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**RETHINKING ESTABLISHED METHODOLOGY IN
MICROMAMMAL TAPHONOMY:
ARCHAEOLOGICAL CASE STUDIES FROM ORKNEY,
UK (4TH MILLENNIUM BC – 15TH CENTURY AD)**

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School of History, Classics and Archaeology

University of Edinburgh

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In the loving memory of my grandfather,

Andrzej Józef Antoni Dyzmański

22.08.1937 – 18.04.2021

DECLARATION OF OWN WORK

I declare that this thesis has been composed solely by myself and that it has not been submitted, in whole or in part, in any previous application for a degree. Except where stated otherwise by reference or acknowledgment, the work presented is entirely my own.

Andrzej Aleksander Romaniuk; 2.07.2021

ABSTRACT

Micromammals (e.g. rodents, shrews), characterised by their small size, short lifespan and high reproduction rate, are known for rapid adaptability to changing conditions, inhabiting all environments besides the most frigid. They form a variety of relationships with other animals as well as humans, from being prey up to mutualism, commensalism and even taming and domestication. Changes occurring short or long-term within micromammal populations can be a useful proxy for natural as well as human-induced changes. However, their remains from archaeological contexts have seldom been investigated, with a scarcity of methodological studies and incomparability of published data often discouraging research.

Human impact on the environment is especially noticeable in the case of insular environments where humans are responsible for the majority of species introductions. This thesis examines a series of case studies from the Orkney islands off north-east Scotland to develop a micromammal zooarchaeological methodology and investigate the micromammal relationships with predators and human activity in this context. Specifically it has two main aims: 1) perform methodological research on obtained data to investigate established methods as well as to suggest new approaches to data analysis given what data are retrievable from studied assemblages; 2) apply the revised methodology to investigate a range of Orcadian sites, covering two main time periods of intensification of maritime contacts: Neolithic (4000 – 2000 BC) and Norse/mediaeval (600 – 1500 AD) ages. Analysis standardisation and reproducibility through coding in R is also introduced to deal with the large breath of obtained data.

The study provides conclusive results, broadening the understanding of micromammal taphonomy and a range of different assemblages and deposition patterns present within and around anthropic contexts. The breath of utilizable data retrievable from micromammal assemblages is comparable with typical zooarchaeological research on the remains of bigger species, for example including information on age of death or non-predatory taphonomic factors. Spatial and contextual data, particularly, proves to be crucial for understanding the impact of dispersal and burial processes on micromammal accumulations. Moreover, the necessity for consistent sieving is confirmed, lower effort sampling or sieving regimes failing to provide representative and comparable samples. The obtained data can be effectively analysed through statistical methods, including classifying algorithms, bypassing problems encountered in the case of multiple comparisons and deposition patterns. However, the results

also show that actualistic research may not be directly comparable with archaeological material without considering non-predatory taphonomic factors and their impact on data representativeness.

Assemblages identified within the studied sites seem to be formed by a variety of factors. Identifiable predatory depositions could be attributed to both owls and diurnal raptors, taxa expected to be found considering modern Orkney fauna and dominant micromammal predators. Cases of non-predatory depositions included deaths of commensal species living and/or nesting within the anthropic environment, self-entrapment in anthropic features such as trenches or pits of single individuals and secondary accumulation in similar features due to dispersal. In general, each site shows multiple different patterns being present, with certain areas or context types (e.g. open/enclosed, natural/usage period/abandonment) exhibiting a predominance of a specific deposition. Intrusiveness is surprisingly rare and, where identified, is characterised by multiple intrusive species within the contexts, with singular species intrusiveness rarely being noted. Some evidence for human interaction with micromammals, direct or indirect, can be noted through additional taphonomic marks such as burning. However, a definitive interpretation of these marks, as of now, cannot be achieved.

LAY SUMMARY

The term “micromammal” refers to very small mammals, such as rodents or shrews. Those species are characterised by a short lifespan, high reproduction rate and high adaptability to changing conditions. Currently micromammals can be found inhabiting the majority of known environments, and form a variety of relationships with other species, including humans. Changes happening within the micromammal populations can be a useful proxy for natural as well as human-induced changes. However, micromammal remains from archaeological contexts have been rarely investigated, with multiple unresolved issues discouraging research.

Human impact on island environments is especially visible, in particular in a form of new species introductions. This thesis examines several archaeological sites from the Orkney islands off north-east Scotland. The research starts from checking the applicability of research methods to the archaeological micromammal material. The methods assessed are primarily ones used in micromammal research on contemporary micromammal remains. However, additional methods common in zooarchaeology are also tested to broaden the possible amount of retrievable information. Following method assessment and validation, the thesis applies these methods to investigate the selected archaeological sites in detail. The sites themselves represent two major periods of Orcadian history, Neolithic and Norse/Mediaeval, both known for the rapid development of human settlements and frequent maritime contacts.

The study provides new information about methods, data and the sites themselves. The amount of data possible to retrieve from archaeological micromammal remains is comparable with typical zooarchaeological research on the remains of bigger species. Spatial and contextual information proved to be of importance when assessing whether remains were scattered over a wider area, remained in the original deposition place or were affected by a transition from the surface to underground. The necessity for consistent sieving of archaeological sites was revealed, with lower effort leading to a significant loss of information. Various statistical methods seem to be working with the obtained data, facilitating comparisons between multiple deposition patterns. The results also show the difference between modern and past micromammal depositions, stemming from processes happening after assemblage creation.

Accumulations of micromammal remains found within the studied sites are a result of a variety of processes. Some of them can be traced to the activity of both owls and diurnal raptors, taxa which currently inhabit Orkney and are the dominant micromammal predators. However, non-

predatory depositions are also present. They are mainly connected to species living next to or nesting within human habitation, being a result of their natural death or accidental self-entrapment. In general, each site showed multiple different patterns being present, with certain areas exhibiting a predominance of a specific deposition. Remains accumulated due to burrowing are surprisingly rare, easy to differentiate from original contexts due to the presence of multiple species introduced to Orkney in later times. Some evidence for human activity could be noted, especially in the form of burn marks, however such finds still lack definitive interpretation.

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1. INTRODUCTION

1.1. RATIONALE BEHIND THE STUDY

The term “micromammal” commonly refers to very small mammals, including rodents, shrews as well as smaller representatives of hedgehogs and lagomorphs. Such animals are usually characterized by a short life span combined with a high turnover rate, resulting in rapid adaptability to different environmental conditions and a tendency towards invasive colonization of new habitats (Stahl 2016, Escudé et al. 2013, Belmaker 2018). Due to their characteristics, micromammals are known to inhabit all terrestrial environments besides coldest ones, such as arctic polar deserts, and consist of the overwhelming majority of all mammals, both in terms of the number of recorded species as well as overall population size (see Wilson & Reeder eds. 2005, 185-529 & 745-752). They can also form a wide range of different relationships with other species and their environment, from being a source of food for predators up to mutual relationships with other species as well as commensal relationships with humans. Being a significant part of the environment biomass, their population dynamics can affect said environment in a number of ways, both positive (e.g. encourage new species to settle, help in biomatter circulation) as well as negative (e.g. causing extinctions by taking already occupied niches). Considering their population dynamics, it is not surprising that a significant part of mammal remains found in natural (Chaline & Mein 1979; Andrews 1990; Kusmer 1990) as well as cultural (Brothwell & Jones 1978; Stahl 1996) deposits often belong to these species.

What prompted researchers to investigate micromammals in detail in the case of the Orkney archipelago was the predominantly anthropogenic nature of Orcadian flora and fauna. It was progressively amassed during the long history of the isles, from first Mesolithic settlers and early Neolithic farmers, through the period of Roman influence, ending on Norse and later Scottish rule (Bullard 1975; Berry 1985, 48-86; Berry 2000: 49-79). Orcadian archaeological sites have been thoroughly sieved or sampled since the 1970s, providing ample materials for further study. The majority of research has concentrated on establishing the origin of micromammal species and the exact date of their introduction to the isles. Results provided strong evidence for multiple introductions during maritime trade intensification periods, with parent populations being found not only in the British Isles but also in Western and Northern Europe (e.g. Corbet 1979; Haynes et al. 2003; Nicholson 2005 & 2007; Martínková et al. 2013).

While providing promising results, research questions more related to zooarchaeology so far have been only briefly investigated. The author's earlier study on Skara Brae micromammal assemblage (Romaniuk & Herman 2016; Romaniuk et al. 2016a;b) shed new light on the spectrum of possible relationships between human and rodent populations. It appeared that Orkney voles might have been intentionally gathered by Neolithic dwellers of Skara Brae and deposited alongside household refuse. The reasons behind this were not fully clear, with food processing and pest control being considered as most likely. The former idea could lead to a solid argument for deliberate human transportation of small animal populations to more remote and isolated regions of the British Isles (Haynes 2003; Martínková 2013), while the latter could stem more from the accidental introduction.

Studies on micromammal assemblages within zooarchaeology remain rare due to multiple issues hindering any research attempt. The most discussed issues are a combination of problematic retrieval and handling of microvertebrate remains, requiring high-effort and systematic sieving and sampling regime (Stahl 1996). Beyond that, micromammal assemblages may consist of multiple species with very similar skeletal and dental morphology. This frequently results in any identification attempt requiring a wide reference collection and/or experienced researcher. As many archaeological excavations are usually restricted in terms of financial backing, time or even storage, micromammal and microvertebrate finds are often excluded from the archaeological investigation if no contextual evidence points towards their importance.

A lack of an established methodological framework specific for archaeological assemblages is also a contributing, if less discussed, issue. Micromammal remains have been intensively studied by quaternary researchers for over half of a century, mostly due to being considered a great proxy for past environmental conditions (e.g. Chaline 1972, Avery 1982a;b) or specific predatory activity (e.g. Andrews & Evans 1983; Andrews 1990). Methodology of micromammal taphonomy has been developing for the most time with research aims and questions specific to biological, especially paleoenvironmental, sciences in mind. The material studied included predominantly natural contexts, especially cave fills, and comparative data coming from modern predatory assemblages or regional zoological studies. As the aforementioned proxy research dominated the subject, studying past populations dynamics (e.g. mortality profiles; population health through pathological finds) has rarely been done. As a result, many elements of the wider taphonomic and osteological field, especially connected to non-predatory factors, have not yet been evaluated for micromammal remains. It is a problem

especially in a setting where human activity might be a biasing factor. While micromammal taphonomy methods have been proven applicable on a technical level to archaeological assemblages (e.g. Weissbrod 2005; Fernández et al. 2009; 2011) such attempts required either further contextual explanation or additional taphonomic research to broaden discussable taphonomic processes with ones often encountered in zooarchaeology (e.g. the impact of dispersal and secondary accumulation, see Weissbrod 2005). The necessity of additional effort being put in methodological studies leads to research not being taken beyond the identification of species or by being handed over to strictly paleoenvironmental or genetic research.

Considering the visible need for wide methodological research on such finds, the author saw a possibility for a larger PhD project on Orkney micromammal archaeological finds. Open access to a number of assemblages from the Orkney isles, successful implementation of current methodology to Skara Brae material and taxonomic diversity related to human activity make proper foundations for the methodological assessment of established methods to archaeological material. Moreover, it would also be possible to assess the applicability of methods more prevalent in zooarchaeology, thus creating a choice better suited for archaeological investigations. Once done, the revalued methodology could be finally applied to the archaeological material itself, hopefully providing better and more accurate answers than micromammal taphonomy previously could. Contextually, the analysis of several sites will definitely provide more details on possible micromammal assemblages that may be encountered within anthropic and mixed contexts as well as possible differences between species across wider periods of time and space.

1.2. RESEARCH AIMS, OBJECTIVES AND QUESTIONS

Two key aims have been identified for this thesis:

- To evaluate, adapt and broaden micromammal methodology to better suit archaeologically retrieved data (**Aim 1**)
- To provide detailed and critical analysis on Orcadian archaeological micromammal material with updated methodology (**Aim 2**)

These aims will be achieved by following eight objectives:

- Review of the current methodology related to micromammal taphonomy in palaeoecology and archaeology (**Objective 1**).
- Selection of a number of sampled or sieved archaeological micromammal assemblages from throughout the Orkney archipelago for analysis (**Objective 2**). The selection should represent main periods of species introduction (Neolithic/Iron Age/Norse/mediaeval) as well as different but comparable (implementation of sieving) retrieval patterns used in archaeology.
- Creation of a reference base for the comparative analysis between known studies and archaeological material as well as broader methodological research (**Objective 3**).
- Investigation of the applicability of established micromammal methodology to Orkney archaeological assemblages using statistical analysis (**Objective 4**)
- Broadening the selection of utilized methods by applying elements of statistical reasoning and by adding ones that obtain data more suitable for zooarchaeological research (**Objective 5**)
- Depending on the outcome of previous points, revaluation of the choice of methods applicable to archaeological, especially Orcadian, sites (**Objective 6**)
- Investigation of the Orkney assemblages (**Objective 7**)
- Discussion of obtained information, with stress put on contextual ramifications of established methodology and different retrieval methods (**Objective 8**)

Chosen aims and objectives in turn can relate to specific research questions:

- How developed is micromammal taphonomy and archaeology and what areas remain omitted or under-researched? (**Research Question 1**)

- Can the application of statistical testing and classification help in the archaeological interpretation of micromammal finds? (**Research Question 2**)
- Can reconstructing mortality profiles and investigating pathological changes help in analysing short-lived micromammal populations? (**Research Question 3**)
- How do different retrieval methods impact obtained datasets? (**Research Question 4**)
- Do different taphonomic factors create similar patterns, or can one factor create multiple patterns over time? (**Research Question 5**)
- Are there any noticeable differences in micromammal accumulations between studied sites and/or between specific time periods? (**Research Question 6**).
- Can differences identified between micromammal assemblages retrieved across chosen sites be attributed to specific factors? (**Research Question 7**).
- How do micromammal assemblages form within different anthropic contexts? (**Research Question 8**)
- How does micromammal data correlate to previous research on Orcadian microfauna? (**Research Question 9**)

1.3. THESIS LAYOUT

Introductory chapters (Literature Review, Materials and Methods) explain the study research background, the current state of methodology (**Objective 1**) as well as materials and methods chosen (including **Objectives 2** and **3**). In the latter case a distinction was made between methods used for methodological evaluation (**Aim 1**) and later sites assessment (**Aim 2**). It is further seen in a division of analysis section into two separate case studies. The first case study (Chapter 4) is methodological, concerned with assessing the utility of the generated data as well as employed or created methods, thus addressing **Objectives 4, 5** and **6**. The second case study (Chapter 5), on the other hand, is a traditional site-based analysis but with the methodological framework refined by the previous case study (**Objective 6**), addressing **Objective 7**. A joint discussion of both case studies follows, with stress being put on **Objective 8**.

The literature review (Chapter 2) is divided into two main sections, with an introduction briefly describing the current state of international micromammal research in archaeology. The first section includes detailed information on the origin and meaning of the term “micromammal” and elaborates on the reasons for studying palaeoecological and archaeological material, the main issues related to performing micromammal research, and the currently utilized methods (**Objective 1**). In contrast, the second part focuses exclusively on the Orcadian natural history and micromammal fauna of the region, alongside any meaningful studies performed on them or their remains relevant to this research. The summary will answer **Research Question 1**.

The methodology chapter (Chapter 3) contains information vital to both case studies. The first section includes basic data on sites chosen for this research (**Objective 2**), with stress being put on methods utilized during the retrieval of micromammal remains. The second section discussed the choice of methods to be applied to the micromammal material as well as obtained references (**Objective 3**) for the sake of data collection for both case studies. The third part, in turn, concentrates exclusively on the methodological investigation in the first case study, including the utilization of the results in sites assessment in a second case study. The summary will briefly discuss key points of each of three sections.

The methodological case study (Chapter 4) contains its own analysis section and a short methodology revaluation, directly related to the analysis results. The analysis section is divided into several parts, each concerned with a different issue, including data distribution and variation, pattern-seeking through correlation and machine learning, sample representativeness

in relation to retrieval methods, exploring the impact of dispersal, evaluating age estimation methods, ending on investigating metric and pathological data (**Objective 4 and 5**). An additional section was dedicated to reevaluating methodology for Case Study 2 in the light of Case Study 1 results (**Objective 6**).

The sites assessment case study (Chapter 5) is fully dedicated to **Objective 7**. Analysis was modelled to discuss each site separately. Data from each site was further divided into specific methods and data, starting from general NISP/MNI/completeness distribution on each site, mortality profiles, NISP related ratios (skeletal frequencies and relative abundances), fragmentation patterns, taphonomic marks (digestion and burning) and results of classification methods.

The final chapter (Chapter 6) concentrates on a joint discussion, additionally reframing findings of both case studies in a broader perspective of archaeological science. Such an approach will help fulfilling the last objective (**Objective 8**) and deliver final answers to **Research Questions 2 - 9**. The discussion is divided into two parts. First part concentrates on the methodological aspect of analysis, predominantly on Case Study 1 and relevant results from Case Study 2. In turn, the second part focuses on sites interpretation, with each site discussed separately, similarly to case study II. The conclusions chapter (Chapter 7) summarises all the key points of the thesis as well as provides a broader outline of further research possibilities.

Due to various different naming conventions in taphonomy, zooarchaeology and palaeoecology, the author tried to follow that established by Peter Andrews (Andrews 1990). It is the most common used in micromammal taphonomy, with only minor differences from mainstream zooarchaeology (for example, using “talus” instead of “astragalus”).

All figures in this thesis were created by the author if not stated otherwise.

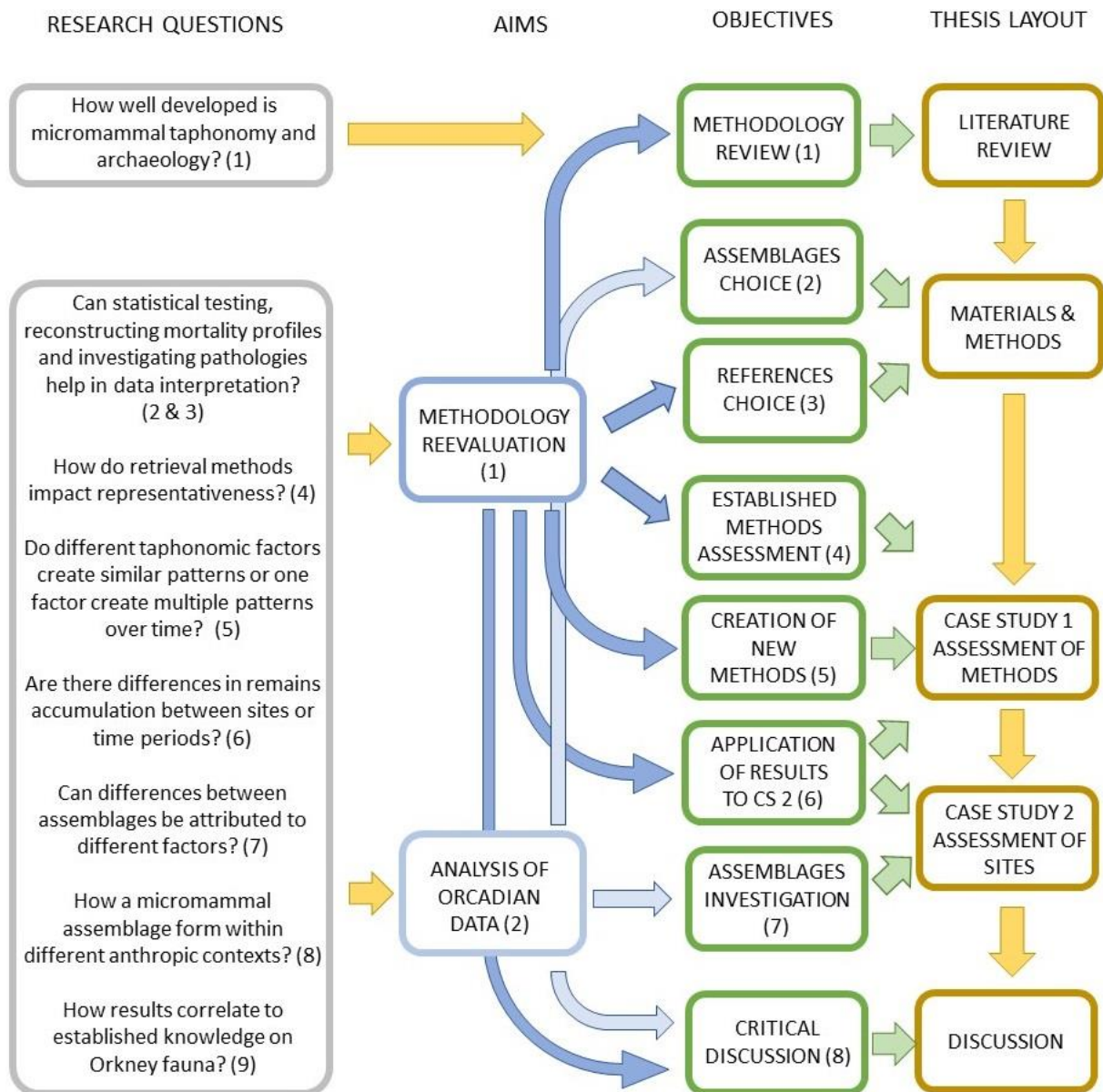


Fig. 1.01 – Graph summarising the relationship between aims, objectives and main chapters of the thesis, with research questions listed.

2. LITERATURE REVIEW

2.1. INTRODUCTION

This review was designed and written to achieve two main goals. One is, simply, to provide as comprehensive review as possible given the obvious gap in the available literature, overall or about specific details, about micromammal archaeology and palaeoecology (**Research Question 1**). Alongside this goal, the natural environment of Orkney and all micromammal species will also be discussed to embed the research in a location-specific context. The second goal is to provide reference material and discuss the methodology that might be of relevance to this research. It will be vital to later identify where new methods can be applied and what has to be investigated in the methodological part of this study (**Aim 1** and **Objective 1**).

In order to achieve those goals, this review will firstly cover relevant terminology and reasons behind studying micromammal finds. Once those points are covered the review will proceed with existing methodology connected to retrieval, handling and studying such remains, ending on a review of Orkney micromammal fauna. Terminology is rarely discussed despite its apparent relation to methodology and different approaches between archaeology and other sciences. The reasons and methods covered will include most vital elements from the perspective of archaeology and related sciences, with some brief discussions from the perspective of general zooarchaeology practice. For the sake of clarity, all key points of this chapter, including references that are going to be used later in the research, are going to be shown in the chapter summary.

2.2. MICROMAMMALS IN ARCHAEOLOGY AND PALAEOECOLOGY

2.2.1. PRIMARY SOURCES

The discipline of micromammal zooarchaeology still lacks a proper, up-to-date and comprehensive literature review. While some publications can be used as reference sources (e.g. Stahl 1996) and handbooks (e.g. Andrews 1990) these are usually several decades old. Only some specific elements of methodology have been summarised in recent publications (e.g. dental wear in Belmaker 2018), sometimes pooled with and presented alongside similar methodological results taken from bigger and/or non-mammal species (e.g. taphonomy in Fernández-Jalvo & Andrews 2016). It is a problem as the reliability of some methods has been put into doubt (e.g. Saavedra & Simonetti 1998; Matthews 2002) while a number of revised (e.g. Fernández et al. 2017) or new (e.g. Lyman et al. 2001) methods have become available. Lack of published reviews is further deepened by the fact, that till today many innovative or otherwise interesting methodological studies, as well as case studies containing comparable data, are hard to find without a great deal of time spent on a literature search due to being published in regional journals, obscure for international reader. Even if archaeologists become involved in micromammal research single case studies are mostly published, with long-term projects, for example of Weissbrod and his team (2005-2013), being a rarity.

Thankfully, in the past two decades the situation has changed for the better. Especially in recent years one can observe a sudden surge in publications about micromammals, either from archaeological contexts or natural sites comparable to the former (e.g. Hawkins et al. 2017; Weissbrod et al. 2017a;b; Luna et al. 2017). Research on small animal remains, also including amphibians and reptiles, is slowly becoming a distinct part of zooarchaeology, with its own methodology and set of objectives. It is especially visible by relatively recent creation of a dedicated working group, called Microvertebrate Working Group, by the International Council for Zooarchaeology (ICAZ- MVWG; see *Microvertebrate Working Group* 2016).

2.2.2. TERM MEANING IN ZOOARCHAEOLOGY

In sciences interested in past and present animal populations and their interactions in specific ecological conditions, it is commonplace to divide species into groups depending on their overall size, especially in the case of mammal species. Such division is a justifiable one due to the physiological (McNab 1990) and behavioural (Eisenberg 1990) impact of size on population dynamics and later taphonomic history (Behrensmeyer et al. 1979; Retallack 1988; more in Lyman 1994a) as well as differences in retrieving and handling remains (e.g. standards described in O'Connor 2000; microvertebrate methods in Andrews 1990; Stahl 1996). However, precise boundaries between size classes as well as the level of their importance to the research are usually an outcome of a methodology internal to a specific science. In zoology, several division lines for mammals have been suggested. Most common is a 5kg living weight threshold for differentiating big and small animals (Boulière 1975), often utilized by scholars from sciences beyond biology (e.g. zooarchaeology: Brothwell & Jones 1978; parasitology: Morand et al. 2006).

