapter has presented the methods used to create a dataset for sampling

simulation, discussed which sample strategies will be evaluated, and described three

specific phases of research which will be investigated. In Chapter 6 I turn to the first of

these phases of research – an investigation of sampling and richness – and present the

results of the sampling simulation.

	Indicator of Status	Explanation given by Ozette archaeologists (Samuels 1994; Huelsbeck 1994; Wessen 1994) based on ethnographic accounts	Pattern observed at Ozette
Inter-house status	Decorative, ceremonial and symbolic (D/C/S) shellfish	Exotic shells were a form of money and a symbol of wealth and prestige.	House 1 had a much higher abundance of these of these species, compared to House 2 and House 5.
	Whale	Known as a high-status food and the hunting of whale was a high-status activity.	House 1 had more whale than House 2 or House 5.
	Relative abundance of salmon and halibut	These fish species have specific ecological habitats and may indicate control of resource locales.	Relative abundance of salmon and halibut higher in House 1 than House 2
Intra-house status	Decorative, ceremonial and symbolic (D/C/S) shellfish	Exotic shells were a form of money and a symbol of wealth and prestige. In particular, the rear corners of the house were considered high-status	D/C/S shellfish was highly clustered within House 1. One cluster occurred near the NE rear corner of the house, and another occurred near the SW corner.
	Whale	Whale consumption and whale hunting were associated with high-status individuals who lived in the rear of the house.	Much of the whale in House 1 found along the rear (east) wall of the house.
	Fish concentrations	Concentrations of fish are indicative of high-status nuclear family consumption and/or feasting, an activity hosted by high-status heads of households.	Distinct clusters of fish occurred near the NE rear corner, indicating that a nuclear family likely consumed more of these taxa. Another cluster occurred near the middle of the house, likely indicating feasting activity.

Table 6. Ozette indicators of status based on faunal data.

Chapter 6: Effects of Sampling on Richness (NTAXA)

The number of fish, mammal and shellfish taxa identified at each house is presented in Figure 11. It is clear that the number of different taxa identified (NTAXA) is not correlated with the absolute quantity of identified specimens. This is a trend that has been observed at other sites: the majority of taxa in an assemblage are identified once NISP values of several hundred have been reached (e.g., Driver 1993; Grayson 1984; Lyman and Ames 2004; Lepofsky and Lertzman 2005; Lyman 2005). These values are much lower than the tens of thousands of bones identified at each house at Ozette. Nearly four times as many specimens were identified at House 2 relative to House 1; however the NTAXA value for each house is very similar (100 and 95). The lower NTAXA value for House 5 (54 taxa) compared to House 1 (95 taxa) and House 2 (100 taxa) is due in large part to the fact that fish remains were not analyzed or identified at this house. Accordingly, any comparison between the absolute number of taxa identified in House 5 and the absolute number of taxa identified in Houses 1 and 2 will be avoided. The primary objective of these analyses is to compare the effect of sample strategies within a single house, and the lack of direct comparability between houses is of less interest in this particular research.

It is also informative to investigate if there are taxa which are consistently present or absent. For instance, one would expect that rare taxa would be less likely to be sampled than abundant taxa, as has been observed elsewhere (Grayson 1984; Lepofsky and Lertzman 2005). However, if abundant taxa are distributed in a highly clustered pattern within a house, then they may be absent from many samples. In order to test this hypothesis, abundant taxa have been arbitrarily defined as the most abundant taxa which,

when their relative abundances are summed, comprise >90% of the faunal assemblage by

NISP for a given house. In contrast, rare taxa are defined as the least abundant taxa

whose combined relative abundance constitutes approximately the remaining 10% of the

assemblage. Each class (fish, mammals and shellfish) was examined independently, since

the NISP for these three groups differs significantly and if combined, would obscure

patterns that exist within each group.

Number of taxa identified to different taxonomic levels at Ozette

☐ Species ☐ Genus ☐ Family ■ Order
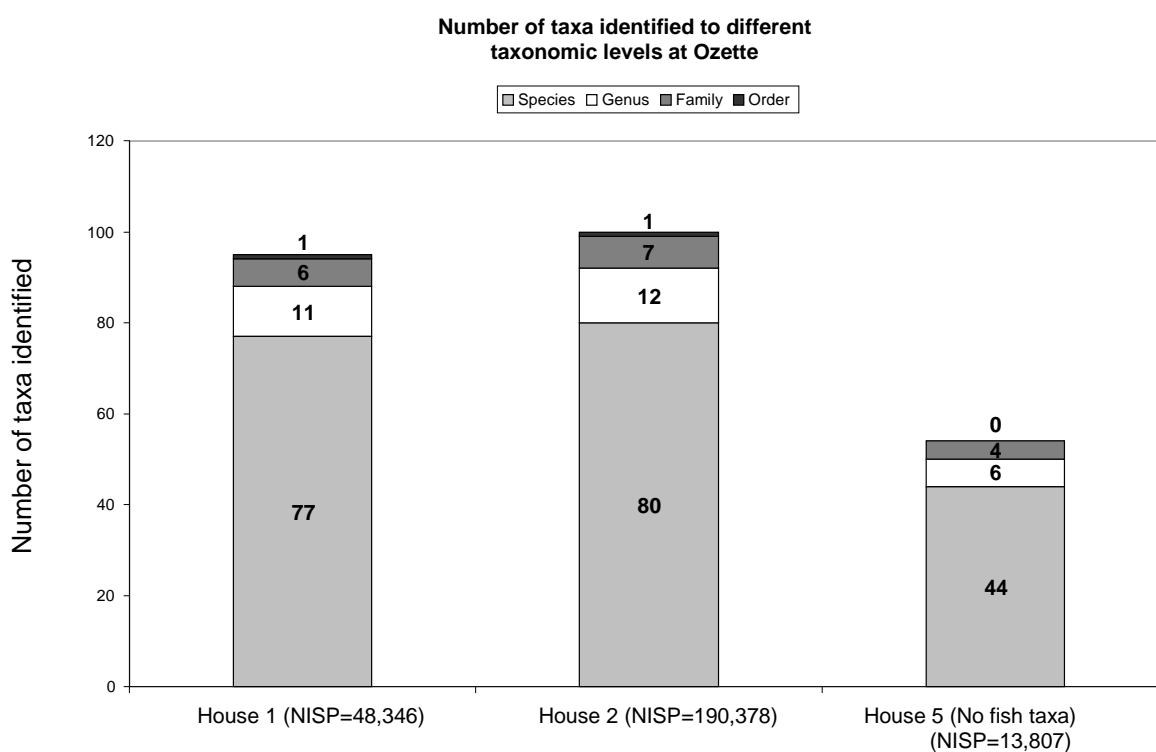
Figure 11. Taxonomic richness at the Ozette houses.

When measuring the NTAXA of a sample from each house, only taxa identified

to the genus and species level were included (as Grayson (1984) suggests). Lyman

(2008:174-175) argues that richness should only be calculated at a single taxonomic level

(i.e. genus *or* species), since summing the richness of both may result in the same

phenomena being counted twice (once at each taxonomic level). In contrast to both

methods above, Monks (2000) included all taxa which could be identified to family,

genus, or species, arguing that important taxa were represented at the family level and therefore should be included. Several taxa which are considered central to subsistence practices, in particular, salmon (*Oncorhynchus* spp.) and rockfish (*Sebastes* spp.) are identified only to genus in the Ozette collection and therefore it was decided that genus-level identifications should be included; however, taxa identified to family and order only were not included. This did present a small problem for the analysis of fish taxa, as two of the most abundant taxa were identified to family only (surfperches and sculpins). Given this fact, when "abundant fish taxa" are described throughout this chapter, they refer to the abundant fish taxa identified to genus and species. These abundant fish (identified to species/genus) are represented by five and six taxa at Houses 1 and 2 respectively. The other classes of data did not suffer from this complication as all abundant taxa were identified to genus or species level.

The NTAXA values are graphed versus sample size (i.e., the percentage of the house floor excavated) rather than NISP. Sample size was selected because it allows for the comparison of the efficacy of a single sample strategy at different houses.[19] If NISP were used, then any sampling strategy at used House 1 would appear to be more optimal when compared to House 2, simply because the former has many fewer bones contained within its house floor. Additionally, describing sample size as a percentage of a house floor is more easily applied in a "real-world" scenario. Researchers are much more likely to wonder "how accurately do the bones contained within 10% of a house floor identify true NTAXA values?" than they are to ask "if I identify X number of bones, what percentage of the true NTAXA value have I likely identified?". This can occur because different taphonomic processes may alter NISP values much more drastically between

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[19] Note that this is *not* the same as comparing the actual richness of each house to one another.

houses than they alter the percentage of a house needed to be excavated in order to assess richness.

6.1.1 House 1 Results

The number of taxa identified to genus or species level using different sample strategies at House 1 are shown in Figure 12. The correlation between sample size and the number of taxa identified is obvious: except for the two largest sampling fractions, for every increase in sample size, there is also an increase in the number of taxa identified. Systematic augering of House 1 revealed the smallest number of taxonomic identifications (14). Using a Dionisio sampling strategy (40% sample size), 77 taxa (87.5% of the taxa identified to genus/species) were identified. The variation between samples of the same size was minimal. The three 1% random samples identified 33, 33 and 39 different taxa, the 5% random samples 56, 57, and 58 taxa, and the 10% random samples identified 64, 65 and 66 taxa.

Sample method does not appear to have a large effect on the number of taxa identified: for every increase in sample size, there is an increase in the number of taxa identified. If there were to be a significant advantage or disadvantage to a specific sample method, one would expect a NTAXA value that could not easily be explained by sample size. For example, if the 10% random samples identified more taxa than the McNichol Creek or Dionisio Point sample strategies, it could be argued that 10% random samples have the potential to perform more optimally in their identification of NTAXA than do these larger judgmental samples. Based on the small number of random samples described thus far, such an argument is not defensible.
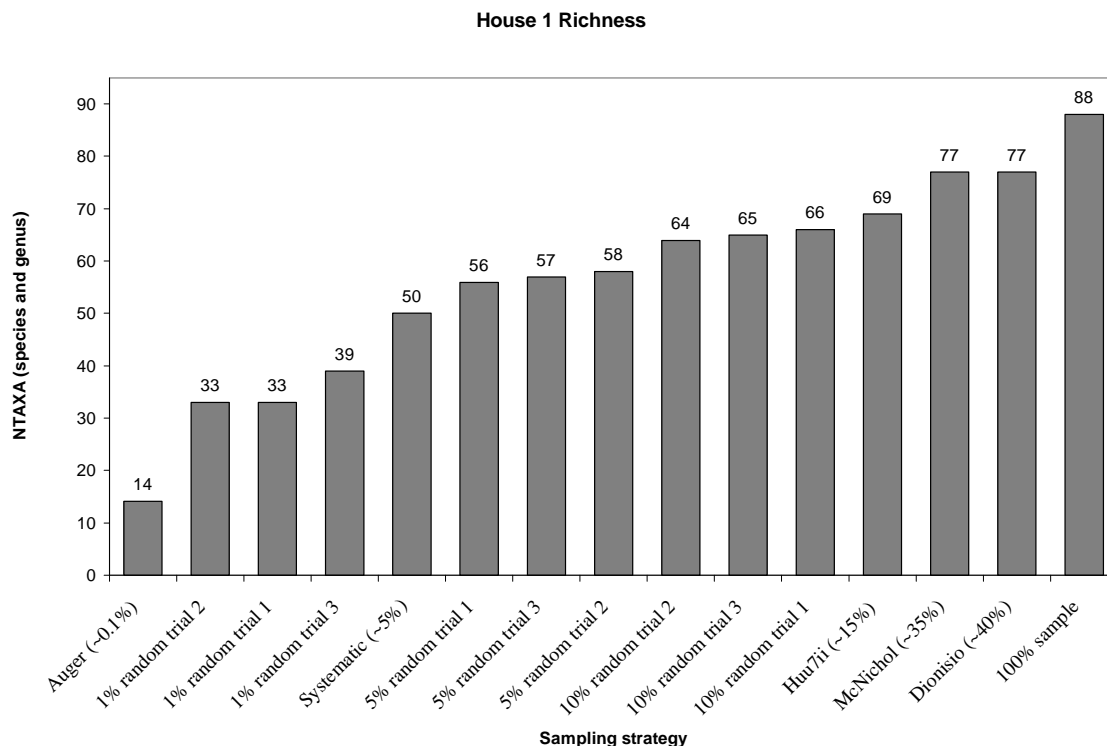
House 1 Richness

Figure 12. Richness (or number of taxa identified) at House 1 using various sample strategies.

When considering which taxa were absent from samples, it was primarily the rare taxa which were not identified, with the exception of the 0.1% auger sample results. Auger sampling failed to identify lingcod (*Ophiodon elongatus*), dog (*Canis familiaris*), and clam (*Tresus* sp.), all of which are abundant[20] taxa. All abundant taxa were present in all other samples except one, suggesting that for House 1, taxa which were not identified in a sample were most likely absent because of their rarity within the house. There is a single exception which requires further explanation. The "1% random trial 2" did not contain any remains of dog, despite the fact that it is the second-most abundant mammalian taxa at House 1. The distribution of this species within the house was highly

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[20] Abundant mammals, fish, and shellfish are represented by only a few taxa at House 1: 2 mammalian taxa, 5 ichthyofaunal taxa (identified to genus/species) and 8 molluscan taxa.

clustered[21], which resulted in its absence from this particular sample despite its relatively high abundance when compared to most other mammalian taxa.

6.1.2 House 2 Results

The results from House 2 exhibit minor variations from the results at House 1 (Figure 13). The fewest taxa (28) were identified using the systematic auger sample; however, the "1% random trial 2" did not identify considerably more taxa (34 taxa) than the auger sample. Unlike House 1, the values for the 1% random samples varied considerably (33, 44, and 49 taxa). In contrast, the differences between most of the 5% and 10% samples were minor. All of these samples except one (the "10% random trial 1", 81 taxa) fell within the range of 65-73 identified taxa.

At House 2, sample size does influence NTAXA values; however, it appears that sample method may also influence this value in the case of one particular method. The Huu7ii sample strategy (15%) did not identify as many taxa as any of the 10% random samples or the 5% systematic sample, indicating that the Huu7ii strategy may be a sub-optimal configuration of excavation units for identifying the NTAXA when compared to probabilistic sample methods. Additionally, the Dionisio Point sample strategy identified fewer taxa than the slightly smaller sampling fraction provided by the McNichol Creek sample strategy.

Much like House 1, the taxa which were consistently identified in all samples are the abundant taxa.[22] Northern fur seal (*Callorhinus ursinus*) accounted for more than 90% of the NISP for mammals at House 2, and therefore all other mammalian taxa were

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[21] The clustered distribution of *Canis familiaris* at House 1 was observed visually and verified statistically using nearest neighbor analysis (p<.01).
[22] Auger samples identified all abundant taxa at House 2, which was not the case at House 1; these differing results are discussed in greater detail Section 6.3.

considered rare. Not surprisingly, this species was identified in every sample, and abundant fish (6 taxa) and abundant shellfish (11 taxa) were also found using every sample strategy.
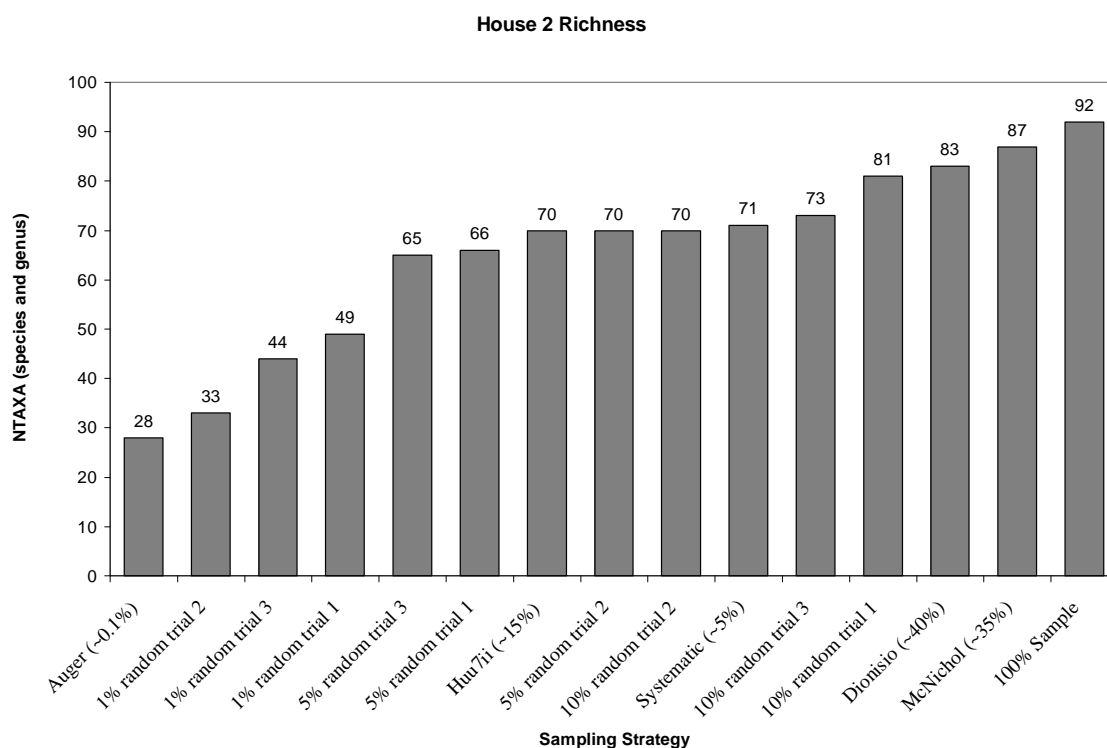
House 2 Richness

Figure 13. Richness (or number of taxa identified) at House 2 for various sample strategies.

6.1.3 House 5 Results

The results from House 5 are shown in Figure 14. As with Houses 1 and 2, systematic augering identified few taxa (6), and, as with House 1, several abundant taxa – – littleneck clam (*Protothaca staminea*), black leather chiton (*Katharina tunicata*), and blue mussel (*Mytilus edulis*) – were not identified using this sample strategy. The 1% random samples from House 5 were similar to the results from House 2 and exhibited some variation in the number of taxa identified (11, 18, and 19); however there was little

variation within or between the 5% random and the systematic samples (29, 29, 30, and

32 taxa) and the 10% random samples (34, 34, and 37 taxa).
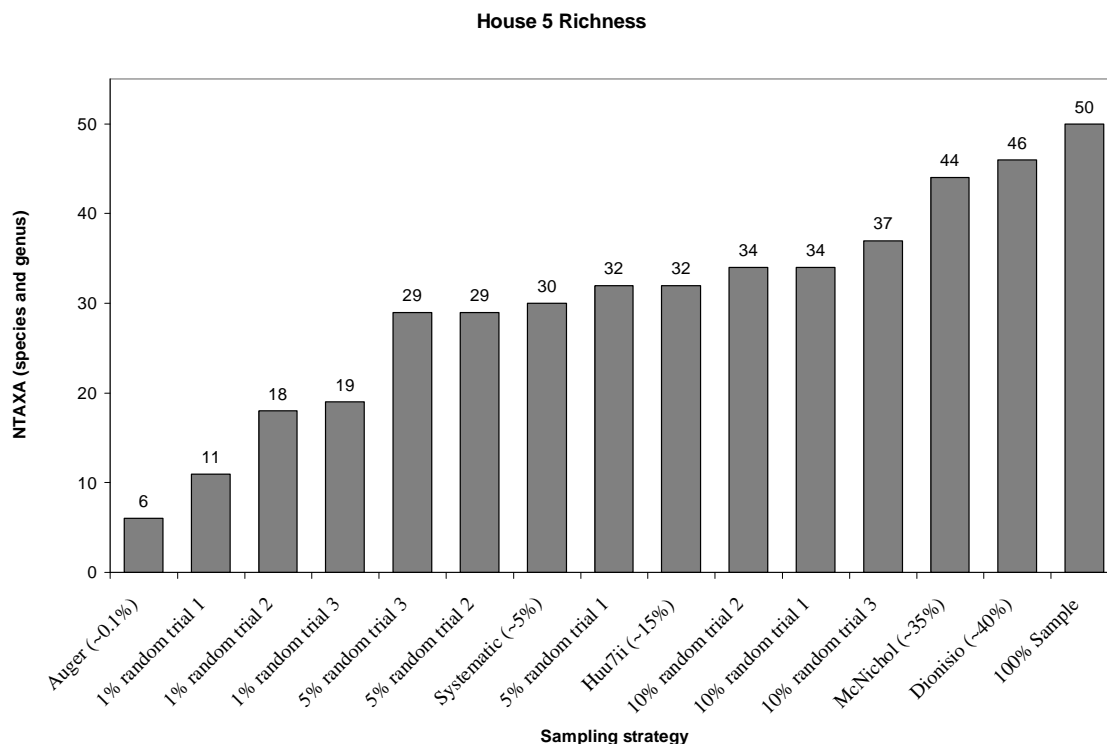
House 5 Richness

Figure 14. Richness (or number of taxa identified) at House 5 for various sample strategies.

There is a distinct correlation between sample size and taxa identified for this

house as well, with one notable exception: the Huu7ii sample strategy, which, as at

House 2, did not identify as many taxa as the 10% random samples. With respect to

abundant taxa, abundant shellfish at House 5 (8 taxa) were identified in all samples, with

the exception of the auger samples and the "1% random trial 1". In this latter sample, the

remains of the abundant taxa blue mussel were not identified because its distribution was

clustered.[23] Northern fur seals accounted for more than 90% of the mammal assemblage

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[23] The clustered distribution of blue mussel was verified statistically using nearest neighbor analysis (p<.01).

and therefore all other taxa were considered rare; all sample strategies identified this abundant species.

6.2 Rarefaction Analysis

As an alternative method of investigating the efficacy of different sampling strategies to identify NTAXA, rarefaction analysis (see Chapter 3; Gotelli and Colwell 2001) was executed for each house. Rarefaction analysis was performed using the rarefaction software *EstimateS* (Colwell 2005). By using the rarefaction software I was able to compare non-random samples to a statistically derived expected mean value for random samples of any size. This is, in effect, a statistical derivation analogous to a Monte-Carlo simulation (Colwell 2005) and has the advantage of including a margin of error of 2 standard deviations above and below the statistical expectation of richness based on a random sample of any size.[24] Non-random samples which fall outside of 2 standard deviations of a random sample of the same size can be considered significantly more or less optimal than a simple random sample. This type of analysis is statistically rigorous, in contrast with the three random samples drawn from each house presented in Section 6.1 above, which are not. However, this rarefaction technique does have one drawback: it does not specify which taxa are present and which taxa are absent for each sample iteration. This type of analysis therefore did not provide information on abundant versus rare taxa, which is precisely what the data in Section 6.1 elucidated.

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[24] Note, however, that the standard deviation above the mean is not accurate as one approaches asymptotic values. The software is meant to be used on samples which could potentially contain additional taxa if more samples were added. The standard deviation above the mean once the asymptotic trend is observed does not apply in this case because it is a known population, and therefore new samples would not produce new taxa. This is of minor concern in this particular case as the sample sizes of interest are smaller than 50% and therefore the standard deviation above the mean is below the total NTAXA value for a given house.

The results of the rarefaction analysis for Houses 1, 2 and 5 are presented below (Figures 15-17). All non-random samples at House 1 fall within 2 standard deviations of a random sample, although they are all below the statistical mean. This appears to

Rarefaction Analysis, House 1
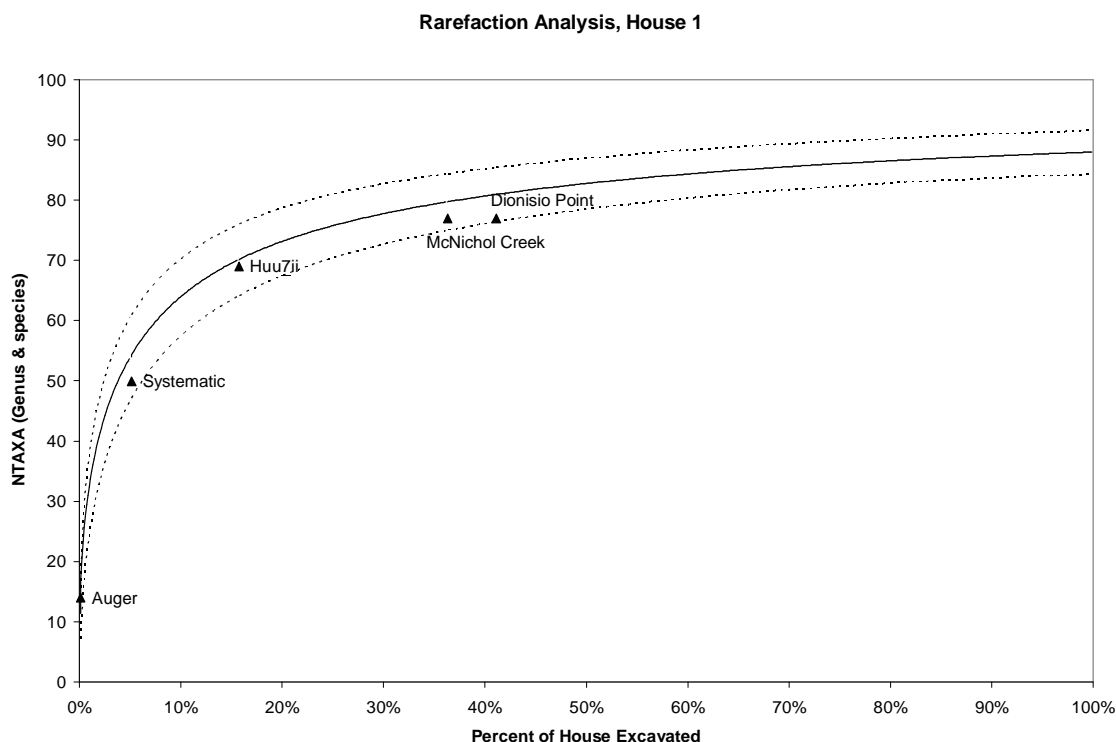
Figure 15. Rarefaction analysis for House 1. The solid line represents the estimated mean richness, the two dotted lines indicate 95% confidence limits for random samples. Other sample results are also listed.

indicate that at House 1, non-random sample methods are likely to perform as well as random sampling methods if the random sample is the same size as the judgmental sample. It was noted in Section 6.1 that no sample method (probabilistic or judgmental) appeared to be more optimal than any other; the results of rarefaction analysis also suggest that this is the case at House 1.

At House 2, the results are somewhat different. The 5% systematic sample identifies more taxa than most random samples of the same size, suggesting it is an optimal sample method to use to identify the NTAXA. It does fall just within two standard deviations, and therefore this result is not statistically significant. The Huu7ii

Rarefaction Analysis, House 2
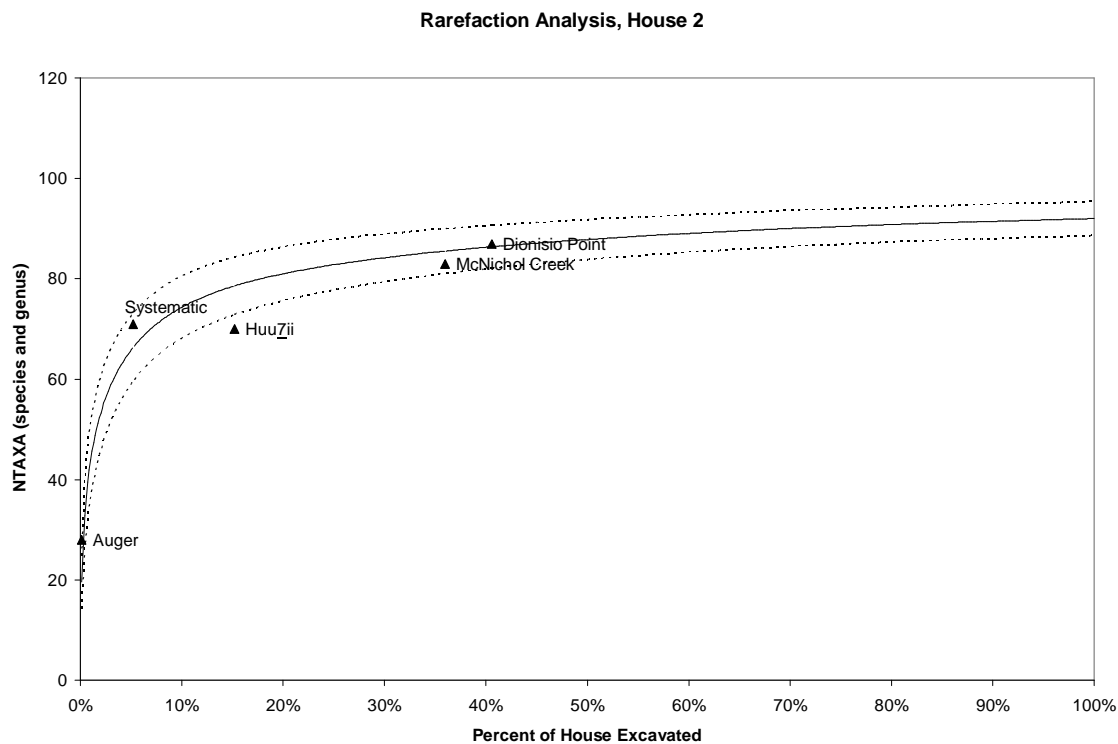
Figure 16. Rarefaction analysis for House 2. The solid line represents the estimated mean richness, the two dotted lines indicate 95% confidence limits for random samples. Other sample results are also listed.

Rarefaction Analysis, House 5
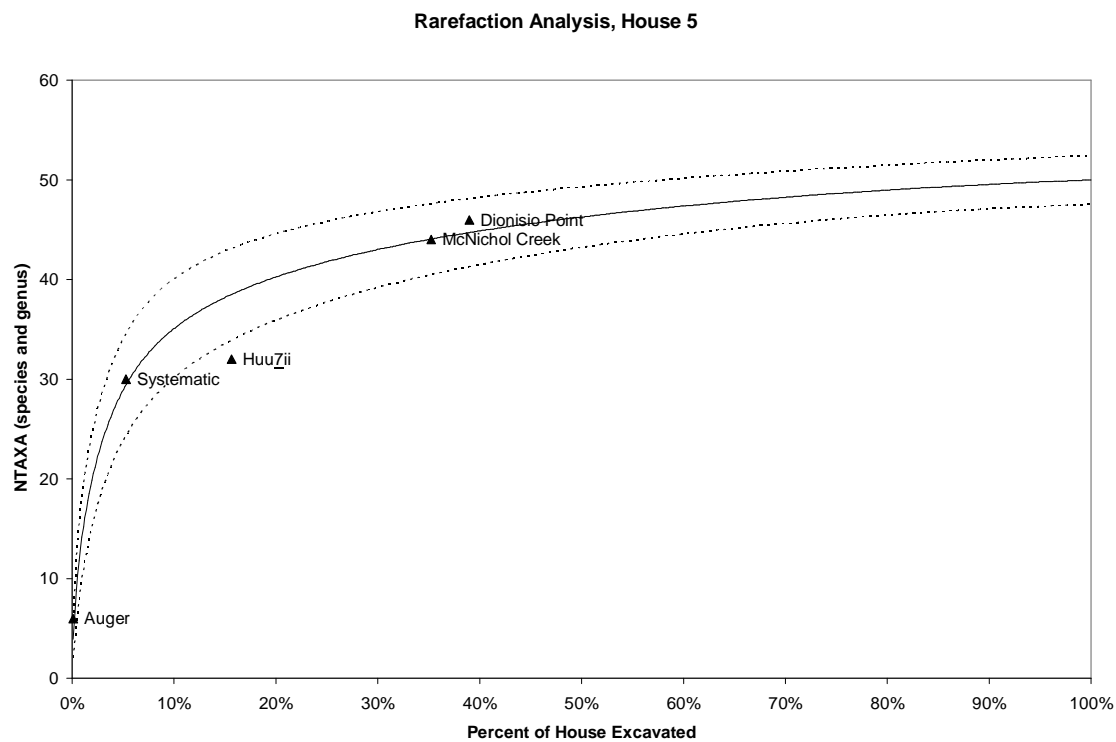
Figure 17. Rarefaction analysis for House 5. The solid line represents the estimated mean richness and the two dotted lines indicate 95% confidence limits for random samples. Other sample results are also listed.

strategy falls outside of 2 standard deviations and is therefore statistically significantly less likely to identify the same number of taxa as a random sample of the same size. Both the Dionisio Point Strategy and the McNichol Creek Strategy fall well within 2 standard deviations for House 2, indicating that they do not perform significantly worse or better than random samples of the same size. These results confirm the trends observed in Section 6.2: at House 2, there are differences in NTAXA values which are attributable to sample method (i.e., the Huu7ii sampling method is sub-optimal when compared to a random sample method) rather than to sample size.

At House 5, the Huu7ii sample strategy identifies significantly fewer taxa than a random sample of the same size is likely to identify, indicating that, as with House 2, the Huu7ii sample method is sub-optimal. This sample was also identified as sub-optimal when compared to the three 10% random samples. The NTAXA values for all other non-random samples were near the mean value derived for random sampling.

As a final analysis, rarefaction curves between all three houses[25] were compared to characterize the ubiquity of all taxa at each house. As illustrated in Figure 18, a smaller number of excavation units (drawn randomly) from House 2 would likely identify relatively more taxa than at Houses 1 and 5, with House 1 slightly more than House 5. While not illustrated in Figure 18, the lower confidence interval of House 2 overlaps with the upper confidence interval of Houses 1 and 5, indicating that no significant difference exists between the distributions of taxonomic richness between houses.

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[25] To compare rarefaction curves, the number of taxa identified was converted to a percentage in order to normalize the different number of taxa found in each house. The sample size had already been normalized to the percentage of the house excavated in terms of area, and therefore did not need to be altered in order to compare between houses. It is important to remember that sample size is relative (i.e., a 10% sample of House 2 is smaller than a 10% sample at House 1).