In the case of zooarchaeology however such division more often than not is based instead on a line between already studied and known domesticates and big game species and lesser-known, smaller species neglected in earlier studies due to technical reasons and/or lack of relevant knowledge (Brothwell & Jones 1978; some remarks in Glyn 1981). “Micro” species separation from other established animal categories correlates to a degree with their small frame but its roots are actually in a different methodological approach to such finds rather than in preestablished, rigid size categories. For example, the term “microvertebrate”, frequently utilized in palaeontology, was invented to denote fossilized remains of small animals which need specific methods of retrieval and analysis to be applied to be successfully studied (Hibbard 1949). With paleoecological and palaeological studies frequently utilizing archaeological material (e.g. Kretzoi & Vertes 1965) it has also become popular in zooarchaeology (Stahl 1996), arguably for similar reasons. However, this term includes species of different biological patterns, possibly requiring different analytical methods, thus being somewhat problematic to properly utilize on a methodological level of the research.

A more specialized and easier to define term is “micromammal”, often utilized by quaternary and related sciences. Micromammals encompass almost exclusively rodents, former insectivores and smaller lagomorphs (Grodzinski & Wunder 1975; Morand et al. 2006). The majority of those mammals share similar biology, with short lifespan, high reproduction rate,

tendency towards burrowing or arboreal lifestyle and nocturnal life, being a prey species to larger predators and prone to establishing commensal-like relations with humans (Hulme-Beaman et al. 2016). There are several weight thresholds suggested for this category (e.g. up to 300g in Grodzinski & Wunder 1975). However, the most widely used is up to 1kg of a living weight. It is due to the majority of rodent and insectivore species do not exceed that size (Morand et al. 2006, 5 Fig. 2). Thanks to distinct biological and morphological traits the methodology between sciences revolving around studying micromammal populations and remains seems relatively similar and, even if interested in different sets of data, to some degree comparable with each other.

Micromammal research can also include bats or compare results to bat-related research (e.g. Morand et al. 2006), but it is debatable whether bats can be considered as micromammals. Similar to Rodentia, order Chiroptera represents a large portion of mammalian biodiversity (Wilson & Reeder eds. 2005 312-524), inhabiting the majority of known environments. In terms of size majority of bat species do not exceed 1kg, qualifying to be included as a micromammal (Morand et al. 2006, 5 Fig. 2). However, beyond ecological importance and general size, their biology is more similar to bigger species, especially when considering long lifespan and related factors (Wilkinson & South 2002). Due to that, even if retrieval and handling methods are roughly similar, analytical approach and results interpretation might differ, in a manner already noted for the microvertebrates.

2.2.3. REASONS TO STUDY MICROMAMMALS

PALEOECOLOGY

In quaternary sciences, micromammal remains are considered as excellent indicators of short and long-term regional climate changes as well as floral and faunal composition. It is due to a short period between the factor occurrence and the subsequent adaptation of micromammal populations (Chaline 1972; Chaline & Mein 1979; Cano et al. 2013; Comay & Dayan 2018a). Most of the early research relied on analysis of taxonomic abundance and the known actualistic studies on the relationship between particular species with their habitat, which in turn provided information about past vegetation and climate (e.g. Avery 1982a, 1982b, 1988; Andrews 1990, 165-177; Reed 2003). Later methods, on the other hand, concentrated on morphometric analysis of micromammal teeth and mandibles, especially vole molars, to notice a correlation in

morphological change with the environment (Escudé et al. 2013, Cucchi et al. 2014). Due to the same factors that enabled paleoenvironment reconstruction methods of chronological dating that utilized species sequencing (e.g. Mein 1989) and later arvicolid teeth morphology were developed (e.g. Martínez et al. 2013). However, their exact accuracy is currently considered debatable (see Martin 2014).

As one of the points of zooarchaeology is to analyse past ecological systems in which humans dwelled it is not surprising that archaeological finds have been studied by quaternary scientists or their methodology has been incorporated in zooarchaeological divagations. It is especially visible in the case of Palaeolithic sites from Europe (e.g. Bennàsar et al. 2016; Carbonell et al. 2008; Belmaker et al. 2016; Luzi et al. 2016; Rey-Rodríguez et al. 2016; López-García et al. 2015 & 2017), Africa (Avery 1982A and B; Stoetzel 2013; Reynard et al. 2016) or Americas (Benton 1999; Teta et al. 2005; López et al. 2016) where assemblages made by hominid activity often mix with natural depositions or predatory remains over a long period of time. Palaeoenvironmental data from micromammals can also be analysed with information obtained from bigger species (Maridet & Costeur 2010; Berto et al. 2016) or palynological studies (van Dam & Utescher 2016) to obtain better results. With the deeper knowledge of human-micromammal relationships not only information about the past environment for a specific period can be assessed to a studied hominid population but also information about possible ecological changes during their presence in the region can be provided (see e.g. Bañuls-Cardona et al. 2017; Weissbrod & Zaidner 2013; Weissbrod et al. 2005 to 2017). Such data can be later utilized in discussion about the environmental impact on human subsistence patterns (e.g. Hillestad-Nel & Henshilwood 2016). Even chronological species sequencing can be to some degree informative – appearance and extinction of various rodent taxa have been utilized as a means to approximate a relative chronological order of hominid appearance and dispersal through Europe (genus *Miomys* and *Arvicola*: Cohen et al. 2012). Recent research also suggests that carbon isotope analysis of modern populations truthfully resembles current environmental conditions (Leichliter et al. 2016) – such information can be of use for studies on the past. However, in Europe archaeological features younger than the Early Bronze Age (e.g. Bañuls-Cardona & López-García 2016) are rarely being integrated into a palaeoenvironmental reconstruction.

Another substantial part of the palaeoecological research is identifying the depositor, especially avian predators or carnivores. Most small animals usually end as prey to bigger species and their remains end up accumulated together in a specific assemblage. Natural death happens

rarely (Andrews 1990, 2-4; Stahl 1996) and can be an indicator of a unique, usually secondary accumulation event (e.g. Tomassini et al. 2017). Owl pellets have already been utilized in palaeoreconstruction (e.g. Davis 1959; unique example on modern material in Love et al. 2000) for some time and with additional research, combined with the analysis of carnivore assemblages and scats (e.g. Andrews & Evans 1983; Montalvo et al. 2012) a methodology of studying such contexts has been established (Andrews 1990). By being able to detect a particular animal deposition one may also identify a predator that may otherwise be physically absent from the assemblage record (e.g. Barn owls, Williams 2001). Avian deposition in archaeological features may be present due to sharing a similar environment to humans (e.g. Hillestad-Nel & Henshilwood 2016; Williams 2001) and should be expected in cases of periods of human absence from the site (Smith et al. 2016). On the other hand, when the pattern of accumulation does not match such criteria, it may be considered as evidence of other factors being involved in accumulation, including fluvial transport of remains or flooding of hibernating animals in their burrows (Tomassini et al. 2017).

MIGRATIONS

Micromammals can also form complex bonds with humans and their environment, from typical commensalism (living nearby humans and taking advantage of the food stored by them) to edificarian (living within human structures but scavenging on their own) or environmental synanthropism (living within a man-made environment, such as crop fields and pastures) (O'Connor 2013, Fig. 57; Hulme-Beaman et al. 2016). Archaeological finds are often incorporated in studying the appearance, habitat change and dispersal of such species. It is especially well researched in relation to human migration. There are a number of modern and historical cases for human involvement in micromammal species dispersal (Long 2003, 45-60, 87-236), especially those considered as pests (e.g. Skokholm isle colonization by house mice: Berry 1964). That is also why data on micromammal finds are often included in major papers (e.g. O'Connor 1988A, 1992 & 2004; Last 2014), with stress being put on identifying commensal species, such as house mouse (*Mus musculus* or *Mus domesticus*, Berry 1991; Berry et al. 2008), brown rat (*Rattus norvegicus*, Taylor et al. 1991; Quy & Macdonald 2008) and black rat (*Rattus rattus*, Taylor 1991; Twig et al. 2008).

Most relevant to such archaeological investigations are studies on the house mouse, a well-known and widespread species of highly commensal rodents that originated in Southwestern

Asia (Suzuki et al. 2013). Contrary to rats, house mouse emergence as a species was from the beginning deeply rooted in ecological niches created by a slow shift in human populations towards a more sedentary lifestyle and subsequent creation of anthropogenically altered environments in the late Upper Palaeolithic (Weissbrod et al. 2017a). Especially archaeological sites containing their remains from the Natufian culture (C.A. 12 - 9 thousand years BC) are well-documented thanks to Weissbrod and colleagues (2005; 2013; 2017a;b). *Mus musculus* was widespread in Near Eastern urban sites in the second and first millennia BC (Weissbrod et al. 2012a; 2014). The nature of this unique self-domestication is still debated (strict parasitism in Dekel et al. 2017 vs commensalism in Weissbrod et al. 2017b), but from this point onwards one can see a slow dispersal of house mice from the Middle East in a number of directions, alongside human migrations (Auffray et al. 1990, O'Connor 2010; Suzuki et al. 2013). Their remains were found within cultural strata in Çatal Hüyük (Brothwell 1981, Jenkins 2012) as well as within Transcaucasian sites related to early farmers (Cucchi et al. 2013, more sites in Auffray et al. 1990, table 1). Cyprus, the first Mediterranean island colonised by house mice and a traditional hub for regional maritime trade, had a population established already in early Neolithic (C.A. 9 - 8 thousand years BC; Cucchi et al. 2002), with mitochondrial DNA providing evidence for multiple subsequent introduction events (García-Rodríguez et al. 2018). Unintentional human transportation of these species on ships, at least since Late Bronze Age, was archeologically confirmed. The investigation of a shipwreck of a Levantine origin, found on the shallows south to the modern Turkish city of Kas, Antalya province, retrieved remains of multiple house mice specimens ("the Uluburun shipwreck", more in Cucchi 2008). House mice colonization of the Western Mediterranean and North-Western Europe took however longer. Slow pace was most likely due to the region being underdeveloped in comparison to Eastern Mediterranean until the second half of first millennium BC (Cucchi et al. 2005; Cucchi & Vigne 2006; O'Connor 2010). House mice dispersal reached Great Britain around the first century BC, if not earlier (Bramwell et al. 1990; see Searle et al. 2009 Appendix 1), with stable populations established soon thereafter (e.g. York: O'Connor 1992 & 2004; Shetland isles: Nicholson et al. 2005; more in: O'Connor 2010). However, house mice were later reintroduced to the Northern and Western end of the British Isles due to Viking, supplanting the original house mice population alongside a new wave of human settlers (Searle et al. 2009; Jones et al. 2012 & 2013).

Apart from house mouse the dispersal of the black rat, a rodent species endemic to South Asia (McCormick 2003; Aplin et al. 2011), has been widely discussed in the past few decades

(Armitage et al. 1984; Armitage 1994). Although encounterable in the wild, black rats strongly prefer a human-altered environment (Harris et al. 1995; Taylor 1991; Twig et al. 2008). The earliest known black rat remains, from the early second millennium BC, were found within the archaeological site of Tell el-Dab'a, Egypt (Boessneck 1976, 34). Roughly similar dating, the middle of second millennium BC, was established for rat bones from the city of Isin, modern Iraq (Boessneck & Ziegler 1987). Signs of black rat presence were also found in Slovenia, dated to 1400 to 400 BC (Toškan & Kryštufek 2006). It reinforced the notion, that the introduction of black rats to an European part of the Mediterranean predated trade intensification during the Ptolemaic period (Armitage 1994) and suggests not a single but a number of such events. Eventually, black rats reached first century BC/AD France (Vigne & Femolant 1991) and Great Britain (as seen in excavations in York: Rackham 1979; O'Connor 1988A; although some may have come earlier, see Bramwell et al. 1990). Later centuries in Great Britain have seen fluctuations and possibly extinctions and reintroductions of this species (Reilly 2010), which highlights the importance of human agency in their survival. Local black rat populations in the UK are present until today, especially in urban areas (Harris et al. 1995).

An introduction of one species may result in the extinction of other animals, especially those in a similar ecological niche. Such indirect impact of humans on the environment has been especially well studied in insular environments, most notably Galapagos islands (Steadman & Ray 1982; Steadman et al. 1991) and other places through Oceania (Harris 2009). The Polynesian rat (*Rattus exulans*) and New Guinea spiny rat (*Rattus praetor*) have been introduced to most of the isles of Oceania with human migrations (Taylor 1982; Roberts 1991; White et al. 2000) and their remains can be found in strata dated to around sixth to fourth millennium BC onwards (e.g. Allen et al. 1989; Spriggs 1989). New Ireland forest Rat (*Rattus sanila*), native to New Ireland, became extinct shortly after first Polynesian rats and New Guinea spiny rats were introduced to their habitats (Flannery & Wicler 1990; Flannery 1995; Leavesley & Allen 1998). Interestingly, their dispersal, apart from osseous remains, was also noted by bite marks on fossilized seeds (Prebble & Wilmshurst 2009).

However, species traditionally considered as non-commensal can also disperse due to human actions, especially if there are no other species to compete with them within the anthropic environment. One of such finds were e.g. remains of Garden dormouse (*Eliomys quercinus*) found during excavations of York (O'Connor 1986; O'Connor 1988b) but a prominent example comes in the form of the isolated population of a common vole (*Microtus arvalis*, Gorman & Reynolds 2008) from Orkney. It will be covered in greater detail later in the paper.

HUMAN & ANIMAL INTERACTIONS

The interaction between humans and micromammals does not end with micromammals simply being moved from one place to another. Although the development of zooarchaeological studies on micromammals differs between regions, being most developed in Africa and the Americas, even in places such as China (Jin et al. 2012) we can lately see new publications emerging about possible human-micromammal relationships in the past.

One of the most obvious is pest control. It is an important issue today (Flint & van den Bosch 1981 *passim*) and was even more vital in the past (Flint & van den Bosch 1981, 51-81). Apart from taking advantage of stored food, rodents may also be vectors of a number of diseases dangerous for humans and other animals (e.g. black rats, McCormick 2003; more about zoonoses in: Acha & Szyfres 1989; Chomel 1992; Meerburg et al. 2009). Some species, for example a domestic cat (*Felis catus*), are believed to be domesticated primarily due to their role as rodent deterrent/catcher in early human agriculture societies. An isotope study on human and animal bones found in a farming village of Quanhucun (Shaanxi, China; 4th millennium BC, Hu et al. 2014) revealed human, cat and rat bones showing very similar values of both carbon and nitrogen isotopes. Interestingly, a recent study (Jenkins 2012) suggests that scats of animals predated on micromammals might have been directly put inside graves by inhabitants of Catal-Höyük, probably as means of a mortuary cult.

Micromammals might have been hunted, bread and eaten in the past, with a possible cultural significance related or not to that role (deFrance 2009). Lagomorphs, especially European rabbits (*Oryctolagus cuniculus*), have been frequently hunted in the past (e.g. Klein & Scott 1986; Hockett & Bicho 2000; Dias et al. 2016). Hunting usually intensified in times when bigger species were absent or temporarily unavailable (Stiner et al. 1999). They are featured in art from ancient times and are until today consumed in various parts of the world. However, rodents also play an important part in human subsistence and their inclusion in a diet can be traced both historically and archaeologically (Fiedler 1990; deFrance 2009; del Papa et al. 2009). For example, Mesolithic rock paintings from Bhimbetka and Jaora, India (Neumayer 1983, 12-28, 90 pl. 45, 91 pl. 46), reveal human activities revolving around hunting rodents (more in Sathe 2017). Various small mammal species might have been utilized by e.g. ancient Maya, including lagomorphs but also endemic opossum species (order *Didelphimorphia*), and played an important role in Mayan iconography (more: Fridberg 2015).

Micromammals are also easily tameable, what can be seen by majority of modern pets being micromammals. Apart from modern laboratory/domestic mice and rats also purely wild specimens can learn various commands. Latest example can be an African giant pouched rat, which has been trained to find landmines as well as diagnose tuberculosis (Poling et al. 2010). Historically, in Late Mediaeval Britain red squirrels were tamed to be used as companion pets (Walker-Meikle 2012).

African archaeological contexts provide the most diverse set of micromammal finds for both zooarchaeology and ethnoarchaeology alike. The earliest known sign of hominid predation on small mammals are cut marks found on a hedgehog's (*Erinaceus broomi*) mandible in Olduvai Gorge Bed-I (Fernández-Yalvo et al. 1999). Signs of micromammal remains can be found in many later archaeological contexts (e.g. Maggs & Ward 1980; Mazel 1989). Among such finds the prominent example is one of the South African burial sites, dated to about 2700 BP. Micromammal remains were found in the stomach-pelvic area of human burial and were identified as being most likely eaten by the deceased shortly before death (Jerardino et al. 1992). Later comparison with other sites, identified as a shell midden and dated to 2490 BP, provided additional information about possible human feeding behaviour on micromammals, most notably Striped field mouse (*Rhabdomys pumilio*) and a number of rat species (Dewar & Jerardino 2007). One of the micromammals endemic to South Africa is a Cape dune mole-rat (*Bathyergus suillus*) which is a common find in archaeological strata (e.g. Schweitzer 1979; Armstrong 2016; Klein & Cruz-Urbe 2016; Reynard et al. 2016), quite often commingled with big game species remains (Henshilwood et al. 2001). Both osteoarchaeological studies and modern ethnographic observations (Henshilwood 1997) points towards intentional human collection and consumption of those rodents. Due to that their remains are usually included in research on subsistence practices, even if other micromammals are excluded (Reynard & Henshilwood 2017). However, there is much ethnoarchaeological evidence for collecting and utilizing small mammal species (e.g. Fancher 2009) with a specific technology, especially by small cone-shaped traps or by hand (more in Lupo & Schmit 2005). A tendency towards small prey is visible especially in temporary camps (Hudson 1991) or in places with a reduced number of bigger or easily encounterable prey (Lupo et al. 2013). Additionally, occupation also seems to be a factor as hunters tend to create most taxonomically diverse refuse (Schmitt & Lupo 2008). The South African Hedgehog (*Atelerix frontalis*), also sometimes found in archaeological contexts (Henshilwood et al. 2001; Armstrong 2016), has recently been utilized as a food source by local populations (Smithers 1986 after Nicoll & Rathbun 1990). Similarly,

African Giant pouched rats (*Cricetomys* sp.) are until today hunted as a prey animal (Lupo & Schmit 2005) and a number of small insectivore species in Africa are currently facing the threat of extinction due to human actions from pest control and food hunt to fur trade (more in Nicoll & Rathbun 1990).

Southern America and Caribbean isles are a prime example of rodent utilization as a food source as well as a cultural impact of such action. The current consumption of a domesticated guinea pig (*Cavia porcellus*) especially bred for eating, called *Cuy*, is deeply rooted in tradition and social interaction of the region (deFrance 2006; deFrance 2009). Domesticated around the second millennium BC with local camelids it soon became widespread through the Andean region (Stahl 2003) and later on Caribbean islands (LeFebvre & deFrance 2014). While in South America *Cuy*, as a rare import, worked as a prestige symbol (Stah 2003) the later utilization on islands suggests a more utilitarian approach to them (LeFebvre & deFrance 2014). Rodents from cavy-like families inhabiting Caribbean islands such as various species of hutias (*Capromyidae*) and extinct *Isolobodon portoricensis* were utilized as a food for feasts until contact with Europeans, but declined with time (Deagan 2004). A number of Pre-Columbian sacrificial burials were found suggesting that Guinea Pigs were utilized as a sacrificial animal and possibly a divination accessory for a long time (Sandweiss & Wing 1997; Rofes 2000; Rofes & Wheeler 2003). Other species of rodents were also included in human subsistence. There has been a number of palaeoecological and archaeological studies concentrated on the lower Negro river valley sites and other Pampean regions from Holocene periods (Quintana et al. 2002; Prates 2008; Fernández et al. 2009; Fernández et al. 2011; Andrade & Fernández 2017). The main issue was the identification of depositors involved in accumulation of various assemblages as well as human activity traces. Some species, such as Brazilian marsh rat (*Holochilus brasiliensis*) and local *Cavia* species, were most likely utilized by humans (Quintana et al. 2002; Santiago 2004; Acosta & Pafundi 2005; Fernández et al. 2011). Two *Cavia* species remains (*Cavia aperea*, Brazilian guinea pig, and *Galea tixiensis*, currently extinct) were found with cut marks that were most likely made by lithic tools (Quintana et al. 2002). Burned bones of various rodent species were also found on archaeological sites from Central Chile (Simonetti & Cornejo 1991). Thermoalteration as well as cutmarks on bones of large rodent species (*M. coypus*, *L. maximus* & *H. hydrochaeris*) is well documented for this region (Escosteguy & Salemme 2012) which further reinforces these finds. Rodents have also been eaten in the past by North American tribes (e.g. Shaffer 1992; Falk & Semken 1990).

Uniquely, in this region human coprolite contents were studied to prove a connection between rodents and humans as a predatory-prey relationship (Reinhard et al. 2007).

Even in Europe and the Middle East archaeologists have encountered signs of sporadic inclusion of micromammals into human subsistence practices. For example, mole rat (*Spalax ehrenbergi*) was most likely utilized as a food source by Natufian foragers (Weissbrod et al. 2012B) while similar evidence from roughly the same time for a variety of micromammals was found on Mesolithic Corsica and Sardinia (Vigne & Balasse 2004). Red Squirrel (*Sciurus vulgaris*) was also mentioned as a potential human prey on the Iberian peninsula (Araújo et al. 2014). Interestingly, evidence from the Western Mediterranean suggests that rodents might have been utilized in periods when larger, more traditional prey was harder to find. The Sardinian example is especially interesting in this regard as it coincides with the human overhunting of currently extinct Sardinian pika (*Prolagus sardus*, small lagomorph of c. 0,5 kg: Moncunill-Solé et al. 2016; Dawson 2014). However, there is no evidence for the continuation of such activities in later periods. The Roman Empire provides us with the sporadic consumption of an edible dormouse (*Glis glis*), as a delicacy and a status symbol, by upper-class Roman families (Fiedler 1990; Brothwell & Brothwell 1969; e.g. passage in Apicius *De re coquinaria: Liber VIII – Tetrapus Quadripedia IX Glires*). However, most of what is known about that tradition come from texts rather than archaeological digs, with dormouse remains from cultural contexts usually considered as food refuse based on written record alone. Still, tradition of edible dormouse hunting from the wild exists in some remote places along the Dalmatian coast till today, with stress being put on obtaining fur and fat rather than edible meat (e.g. Slovenia: Peršič 1998).

As the inclusion of micromammals into subsistence has only recently become deeply studied which resulted in some previously established explanations being challenged – most notably “accidental” human introduction of micromammals in some areas of the World. Earlier studies considered human involvement in the dispersal of Polynesian rats through Oceania as unintended, with introduced species being stowaways (e.g. Kirch 1985, 291). However, newer studies on these species rules out such possibility due to both ethnographic reference and genetic studies suggesting intentional transportation (Matisoo-Smith 1994; Matisoo-Smith et al. 1998; Matisoo-Smith & Robins 2004). A similar pattern of dispersal may be observed in New Guinea Spiny Rat (White et al. 2000). Humans most likely transported those animals as an easily manageable source of meat (Matisoo-Smith 1994; Matisoo-Smith et al. 1998). Similar re-evaluation has also occurred in studies concerned with the previously mentioned Orkney

vole introduction to the Orkney isles. It was originally suggested that voles were accidentally introduced to the isles during the intensification of human maritime trade and migrations in Neolithic times (e.g. Corbet 1961). However, later studies put this idea into doubt, reasoning that in case of accidental introductions there should be evidence for repeated introductions as well as the presence of common vole populations along the coast of Mainland Britain (e.g. Thaw et al. 2004). The outcome of genetic and morphological studies excludes any later introduction, suggesting a single crossing of a genetically diverse population around 4000 BC and rapid adaptation with a subsequent long period of evolutionary stabilization, with only a single period of evolutionary response to new species being introduced to islands (Martínková et al. 2013; Cucchi et al. 2014). Moreover, among dozens of Orkney islands voles inhabit at most only ten of them, all connected to main hubs of human habitation (e.g. Mainland, Westray, Sanday, Rousay, South Ronaldsay, more in Berry 1985, 2000; Booth & Booth 1994, 2005). Considering their presence in abundance in archaeological rather than natural strata suggests intentional human or related species accumulations during the Neolithic (Romaniuk et al. 2016), a pattern so far only visible during this time period and, considering ongoing studies in National Museums of Scotland, disappearing with the transition to Bronze age in late 3rd millennium BC.

Pest control as such is not a well-researched topic in zooarchaeology. There is valid archaeological evidence for utilization of animals for pest control in ancient Egypt, with black rat remains found in stomach content of mummified birds as well as buried cats (von den Driessh & Boessneck 1983). However, until today studies on past pest control techniques are mostly loose interpretations of historical or archaeological finds, with the scope being shifted to other aspects of human life (e.g. religious significance in Mesopotamian prayers against pests: George et al. 2010). Only a few case studies on archaeological remains consider pest control as such (e.g. Jenkins 2012; Romaniuk et al. 2016). Still, due to commensalism rodent remains of some species can be utilized as a proxy for food-related human activities. Isotope studies so far successfully incorporated such information sources to gain additional insight into the human diet (e.g. Guiry & Gaulton 2016), establish a network of dependencies between species (e.g. rodents, cats and humans in Hu et al. 2014) and improve palaeoenvironmental reconstruction attempts (e.g. Swift et al. 2017). Unintentionally burned bones of rodent species have also been used as indicators of human-induced fires (Rhodes et al. 2016).