The comparison of rarefaction curves between houses should be considered in light of what is hypothesized about the cultural site formation processes at each house. At House 1, the floor was likely swept to keep it clean (Huelsbeck 1994), thereby reducing
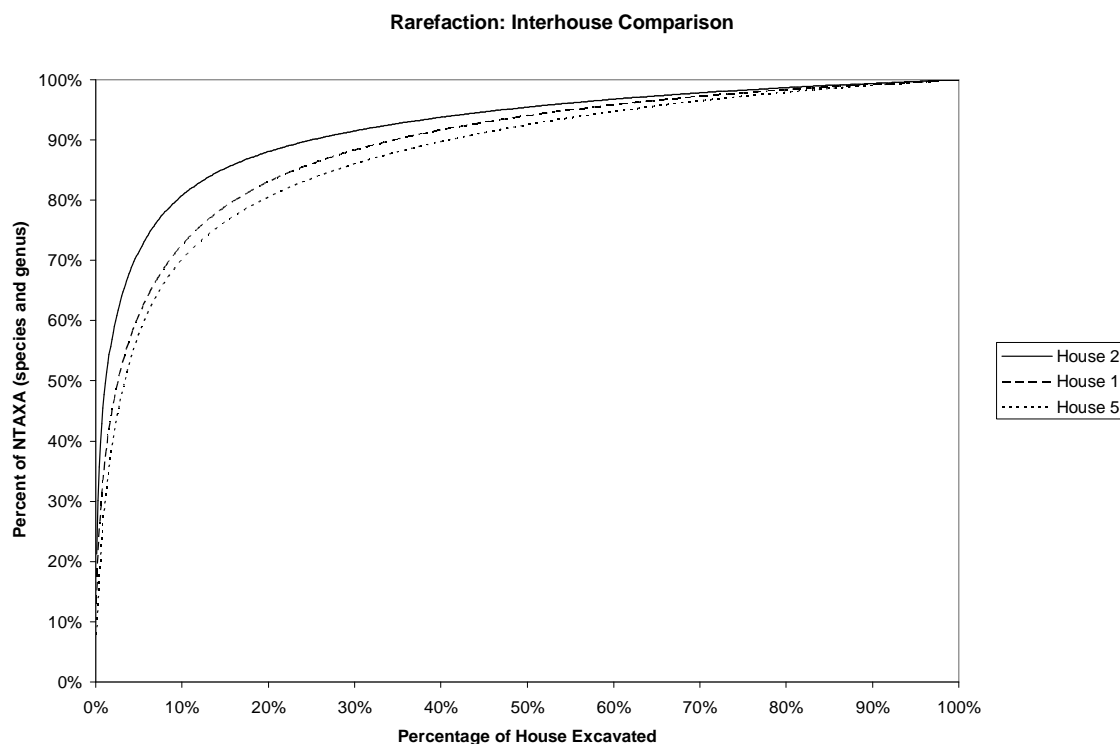

Figure 18. Comparison of rarefaction curves from House 1, House 2 and House 5.

the ubiquity of many species throughout this house. Similarly, House 5 was purposefully abandoned which may have resulted in a "patchy" distribution of taxa throughout this house, although a lack of analysis for the ichthyofauna requires that these results be interpreted cautiously, as the distribution of this class of data in House 5 could alter the rarefaction curve. Unlike House 1 and House 5, different cultural formation processes at House 2 (i.e. a lack of housefloor sweeping) would have produced a different faunal assemblage which, based on the rarefaction curve, indicates that taxa were more ubiquitously distributed at House 2 than they were at House 1 or House 5. House floors

which are not cleaned could easily result in many taxa being more ubiquitously distributed throughout the house.

6.3 Discussion

Several key points can be developed when comparing sampling methods and sample sizes, all of which indicate that sampling has a large effect on NTAXA values. The effectiveness of the 0.1% systematic auger sample strategy varies considerably between houses, making the utility of such a strategy difficult to predict for future excavations. At Houses 1 and 5, this sample method identified 16% (14 taxa) and 12% (6 taxa) respectively, values which appear fairly similar when compared with the NTAXA value for the 0.1% systematic auger sample at House 2, at which quite a few more taxa 30% (28 taxa) were identified. House 2 auger samples also identified all abundant taxa, while this strategy, applied at the other two houses, did not. Overall, this strategy identified the fewest taxa at every house; however, the value of utilizing this technique to identify taxonomic richness at future house excavations is hard to predict as explained above, and because of the reasons discussed below.

Auger samples, like all other samples in this simulation, are only identifying fauna which were screened through 6.4mm mesh (see Chapter 5). In reality, fauna from auger samples would likely be processed through much smaller mesh, and therefore it would be likely that faunal elements which are smaller than 6.4mm would be identified. Furthermore, auger samples are designed to sample vertical deposits, and therefore the spatial heterogeneity (in terms of taxonomic richness) of a discrete house floor is unlikely to be represented well by this strategy which excavated only 0.1% of the area of a house floor. If behavioural patterns persist within a house over long periods of time (e.g., long-

term and/or reoccupation of the house), then auger samples have the potential to identify more taxa which are inadvertently incorporated into house floor deposits during its occupation. However, if cultural site formation processes (such as house floor cleaning/sweeping) also persist during the occupation of the house, the ubiquity of different taxa may not increase over time.

The Huu7ii strategy is another strategy for which the efficacy is hard to predict. Like the auger strategy, this strategy also appears to perform sub-optimally at Houses 2 and 5 (see Figure 16 and Figure 17). The most likely reason that fewer taxa were identified using this strategy compared to random samples of the same size is that taxa were heterogeneously distributed throughout Houses 2 and 5, and therefore sampling only the rear of the house failed to identify taxa which were distributed in the middle or front of the house. Interestingly, this strategy performed more optimally at House 1, possibly indicating that, overall, taxa were distributed more ubiquitously at the rear of House 1 than they were at the rear of the other two houses.

The rarefaction technique has provided a useful method to statistically evaluate random versus non-random samples. It indicated that the Huu7ii sample was sub-optimal compared to random samples and that both McNichol Creek and Dionisio Point sample strategies performed as well as the random samples of the same size. These trends were also observed, albeit qualitatively, prior to rarefaction analysis using the three random samples drawn from each house.

The clustered distribution of an abundant taxon within a house floor that results in that taxon's exclusion from the sample is a practical problem that cannot be circumvented, nor tested for during actual archaeological investigation. How substantial

is this problem? Based on the above data from Ozette, and despite the fact that abundant taxa were observed to often be distributed in a clustered fashion, they were still identified in all non-random samples (except auger samples) and in the majority of the random samples. In fact, the omission of abundant taxa only occurred in two samples (not counting auger samples): once in a 1% random sample at House 1, and once in a 1% random sample at House 5. Based on these results, it appears that abundant taxa within a house are likely to be identified, assuming that at least 1% of a house is excavated.

None of the sample strategies tested above identified the overall richness for each house, a result determined in part by the many rare taxa found within each house. Nevertheless, several arbitrary thresholds, which may be of heuristic value for future excavations, can be delineated. Firstly, a 10% random sample identified more than 70% of the taxa at House 1 and House 2. At House 5, 60% of the taxa were identified by any sample of size 10% or greater. Secondly, sample sizes of 40% and greater seldom identified fewer than 90% of the different taxa at every house. Whether the extra sampling effort is warranted in order to identify many of the additional taxa ultimately depends on the research design and specific research questions, and I return to this point in Chapter 9.

In summary, a general trend exists for all sample strategies in which an increase in sample size results in an increase in NTAXA values. The majority of judgmental and systematic sampling strategies perform no better or worse than expected when compared to the random samples and to each other. Having investigated how sample size and method affects the number of taxa identified, I now investigate how sample strategies affect the relative abundance of various taxa.

Chapter 7: Effects of Sampling on Relative Abundance

Chapter 7 presents the results of sampling simulations in order to measure the effect of sampling on the relative abundance of taxa. Initially, evaluating differences between sample abundances and population abundances proved difficult, as no one technique, statistical or otherwise, was ideal in all respects (see Table 7 and Agresti and Finlay 1996; Grayson 1984; Lyman 2008). Based on the advantages and disadvantages presented in Table 7, three methods have been selected in order to evaluate the relative abundance between samples and the complete assemblage for each house.[26] Section 7.1 presents the results of Spearman's rank correlation. Section 7.2 discusses the usefulness of arbitrary threshold values in defining sample optimality, and subsequently analyzes the samples based on a defined threshold value. Histograms are also employed in this section to illustrate the congruence between sample relative abundance and actual relative abundance. Following this, the ineffectiveness of auger samples to accurately detect relative abundances of taxa is discussed. The chapter concludes with a discussion of the results presented.

7.1 Spearman's Rank Correlation

Spearman's rank correlation (Blalock 1960) can be used to measure to what extent the ranking of a taxon between the complete assemblage and a sample is comparable. Rank is determined by the relative abundance of a given taxon; the most abundant taxon is given a rank of 1, the second most abundant taxon is given a value

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[26] The absolute number of taxa identified in each sample is presented in Appendix 4.

Analysis method	What is measured?	Advantage(s)	Disadvantage(s)
Tables of NISP values (see Appendix 4) or tables of %NISP values	The number of bones from a given species in a sample or population.	Easy to understand the raw data.	Cannot tell if differences are statistically significant, hard to interpret general trends quickly.
Histograms (see Section 7.2)	Differences in relative abundance between samples and population are displayed.	Visual display is easy to interpret.	Cannot tell if differences are statistically significant; open to interpretation. Cumbersome to display if many taxa or many different samples are compared.
Spearman's rho rank correlation (see Section 7.1)	The correlation between ranks of taxa in a given sample and rank of same taxa in the complete assemblage.	Statistical; sensitive to changes in relative abundance of taxa providing that their ranks change.	Does not consider the magnitude of the difference in relative abundance for a given taxon unless it results in a different rank between the sample and the assemblage (i.e. it is an ordinal-scale measure rather than a ratio or interval measure).
Arbitrary thresholds (see Section 7.2)	Defined arbitrary values which, when exceeded, are considered to represent a sub-optimal sample.	Transparent, easy to evaluate and easy to understand.	Non-statistical and arbitrary, and therefore open to criticism that the defined thresholds are not indicative of 'real-world' differences. However, if presented clearly, the results can be evaluated using different thresholds in order to observe if (how) interpretations would differ based on different thresholds.
Chi-square test	Similarity between expected values (i.e. population) and observed values (i.e. sample).	Simple statistical test with levels of significance; analysis of residuals can be used to indicate which taxa are producing statistically significant results (see Lyman 2008:188-189).	Statistical significance is sensitive to population size. This statistic is therefore difficult to compare between different samples, as large differences in NISP values exist between houses, between samples and between classes. For the Ozette fauna, rare taxa must be grouped together because this test does not work for very small expected values (n<5) (Agresti and Findlay 1996).
Diversity indices (e.g., Shannon or Simpson Index)	Combined measure of evenness and richness (e.g. Lyman 2008)	Easy to measure and interpret; statistical significance of results can be derived.	Since it is a combined measure, it is hard to know whether it is evenness or richness (or both) that is causing diversity indices to change (Lepofsky and Lertzman 2005).
Kolmgorov-Smirnov	Measures whether cumulative frequency distributions could have come from the same population (e.g. Grayson 1984:152-153)	Indicates similarities in data structure and to what extent the evenness (or lack thereof) of a sample corresponds to its parent population. Statistical significance of the results can be derived.	In this method, frequencies of taxa (from least abundant to most abundant) are compared between the population and the sample. However, this distribution is derived independently of class. Therefore, the relative abundance of a specific taxon in a sample cannot be compared to its relative abundance in the population.

Table 7. Advantages and disadvantages of various methods of comparing the sample relative abundance to its actual relative abundance in the population.

of 2, etc., until all taxa have been given a rank. If two or more taxa have the same relative abundance, their collective ranks are averaged so that every taxon with the same relative abundance is given the same rank. Taxa are ranked both within the sample and within the population and then their ranks are compared. Rank correlation is useful in this instance because each rank has an equal weight, and therefore any changes in the ranks of abundant taxa, rare taxa, or both, will result in a lower correlation coefficient.

Values for Spearman's rank correlation vary between 1 and -1: A value of 1 indicates a perfect positive correlation between the ranks of all taxa in the sample compared to the population, a value of -1 indicates a perfect negative correlation, and a value of 0 indicates that no correlation exists. The significance level used for rank correlations in this thesis is two-tailed, as there is no *a priori* reason to assume that the relative abundance of a given taxa will increase rather than decrease (or vice versa) in any sample. Therefore, for all Spearman's rank correlations, two-tailed significance to the .01 level is implied unless otherwise noted.

The results of the correlation are remarkably similar for all samples and all houses (see Table 8). For all fish and shellfish at all three houses, there is significant correlation (p<.01) between the ranks of species in the complete assemblage and their ranks in all samples. Correlation values did tend to decrease as sample size became smaller, although in most cases correlation was still significant. These results are somewhat unexpected given that the relative abundance of many rare taxa (as defined in Chapter 6) was expected to fluctuate considerably between samples because of their rarity, thus changing their rank in a given sample. While fluctuations in relative abundances were

Sample Strategy	H1 Mammals	H1 Fish	H1 Shellfish	H2 Mammals	H2 Fish	H2 Shellfish	H5 Mammals	H5 Shellfish
1% RT#1	0.893	0.850	0.699	**0.623**	0.903	0.913	**0.611**	0.682
1% RT#2	**0.658**	0.899	0.805	0.733	0.885	0.768	**0.710**	0.655
1% RT#3	0.821	0.836	0.735	0.735	0.956	0.881	**0.702**	0.755
5% RT#1	0.884	0.982	0.906	0.914	0.960	0.927	0.859	0.880
5% RT#2	0.935	0.960	0.871	0.956	0.989	0.920	**0.610**	0.915
5% RT#3	0.869	0.971	0.915	0.771	0.977	0.961	0.834	0.905
5% Systematic	0.958	0.989	0.847	0.886	0.977	0.971	0.896	0.924
10% RT#1	0.941	0.989	0.927	0.731	0.990	0.974	0.918	0.918
10% RT#2	0.969	0.991	0.925	0.870	0.996	0.968	0.896	0.893
10% RT#3	0.947	0.988	0.932	0.835	0.957	0.979	0.907	0.900
Huu7ii	0.90	0.950	0.893	0.737	0.968	0.950	0.865	0.767
McNichol Creek	0.892	0.954	0.932	0.900	0.961	0.979	0.909	0.962
Dionisio Point	0.974	0.963	0.881	0.961	0.983	0.990	0.957	0.980

Table 8. Results of correlation analyses for various sample strategies when comparing the ranks of taxa based on their relative abundance. Values in '**bold**' indicate that the correlation between the sample and the complete assemblage was not statistically significant (p<.01). None of the samples exhibited a complete lack of correlation (i.e. values approaching zero), and none of the samples exhibited a negative correlation. Note: "RT" refers to "random trial".

observed, these were evidently not large enough to change the correlation values to a great extent.

The sampling of mammals was the only class for which the correlation was not significant in all cases.[27] At House 1, the "1% random trial 2" showed no significant correlation to the rankings of the same taxa in the complete assemblage. As noted in Chapter 6, no dog remains were found in this sample, resulting in a large change in its rank and therefore a lack of significant correlation. The "5% random trial 2" at House 2 also did not exhibit significant correlation when compared to the entire collection. In this sample, the second-most abundant mammalian taxa at the house, sea lion (*Eumetopias jubata*), was represented by very few specimens and this resulted in a non-significant correlation.

The "1% random trial 1" at House 1 and all of the 1% random samples from House 5 exhibited no significant correlation with the entire collection. In all of these cases, the absence of many rare taxa is the reason for the lack of significant correlation, rather than the fact that one specific taxon was absent. Their absence in a sample results in their equal ranking since they have the same abundance (0); however, each rare taxa had a different rank in the complete assemblage, and as a result their ranks in the sample differ from their expected ranks.

Based on the results above, the ranks of the relative abundance of taxa in samples show an overwhelming positive significant correlation with the ranks of the relative abundance of the complete sample. The reasons for this most likely lie in the structure of the faunal data, which consist of a few abundant taxa and many rare taxa. By virtue of being rare, these taxa are never identified in greater quantities than abundant taxa, and

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[27]In these cases correlations were still positive, however they lacked statistical significance.

therefore their ranking never exceeds that of abundant taxa. Similarly, abundant taxa are identified in large enough quantities that their NISP values almost always exceed the NISP of rare taxa, (although two samples of mammalian taxa were not statistically correlated because relatively abundant taxa were either rare or entirely absent from the sample). Small changes within the ranks of abundant taxa or within the ranks of rare taxa, do not appear to affect the overall ranking to the point where correlation is not significant.

As noted in Table 7, one drawback of using this method to indicate sample effects on relative abundance is that changes in relative abundance which do not alter the rank of a taxon are not identified. Consider a hypothetical population which is comprised of three species: 80% species A, 15% species B, and 5% species C. A sample of this population whose constituent members were 40% species A, 35% species B, and 25% species C would have a correlation value of when 1 compared to the population, yet the difference in relative abundance between the sample and the population would arguably be quite large, especially from an interpretive perspective. Because of this fact, and because most samples appeared to be optimal based on correlation analysis, another method of analyzing these results was desired. In order to do so, the taxon which accounted for the greatest variability in a given sample was identified as another method of evaluating all of the samples.

7.2 Maximum Variability in a Sample

A further investigation was carried out to identify samples that "work". In order to do so, the taxon in each sample which deviated the most from its actual relative

abundance was identified, and the magnitude of this deviation quantified (LMOD[28]) (see Tables 9-11). Since, by definition, this value is the largest deviation, all other taxa in the sample must deviate from their actual relative abundance by less than this value. Analysis of this type allows for the examination of a specific taxon which exhibits the most variability in its relative abundance in each sample. If the same taxon continually has the largest magnitude of deviation (LMOD) value across numerous samples, then this may prompt further investigation into the distribution of this particular taxon and the reasons why its variance is continually greater than for any other taxon. A criterion has been developed below which indicates which samples are optimal and which samples are sub-optimal based on a specific threshold value for the LMOD.

In this thesis, those samples for which the LMOD exceeded 4.0% will be considered sub-optimal. While this is an arbitrary value, its implementation and use were selected for several reasons. Values larger than this value may result in too great a source of error, especially if the relative abundance of the LMOD taxon is small. For example, if the taxon which accounts for the most variation in a sample has an actual relative abundance of 12% within the population, a change of 5% would result in this taxon's relative abundance becoming over 40% smaller or larger (7% or 17%), which may (or may not) affect the interpretation of the importance of this taxon. Conversely, a taxon with a much higher relative abundance will be affected to a lesser degree. Thus, the 4.0% threshold was employed because some variation away from the actual relative abundance is permitted under this threshold; however, it is also hypothesized that this value is not so

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[28] LMOD refers to the value associated with the taxon taken from a sample which has the **l**argest **m**agnitude **o**f **d**eviation in relative abundance from its known relative abundance in the population. What this acronym lacks in eloquence it makes up for in clarity when results are presented and discussed.

large that valid interpretation of general, macro-scale observations about the relative

quantities of different faunal constituents in a sample are no longer possible.

I believe that this value (4.0%) is an acceptable margin of error when describing

the general composition of faunal data from house floors. Of course, whether this is the

case in a particular instance depends both on the analyst and the research objectives

involved. Researchers can decide for themselves if they think that 4% is acceptable, and

if not, they can assess the data (see Appendix 4) using a different threshold. This allows

one to move forward productively, rather than debate arbitrary threshold values.

7.2.1 House 1 Results

At House 1, all of the sample strategies except the Dionisio Point sample strategy

failed to meet the 4% threshold level for all classes in a sample (Table 9). All 1% random

samples exhibited LMOD values considerably larger than 4.0%. These results are not the

result of one particular class of data being sub-optimal, as each class of data was well

Sample Strategy	Mammals		Fish		Shellfish	
1% RT#1	Dog	(3.32%)	Salmon	(6.63%)	Littleneck clam	(11.34%)
1% RT#2	Northern fur seal	(8.11%)	Salmon	(7.19%)	Sitka periwinkle	(7.22%)
1% RT#3	Porpoise	(7.25%)	Halibut	(13.43%)	Sitka periwinkle	(9.90%)
5% RT#1	Dog	(1.86%)	Surfperch	(3.22%)	Dentalia	(1.68%)
5% RT#2	Northern fur seal	(7.56%)	Lingcod	(5.96%)	Sitka periwinkle	(2.19%)
5% RT#3	Northern fur seal	(3.07%)	Cabezon	(1.98%)	Sitka periwinkle	(2.25%)
5% Systematic	Northern fur seal	(3.36%)	Lingcod	(4.50%)	Littleneck clam	(2.88%)
10% RT#1	Dog	(1.68%)	Lingcod	(2.62%)	Sitka periwinkle	(6.50%)
10% RT#2	Northern fur seal	(0.83%)	Lingcod	(2.13%)	Sitka periwinkle	(3.19%)
10% RT#3	Northern fur seal	(3.01%)	Salmon	(3.48%)	Sitka periwinkle	(6.23%)
Huu7ii	Dog	(5.71%)	Salmon	(6.57%)	Sitka periwinkle	(10.53%)
McNichol Creek	Northern fur seal	(6.74%)	Salmon	(6.60%)	Sitka periwinkle	(9.67%)
Dionisio Point	Dog	(0.81%)	Greenling	(2.19%)	Sitka periwinkle	(3.23%)

Table 9. Taxa whose relative abundance varied the most in a sample compared to the complete assemblage at House 1 (i.e. LMOD values). Percentage change in relative abundance is listed in brackets, however the direction of change (i.e. increase or decrease) is not noted. Note: "RT" refers to "random trial".

above 4.0% in all cases except one. For the "1% random trial 1", the abundance of littleneck clam deviated 11.34% when compared to the actual abundance of this species at House 1; for the "1% random trial 2", the relative abundance of halibut (*Hippoglossus stenolepis*) was 13.43% different than its expected value; for the "1% random trial 3", northern fur seal was 8.11% different than expected. At the 5% random sample size, analysis of shellfish taxa LMOD values indicates that they are all below the 4.0% threshold; however, larger LMOD values for fish and mammals indicate that for no one sample are all taxa from every class below 4.0% in LMOD values. The LMOD values for the 5% systematic sample for shellfish and mammals were below 4.0%, while this value for fish (4.50%) was just above the threshold value. The 10% random samples were below 4% for mammals and fish. Shellfish, which did not exceed 4.0% LMOD values in any of the 5% random trials, were above this value two out of three times in the 10% random samples. This result is somewhat difficult to explain, but may be the result of three optimal[29] 5% random samples being selected by chance, or two poor 10% random samples being selected. Judgmental strategies exhibited considerable variability in their LMOD values between samples and between classes. The Huu7ii and McNichol Creek strategies had taxa which varied by as much as 6-10%, indicating that they are sub-optimal, while the Dionisio Point strategy was optimal for all classes of data.

The taxa which accounted for LMOD variables in each sample can be examined for trends as well. In mammals, the two most abundant taxa – northern fur seal and dog – are the most variable taxa in all samples except one (the "1% random trial 2"). For the fish, no particular species is consistently the most variable, although all of the taxa

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[29] Optimal in this case refers only to shellfish taxa, as these sample strategies were not optimal for mammals or fish.

represented are abundant taxa. For shellfish, Sitka periwinkle (*Littorina sitkana*) is generally the most variable taxa when all samples are considered, although there are three exceptions to this trend.

Based on all of the above observations, the 5% systematic sample for all classes of data and the 10% random samples for mammals and fish are the most optimal strategies used at House 1, although even they are still above the threshold value. Although the Dionisio Point strategy identified all taxa with LMOD values under 4.0%, such a large sample taken from a house is unlikely to be analyzed in its entirety with respect to faunal data. The optimal results presented by all 5% random samples for shellfish is hypothesized to be a statistical anomaly, although the current research for this thesis is unable to address whether or not this is the case. In order to err on the side of caution, it seems as if no sample strategy "works" for shellfish except the Dionisio Point and 5% systematic strategy. The 5% systematic samples and the 10% random samples for fish and mammals are the most likely strategies to be applied in the future because they significantly reduce the amount of fauna that needs to be excavated in order to identify the general composition of fauna at House 1.

Histograms provide a final method of demonstrating similarities and differences between datasets. Histograms are employed because they indicate the fluctuation of all taxa, not just the taxon with the greatest fluctuation. Figures 19-21 present data in histogram form for the 5% systematic sample and the 10% random samples for mammals and fish at House 1; the 5% systematic sample for shellfish is also provided. After observing these histograms, it is my opinion that this final line of evidence demonstrates that none of the samples presented would have resulted in a different interpretation
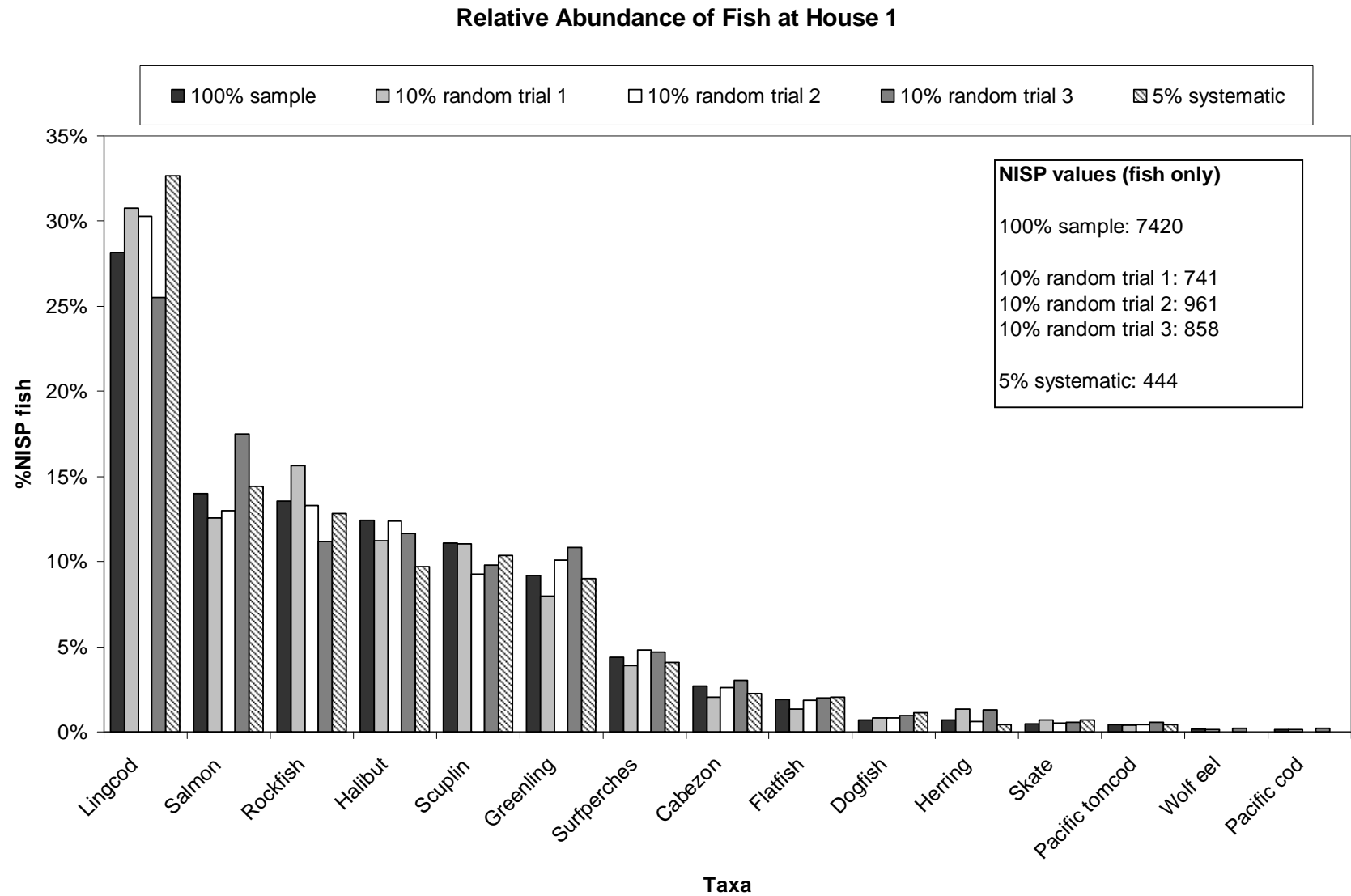
Figure 19. Relative abundance of fish using different samples at House 1.

Relative Abundance of Mammals at House 1
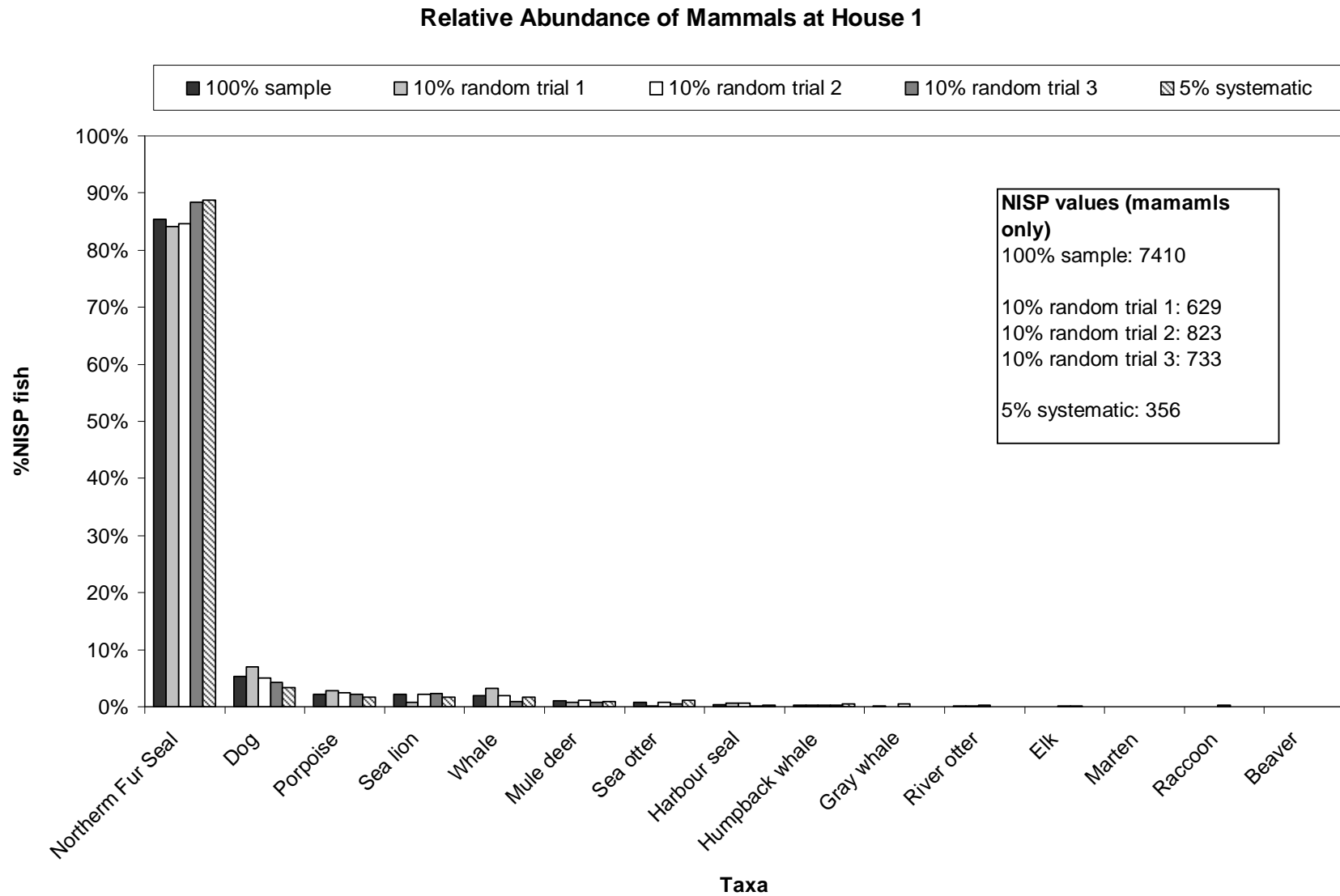
Figure 20. Relative abundance of mammals using different samples at House 1.

Relative Abundance of Shellfish at House 1

■ 100% sample   ⊠ 5% systematic sample

NISP values (shellfish only)
100% sample: 33517
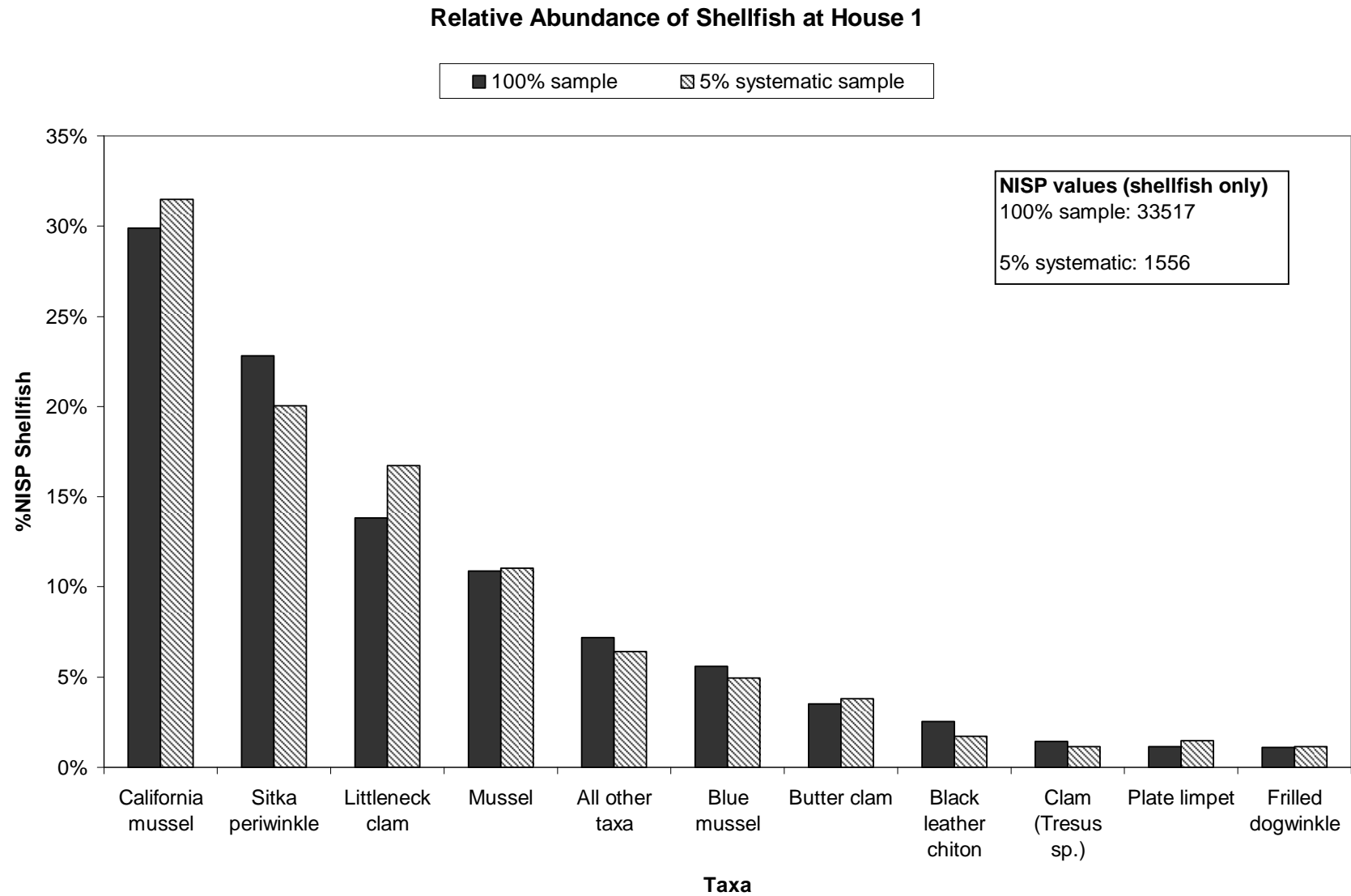
5% systematic: 1556

Figure 21. Relative abundance of shellfish in the complete assemblage compared to the 5% systematic sample at House 1.

with respect to the importance of abundant taxa when compared to the assemblage. In all cases some rare taxa were not identified in samples; however, this did not affect general trends in faunal abundances when compared to the entire faunal population.