IMPACT ON OTHER SPECIES TAPHONOMY

Rodent activity may play an important role as a taphonomic process of other species' remains. The impact of rodent scavenging on human remains (Haglund et al. 1988; Haglund 1992; Kippel & Synstelien 2007; Gapert & Tsokos 2013; Pokines 2015) and in extension on animal bones (Pokines et al. 2016; Pokines et al. 2017) has been studied relatively recently by forensic anthropology (Haglund & Sorg eds. 1996, 405-414; Haglund & Sorg eds. 2001, 409-411). Incisal gnawing creates characteristic, long gnaw marks appearing in a set of two, that due to repeated gnawing can produce a specific pattern of very thin cuts (Haglund & Sorg eds. 1996, 406 Fig 1); molar gnawing is less specific but can also happen (Pokines 2015, fig. 5). The reason for gnawing can be connected to the need of providing constant attrition to ever-growing incisors as well as scavenging corpses for food (Haglund 1992; Haglund & Sorg eds. 1996, 405-406; Klippel & Synstelien 2007). Lack of gnawing in the case of periodically exposed remains may suggest short periods of exposure in a problematic environment (e.g. Mollerup et al. 2016). Burrowing rodents are also known for entering archaeological contexts, disturbing their content and accumulating additional material there. A good example are the Neanderthal burials from Shanidar IV, thought to showcase the earliest known treatment of buried by adding flowers to their graves (Solecki 1975). However, it seems more likely that Persian jirds, *Meriones persicus*, accumulated these flowers through frequent burrowing through the archaeological stratigraphy (Sommer 1999).

2.2.4. RESEARCH METHODS – RETRIEVAL AND HANDLING

Micromammal retrieval by hand excavation is heavily problematic due to their small size and sheer numbers of such finds in archaeological contexts, sometimes going up to tens of thousands of fragments (e.g. Romaniuk 2016A, see Fig. 2.01). That is why sieving of archaeological content as means to retrieve such finds has been widely discussed (Stahl 1996; e.g. Barker 1975; Ball & Bobrowsky 1987; Payne 1992; Shaffer 1992B; Shaffer & Sanchez 1994). Especially wet sieving of the whole content of a studied context is favoured if possible (Payne 1992; Stahl 1996). The mesh size is also crucial as the smaller the mesh the more osseous remains of small animals can be retrieved. While utilizing a smaller mesh size for larger animals produce diminishing results in the case of small ones results gradually rise – technically the mesh size should be as small as possible in order to properly represent all vertebrates and

thus prevent misrepresentation of the species importance to the site (figure 1 in Ball & Bobrowsky 1987, based on Thomas 1969). In studies interested in small finds there has been a change in mesh size utilized. For example, older samples from Great Britain were retrieved by utilizing 3, 2 and 1mm meshes (e.g. O'Connor 1988A), while more recent studies utilize as small as 300 micrometers (Jenkins 2012) for the majority of their samples.

However, the application of sieving on finer meshes increases the time needed to process a context, thus creating additional expenses (Ball & Bobrowsky 1987; Payne 1992). Consequently, arguments against using regular sieving and utilization of smaller mesh sizes have been raised if the situation does not require such methods. From the micromammal archaeology perspective this may create a false negative feedback loop. The lack of standardised approach would lead to less informative samples incomparable with each other, leading to the lack of significant results being used as an excuse to completely omit micromammals from archaeological consideration. Such a situation, in conjunction with other factors, has been noticed many times (Stahl 1996), from Canada (e.g. Semken & Falk 1991; Morlan 1994) to Oceania (Matisoo-Smith & Allen 2001), in places where such studies would be, at least potentially, beneficial.

There are various problems associated with on-site sampling and how this translates into recovered data. Micromammal taphonomy was developed to analyse micromammal assemblages retrieved in whole (Andrews 1990) but studies that encompass all studied contexts fully sieved (whole-earth approach, e.g. Skara Brae in Clarke 1976a, see Romaniuk 2016a) are so far extremely rare and usually restricted to Palaeolithic sites (e.g. Fernández-Yalvo & Avery 2015). More often only specific contexts are investigated partially or in full (e.g. Jenkins 2012), which is statistically similar to sampling for bigger species, predominantly domesticates or big game, in features of human origin (e.g. storage pits or hearth, see Reitz & Wing 2008: 117-152). Archaeology has adapted or developed a number of sophisticated approaches to sampling archaeological sites (see e.g. Orton 2000; for environmental archaeology see Reitz & Shackley 2012) but inconsistent sampling remains a huge issue, especially for zooarchaeology, biasing the results towards excavator's own, sometimes unrecorded, judgement rather than a quantifiable constant. Often micromammal research is an afterthought after sampling provides large quantities of their remains. Sometimes sampling may be adjusted to avoid redundancy (see e.g. shells in Mitchell et al. 2016) for very specific material types but may in turn negatively affect the retrieval of micromammal bones. The impact of different sampling regimes on the retrievability of specific data types, such as age distribution, is currently unknown. To retrieve

data about the micromammal connection to the wider ecosystem as well as possible human-animal interactions either a different, standardised approach must be adopted or differences between different sampling methods at least studied and understood.

Another issue is the fragility of small osseous finds. Studies on micromammal bone fragmentation and abrasion (Korth 1979; Andrews 1990; Fernández-Jalvo & Andrews 2003) suggests a high risk of *in situ* breakage, especially on the sieving stage of retrieval. However, apart from the acknowledgement (Stahl 1996) not much has been done to assess such bias. Additionally, while there have been studies on the impact of structural density of bones for some lagomorphs (Pavao & Stahl 1999) and bigger rodents such as marmots (Lyman et al. 1992) on taphonomic history and the correlation between density and survivorship in archaeological contexts, this has not yet been studied in smaller species of rodents or insectivores. However, as fragility is a factor that has to be considered it seems that studies should be performed on freshly excavated material to minimize movement that the sample has gone through before analysis and by that possible fragmentation bias. The issue is however that many micromammal samples are studied many decades after excavation, possibly undergoing additional fragmentation while being transported and stored in museum collections, which diminishes their reliability.

As micromammal remains are rarely studied on-site, relevant data have to be included either in the site report or delivered with the sample. One of such details is the evidence for or lack of burrowing within studied contexts and the possible identification of burrowing species that may intrude into the archaeological context. The common notion is that rodents are as such intrusive species and leave their own remains in contexts they burrow through. However, the notion is an oversimplification. Micromammal burrowing is a form of survival adaptation and the presence of their own bones in a context may only mean the failure of such strategy (Morlan 1994, Stahl 1996). Such failure does not happen often as even complex systems of rodent burrows rarely bear significant finds (e.g. only 23 fragments in Joeckel & Tucker 2014) or high densities (e.g. uniformly low density in Weissbrod & Zaidner 2013) if additional factors are not included. Such factors are e.g. flooding (Szafer 1957; Tomassini et al. 2017), intraspecific violence or hibernation failure (more in Morlan 1994 and Stahl 1996). Post-predation assemblages can also be intrusive if left by a burrowing predator (Shaffer 1992A; Morlan 1994). Single specimens can also enter contexts due to actions of other small scavenging animals (e.g. Milne & Milne 1976). Further contextual information worth mentioning is the presence or lack of dense layers of micromammal deposits in pit-like contexts. Open pits, both natural and man-

made, can trap a significant number of animals by accident or by luring them in due to their contents (more in Whyte 1988; 1991). Especially the latter creates a specific pattern of deposition on the pit bottom or on top of already deposited content. Similarly, in the case of human traps, trapability between live or snap traps and pit-falls may significantly differ, giving recognisable samples (e.g. *Myodes glareolus* in Andrzejewski & Rajska 1972; *Microtus townsendii* in Boonstra & Krebs 1978). Additionally, due to the susceptibility to fragmentation, it is beneficial to know if contexts were subject to past or present soil turbation.



Fig. 2.01 – Whole-sieved context example from Romaniuk et al. (2016) research. Material from context 110, Trench I, Skara Brae, presented against an A4 paper. With over 6000 NISP it was the biggest concentration of micromammal bones found within the site.

2.2.5. RESEARCH METHODS – IDENTIFICATION AND MEASUREMENTS

The identification of micromammal bones is a challenging task and the level of identification possible depends on a number of factors. Inferring basic animal order (e.g. *Rodentia*) and anatomical provenience (e.g. *humerus*) of remains does not pose additional issues besides the size of the remains, which can be overcome by the use of a hand lens or microscope (or even a trained eye) and desirably a reference collection. However, identification of genus (e.g. *Microtus*) or species (e.g. *M. arvalis*) is highly challenging due to a number of reasons. Apart from the well-studied micromammal teeth (Chaline 1974; Hillson 2005) and skulls (e.g. Lawrence & Brown 1973; Chaline 1974; Osborn & Helmy 1980; Nagorsen 2002), there are relatively few osteological references available for researchers. Moreover, those are widely scattered across a number of osteological atlases and papers (e.g. rats in Amorosi 1989; an appendicular skeleton of selected species in Vigne 1995, Ronniger 2009) as well as other, heavily obscure sources (e.g. scapulae in selected species in Lehmann 1961, fig 4.). Some identification charts or bone sorting guides are available publicly online, but they lack a description of a proper identification methodology as well as sufficient depth for species identification. Also, in contrast to other animals (e.g. fish, von Busekist 2008) no regional or global internet database for micromammal species currently exists. Such difference between references available for cranial and postcranial bones is primarily due to the fact, that purely biological studies on rodents, predating archaeological interest in such material, heavily differs in the sample choice and utilizes a different set of methods to achieve its goals (e.g. cranial measurements for Polynesian rats in Taylor et al. 1982 and studies on mainly postcranial remains in Matisoo-Smith & Allen 2001; discussed more in Stahl 1996).

Moreover, the sheer number of micromammal taxa (Wilson & Reeder eds. 2005, 185-311 & 745-752), with often similar skeletal construction, makes the task even more problematic. In the case of some species, similarities in skeletal structure require cranial morphometrics to be performed in order to distinguish them from each other (e.g. Barčiová & Macholán 2009). Issues also include species that have seemingly been studied for many years, such as black and brown rats, which require in-depth analysis to be sure of their proper identification (e.g. skulls and teeth morphology in Osborn & Helmy 1980, 266-274; Yiğit et al. 1998; Pagès et al. 2011). Even references produced so far are highly localized and cannot easily be applied to samples from different regions (noted in Matisoo-Smith & Allen 2001; a similar issue was encountered in adapting Ronniger identification methods for Skara Brae sample in Romaniuk et al. 2016A).

That is why most studies rely predominantly on local reference collections, already studied samples and external specialists (e.g. Dewar & Jerardino 2007). Usually, zooarchaeological investigations only utilize teeth as well as maxillae and mandibles for the sake of identifying and quantifying taxa (e.g. Corbet 1979; Weissbrod et al. 2005). However, other bones are sometimes assessed to a specific order or family, especially in recent research (e.g. Hillestad-Nel & Henshilwood 2016). There are studies that attempt a taxonomic identification for both cranial and postcranial remains (e.g. Weissbrod et al. 2014; Romaniuk et al. 2016a;b) but usually only about 60% of all remains can be successfully assigned to species, even if only a few species are present within the sample (Romaniuk et al. 2016a;b). A near 100% success rate can be achieved only in unique cases, such as the presence of species that differ so much that they cannot be misidentified (e.g. Souttou et al. 2012). Such a situation is predominantly due to additional factors that prevent proper identification, especially a big impact of taphonomic history on bone identification - erosion and fragmentation easily blur bone features unique for taxa (Korth 1979; Andrews 1990; Stahl 1996).

Some studies suggest dropping traditional identification based on morphological examination in favour of other methods, most notably molecular analysis (Matisoo-Smith & Allen 2001). Ancient DNA (aDNA) has been successfully retrieved from archaeological micromammal remains, studied through different methods and compared to modern samples (Matisoo-Smith & Robins 2004, Jones et al. 2012 & 2013; Martínková et al. 2013). aDNA enables not only certain species identification but also establishing kinship between specific populations, in a result tracking species migrations, populations divergence and the process of adaptation to new environments. Moreover, a correlation of specific factors between different species may show shared past (e.g. genetic diversity between humans and house mice, due to both relying on human transportation, Jones et al. 2012 & 2013). However, aDNA methods are still too expensive to be used on regular basis for zooarchaeological research (Gifford-Gonzales 2018, 105), with DNA degradation being an additional issue (Reitz & Shackley 2012, 442). Another, more affordable option, is ZooMS – Zooarchaeology by Mass Spectrometry (Buckley et al. 2009). Instead of DNA it uses collagen as a source of information, which is more durable and can be preserved for much longer in archaeological contexts. The method has been utilized a number of times on the archaeological material, including worked bone and antler samples (Hounslow et al. 2013), and provided satisfactory results. Although this method firstly needs a molecular sample from one species in order to be able to identify it in a studied material, samples for some murid rodents are currently available (Buckley et al. 2016; Buckley et al.

2018). Newer and newer approaches are announced yearly (e.g. Guimaraes et al. 2017) but commonplace usage of molecular analysis is yet to be seen in zooarchaeological science.

Assessing the sex of micromammal remains is rarely discussed (e.g. lack of comment on sex in Andrews 1990 or Stahl 1996) and almost never done. Technically pelvic bones can be used for such assessment (see Lawrence & Brown 1973) but it is often impossible to do so for the overwhelming majority of finds due to fragmentation, with morphological variation between populations being a contributing factor. However, in cases where micromammal sexual dimorphism was investigated, mostly zoological studies, it turned out not to be of significance for research (e.g. complete lack of dimorphism in red squirrel *Sciurus vulgaris* skull measurements in Sidorowicz 1958; Hale & Lurz 2003).

The identification of taphonomic alterations on micromammal bones has been considered as crucial for their analysis (Andrews 1990; Morlan 1994; Stahl 1996) and recently micromammal remains have been included in a comprehensive book on taphonomy written as an aid for such investigations (Fernández-Jalvo & Andrews 2016). The possible relationship between various taphonomic marks, assemblage context and completeness has already been suggested in Morlan (1994, table 1) and discussed for some context types in Andrews (1990). While especially early studies on taphonomy have been performed on non-statistical samples without consideration of replicability (as noted in Denys 2002) the current state can be considered as the most thoroughly investigated segment of micromammal methodology, most likely due to the similar development in taphonomic studies on bigger species remains. Most notably, marks suggesting staining, digestive or diagenetic corrosion, weathering, etching, fragmentation and charring should be taken into account (Andrews 1990; Morlan 1994; Stahl 1996; Denys 2002; Fernández et al. 2009; 2011; Romaniuk 2016a). Digestion is a feature well known from micromammal assemblages. Smaller species can be eaten whole, and thus all bones as well as teeth can be introduced to stomach acids. However, it can be problematic to differentiate from other forms of taphonomic alteration, especially from abrasion. Digestion firstly dissolves highly-mineralized regions such as enamel coating on teeth as well as having a specific pattern under the microscope resembling a distorted surface with specific “collapsed” areas within it, visible especially on teeth and long bone epiphyses (Andrews 1990; Fernández-Jalvo & Andrews 1992; Crandall & Stahl 1995; Fernández-Jalvo & Dauphin 1995; Jenkins 2012; Fernández-Jalvo et al. 2014; Fernández-Jalvo & Andrews 2016; Fernández et al. 2017). On the other hand, abrasion seems to affect all the bone surfaces in a similar fashion, creating a regular pattern of long and rounded shallow lines, usually aligned with each other (Fernández-Jalvo & Andrews 2016). As

the morphology of micromammal species differs between each other taxonomic diversity has to be acknowledged in order to properly interpret such features (see Fig 6 in Fernández et al. 2017). Additionally, food hardness variation may result in severe mesowear (see Smirnov & Kropacheva 2015; Kropacheva et al. 2017; Zykov et al. 2018), possibly resembling one-sided digestion. Dental shape and wear study can help to understand the relation between tooth morphology and diet (e.g. Firmat et al. 2011). Recently issues related to dental wear in micromammal paleobiology were tackled in a comprehensive review of the subject (Belmaker 2018). As identification of some marks is impossible without microscopes and it is advisable to utilize SEM micrographs (as seen in Andrews 1990 and other works) and other similar methods in order to properly work with key taphonomic elements.

Fragmentation due to trampling, soil turbation and other factors will also be to some degree present in every archaeological sample (Korth 1979; Andrews 1990; Stahl 1996). On the other hand percussion/blow, cut or teeth marks, crucial for the reconstruction of the taphonomic history of bigger species (Johnson 1985 & 1989; Marshall 1989; Noe-Nygaard 1989; Lyman 1994a), will most likely be completely absent from micromammal assemblages. The smaller the animal is the less force is needed to disarticulate it, leading to smaller animals, such as *Cavia*, being easily torn apart without or with minimal use of tools (Quintana 2005). Avian predators tend to swallow such small prey whole, which will not leave any teeth or corresponding marks on bones, while canids and other species may leave significant teeth marks (Andrews & Evans 1983; Andrews 1990, table 2.6.; fossil shrews in Bennàsar et al. 2015 & 2017). However, even in the case of chewing micromammal bones will rather break and splinter than withstand the imprinting of their surface, thus making fragmentation studies more important than teeth marks.

Similarly to taxon identification, micromammal measurements utilized are confined to cranial elements, with postcranial remains being utilized on rare occasions. Most popular are molar teeth measurements (e.g. Korth & Evander 1986), especially those utilized in the molar morphometrics method (e.g. Escudé et al. 2013; Cucchi et al. 2014). The method is utilized in reconstructing the microevolutionary history of species, up to separate populations, and to trace their response to known external factors. Molar morphometrics can work in conjunction with other methods such as molecular analysis for better results (e.g. Renvoisé et al. 2012). In such a method first molar teeth' occlusal surface is mapped and measured, sometimes with an aid of dedicated software or software packages (e.g. TPSdig2 in Cucchi et al. 2014). On the other hand, cranial measurements have been routinely taken by zoologists for over a century (e.g.

Miller 1912) and regularly studied (e.g. Taylor et al. 1982) but archaeological strata rarely provide crania complete enough that can be studied in this way, rendering craniometrics useless besides some natural contexts. However, mandibular measurements may help in distinguishing between Brown and Black rats (Armitage et al. 1984).

When it comes to postcranial measurements some zoological morphometric studies on modern (e.g. Ventura 1992) and fossil (Casinos et al. 1993) samples have been performed, but no standards have been widely adopted for micromammal bones coming from archaeological contexts. The few studies that include postcranial measurements (eg. Matisoo-smith & Allen 2001; Lyman et al. 2001; Romaniuk 2016A) usually follow general outlines for bigger species (von den Driessh 1976). Measurements recorded from these studies include exclusively maximal humeral and femoral length (Lyman et al. 2001; Romaniuk 2016a) and occasionally proximal and distal width (Matisoo-Smith & Allen 2001). Additionally, due to short lifespan – and in extension demographic structure consisting predominantly of still growing specimens, skeletal ontogeny has to be taken into account when performing research on micromammal research.

The identification of pathological changes on rodent bones has only been done in a handful of studies worldwide (Arrizabalaga & Montaugut 1990; Ventura & Götzens 2005; Luna et al. 2017). While macrofaunal remains have been for some time studied from that perspective (more in Bartosiewicz 2008 & 2013) micromammal bones are usually avoided, mainly due to the lack of any comparative studies and the necessity to utilize sources for human and larger species pathology (e.g. Baker & Brothwell 1980; Aufderheide & Rodríguez-Martín 1998; Bartosiewicz 2013). However, studies performed so far suggest the need for data to understand various stress-related behaviours within small animal populations (Ventura & Götzens 2005; Luna et al. 2017). The author has not seen any paper mentioning dental pathologies but a number of references exist in current veterinary dentistry (see Böhmer 2015).

Not only bones but also biological residues left on artefacts can be assessed to a specific taxon. The immunoassay method seems to be able to identify micromammal remains on human lithic tools (Yohe et al. 1991). This method originated from medical and forensic research and has a long, although controversial history, mainly due to a number of unknown factors such as the impact of time and contamination of proteins from various sources on the results (Downs & Lowenstein 1995, Reuther et al. 2006). The methodology, however, constantly develops and the improved pRIA technique seems to yield far more reliable results than previous ones, including with mixed samples (Reuther et al. 2006).

2.2.6. RESEARCH METHODS – DATA QUANTIFICATION

A number of quantification units have so far been utilized, often resembling ones used by other branches of zooarchaeology and taphonomy (Lyman 1994a;b; Lyman 2008), with relative abundances being most commonly used (See table 2.01 for key equations discussed). Due to the relatively young age of micromammal zooarchaeology, the choice of methods is usually heavily tailored towards local conditions (Saavedra & Simonetti 1998). One of the main ideas behind studying archaeological bone assemblages is to identify patterns due to specific taphonomic agents that could be quantified and later utilized to identify contexts affected by them (more in Lyman 1994a; 2008; Reitz & Wing 2008; see Binford 1981). In the case of micromammal assemblages, the work of Dodson & Wexler in 70s (1979) and later Andrews and other researchers (Andrews & Evans 1983; Andrews 1990; Kusmer 1990; Fernández-Jalvo & Andrews 1992) led to the widespread utilization of relative abundance (Shotwell 1955), sometimes called relative completeness (e.g. Saavedra & Simonetti 1998). The popularity of the method is partially due to the ease of its graphical depiction (e.g. Fig 4 in Hillestad-Nel & Henshilwood 2016 or Fig 4 in Romaniuk et al. 2016a), greatly helping in sample analysis against references and comparisons between contexts. The relative abundance of a specific skeletal element is calculated by dividing the number of said elements found in an assemblage by the expected number of those, considering the estimated minimum number of individuals (MNI). The outcome is usually a ratio between 0 and 1, though can exceed 1 in specific situations. Additionally, it can be multiplied by 100% to obtain a percentile value. Relative abundance is separately calculated for mandibular and maxillar bones, incisors (loose), molars (loose), scapulae, humeri, radii, ulnae, pelves, femora, tibiae, vertebrae, metacarpals, phalanges, calcanei and talus (Andrews 1990; e.g. Fernández et al. 2011; Hillestad-Nel & Henshilwood 2016; Romaniuk et al. 2016a). All these bones are quite easy for anatomical identification, even if fragmented. The number of vertebrae, as well as ribs, may differ from species to species and studies may utilize different values as their default number in a single individual. Other cranial bones are usually not included in that quantitative method (e.g. Dewar & Jerardino 2007; Romaniuk 2016a) albeit it is not a strict rule (e.g. Fernández et al. 2011).

However, there have been several disagreements with relative abundances interpretation and utilization. As noted by Lyman (1994b), the number of an element “i” stated in the abundances equation was most likely Number of Identified Specimens (NISP, Lyman 2008) and was utilized in this way in most cases (e.g. Saavedra & Simonetti 1998; Dewar & Jerardino 2007).

However, some studies, for example Kusmer (1990), actually used the Minimum Number of Elements (MNE, Lyman 2008) to calculate relative abundance (see Lyman 1994b for explanation). It is especially visible in studies from Argentina, in one case even providing equation with MNE stated (Fernández et al. 2011; similar to %MAU, see Lyman 2008). The difference between utilizing NISP and MNE counts may not be that great for larger assemblages (e.g. NISP and MNE tables in Romaniuk et al. 2016B). However, when utilized on small, fragmented samples (Dewar & Jerardino 2007) some values in the case of NISP may exceed those suggested by $MNI \times E_i$, resulting in values beyond 1. Moreover, due to both issues with taxonomic identification and the methodology centred around finding a taphonomic agent, relative abundances usually are disjoined from specific species analysis and calculated for all micromammal elements present in the sample (e.g. Andrews 1990; Fernández-Yalvo & Andrews 1992). Even if MNI is often calculated separately for each species present in the sample, similar to larger species, it does not help in removing possible bias and may even add yet another one. It is due to remains unidentified to taxa sometimes denotes a possibility of additional individuals in the sample (e.g. Dewar & Jerardino 2007).

Apart from relative abundances a number of methods relying on NISP/MNE have been suggested for micromammals and occasionally utilized as means of comparison between samples. One of Andrews's (1990, 45) ideas was to bypass MNI estimations and utilize skeletal elements proportions in order to express how much of the whole bone assemblage is represented by a specific skeletal element. However, in contrast to relative abundance, this method, to the author's knowledge, has been ignored by researchers and all recent studies rely on relative abundance and MNI calculation (Dewar & Jerardino 2007; Fernández et al. 2011; Hillestad-Nel & Henshilwood 2016; Romaniuk et al. 2016A). Beyond skeletal methods, Andrews (1990, 49-55) suggested investigating skeletal proportions between two or more specific elements, such as proportions of postcranial to cranial elements or distal to proximal limb bones, occasionally named indices by other researchers. Three separate indices were also introduced by Andrews for teeth and utilized the number of teeth found intact, teeth found loose (isolated) and a number of empty alveolar spaces. Such proportions could be utilized in conjunction with relative abundance as additional data. However, all those methods also include a bias noted in the case of abundances, with specific element numbers designed for NISP but with MNE also being used by many researchers (e.g. Fernández et al. 2011; Romaniuk et al. 2016a).

The breakage pattern of cranial as well as postcranial bones has been extensively studied and quantified for the sake of analytical comparisons (Andrews & Evans 1983; Andrews 1990;

Fernández-Jalvo & Andrews 1992; Comay & Dayan 2018b; see Fig. 2.02). The method for long limb bones relies on counting complete humeri, ulnae, femora, and tibiae as well as proximal and distal fragments as well as shafts present in the sample (Andrews 1990, Fig 3.7, t.3.3). However, the method can be problematic as some fragments can be counted twice, e.g. one bone end with a shaft longer than 50%. Similar issue was originally found for skull and mandible breakage (Andrews 1990, Fig. 3.11 & 3.12), but later studies divided it into four stages (Fernández-Jalvo & Andrews 1992; Fernández et al. 2011). Mandibular breakage is relatively simple to explain as only two markers are considered, ascending ramus and inferior edge:

- 1) Complete mandible
- 2) Mandible with ascending ramus broken (>50% of ascending ramus present)
- 3) Mandible with ascending ramus missing (<50% of ascending ramus present)
- 4) --/-- and inferior edge broken

In the case of skulls, it is more complex as there are multiple bones, but the most crucial is the state of the maxillozygomatic region:

- 1) Complete skull (>75%, with maxillary and zygomatic region intact)
- 2) Broken skull/maxillae with zygomatic (<75%, braincase missing but with maxillary and zygomatic region intact)
- 3) Maxillae without zygomatic (intact maxillary bones only)
- 4) Minor skull fragments (isolated and fragmented skull bones)

In the case of incisors and teeth, two sets of dichotomic values are recorded: either the tooth is broken or not and if it was found isolated or in the mandible/maxilla (e.g. Fernández-Jalvo & Andrews 1992; Fernández et al. 2011). However, a different approach is present within the literature. Terry (2007) utilized a simple complete/broken long bone count for use in statistical analysis and algorithm training. A more specific approach to breakage pattern, in the context of specific owl species deposition patterns, has recently been suggested by Comay & Dayan (2018b).