7.2.2 House 2 Results

The results from House 2 exhibit both similarities and differences when compared to the House 1 results. Just as with House 1, the 1% random samples were sub-optimal in every category, although one sample ("random trial 1") was below the threshold for mammals. All 5% random samples appear to 'work' for mammals, as does one of the 5% random samples for fish and shellfish taxa. However, at the 10% random sample size, all samples and all classes are below the 4% LMOD threshold, indicating that this sample size and method is optimal regardless of which faunal class is of interest. Systematic sampling also appears to be adequate as well: all LMOD

Sample Strategy	Mammals		Fish		Shellfish
1% RT#1	Northern fur seal	(4.44%)	Greenling	(4.31%)	Sitka periwinkle (11.14%)
1% RT#2	Northern fur seal	(6.21%)	Greenling	(12.54%)	Sitka periwinkle (12.35%)
1% RT#3	Northern fur seal	(2.70%)	Salmon	(5.43%)	California mussel (4.92%)
5% RT#1	Dog	(1.78%)	Greenling	(5.70%)	California Mussel (6.00%)
5% RT#2	Sea lion	(0.54%)	Greenling	(3.54%)	Leather chiton (1.63%)
5% RT#3	Dog	(1.17%)	Rockfish	(2.08%)	Sitka periwinkle (3.06%)
5% Systematic	Northern fur seal	(0.77%)	Rockfish	(2.34%)	California mussel (2.30%)
10% RT#1	Sea lion	(2.12%)	Lingcod	(2.80%)	Blue mussel (0.83%)
10% RT#2	Skunks	(2.39%)	Lingcod	(1.84%)	California Mussel (1.34%)
10% RT#3	Whale	(2.39%)	Salmon	(2.59%)	Mussel sp. (0.83%)
Huu7ii	Northern fur seal	(3.15%)	Rockfish	(2.94%)	California mussel (6.34%)
McNichol Creek	Northern fur seal	(2.05%)	Greenling	(10.06%)	Leather chiton (2.55%)
Dionisio Point	Dog	(0.63%)	Rockfish	(4.73%)	Littleneck clams (0.65%)

Table 10. Taxa whose relative abundance varied the most in a sample compared to the complete assemblage at House 2 (i.e. LMOD values). Percentage change in relative abundance is listed in brackets; however, the direction of change (i.e. increase or decrease) is not noted.

Relative Abundance of Fish at House 2
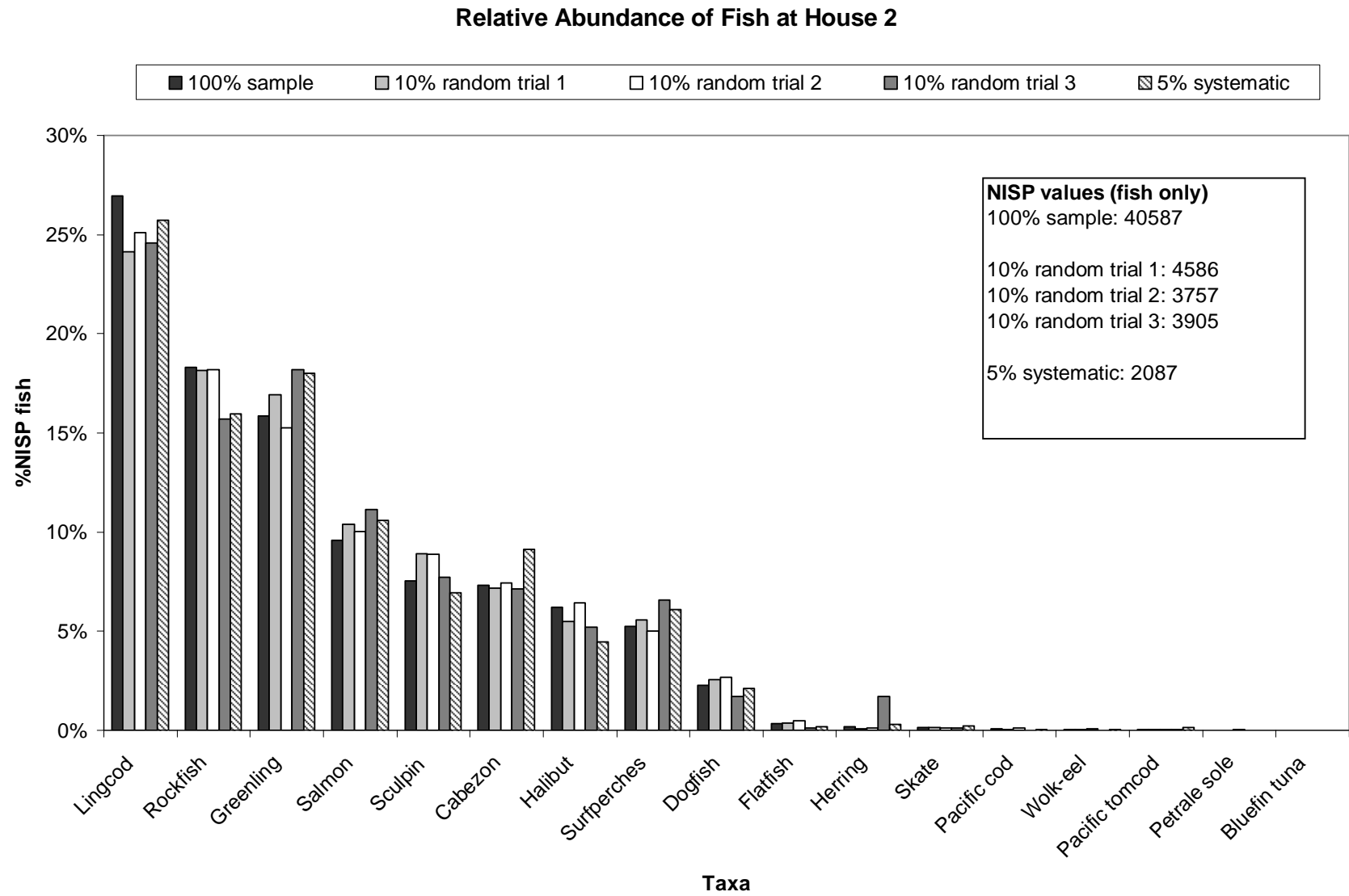
Figure 22. Relative abundance of fish obtained using different samples at House 2.

Relative Abundance of Mammals at House 2
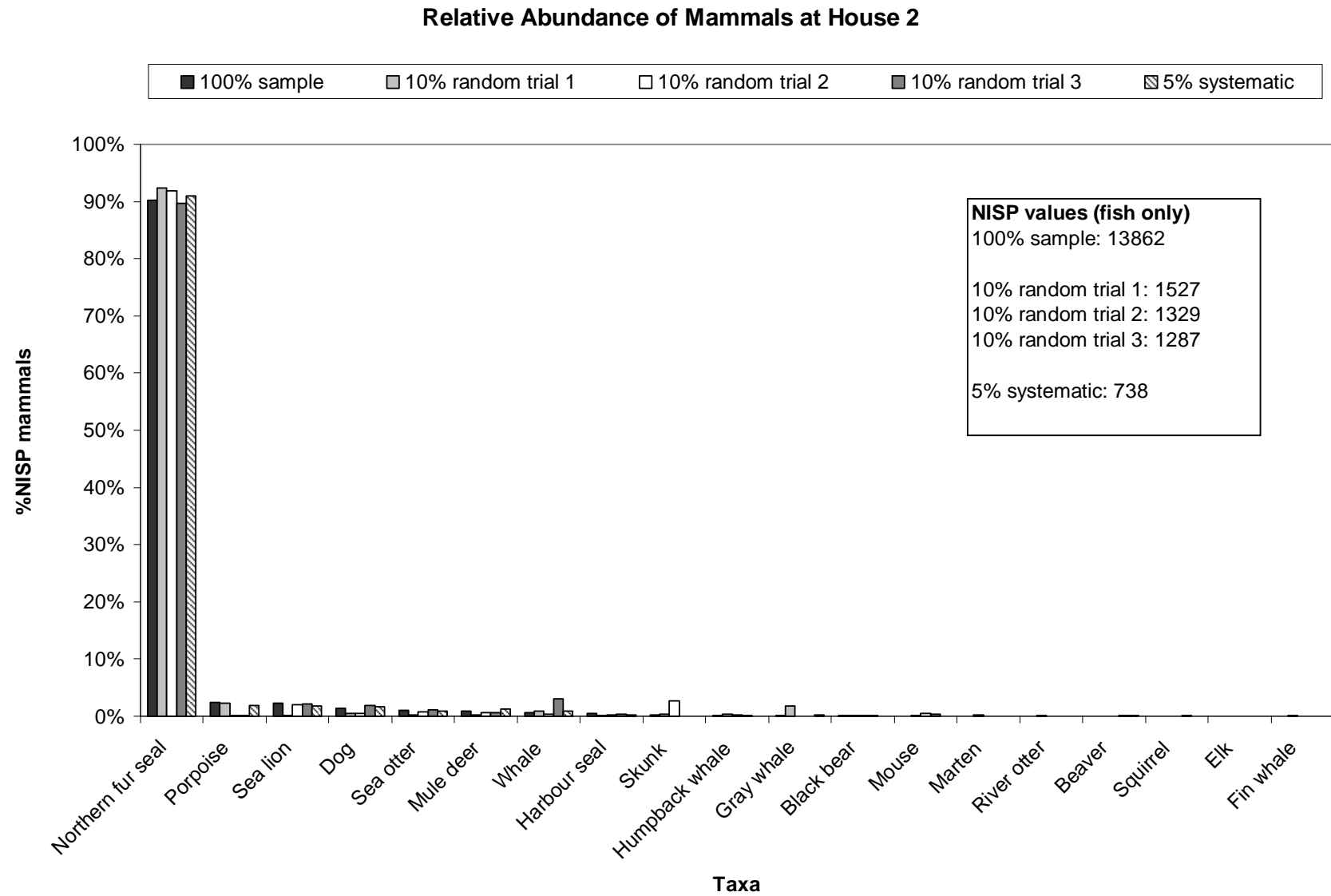
Figure 23. Relative abundance of mammals obtained from different samples at House 2.
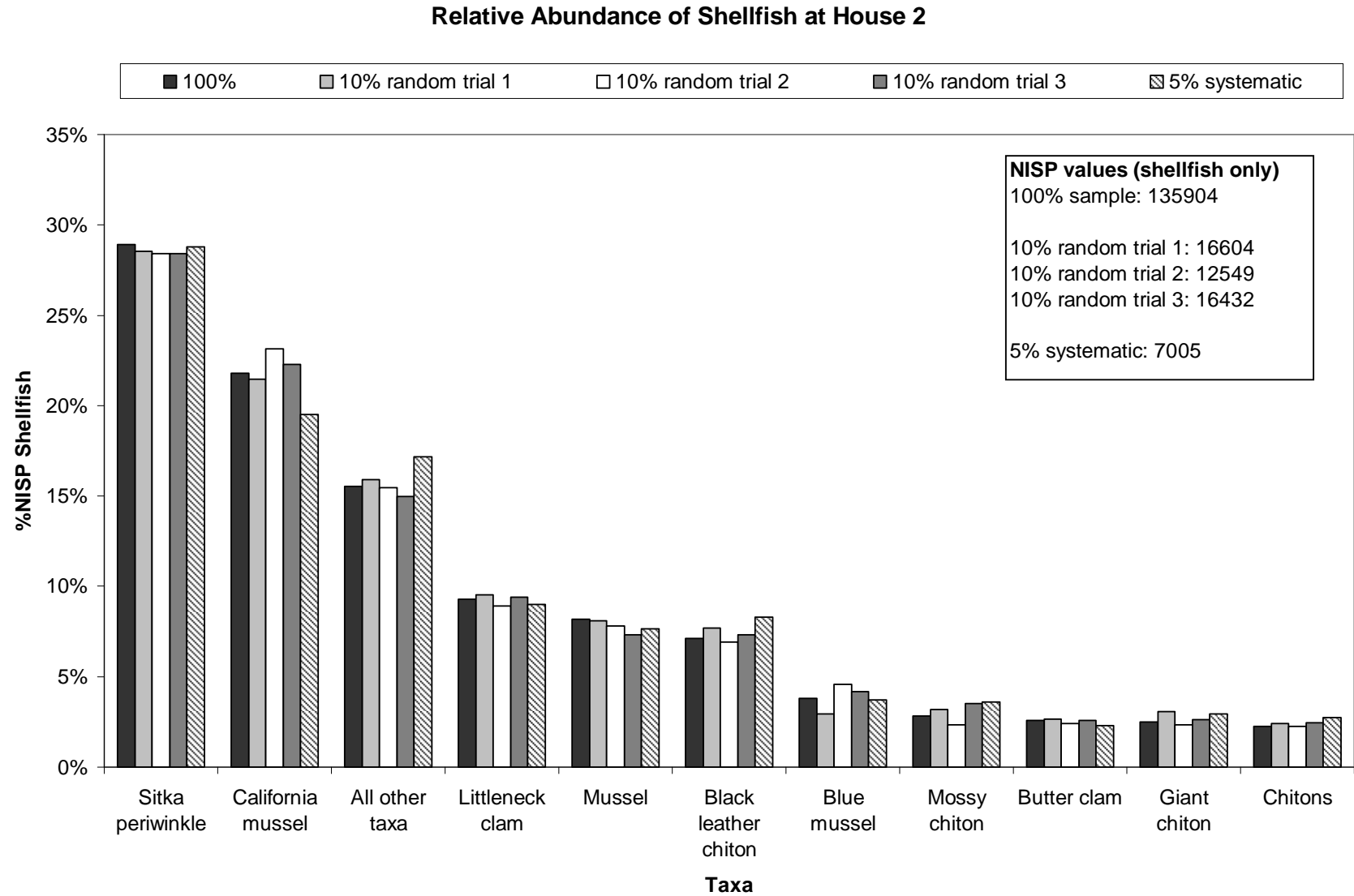
Figure 24. Relative abundance of shellfish obtained using different samples at House 2.

values fall below 4.0%. The LMOD values for judgmental samples are generally lower than at House 1; however, they were still above the threshold value for at least one out of the three classes of data using the Huu7ii or McNichol Creek Strategies. The LMOD value for the fish taxon (greenling; *Hexagrammos* sp.) using the McNichol Creek strategy (10.06%), and for shellfish (California mussel; *Mytilus californianus*) using the Huu7ii strategy (6.34%) were still considerably above the threshold value. As at House 1, the Dionisio Point strategy produced accurate results at House 2. In contrast to House 1, the taxon which was responsible for the variation, rather than being represented by the same specific taxon in difference samples.

Based on the above observations, the 10% random samples for all classes and the 5% systematic sample require further exposition, as these samples are small and yet and produced optimal results. The Dionisio Point Strategy also produced optimal results, but the likelihood of such a large sample being completely identified is remote, and therefore this strategy will not be investigated further at this juncture. Histograms based on the 5% systematic sample and the 10% random samples indicate that general trends in relative abundance are accurately identified by these sample strategies (Figures 22, 23 and 24).

7.2.3 House 5 Results

House 5 results do not differ markedly from those of House 1 or House 2. When considering mammalian species, samples that were 5% or larger, regardless of whether they were derived from systematic, judgmental or random sampling, were below the 4.0% LMOD value for mammals. Conversely, shellfish taxa had sub-optimal LMOD values that exceeded 4.0% in all but two cases: the systematic strategy and the Dionisio Point strategy. This indicates that very few strategies "work" for this class of data. The

abundance of northern fur seal varied the most (relative to other mammalian taxa) in many of the samples, while either mussels or Sitka periwinkles accounted for the highest variability in shellfish taxa in each sample. As with Houses 1 and 2, the most optimal strategies, in this case the systematic sample and the 5% random sample of mammals, were presented in histogram form to illustrate their congruence with the complete assemblage. As is the case at the other houses, histograms confirm that these sample strategies identify the approximate relative abundance of abundant taxa (Figures 25 and 26).

Sample Strategy	Mammals		Shellfish	
1% RT#1	Northern fur seal	(8.57%)	California mussel	(25.74%)
1% RT#2	Northern fur seal	(2.47%)	Sitka periwinkle	(16.84%)
1% RT#3	Northern fur seal	(3.98%)	Sitka periwinkle	(5.60%)
5% RT#1	River otter	(0.93%)	Sitka periwinkle	(7.84%)
5% RT#2	Northern fur seal	(3.97%)	California Mussel	(7.71%)
5% RT#3	Sea lion	(1.57%)	Sitka periwinkle	(3.59%)
5% Systematic	Northern fur seal	(1.39%)	California Mussel	(2.23%)
10% RT#1	Harbor seal	(1.76%)	Mussel (Mytilus sp.)	(5.43%)
10% RT#2	Northern fur seal	(1.62%)	Mussel (Mytilus sp.)	(9.06%)
10% RT#3	Northern fur seal	(2.42%)	Mussel (Mytilus sp.)	(5.43%)
Huu7ii	Northern fur seal	(0.78%)	Mussel (Mytilus sp.)	(16.58%)
McNichol Creek	Northern fur seal	(1.12%)	Sitka periwinkle	(8.74%)
Dionisio Point	Northern fur seal	(1.38%)	Mussel (Mytilus sp.)	(3.85%)

Table 11. Taxa whose relative abundance varied the most in a sample compared to the complete assemblage at House 5. Percentage change in relative abundance is listed in brackets.

Relative Abundance of Mammals at House 5
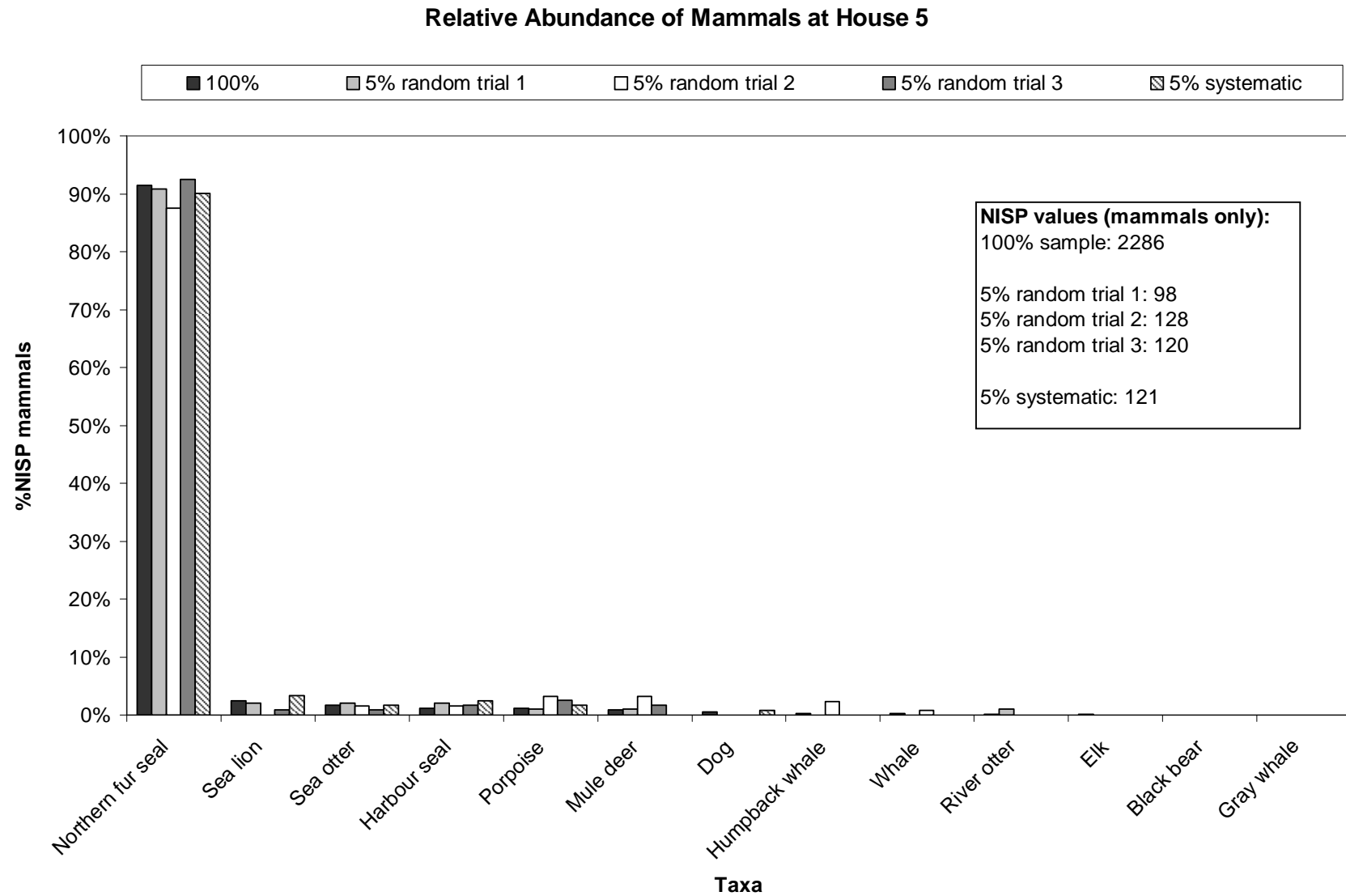
Figure 25. Relative abundance of mammals obtained using different samples at House 5.

Relative Abundance of Shellfish at House 5
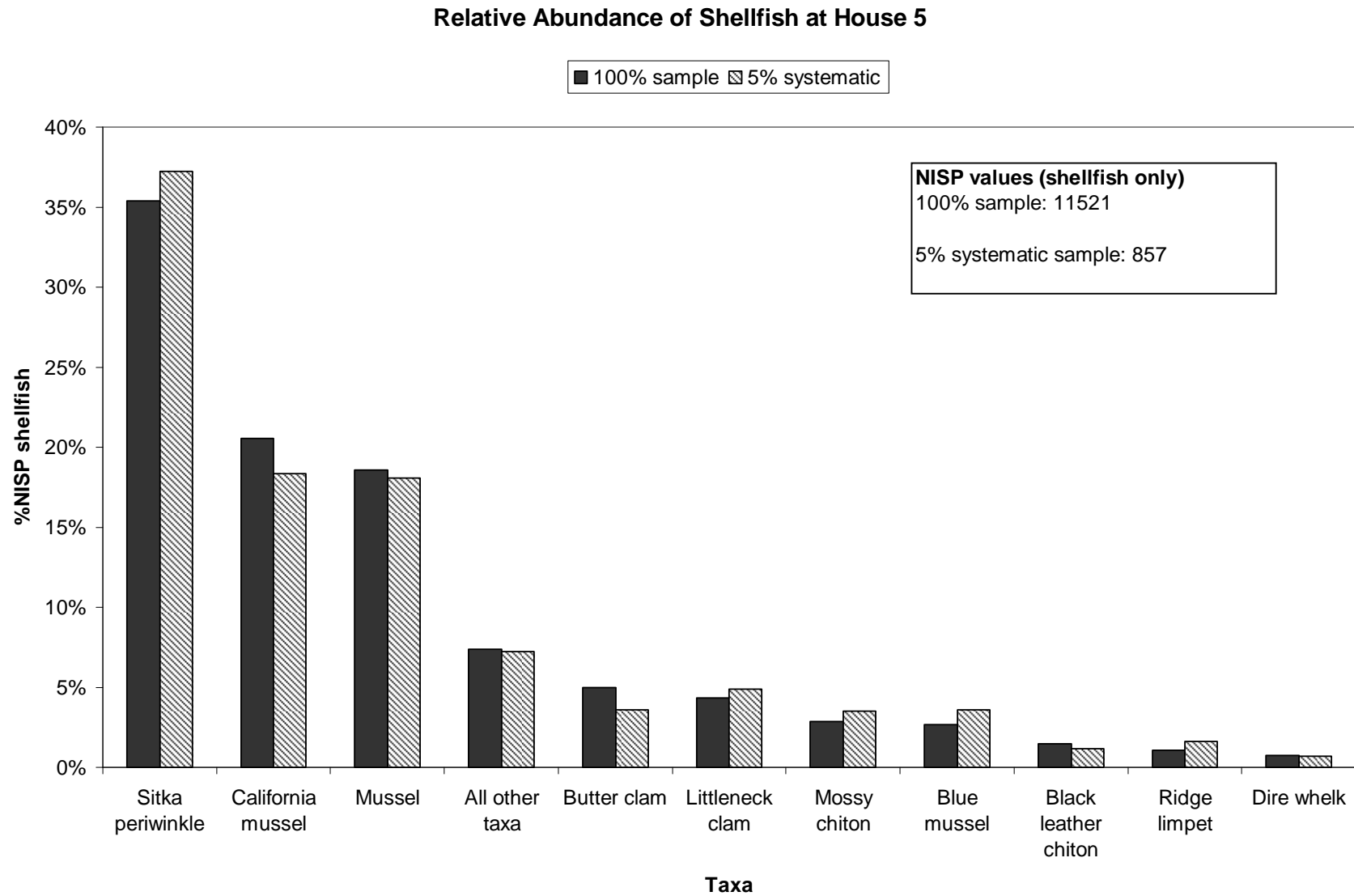
Figure 26. Relative abundance of shellfish obtained using different samples at House 5.

7.3 A Note on Auger Samples

An analysis of the data gathered from the auger samples has yet to be presented. The reason for the lack of in-depth analysis of the data from these samples is that the number of bones found within these samples was very small, and therefore it seems unlikely that these 0.1% auger samples would be used to infer the relative abundance of taxa at any house. All of the results from each house are presented in Table 12. The reason why these particular auger samples identify so few taxa was discussed in Chapter 6, but it is worth briefly reiterating here. Auger samples are primarily used when sampling vertical deposits and as such they are not as effective when sampling large horizontal areas. House floors are much more productively investigated using larger excavation unit sizes which allow for identification of feature and artifact densities much more easily than bucket-augering. If there is an accretion of fauna that has occurred as a result of deposition over many generations living on a single house floor, then auger samples may be of more use than is indicated by these results. However, House 2 had a large faunal sample (NISP=190,378), and the 0.1% auger sample identified very few bones within this house (Table 12). Similarly, House 1 was occupied for at least two generations (50 years), and yet the rate of accumulation of fauna within this house was relatively low due to house cleaning activities. As a result, even less fauna was identified using the auger strategy at this house when compared to House 2 results.

7.4 Discussion

Having presented the results, they can now be discussed in terms of the effects of sample size and sample method. The sample size effect appears unpredictable. Extremely small samples (i.e., 0.1% auger samples) are sub-optimal, and while increasing sample

Taxa	NISP H1	%NISP H1	NISP H2	%NISP H2	NISP H5	%NISP H5
Butter clam	3	6.38%	5	2.56%	1	5.26%
Mossy chiton	0	0	6	3.08%	1	5.26%
California mussel	10	21.28%	38	19.49%	2	10.53%
Northern fur seal	2	4.26%	6	3.08%	4	21.05%
Mussel sp.	0	0	11	5.64%	4	21.05%
Sitka periwinkle	8	17.02%	42	21.54%	7	36.84%
Halibut	1	2.13%	4	2.05%	0	0.00%
Black leather chiton	1	2.13%	14	7.18%	0	0.00%
Herring	1	2.13%	0	0	0	0.00%
Sculpin	1	2.13%	0	0	0	0.00%
Flatfish	1	2.13%	0	0	0	0.00%
Emarginate dogwinkle	1	2.13%	0	0	0	0.00%
Greenling	2	4.26%	5	2.56%	0	0.00%
Chitons	2	4.26%	7	3.59%	0	0.00%
Salmon	2	4.26%	2	1.03%	0	0.00%
Rockfish	2	4.26%	3	1.54%	0	0.00%
Porpoise	2	4.26%	0	0	0	0.00%
Blue mussel	2	4.26%	3	1.54%	0	0.00%
Littleneck clam	6	12.77%	16	8.21%	0	0.00%
Ridge limpet	0	0	2	1.03%	0	0.00%
Limpets	0	0	1	0.51%	0	0.00%
Plate limpet	0	0	2	1.03%	0	0.00%
Giant chiton	0	0	4	2.05%	0	0.00%
Surfperches	0	0	3	1.54%	0	0.00%
Sea lion	0	0	1	0.51%	0	0.00%
Northern chink shell	0	0	1	0.51%	0	0.00%
Bent-nose clam	0	0	1	0.51%	0	0.00%
Lingcod	0	0	8	4.10%	0	0.00%
Cabezon	0	0	3	1.54%	0	0.00%
Dire whelk	0	0	1	0.51%	0	0.00%
Dogfish	0	0	1	0.51%	0	0.00%
Urchin	0	0	2	1.03%	0	5.26%
Frilled dogwinkle	0	0	1	0.51%	0	0.00%
File dogwinkle	0	0	1	0.51%	0	0.00%
Clam (Tresus sp.)	0	0	1	0.51%	0	0.00%
Totals	**47**	**100%**	**195**	**100%**	**19**	**100%**

Table 12. Results of augering at Houses 1, 2 and 5.

size generally did reduce the amount of variation between actual relative abundance of a taxon and its value in the complete assemblage as sample size increased, there were many exceptions to this trend. For example, at House 1, all 5% random and systematic samples for shellfish performed more optimally than the 10% random samples, and at House 2, 5% random samples were more optimal for mammals than the 10% random samples. Similarly, the strategies which consistently produced results closest to the actual relative abundance of all taxa were the 5% systematic strategy and the Dionisio Point Strategy (~40% sample size). These samples fall near or at the opposite ends of the spectrum with respect to the sample sizes investigated in this thesis. The Huu7ii strategy (~15% sample size) produced results which in some case were more accurate than McNichol Creek (~35% sample size) results: the LMOD value for fish at House 2 was approximately 10% (this occurred for greenling) using the McNichol Creek strategy, while the Huu7ii strategy had a maximum LMOD value of approximately 3% (for rockfish). Neither of these samples performed optimally for all classes of data, while the Dionisio Point strategy, which was only slightly larger than the McNichol Creek strategy, was much more accurate overall when compared to either of the other judgmental strategies.

What the above discussion suggests is that sample method affects the precision of a particular strategy to a much greater extent than does the size of a sample, although the relationship between the two is still complex. It appears that a 5% systematic sample is the most optimal sample method, as its performance has demonstrated. In all cases, with the exception of fish at House 1, for all houses and all classes of data, the 5% systematic samples were the most optimal as evidenced by correlation values, LMOD values and histograms. Other samples were also optimal; however, the precision of the results

depended on which class of data was of interest. For example, at House 2, a 5% random sample worked for mammals, but for only two of the three shellfish and fish 5% random samples.

As a result of the data above, the possibility exists that the amount of a house excavated and the amount of time required to analyze fauna can be significantly reduced. For small samples that seemed to "work", the number of bones identified for each class is documented in Table 13. Each of the systematic samples contained under 10,000 bones, and in the case of House 1 and House 5, values were considerably lower than this number, suggesting that much can be learned about relative abundance with much less analysis and excavation of less than 100% of the house floor. Other probabilistic sample strategies (i.e., 10% random samples) also offer a significant reduction in the number of faunal elements identified while providing much information about the relative abundances of abundant taxa within a house. The implications of these findings for future research and household archaeology on the NWC are discussed in Chapter 9.

House	Strategy	Mammal NISP	Fish NISP	Shellfish NISP	Total NISP Identified
House 1	5% systematic	356	444	1556	2356
House 2	5% systematic	738	2087	7005	9830
House 5	5% systematic	121	N/A	857	978[b]
House 1	10% random #1	629	741	N/A	1370[a]
House 1	10% random #2	823	961	N/A	1784[a]
House 1	10% random #3	733	858	N/A	1591[a]
House 2	10% random #1	1527	4586	16604	22717
House 2	10% random #2	1329	3757	12549	17635
House 2	10% random #3	1287	3905	16432	21624
House 1	Dionisio Point	2264	2833	12279	17376
House 2	Dionisio Point	5241	13454	57680	76375
House 5	Dionisio Point	1112	N/A	5257	6369[b]

Table 13. NISP values associated with specific sample strategies at specific houses. Note the large difference in NISP between the accurate judgmental samples (Dionisio Point) and the accurate probabilistic samples.
[a]Shellfish values not included because this sample strategy did not identify shellfish accurately.
[b]Fish values not included as they were not identified at this house.

Throughout this chapter, much of the discussion has focused on trends in the relative abundance of abundant taxa in a sample. Comparison of taxonomic abundance between population and samples described in this chapter has highlighted the variability (or lack thereof) in abundant taxa between samples and the population, since this analytical scale (that of the entire assemblage) obscures changes in the numbers of individual rare taxa. On the one hand, this is acceptable, as many questions about past life on the NWC, such as the dietary contribution of a particular taxon to one household, or the differences and similarities in subsistence strategies between households, can be answered by these more abundant taxa. On the other hand, rare taxa are also used to interpret how these households functioned – especially with respect to inter- and intra-house variation in status. I will now consider how sampling designs may influence the observed quantity and spatial location of specific taxa, and how this may alter our interpretation of inter- and intra-house status.

Chapter 8: Effects of Sampling on the Interpretation of Inter- and Intra-house Status

Previous chapters have focused on the Ozette data from a methodological

perspective. These methodological questions, while important, are considerably more

interesting when used as evidence to interpret human behaviours. As such, this chapter

presents the results of the effects of sampling on the interpretation of status for Houses 1,

2 and 5 at Ozette. In doing so, I integrate and expand on the results from the previous two

chapters, demonstrating how differences in the reliability of results are dependent in part

on whether or not the taxa in question are rare or abundant. I begin with a brief overview

of how status is defined and outline an arbitrary set of criteria which can be used to

measure status. Subsequently, I consider three faunal indicators which were used at

Ozette to infer inter-house status differences: the use of shellfish for decorative,

ceremonial, and symbolic (D/C/S) purposes; the abundance of whale[30]; and the relative

abundance of salmon and halibut. I then examine intra-house differences in status and

discuss whether the differences that are evident at House 1 are observable using

judgmental sampling methods.

8.1 Defining and Interpreting Status

The NWC house is a location where evidence of status differentiation between

and within households is thought to be visible archaeologically, and as such status is

often a central research focus when houses are excavated (e.g., Ames 1996; Ames et al.

1992; Archer 2001; Coupland 2006; Grier 2006). Specific artifacts (e.g., nephrite adzes,

seated figure bowls, exotic lithic tools) that were incorporated into house deposits are the

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[30] When whales are discussed, I am referring to fauna identified to taxa which were identified to family (Balaenopteridae), as well as to species.

most commonly accepted indicators of status of a household or high-status family living area, although the size of a house, its location within a village, its construction and maintenance costs have also been used as proxy evidence for indicating which households had higher status (e.g., Ames 1996, Archer 2001). Faunal data are an alternative source that can be used in conjunction with these other lines of evidence to infer status. The congruence between the rich ethnohistoric record (which indicates that certain fauna were associated with high-status individuals or households) and the proto-historic archaeological record at Ozette suggests that the Ozette data are representative of an ethnohistorically-observed pattern. Sampling designs, as discussed in Chapter 4, commonly target the rear of the house and/or the rear corners. Evaluating whether or not these sample strategies actually identify inter- and intra-house differences when they do exist – as is the case at Ozette – allows one to consider whether the use of such strategies provide data which would result in the same interpretation, had the whole house been excavated.

In order to evaluate a sample according to this premise, two components must be considered. Given a specific sample strategy, does the chosen sample strategy correctly identify House 1 as the high-status house, and are there significant differences between House 2 and House 5? To answer these questions, the data gathered from different sample strategies are categorized according to those strategies which correctly identify House 1 as the high-status house, those which incorrectly identify the high-status house (those which identify House 2 or House 5 as the high-status house), and those which fail to uncover significant differences of status between all or some of the houses. Since status and hierarchy lack defined empirical correlates, arbitrary criteria have been created

in order to classify the results from each sample strategy. The thresholds used in

identifying the differences in status are as follows:

1. For (D/C/S) shellfish, a difference between houses which exceeded a NISP of 25
   was considered to be indicative of a difference in status between houses.

2. For whale, a difference exceeding a NISP of 15 was considered to indicate
   differences in status.

3. In comparing the relative abundance of salmon and halibut at House 1 and House
   2, a difference of 7% or greater between each house was considered indicative of
   a difference in status.