Apart from fragmentation, a number of taphonomic marks should also be quantified. In contrast to breakage, digestion analysis is mainly confined to teeth, with the rare exception of distal humeral ends and proximal femora (Andrews 1990; Fernández-Jalvo & Andrews 1992; Fernández et al. 2017). While for long limb bones only the percentage of specimens with digestion marks are noted (e.g. Fernández-Jalvo & Andrews 1992) teeth digestion marks are

usually assessed to four values: light (usually microscopical marks), moderate, heavy and extreme digestion (all enamel gone, heavy and irregular pitting and torsion of dentine surface; Fernández et al. 2017; see Fig. 2.03). Apart from digestion, each occurrence of taphonomic marks should be noted and the number of bones affected calculated for each type of surface alteration (e.g. table 3 in Fernández-Jalvo et al. 1998). The presence of thermal alteration has been investigated on a number of sites (Simonetti & Cornejo 1991; Fernández et al. 2009; 2011; Rhodes et al. 2016; Romaniuk 2016a) and at least the number of bones affected has been noted. However, due to the variety of natural and anthropic sources of burning it is worthwhile to follow methods suggested for larger species and noting anatomical elements, calculating the amount of surface burnt as well as a stage of charring (e.g. partially carbonated, fully carbonated, partially calcinated, fully calcinated, more in Buikstra & Swegle 1989; Marshall 1989; Lyman 1994a, 384-392; Fernández-Jalvo & Avery 2015; Rhodes 2016; see Fernández-Jalvo & Andrews 2016, 155-158).

As the number of micromammal species identified is usually high in the case of continental assemblages (e.g. 25 taxa in Hillestad-Nel & Henshilwood 2016), methods tailored for biodiversity exploration can provide valuable information for palaeoecology and archaeology alike, especially for regions with published comparative biological studies. Most basic are taxonomic richness and abundance, which can work as comparative data on its own or being a part of a specific index. Both are usually used in one way or another in each study, even if not directly stated. Taxonomic richness is a number of all identified taxa, often expressed as S or $\Sigma TAXA$ (e.g. Belmaker & Hovers 2011; Lupo et al. 2013). It can be used to compare assemblages, contexts or sites (e.g. Weissbrod et al. 2014, fig. 3). In turn, taxonomic abundance, often denoted as P , is a ratio calculated for a specific taxon. It showcases how big part of a general assemblage size it represents, relying on either NISP/MNE or MNI as its basis (e.g. Morlan 1983; Lupo & Schmitt 2005).

In order to provide information and guarantee better comparability, in-depth research on past micromammal biodiversity often makes use of indices provided by biological and related studies (see Grayson 1984, 131-167; Hammer & Harper 2006, 183-207; Lyman 2008, 172-202). Among the frequently used are Shanon index of diversity (H or H'), richness index (dI), evenness index (E) and Simpson or dominance index (D) (e.g. Cruz-Urbe 1988; Schmitt & Lupo 1995; Fernández et al. 2011; Hillestad-Nel & Henshilwood 2016; see table 2.02). Shannon index, which takes into account both taxonomic richness and taxonomic abundances, is the most commonplace way of comparing general taxonomic diversity between and within the

sites. Similar Shannon index values across contexts/sites denote a long period of climate stability (e.g. Avery 1982A) while shifts between contexts or sites may suggest changing environmental conditions. However, in order to understand how species presence relates to an assemblage, indices of evenness and dominance are frequently used. By evenness, most researchers will refer to a Shannon index result divided by a natural logarithm of all species identified, while Simpson index will be considered as a dominance index (e.g. Hillestad-Nel & Henshilwood 2016; Bañulus-Cardona et al. 2017). However, evenness as a reciprocal of a Simpson index often appears in ethnoarchaeological studies related to micromammal research (e.g. Lupo & Schmitt 2013).

A number of index-based methods have also been either developed or adapted specifically for micromammals in order to be used specifically for studying past environmental conditions. Most common out of these are Taxonomic Habitat Index (THI), a part of so-called Habitat Weighting Method (Evans et al. 1981; Andrews 1990, 167-169; e.g. Matthews et al. 2005; Hillestad-Nel & Henshilwood 2016), and Climatic Restriction Index (CRI), based on a Bioclimatic Model (Hernández-Fernández 2001; Hernández-Fernández & Peláez-Campomanes 2005; Hernández-Fernández et al. 2007). In both, each species is represented by a value of 1. However, in THI the value is divided into a number of habitats this animal can be naturally found within, often associated with specific vegetation or lack of this. In turn, CRI is divided into specific climatic zones the species appear in, essentially existing climates with known values of e.g. average yearly temperature or precipitation. THI considers the abundance of species by weighting divided values accordingly, while in the case of CRI value is equally distributed across all relevant climatic zones. Currently encountered and well-researched species preference is assessed directly to species while for extinct animals (or rarely studied) the approximation from the known data for these specific genera (in the case of insufficient data for family) is usually used (e.g. THI in Evans et al. 1981; Andrews 1990, 168). THI values taken from all species are later used to calculate the total value for each habitat and then recalculated through the cumulative index to show a ratio or percentile ($X/100\%$) importance of each habitat. CRI can be also used through its own version of a cumulative index called a Bioclimatic component. However, the Bioclimatic component is rarely a final stage of analysis and is often further analysed or used as entry data for more elaborate methods. Both habitat and climate-based methods can be used separately but for strictly palaeoenvironmental reconstruction it is best to combine both approaches (e.g. López-García et al. 2017). Other methods of inferring data about the past environment also exist (e.g. Mutual Ecogeographic

Range method, MER, in Blain et al. 2016, e.g. Fagoaga et al. 2017) and many researchers currently work on improving existing or creating new methods.

Age frequency (e.g. mortality profiles) in micromammal samples may be highly relevant to determine their taphonomic history (Korth & Evander 1986; Lyman et al. 2001) though archaeological finds are rarely studied in such way. In most mammal species (see Reitz & Wing 2008, 172-178) it can be done by scoring eruption and wear of molar teeth (e.g. house mouse in Lidicker 1966; Brothwell 1981; Valenzuela-Lamas et al. 2011; striped fieldmouse *Rhabdomys pumilio* in Henschel et al. 1982; black rats in appendix by Armitage in Morales & Rodríguez 1997) as well as stages of epiphyseal fusion (e.g. rats in Dawson 1925). Those methods can be further combined with additional measurements if necessary (Korth & Evander 1986), what is especially of use for animals with ever growing teeth such as voles (Lyman et al. 2001). Cranial suture closure may be utilized but the chance of finding crania complete enough for assessment is at best very low. However, similarly to larger animals, methods have to be created or adjusted separately to species due to differing biology and population dynamics in each case. In the case of micromammals it is further complicated by their sheer numbers. Only rarely species are comparable with each other, like in the case of a long-tailed field mouse (*Apodemus sylvaticus*) which is so similar to the Yellow-necked mouse (*Apodemus flavicollis*) that the eruption and wear of their teeth can be scored successfully by methods created for the latter (Adamczewska-Andrzejewska 1967; Steiner 1967; Herman, pers. comm). Moreover, most ageing methods for micromammals were developed to fit typically biological studies on a living population and finding relevant one for their skeletal remains may be highly problematic, especially when average tooth wear, as a continuous variable, is a less reliant indicator of age for zoologists and comparative biologists than other quantifiable parameters (Bellamy 1981; Frynta & Zizková 1992). One thing more to consider is that bones of juveniles or sub-adults may have a lower survivorship in contrast to denser bones of older, fully developed individuals. It may impact the frequency of finds (Lyman 1994a, 234-280), with an archaeological population looking older than the actual population it originated from.

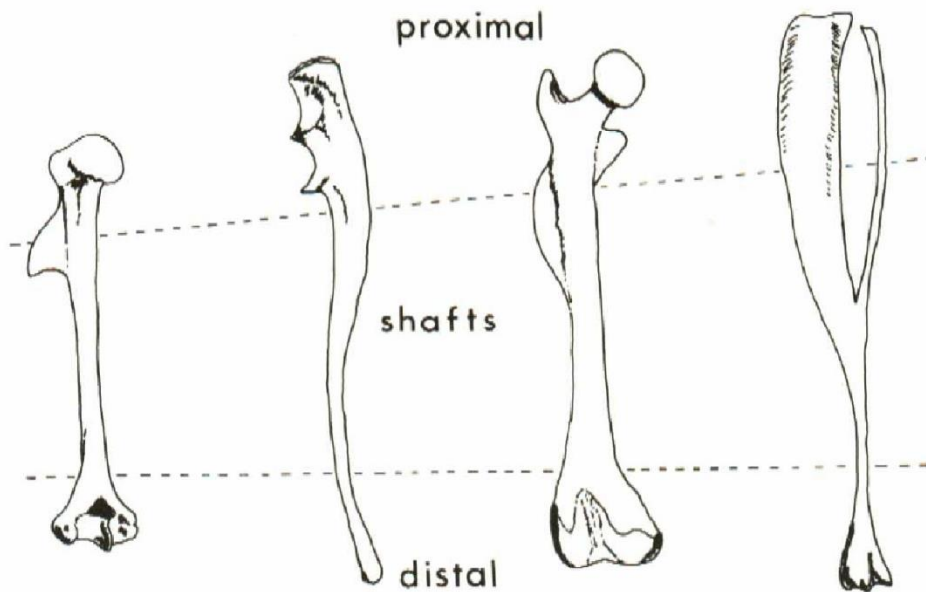
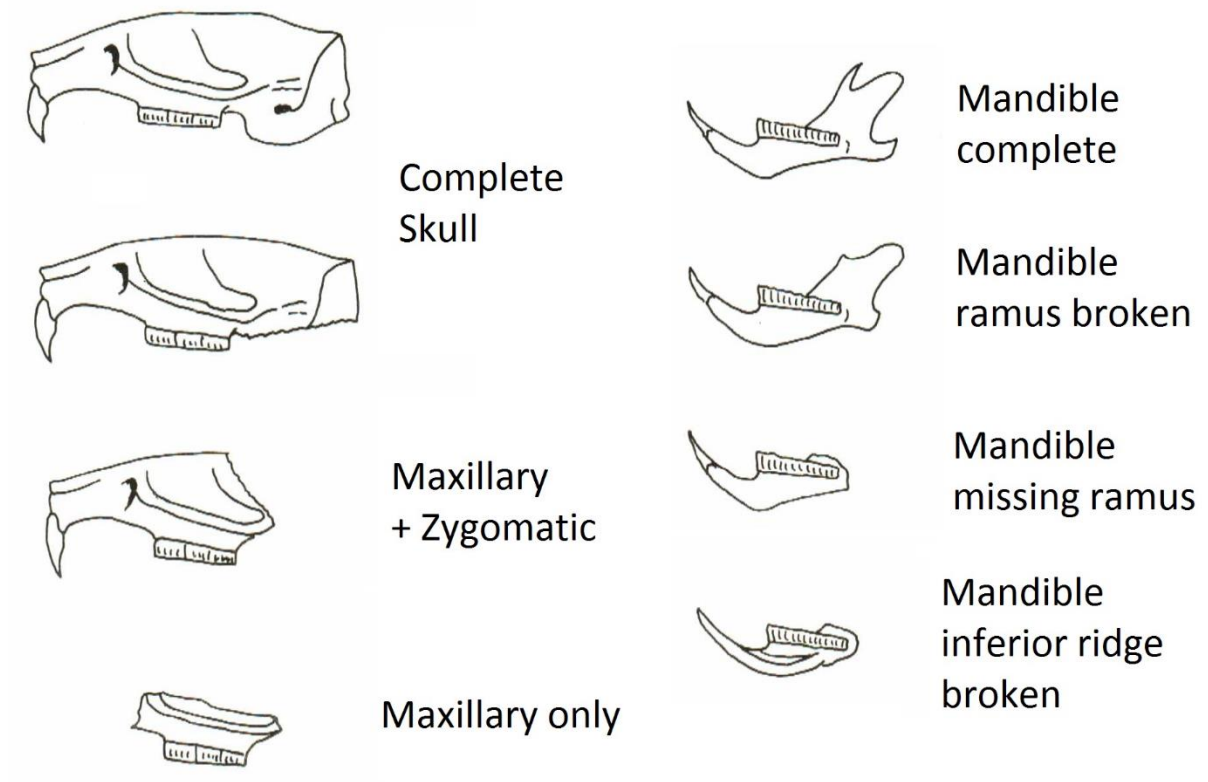


Fig. 2.02 – Visual explanation of fragmentation stages of a skull (upper) and main long bones (lower) from Andrews 1990 (Fig. 3.7,3.11, 3.12).

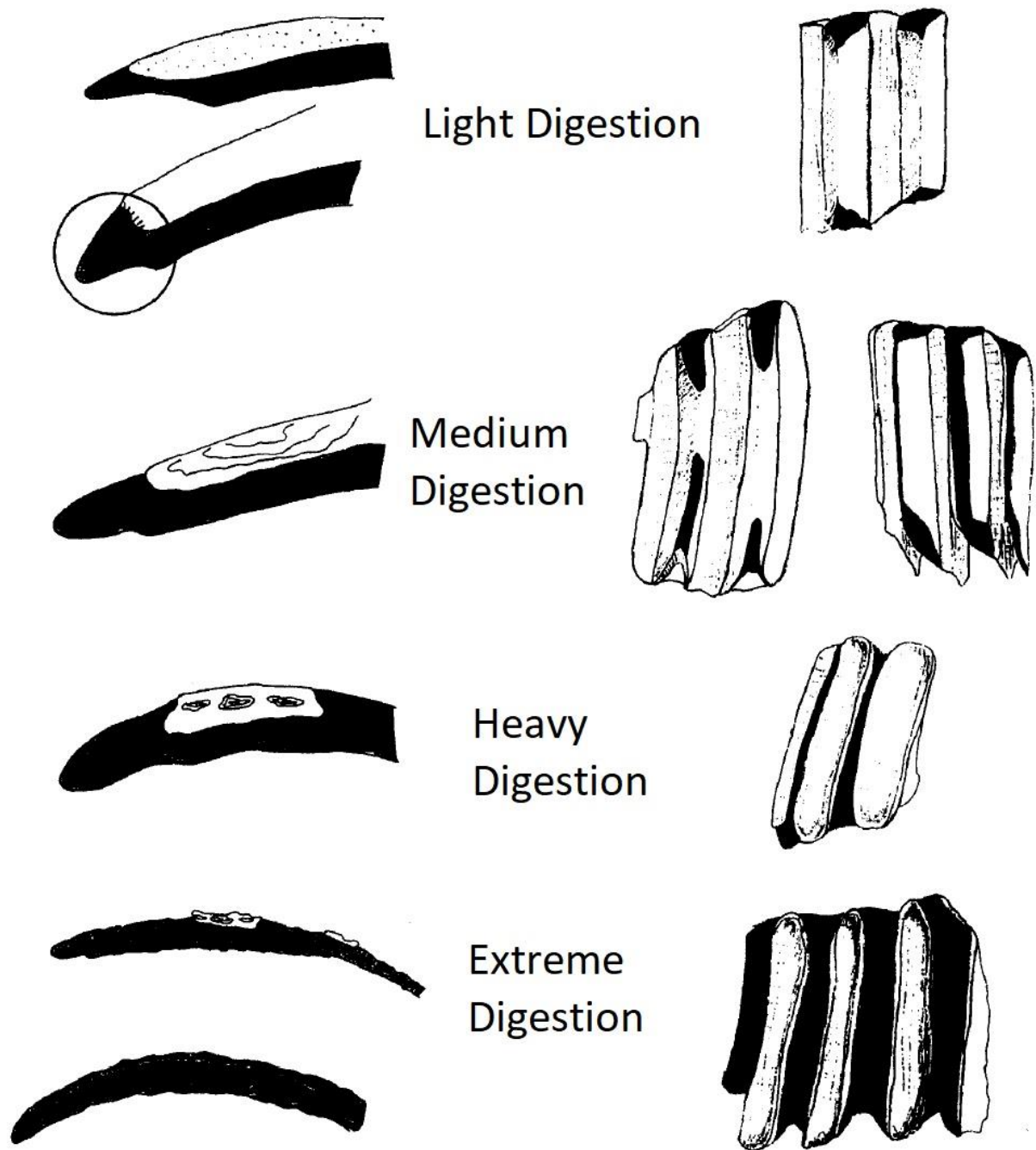


Fig. 2.03 – Visual explanation of digestion stages for incisors (left) and vole molars (right) from Fernández-Jalvo & Andrews 1992 (Fig. 2a;b).

Table 2.01 – Table summarizing major equations presented in Andrews (1990) and utilized in micromammal taphonomy related to predator identification. All can be multiplied by 100% to get percentile values.

Type	Equation	Full Term	Explanation
Ratios	$R_i = N_i / (MNI \times E_i)$	Relative abundance	Ratio of a specific element (i) finds (N_i) to expected anatomical elements numbers (MNI multiplied by a number of elements in an average skeletons, E_i)
	$SK_i = N_i / N$	Skeletal elements proportions	Ratio of a specific element (i) finds (N_i) to all finds (N)
Indices	$(\text{femurs} + \text{humeri} + \text{tibiae} + \text{radii} + \text{ulnae}) \times 8 / (\text{mandibles} + \text{maxillae} + \text{isolated molars}) \times 5$		Proportions of postcranial to cranial elements (Complex)
	$\text{femurs} + \text{humeri} / \text{mandibles} + \text{maxillae}$		Proportions of postcranial to cranial elements (Simple)
	$\text{tibiae} + \text{radii} / \text{femurs} + \text{humeri}$		Proportion of distal limb elements
Indices, teeth only	$E(i, \text{isolated}) / \text{empty alveoli of } E(i)$	Isolated Incisors/Molars (%)	Ratio of isolated teeth against empty alveolar spaces
	$\text{empty alveoli of } E(i) / E(i)$	Incisor/Molar loss (%)	Ratio of empty alveolar spaces against expected number of specific teeth
	$E(i, \text{in situ}) / E(i)$	Incisors/Molars <i>in situ</i> (%)	Ratio of teeth present against their expected number

Table 2.02 – Table summarizing major equations related to taxonomic richness, abundance and diversity and used in micromammal or related research (Cruz-Urbe 1988; Andrews 1990; Schmitt & Lupo 1995; Hillestad-Nel & Henshilwood 2016; López-García et al. 2017).

Type	Equation	Full Term	Explanation/Calculation
General values and indices	S or $\Sigma TAXA$	(Taxonomic) Richness	Total number of taxa found in assemblage
	$P_i = N_i / N$	(Taxonomic) Abundance	Proportion (P) of specific taxon (i) finds or individuals (N_i) to all finds or individuals within studied assemblage (N)
	$H' = - \sum P_i \log_e(P_i)$	Shannon index of diversity (Shannon-Wiener information function)	Calculated for a whole assemblage, firstly by calculating P multiplied by a natural logarithm of P for each taxon(i), then summing all results together and multiplying by - 1 to obtain a positive value
	$d1 = (S - 1) / \log_e N$	Richness index	Calculated by dividing the total number of taxa (S) - 1 by a natural logarithm of all finds or individuals within studied assemblage (N)
	$D = \sum (P_i)^2$	Dominance index (Simpson index)	Calculated by firstly multiplying proportions (P) for each taxa by itself and then summing obtained results
	$E = H' / \log_e(S)$	Evenness index	Calculated by dividing Shannon index of diversity by a natural logarithm of the total number of taxa (S)
	$E = 1 / D$		or Calculated as reciprocal of Simpson index
Strict environmental and climatic research	$THI_i = n_i / n$	Taxonomic habitat index	Calculated for specific species in a specific habitat (i), where n_i is a weight of this habitat for the species and n a cumulative weight for all habitats
	$CR_i = 1/n$	Climatic restriction index	Calculated for specific species in a specific climate zone (i), where n is the number of climatic zones species are represented and i is a specific climate zone
	$CI_i = \Sigma THI_i / \Sigma THI$	Cumulative Index	Calculated for a specific habitat (i), with a sum of species weights appearing in this habitat divided by a total sum of weights in all habitats
	$BC_i = \Sigma CR_i / S$	Bioclimatic Component	Calculated for a specific climatic zone (i), with a sum of species weights appearing in this climatic zone divided by a total number of species

2.2.7. RESEARCH METHODS – STATISTICAL AND COMPUTATIONAL

Quantification methods used in micromammal research provide plenty of avenues for the utilization of statistical and computational methods. Especially palaeoecological and paleontological studies heavily rely on these for inferring more about past environmental conditions from obtained samples, such as mean precipitation or temperature (see MAT and MAP values in López-García et al. 2017). Standard statistical methods are frequently used, from simple t-test (Belmaker & Hovers 2011; Hillestad-Nel & Henshilwood 2016) up to complex techniques like multiple linear regression (López-García et al. 2017). Those are often combined together or reworked in order to provide clearer results. Palaeoecological and paleoclimatic indexes and related statistical and computational methods are often complex enough to justify using a dedicated software, for example Paleontological Statistics Program (PAST, Hamer et al. 2001).

In contrast, micromammal taphonomy only occasionally makes use of statistical methods. Andrews himself (1990, 45-46 & fig. 3.1) utilized χ^2 analysis as means of proving that differences between skeletal proportion patterns of owls and diurnal predators are statistically significant. In the case of raw skeletal element counts, Pearson's correlation coefficient was also used (1990, 47 table 3.1) as means of showing similarities and differences between assemblages beyond abundances visualisation. However, the majority of work done by Andrews relies on direct visual and descriptive comparison of patterns found in quantified data. The reasoning behind this can be most likely related to general trends in the early 1990s. Andrews manner of creating a large dataset of all possibly relevant data (e.g. Andrews 1990, 33 table 2.2) shows similarity to a point of Lyman discussion – a need of creating complex datasets that take into account all possible data, usable for different purposes by different branches of science (Lyman 1994a, 455-462 table 13.1-2 and fig. 13.1). However, since then taphonomy and related sciences have generally amassed large quantities of such datasets, with the trend moving on from descriptive, even if thorough, data display towards making more frequent use of standardised statistical analysis (taphonomy in Lyman 2008, biology in Whitlock & Schluter 2015, zooarchaeology in Gifford-Gonzales 2018). Still, later micromammal work, even if incorporating some form of standardised statistical methods, stayed mostly within Andrews's pattern of analysis (e.g. tables in Fernandez-Jalvo & Andrews 1992; Fernández et al. 2011), possibly reflecting lack of larger methodological projects in the last three decades.

As a result, there are no field-specific guidelines on what data should be statistically analysed and by what methods specifically. Basis of the specific method usage is usually based on assumption, and the author did not find any research where data distribution was actually checked prior to method choice. The only example where distribution was considered, through the Shapiro-Wilk normality test, was to ensure normality of data and a necessity of using arcsine transformations for that sake (Terry 2007), not to investigate the actual distribution within the wider population. Hoffman's research on raptor pellets (1988), predating Andrews's work, made use of spearman rank-correlation for comparing skeletal elements from different assemblages. Moreover, Kendall's Tau rank-order correlation was used for the comparison of fragmentation categories. In the case of more recent research, the beforementioned χ^2 method was used to prove differences twice in Romaniuk et al. (2016a;b), in each case differently from its original utilization in Andrews work. The first case compared trenches in order to reject the null hypothesis of even distribution of finds. The second case in turn compared trenches between each other and with known references, using relative abundance (here named as frequencies) and fragmentation patterns. The second case approach was inspired by Tables 2 and 5 in Saavedra & Simonetti (1998), which used similar data but compared specific elements/fragmentation patterns separately in each case.

More complex approaches requiring computational methods are essentially absent from micromammal taphonomy. Two prominent exceptions are Terry's (2007 & 2008) work, first on the application of machine learning for the sake of studying micromammal assemblages and second on how to use long-term modelling to better the representativeness of predatory assemblages of a micromammal community. Especially the first research included two machine learning models applied separately to abundances and fragmentation data of selected species – a pool represented by owls, diurnal raptors and mammalian carnivores. First, principal component analysis (PCA), a dimensionality-reduction method, was used to establish the existence of significant differences between major groups of species. Subsequently, the linear discriminant function (LDA), a learning technique for parametric data, was utilized to first assess the accuracy of the LDA-based predictive model and later to identify natural depositions from Homestead cave (Utah). Accuracy ranged from 70% to over 90%, being on the lower end of the spectrum when differentiating between owls, diurnal raptors and mammals but on the higher end when comparing only owls to other assemblages. When the predictive model was applied to Homestead cave contexts it returned owls as most likely depositors, confirming previous hypotheses (see Fig. 2.04).

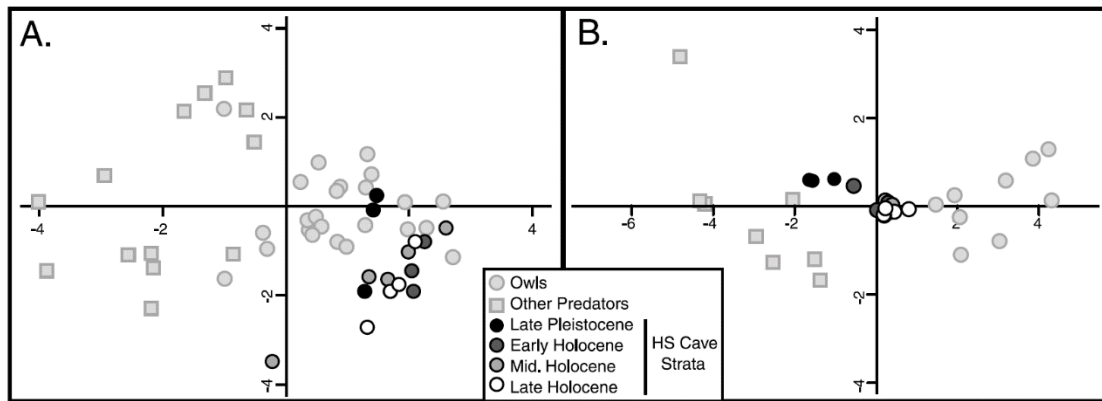


Fig. 2.04 – Visual representation of the Linear Discriminant Analysis for relative abundances (A) and fragmentation (B) data (from Terry 2007, Fig. 5). In the case of relative abundances Homestead cave deposits fit completely with owl assemblages cluster while in the case of fragmentation older contexts, with more severe fragmentation, lean towards other predators such as diurnal raptors and mammalian carnivores.

2.2.8. RESEARCH METHODS – CONTEXTUAL INTERPRETATION

From a zoological perspective, micromammals are challenging to study due to a wide number of biological and environmental factors affecting their population (e.g. Elliot's short-tailed shrews, *Blarina hylophaga*: Kaufman et al. 2012). While rodents are traditionally divided into herbivores, omnivores and rarely carnivorous they can adapt their feeding preferences to food availability (Verde Arregoitia 2016). For example, a long-tailed field mouse, a non-hibernating species with a tendency toward herbivore behaviour (more in Flowerdew 1991) can predate on hibernating bats during winter (pond bat, *Myotis dasycneme*, Daubenton's bat, *M. daubentonii*, whiskered bat, *M. mystacinus*, Natterer's bat, *M. nattereri*, and brown long-eared bat, *Plecotus auratus*: Haarsma & Kaal 2016) while rats may kill and eat other micromammals (e.g. house mice: Bridgman et al. 2013) and predate on bird and tortoise nests (Caut et al. 2008; Harper & Bunbury 2015). On the other hand, some species may have a very rigid approach to subsistence and habitat preference and avoid non-optimal areas as long as the saturation in the preferred area is tolerable (e.g. common voles in Jacob et al. 2013). Micromammals can also fiercely compete with each other in some habitats (house and field mouse competition in Smirin & Smirin 1999) while in the other antagonisms will be minimised by e.g. choosing different microhabitat (bank vole, *Clethrionomys glareolus*, and wood mouse: Canova 1993).

Additionally, the population density of some species can heavily oscillate through the year, which may result in overpopulation and population movements. Common voles are known to have an oscillating population in continental habitats (e.g. Mackin-Rogalska 1979) but insular populations may differ in this regard (Berry 1985, 160; Reynolds 1992; Reynolds & Gorman 1994; Gorman & Reynolds 2008) with diminished yearly oscillations and lack of evident overpopulation. This situation suggests that other factors are involved, such as stabilization of population through time in an isolated area (as seen in later years in Mackin-Rogalska 1979), environmental conditions that stabilize the reproduction cycle (such as food supply or yearly temperature changes, more in Gromov & Polyakov 199, 483-490 & 494-561) or predation that both lowers the population count as well as suppresses reproduction due to vicinity of a predator noticeable by prey species (Jochym & Halle 2013).

As most methods rely on identifying the depositor (Andrews 1990) predator behaviour introduces new factors to be considered in the micromammal taphonomic history. Some predators may prefer a specific species or a specific size of prey as their main food source (e.g. Tawny owl, *Strix aluco*, and long-eared owl, *Asio otus*: Balčiauskas & Balčiauskienė 2014). That is why low diversity of richness index may suggest selectivity expected from predatory or human assemblages (Fernández et al. 2011). Pellets or scats containing rodent remains can be left either randomly (Falk & Semken 1990), in specific areas (e.g. area marking as described in Andrews & Evans 1983) or large assemblages (e.g. Fig 2 in Andrews & Evans 1983), depending on preferences of the predator. Different predators ingest their prey in a number of ways, thus creating fractures and teeth marks or leaving remains intact (whole, with head bitten off, in parts: Andrews 1990). Additionally, primary bone accumulations can be deposited in places that may cause dispersal and appearance of secondary accumulations through the wider area (Fig. 15 in Weissbrod et al. 2005) and without proper knowledge such situation may be indistinguishable from e.g. fluvial transport (opposite situation in Klein et al. 1999). In-depth consideration about bone dispersal from owl pellets has been given in a number of recent papers (e.g. Terry 2004; Weissbrod et al. 2005). Remains of the same animal can be split by a predator during feeding (Andrews & Evans 1983; Andrews 1990) and may end up in different scats. As predators may not end up in assemblages studied by archaeologists and therefore avoid identification (Morlan 1994) there is also a risk of misidentification of the predator due to assessing remains to a pool of known species. The original idea of context comparison relied on the notion that each predator creates its own distinctive pattern through fragmentation, digestion and completeness (Andrews & Evans 1983; Andrews 1990, 45-90; Fernández-Jalvo

& Andrews 1992). However, it is currently understood that individuals of the same species may produce patterns differing from each other (e.g. Saavedra & Simonetti 1998; Matthews 2002). Factors that contribute to these differences are still vaguely understood, but in cases of some animals could be successfully identified and evaluated (e.g. Tawny owls, *strix aluco*, seasonal variation in digestion in Andrews & Fernández-Jalvo 2018; see Comay & Dayan 2018b for discussion on postcranial breakage and digestion). Many issues noted by newer studies are currently being discussed in revisions of established methods (e.g. Fernández et al. 2017) and the number of references for newer species is steadily increasing (e.g. data on Black-shouldered kite *Elanus caeruleus* for African assemblages in Souttou et al. 2012). Microbial and invertebrate action may affect a decomposition of an assemblage (e.g. for owl pellets see Levinson 1982) and add yet another layer of taphonomic alterations on the bone (see Fernández-Jalvo & Andrews 2016 for multiple examples).

The possibility of human involvement in micromammal deposition, especially consumption, adds yet another layer of factors that needs to be addressed. While the burn marks have been considered as evidence of hominid actions the issue is quite complex and needs elaborate research to be done to be sure of its proper identification (Johnson 1989; Buikstra & Swegle 1989; Noe-Nygaard 1989; Marshall 1989; Lyman 1994a, 384-392). Naturally occurring fire will have a specific impact on a sample (David 1990; Lyman 1994a), with most bones being carbonized but not calcinated. On the other hand, human-induced fire may reach temperatures necessary for the calcination of bony tissues (Johnson 1989; David 1990). Additionally, the number of bones affected will differ depending on if the sample was already deposited, skeletonized but not yet deposited or belonged to a carcass caught in fire (more in Buikstra & Swegle 1989; Gifford-Gonzalez 1989). The most important is however to understand, that humans do not “burn” their food to a carbonized state and too many bones burned, especially to a calcinated state and without a clear pattern, suggest rather unintentional fire alteration (Lyman 1994a; e.g. Rhodes et al. 2016). On the other hand, a number of carbonized bones suggests thermal alteration of a carcass, and possibly similar in pattern with ethnoarchaeological knowledge from the studied region (e.g. South Africa in Henshilwood 1997), on a human settlement site may indeed suggest intentional human action. Correlation of spatial and temporal location of remains with regions of human daily activity (e.g. Falk & Semken 1990; Dewar & Jerardino 2007; Romaniuk et al. 2016a) would further reinforce such interpretation. Finally, not all human food preparation will leave burn marks (e.g. boiling in water) or even requires fire (e.g. smoking). For example, there is no verifiable evidence for

burning and consuming rodents in the archaeological context in India, yet rock paintings from the Palaeolithic era clearly suggest such activities (Sathe 2017).

Directly tied to the issue of burning is bone surface decolouration, which if unassessed may lead to wrong conclusions. Overall, there are a few possibilities of a stain similar to burning to appear on a bone or tooth, including manganese oxidation, carbon stain, fungi growth, soil acidity and so on (Fernández-Jalvo & Andrews 2016, table 1.1 & 155-158). One of the most common chemical staining present on the bones is due to the crystallization of the manganese present in the soil. However, teeth crowns are not usually stained by manganese apart from cracks or other alterations affecting the tooth (Fernández-Jalvo & Avery 2015, Fig 5&6; Fernández-Jalvo & Andrews 2016, see Fig. A.514, 515, 516) while burning affects both enamel and dentine (Fernández-Jalvo, Y. & D. M. Avery 2015, Fig 5&6; Fernández-Jalvo & Andrews 2016, Fig. A.710) as well as bone proper (Fig. A511). Scanning Electron Microscopy (SEM) with EDS (Energy Dispersive X-Ray Spectroscopy) can establish the chemical element composition of the studied element (more in Goldstein 2003). Since early 1980s (e.g. Shipman 1981) is occasionally used in general taphonomic (e.g. Bendrey 2011; Fernández-Jalvo & Avery 2015) and forensic (Schmidt & Symes 2011, 65-66; e.g. Schmidt & Uhlig 2012) studies. From a zooarchaeological perspective, is especially good at differentiating between chemical staining and proper burning (Fernández-Jalvo & Avery 2015; Fernández-Jalvo & Andrews 2016). Additionally, some experiments were performed to assess how various skeletal preparation methods affect rodent bone colour (see Onwuama et al. 2012), which may to some degree be utilized for taphonomic investigations, but there are no more specific studies on micromammal bone discolouration.

Properly identifying commensal relationships as well as interpreting human impact on species evolution requires data beyond taxonomic or taphonomic information. Apart from (a)DNA method usage for establishing migration patterns, already mentioned in **Chapter 2.2.5.**, especially the isotopes seem important for both palaeoenvironmental reconstruction (Leichliter et al. 2016 & 2017) as well as identifying species consuming food gathered by humans (e.g. Hu et al. 2014; Guiry & Gaulton 2016). Apart from stable carbon analysis nitrogen analysis could also theoretically show food quality consumed by micromammals as it is not affected by age, size or other internal biases (e.g. common voles and field mice in Janova et al. 2016), but so far no studies including both methods have been done. Measurements encompassing whole skeleton can be also a potential source of information on changes of the external and cranial bodily dimensions due to environmental or human-mediated factors (e.g. overall size reduction

with the single value increase: Balčiauskas et al. 2016). Allometric analysis may show changes reflecting important changes in lifestyle, such as the importance of burrowing (more in Casinos et al. 1993) or change of a food source as well as locomotion type of specific animal (Verde Arregoitia et al. 2017). However, micromammal zooarchaeology lacks such investigations, with lagomorphs are a rare exception to this (Moncunill-Solé et al. 2016).

The cultural sphere of interaction between micromammals and humans remains only barely explored. While there are significant works in this field (e.g. Sathe 2017) such analyses are just too scarce to create a proper, standardised framework for the zooarchaeologist to work with. The only place where the cultural significance of small animals is well known in South America (deFrance 2006; de France 2009; as previously mentioned) and can be considered as good reference material for scholars interested in micromammal iconography and symbolism.

2.3. MICROMAMMAL POPULATIONS ON THE ORKNEY ISLES

2.3.1. ORKNEY ENVIRONMENT

The Orkney archipelago is a group of over 50 islands north to northeast from the Scottish mainland, almost completely composed of sedimentary and volcanic rocks (Mykura 1975; Berry 1985: 35-45; Berry 2000: 31-43). The coastline is long (800km) and features high as well as till cliffs, sandy or shingle beaches, low rocky shores, manmade seawalls and causeways (Mather et al. 1975; Berry 1985: 46-47; Berry 2000: 44-46). Most of the islands, including the biggest, Orkney mainland, are relatively flat, with low, gently sloped or terraced hills (up to 275m) but steep hills and rough cliffs appear on some islands, most notably Hoy (Mykura 1975). The climate is very windy and wet, but, thanks to the effect of the North Atlantic Drift, relatively warm and with minor yearly variation (Bullard 1975; Berry, 1985, 13-24). Palynological studies suggest that in the early Neolithic period some islands had a cover of birch-hazel scrub, but in a period of just two centuries (3000 to 2800 BC) most had disappeared (Keatinge & Dickson, 1979). Deforestation is attributed to both the increasing impact of hyperoceanic climate as well as human activity at that time (Bullard 1975; Keatinge & Dickson, 1979; Berry 2000: 52-54). The current landscape is devoid of high vegetation besides high shrubs and ferns as well as tree species recently introduced to the Orcadian environment by farmers (Berry, 1985, 51; Berry 2000: 52-54 & 201-206; Davidson & Jones 1985). Prominent habitats are either anthropogenic (e.g. arable land and pastures) or naturally open (wetlands, fern, heath & peat vegetation; more in Bullard 1975; Berry 1985, 48-86; Berry 2000: 49-79).

During the last glacial period the Orkney isles were completely covered by the ice sheet and the rise of the sea level at the beginning of the Holocene occurred relatively fast, flooding the post-glacial landscape of the region (Berry 1985, 42-45; Berry 2000, 38-43). If there was a land connection between Orkney and Scotland it was most likely short-lived, disappearing at latest in the first half of the eight millennium BC, before the climate was warm enough for small mammals to reach Scotland (Corbet 1961; Berry 1985, 26-31). Modern evidence (e.g. genetic: Martínková et al. 2013; Herman et al. 2017, archaeological: Corbet 1961; Corbet 1979; Nicholson 2007, Romaniuk et al. 2016a) points towards human agency being crucial in the introduction of the majority of mammals species ever recorded on Orkney. The first introductions were most likely herbivores, followed about three to four thousand years later by carnivores such as red foxes, *Vulpes vulpes* (Fairnell & Barrett, 2006, Cucchi et al. 2014), but

the exact sequence of introductions is still being debated. Bat species might have colonized Orkney on their own (Booth & Booth 1994, 5-7). While some older sources suggest ship-related introduction in at least one case (*Vespertilio* sp. occurrence in 1847 in Buckley & Harvie-Brown 1891, 62-64) but the lack of studies prohibits any meaningful analysis.

The majority of the current terrestrial micromammal population present on Orkney belongs to just four different species of rodents, two shrew taxa and one representative of hedgehogs (Booth & Booth, 1994; Berry 1985, 132; 2000, 142-143). It seems that, once introduced, each micromammal species population remained on the isles until today. The only known exceptions are two major rat species. Some introductions can be traced archaeologically or/and genetically, but in general one can divide those species into two classes: prehistoric introductions, and those that occurred in the past 300 years.

2.3.2. ORKNEY VOLE (*MICROTUS ARVALIS*)

The first written reference to Orkney voles can be found in “The History of Orkney Islands” (Barry 1805), although no further information besides their presence on Orkney was given. Until the beginning of the twentieth-century writers considered Orcadian populations to belong to the field vole, *Microtus agrestis*, present on the Mainland Britain and a number of other islands (Gipps & Alibhai 1991). However, Millais (1904) noted the visible physical differences between Orkney voles and field voles and concluded, that the Orcadian population belongs to an entirely different species. Later studies (Matthey 1956; Zimmermann 1959) confirmed Orkney voles to be an isolated form of common voles, *Microtus arvalis*, a species widespread on continental Europe but absent from Britain apart from the Channel Islands (Gorman 1991; Gorman & Reynolds 2008; Lawrence & Brown 1973; Berry 1985, 125-127; 2000, 131-135).

Common voles are a species of non-hibernating, non-commensal, herbivorous rodents, preferring open spaces like meadows and pastures where they can easily create a net of burrows and roam for food available at ground level, predominantly green parts and fruits of local flora (Gorman 1991; Gorman & Reynolds 2008). Common voles can rapidly invade and settle preferable habitats (e.g. Luque-Larena et al. 2013; Jareño et al. 2015) but will wait with settling non-optimal habitats as long as there is space and resources left in a preferable one (Jacob et al. 2013). Studies on Orkney voles reaffirm that high population density is confined to rough grass (Reynolds 1992; Reynolds & Gorman 1999) and other habitats are either sparsely saturated or

completely devoid of voles. Common voles are widely considered as agricultural pests (e.g. Jacob et al. 2013) and indeed crop fields on Orkney used to be inhabited by voles (Millais 1904) before the agricultural intensification but are currently devoid of vole nests (Booth & Booth 1994; Reynolds 1992; Reynolds & Gorman 1999). It is likely due to a shift towards new seed mixtures and reduction of previously cultivated crops (Davidson & Jones 1985) as some crop types render the land unsuitable for vole habitation (Janova et al. 2011), especially if their farming requires deep and/or intense ploughing (Bonnet et al. 2013; deeper analysis of Orkney vole habitation in Reynolds 1992). While Orkney voles may be sometimes found on fields their presence is usually ignored as the main pest of the isles is the rabbit, *Oryctolagus cuniculus* (Berry 2000, 200). Orkney voles can be also occasionally found in abandoned buildings. Their current populations can be found on islands of Burray, Hunda, Mainland, Rousay, Sanday, South Ronaldsay, Westray and recently on Eday (Berry 1985, 132; 2000, 142-143; Booth & Booth 1994, 12-13; 2005, 82-84).

All vole species are known for their high fertility and rapid reproduction rates which is also directly connected to their energy management strategy, similarly to their habitat preference (more in Gromov & Polyakov 1992, 509-531). Among them common voles are one of the most extreme examples, being able to mate as early as 12 days after birth and delivering their first litter around 20-22 days later (Tkadlec & Zejda 1995). Moreover, they are heavily susceptible to short-term variations in environmental factors (Tkadlec & Zejda 1995), especially fluctuations in temperature (Gromov & Polyakov 1992; also related to altitudes settled: Reynolds 1992; Pikula et al. 2002) – a short period of especially favourable conditions may, in the long run, result in rapid population increase followed by a swift decline due to lack of resources and/or the overpopulation stress. It creates a specific yearly pattern of population fluctuation in a temperate climate (e.g. Mackin-Rogalska 1979) and, depending on a region, may result in a multi-annual cycle of population density (known from e.g. Western and Central Europe common voles, Mackin-Rogalska & Nabagło 1990; Pinot et al. 2016). However, it seems that the current Orkney vole population do not show such extremes as continental ones (Berry 1985, 160; Reynolds 1992; Reynolds & Gorman 1994; Gorman & Reynolds 2008), even in a preferred habitat (e.g. compare Reynolds 1992 and Mackin-Rogalska 1979), and seems to oscillate between a million and four million yearly (Reynolds 1992), without multi-annual variation (Reynolds & Gorman 1994). Interestingly, their population is on the decline since the agricultural intensification due to the loss of preferred habitats and what is currently observable are the disjointed colonies of previously uniform, islands-wide populations (Reynolds 1992).

Older studies (e.g. Millais 1904) have also mentioned the lack of overpopulation periods within the Orkney vole population – or at least overpopulation that is a threat to local farmers. It is possible that small temperature and moisture variations through the year (Berry 1985, 18-24; 2000, 7-12) combined with a long-term optimization of a burrow and population system (as seen in Mackin-Rogalska 1979) and the suppressed breeding in a presence of predators (Jochym & Halle 2013) are factors stabilizing the vole population density in a long-term period. Additionally, it seems that female Orkney voles breed in older age and in average have a smaller litter (about three young) than other voles, delivered on average three times per year, albeit due to the life longevity they have more offspring in general (Leslie et al. 1955; Rose 1975).

Orkney voles are larger than their continental European brethren, being up to twice as heavy (up to 86g, Reynolds 1992) and having about 20% longer body and extremities (Millais 1904; Miller 1912, 700). As it can be inferred from teeth measurements (Corbet 1986; Cucchi et al. 2014) the difference was most likely bigger in the past. The initial increase in size can be attributed to the founder effect around 4000 BC. It could also be aided by the lack of natural predators and abundance of food at that time, prompting a natural selection to favour bigger specimens (e.g. Moncunill-Solé et al. 2014). However, a gradual reduction in size occurred around the time of the introduction of new predator species around 1200 AD (Cucchi et al. 2014). Physically they are most similar to Guernsey voles (Miller 1912. 694-700; Cucchi et al. 2014) but genetically are distant from most of the current common vole populations (Martínková et al. 2013). Similar to their continental brethren, their diet is completely herbivorous (Rose 1975).

Common voles are a preferred prey for a wide range of avian predators and the Orkney population is a major food source for short-eared owls, *Asio flammeus*, and kestrels, *Falco tinnunculus*, (Reynolds 1992; Reynolds & Gorman 1999; Berry 1985, 127 & 150-151; 2000, 135 & 157-160). Some archaeological rodent assemblages have been identified as short-eared owl pellets (e.g. Nicholson 2007). Voles are also a minor addition to hen harriers, *Circus cyaneus*, diet (Reynolds 1992; Berry 1985, 127; 2000, 135) and may be opportunistically hunted by common ravens, *Corvus corax* (Marquiss & Booth 1986). Interestingly, recent hen harrier decline may show some correlation with less abundant voles (Berry 2000, 158). Domestic cats and dogs may hunt them but are rarely reported to be eaten (Rose 1975). However, current Orkney feral and domestic cats are considered as one of the main vole predators (Booth & Booth 2005, 83). While their trapability does not show any significant bias (Grunwald 1975) some predators may aim for specific prey size and/or sex (e.g. bigger voles by tawny owls and

long-eared owls, Balčiauskas & Balčiauskienė 2014). Interestingly, vole presence in a habitat can aid in biomass and moisture circulation through the soil (Goszczyńska & Goszczyński 1977; Gromov & Polyakov 1992, 509-531). Voles can carry zoonoses, but their populations are rarely considered as the main vectors (e.g. tularaemia in Pikula et al. 2002).

The anomalous localization of common vole populations in the UK has been a subject of research for over a century now. Initially, Orkney voles were considered as a relict population, but later studies debunked this idea and suggested human involvement in their introduction during the Neolithic instead (Corbet 1961, 1986; Berry & Rose 1975; Haynes et al. 2003; Martínková et al. 2013). While analysis of non-metrical skull traits pointed towards South Europe (Berry & Rose 1975) later genetic studies suggest Western Europe, Northern France and Belgium, as the origin of vole population (Haynes et al. 2003; Martínková et al. 2013) although the Belgian source is highly debatable (Sheridan & Pétrequin 2014). The correlation of vole remains and human activity has its roots in archaeological finds. The earliest vole bone assemblages come from early/middle Neolithic settlements of Skara Brae (Clarke 1976a, 1976b, 2003) and Links of Noltland (Moore & Wilson 2011) and other Neolithic and Early Bronze sites (Corbet 1979; Nicholson 2007). The oldest assemblages were dated to around 3100-2800 BC (Hedges et al. 1987; Sheridan et al. 2013). Due to this, it was originally suggested that voles were accidentally introduced to the isles during the intensification of human maritime trade and migrations in Neolithic times (e.g. Corbet 1961). Later studies, however, put this idea into doubt, reasoning that in the case of accidental introductions there should be evidence for repeated introductions as well as the presence of common vole populations along the Mainland Britain coast (e.g. Thaw et al. 2004). The outcome of genetic and morphological studies excludes any later introduction, suggesting a single introduction of a genetically diverse population around 4000 BC and rapid adaptation with a subsequent long period of evolutionary stabilization, with only a single period of evolutionary response to new species being introduced to islands (Martínková et al. 2013; Cucchi et al. 2014). Moreover, among dozens of Orkney islands voles inhabit at most only ten of them, all connected to main hubs of human habitation (e.g. Mainland, Westray, Sanday, Rousay, South Ronaldsay, more in Berry 1985, 2000; Booth & Booth 1994, 2005) and present in abundance in archaeological rather than natural strata (Romaniuk 2016A).

According to recent studies (Romaniuk 2016a), Neolithic Orcadians could intentionally accumulate Orkney vole remains alongside house refuse. The most plausible explanation, aided by the presence of a few charred bones, is that they were either eaten or getting rid of them as

a part of some form of pest control. Both are to some degree problematic. Especially the latter, though at first more probable, may not be true due to the fact, that during the Neolithic agriculture was just an addition to hunting/fishing and cattle and possibly sheep stockbreeding (Clarke 1976a; Clarke & Skarples 1985). Known remains of agriculture suggest the utilization of flattened middens as new places for fields (Guttmann et al. 2006) and human manure as a fertilizer (Clarke & Skarples 1985). Voles could react to such environments as they react to pellets or scats of other predators (Jochym & Halle 2013) and just be absent. Even if not the lack of pest control in the known historic period (Millais 1904) may suggest a lack of such necessity also in the past. Some previous studies have suggested that those rodents might have been utilized as a cheap meat source during long voyages (e.g. Thaw et al. 2004), similarly to Polynesian and spiny rats in Oceania (Matisoo-Smith 1994; Matisoo-Smith et al. 1998). Voles could be also utilized as fodder for other animals as dogs were present on Neolithic Orkney (Carrot 2011; Fraser 2011).