These thresholds were created for reasons similar to those outlined in Chapter 7,

but it is worth mentioning how and why thresholds were chosen in this instance. There is

no value that is intrinsically correct for all houses in every case on the NWC; any value

selected will depend largely on each individual researcher's prerogative. For example, the

archaeologists working at Ozette interpreted status differences based on empirical

differences between houses (as discussed below), although they did not consider any

specific values which, once reached, indicated status differences. At the McNichol Creek

site, 67% of the fauna from the high-status house were mammalian, while at another

house mammalian remains accounted for only 25% of the fauna (Coupland 2006:91), and

therefore the latter house was considered to be of lower status. However, at what point

the ratio of mammal to fish bones would be indicative of status differences were not

defined prior to analysis. Chatters (1989) interpreted differences in the taxonomic

composition of fish within different family areas within a household based solely on

statistical (chi-squared) values. Since he did not report the actual numbers of different

taxa in different nuclear family living areas, no definitive threshold values can be derived

from this research. The actual difference in the number of specific taxa (or even artifacts)

between houses appears less important than the fact that the difference is congruent with other lines of evidence. For example, small numbers in the difference of whale remains at Ozette between Houses 1 and 2 were interpreted as indicative of status differences primarily because other lines of evidence also indicated status differences (Samuels 1994). Rather than debate the appropriateness of the interpretations based on empirical evidence that have been used by others, I present my own as part of a heuristic exercise in the interpretation of status. I recognize that changing these values would likely change the results of the sampling simulation considerably.

It is my opinion that these numbers are very conservative, and I expect that only a few researchers would be likely to interpret differences in status based on these differences. However, these values do provide a starting point for thinking about sampling and its effect on the interpretation of status: if all (or most) sample strategies accurately interpret status based on these values, the values can be increased in order to observe which samples are still producing accurate interpretations. Alternatively, if none (or only a few) of the samples are able to identify status differences based on these conservative indicators of status, then this can also be used to evaluate the usefulness of sample strategies. Absolute differences rather than ratio differences were utilized for the reasons discussed below.

Since samples of different sizes are not directly comparable, the data derived from each sample strategy have been compared to the data derived using the same sample strategy at other houses. For both D/C/S shellfish and whale, the absolute values (NISP) for each sample strategy were included so that readers can get a sense of the magnitude of the difference. While normalizing the values from each sample strategy in order to

provide directly comparable ratios would be useful, the data were not presented in this way because the absolute number of items is in part reflective of status. For example, if six D/C/S shellfish were found using a given strategy at House 1, compared to two D/C/S shellfish at House 2, this is unlikely to be considered indicative of a significant difference in status, even though the ratio of their abundances is 3:1. However, a difference of 100 D/C/S shellfish at House 1 compared to 50 D/C/S shellfish at House 2 arguably represents a significant difference in status, despite the lower ratio (2:1). It is important to recognize one drawback of using an absolute difference: small sample sizes such as the 1% and 5% may not indicate differences, simply because the overall quantity of fauna identified using this strategy is small, and therefore less likely to identify enough fauna to reach the 25 or 15 NISP threshold values.

8.2 Status Indicators

8.2.1 Decorative, Ceremonial, Symbolic Shellfish

Differences in the quantity of D/C/S shellfish at different Ozette houses provided some of the most compelling faunal evidence that some houses contained more status goods than others, and by extension, that these were the dwellings of status individuals (Wessen 1994; see Figure 27). In the complete assemblage (100% sample), nearly two and a half times as many D/C/S shellfish were found in House 1 when compared to House 2. At House 5, very few of these taxa were identified at all. Given the large differences in NISP values for these taxa at each house, it is hypothesized that the 25 NISP threshold value would be achieved by most sample strategies except perhaps the smaller random samples.

The results of different sample strategies differ somewhat from this expectation. It is obvious that the auger sample strategy is sub-optimal because no D/C/S shellfish were identified at any house using this sample strategy. The systematic sample strategy shows

Identification of D/S/C Shellfish using various Sample Strategies at House 1, 2 & 5
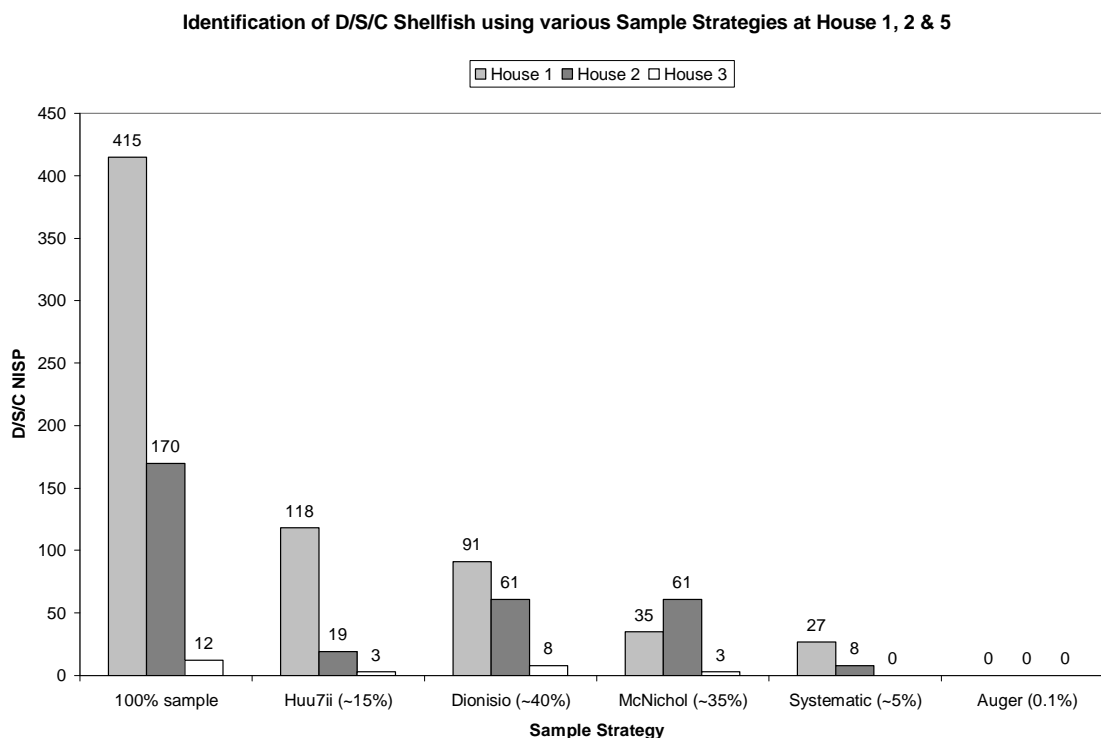
Figure 27. NISP for decorative shellfish recovered from Houses 1, 2 and 5 based on several non-random sample strategies. The actual numbers of these taxa recovered at each house was shown on the far left (100% sample). All numbers indicate absolute values rather than ratios for reasons described above.

differences in quantities which are similar (in ratio) to the complete assemblage; however, the absolute NISP values between House 1 and House 2 are not large enough to surpass the 25 NISP threshold. All of the other sample strategies, with the exception of the McNichol Creek strategy, produced quantities of shellfish which would correctly identify House 1 as the high-status house. However, the Huu7ii sample strategy did not provide precise information: the ratio of the taxa between House 1 and House 2 is significantly different than in reality (6.2:1 using the Huu7ii method rather than 2.3:1 in reality). If a McNichol Creek sample strategy had been used, nearly two times as many

D/C/S shellfish would have been uncovered at House 2 (an increase of 29), which would result in the incorrect assumption that House 2 was the high-status house.

Comparison	10% RT#1	10% RT#2	10% RT#3	5% RT#1	5% RT#2	5% RT#3	1% RT#1	1% RT#2	1% RT#3
H1 to H2	-6	39	38	38	9	18	-2	1	0
Status diff.?	No	Yes	Yes	Yes	No	No	No	No	No
H1 to H5	18	54	52	41	21	22	2	2	2
Status diff.?	No	Yes	Yes	Yes	No	No	No	No	No
H2 to H5	24	15	14	6	12	4	4	1	2
Status diff.?	No	No	No	No	No	No	No	No	No

Table 14. Comparison of samples drawn from each house for D/C/S shellfish. Note: "RT" refers to "random trial".

The three random samples drawn from each house are more difficult to evaluate than the non-random samples. One method of evaluating samples is from the perspective of a "real-world" scenario: compare all of the first random samples from each house to each other, compare the second random samples from each house to each other, etc. If such a comparison is undertaken, differences between House 1 and Houses 2 or 5 are observable only when the "10% random trial 1" or the "10% random trial 2" or the "5% random trial 1" is applied at each house (Table 14). No differences between House 2 and House 5 were observed for trials 1, 2 or 3 of any size.

While the above method is analogous to actual excavation, there is an equal probability that any random sample for a given sample fraction can be compared to any other sample of the same size at another house. Therefore, three random samples from each house can be evaluated on the basis of 27 different combinations by extracting any one sample from each of Houses 1, 2 and 5. If all the combinations of 10% random samples from House 1 are compared to those of House 2 (at the 10% fraction), only five of nine possible combinations (55.6%) resulted in an accurate interpretation of status. A similar problem is observed at the 5% sample size: only three of the nine possible combinations (33.3%) of House 1 to House 2 comparisons were able to identify House 1

as high-status, while all other samples from all houses indicated no significant differences between these houses. This problem was magnified at the 1% sample size, where no differences were apparent (Figure 28).
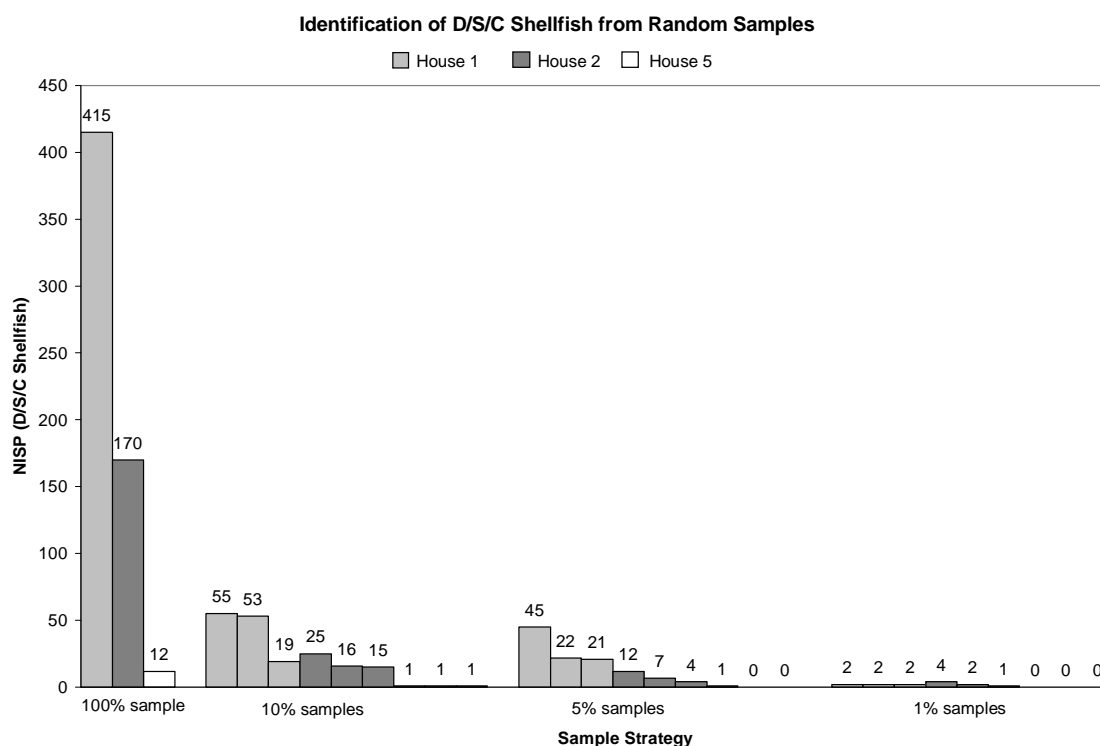
Figure 28. NISP of D/C/S shellfish for three random samples drawn from each house for different sample fractions.

These individual random samples indicate that the possibility of success exists for this method to be used to identify status differences for all sample sizes tested except for the 1% random samples. Only three samples were drawn for each sample fraction, and estimating the probability of success on only three samples is hazardous, as it is unknown to what extent these samples represented typical samples for that sample fraction. By repeatedly drawing random samples of the same size from each house and then comparing the results to the results from other houses, probabilities of success can be more accurately determined. Monte-Carlo simulation was performed in order to produce

such probabilities for both D/C/S shellfish and whale. These probabilities were generated by drawing a random sample from each house and then comparing the results from each house to the other two houses in order to determine into which category the results fell; this procedure was repeated 500 times. At first glance, the 10% sample fractions failed to identify House 1 as high-status in every case; therefore, a larger 25% sample was also tested to observe if the greater sample size would produce more reliable results. The results for the Monte-Carlo simulation of D/C/S shellfish are presented in Table 15.

Based on the results of the Monte-Carlo simulation, several observations can be made about random sampling and the probabilities of detecting status differences using D/C/S shellfish. None of the comparisons, regardless of sample size, resulted in a mis-identification of the high-status house, i.e., no sample had more than 25 D/C/S shellfish at House 2 compared to House 1, House 5 compared to House 1, or House 5 compared to House 2. However, only at the 25% random sample size do probabilities exceed a 90% likelihood of an accurate interpretation of status. Secondly, the largest increase in accurate status interpretations of House 1 compared to House 2 occurred between the 10% sample fraction and the 25% sample fraction. Accurate interpretations of the status of House 1 compared to House 2 rose from 263 correct iterations (52.6% probability of getting data which results in an accurate interpretation) for a 10% sample[31], to 466 correct iterations, (93.2% chance of getting data which is accurate) at the 25% sample size. Thirdly, because the magnitude of difference between House 1 and House 5 is great, these differences were identified more frequently (76% percent of the iterations were accurate) at the 10% sample fraction than for differences between Houses 1 and 2 or

---

[31] Interestingly, the percentage of accurate samples at the 10% sample size using Monte-Carlo simulation (52.6%) is very similar to the rough estimate provided by the comparison of the three specific random 10% samples (55.6%).

Houses 2 and 5 at the same sample fraction. The increased frequency of accurate

interpretations for this comparison (H1 to H5) occurred between 5% and 10%, rather than

between 10% and 25%, as was the case for H1 to H2 comparisons (Table 15). Finally,

despite the large difference in the NISP of D/C/S shellfish between House 2 and House 5

(a difference of NISP of 152), a 25% sample was only accurate 418 times out of 500

(83.6%).

Sample	Comparison	Accurate interpretation % (# of runs)	Mis-identification of high-status house % (# of runs)	No difference between houses % (# of runs)
1% Random Samples	H1 to H2	2.0% (10)	0.0% (0)	98.0% (490)
	H1 to H5	4.0% (20)	0.0% (0)	96.0% (480)
	H2 to H5	0.0% (0)	0.0% (0)	100.0% (500)
5% Random Samples	H1 to H2	14.8% (74)	0.0% (0)	85.2% (426)
	H1 to H5	25.6% (128)	0.0% (0)	74.4% (372)
	H2 to H5	0.0% (0)	0.0% (0)	100.0% (500)
10% Random Samples	H1 to H2	52.6% (263)	0.0% (0)	47.4% (237)
	H1 to H5	76.0% (380)	0.0% (0)	24.0% (120)
	H2 to H5	0.6% (3)	0.0% (0)	99.4% (497)
25% Random Samples	H1 to H2	93.2% (466)	0.0% (0)	6.8% (34)
	H1 to H5	100.0% (500)	0.0% (0)	0.0% (0)
	H2 toH5	83.6% (418)	0.0% (0)	16.4% (82)

Table 15. Results of Monte-Carlo Simulation for D/C/S shellfish. Values indicate percentage of trials which fell within a given category. The actual number of trials for each category is listed in brackets.

8.2.2 Whale

At Ozette, the differences in the quantity of whale between Houses 1, 2 and 5 are

not as pronounced as the results for shellfish were; nevertheless, the difference is

suggestive of differences in status (Huelsbeck 1994; Figure 29). The McNichol Creek

and Huu7ii sample strategies would both identify House 1 as high status, as these

strategies identified a difference of more than 15 NISP between House 1 and the other

two houses. The Dionisio Point sample strategy and the systematic strategy did not reflect

differences of a NISP of 15 or greater between Houses 1 and 2, indicating that these

strategies were sub-optimal when considering this question. However, neither of these

strategies identified any other house as high-status.

How precise are the above strategies when considering the relative amounts of whale between houses? In the complete assemblage (100% sample), there is approximately 26% less whale in House 2 when compared to House 1. However, the non-random sampling strategies did not reflect similar relative differences. Using the

Identification of Whale using various Sample Strategies at House 1, 2 and 5
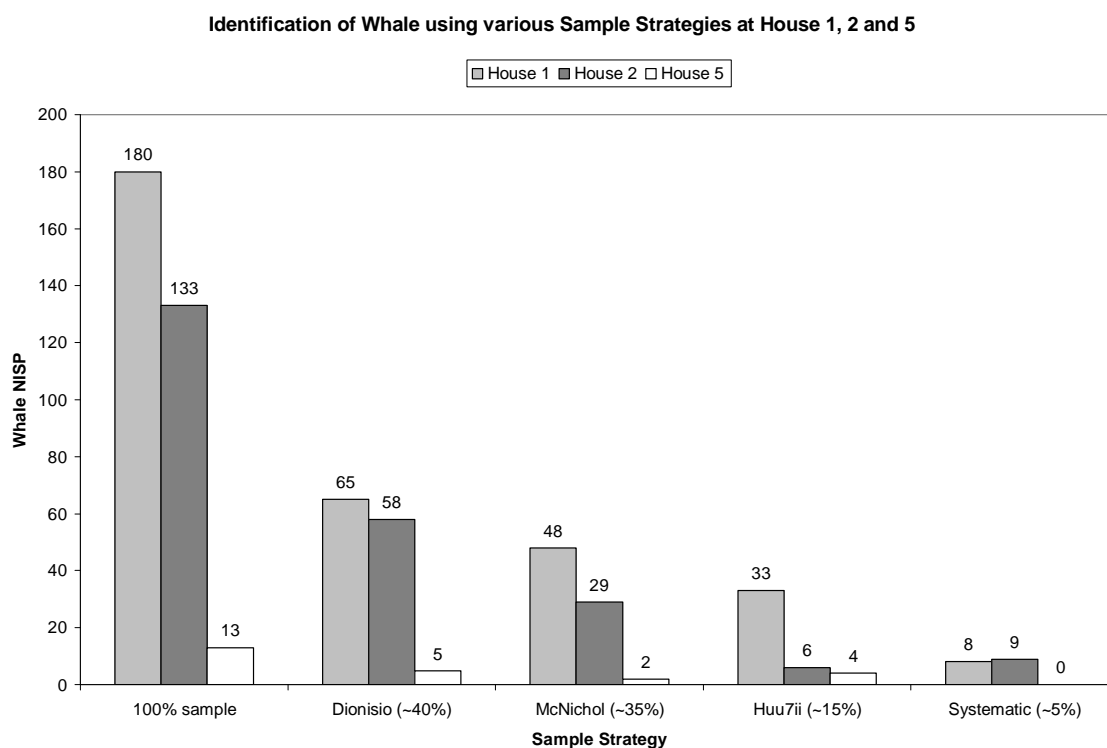
Figure 29. NISP for whale remains recovered using different non-random sample strategies.

Dionisio Point sample strategy, the difference between H1 and H2 is underrepresented (11% less whale), and drastically exaggerated using the Huu7ii sample strategy (81% less whale). The McNichol Creek sample strategy was the most precise, identifying 40% fewer whale bones at House 2 compared to House 1. When houses were sampled using a 5% systematic sample strategy, more whale (13%) was recovered from House 2 than House 1. The small number of whale at House 5 was represented well in all sample strategies except the systematic strategy, which identified no whale whatsoever. However, this result is arguably not important from an interpretive perspective, as the

actual number of whale bones found in the entire house is very small to begin with. The same cannot be said of the Huu7ii sample strategy, because, while the small values at House 5 were well represented, House 2 values were also low, indicating a similarity between these two houses which is inaccurate when the 100% samples are examined. The 0.1% auger strategy, while not presented in Figure 29, did not identify any whale. In any case, real-world excavation of whale using auger samples is somewhat far-fetched, given that whale bones would not fit within a 10cm diameter bucket auger, or would be highly fragmented and unable to easily identified.

Rather than compare individual samples from a "real-world" perspective as was done for the D/C/S shellfish results, I will proceed directly to the results of the Monte-Carlo simulation of random samples in order to determine success rates for whale as an indicator of status. The reason for doing so is primarily heuristic: an investigation of specific samples from a real-world perspective is interesting; however, probabilities of success are much more useful in the planning of future excavations. For instance, it is possible that researchers would use a 10% random sample strategy if, hypothetically, it worked 480 times out of 500, as the researcher would have a high degree of confidence that the results were accurate. However, a 5% random sample strategy which produced accurate samples in 2 out of 3 trials may not be adopted simply because researchers do not know whether these three 5% samples are typical or atypical, and therefore are not sure whether such a strategy will produce reliable results consistently. As such, I address only the Monte-Carlo simulation results for whale, although comparison of the number of whale bones found in the three individual samples from each house could be undertaken using the data provided in Appendix 4.

Firstly, like the D/C/S shellfish simulations, none of the simulations produced data which would result in another house being interpreted as the high-status house. Secondly, in order to observe differences in status between House 1 and House 2, a random sample larger than 25% would be required, as this strategy only produced a correct interpretation 34.6% of the time. Thirdly, the largest increase in accurate samples for H1 to H5 comparisons occurred when the sample size was increased from 5% to 10%, while the largest increase in accurate samples for H1 to H2 comparisons occurred between 10% and 25% sample sizes. The low overall quantity of whale resulted in a larger percentage of correct samples when House 5 was compared to House 1 or House 2, but this situation was only observable with any consistency once a sample size of 25% had been reached.

Sample	Comparison	Accurate interpretation % (# of runs)	Mis-identification of high-status house % (# of runs)	No difference between houses % (# of runs)
1% Random Samples	H1 to H2	0.0% (0)	0.0% (0)	100.0% (500)
	H1 to H5	0.0% (0)	0.0% (0)	100.0% (500)
	H2 to H5	0.0% (0)	0.0% (0)	100.0% (500)
5% Random Samples	H1 to H2	0.0% (0)	0.0% (0)	100.0% (500)
	H1 to H5	1.4% (7)	0.0% (0)	98.6% (493)
	H2 to H5	0.2% (1)	0.0% (0)	99.8% (499)
10% Random Samples	H1 to H2	2.8% (14)	0.0% (0)	97.2% (486)
	H1 to H5	58.4% (292)	0.0% (0)	41.6% (208)
	H2 to H5	22.8% (114)	0.0% (0)	77.2% (386)
25% Random Samples	H1 to H2	34.6% (173)	0.0% (0)	65.4% (327)
	H1 to H5	100.0% (500)	0.0% (0)	0.0% (0)
	H2 to H5	97.4% (487)	0.0% (0)	2.6% (13)

Table 16. Results of Monte-Carlo simulation for whale. Values indicate percentage of trials which fell within a given category. The actual number of trials for each category is listed in brackets

8.2.3 Salmon and Halibut

The intensive fishing of salmon and halibut occurs in localized habitats such as rivers with spawning runs or offshore banks; ownership of these resource locales by a lineage or a chief was seen as indicative of status within a village, which it is argued was

the case at Ozette (Huelsbeck 1989). Evidence of resource locale ownership is potentially observable in the relative abundance of these taxa in different houses. Huelsbeck (1989) argues that the higher relative abundance of salmon and halibut at House 1, compared to House 2, is indicative of resource ownership by the former household. Since fish from House 5 were never identified, the comparison between this house and the others cannot be undertaken.

The relative abundance of salmon and halibut compared to all fish at House 1 is approximately 11% higher than at House 2 when comparing complete assemblages (100% sample). While this may not seem like a large difference, the importance of this fact can be considered from another perspective. At House 2, salmon and halibut together accounted for 15% of the fish assemblage; therefore the 26% of salmon/halibut at House 1 may indicate that salmon and halibut together were nearly twice as important to household members at this house when compared to House 2 household members (ratio of 1.73:1). Even if the threshold value identified at the start of the chapter were used (7%), it still represents an increase of almost 50% regarding the importance of the two taxa, a ratio of 1:1.47.

Investigation of this indicator of status necessitated a slightly different approach than was used for the D/C/S shellfish or whale. As shown in Chapter 7, abundant taxa (which include salmon and halibut) were fairly accurately represented by the 10% random samples at each house. Based on this observation, and because of the logistical difficulties of undertaking Monte-Carlo simulation for all of the fish taxa, Monte-Carlo simulation was not performed for this analysis. While this would be interesting, it is beyond the scope of this thesis.

Relative Abundance of Salmon and Halibut, House 1 and 2
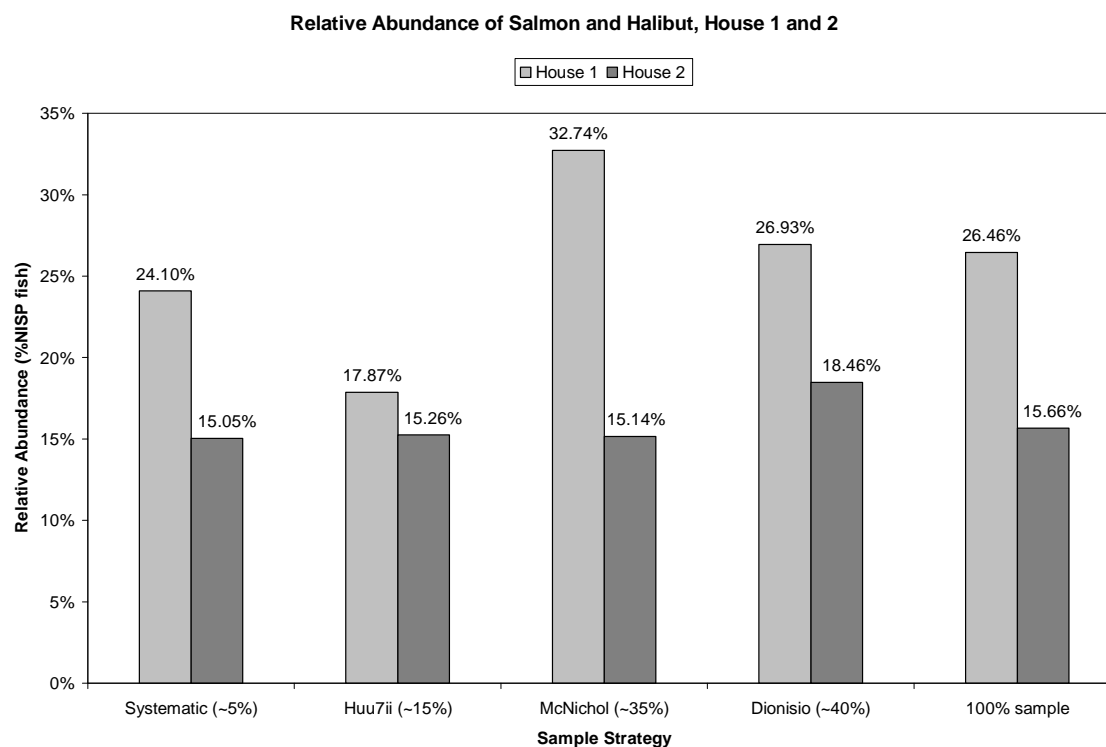
Figure 30. Relative abundance of salmon and halibut for Houses 1 and 2 identified using various sample strategies.

The results of non-random samples are presented in Figure 30. Regardless of which non-random sampling strategy was used, the relative abundance of salmon and halibut was higher at House 1. The systematic sample and the Dionisio Point sample were very similar to the complete sample (9% and 8% difference between houses respectively). The McNichol Creek sample strategy would not change the interpretation of House 1 as a high-status house; however, it was imprecise and over-represented the relative abundance of salmon and halibut at that house. The Huu7ii sample strategy recovered very similar relative abundances of these species at each house, and utilizing this strategy at Ozette would not have indicated any significant differences for these two taxa between these two houses.

When random samples of varying fractions are considered, major variations are visible at the 1% sample fraction only (Figure 31). The three 1% random samples drawn

from each house overlap, indicating that this sample fraction is probably sub-optimal for indicating differences in status between houses.
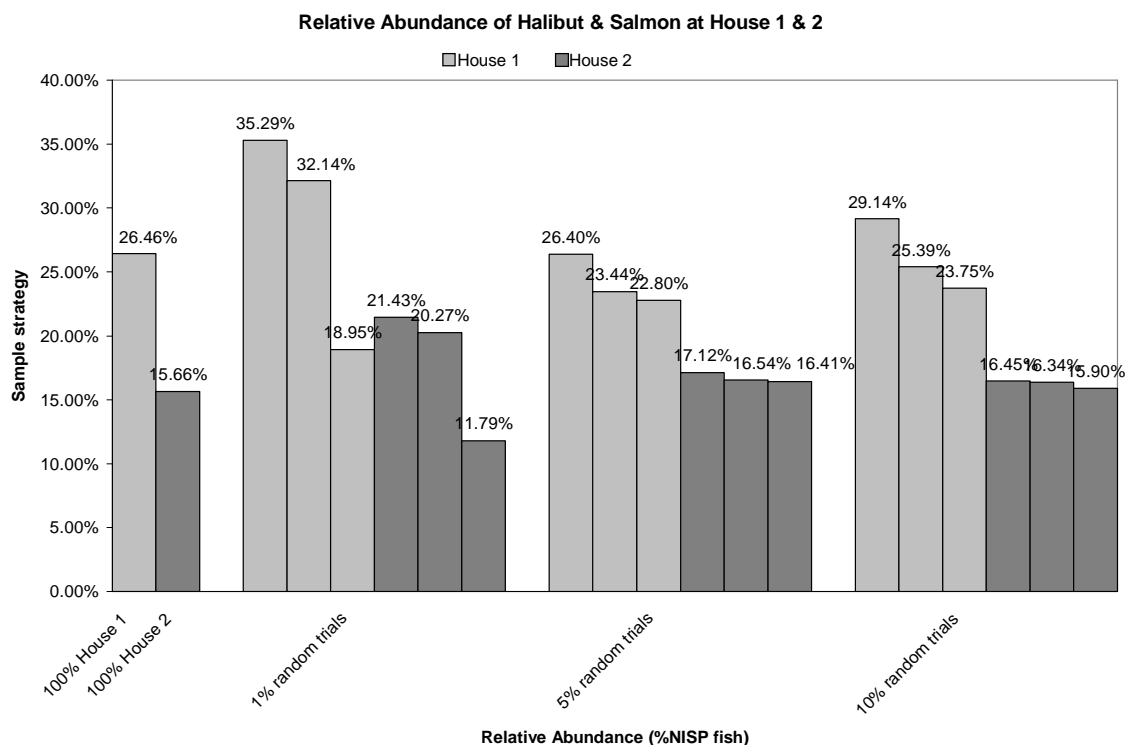
Figure 31. Relative abundance of salmon and halibut combined from House 1 and House 2.

This is expected, as abundant taxa were not identified in their correct relative abundances at this sample fraction (see Chapter 7, Section 7.2). The 5% random samples, while they did consistently indicate differences between House 1 and House 2, only exceeded the 7% threshold value in 4 out of 9 possible comparisons. The 10% samples do in fact identify the correct high-status house for every possible combination of H1 to H2 comparisons (9 possibilities). The smallest difference in relative abundance between samples from H1 and H2 was 7.3%.

8.3 Inter-house Status: Evaluating Multiple Lines of Evidence

It is usually the case that multiple lines of evidence together form a strong argument for the existence of inter-house status, rather than a single faunal indicator of status. Even though it is only faunal evidence that has been discussed in this thesis, one can still consider to what extent a given strategy shows congruence between different classes of fauna. Based on Table 17, it is apparent that no one sample strategy, applied to all three houses, is optimal. Random samples are sub-optimal at any sample fraction when used to identify House 1 as high-status using whale and D/C/S shellfish remains, although they did produce useful information about the relative abundance of salmon and halibut. When D/C/S shellfish are used as a proxy for status, the McNichol Creek strategy incorrectly identified House 2 as the high-status house.

| Sample method | Faunal Indicator of Status | | |
	D/C/S Shellfish	Whale	Salmon/Halibut
1% random	None	None	None
5% random	None	None	None
10% random	None	None	House 1 only high-status house
25% random	House 1 only high-status house	None	Not tested
Systematic (5%)	None	None	House 1 only high-status house
Huu7ii	House 1 only high-status house	House 1 only high-status house	None
McNichol	House 2 only high-status house	House 1 only high-status house	House 1 only high-status house
Dionisio	House 1 only high-status house	None	House 1 only high-status house

Table 17. Summary of sample strategies and the results if applied to all three houses.

When whale remains are used as a proxy for status, the Dionisio Point Strategy did not uncover significant differences between the two houses, nor did the 5% systematic sample. Identifying House 1 as a high-status house using the relative abundance of salmon and halibut did not occur using the Huu7ii sampling strategy; however this sample method worked well for the other classes of data. Systematic

samples did not indicate significant differences except for the relative abundance of halibut and whale.

It would be unlikely that one strategy alone used at all houses during any future excavations would result in accurate information about all types of fauna, especially if the spatial organization of fauna of interest differed between houses. For instance, the Huu7ii sample strategy uncovered a large percentage of whale and D/C/S shellfish at House 1 even though only 15% of the house was excavated using this strategy. This occurred because these high-status taxa were more abundant at the rear of the house. However, by the same token, this strategy recovered relatively fewer of these taxa at House 2 because their distribution was not clustered in the rear of the house. The reverse situation was apparent when the systematic sample strategy was used: although there was significantly more whale in House 1 than in House 2, the frequency of whale in a systematic sample from either house is approximately equal, as a higher percentage of the whale was identified at House 2 because of its more even distribution. Based on these observations, any inter-house comparisons between rare taxa, even when using identical sample strategies should be undertaken very carefully.

Using random samples to identify status differences between houses is only feasible if one uses large sample fractions: 25% for D/C/S shellfish, and even larger samples for whale. That the results from salmon and halibut appear to be accurate at 10% random or 5% systematic sample sizes is not surprising. Halibut and salmon are abundant taxa, and therefore their relative abundances are more likely to be accurately identified (see Chapter 7). Unfortunately, accurate results for abundant taxa from all judgmental samples did not occur, as evidenced by the Huu7ii sample method which returned similar

relative abundances for each house. In contrast to salmon and halibut values, D/C/S

shellfish and whale, by virtue of their rarity, may not be identified at all (as was observed

for rare taxa in general in Chapter 6), or were identified in widely fluctuating abundances.

A caveat needs to be added here to these results: changing the threshold values for

distinguishing status differences will affect the probability of getting an accurate

interpretation. It was argued at the start of the chapter that differences in NISP of 25 and

15 (for D/C/S shellfish and whale) and a 7% difference in relative abundance for salmon

and halibut between houses are all conservative indicators of status. Many researchers

would require larger differences in order to state categorically that differences in status

between houses exist. If the threshold values were increased, then an even greater

percentage of the random samples would be sub-optimal. However, such concerns may

be moot, as a random sample of 25% or larger is unlikely to be implemented because of

logistical issues. If the resources are available to excavate at least 25% of the house,

maximizing exposed floor surface areas is far more likely to be undertaken than 50cm X

50cm evaluative units, since the former method aids in the identification of features. For

these reasons, random sampling does not appear to be an optimal method of identifying

differences in status between households when the taxa in question are rare.

8.4 Intra-house Status at House 1

The internal organization within a single plankhouse may also be highly

structured according to the inhabitants' status, and this is visible archaeologically at

Ozette. Typically, high-status individuals occupied the rear corners of the house and other

ranking families occupied the spaces around the perimeter of the house (in particular the

other two corners of the house), while the area near the doorway was often reserved for

slaves (Drucker 1951, see also Chapter 2, Section. 2.1). A central hearth house was often interpreted as a hearth that was used for feasting, an activity often hosted by a chief in order to demonstrate his status or that of his lineage.

Some of these patterns have been observed at House 1 at Ozette, although the front of this house was removed by wave action and therefore it is unknown if the front corners of the house contained any high status items. For example, the quantity of whale remains was found predominantly in the rear of House 1. Similarly, the distribution of D/C/S shellfish was concentrated along the periphery of the house. In particular, two concentrations were found, one in the northeast (rear) corner, and one near the southwest corner. The distribution and clustering of all fish were concentrated in two distinct but contiguous areas. The cluster in the northeastern corner (in the same location as one of the D/C/S shellfish concentrations) is hypothesized as evidence for the consumption of fish by the high-status head of the household. The concentration of fish near the centre of the dwelling is hypothesized as evidence of feasting, an activity which high-status individuals often engaged in to further increase their status (Hayden 2001). Concentrations in the southeast (rear) corner may be indicative of consumption by another high-status family, while the concentrations of bones near the northwest wall is hypothesized as evidence of sweeping and housecleaning activities near the door of the house (Figure 34).

These separate lines of evidence can be examined to see if sampling strategies identify intra-house differences. Only judgmental and systematic sample strategies will be investigated, as random samples vary too much in their location to be used as reliable indicators of intra-house differences. In addition to the judgmental strategies tested in

previous sections, another stratified sampling design was also investigated. This strategy involved dividing up the house into nuclear family living areas in approximately the same divisions as used by the Ozette researchers (see Figure 32 and Wessen 1994:109) and then sampling these areas. It was hypothesized that the fauna would be distributed evenly enough within each nuclear family living area such that a 1m X 1m unit in each family area would identify some of the differences between these areas. A synopsis of some of the results is shown in Table 18.
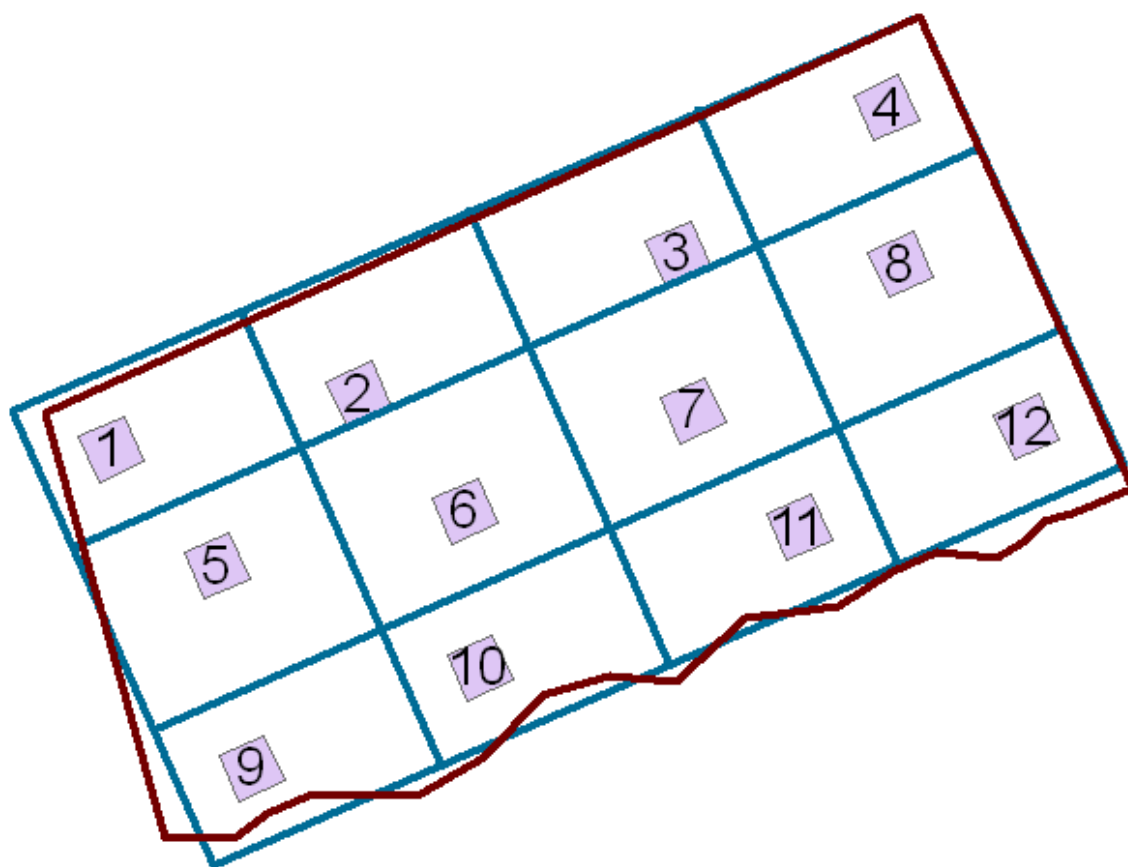
Figure 32. Stratified systematic sampling design with excavation unit designations at House 1. The grid system was created based on hypothesized nuclear family living areas within the house. Sections which contain excavation units number 6 and number 7 are meant to infer a central feasting and/or low status individuals' living area.

Unit Number	NISP (all taxa)	Mammal NISP	Fish NISP	Shellfish NISP	D/C/S Shellfish	Whale NISP	Salmon NISP	Halibut NISP
1	116	15	14	87			2	
2	1187	80	82	1025	2		7	10
3	108	18	15	75			4	2
4	380	74	65	241		3	10	11
5	166	55	18	93	1		1	1
6	201	26	43	132			8	4
7	92	17	17	58	2		2	2
8	200	24	3	173		1	1	
9	265	63	61	141			1	3
10	457	122	105	230			25	10
11	78	18	16	44			1	11
12	57	13	12	32	2			

Table 18. Synopsis of faunal data from stratified systematic sampling design.

When using a stratified systematic sampling strategy, the quantity of fauna from each unit varied significantly: unit 2, adjacent to the left rear corner, had more than twice as much fauna as the second most productive unit, likely because unit 2 was a feasting/high-status area. The low numbers and lack of concentrated distributions of both whale and D/C/S shellfish provided little evidence to indicate status areas using this sample strategy (see also Figure 33). It may also be difficult to know whether the samples taken from each nuclear family living area represent the same types of deposits. Nevertheless, the above data indicate that at Ozette, high-status fauna are not distributed evenly enough within the nuclear family living area so that a 1m X 1m excavation unit can reliably identify differences between these areas.

Judgmental sample strategies can also be evaluated to observe whether they indicate intra-house differences in status at House 1. Once again, the results are mixed depending on the strategy. Figure 33 demonstrates that judgmental sample strategies can identify clustered distributions of whale and D/C/S shellfish. The Dionisio Point sample strategy clearly identified the concentration of D/C/S shellfish in the southwest corner of the house, and arguably identified two other clusters in the northeast and southeast

corners as well. However, this sample strategy missed a significant portion of the D/C/S shellfish in the northeast corner, which potentially might alter the interpretation of which area of the house was of the highest status. Based on the Dionisio Point sample strategy, it was the southwest corner, not the northeast corner that was high-status. Furthermore, similar numbers of these rare taxa were found in the northeast corner (n=12) and southeast corner (n=18), when in actuality the northeast corner contained hundreds of D/C/S shellfish while the southeast corner did not. The status of these areas appears similar, when in fact the northeast corner had considerably more status-related fauna. The McNichol Creek strategy did not show any significant clusters of these taxa, although arguably there were two small concentrations along the north and east walls. At the very minimum, this strategy did indicate that these taxa were located more frequently at the margins of the house rather than in the middle spaces. The Huu7ii sample strategy clearly identified the high-status corner of the house, although it did not identify the concentration of D/C/S shellfish in the southwest corner of the house. A systematic sample strategy identified one high-status area in the northeast corner, but failed to identify any other clusters.

Dionisio Point sample strategy:
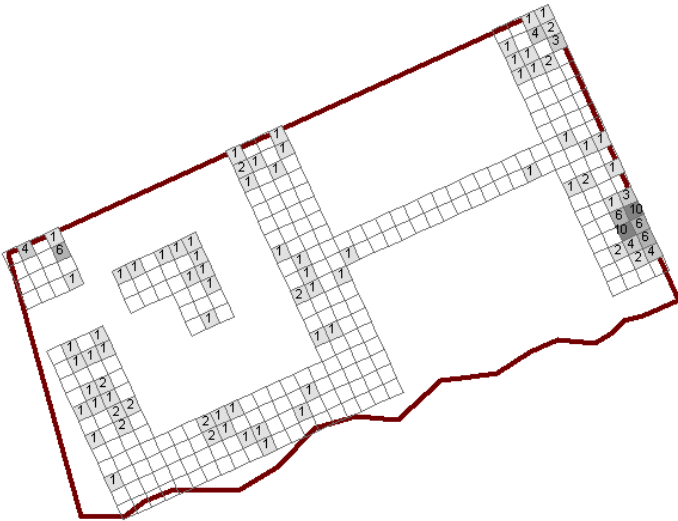
Huu7ii sample strategy
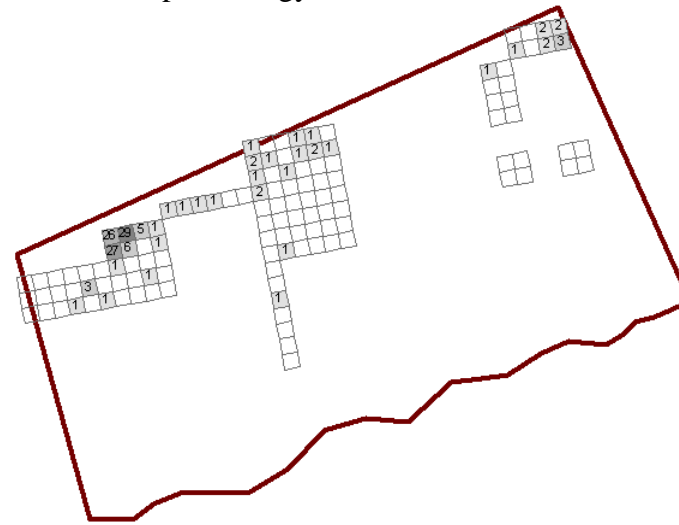
McNichol Creek sample strategy:
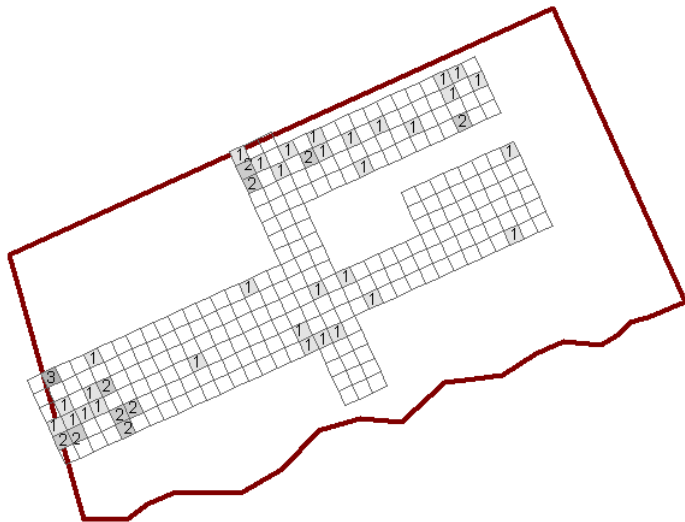
N ←——————

Systematic (5%) sample strategy:
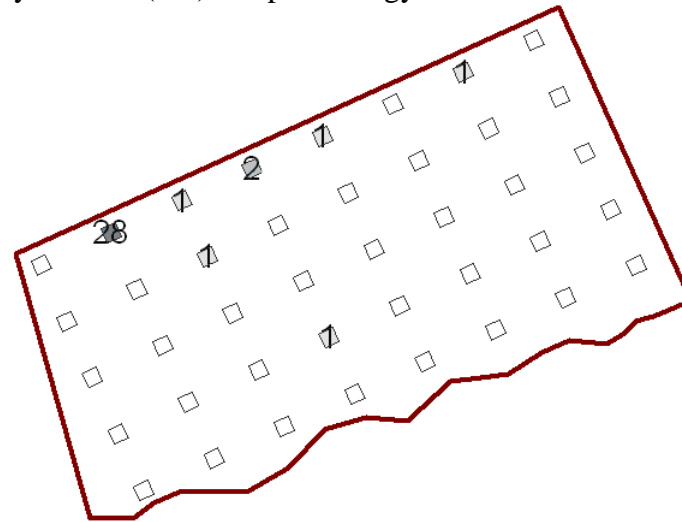
Figure 33. Number of D/C/S shellfish and whale found in each excavation unit for a given sample strategy (stratified sample on next page)

Stratified sample strategy:
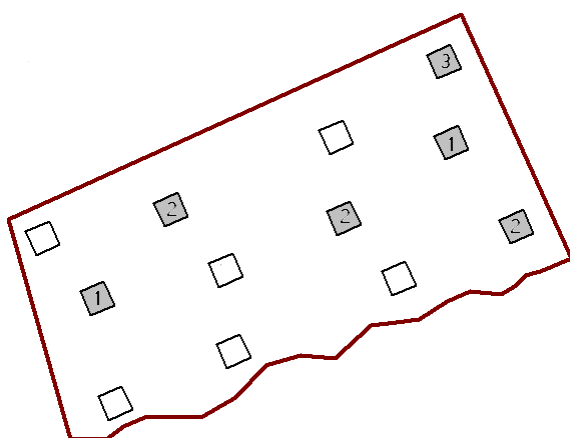
The judgmental sample strategies can also be examined to determine whether any strategy would reveal any of the differences in consumption practices or feasting activities based on the concentrations of fish bones (Figure 34). The Dionisio Point sample strategy did uncover some of the ichthyofaunal debris near the front door (northwest wall) which had accumulated there as a result of housecleaning activities. It also identified a concentration of fish bones in the southeast corner; however, a significant number of the bones from the central feasting hearth were missed. This is partly a result of the slightly skewed location of the hearth which is actually 2-3 metres north of the centre of the house, and as a result the majority of the feasting remains were not sampled using this strategy despite the fact that the middle of the house was sampled. This sample strategy also missed the concentration of bones near the high-status northeast corner of the house. Unlike the Dionisio Point strategy, the McNichol Creek strategy clearly identified the central feasting area in the house; however, it failed to uncover the concentration of bones associated with the high-status family in the rear of the house. The Huu7ii strategy identified the abundance of fish associated with the high-status northeast corner, as well as a minor concentration of bones near the southeast corner. However, the

central hearth was not identified because the sample unit placement had been biased in favour of the rear of the house. If the stratified sample design had been employed, higher concentrations of fish bones were observable in units #2 and #10, which corresponded with two of the three concentrations within the house.

Identifying intra-house differences in status using judgmental strategies appears to be less problematic than identifying inter-house differences in status. While no one sample strategy identified all socially-significant spaces, all strategies were able to pinpoint at least one of the predicted indicators of intra-house status differences. The McNichol Creek strategy was only able to identify the central hearth area, likely because this sample design was not developed for a shed-roof house, but rather for a northern house type, and therefore the configuration of the units was different.

In all cases, rare taxa were observed more frequently near the perimeter of the house although it is clear that the entire perimeter must be sampled in order to identify specific status areas based on rare taxa. For example, the Dionisio and Huu7ii strategies each identified one out of the two concentrations of D/C/S shellfish but missed the other because the entire perimeter was not excavated. The McNichol Creek strategy uncovered neither of these concentrations, although it did identify one concentration along the north wall. Differences in distributions of the fauna described above indicate some of the spatial structure of the house as well as differences between high and low status. At Ozette, all sampling designs clearly identified a difference between the perimeter areas of the house and the central space using rare, high-status fauna. However, when a higher

100% sample
strategy:
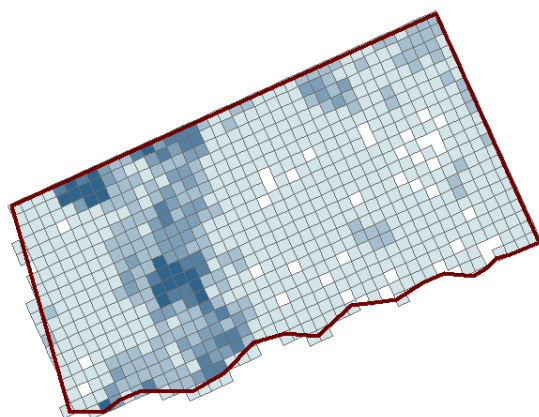
McNichol Creek sample strategy:
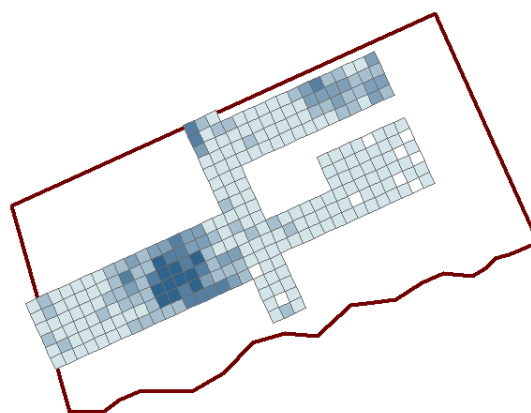
Dionisio Point sample strategy:
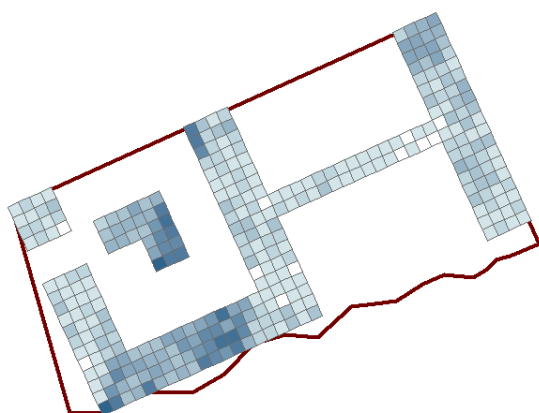
Huu7ii sample strategy:
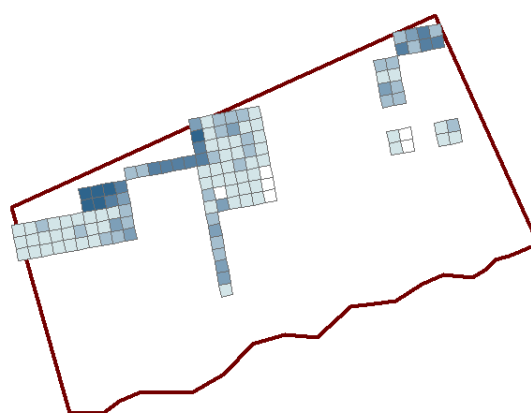
N ←

Figure 34. Abundance of fish using different excavation strategies at House 1. Darker shading represents units with higher abundance of fish remains. The number of fish bones for each sample unit has been normalized as a percentage of the total number of fish excavated according to the particular sample strategy being tested.

resolution of difference is desired (e.g. differences between nuclear families throughout the house), the results are much harder to predict and may require that even larger areas of the house be excavated.

In summary, inter-house differences are hard to identify regardless of sample strategy when the taxa in question are rare; however, when such taxa are abundant, many of the strategies will detect such differences. For intra-house differences, large areal excavations do identify difference status areas within the house, although it appears that the entire house would have to be excavated in order for one to be confident that a status area was not missed. Inter- and intra-house differences are affected both by sample method and sample size. Probabilistic (random and systematic) samples can be used to identify inter-house differences in status, although larger sample sizes than the ones used in this thesis would be required for rare taxa to be identified with certainty. Using the same judgmental sample at each house is very hazardous, and an increase in size does not appear to result in more accurate information; the sample method chosen appears much more important. When intra-house differences are considered, both size and method will affect the outcome: an increase in sample size will likely identify more of the status areas, although this is dependent on fortuitously identifying status indicators within each nuclear family area.

Chapter 9: Discussion and Conclusion

This chapter begins with a synthesis and discussion of critical sample sizes needed to investigate a variety of research questions. The implications of this research for household archaeology and for cultural resource management will then be outlined, followed by a discussion of the limitations of this research. Finally, future avenues of research are considered.

9.1 The Optimal Sample Strategy

The title of this section is purposefully a tongue-in-cheek comment, as the results of sampling simulations indicate that no one sample strategy is appropriate for all three research questions that were investigated in this thesis. Nevertheless, based on the results of sampling simulations, several generalizations can be made. Although the statements below do not hold true in every case, they are trends that were clearly evident for the majority of the sampling simulations.

1. Most samples, regardless of size or method, identified the presence of abundant taxa in each of the houses.

2. A large sample size was needed – approximately 40% – in order to identify most, i.e., 90% or more, of the taxonomic richness of a house.

3. If the total richness of a house is the central research question, then an extremely large sample of the house would need to be excavated.

4. Richness values were affected more by sample size than by sample method.

5. A 5% systematic sample identified general trends in the relative abundance of most taxa. Random samples of 5-10% were also able to identify general trends in relative abundance, with one exception (shellfish taxa at House 1).

6. The relative abundance of a taxon depended more on the sample method than on the sample size.

7. Inter-house differences in status were difficult to ascertain accurately using any of the sample strategies tested in this thesis. This was especially true if the taxa in question were rare.

8. Large areal excavations that targeted high-status areas were able to detect some intra-house differences in status, but they also failed to identify all of these areas as well.

9. Despite considerable differences in cultural site formation processes and different faunal distributions at each Ozette house, all of the sample strategies performed similarly regardless of the house at which they were being tested.

10. Very small (0.1%) systematic auger samples appeared to be an inappropriate method to use in sampling house features if one wishes to answer the questions posed in this thesis regarding richness, relative abundance and indicators of status.

While it is impossible to be certain that houses at other shell-midden rich sites will have exactly the same distribution of taxa as the ones at Ozette, many similar cultural site formation processes that were observed at Ozette have been observed at other sites. It is plausible that they share at least some similarities in the structure of their faunal data with houses at Ozette. As such, this research provides viable alternative methods of excavating houses in the future which can address some of the issues raised in Chapter 2 and Chapter 4. These issues include data-overload, the small number of house excavations undertaken, and sampling designs which implicitly or explicitly invoke the ethnographic record when selecting which house and where within the house to excavate. .

Based on points #5 and #6 above, it is clear that the issue of faunal data-overload can be addressed by using small probabilistic samples. As noted in Chapter 7, a 5% systematic sample fairly accurately identified general trends in the composition of fauna within a house and as such, this sampling method could drastically reduce the number of specimens that need to be identified in future excavations. For example, at House 2 – a house which contained over 190,000 faunal specimens – a 5% systematic sample

required the analysis of fewer than 3,000 mammal and fish bones (Table 13) from $8.5m^2$

of excavation. The results from this sample were fairly representative of the relative

abundance of abundant taxa in this house and deviated by less than 4.0% from their

actual relative abundance (Figure 22 and Figure 23). Even if the shellfish specimens from

the sample are added to this total, the total number of identified specimens is still under

10,000. At the other two houses, a 5% systematic sample by area required even fewer

bones to be identified (Table 13).

Implementing such a small sample strategy does not necessarily exclude the

possibility that large areal excavation may also be undertaken. In some cases, large areal

excavation may be desired because other lines of evidence, including features and

artifacts, provide valuable information about the organization of space within these

dwellings. One could apply a systematic or random sample strategy to the entire house,

and then add additional units which are contiguous to the existing randomly- or

systematically-placed units in order to sample for features and artifacts, although it is

important to recognize that these additional units should be interpreted with caution since

they form part of a judgmental sampling strategy.

If judgmental sampling were the only sample method chosen, then randomly or

systematically selected units within this judgmental sample might allow researchers to

decrease the number of specimens identified. Whether this strategy would provide

accurate results at Ozette, based on the Huu7ii, McNichol Creek or Dionisio Point

strategies is one avenue for future research. Since faunal data collected from data-rich

shell middens are rarely analyzed in their entirety, the research presented in this thesis

may provide a rationale for selecting specific excavation units to sample, according to

random or systematic procedures. Other considerations, such as the proximity to a hearth may also be guiding factors to consider when selecting excavation units for faunal analysis (Ewonus 2006).

When considering statements #5 and #6 above, it is clear that more houses within a village can be excavated, thereby addressing the second issue raised above, namely that only a small number of houses have been excavated within a single village. Furthermore, using the same sample strategy at each house is advantageous, since the faunal data generated from each sample from one house can be compared directly with the data from another house. Generalized trends in the faunal data derived from these units at different houses may in fact indicate socioeconomic differences. At McNichol Creek, for example, the higher proportion of mammalian taxa at House O, when compared to faunal data at House D, was used to support the argument that House O was the high-status house (Coupland et al. 2003). A 5% systematic sample taken from 3-4 houses within a single village and subsequently analyzed could elucidate information about patterns that are similar or different to the ones at McNichol Creek, and researchers should have greater confidence in their results. The outcome of such research is likely to result in a greater understanding of both village dynamics and differences in household subsistence practices.

Finally, it is important to comment on the concern outlined in Chapter 4 regarding the use of ethnographic literature to decide upon the sample strategy to be used. Ethnographically, the largest house is generally the highest status house, and the space within each house is also assumed to be structured according to status (see Chapter 2). As such, large houses are often investigated in a more in-depth fashion than other houses,

and supposed high-status areas within these houses are also tested (see Chapter 4). This reinforces, rather than tests whether archaeological data reflect ethnohistoric observations. The solution to the first part of this issue – the emphasis on excavation directed towards the largest house – can be addressed by sampling additional houses in a village, provided that houses which are smaller or on the periphery of a village are tested. As observed above, this may be possible using small systematic samples, and will allow for the direct comparison of faunal data from both high-status and commoner households, and therefore evaluate whether the faunal data indicates congruence with ethnographic patterns or not.

The other aspect of ethnographic observations often utilized within sampling strategies was the assumption that practices within the house were structured in a specific manner. Based on the samples tested in this thesis, there appears to be no simple sample solution to this issue. Based on point #7 above, identifying the amount of high-status fauna in a house, even when this house conforms to ethnographic patterns, as is the case at Ozette, is not reliably accomplished for all types of fauna using any one of the sample strategies tested in this thesis. Similarly, as a result of point #8 above, it appears as if the spatial organization of the entire house, as interpreted using faunal distributions, is also difficult to ascertain without large-scale excavation. Even if this type of excavation is undertaken, it is likely that some of the status areas will be missed.

Examination of this issue from the perspective of the MAUP may suggest a possible method of addressing the link between ethnographic accounts of the household and archaeological interpretation of status areas, and may also prompt researchers to consider how their sample designs are guided by ethnohistoric accounts. The MAUP, as

noted in Chapter 3, results from the creation of artificial boundaries which are not meaningful, and therefore results in excavation units that could be aggregated according to a number of different configurations. In current practice, "meaningful" boundaries are almost always developed using ethnographic sources in conjunction with features such as hearths and house posts (e.g., Grier 2006). The latter methods are extremely useful, although in some cases it does appear as if the presence of features is utilized as a teleological argument for the existence of an ethnographic pattern. More research is required in which these multiple lines of archaeological evidence, rather than ethnographic evidence, are used to meaningfully identify differences in the spatial organization of household activities.

Another method of addressing the link between ethnographic and ethnohistoric sources and archaeological examples would be to investigate more houses which do not date to the contact period, since some of those which do date to this period do appear to reflect ethnohistorically documented patterns. In doing so, archaeologists may be able to more fully comprehend changes to NWC society and observe points of similarity and difference between ethnohistoric accounts and archaeological data which predate European contact.

Finally, while this argument is not developed within the scope of this thesis, an informed critical discussion on the accuracy of ethnohistoric accounts may help archaeologists decide how reliable and applicable such accounts are as analogues for the sites they are excavating and whether they wish to use these accounts when deciding on a particular sample strategy.

The research in this thesis can also be fruitfully applied to issues not directly investigated in this thesis. For example, the heuristic value of this research may apply not only to ecofacts but also to artifacts, as the distribution of the latter may be similar to the distribution of rare fauna. As such, this may force researchers to question the validity of their conclusions regarding similarities and differences between houses based on artifactual evidence, given that such comparisons between samples from each house failed to accurately predict inter-house differences for rare fauna at Ozette.

This research has focused on the issue of sampling and household archaeology on the Northwest Coast, and similar issues must exist elsewhere in the world when the focus of excavation directed towards domestic structures. It is likely that some of the issues addressed in this thesis are analogous to problems in other areas of the world faced by household archaeologists. Using some of the observations made in this thesis as a point of departure, other archaeologists could examine the effects of sampling on their interpretation of houses and households in other regions.

Finally, this research may also have implications for cultural resource management (CRM) archaeology. Although house deposits are rarely investigated specifically during CRM work, the results from previous chapters indicate that a 10% random sample or a 5% systematic sample may provide adequate information in order to understand the general composition of fauna from a house. This research can be used as a rationale for the sample strategy employed, and subsequently as an estimation of the time and expense required to adequately excavate and analyze faunal data from the house(s). Future research on the Ozette data (elaborated in Section 9.3) may be able to suggest how

much of the exterior midden would need to be excavated in order to understand the fauna from this part of the village.

9.2 Limitations

There are several limitations concerning this research that should be articulated. This research is predicated on the fact that house floors can be defined. As noted in Chapter 2, midden ridges behind, in front and between houses can help to identify the spatial extent of houses. In situations where house platforms are not defined and sub-surface testing is required in order to define house boundaries, systematic sampling may be a useful technique. If 50cm X 50cm units are used, such units may allow the researcher to identify features more easily than auger or core testing, and once house features are defined based on these units, excavation units located within the house can be integrated into a house floor-specific sampling design. Another issue which archaeologists at other sites will likely have to contend with (which was not an issue at Ozette) is the identification of house floor deposits. The mixing of material from occupation of the site both prior to house construction and after house abandonment can make the identification of discrete house floors difficult. Stratigraphy, compaction, and the presence of features may aid in the identification of house floors and allow for samples to be taken from a specific house floor.

This particular project was also limited by the fact that avifaunal remains were not identified. While this often represents the smallest proportion of fauna recovered from a site (as was the case at Ozette, McNichol Creek, Shingle Spit, Huu7ii, etc.) the distribution of bird remains could be significantly different from that of other types of

fauna, and therefore could change the results derived in this thesis. At present, there is no way to predict how accurate the results for avifaunal remains will be.

9.3 Future Avenues of Research

The Ozette dataset, by virtue of its size and relative completeness, has many potential avenues for further exploration, especially with respect to sampling. In order to maintain focus, this thesis focused on a small number of sampling issues that could be investigated using this dataset. Other avenues of research are listed below, although this is by no means a comprehensive list. These possibilities have been divided into two categories: future sampling research based on the extensive Ozette dataset, and future research based on the results of this thesis.

Future sampling research using Ozette dataset:

1. Exterior midden data from Ozette could be analyzed to observe what sample sizes and methods provide accurate results for exterior contexts. These results could then be compared with the interior of houses in order to observe what similarities and differences exist between sampling requirements for the interior versus the exterior of a house.

2. Different sample strategies could be analyzed. These could include judgmental samples from other NWC house excavations or stratified systematic samples. Additionally, different sample sizes could be tested in order to address the effect of the MAUP. Excavation units of varying sizes (e.g. 50cm^2, 1m^2 or 2 m^2 units) could be compared to observe the decrease in resolution as excavation units become larger (i.e., the aggregation issue of MAUP noted in Chapter 3). This in turn could be investigated to determine if larger excavation units obscure too much of the variability in faunal concentrations and make it difficult to determine the spatial organization of a house based on faunal data.

3. Data could be added to the GIS such as hearth features and artifacts, and then the houses re-sampled. The congruence between these different lines of evidence in the interpretation of inter-house and intra-houses differences could then be re-examined, focusing on which strategies provide the most accurate results for these different lines of evidence.

4. The complete dataset could be analyzed in-depth by investigating the degree of spatial clustering for each and every taxon. This clustering could be compared

between and within houses for a given taxon in order to interpret the range of behaviours which occurred in each house and the spatial location (if any) of such behaviours in the house.

5. Monte-Carlo simulation of entire assemblages could be investigated in order to identify the probabilities of getting an accurate sample for a given sample size using random or systematic sampling.

Applied research based on the results from this thesis:

6. One could excavate part of a village and test four or more houses according to a 5% systematic sample strategy to understand village dynamics.

7. The fauna from different sites could be evaluated based on sampling designs generated from this thesis. The results based on these sample strategies could be compared to the sample of fauna identified using the actual strategy employed. Essentially, this type of research would evaluate and compare the efficacy of sample strategies at Ozette versus the efficacy of the same sample strategies at other sites to identify similarities and differences.

9.3 Conclusion

Sampling is an issue which is often ignored or overlooked with respect to household archaeology on the Northwest Coast. At the very least, this thesis should prompt researchers in NWC household archaeology to recognize the importance of sampling and therefore to consider much more carefully their choice of sampling strategy. The results of the sampling simulation of Ozette data indicate that significant reduction in the quantity of faunal analysis may result in only minimal loss of information, although an accurate interpretation of status may be difficult to ascertain using these smaller samples. Nevertheless, in an era where funding and labour for archaeological projects are scarce, and given the large quantity of data contained in archaeological deposits, I hope to have shown that certain avenues of research can productively be investigated using relatively small sample sizes.