2.3.3. LONG-TAILED FIELD/WOOD MOUSE (*APODEMUS SYLVATICUS*)

The long-tailed field mouse, *Apodemus sylvaticus*, is a species of mostly nocturnal, solitary and opportunistic rodents, inhabiting most of Central Asia, Europe and many nearby islands, including Great Britain and Iceland (Flowerdew 1991; Flowerdew & Tattersall 2008). In mainland Britain their size ranges from about 8 cm and 13 gr to up to 11 cm and 27 g (excluding tail length, Flowerdew 1991, table 8.18) but on smaller islands with no significant competition and/or predation their size may significantly increase (Angerbjörn 1986). Their choice of habitat is rather broad, from woodland (e.g. Montgomery 1989a;b), grassland (including pastoral farmland and field margins, e.g. Montgomery & Dowie 1993) up to sand dunes (e.g. Attuquayefio et al. 1986), man-made features (Healing 1980) and up to treeline in the mountains (e.g. Wilkinson 1987). While it seems that field mice, similarly to voles, do not prefer intensive agricultural regions (Montgomery & Dowie 1993) they can be found in significant numbers on most known field types (more in Flowerdew & Tattersall 2008). Occasionally these species can roam for food and seek shelter in manmade environments during winter and in the absence of house mice they may settle in human habitats. They will also take advantage of any abandoned buildings. The extreme example of this is the colonization of abandoned villages in St. Kilda by field mice, where all original populations of house mice died shortly after people left the islands (Boyd 1956; Berry & Tricker 1969). While the initial suggestion of the event was that

house mice could not survive without the human population (Boyd 1956) it is more plausible that they were unable to successfully compete for available food sources when bigger *Apodemus* entered abandoned human buildings (Berry & Tricker 1969). Field mice can also penetrate urban environments through semi-natural areas, such as parks or gardens, and possibly through that creating a competitive stress factor on house mouse population thus restricting the latter species range strictly to occupied housing (Yalden 1980). Despite being frequently seen around crops and feeding on grains and seeds their impact on agriculture as a pest is currently considered minor or non-existent (more Flowerdew & Tattersall 2008) but could have been greater in the past.

All populations are quite closely related to each other and most likely originated from the area of Dordogne, France, around 12 000 BC and dispersed from their refugium in the early Holocene (Herman et al. 2017). Judging from archaeological remains, first field mice came to Orkney around Early Neolithic, probably alongside human migrations (Corbet 1979; Nicholson et al. 2005 & Nicholson 2007; Romaniuk et al. 2016A). Previous studies suggested Norway (Berry 1985, 27 & 131) or Mainland Europe (Nicholson et al. 2005) as a source of the initial population, but current genetic knowledge about the species suggests gradual colonization of the British isles and Orcadian specimens coming from already established Mainland Britain populations (Herman et al. 2017). Field mice can be currently found on many Orcadian islands, including Copinsay, Eday, Graemsay, Hoy, Linga Holm, Mainland, North Ronaldsay, Sanday, Shapinsay and Stronsay (Berry 1985, 132; 2000, 142-143; Booth & Booth 1994, 14; 2005, 83). While not reported in official publications, Westray also seems to currently have a stable albeit completely unresearched field mouse population (J. Herman *pers. comm.*).

As far as the author and other sources can tell (e.g. Booth & Booth 1994, 15) *Apodemus* population dynamics on Orkney has not yet been a subject of a detailed study. In England, studies that utilized live traps reported male overrepresentation in the mouse population and substantial differences in winter population size between similar environments and a narrow age structure (e.g. Boyd 1956; Montgomery 1989a;b, Montgomery & Dowie 1993). The territory size depends on food availability and in impoverished areas can be significantly bigger (Attuquayefio et al. 1986). Density and yearly population cycles also highly depend on food availability, ranging from 0.5 per ha up to 200 (more in Flowerdew 1991, densities). *Apodemus* can be found in a diet of a number of different species, including mustelids, foxes, cats and a wide variety of owls, but usually not as the main prey (more in Flowerdew & Tattersall 2008, mortality). Especially avian predators prefer voles to field mice (e.g. Halle 1988) but a decline

of major prey population can force them to prey on *Apodemus* more often (e.g. Love et al. 2000). On Orkney field mice were found in hen harrier, kestrel and short-ear owl pellets, but only as an addition to their diet (at most 10% for kestrels during the breeding season, usually 1-1.5%: Reynolds 1992).

2.3.4. HOUSE MOUSE (*MUS MUSCULUS*)

One of the most known and commonplace rodent species, house mice are highly diverse from a morphological, behavioural and organizational standpoint to the point of each population being highly specific and recognizable (Berry 1991; Berry et al. 2008). The size differs, from as small as 7 cm without a tail to above 9 cm, while weight is not deeply related to length and can vary from 13 to just below 20 g (Berry 1991; table 8.21). House mice are considered a highly commensal species and indeed they are the main pest throughout Britain (e.g. Langton et al. 2001). However, contrary to the prevailing notion on their over-reliability on human activity, strengthened by some extinction events (as mentioned before, see Boyd 1956), their populations can actually adapt to wild areas, especially isolated islands (e.g. Skokholm in Berry 1968 or Lewis in Elton 1934). Depending on habitat house mice population dynamics may be vastly different, from a relatively stable in-house population with a restricted territory and breeding season encompassing most of the year (e.g. Pocock et al. 2004), usually skewed towards females (e.g. Khanam et al. 2017), to free and long-distance roaming, young population without visible sexual bias but with a breeding season restricted by environmental factors (e.g. Pearson 1963; Berry 1968). Mice may migrate towards shelters during the winter and resettle open areas during late spring and summer (e.g. Skokholm island in Berry 1968).

In nature their population may be scarce and irregularly distributed (Pearson 1963). Some house mice populations on Orkney have survived the isle abandonment by humans, but existing examples, such as Faray abandoned in the late 1940s, have been greatly reduced in size to the point of a significant genetic drift each winter (Berry et al. 1992). While having a relatively fast reproduction rate in comparison to e.g. *Apodemus* (Berry & Tricker 1969) house mice population is more susceptible to yearly variation of temperatures than other rodents. A direct relation between the % of population survivorship rates during the winter and climatic variation, especially temperature during the preceding year, can be inferred from previous studies (Pearson 1963; Berry 1968). However, house mice may sometimes adapt to harsh conditions

and the presence of other competitors (e.g. Sub-Arctic in Renaud et al. 2013) and environmental changes may have a major impact on social behaviour and structure of the house mouse population (Wolff 1985; Perony et al. 2012) which contributes to their chances of survival.

House mice seem to be present on all major landmasses of the Orkney archipelago and there are records of sighting from 20 different isles (Berry 1985, 132; 2000, 142-143; Booth & Booth 1994, 15; Booth & Booth 2005, 83-84). Not much is known about the history of house mice on Orkney apart from historic references from the eighteenth century AD onwards (Booth & Booth 1994, 15; Booth & Booth 2005, 83-84). In the nearby Shetland isles archaeological digs unravelled house mice bones in contexts from around the middle Iron age (circa second century BC – fourth century AD, Nicholson et al. 2005), suggesting a stable population roughly correlating the established timeframe of house mice colonisation of Great Britain (Connor 2010; Searle et al. 2009 Appendix 1). Still, later human migrations and Atlantic trade intensification during the Norse period (late eighth to twelfth century AD) resulted in a Scandinavian population of a house mouse being introduced to various Atlantic isles, including Ireland, the northern end of Great Britain (Caithness), Outer Hebrides as well as Orkney and Shetland isles (Searle et al. 2009). The impact was severe as current *Mus* mtDNA vastly differs from one found in the rest of Great Britain, being its own kinship group with Norway and Iceland populations (Searle et al. 2009; Jones et al. 2012, 2013).

In the wild, house mice may fall prey to other rodents (e.g. black rat, Bridgman et al. 2013) as well as small carnivores (e.g. weasels, *Mustela nivalis*, Tattersall et al. 1997). However, while usually considered as harmless to other species, house mice in the wild may actually affect the distribution of some of them, most notably bird nesting's due to predation on eggs (Cuthbert & Hilton 2004). House mice population may also transmit diseases dangerous for humans and their animals, e.g. lymphocytic choriomeningitis virus or cowpox, especially through contaminating the area with their feces (more in Meerburg et al. 2009). However, the Orcadian isles are scarcely populated and due to single at most cases of such illnesses there is no available data for tracking and comparing (e.g. lack of information about *Campylobacter* infections, Miller et al. 2004; Bessell et al. 2010). Judging from the study on the cause of death of sheep population on North Ronaldsay (Britt & Baker 1990) there are parasites present on Orkney isles that may be transmitted between mammals, including rodents (see Flowerdew 1991; Flowerdew & Tattersall 2008, parasites), but prominent cases are usually either species-related (in this case sheep) or shared by predominantly domestic animals (e.g. in this case by sheep and dogs).

2.3.5. PYGMY SHREW (*SOREX MINUTUS*)

Pygmy shrew is one of the smallest mammals in existence, with head and body length up to 6 cm and weighting up to 6 g (Churchfield 1990, 108, fig. 5.1; Churchfield 1991a, table 5.4.). This species of solitary insectivores is widespread and relatively uniform through Eurasia, including the British Isles, except for Shetlands, Channel Islands and the Isle of Scilly (Churchfield 1991b; Churchfield & Searle 2008a). In contrast to their bigger brethren, common shrews (*Sorex araneus*, Churchfield 1991a; Churchfield & Searle 2008b), pygmy shrews exhibit far higher tolerance towards extreme and non-optimal environments in conjunction with wider roaming territories, broader diet, utilizing burrows of other species instead of creating ones and general lower population density (Michielsen 1966; Yalden 1981; Churchfield, S. 1990, 92, 101; Churchfield 1991b). They are known to inhabit grassland, marshland, stone walls, and buildings vicinity, occasionally entering human habitation as well as man-made nesting boxes (Yalden et al. 1973; Churchfield 1990, 149; Churchfield & Searle 2008a). Pygmy shrews can carry zoonotic diseases but rarely engage humans in a way that would enable their transmission (Churchfield 1990, 151).

Considering genetic and morphological studies, pygmy shrews were most likely introduced to Orkney through Great Britain from South-Western Europe and in contrast to Orkney voles show low genetic variation thus suggesting a small initial founder population (Vega Bernal 2010). The initial introduction event, from Great Britain to Orkney isles, occurred most likely due to human agency but later introductions to other islands, especially through narrow water corridors (Hanski 1986; considered as good swimmers, Churchfield, S. 1990, 149-150; Churchfield 1991b), were most likely natural and spontaneous (Vega Bernal 2010). While there is no archaeological evidence known for this species the Neolithic period is suggested as the most relevant time from a genetic perspective (Vega Bernal 2010). Single pygmy shrew bone find was reported from Howe, broch site and later farmstead, layer 8 (Late Iron Age, on-site from fourth century AD till seventh to ninth century AD; Smith 1994, table 11), as well as within the Birsay sites (Rackham 1996).

Pygmy shrews seem to be rarely seen on Orkney, but most of the isles, apart from the North-eastern end of the archipelago (Sanday, North Ronaldsay), contain at least a small population of them and are considered as relatively common (Booth & Booth 1994, 4; 2005, 78; Churchfield 1991b). Known data from English grasslands suggest a mean density of 12 per ha and a maximum up to 30 (Pernetta 1977; Churchfield 1984; Churchfield & Brown 1987) and

considering habitat should be roughly similar to those on Orkney. They may be sometimes caught by kestrels, hen harriers and short-eared owls but consist of a minority of their diet (at best <3,1%, Reynolds 1992).

2.3.6. BLACK RAT (*RATTUS RATTUS*) AND BROWN RAT (*RATTUS NORVEGICUS*)

Black rats are omnivorous rodents well adapted to the anthropogenic environment and, depending on environmental conditions, dependent to highly dependent on human presence. (Taylor 1991; Twig et al. 2008). Head and body can reach a length of 24cm and a tail of about the same length as well as 200 to 280 g live weight (Taylor 1991; Twig et al. 2008). In the wild population density fluctuates similar to other rodent species and the general densities depend on the environment, from less than one specimen per hectare up to almost 50 during late summer peaks (e.g. Harper & Rutherford 2016, table 3). In urban areas densities are usually high (Leslie & Davis 1939) but depend if brown rats, *Rattus norvegicus*, are present. If yes, the black rat population, being outcompeted by brown rats, will most likely be confined to the city port and avoid residential blocks (Himsworth et al. 2014). Especially rats living within the urban environment are prone to contract and carry various diseases. However, the actual risk of infection depends on the density and size of rat colonies, flea infestation and other variables – if specific thresholds are not reached there is no risk of plague (e.g. *Yersinia pestis* in Durham & Casman 2009).

As previously noted the first black rats came to the UK around the first century AD, as archaeological evidence suggest (Rackham 1979; O'Connor 1988A), and are present to this day (Harris et al. 1995), but the distribution and size of their population fluctuated heavily during the past twenty centuries (Reilly 2010). Confirmed archaeological remains of these rats have so far been reported only from Birsay Bay (Rackham 1996) although not much consideration was given to their presence. In most cases no identification was attempted, with bones just identified as a “rat” (e.g. Burgh of Birsay. Seller 1982). It is widely accepted that their decline in the past two to three centuries was due to the introduction of the larger-bodied brown rat to the UK and the current population most likely survived due to occasional reintroduction through maritime travel (Lawrence & Brown 1973, 100-102; Taylor 1991; Twig et al. 2008). According to a couple of sources (e.g. Baikie & Heddle 1848, 15) black rats were present on at least some Orkney isles at the end of eighteen till middle nineteen century but their population was swiftly

declining; the only record from the twentieth century mentions accidental introduction to Westray, but this population is most likely completely extinct by now (Booth & Booth 1994, 17; Booth & Booth 2005, 84). It cannot be excluded, that an introduction occurred in the past, but so far no relevant archaeological data have been retrieved from contexts dating from the first to eighteenth century AD.

So-called brown, common or Norway, rats are one of the largest omnivorous and burrowing rodents living near or within the man-made environment, sometimes measuring over 28cm in length (excluding tail) and 600 g in weight (Taylor et al. 1991; Quay & Macdonald 2008). In urban areas the density may heavily fluctuate, from regions devoid of infestation to those suggesting populations well above 100 specimens per ha (Himsworth et al. 2014). Similarly to other British populations (Lawrence & Brown 1973, 102-103; Taylor et al. 1991; Quay & Macdonald 2008) brown rats were introduced to Orkney around eighteenth century, most likely as stowaways, and established populations on main isles except for Westray, North Ronaldsay but Papa Westray population is most likely currently extinct (Booth & Booth 1994; Booth & Booth 2005, 84). Currently their colonies can be found in most urban environments as well as those, where there is no significant competition from other species (Taylor et al. 1991; Quay & Macdonald 2008). On Orkney known habitats include seashore, ditches, dykes and barns as well as refuse heaps and, during winter, human habitation (Booth & Booth 1994, 16). While some are occasionally hunted by ravens (Marquiss & Booth 1986) the presence or absence of rats may impact establishing nests by some bird species. Most notably Storm petrels, *Hydrobates pelagicus*, nest exclusively on small Orkney islands devoid of any signs of rat activity (León et al. 2006) while a nesting location of Black Guillemots, *Cephus grylle*, depends on the presence or absence of brown rats and stoats, *Mustela erminea* (Ewins & Tasker 1985).

While there are no archaeological finds of these species from the Eighteenth century AD onward, at the archaeological site (broch) of Howe a rat skull from the Iron Age for Phase 7 (first to fourth century AD) was identified as a brown rat (Smith 1994, 142, 147). It was however acknowledged, that such remains are most likely intrusive, though how a single individual penetrated about 1,5 m of archaeological rubble layers is currently unknown (Smith 1994, 147). A similar issue was also found in the case of Holm of Papa Westray site (Cucchi et al. 2009).

2.3.7. AMBIGUOUS INTRODUCTIONS

Water shrews (*Neomys fodiens*) were only reported on Hoy in the nineteenth and twentieth century AD. (Baikie & Heddle 1848, 14; Buckley & Harvie-Brown 1891, 65; McMillan 1965) but are considered now as either as a temporary introduction or misidentification (Booth & Booth 1994, 4; Booth & Booth 2005, 79). *N. fodiens* specimens are definitely bigger than pygmy shrews, up to 10cm of body and head length and weight up to 18 g and create specific burrows or utilize ones created by field mice (Churchfield 1991c; Churchfield & Searle 2008c). Once caught, their identification should be relatively easy. However, densities are even lower than pygmy shrews, around two or three per ha (Churchfield 1984), and, along with the feeding behaviour that includes foraging shallow waters (Churchfield 1991c), it may be the point why their population is so elusive. However, even if present the substantial lack of data for this species suggests at most minor and highly restricted impact on Orcadian environment, rendering this species of minimal relevance to archaeological investigation.

The most recent introduction is most likely the European hedgehogs (*Erinaceus europaeus*), a species of mostly nocturnal omnivores. Up to 26cm long, excluding the tail, and weighing sometimes up to 2kg, hedgehogs are solitary animals fond of high vegetation habitats, where they can build their nests and hibernate during winter (Morris 1991; Morris & Reeve 2008). The sequence of introductions on Orkney is well established and spans from 1870 to 1980. In most of these cases the introduction was deliberate: from the need of pest-eaters to be introduced to gardens to simply handing them as pets to children (more in Booth & Booth 1994, 1-3; Berry, 1985, 130-131; 2000, 137-138; example in Buckley & Harvie-Brown 1891, 64). Population densities are low, around 1 to 2 per ha depending on the habitat (more in Morris & Reeve 2008). Hedgehogs can prey on bird eggs and their presence can have a negative impact on the seabird population (e.g. Jackson & Green 2000). There is some correlation present on Orkney (e.g. León et al. 2006) that may have some impact on bird colonies, but even if they are not considered as a serious threat (Berry 2000, 138; e.g. Amar & Redpath 2002). Similar to water voles, those animals show no importance to archaeological studies due to their recent introduction and lack of burrowing capabilities, although they can sometimes use burrows of bigger species and enter archaeological context in that way.

2.3.8. MICROMAMMAL REMAINS AND OTTER SPRAINT

The presence of rodent bones on sites nearby watery habitats is sometimes considered in casual conversation between archaeologists as a side effect of European otter, *Lutra lutra*, predation. However, it is rarely discussed in the available literature, usually as one of many suggestions towards assemblage formation (e.g. Barber 1997, 52). Indeed, the presence of micromammals in otter spraint is occasionally visible. However, their bones consist of less than 5% of such assemblages and predominantly include rabbits and water voles, species that live next to or in similar habitats as otters (e.g. Erlinge 1967; Wise et al. 1981; more in Chanin 1985). Orkney otters were found occasionally hunting wild birds or entering hen houses during winter months, but in similar environments in Shetland all of their diet consisted of marine species (Berry 1985, 107). There is no paper on this phenomenon that could be used for a proper comparison. However, as known from carnivores (e.g. Andrews & Evans 1983; Andrews 1990), micromammal bones in otter spraint should be heavily fragmented, digested and skeletally incomplete, similarly to foxes and dogs. Therefore, contexts similar in composition to red fox assemblage but from different habitats than those usually inhabited by foxes may show otter activity.

2.4. SUMMARY

Zooarchaeology, paleoecology and paleontology of micromammals is thematically and methodologically as complex as for larger species. Interests of researchers range from typically biological questions, such as species evolution and impact of paleoenvironmental/palaeoclimate factors on it, to zooarchaeological investigations into human-animal relationships, especially between human migrations and subsequent introductions of micromammal species to new environments. In some cases, such as palaeoenvironmental reconstruction, micromammals are a far better source of information than other types of animals due to their population dynamics. In consequence, methods available for studying micromammal remains, even if not commonly used, are also as varied as ones used for larger taxa and reflect faithfully a wide range of thematic approaches. Research on digestive marks especially reached its current state partially thanks to research on micromammal remains, which quite often provide signs of being swallowed as a whole by a wide range of different predators. Workable methods include retrieval and handling, species identification, measurements, data quantification and contextual information. The type of primary data that can be retrieved includes contextual information, basic quantification units (e.g. NISP), age in broad categories (juvenile/subadult/adult) and different types of taphonomic changes (e.g. fragmentation, burning). Secondary data includes the estimation of minimal number of individuals (MNI), indexes, including ones specifically created to study rodent populations, (based on a number of identified species, specific bones NISP, taphonomy etc.) and skeletal frequencies/abundances.

From a methodological view, micromammal zooarchaeology is however plagued with problems that hinder its development. Some of the issues are similar to those encounterable when studying bird or fish remains (e.g. identification). However, where solutions have been suggested and are currently being introduced in those two fields, micromammal zooarchaeology lacks such long-term projects. The proper application of many methods beyond simple identification requires sieving, which may be heavily problematic to achieve and/or fund. Even if rigorous sieving is employed it may not be optimised towards retrieving small mammals but rather bird or fish bones or even shell remains. Moreover, the impact of different approaches to sieving or sampling on the retrievability and representativeness of various types of data has been rarely discussed. Discussion so far was concerned with only the number of retrievable bone fragments and possibly the size of retrieved elements (e.g. Stahl 1996) but the

impact of sampling/sieving on e.g. frequencies or age distribution was never estimated. In a similar manner, the impact of many taphonomic factors on established methods has not yet been properly assessed. While recent research starts to understand the presence and pattern of such factors it is still largely on a contextual rather than quantifiable level. As a result, statistical and computational methods are well developed only for research questions treating micromammals as a proxy, remaining underdeveloped for more taphonomy-related research.

At a larger scope, the overall sparseness of research centres working regularly with micromammal remains from archaeological sites significantly slows the research development. Overall reliance on zoology and paleoecology of existing research centres also does not help. African and American micromammal research can be considered as highly varied, tackling all approaches described in the paper above. It is not surprising considering the wealth of micromammal species present on those continents but is also motivated by human-animal interactions currently present or historically known in those regions. In turn, Europe is represented by both highly detailed palaeoenvironmental and migratory research, but deeper insight into other forms of human-animal relationship, or past population dynamics besides prey-predator, is visible in only a handful of publications. Some regions, most notably Asia, remain mostly unknown, with only a handful of studies available from wildly different regions. However, this situation may be a sign of the obscurity of existing published studies and the lack of sources available for the worldwide audience rather than just a lack of research. In many studies known to the author micromammal remains analysis are also thematically detached from other faunal remains, such as bigger mammals but also birds and fish and even other small animals, that could share similar or even the same taphonomic history, as well as floral finds that could aid in such research. Rarely do the environmental and human-animal relationship questions overlap in one paper, typically being treated separately from each other. Thankfully, recent papers challenge this situation and try to bring mainstream zooarchaeology and palynology closer to worthwhile micromammal research.

When it comes to the scope of Orkney and its fauna and natural history, one can see a desirable testing ground for more archaeology-related micromammal studies. Most terrestrial species inhabiting Orkney, including all terrestrial mammals, have been introduced by humans, intentionally or not, during the span of several thousand years. Introduction events occurred most likely during periods of intensive maritime contacts, resulting in the establishment of several micromammal species populations of commensal or quasi-commensal nature. Additionally, some predators, e.g. kestrels, most likely started inhabiting Orkney once the

population of Orkney voles had been established, suggesting gradual enrichment of Orkney fauna and the appearance of more and more complex chain of dependencies between various species. Considering those possibilities more detailed studies on micromammal taphonomy may help in establishing relations between micromammals, their predators and humans and their changes over the span of several millennia. The more exact dating of introduction events may be also possible when archaeological material will be explored in depth. A small pool of species inhabiting Orkney however offers both opportunities and challenges. Several methods related to tracking environmental changes are not applicable but at the same time taphonomic histories of those species should be easier to differentiate and research.

3. MATERIALS AND METHODS

3.1. INTRODUCTION

The initial choice of methods concentrated on ones developed specifically for micromammal taphonomy. Considering the restricted number of species on Orkney, sharing strong connections to human activity, analysis of diversity or richness could be done by simplest means; more complex approaches would most likely return no valuable information. Moreover, studies on taphonomy are more relevant to zooarchaeological research and much more needed due to a lack of significant development over the past several years. The methodology established for Romaniuk et al. (2016a) paper, built mostly on Andrews (1990) work, was broadened by alternative approaches more akin to zooarchaeology, notably scoring age-related markers, investigating pathologies and researching taphonomic marks of burning, staining and weathering. A number of sites have been investigated (**Objective 2**), alongside a wide selection of references have also been established for further study (**Objective 3**). Visualisation, when possible, followed pre-established standards (e.g. linear graphs for comparing abundances, see Andrews 1990).

However, the biggest challenge was to deliver methodological research split into two thematic parts, following both thesis aims. Especially including the results of the first, methodological case study in later sites assessment proved to be a complex task. That is why the chapter was divided into three parts. First concentrates on all the materials used in both case studies (**Objectives 2 and 3**), including reasons behind their choice. The second part proceeds with describing methods utilized for obtaining data from chosen materials and constructing a database of possible references. The third part continues with outlining the methodological approach used for investigating and developing established methodology in the first case study, with a description on how first case study results can be used to improve the methodology used in later sites assessment.

All micromammal material used for this thesis was stored in the NMS Vertebrate Collection (National Museums Collection Centre) and studied within the centre's facilities with the help of Dr Lore Troalen and Dr Jeremy Herman. The only exception to this is a small number of bones sent to the University of York, Archaeology Department (see **Chapter 3.3.2.**).

3.2. MATERIALS

3.2.1. SITES SELECTION

Choosing comparable sites that would faithfully represent Orkney over two main time periods was a complex one. Due to the importance of proper sieving, elaborated on in the literature review, predominantly sieved samples or contexts had to be included in the study. Beyond that for the sake of contextual comparability with Skara Brae (Romaniuk et al. 2016a;b), the material should have been coming from settlement sites. The point of the research was also to investigate differently retrieved archaeological material. The issue was that the choice of methods often differs along the lines of better and lesser understood time periods. Neolithic and Early Bronze sites were often thoroughly sieved while Norse and Medieval ones were mainly investigated through sampling or a combination of it with a whole-earth approach to specific contexts/areas. The situation has changed in recent years and currently ongoing excavations on sites from different time periods differ less in their sampling strategy. However, newly excavated material was not available to the author. As a result, excavation material from the 1970s to 1990s had to be employed for the research.