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Appendix 1: Sampling Designs Used in Northwest Coast Household Archaeology
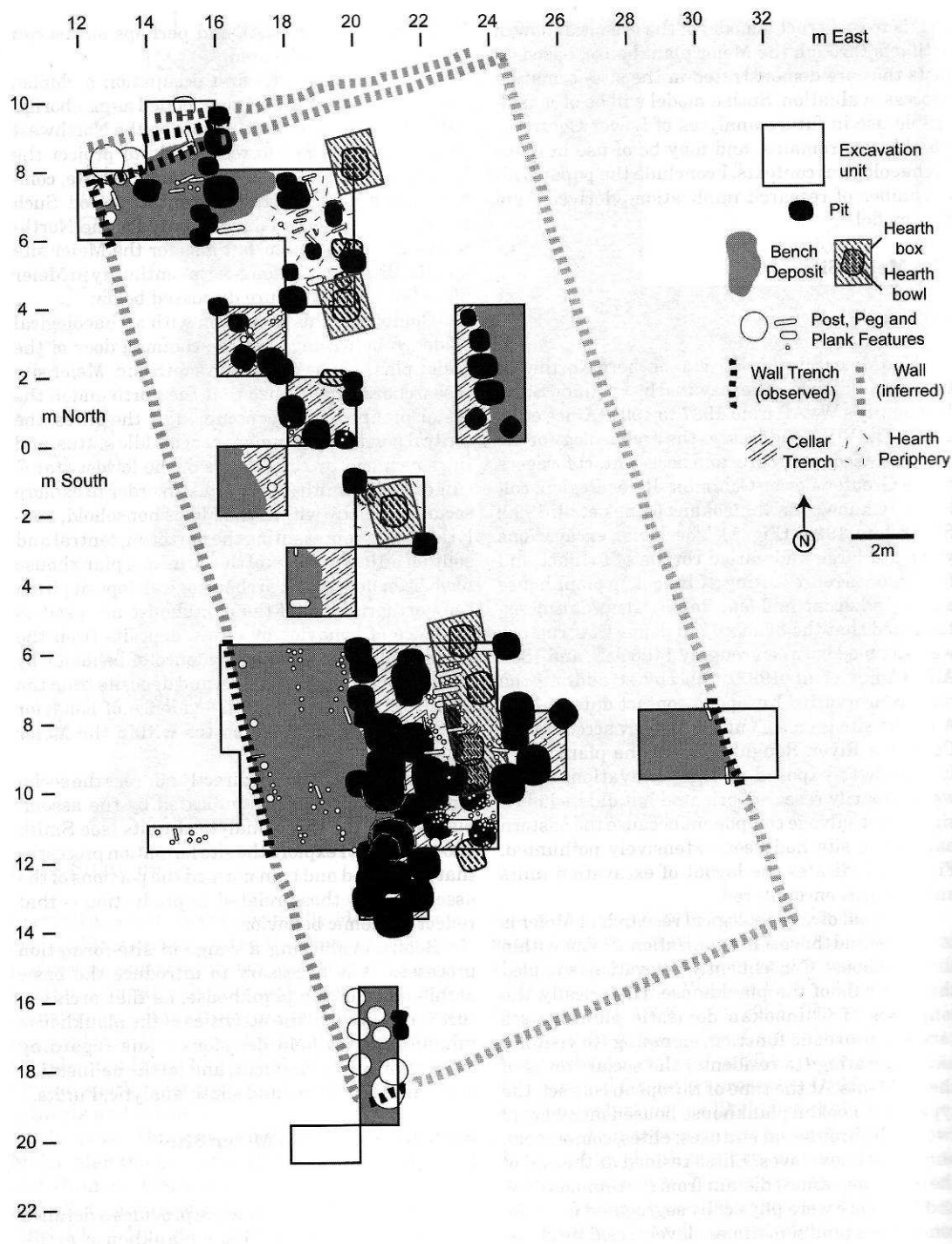
Excavated areas of the Meier house (Smith 2006:236).
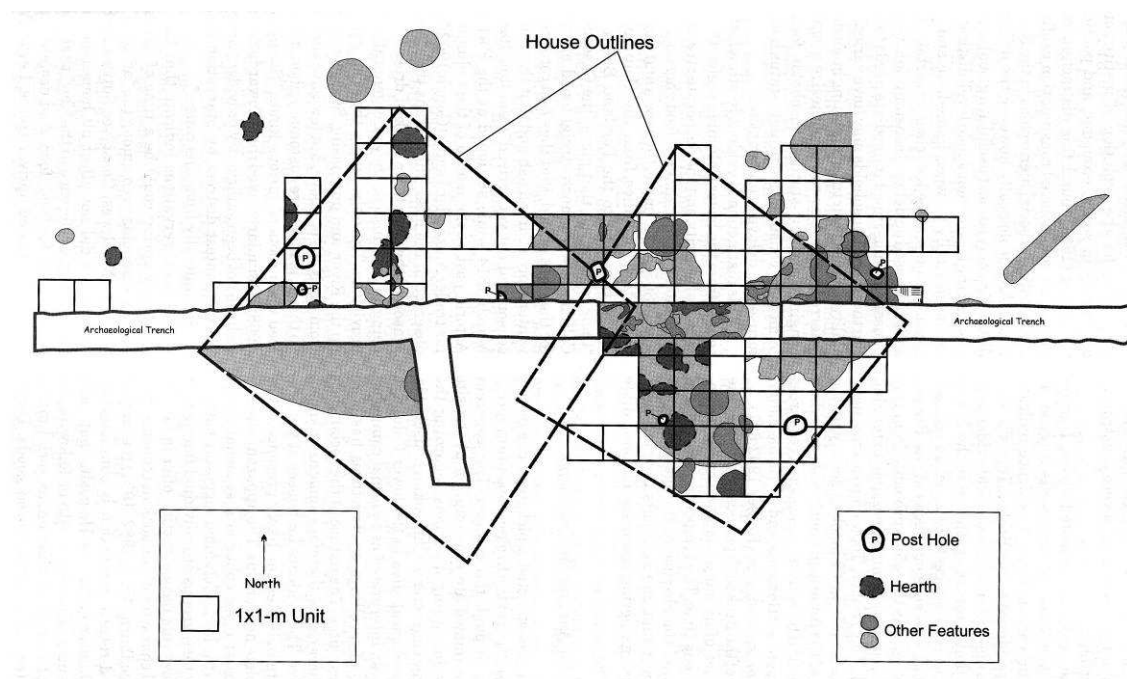
Excavation of two small houses from the Broken Tops site (Ellis 2006:131).
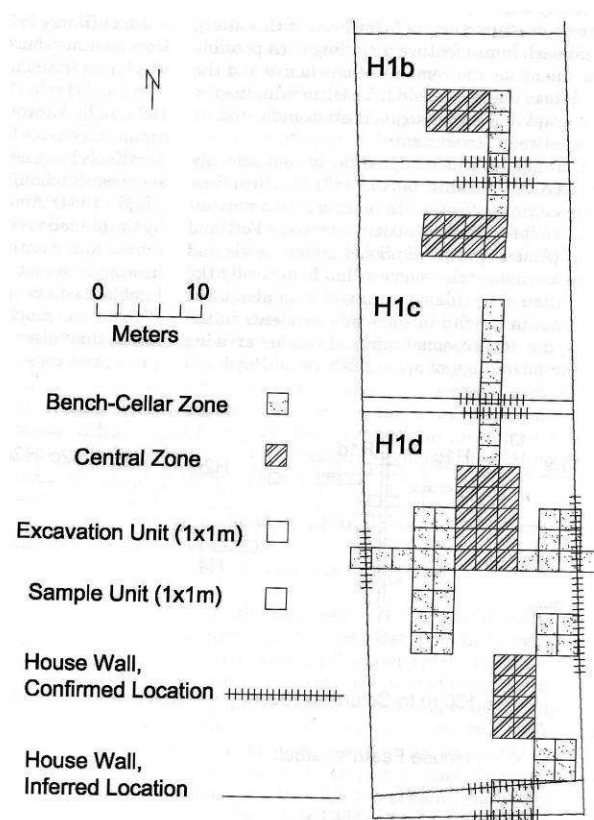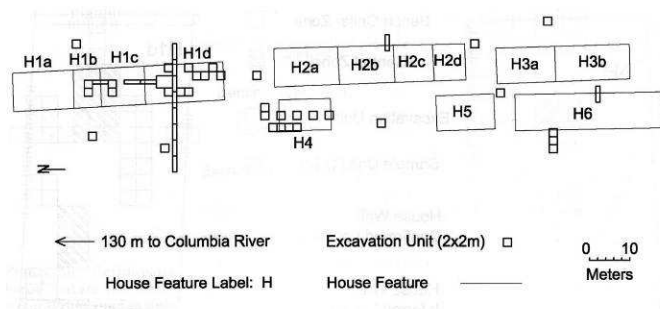
Excavation of several houses at the Cathapotle site (Sobel 2006:167-168).
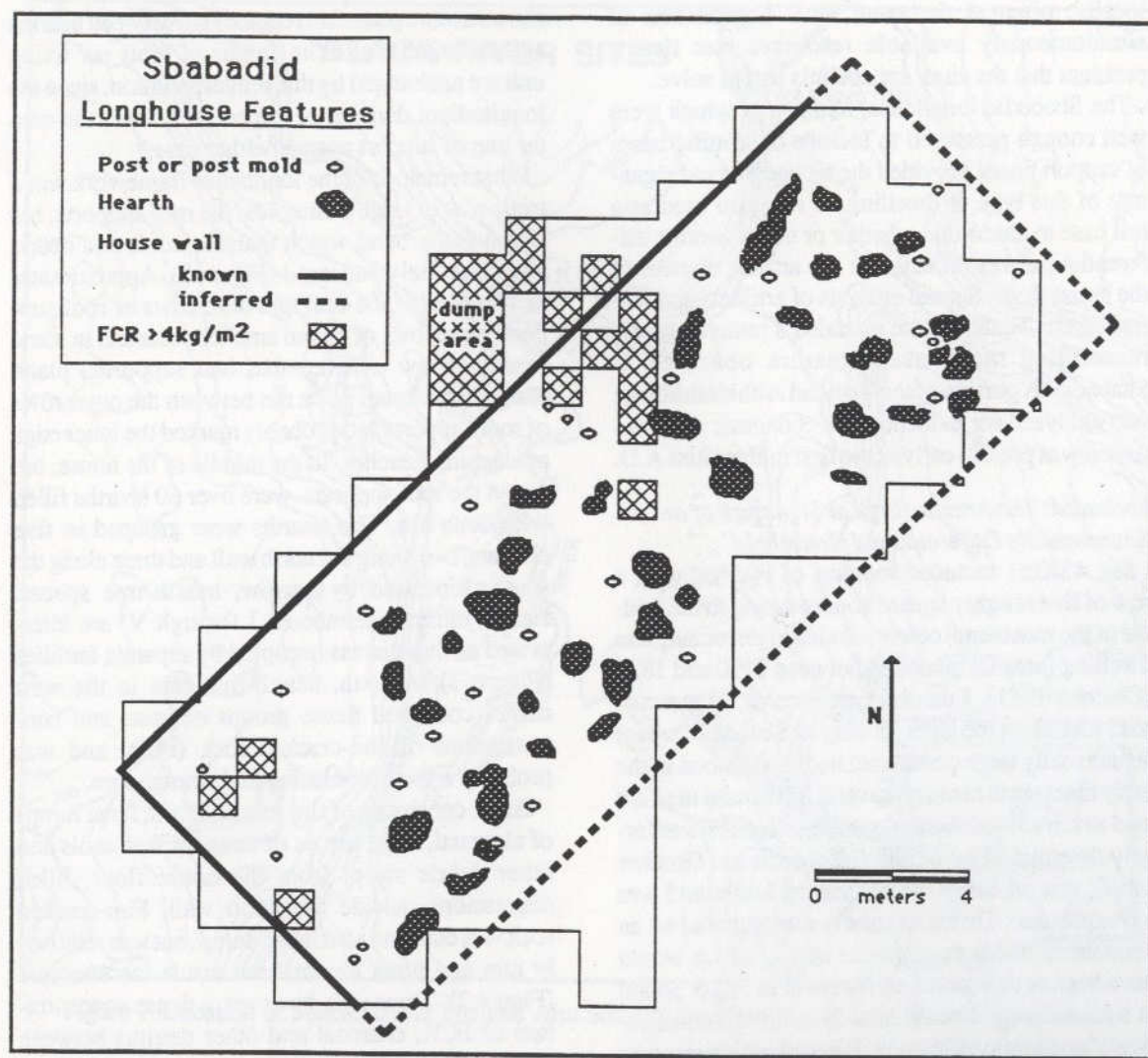
Excavation of a house at the Sbabadid site (Chatters 1989:172).
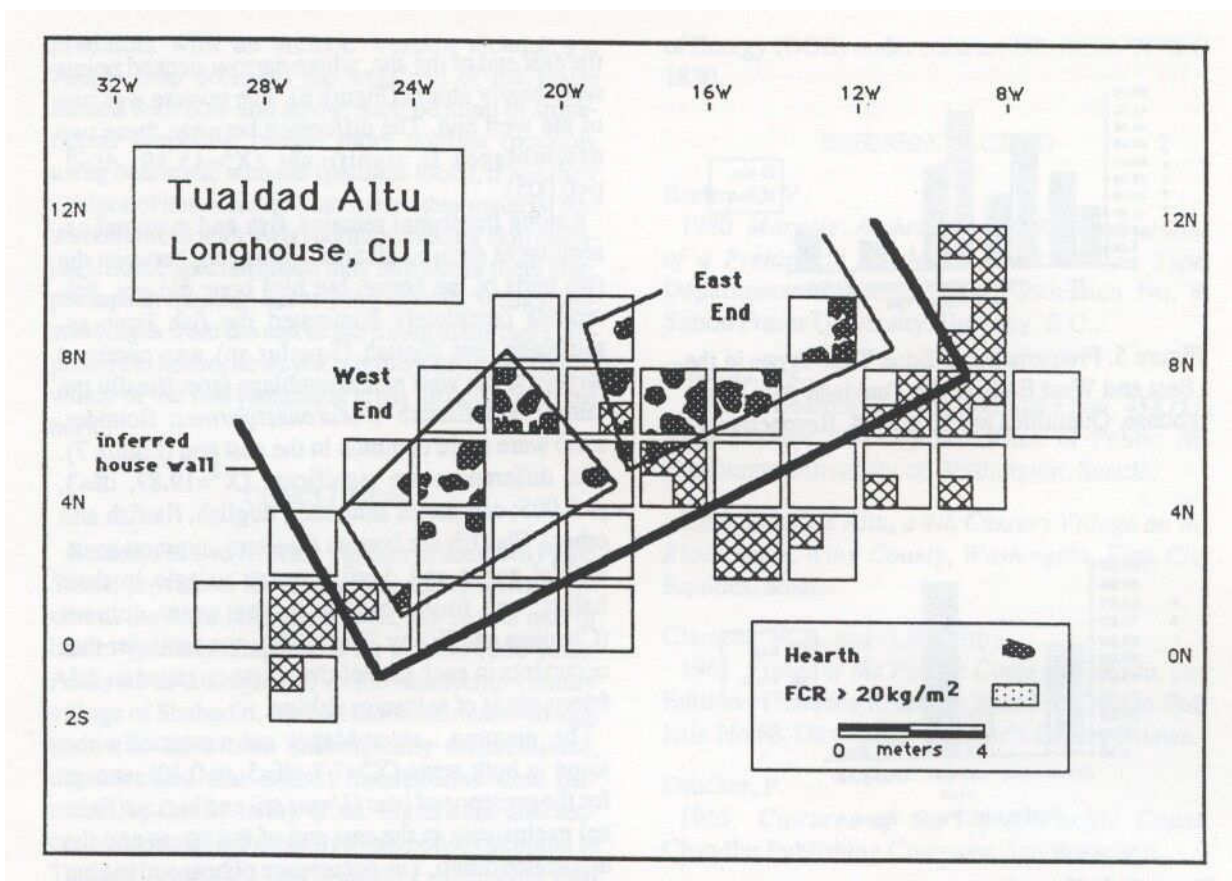
Excavation of a house at the Tualdad Altu site (Chatters 1989:175).
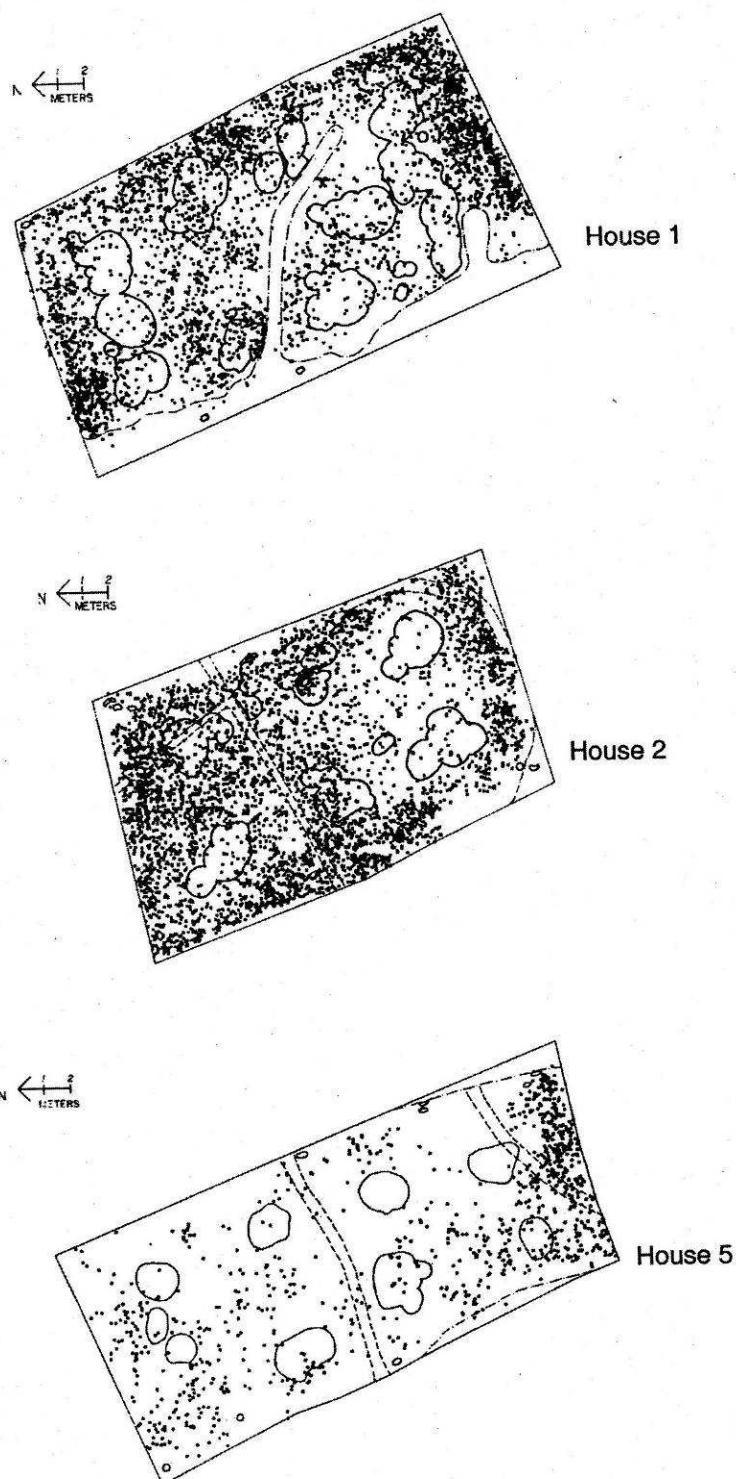
Excavation of 3 houses at Ozette (spatial relationships between houses not shown). The dots represent artifacts, solid lines represent hearth complexes. Dashed lines represent drainage trenches and dot-dash lines represent *in situ* house floor midden (Samuels 1994:215).
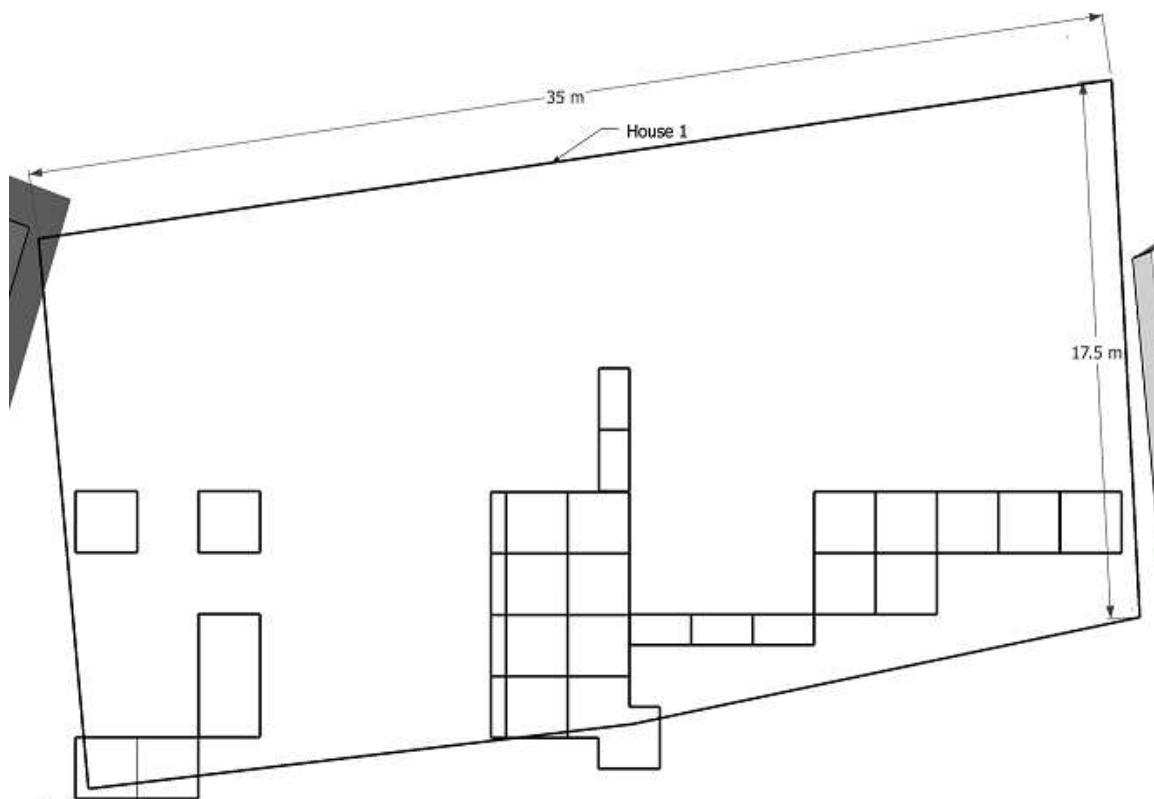
Excavated areas at the Huu7ii site (Courtesy Alan MacMillan and Iain McKechnie).
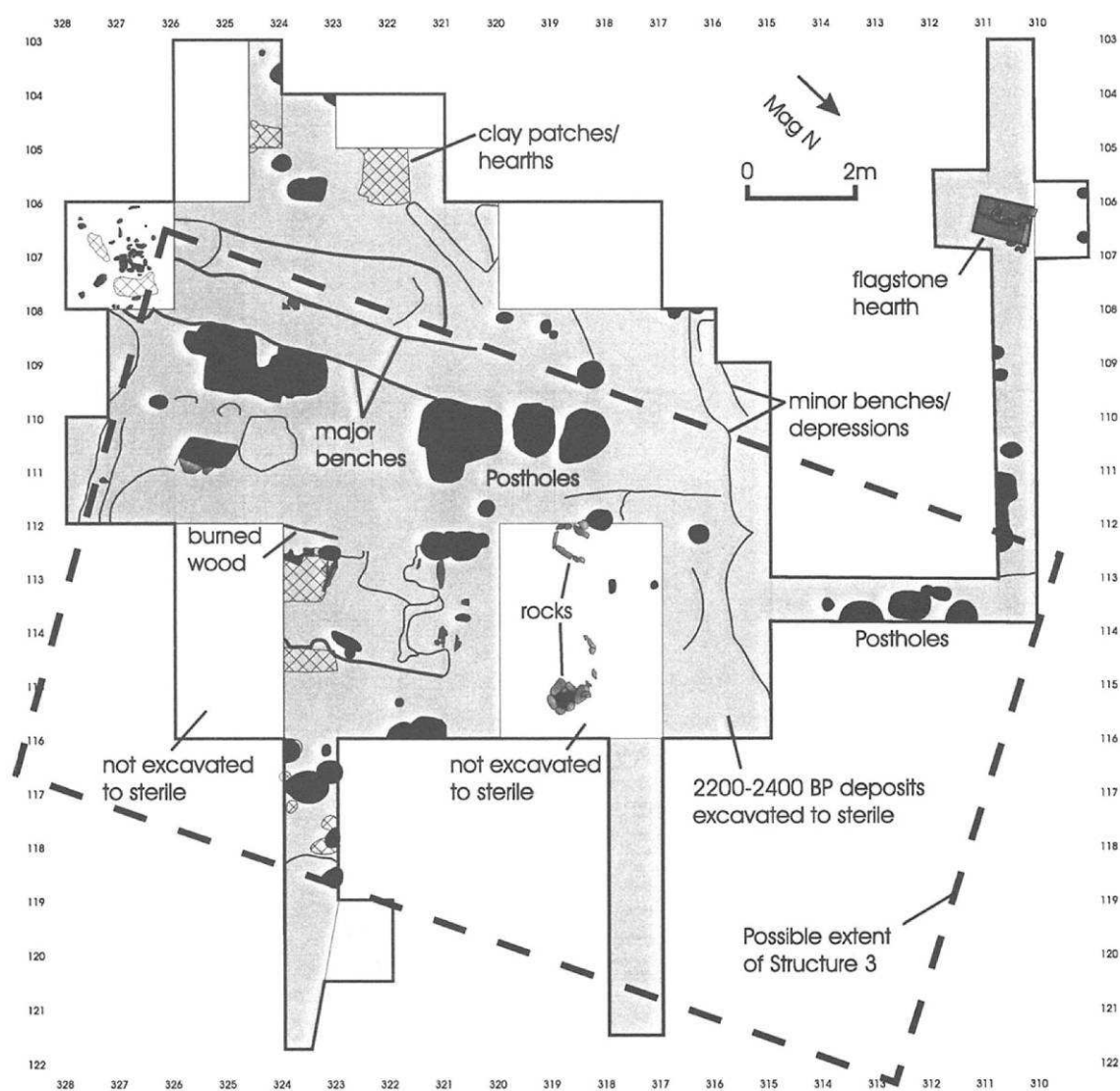
Excavation of Structure 3 at the Scowlitz site (Lepofsky et al. 2000:401).
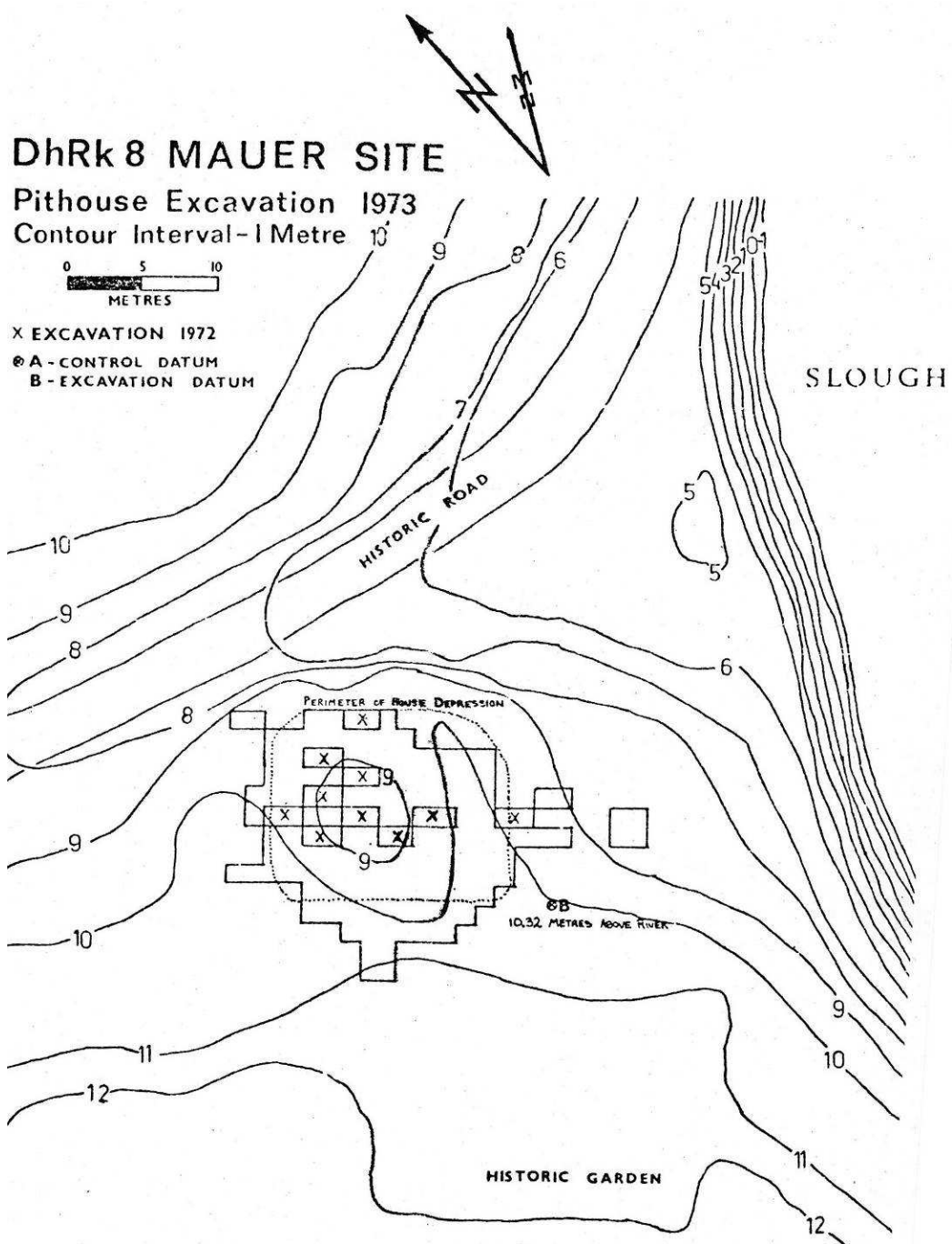
Excavations at the Mauer site (LeClaire 1973:36).
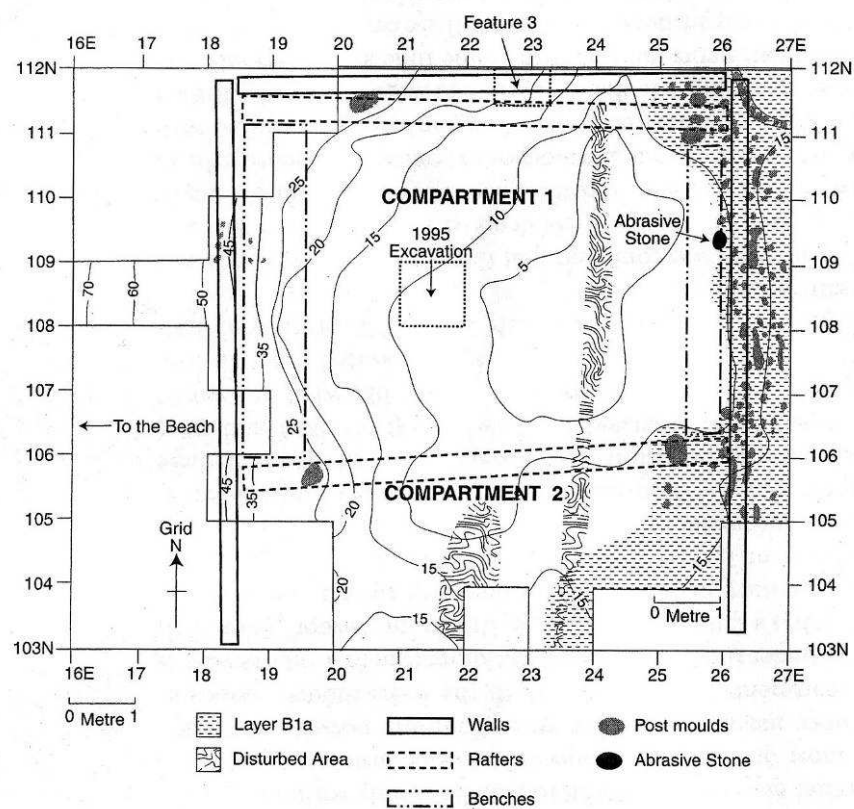
Excavations at Shingle Point (Matson 2003:84).
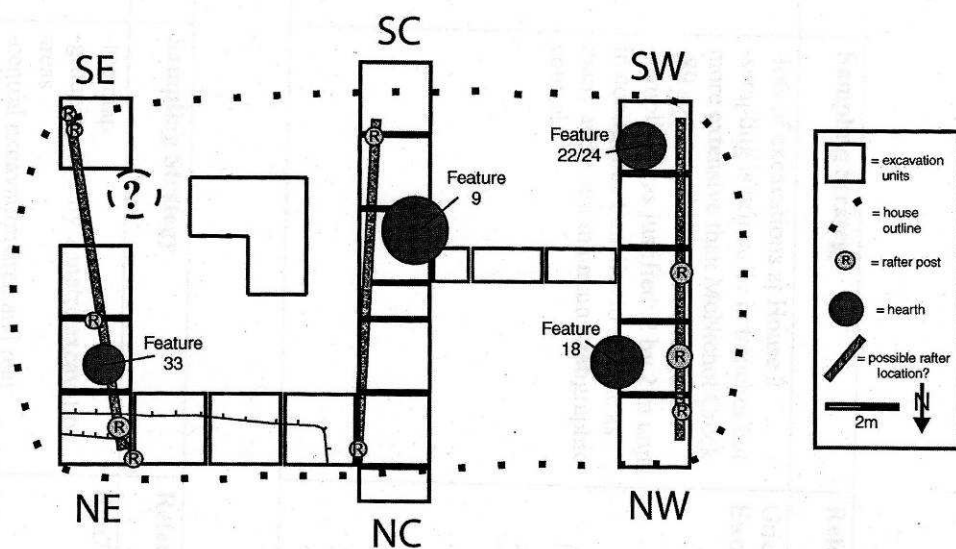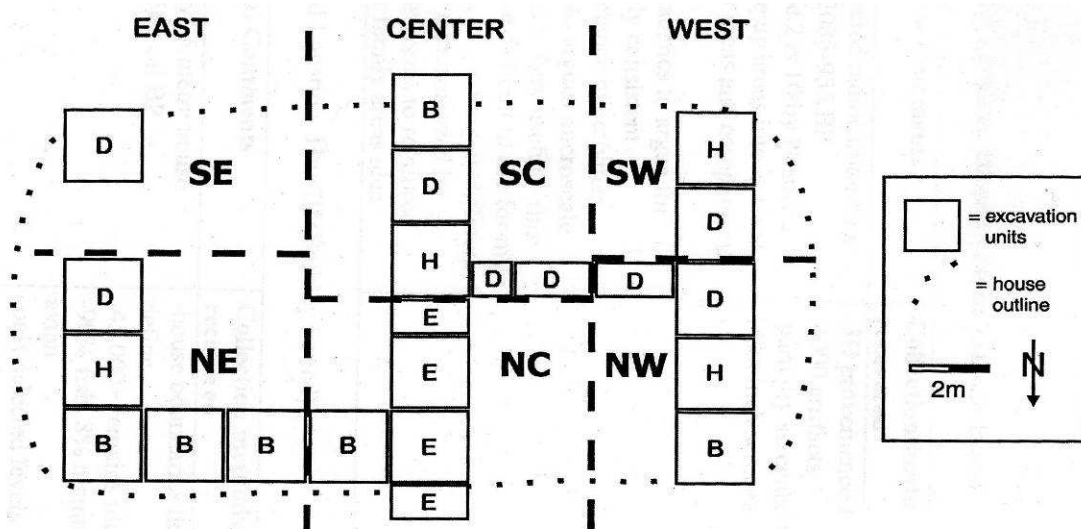
Excavated areas of House 2 at the Dionisio Point Site. The upper diagram divisions of space within the house: Bench area; D=open domestic space; H=hearth area; E=entranceway space. The lower diagram indicates the different domestic areas and some of structural elements of the house (Grier 2006:106).
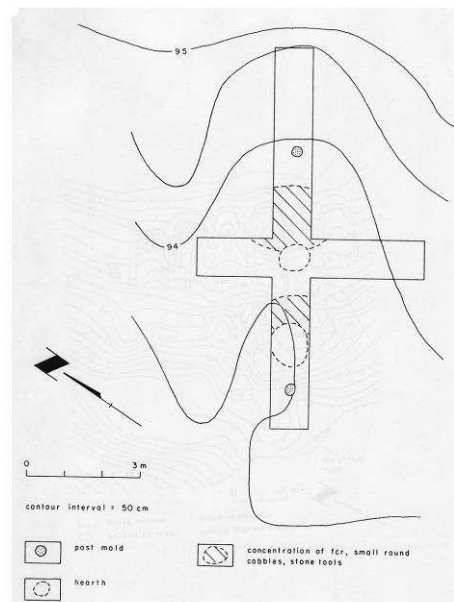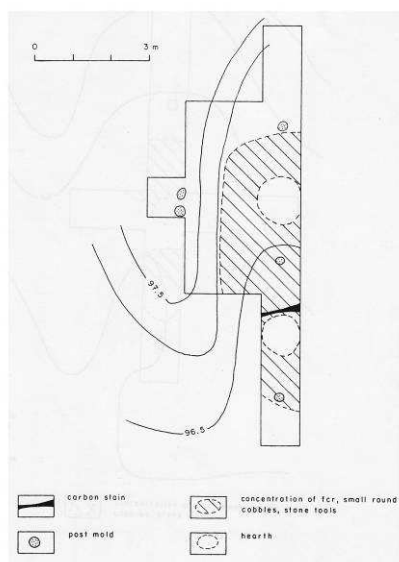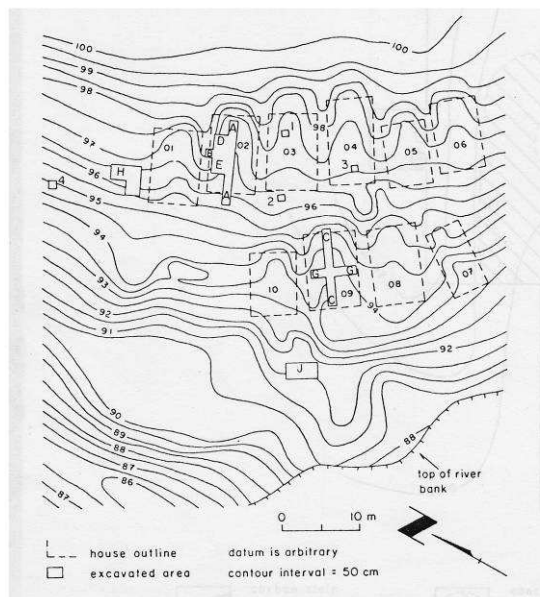
Excavated areas of the Paul Mason Site. The upper diagram demarcates all the excavated areas at the site. The lower left diagram shows more detail of the excavation at House 2, while the lower right diagram shows more detail of the excavation at House 9 (Coupland 1988:133, 140, 141).
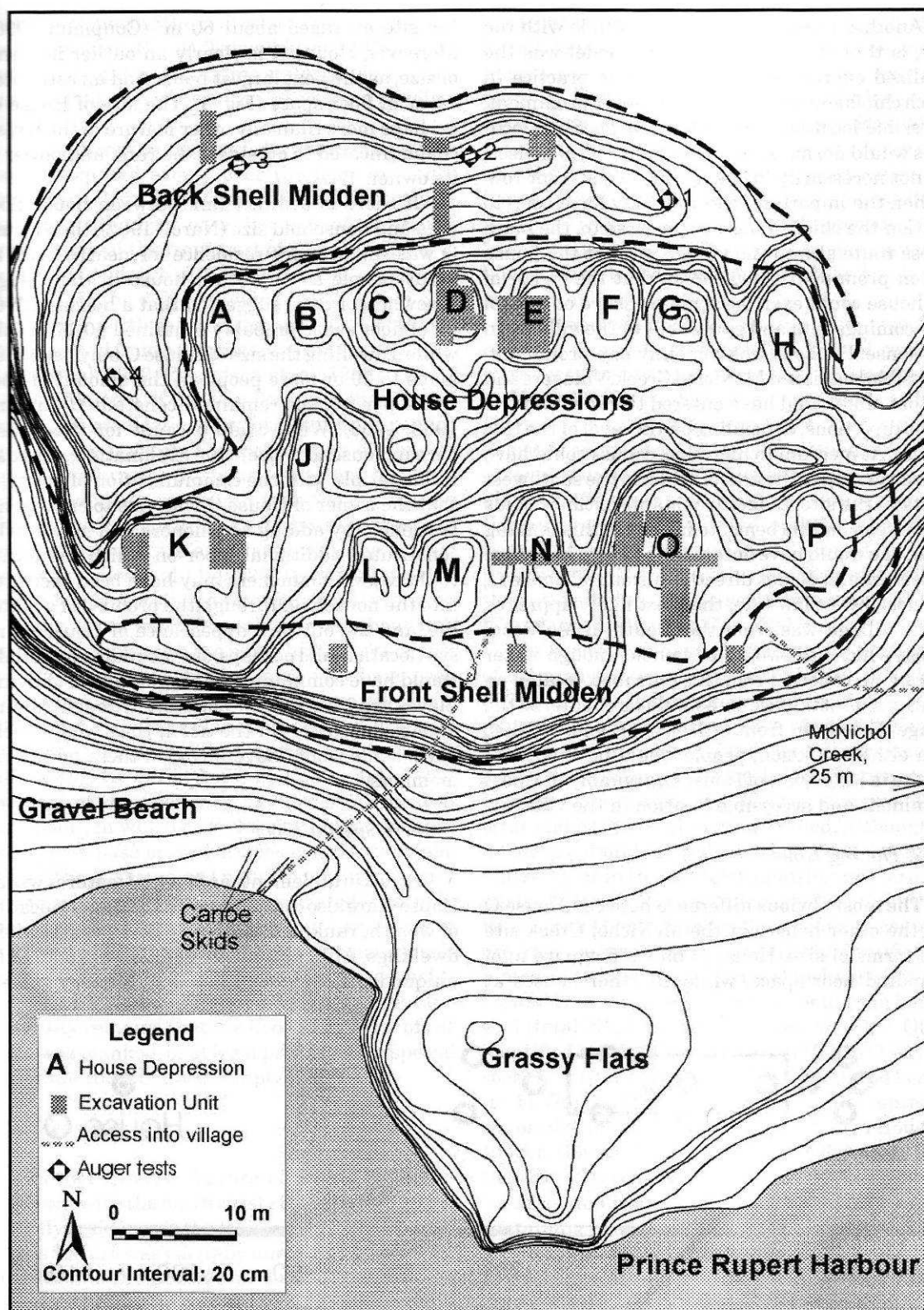
Excavated areas at the McNichol Creek Site; see also page below (Coupland 2006:87).
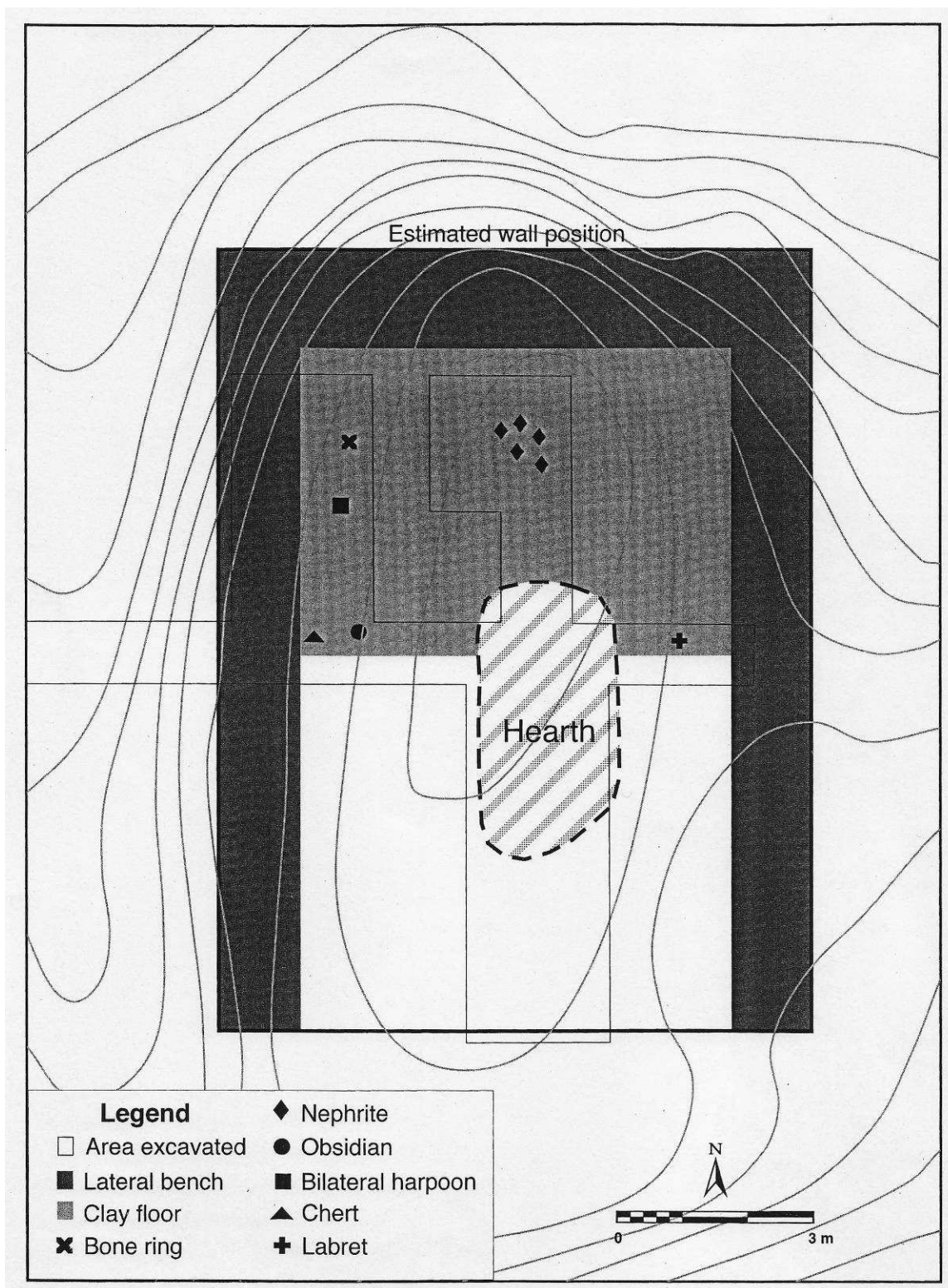
Excavation at House O at McNichol Creek; see also page above (Coupland 2006:90).