Six sites were available to study between 2017 and 2020 (see Table 3.01 for the summary data for each site and Fig. 3.01 for their location). All have included sieving in their methodology, though differing in detail. Methodological differences noted, as expected, showed a division between whole-sieved Neolithic and later sampled sites. In turn, contextual comparability could be fully achieved with five out of six sites being settlements with little to no intrusive burrowing identified. Samples from those sites came from both the site centre as well as its peripheries or even off-site natural accumulations, possibly providing foundations for more complex comparisons. Mainland, the biggest, most populated and economically important island, was represented by three sites, with the remaining two coming from the fringe island of Westray, located on the maritime route to the Shetland isles. Finally, in order to compare those sites with likely intrusive assemblages, the author included a Norse boat burial from Sanday. Two sites were already part of NMS collection while the other four were loaned to NMS by Dr Gail Drinkall (Orkney Museum), Dr Olwyn Owen and Dr Catherine Smith (Adler Archaeology) for the duration of this research.

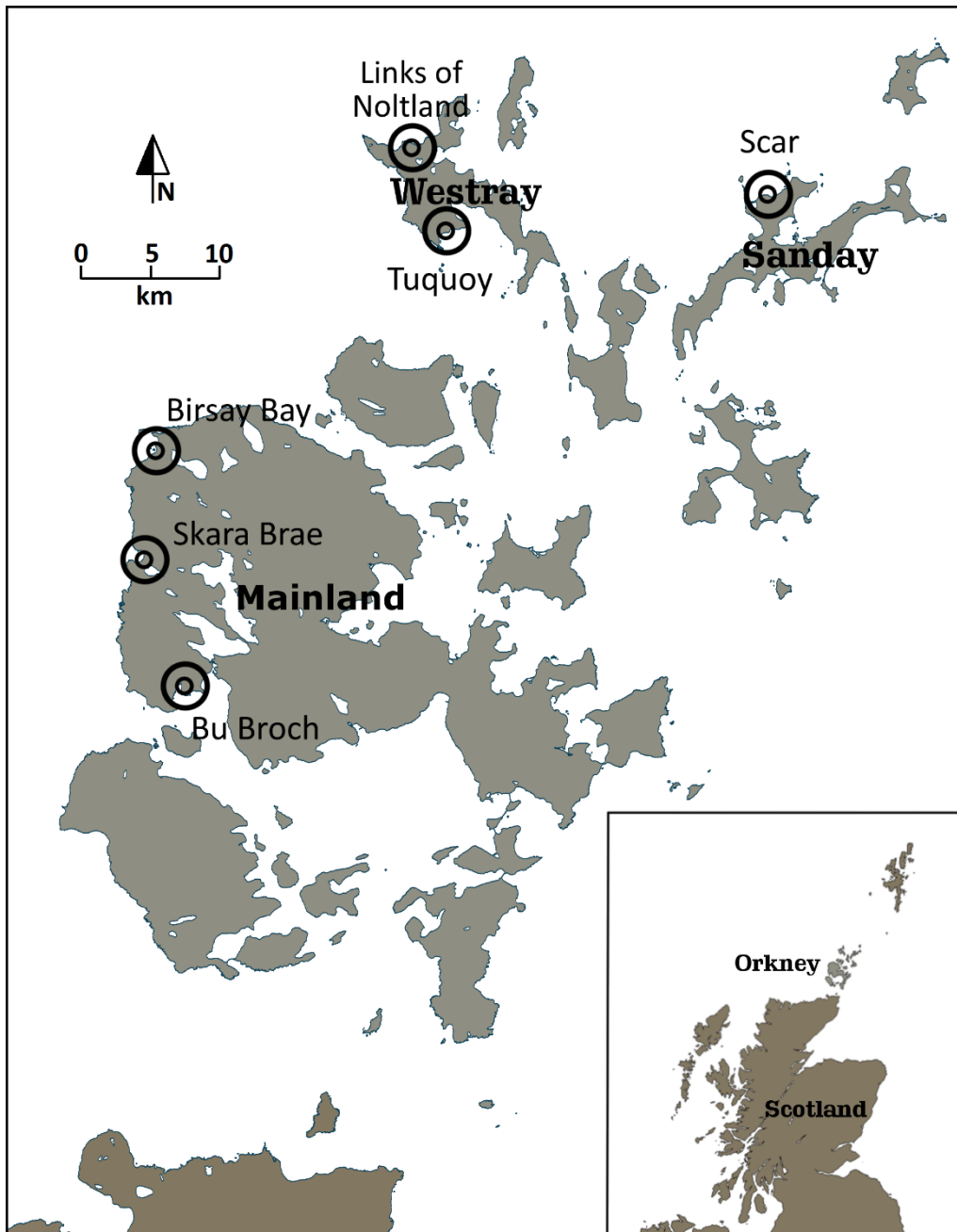


Fig. 3.01 – Map of the Orkney archipelago with the location of six studied sites.

Table 3.01 – Summary of key information about the chosen sites, including sampling/sieving strategy used (Hedges 1987; Owen 1993; Morris & Ballin Smith 1996; Owen & Dalland 1999; Moore & Wilson eds. 2011; Marshall et al. 2016; Shepherd 2016; Clarke et al. 2017; Bayliss et al. 2017; Krus 2017; Owen 2017).

Site	Skara Brae	Links of Noltland	Tuquoy	Bu Broch	Birsay Bay	Scar
Location	Mainland	Westray	Westray	Mainland	Mainland	Sanday
Type	Settlement	Settlement	Settlement	Settlement	Settlement	Boat Burial
Date	3500 - 2450 BC	3160 - 1930 BC	700 - 1300 AD	850 - 450 BC (?)	980 - 1210 AD	895 - 1030 AD
Periods Represented	Neolithic		Norse/Mediaeval	Early Iron Age	Pictish/Norse/Mediaeval	Norse
Originally Stored	National Museums of Scotland (NMS) Alder Archaeology Ltd					
Time Excavated	1972-3 & 1977	1978-81	1982-3 & 1988	1978	1978-80	1991
Supervisor	David V. Clarke		Olwyn A. Owen	John W. Hedges	Christopher D. Morris	Magnar Dalland
Sampling strategy	Whole sieving	Whole sieving, grid coordinates considered	One up to four samples per context	One sample per archaeological context	Depending on area, either key contexts or selected grid square sampled in full	Multiple samples per context
Sample size			~10 l samples	unknown	~14 l samples	~10 l samples
Sieving	Meshes utilized jointly: 5, 3 and 1.5 mm	grid-reliant	1982-3: 1 mm (all samples) 1988: 4mm (all) and 0.5 mm (1 out of 10 samples)	Utilized but mesh unknown	Meshes utilized jointly: 2, 0.895 and 0.5 mm	1 mm for samples, bigger meshes for entirety of contexts

3.2.2. SKARA BRAE

Skara Brae is a famous Orcadian Neolithic settlement site located on the western shore of Mainland, near the Bay of Skail (Fig. 3.02). It was initially investigated by V.G. Childe in the 1920s (Childe 1930; 1931). However, during that time only the latest layers of the site were investigated, with little to no insight into stratification and no sieving done. However, later archaeological research, of D. Clarke and his colleagues in 1972-3 (Clarke 1976a; 1976b) and later in 1977, provided far more data to work with. During that dig four trenches were opened, located in different parts of the site – one in the centre, one in the peripheral area and two outside of the settlement (Clarke 1976a; 1976b; D. Clare and A. Sheridan pers. comm.). All material excavated was thoroughly sieved through a set of 5mm, 3mm and 1,5 mm mesh sieves. While site monograph has not yet been published materials from Clarke's work has been frequently discussed and a large amount of data are available in different papers or book chapters (Clarke & Sharples 1985; Clarke 2003; Shepherd 2016; Romaniuk et al. 2016a;b; Bayliss et al. 2017) as well as from the researchers themselves (D. Clarke, A. Shepherd and A. Sheridan, pers. comm.).

Official dating underwent a number of changes, from the initial assumption of the site belonging to the Iron Age (due to the presence of stone architecture, more: Childe, 1930; 1931) and later reconsideration as Neolithic (Childe 1935, 176-181; Childe, 1946, 25-34) to proper radiocarbon dating and placing the period of site occupation in a span of roughly 3500 – 2450 BC (Renfrew & Buteux 1985; Sheridan et al. 2013). Three phases of occupation with hiatuses in-between were identified (Clarke 1976a; Martínková et al 2013; Sheridan et al. 2013) and later incorporated into the study of Orcadian sites using Bayesian framework (Bayliss et al. 2017, especially Fig .5). Phase 0 (lowest contexts), dated to 3500 – 3100 BC and associated with round-based pottery, was followed by a long hiatus of two centuries, ending on the century-long Phase 1 representing flat-based pottery (2900 – 2800 BC). After that another hiatus of less than a century was present, ending on a continuous occupation from 2750 to 2450 BC.

The site is especially known for its architecture but the notion about its significance changed over time as more data became available with later archaeological work. All constructions were made out of stone, with some parts mimicking what is usually seen in wooden architecture like e.g. room furnishing (Childe, 1931; 1935; 1946; Clarke, 1976a; 1976b; 2003; Shepherd 2016). Originally it was thought, that Skara Brae was a unique case of a whole site being created in stone and along with specific planning, but later finds of stone architecture on Orkney or re-

dating already found stone architecture sites to the Neolithic (e.g. Knap of Howar: Renfrew 1979) and a better understanding of stratigraphy and proofs of gradual creation of such sites (Shepherd 2016) proved original notions wrong. In a similar way, it was thought that the site buildings and passages between them were dug into pre-existing midden deposits, but properly analysed data from the 1970s digs suggest that middens associated with specific buildings appear later than their construction, being most likely deposited by inhabitants during the site occupation (Shepherd 2016).

As in the case of architecture, the notion about ancient Skara Brae dwellers' subsistence also underwent changes as new finds emerged. Zooarchaeological finds from Childe's investigations pointed almost exclusively towards cattle and sheep stockbreeding and possibly hunting (Watson 1931). However, such conclusions were most likely due to a lack of sieving as a half-century later evidence for intensive fishing was found (Clarke 1976a; Clarke & Skarples 1985). While some evidence for farming has been found in Skara Brae better and well-dated finds were excavated on other Neolithic sites, suggesting intentional usage of manure as a fertiliser (Clarke & Skarples, 1985). Later studies revealed, that arable lands were created artificially by flattening former midden heaps (Guttmann et al., 2006). Apart from large domesticated animals, dogs were also present in Skara Brae (A. Shepherd & A. Sheridan pers. comm.) and their remains and/or coprolites are known from a number of different sites, including e.g. Links of Noltland (Carrot 2011; Fraser 2011).

The site stratigraphy is faithfully represented by Trench I, located near the centre of the site, and supplemented by Trench II, representing site periphery (Fig. 3.03 and 3.04 respectively). Beyond 4 meters deep, Trench I provided data about all three major phases of occupation and hiatuses in between (Clarke, 1976a; Shepherd 2016). Contexts from Phase 0 contain mainly clay with ash inclusions while Phase 1 provided mostly mixed contexts, containing sand, clay, ash, refuse and household refuse. The intermediate phase, between Phase 1 and 2, contained mostly sand accumulations, with lenses of clay, ash and refuse in between, suggesting the site was still occupied to some extent. Phase 2, most complex in terms of evidence, contained contexts similar to phase 1 but richer in household waste. Clay deposits are evidence for walls of Skara Brae building being most likely encased in them; such layers later crumbled down and were included in midden deposits around constructions (Shepherd 2016). No visible traces of burrowing were recorded while soil studied on selected samples showed no bioturbation present (Simpson et al. 2006). Trench II deposits correlate with both Phase 1 and 2 and are filled with

sand, clay, household refuse but also remains of animal dung (Simpson et al. 2006). Especially context 213 provided a variety of organic finds due to being a water-logged midden.

Trenches III and IV represent off-site, relatively undisturbed natural accumulations, with quite a simple stratigraphy and a small number of contexts representing wider time periods. Contexts excavated contained predominantly sand with a minor addition of clay and turf, with some evidence of plough marks and redeposited or eroded occupation deposits in Trench IV. The only evidence for intrusive burrowing found was a rabbit hole in Trench IV, filled with sand. However, finds from off-site contexts have rarely been discussed in the currently available literature.

Lack of burrowing and whole-earth approach sieving makes Skara Brae a great site to study micromammals. The sample was firstly studied in 2015 as a part of the author's MSc dissertation (Romaniuk 2015; Romaniuk & Herman 2016; Romaniuk et al. 2016A; Romaniuk et al. 2016B). Micromammal remains were found in all four trenches, with all the content weighting about 822g.

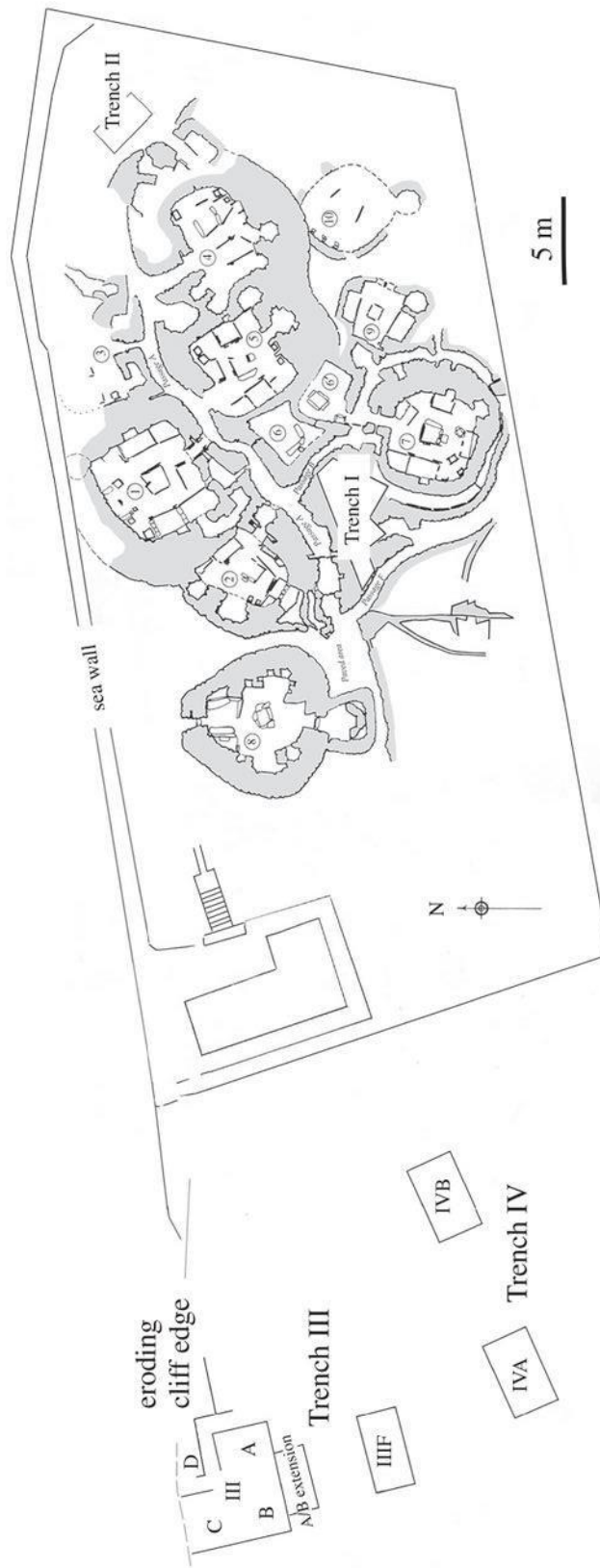


Fig. 3.02 –Skara Brae, site plan. Places of 1972-3 trenches can be seen within the site (Trench I) and its north-eastern end (Trench II) while all 1977 trenches (IIIa-d&f and IV) are located beyond the western end (Romaniuk et al. 2016A, fig. 1).

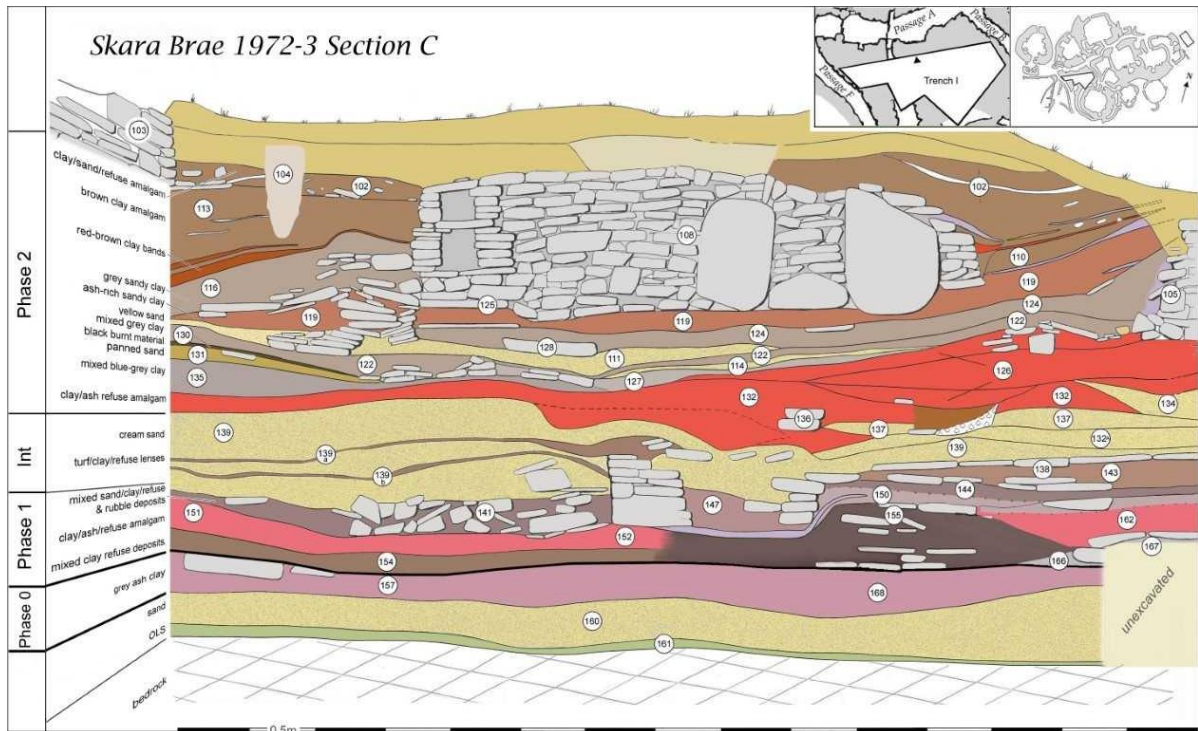


Fig. 3.03 – Stratigraphy of Skara Brae Trench I. The stratigraphy plan shows the northern face of the area, with main phases and context details present (Shepherd 2016, 223 fig. 5).

Skara Brae 2006-7 C14 dates BP Trench II

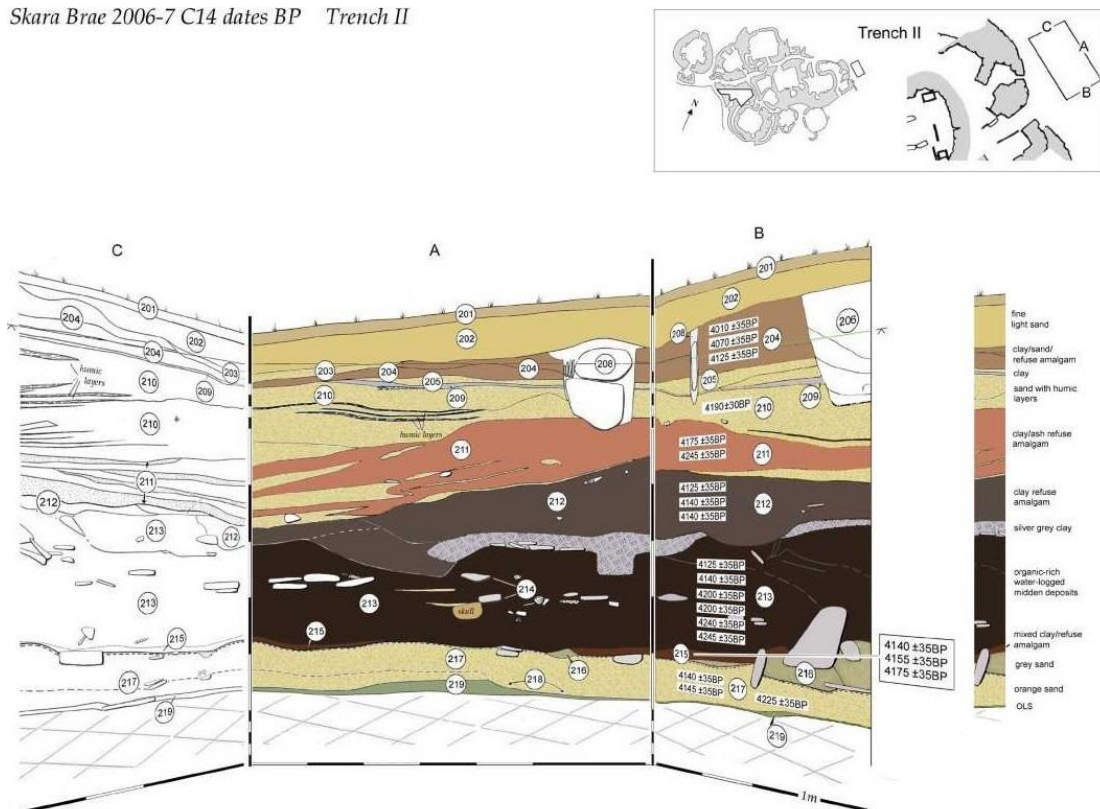


Fig. 3.04 – Stratigraphy of Skara Brae Trench II. The stratigraphy shows north-eastern, north-western and south-eastern faces of the area, with main phases and context details present (A. Shepherd pers. comm.).

3.2.3. LINKS OF NOLTLAND

Links of Noltland is a settlement site located on the Northern shore of Westray, Orkney. It was firstly excavated in 1978-1981 by Prof. D.V. Clarke (Clarke et al. 1978, Clarke & Sharples 1985). However, due to rapid erosion, rescue digs had to be arranged. From 2000 the assessment of the site began, with regular archaeological investigations from 2007 onwards (Moore & Wilson eds. 2011). Trenches from the late 1970s dig encompassed Neolithic material, roughly contemporary to Skara Brae (Ashmore 2000), Barnhouse (Richards 2005) and Phase 3 at Pool (Hunter 2007; sequence of all sites in Bayliss et al. 2017). However, later digs also found remains from the Early Bronze Age (Moore & Wilson eds. 2011, 24-28). While the radiocarbon dating is highly problematic and final dating has not been published yet for both excavations it seems, that, contrary to Skara Brae, Links of Noltland had been continuously occupied from about thirty-fourth/thirty-second century BC till eighteenth century BC (Moore & Wilson eds. 2011, 38-39; Bayliss et al. 2017, fig. 5). Links of Noltland provided finds such as ploughmarks (Clarke & Sharples 1985, 74 Pl. 4.10.) which suggested that agriculture might have been more important to Neolithic Orcadians than previous investigations have established (Clarke & Sharples 1985). Apart from that the settlement itself represents a loose concentration of various buildings of evidently different utilization (Moore & Wilson eds. 2011, 29-32).

Both 1970-80s digs and modern investigations provided a significant amount of finds but only Clarke's material could be covered in this study. While the sieving process during Clarke's digs is never officially stated in any publication, the method was in essence identical to that utilized in Skara Brae, including mesh sizes. Also, similarly to Skara Brae, Clarke's excavations at Links of Noltland lacks a final monograph. However, a number of publications covering details of their work are available (Moore & Wilson eds. 2011; Marschall et al. 2016; Clarke et al. 2017). Additionally, the author could obtain unpublished data from the researchers (D. Clarke, A. Shepherd and A. Sheridan, pers. comm.). In newer studies both dry and wet sieving have been employed but only archaeologically rich deposits were screened in full (Moore & Wilson eds. 2011, 35-36). The size of the mesh is unknown, but a taxonomic identification of some smaller finds revealed the presence of an Orkney vole (Fraser 2011). The excavations are still ongoing, but the author could not obtain permission to study already excavated materials.

Two trench areas could be taken into consideration during this research. Clarke's excavations investigated mainly in the coastal, Neolithic part of the site, exposed to sea erosion and requiring immediate archaeological intervention. Six trenches, named after first letters of the

alphabet, were opened in two broader regions of the site where structural remains were unearthed by the erosion (see Fig. 3.05). Apart from Trench B, all provided micromammal material. However, stratigraphic and contextual data are currently available only for the two biggest trenches excavated, Trench A and D, each representing a different region of the site but of roughly the same occupation periods.

Most varied and well documented is Trench D (Fig. 3.06), located on a verge of Area 4 Neolithic occupation deposits. As only one of six trenches it was excavated up to the natural bedrock revealing layers of cultivation, refuse deposition and minor constructions such as stone walls (Clarke et al. 2017). It is also the place where carcasses of several red deer were found piled in a single context, prompting questions about Orcadian ritual practices (Sharples 2000, Clarke et al. 2017). Later research revealed that trench is located next to a so-called Structure 7, a rectilinear stone building containing multiple midden deposits and being most likely the centre of Neolithic activity for the whole area 4 (Moore & Wilson eds. 2011, 22).