Excavations at the Psacelay site (Martindale 2006:149).

plan of
CORNER POST HOUSE

letters indicate excavated
one-meter units.

beach
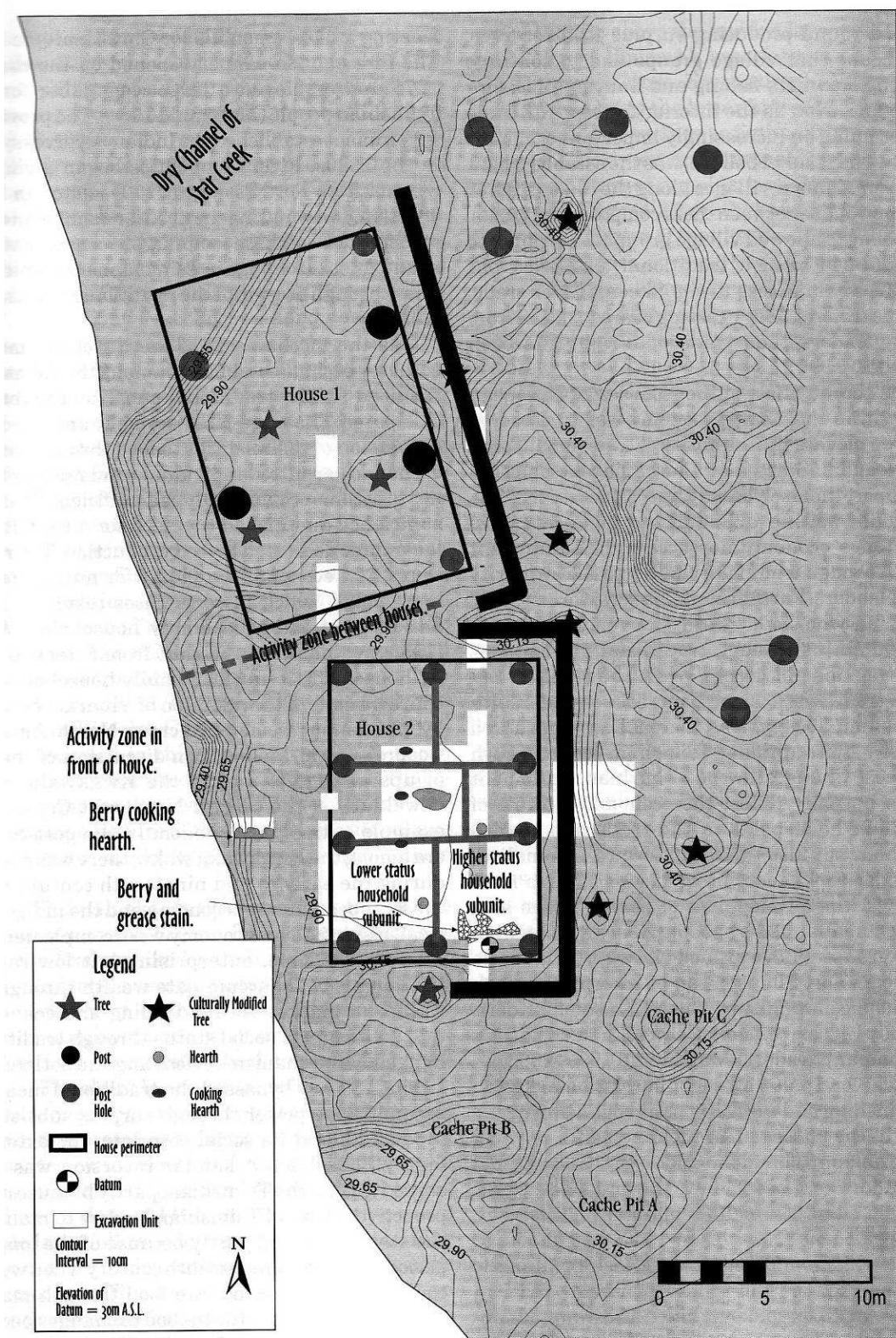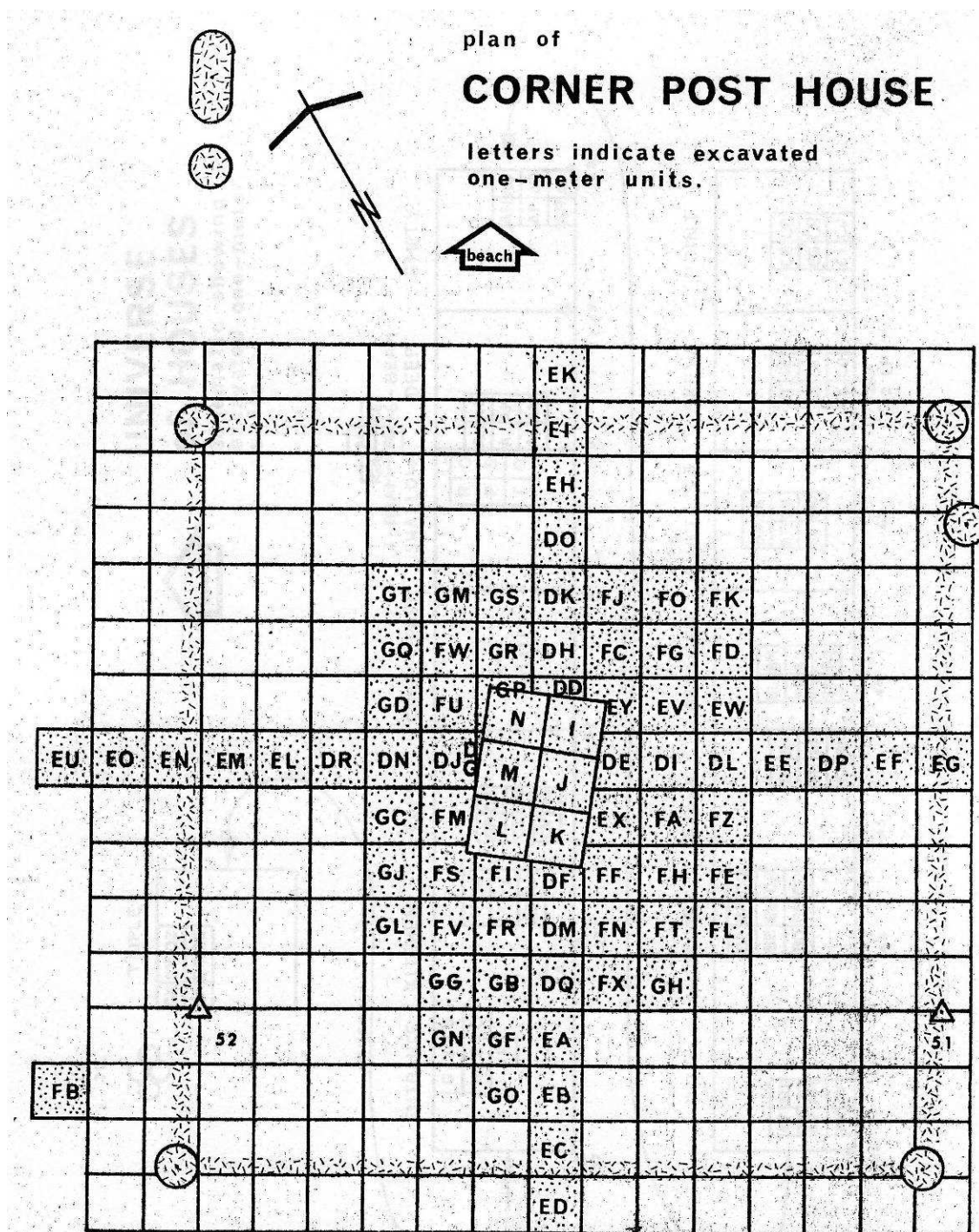
Excavations of a single house at the Kiusta site (Gessler 1975).
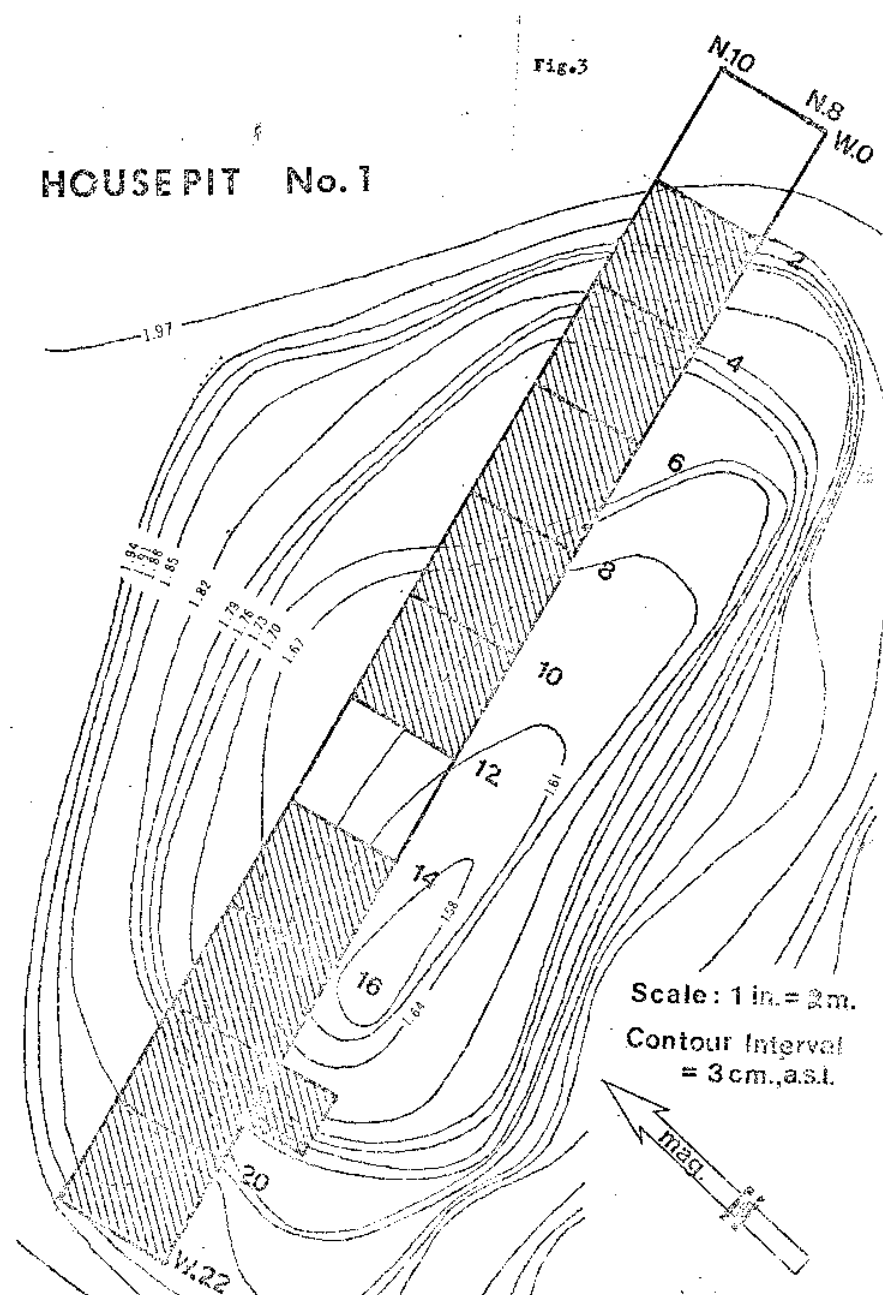
Excavation of the largest house at the Richardson Ranch site (Fladmark 1972:Figure 3).

Appendix 2: Corrected Faunal Database

House 1

Taxa (Fish)	Common Name	NISP	% NISP (fish)
Ophiodon elongatus	Lingcod	2089	28.15%
Oncorhynchus spp./*Salmo* sp.	Salmon	1039	14.00%
Sebastes spp.	Rockfish	1007	13.57%
Hippoglossus stenolepis	Halibut	924	12.45%
Cottidae	Scuplin	822	11.08%
Hexagrammos sp.	Greenling	681	9.18%
Embiotocidae	Surfperches	325	4.38%
Scorpaenichthys marmoratus	Cabezon	200	2.70%
Pleuronectiformes	Flatfish	140	1.89%
Squalus acanthias	Dogfish	52	0.70%
Clupea harengus pallasi	Herring	50	0.67%
Raja sp.	Skate	35	0.47%
Microgadus proximus	Pacific tomcod	33	0.44%
Anarrhichthys ocellatus	Wolf eel	13	0.18%
Gadus macrocephalus	Pacific cod	10	0.13%
Totals		**7420**	**100%**

Taxa (Mammals)	Common Name	NISP	%NISP (mammals)
Callorhinus ursinus	Northern fur seal	6328	85.40%
Canis familiaris	Dog	394	5.32%
Delphinidae	Porpoise	164	2.21%
Eumetopias jubata	Sea lion	159	2.15%
Balaenopteridae	Whale	147	1.98%
Odocoileus hemionus	Mule deer	78	1.05%
Enhydra lutris	Sea otter	60	0.81%
Phoca vitulina	Harbour seal	32	0.43%
Megaptera novaeangliae	Humpback whale	20	0.27%
Eschrichtius gibbosus	Gray whale	13	0.18%
Lutra canadensis	River otter	5	0.07%
Cervus canadensis	Elk	4	0.05%
Martes americana	Marten	3	0.04%
Procyon lotor	Raccoon	2	0.03%
Castor canadensis	Beaver	1	0.01%
Totals		**7410**	**100%**

Taxa (Shellfish)	Common Name	NISP	%NISP (shellfish)
Mytilus californianus	California mussel	10022	29.90%
Littorina sitkana	Sitka periwinkle	7652	22.83%
Protothaca staminea	Littleneck clam	4636	13.83%
Mytilus sp.	Mussel	3651	10.89%
Mytilus edulis	Blue mussel	1879	5.61%
Saxidomus giganteus	Butter clam	1177	3.51%
Katharina tunicata	Black leather chiton	848	2.53%
Tresus sp.	Tresus clam	484	1.44%
Acmaea t. scutum	Plate limpet	383	1.14%
Thais lamellosa	Frilled dogwinkle	375	1.12%
Dentalium pretiosum	Dentalia	266	0.79%
Acmaea sp.	Limpet	239	0.71%
Cryptochiton stelleri	Giant chiton	225	0.67%
Acmaea pelta	Ridge limpet	196	0.58%
Searlesia dira	Dire whelk	145	0.43%
Mitella polymerus	Stationary gooseneck barnacle	120	0.36%
Strongylocentrotidae	Urchin	104	0.31%
Lacuna variegata	Northern chink shell	104	0.31%
Mopalia muscosa	Mossy chiton	99	0.30%
Acmaea mitra	Nookta cap limpet	87	0.26%
Macoma nasuta	Bent-nose clam	83	0.25%
Astraea gibberosa	Red turban shell (opercula)	79	0.24%
Mopalia sp.	Chitons	73	0.22%
Thais lima	File dogwinkle	69	0.21%
Thais emarginata	Emarginate dogwinkle	66	0.20%
Olivella biplicata	Purple olive shell	44	0.13%
Veneridae	Venus clam	40	0.12%
Tegula funebralis	Black turban shell	30	0.09%
Macoma secta	White sand clam	26	0.08%
Siliqua patula	Pacific razor clam	24	0.07%
Clinocardium nuttalli	Pacific basket cockle	20	0.06%
Diodara aspera	Rough keyhole limpet	20	0.06%
Strongylcentrotus drobachiensis	Green sea urchin	19	0.06%
Thais sp.	Dogwinkle	18	0.05%
Cancer productus	Red rock crab	18	0.05%
Haliotus kamtschatkana	Northern abalone	17	0.05%
Calliostoma ligatum	Blue top shell	16	0.05%
Chyamys icelandicus	Icelandic scallop	16	0.05%
Hipponix cranoides	Flat hoof shell	15	0.04%

Taxa (Shellfish)	Common Name	NISP	%NISP (shellfish)
Octopus dofleini	Octopus	13	0.04%
Acmaea persona	Mask limpet	13	0.04%
Tresus capax	Horse clam	11	0.03%
Littorina sp.	Periwinkle	10	0.03%
Macoma irus	Polluted macoma	9	0.03%
Pecten caurinus	Weathervane scallop	8	0.02%
Thais canaliculata	Channeled dogwinkle	8	0.02%
Tellina bodegensis	Bodega clam	8	0.02%
Fustritriton oregonensis	Oregon triton	6	0.02%
Tellina sp.	Tellin clam	5	0.01%
Scapellum columbiaum	Not listed	5	0.01%
Littorina planaxis	Flat periwinkle	5	0.01%
Crepidula adunca	Hooked slipped shell	4	0.01%
Tresus nuttallia	Horse clam	3	0.01%
Hinnites mutlirugosus	Purple-hinged rock scallop	3	0.01%
Pododesmus macroschisma	Rock oyster	3	0.01%
Glycymeris suboboleta	Bittersweet / Ark shell	3	0.01%
Penitella penita	Piddocke clam	3	0.01%
Natica clausa	Arctic moon snail	2	0.01%
Opalia wroblewskii	Wrobleski's wentletrap	2	0.01%
Littorina scutulata	Checkered periwinkle	2	0.01%
Chyamys hastata	Pacific spear scallop	1	0.01%
Acmaea instabilis	Instable limpet	1	0.01%
Mopalia lignosa	Woody chiton	1	0.01%
Crepidula nummaria	White slipper shell	1	0.01%
Acmaea digitalis	Finger limpet	1	0.01%
Totals		**33516**	**100%**

House 2

Taxa (Fish)	Common name	NISP	%NISP (fish)
Ophiodon elongatus	Lingcod	10935	26.12%
Sebastes spp.	Rockfish	7424	17.74%
Hexagrammos sp.	Greenling	6428	15.36%
Oncorhynchus spp./*Salmo* sp.	Salmon	3884	9.28%
Cottidae	Sculpin	3063	7.32%
Scorpaenichthys marmoratus	Cabezon	2964	7.08%
Hippoglossus stenolepis	Halibut	2513	6.00%
Embiotocidae	Surfperches	2121	5.07%
Squalus acanthias	Dogfish	923	2.21%
Pleuronectiformes	Flatfish	140	0.33%

Taxa (Fish)	Common name	NISP	%NISP (fish)
Clupea harengus pallasi	Herring	69	0.16%
Raja sp.	Skate	65	0.16%
Gadus macrocephalus	Pacific cod	23	0.05%
Anarrhichthys ocellatus	Wolf-eel	19	0.05%
Microgadus proximus	Pacific tomcod	13	0.03%
Eopsetta jordani	Petrale sole	2	0.01%
Thunnus thynnus	Bluefin tuna	1	0.01%
Totals		**40597**	**100%**

Taxa (Mammals)	Common name	NISP	%NISP (mammals)
Callorhinus ursinus	Northern fur seal	12497	90.15%
Delphinidae	Porpoise	327	2.36%
Eumetopias jubata	Sea lion	312	2.25%
Canis familiaris	Dog	188	1.36%
Enhydra lutris	Sea otter	145	1.05%
Odocoileus hemionus	Mule deer	120	0.87%
Balaenopteridae	Whale	95	0.69%
Phoca vitulina	Harbour seal	70	0.50%
Mephitis sp.	Skunk	44	0.32%
Megaptera novaeangliae	Humpback whale	21	0.15%
Eschrichtius gibbosus	Gray whale	16	0.12%
Ursus americanus	Black bear	10	0.07%
Cricetidae	Mouse	4	0.03%
Martes americana	Marten	3	0.02%
Lutra canadensis	River otter	3	0.02%
Castor canadensis	Beaver	3	0.02%
Tamiasciurus douglasii	Squirrel	2	0.01%
Cervus canadensis	Elk	1	0.01%
Balaenoptera physalus	Fin whale	1	0.01%
Totals		**13866**	**100%**

Taxa (Shellfish)	Common name	NISP	%NISP (fish)
Littorina sitkana	Sitka periwinkle	39290	28.91%
Mytilus californianus	California mussel	29641	21.81%
Protothaca staminea	Littleneck clam	12601	9.27%
Mytilus sp.	Mussel	11097	8.16%
Katharina tunicata	Black leather chiton	9667	7.11%
Mytilus edulis	Blue mussel	5158	3.80%
Mopalia muscosa	Mossy chiton	3818	2.81%
Saxidomus giganteus	Butter clam	3491	2.57%
Cryptochiton stelleri	Giant chiton	3385	2.49%
Mopalia sp.	Chitons	3048	2.24%

Taxa (Shellfish)	Common name	NISP	%NISP (fish)
Acmaea t. scutum	Plate limpet	3040	2.24%
Acmaea pelta	Ridge limpet	1692	1.24%
Thais lamellosa	Frilled dogwinkle	1577	1.16%
Acmaea sp.	Limpet	1055	0.78%
Searlesia dira	Dire whelk	1005	0.74%
Strongylocentrotidae	Urchin	888	0.65%
Thais lima	File dogwinkle	852	0.63%
Tresus sp.	Clam	595	0.44%
Mopalia lignosa	Woody chiton	466	0.34%
Lacuna variegated	Northern chink shell	366	0.27%
Veneridae	Venus clams	356	0.26%
Strongylocentrotus drobachiensis	Urchin	334	0.25%
Thais emarginata	Emarginate dogwinkle	308	0.23%
Acmaea persona	Mask limpet	304	0.22%
Tegula funebralis	Black turban shell	201	0.15%
Acmaea mitra	Nootka cap limpet	175	0.13%
Mitella polymerus	Stationary gooseneck barnacle	161	0.12%
Thais sp.	Dogwinkle	156	0.11%
Littorina planaxis	Flat periwinkle	116	0.09%
Thais canaliculata	Channeled dogwinkle	116	0.09%
Tellina sp.	Tellin clam	90	0.07%
Octopus dofleini	Octopus	87	0.06%
Macoma nasuta	Bent-nose clam	71	0.05%
Littorina sp.	Periwinkle	59	0.04%
Acmaea digitalis	Finger limpet	51	0.04%
Calliostoma lignatum	Blue top shell	47	0.03%
Clinocardium nuttalli	Pacific basket cockle	45	0.03%
Diodara aspera	Rough keyhole limpet	43	0.03%
Hipponix cranoides	Flat hoof shell	42	0.03%
Pecten caurinus	Weathervane scallop	42	0.03%
Olivella biplicata	Purple olive shell	39	0.03%
Chyamys hastata	Pacific spear scallop	36	0.03%
Hinnites multirugosus	Purple hinged rock scallop	35	0.03%
Littorina scutulata	Checkered periwinkle	33	0.02%
Astraea gibberosa	Red turban shell (opercula)	30	0.02%
Tellina bodegensis	Bodega clam	25	0.02%
Macoma secta	White sand clam	24	0.02%
Cancer productus	Red rock crab	20	0.01%
Haliotis kamtschatkana	Northern abalone	20	0.01%

Taxa (Shellfish)	Common name	NISP	%NISP (fish)
Scalpellum columbiaum	N/A	17	0.01%
Macoma irus	Polluted macoma	16	0.01%
Opalia wroblewskii	Wrobleski's wentletrap	12	0.01%
Siliqua patula	Pacific razor clam	11	0.01%
Tresus nuttalli	Horse clam	10	0.01%
Chyamus rubidus	Hinds scallop	8	0.01%
Glycymeris suboboleta	Bittersweet / Ark shell	7	0.01%
Crepidula adunca	Hooked slipped shell	5	0.01%
Nassarius fossatus	Channeled dog whelk	5	0.01%
Chyamys icelandicus	Icelandic scallop	4	0.01%
Crepidula nummaria	White slipper shell	3	0.01%
Dentalium pretiosum	Dentalia	3	0.01%
Fusitriton oregonensis	Oregon triton	2	0.01%
Pododesmus macroschisma	Rock oyster	1	0.01%
Tresus capax	Horse clam	1	0.01%
Totals		**135915**	**100%**

House 5

Taxa (Mammals)	Common name	NISP	%NISP (mammals)
Callorhinus ursinus	Northern fur seal	2091	91.47%
Eumetopias jubata	Sea lion	55	2.41%
Enhydra lutris	Sea otter	38	1.66%
Phoca vitulina	Harbour seal	26	1.14%
Delphinidae	Porpoise	25	1.09%
Odocoileus hemionus	Mule deer	21	0.92%
Canis familiaris	Dog	12	0.52%
Megaptera novaeangliae	Humpback whale	6	0.26%
Balaenopteridae	Whale	6	0.26%
Lutra canadensis	River otter	2	0.09%
Cervus canadensis	Elk	2	0.09%
Ursus americanus	Black bear	1	0.04%
Eubalaena sieboldii	Gray whale	1	0.04%
Totals		**2286**	**100%**

Taxa (Shellfish)	Common name	NISP	%NISP (shellfish)
Littorina sitkana	Sitka periwinkle	4076	35.38%
Mytilus californianus	California mussel	2368	20.55%
Mytilus sp.	Mussel	2140	18.57%
Saxidomus giganteus	Butter clam	575	4.99%

Taxa (Shellfish)	Common name	NISP	%NISP (shellfish)
Protothaca staminea	Littleneck clam	501	4.35%
Mopalia muscosa	Mossy chiton	327	2.84%
Mytilus edulis	Blue mussel	306	2.66%
Katharina tunicata	Black leather chiton	170	1.48%
Acmaea pelta	Ridge limpet	124	1.08%
Searlesia dira	Dire whelk	87	0.76%
Strongylocentrotidae	Urchin	87	0.76%
Acmaea t. scutum	Plate limpet	85	0.74%
Cryptochiton stelleri	Giant chiton	85	0.74%
Acmaea persona	Mask limpet	68	0.59%
Thais lamellosa	Frilled dogwinkle	56	0.49%
Mopalia lignosa	Woody chiton	53	0.46%
Lacuna variegated	Northern chink shell	51	0.44%
Octopus dofleini	Octopus	48	0.42%
Thais emarginata	Emarginate dogwinkle	46	0.40%
Acmaea mitra	Nootka cap limpet	38	0.33%
Mitella polymerus	Barnacle	38	0.33%
Mopalia sp.	Chitons	34	0.30%
Veneridae	Venus clam	26	0.23%
Tresus sp.	Clam	23	0.20%
Acmaea sp.	Limpet	20	0.17%
Modiolus modiolus	Horse mussel	13	0.11%
Diodara aspera	Rough keyhole limpet	11	0.10%
Thais sp.	Dogwinkle	11	0.10%
Strongylocentrotus drobachiensis	Green sea urchin	10	0.09%
Thais lima	File dogwinkle	9	0.08%
Astraea gibberosa	Red turban shell (opercula)	8	0.07%
Littorina planaxis	Flat periwinkle	6	0.05%
Pecten caurinus	Weathervane scallop	4	0.03%
Hinnites multirugosus	Northern abalone	3	0.03%
Macoma sp.	Macoma clam	3	0.03%
Pododesmus macroshisma	Rock oyster	3	0.03%
Clinocardium nuttalli	Pacific basket cockle	2	0.02%
Opalia wroblewskii	Wrobleski's wentletrap	2	0.02%
Thais canaliculata	Channeled dogwinkle	2	0.02%
Macoma nasuta	Bent-nose clam	1	0.01%
Modiolus rectus	Horse mussel	1	0.01%
Totals		**11521**	**100%**

Appendix 3: Sample Designs Applied to Ozette

Note: Each ☐ represents a single 50cm X 50cm unit.

House 1

10% random trial 1:
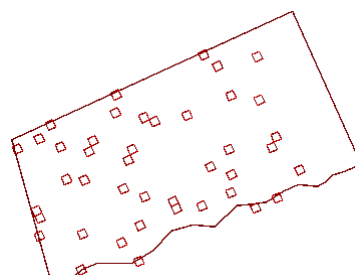
10% random trial 2:

10% random trial 3:

5% random trial 1:

5% random trial 2:

5% random trial 3:

1% random trial 1:

1% random trial 2:

1% random trial 3:

McNichol Creek Strategy:

0.1% Systematic Auger Strategy:

Dionisio Point Strategy:

5% Systematic Strategy:

(~6%) Stratified Systematic Strategy:
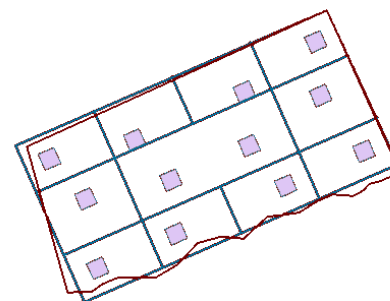
Huu_7ii Strategy:

House 2

10% random trial 1:
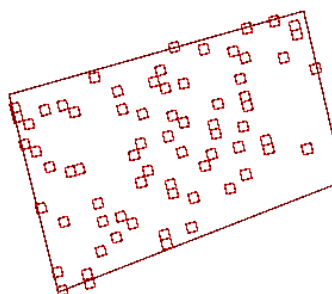
10% random trial 2:
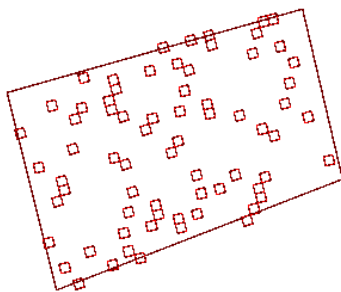
5% random trial 3:
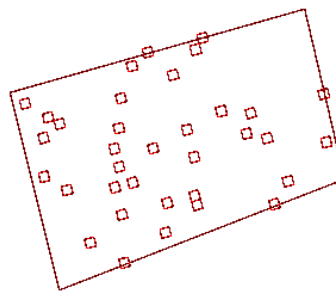
10% random trial 3:
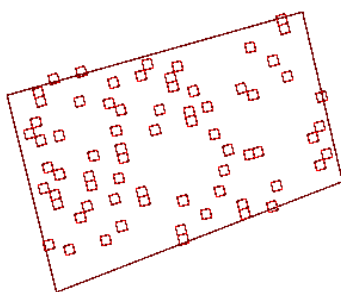

1% random trial 1:
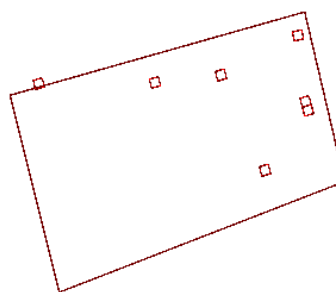
5% random trial 1:
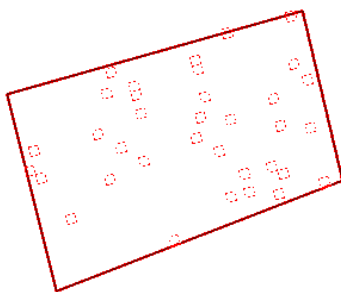

1% random trial 2:
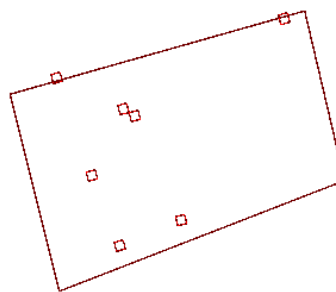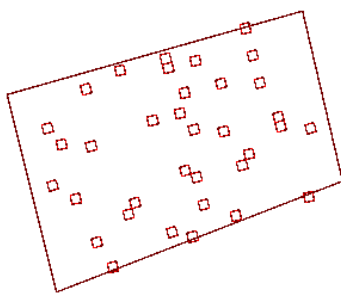
5% random trial 2:
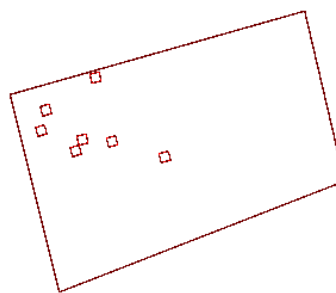
1% random trial 3:

0.1% Systematic auger strategy:

5% Systematic strategy:

Huu<u>7</u>ii strategy:

McNichol Creek Strategy:
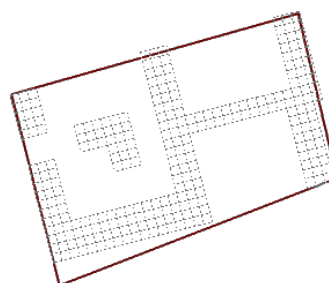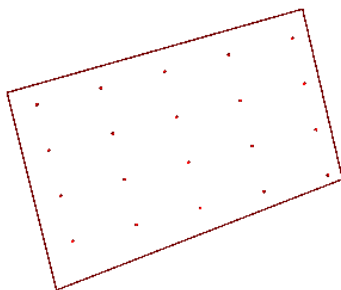
Dionisio Point Strategy:

House 5

10% random trial 1:
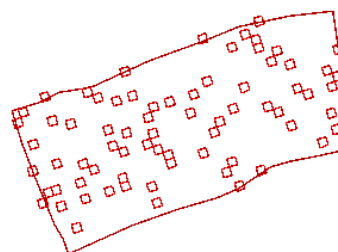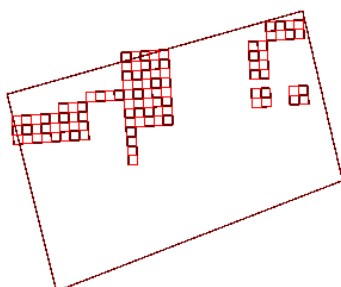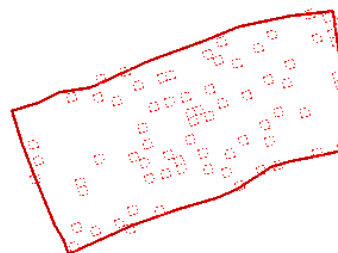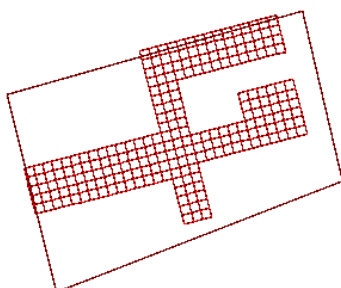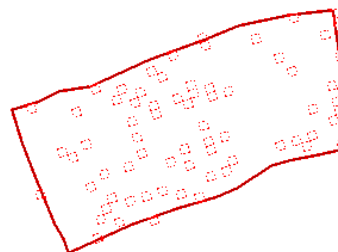
10% random trial 2:

10% random trial 3:
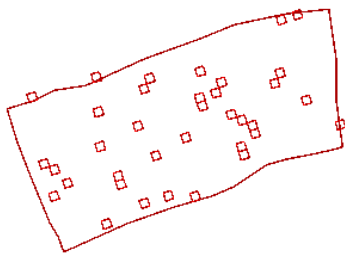
5% random trial 1:
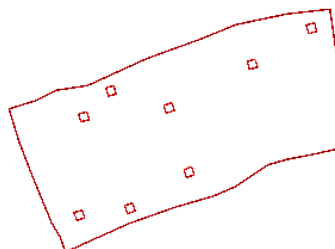
1% random trial 2:
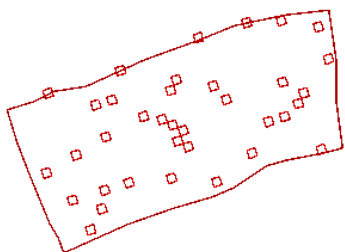
5% random trial 2:
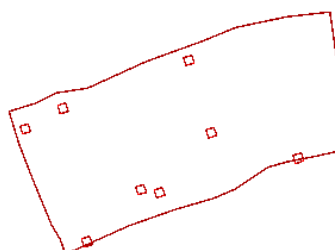
1% random trial 3:

5% random trial 3:
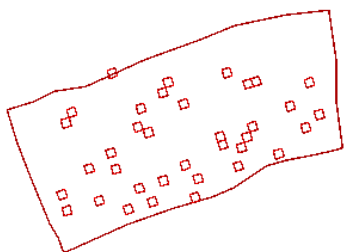
0.1% Systematic Auger Strategy:
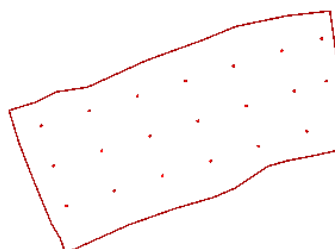
1% random trial 1:
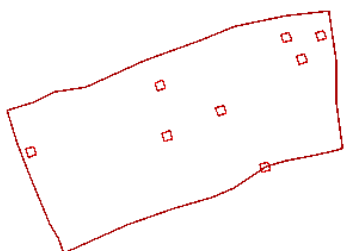
5% Systematic Strategy:
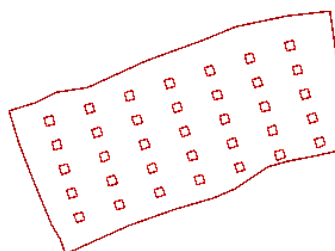
Huu_7ii Strategy:
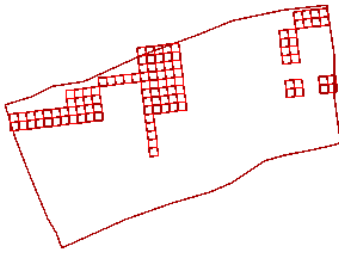
Dionisio Point Strategy:
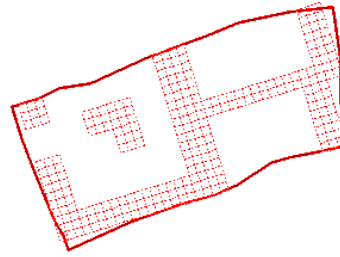
McNichol Creek Strategy:
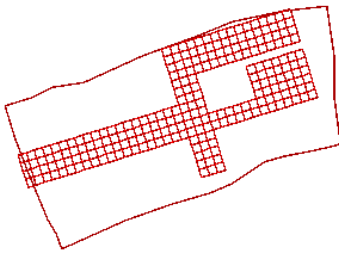
Appendix 4: NISP Values for Samples

Note: "RT" refers to "random trial"

House 1

House 1 Fish Samples

Taxa	100%	Dionisio	McNichol	Huuȥii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Lingcod	2089	788	675	300	228	291	219	145	117	131	121	23	17	28
Salmon sp.	1039	372	540	79	93	125	150	64	49	40	63	7	7	8
Rockfish sp	1007	400	274	209	116	128	96	57	59	58	53	11	6	5
Halibut	924	391	318	111	83	119	100	43	47	50	50	11	11	22
Scuplin	822	367	276	124	82	89	84	46	36	28	45	10	6	11
Greenling sp.	681	198	264	99	59	97	93	40	42	36	38	14	2	2
Surfperches	325	144	74	53	29	46	40	18	32	16	21	9	1	4
Cabezon	200	78	85	23	15	25	26	10	12	7	20	3	5	0
Flatfish spp.	140	26	26	45	10	18	17	9	12	10	7	1	0	0
Dogfish	52	30	14	7	6	8	8	5	4	4	3	0	0	1
Herring	50	5	38	6	10	6	11	2	7	0	1	5	0	2
Skate sp.	35	13	14	6	5	5	5	3	3	2	0	0	1	2
Pacific tomcod	33	9	18	0	3	4	5	2	0	2	6	0	0	0
Wolf eel	13	9	1	1	1	0	2	0	1	0	0	1	0	0
Pacific cod	10	3	4	0	1	0	2	0	0	0	0	0	0	0
Totals	7420	2833	2621	1063	741	961	858	444	421	384	428	95	56	85

House 1 Mammal Samples

Taxa	100%	Dionisio	McNichol	Huuȥii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Northern Fur Seal	6328	2868	2086	749	529	696	648	316	274	267	353	85	72	62
Dog	394	207	9	103	44	41	31	12	9	43	4	2	0	1
Porpoise	164	60	40	23	18	20	16	6	4	4	3	3	1	7
Sea lion	159	74	37	7	5	18	17	6	14	5	11	3	1	1

Taxa	100%	Dionisio	McNichol	Huuẕii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Whale	147	54	34	29	20	16	7	6	10	10	17	2	0	2
Mule deer	78	40	16	2	5	10	6	3	6	5	4	3	2	0
Sea otter	60	39	14	11	1	6	4	4	2	2	5	1	0	0
Harbour seal	32	15	10	3	4	5	1	1	1	4	1	0	1	1
Humpback whale	20	7	9	1	2	2	2	2	2	1	0	1	0	0
Gray whale	13	4	5	3	0	4	0	0	6	2	1	0	0	0
River otter	5	1	1	0	1	2	0	0	0	0	0	0	0	0
Elk	4	3	2	1	0	1	1	0	0	0	0	0	0	0
Marten	3	3	0	1	0	0	0	0	0	0	0	0	0	0
Raccoon	2	2	0	1	0	2	0	0	0	0	0	0	0	0
Beaver	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Totals	7410	3377	2264	934	629	823	733	356	328	343	399	100	77	74

House 1 Shellfish Samples

Taxa	100%	Dionisio	McNichol	Huuẕii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
California mussel	10022	3717	2783	2108	1057	1111	944	490	538	583	478	65	74	153
Sitka periwinkle	7652	3200	2423	993	554	724	942	312	397	405	328	47	42	60
Littleneck clam	4636	1620	1158	995	533	574	378	260	258	250	221	74	46	61
Mussel	3651	1150	1157	722	420	391	294	172	174	252	195	45	41	56
Blue mussel	1879	663	541	446	218	214	139	77	81	113	87	24	16	35
Butter clam	1177	483	315	276	131	150	101	59	47	68	49	5	13	11
Black leather chiton	848	242	184	147	106	106	74	27	42	65	42	2	12	35
Clam	484	179	139	85	54	45	49	18	23	38	20	3	3	5
Plate limpet	383	129	107	69	42	42	47	23	20	25	19	2	2	7
Frilled dogwinkle	375	161	95	73	50	49	28	18	20	31	20	0	3	5
Dentalia	266	2	4	102	7	42	38	26	43	17	18	0	0	0
Limpet	239	44	70	46	25	32	26	7	10	14	15	4	1	4
Giant chiton	225	56	60	41	24	27	14	10	9	17	19	4	2	6

Taxa	100%	Dionisio	McNichol	Huu7ii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Ridge limpet	196	54	64	31	22	18	21	10	9	12	12	1	3	2
Dire whelk	145	44	70	26	14	11	15	5	8	7	6	6	2	0
Stationary gooseneck barnacle	120	49	47	26	10	16	12	6	6	3	10	3	1	0
Urchin	104	58	23	23	4	8	10	4	5	1	4	0	0	0
Northern chink shell	104	40	44	18	10	13	13	3	4	2	6	1	0	3
Mossy chiton	99	40	21	23	10	11	10	2	3	7	9	0	1	5
Nootka cap limpet	87	38	30	12	9	17	10	0	8	2	4	0	2	1
Bent-nose clam	83	28	17	30	11	11	0	5	3	3	3	2	0	2
Red turban shell (opercula)	79	65	12	3	4	3	6	0	0	0	2	0	1	0
Chitons	73	35	10	16	8	12	3	1	4	4	1	0	1	1
File dogwinkle	69	25	33	9	9	8	7	0	5	3	3	0	1	1
Emarginate dogwinkle	66	18	35	5	6	10	10	1	1	3	1	0	1	0
Purple olive shell	44	21	16	10	3	6	5	1	1	4	2	0	0	1
Venus clam	40	8	18	3	3	1	4	0	2	1	0	0	0	0
Black turban shell	30	9	11	7	3	3	2	2	3	5	1	0	0	0
White sand clam	26	5	8	7	2	4	1	2	1	3	2	0	0	1
Pacific razor clam	24	9	6	0	1	2	4	2	5	1	1	0	0	0
Pacific basket cockle	20	0	11	2	2	2	4	2	1	0	3	1	0	0
Rough keyhole limpet	20	8	3	4	2	3	3	0	2	2	1	0	0	1
Green sea urchin	19	5	12	2	3	3	2	2	1	2	1	0	0	1
Dogwinkle	18	10	12	0	3	3	4	0	0	1	2	0	0	0
Red rock crab	18	2	14	2	0	0	1	1	1	2	1	0	0	0
Northern abalone	17	2	1	1	4	2	3	0	1	0	0	0	1	1
Blue top shell	16	0	8	1	6	1	3	0	2	1	1	2	0	0
Icelandic scallop	16	0	5	0	6	0	4	0	0	5	1	0	0	2
Flat hoof shell	15	9	4	2	1	2	1	3	1	1	0	0	0	0
Octopus	13	9	9	5	3	2	3	1	0	1	2	0	0	0
Mask limpet	13	3	2	3	0	0	0	2	3	2	1	0	0	0
Horse clam	11	5	4	1	2	1	1	1	1	0	0	0	0	1
Periwinkle	10	3	5	1	1	1	1	0	2	0	0	0	0	0
Polluted macoma	9	1	1	2	2	0	1	0	0	2	0	0	0	0
Weathervane scallop	8	0	2	2	1	1	1	0	0	0	0	2	0	0

Taxa	100%	Dionisio	McNichol	Huuꞥii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Channeled dogwinkle	8	3	5	0	1	0	1	0	0	0	0	0	0	1
Bodega clam	8	3	2	0	1	0	0	0	0	0	0	0	0	0
Oregon triton	6	3	0	0	0	0	1	0	1	0	1	0	0	0
Tellin clam	5	4	0	1	0	0	0	0	0	0	0	0	0	0
Not listed	5	2	2	1	0	1	0	0	0	1	1	0	0	2
Flat periwinkle	5	1	1	0	0	1	0	1	0	0	0	1	0	0
Hooked slipped shell	4	2	1	0	0	1	0	0	0	0	0	0	0	0
Horse clam	3	2	0	1	2	0	0	0	0	1	0	0	0	0
Purple-hinged rock scallop	3	3	0	0	0	0	0	0	1	1	1	0	0	0
Rock oyster	3	1	1	2	0	0	0	0	0	0	0	0	0	0
Bittersweet / Ark shell	3	2	3	3	0	0	0	0	0	1	0	0	0	0
Piddocke clam	3	1	0	1	0	0	0	0	0	0	0	0	0	0
Arctic moon snail	2	0	2	0	0	0	0	0	0	0	0	0	0	0
Wrobleski's wentletrap	2	2	0	2	1	0	0	0	0	0	0	0	0	0
Checkered periwinkle	2	0	0	1	1	0	1	0	0	0	0	0	0	0
Pacific spear scallop	1	0	1	0	0	1	0	0	0	0	0	0	0	0
Instable limpet	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Woody Chiton	1	1	0	0	0	0	0	0	0	0	0	0	0	0
White slipper shell	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Finger limpet	1	0	0	0	0	1	0	0	0	0	0	0	0	0
Totals	33516	12279	9614	6392	3392	3687	3242	1556	1747	1962	1594	294	269	464

House 1 Stratified Systematic Sample

Fish	NISP fish	Mammalian Taxa	NISP Mammals	Shellfish	NISP
Lingcod	110	Northern Fur Seal	457	California Mussel	833
Rockfish	82	Dog	30	Sitka Periwinkle	390
Salmon	62	Sea lion	13	Littleneck clam	284
Sculpin	55	Porpoise	7	Mussel	266
Halibut	47	Sea otter	7	Blue mussel	145
Greenling	35	Habour seal	5	Black leather chiton	100
Surfperches	30	Whale	4	Butter clam	90
Cabezon	14	Marten	1	Frilled dogwinkle	45

Herring	7	Deer		1	Tresus clams	36
Skate	4				Plate limpet	25
Wolf-eel	3				Limpet	19
Dogfish	2				Ridge limpet	11
					Giant chiton	10
					Stationary gooseneck barnacle	10
					Dire whelk	7
					Nootka cap limpet	6
					Mossy chiton	6
					Urchin	5
					Chitons	5
					Bent-nose clam	4
					Purple olive shell	4
					File dogwinkle	4
					Red turban shell (opercula)	3
					Black turban shell	3
					Rough keyhole limpet	2
					Flat hoof shell	2
					Checkered periwinkle	2
					White sand clam	2
					Venus clam	1
					Periwinkle	1
					Tellin clam	1
					Dogwinkle	1
					Bittersweet/ Ark shell	1
					Flat periwinkle	1
					Polluted macoma	1
					Octopus	1
					Pacific razor clam	1
					Channelled dogwinkle	1
					Emarginate dogwinkle	1
					Horse clam	1

Totals	451		525			2331

House 2
House 2 Fish Samples

Taxa	100%	Dionisio	McNichol	Huu_7_ii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Lingcod	10935	3407	666	4539	1107	943	960	537	491	584	572	61	43	121
Rockfish	7424	1913	467	2513	833	684	613	333	256	479	323	51	22	80
Greenling sp.	6428	2404	889	3023	776	574	711	376	422	278	308	53	63	48
Salmon sp.	3884	1628	405	1857	477	377	435	221	228	219	218	18	21	63
Sculpin	3063	984	333	1167	408	334	302	145	126	215	145	31	12	16
Cabezon	2964	1162	211	1298	329	279	279	191	158	137	178	17	15	42
Halibut	2513	856	119	620	252	241	203	93	96	168	109	13	24	27
Surfperches	2121	768	294	1072	255	189	257	127	143	86	108	17	19	12
Dogfish	923	255	28	153	117	100	67	44	25	69	26	1	3	8
Flatfish	140	16	6	19	17	18	5	4	4	15	1	1	0	1
Herring	69	36	5	58	4	4	67	6	3	4	3	0	0	0
Skate sp.	65	9	6	24	6	4	5	5	5	2	1	0	0	0
Pacific cod	23	2	2	5	2	4	0	1	0	2	1	0	0	0
Wolf-eel	19	12	0	4	1	3	0	1	0	2	0	0	0	2
Pacific tomcod	13	2	2	9	2	2	1	3	2	0	0	0	0	0
Petrale sole	2	0	0	2	0	1	0	0	0	0	0	0	0	0
Bluefin Tuna	1	0	0	1	0	0	0	0	0	0	0	0	0	0
Totals	40587	13454	3433	16364	4586	3757	3905	2087	1959	2260	1993	263	222	420

House 2 Mammal Samples

Taxa	100%	Dionisio	McNichol	Huu_7_ii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Northern fur seal	12497	4752	3784	878	1411	1220	1154	671	358	741	575	105	53	169
Porpoise	327	121	85	13	35	1	1	14	12	20	15	3	0	4
Sea lion	312	118	72	16	2	27	28	13	6	14	14	0	0	3
Dog	188	38	26	4	8	7	25	12	13	8	16	0	0	1
Sea otter	145	70	37	9	3	10	15	7	9	7	4	1	1	2

Taxa	100%	Dionisio	McNichol	Huuẕii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Mule deer	120	46	36	0	4	8	9	9	7	5	3	0	0	0
Whale	95	42	21	6	13	5	39	7	5	5	4	0	1	0
Harbour seal	70	23	26	10	2	3	5	2	3	5	0	0	0	0
Skunk	44	3	0	0	6	36	0	0	0	4	0	0	0	0
Humpback whale	21	9	3	0	6	3	2	0	1	1	1	2	0	1
Gray whale	16	7	5	0	28	0	0	2	1	3	0	0	0	0
Black bear	10	4	1	2	2	2	2	0	0	0	0	0	0	2
Mouse	4	2	3	1	1	7	5	0	0	1	0	0	0	0
Marten	3	3	1	0	3	0	0	0	0	0	1	0	0	0
River otter	3	1	2	0	2	0	0	0	0	0	0	0	0	0
Beaver	3	2	2	0	0	0	1	1	0	2	0	0	0	0
Squirrel	2	0	0	2	0	0	1	0	0	0	1	0	0	0
Elk	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Fin whale	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Totals	13862	5241	4104	941	1527	1329	1287	738	415	816	634	111	55	182

House 2 Shellfish Samples

Taxa	100%	Dionisio	McNichol	Huuẕii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Sitka periwinkle	1	0	1	0	1	0	0	0	0	0	0	0	0	0
California mussel	1	0	1	0	0	0	0	0	1	1	0	0	0	0
Littleneck clam	2	1	0	2	0	0	0	0	0	0	0	0	0	0
Mussel	3	1	1	0	1	0	0	1	0	0	0	0	0	0
Black leather chiton	3	1	3	0	2	0	0	0	0	0	0	0	0	0
Blue mussel	4	2	2	0	0	0	0	1	2	0	0	0	0	0
Mossy chiton	5	3	1	0	1	0	1	1	1	0	0	0	0	0
Butter clam	5	0	4	0	1	0	0	0	0	0	0	0	0	0

Taxa	100%	Dionisio	McNichol	Huuẕii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Giant chiton	7	0	3	0	1	0	0	0	0	0	0	0	0	0
Chitons	8	2	7	0	1	0	0	0	1	1	0	0	0	0
Plate limpet	10	5	5	5	3	1	1	0	0	1	1	0	0	0
Ridge limpet	11	7	9	2	1	0	1	1	1	0	0	0	0	0
Frilled dogwinkle	12	5	8	1	0	0	1	1	0	6	0	0	0	0
Limpet	16	9	5	3	2	1	1	0	0	1	0	1	0	0
Dire whelk	17	4	2	9	0	1	3	1	1	0	3	0	0	0
Urchin	20	2	11	5	0	3	2	1	0	0	2	0	0	0
File dogwinkle	20	9	11	3	2	2	4	0	3	3	0	1	0	1
Clam	24	9	8	8	8	3	4	2	1	3	3	0	1	0
Woody chiton	25	8	7	2	4	2	3	0	1	1	3	0	1	1
Northern chink shell	30	6	2	4	5	4	2	1	1	2	0	2	0	0
Venus clam	33	14	11	0	4	5	1	1	0	1	4	0	0	0
Urchin	35	11	5	2	3	2	2	1	0	2	2	0	0	0
Emarginate dogwinkle	36	12	19	8	7	3	3	1	1	1	2	0	1	0
Mask limpet	39	22	20	4	3	0	2	4	1	2	1	0	0	0
Black turban shell	42	20	8	3	7	7	4	1	1	4	1	1	0	1
Nootka cap limpet	42	22	36	4	5	4	2	2	0	2	3	4	0	0
Stationary gooseneck barnacle	43	15	19	2	6	0	1	3	2	4	2	2	0	0
Dogwinkle	45	18	14	10	5	3	4	4	7	0	2	0	0	0
Flat periwinkle	47	10	11	28	7	2	5	2	0	1	2	3	0	0
Channeled dogwinkle	51	14	14	20	6	4	8	3	2	0	3	3	0	2
Tellin clam	59	27	54	2	9	4	3	4	3	1	1	2	0	0
Octopus	71	28	51	5	7	11	8	9	6	1	5	1	0	0
Bent-nose clam	87	33	26	22	7	5	18	6	4	4	2	1	0	1
Periwinkle	90	32	31	26	10	6	9	5	5	6	7	4	0	0
Finger limpet	116	32	86	9	21	13	19	6	11	6	7	0	0	0
Blue top shell	116	46	65	14	10	16	19	8	2	2	9	2	1	0
Pacific basket cockle	156	81	51	45	15	17	15	8	9	3	8	6	1	1
Rough keyhole limpet	161	74	60	23	17	12	20	7	9	9	11	3	0	1

Taxa	100%	Dionisio	McNichol	Huu7ii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Flat hoof shell	175	52	67	22	26	15	12	5	11	9	8	3	0	4
Weathervane scallop	201	102	98	27	19	16	19	12	3	15	4	9	1	0
Purple olive shell	304	145	178	17	36	28	31	11	21	16	25	3	0	2
Pacific spear scallop	308	106	125	50	47	40	19	15	10	11	10	1	8	6
Purple hinged rock scallop	334	130	132	86	41	26	53	16	20	14	28	6	1	4
Checkered periwinkle	356	164	120	112	53	25	52	14	14	15	23	16	1	1
Red turban shell (opercula)	366	177	138	29	31	37	47	20	35	29	17	5	2	4
Bodega clam	466	143	186	68	52	27	68	24	20	6	27	7	1	5
White sand clam	595	246	224	75	62	54	68	43	36	34	28	10	2	7
Red rock crab	852	284	522	117	133	76	109	38	52	30	58	1	0	15
Northern Abalone	888	369	486	133	116	71	108	42	70	45	70	5	5	9
Scappelum columbiaum	1005	409	239	272	104	123	105	55	58	40	62	27	0	42
Polluted macoma	1055	422	429	64	125	99	102	57	31	57	78	9	1	12
Wrobleski's wentletrap	1577	550	748	224	207	188	152	84	87	63	64	8	12	9
Pacific razor clam	1692	767	808	112	183	143	168	99	62	87	97	25	2	31
Horse clam	3040	1369	1765	211	317	268	348	183	171	177	190	37	2	46
Hinds scallop	3048	1368	1765	247	398	283	403	193	354	206	202	11	0	24
Bittersweet / Ark shell	3385	1387	2640	462	511	290	428	207	261	56	274	35	3	32
Hooked slipped shell	3491	1420	1319	452	443	305	426	160	160	173	209	73	4	28
Channeled dog whelk	3818	1623	2394	460	528	293	580	252	361	136	280	32	2	23
Icelandic scallop	5158	2336	2644	706	492	573	683	260	274	296	307	80	23	51
White slipper shell	9667	4012	6131	1235	1278	868	1204	580	779	344	676	109	9	93
Dentalia	11097	4514	4644	1703	1343	980	1206	537	574	571	534	213	80	87
Oregon triton	12601	5725	5069	1885	1580	1117	1543	629	655	537	752	308	23	115
Rock oyster	29641	12722	12658	5545	3561	2905	3660	1367	1290	1464	1788	708	75	217
Horse clam	39290	16553	17267	5110	4736	3568	4672	2017	2673	1779	2055	384	184	410
Totals	135903	57680	63468	19695	16604	12549	16432	7005	8158	6278	7950	2161	446	1285

House 5

House 5 Mammal Samples

Taxa	100%	Dionisio	McNichol	Huu7ii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Northern fur seal	2091	1008	457	246	219	177	244	109	89	112	111	8	31	21
Sea lion	55	29	10	5	8	4	6	4	2	0	1	0	0	1
Sea otter	38	21	18	6	3	5	6	2	2	2	1	0	1	0
Harbour seal	26	17	2	2	7	5	2	3	2	2	2	0	1	0
Porpoise	25	13	3	3	3	3	3	2	1	4	3	0	0	0
Mule deer	21	12	3	1	2	1	8	0	1	4	2	0	0	0
Dog	12	4	3	3	0	0	2	1	0	0	0	0	0	0
Humpback whale	6	4	1	4	0	2	2	0	0	3	0	0	0	0
Whale	6	1	1	0	0	0	1	0	0	1	0	0	0	0
River otter	2	2	0	0	0	0	0	0	1	0	0	0	0	0
Elk	2	0	2	0	0	0	0	0	0	0		0	0	0
Black bear	1	1	0	0	0	0	0	0	0	0	0	0	0	0
Gray whale	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Totals	**2287**	**1112**	**500**	**270**	**242**	**197**	**274**	**121**	**98**	**128**	**120**	**8**	**33**	**22**

House 5 Shellfish Samples

Taxa	100%	Dionisio	McNichol	Huu7ii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Sitka periwinkle	4076	1950	1456	202	514	278	301	319	157	206	288	12	94	50
California mussel	2368	1129	902	213	287	200	176	157	153	158	177	25	30	23
Mussel	2140	774	1370	304	368	273	218	155	127	61	192	6	9	21
Butter clam	575	202	363	70	96	62	52	31	35	8	49	2	7	6
Littleneck clam	501	235	160	37	56	23	24	42	18	27	30	3	11	2
Mossy chiton	327	154	142	24	64	41	12	30	14	14	30	1	6	6
Blue mussel	306	185	88	32	26	18	24	31	10	22	25	0	3	1
Black leather chiton	170	72	62	6	16	6	12	10	7	13	12	2	2	1
Ridge limpet	124	72	43	15	9	6	10	14	6	11	26	0	0	1
Dire whelk	87	45	34	2	9	6	9	9	3	2	12	0	6	1
Urchin	87	57	12	2	4	3	6	6	1	3	8	0	2	0
Plate limpet	85	41	29	13	5	8	1	5	4	7	15	0	0	0
Giant chiton	85	52	55	0	12	9	15	3	3	2	5	0	1	3
Mask limpet	68	14	22	0	12	6	2	4	2	4	2	0	0	1
Frilled dogwinkle	56	29	21	3	3	4	1	7	5	4	5	0	0	0

Taxa	100%	Dionisio	McNichol	Huu7ii	10% RT 1	10% RT 2	10% RT 3	5% Syst.	5% RT 1	5% RT 2	5% RT 3	1% RT 1	1% RT 2	1% RT 3
Woody Chiton	53	26	29	0	5	7	6	2	3	1	3	0	0	0
Northern chink shell	51	32	11	6	6	4	4	7	1	2	5	1	0	0
Octopus	48	20	10	7	5	12	4	1	1	1	0	1	0	1
Emarginate dogwinkle	46	32	20	7	8	1	4	5	3	5	4	0	0	0
Nootka cap limpet	38	25	17	7	0	0	1	3	5	1	5	0	0	0
Barnacle	38	18	15	3	6	3	7	6	3	3	3	0	0	2
Chitons	34	18	9	0	5	1	2	2	0	1	2	0	1	1
Venus clams	26	15	10	2	3	2	3	3	1	0	2	0	3	0
Clam	23	10	4	3	2	3	5	0	0	1	0	1	0	0
Limpet	20	12	10	2	3	2	1	0	2	1	0	0	0	1
Horse mussel	13	3	10	3	2	3	1	0	2	0	3	0	0	0
Rough keyhole limpet	11	4	5	3	2	2	1	0	1	0	1	0	2	1
Dogwinkle	11	5	6	0	1	0	0	1	0	0	0	0	0	0
Green sea urchin	10	4	1	1	0	0	1	1	0	0	0	0	1	0
File dogwinkle	9	3	1	0	0	1	2	1	0	0	1	0	0	0
Red turban shell (opercula)	8	5	2	1	0	0	1	0	1	0	0	0	0	0
Flat periwinkle	6	3	0	0	0	0	0	2	0	0	0	0	1	0
Weathervane scallop	4	3	1	2	1	1	0	0	0	0	0	0	0	0
Northern abalone	3	2	1	0	1	0	0	0	0	0	0	0	1	0
Macoma clam	3	1	2	0	1	0	0	0	1	0	0	0	0	0
Rock oyster	3	2	2	0	0	1	1	0	1	0	0	0	0	0
Pacific basket cockle	2	1	0	1	0	0	0	0	0	0	0	0	0	0
Wrobleski's wentletrap	2	0	1	0	0	0	1	0	0	0	0	0	0	0
Channeled dogwinkle	2	0	1	0	1	2	0	0	0	1	0	0	0	0
Bent-nose clam	1	1	1	0	0	0	0	0	0	0	0	0	0	0
Horse mussel	1	1	0	0	0	0	0	0	0	0	1	0	0	0
Totals	**11521**	**5257**	**4928**	**971**	**1533**	**988**	**908**	**857**	**570**	**559**	**906**	**54**	**180**	**122**