The stratigraphy of Trench D is complex (Fig. 3.07) and in some cases impossible to establish fully (Clarke et al. 2017). Oldest unearthed cultural phases (Phases 1 and 2) showed signs of arid cultivation on midden-enriched soils, with repeating episodes of cultivation and refuse deposition over a period of at least 55 - 330 years (from 3160/2870 to 2850/2640 cal. BC, Clarke et al. 2017, Ill. 11). Subsequent Period 3, however, did not represent cultivation but only refuse dumping in large quantities, especially of organic material and shells, and occasional in-situ activity (e.g. flint knapping in context 21). Considering carbon dating, refuse accumulation seemed to start as soon as cultivation stopped and continued for a considerable time (Phase III itself till about 2550-2300 BC, see Clarke et al. 2017, Ill. 11). Around 2500-2225 cal. BC a stone wall was constructed (Phase IV), possibly as a boundary rather than an element of any structure. Contexts around Phase IV were disturbed by the construction work to the point it is currently impossible to be certain whether refuse deposition continued some time after or ended before or alongside the wall creation. However, the next phase (Phase V) saw a deposition of 15 deer carcasses, parts of other animal body parts and shed antlers, possibly as a single event (2280-2245 cal. BC, see Clarke et al. 2016, Ill. 11), additional layers of sand covering the deposition and marker-like structure of several stone slabs. Following contexts, belonging to Phase VI, represent temporary abandonment of the site and is followed by a return to cultivation (Phase VII). The latest finds from recent cultivation layers were vole remains, dated to 2200-1930 cal. BC (Clarke et al. 2016, Ill. 11). The final sign of human activity before complete site

abandonment was the construction of another wall in Phase VIII, though an exact date is unknown.

Trench A covered a bigger area than D but only a part of its stratigraphy has been reconstructed. The robust structure consists of two main areas, a main chamber on the south and a room or rooms on the north, connected with a long passage (“C” on the map, see Fig. 3.08). However, floor levels were not reached during Clarke’s excavations (see Moore & Wilson eds. 2011, 19) and the full extent of stratigraphy was never established. Currently only context data are considered as fully integrated though the relationship between bigger or lesser context groups is unknown (D. Clarke, A. Shepherd and A. Sheridan, pers. comm.). However, four radiocarbon samples provided a relatively similar timeframe to Phases 3,4 and 5 of Trench D, around 2480 (up to 2855 considering otter bones) to 2005 cal. BC (Marshall et al. 2016, table 4).

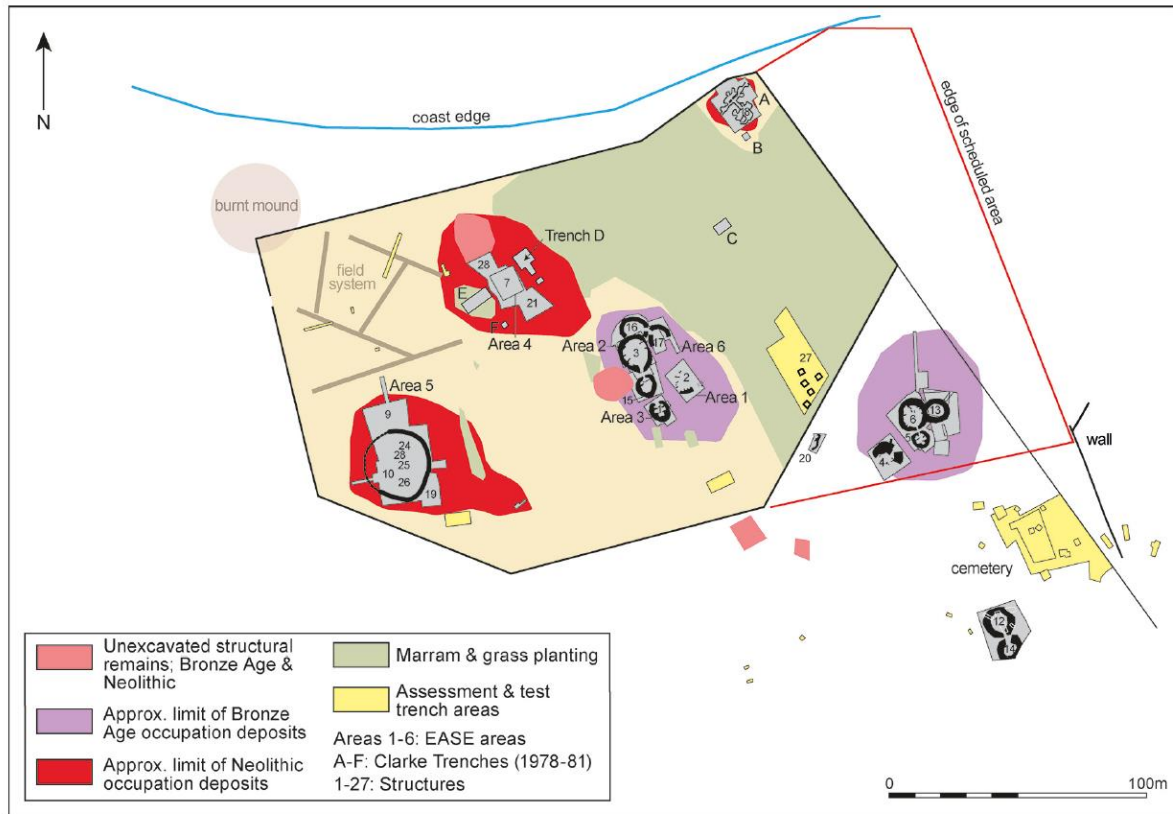


Fig. 3.05 – Plan of the Links of Notland site, areas covered by Clarke's trenches named from A to F (Clarke et al. 2017, Ill. 2).

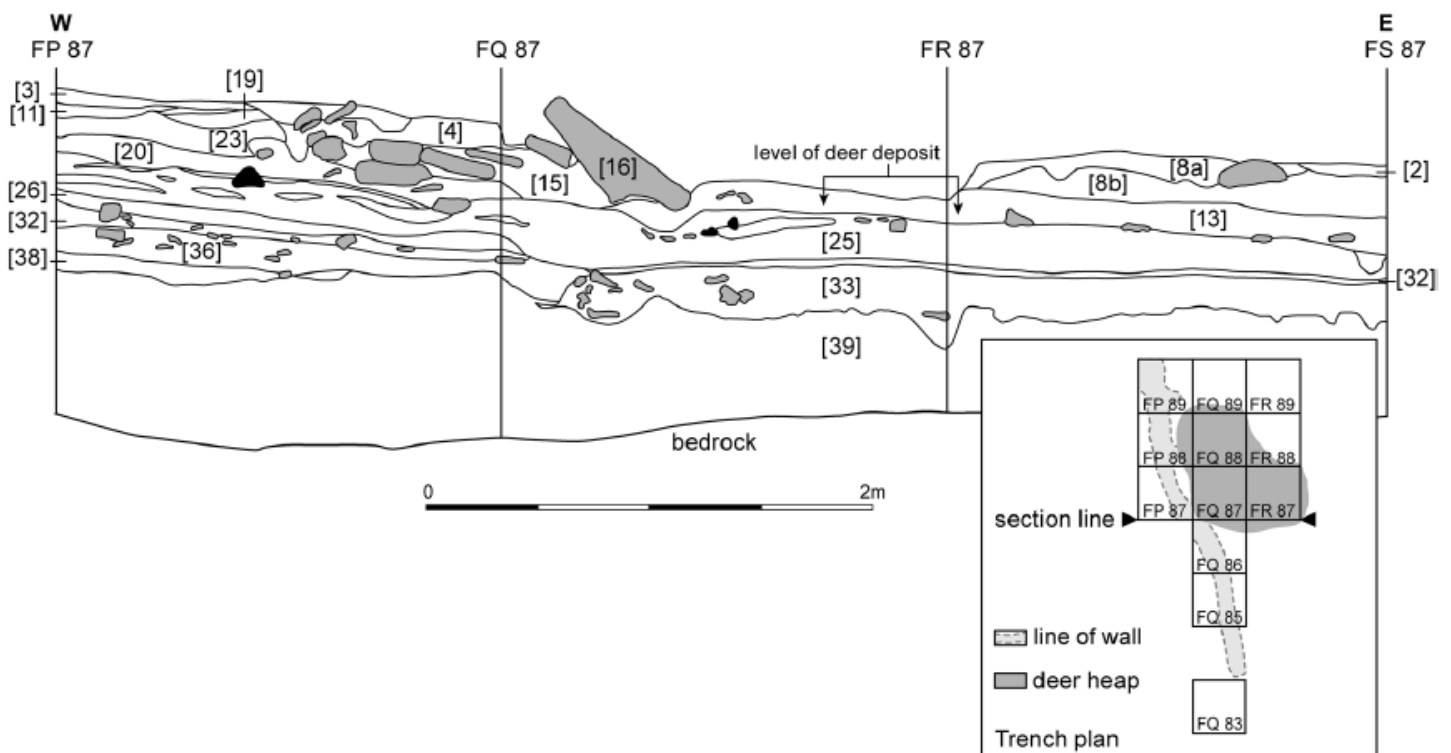


Fig. 3.06 – Plan and stratigraphy of Links of Notland Trench D (Clarke et al. 2017, Ill. 6).

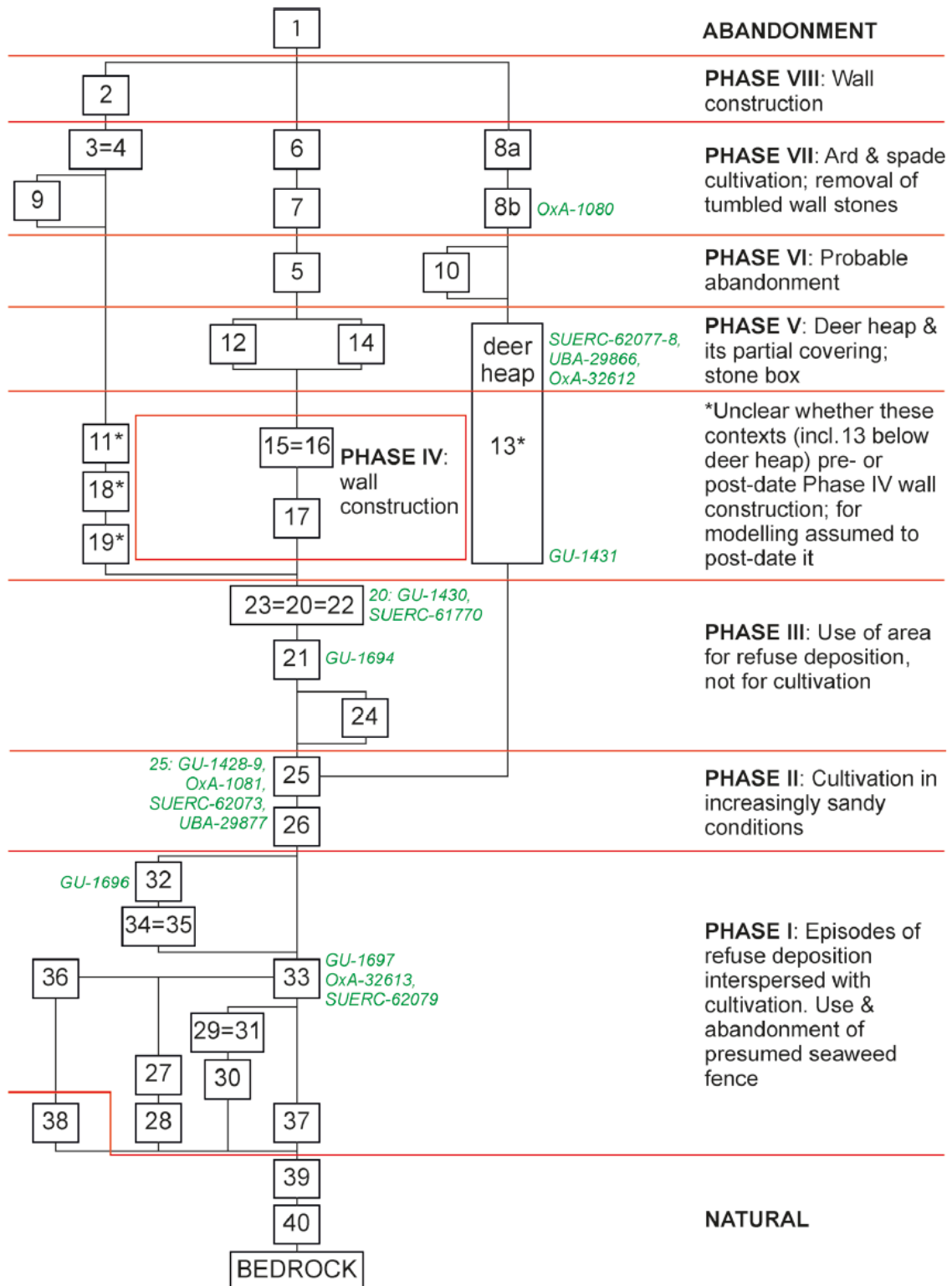


Fig. 3.07 – Harris matrix for Trench D stratigraphy (Clarke et al. 2017, Ill. 5).

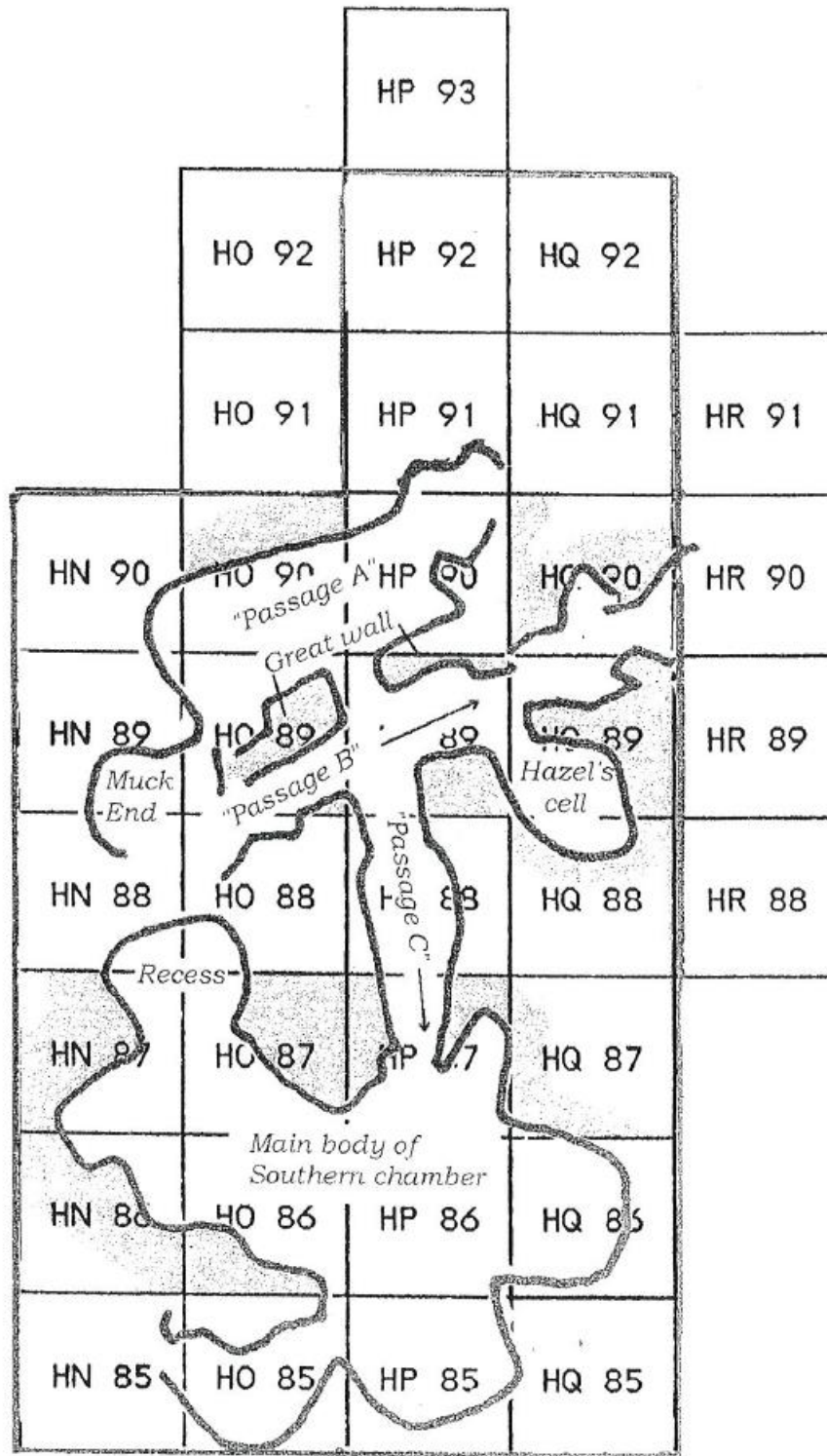


Fig. 3.08 – Plan of Links of Noltland Trench A (D. Clarke, A. Shepherd and A. Sheridan, pers. comm.).

3.2.4. BU BROCH

Located within the Stromness parish of Mainland, Bu Broch was studied during emergency excavations in 1978, undertaken by the now-defunct North of Scotland Archaeology Services. Originally thought to be a burial mound, and classified as such in the 1946 survey, it turned out to be a classical broch structure, which was at that time relatively understudied. Due to a lack of time for preparations and restricted financing as well as manpower available the judgement was made to approach the site in a way that would help to understand the nature of broch structures not answered by previous studies (Hedges & Smith 1979; Hedges & Bell 1980; Hedges 1987, 2-4).

While it is accepted that the site should be dated to the Early Iron Age exact dating may be quite problematic. The site main phases (Phase IIa, IIb and IIIa) were radiocarbon dated to around 850-450 cal. BC (Hedges 1987, 117), which is one of the earliest dates for such structures in Scotland (Hedges 1987, 93; see Dockrill et al. 2006, table 1). However, due to the small number of samples, taken from different animals, and general issues when working with ^{14}C samples in a marine-influenced environment it is possible that obtained data may be overshoot (Dockrill et al. 2006). Research in Howe, Orkney, provided a number of different samples for local broch structure, ranging from 760 BC to 230 AD for the Iron Age periods, suggesting the timespan of construction and usage somewhere between 500 BC to 100/200 AD (Carter 1994). Best dated broch so far, Old Scatness Broch in Shetland, provided range between 390 and 200 BC as a period of its construction and 40 BC to 140AD for its abandonment (Dockrill et al. 2006). Considering other sites and known dating it seems possible, that Bu Broch was constructed around the 6th/5th century BC although lengths of later utilization and abandonment periods are impossible to be established.

General stratigraphy of the site seems well understood, despite possible robbing of the site and removal of top layers in more recent periods (Fig. 3.09, more about stratigraphy: Hedges 1987, 5-38). The initial occupation started well before the broch construction (Phase Ia) and plough marks were present on the site (Phase Ib). Phase IIa represented proper broch construction and usage, followed by a hiatus between phases (Phase IIb), with evidence of abandonment and slow disintegration. The next and last period of utilization, IIIa, included re-using and/or robbing of original broch but also the inclusion of subterranean constructions within and around the site, possible in a sequence. Phase IIIb marks the final abandonment of the site and later

usage as a burial place for two skeletons and additional 90 disarticulated human bones, possibly redeposited either by humans and/or rabbit burrowing (Hedges 1987, 123-125).

The excavators found well preserved finds, including e.g. wooden furnishing and human remains (Hedges & Bell 1980; Hedges 1987, 96-116 & 123-125). Obtaining environmental evidence was one of the main objectives for excavators (Hedges 1987, 4) and indeed some were retrieved. Few micromammal samples collected and later stored in Orkney museum storage seemed to be sieved and in big enough numbers to be included in any research. However, the monograph mentions that many hand-retrieved bone finds were not recorded at all (Hedges 1987, 89). Two samples from Phase IIa came from middens, one beneath the eastern wall (Context L80) and one beneath constructions of the western broch end (Context L43), latter located over the plough mark horizon of Phase Ib (Hedges 1987, 23). Next three samples, from abandonment Phase IIb, are silt deposits with rubble (Context L50, L17), representing early abandonment, and one of general rubble contexts of the phase located near the entrance (Context L 68) (Hedges 1987, 24). Only one sample available from later utilization phase, Phase IIIa, was a floor deposit from earth-house, located to the east of the original broch structure (Context L 65, Hedges 1987, 26 fig. 1.11). Later two samples, similarly to Context L68, were rubble Context L2 (Phase IIB/IIIB; Hedges 1987, 24 & 29) and Context L14 (Phase IIIB; Hedges 1987, 29), latter with two human skeletons. One sample also came from unstratified deposits, including topsoil (Context L1).

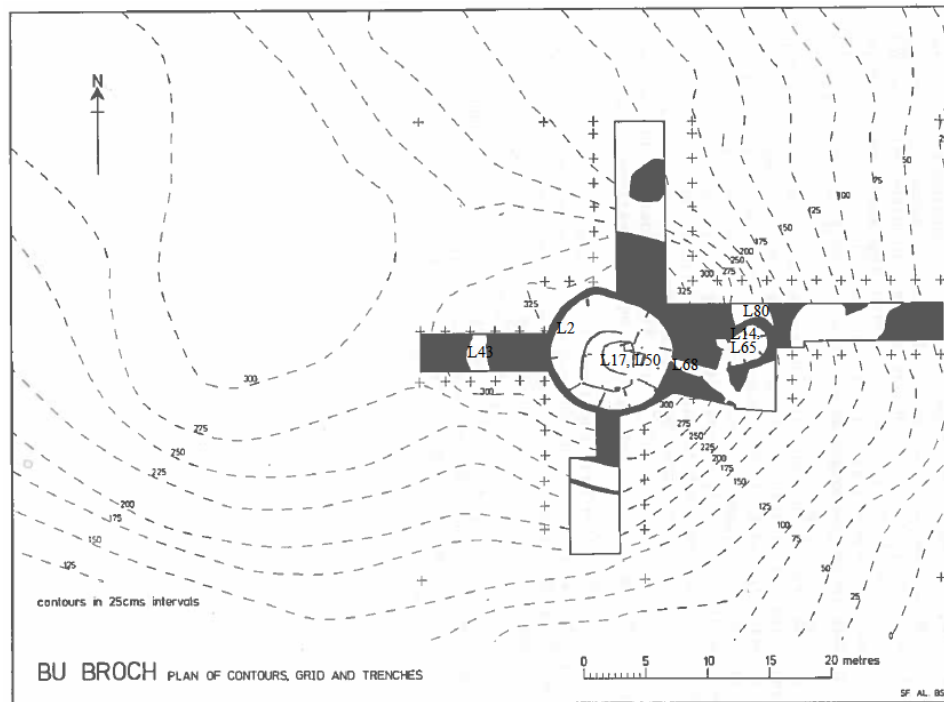


Fig. 3.09 – Bu Broch site plan, showing its interior structure as well as contents of the western, eastern, northern and southern trench as well as the approximate location of sampled contexts (Hedges 1987, 3 Fig. 1.2).

3.2.5. BIRSAY BAY

Birsay is a parish located in the North-western end of the Mainland, Orkney, famous for its wealth of historical monuments and archaeological sites. In the modern Birsay village, located near a small river estuary, one can notice St Magnus Kirk, a parish church dating back to the 9th century AD and still utilized today (Morris & Ballin Smith 1996, 12-13, 22-23), and the remains of so-called Earl's Palace, with foundations dated back to the beginning of sixteenth century AD (Morris & Ballin Smith 1996, 193). However, one of the most important sites is Burgh of Birsay, located on a small tidal island northwest of the village. It was originally thought to be a simple fortified settlement site with visible remains of a church but excavations in the 1930s and later in 1974-82 proved it to be a much more complex case than previously thought. Settlement site changed over time, with clusters of different buildings, both secular and sacral in nature, spanning from late Pictish (*c.* 6th to 9th century AD) to Upper Norse period (second half of the 10th to 12th century AD) (Curle 1982, 11-17; more in Hunter 1986), with finds suggesting the high importance of the site during that time (more in Curle 1982; Morris & Ballin Smith 1996, 209-255). Rescue excavations in the late 70s and early 80s provided some evidence for the presence of micromammals, including rat bone finds within kitchen refuse deposits from Room 5, in a clifftop settlement (Seller 1982; 1986). However, apart from Orkney vole, no attempt of further identification was undertaken not only for rats but also mouse remains. With no sampling strategy undertaken and only rudimentary sieving of clay soils most finds were hand-retrieved, which most likely led to significant data loss. However, due to the presence of hare bones it is also possible that micromammals deposited were mostly intrusive, which can also explain the lack of voles in earlier contexts (Seller 1982).

Due to monuments as well as remains from different time periods suggesting the ongoing importance of the region a number of survey excavations were undertaken within the vicinity of the modern village in the late 1970s, resulting in the discovery and excavations of Beachview Burnside (Area 2 & 3) and Beachview "Studio" (Area 1) sites (Fig. 3.10, Morris & Ballin Smith 1996, 1-8). Beachview sites represent a number of different activities in the vicinity of the village, radiocarbon dated to 980 - 1210 AD (Cook 1996). Moreover, all sites were sampled and soil samples were wet-sieved through a selection of meshes, resulting in retrieval of a substantial assemblage of small mammal skeletal remains (more in Rackham 1996 and Morris & Ballin Smith 1996 in relevant sections). With additional information from sites monograph (Morris & Ballin Smith 1996) and unpublished reports as well as site notebooks (especially

Viking and Early Settlement Archaeology Research Project 1979-1980a;b) it was possible to work with samples from Birsay Bay. However, while some data on micromammals was included in the monograph (see Morris & Ballin Smith 1996, 64-67 96-100, 147-156, 161-191) only minor attention was given to micromammal remains (see Rackham 1996, 170-171) leaving much data yet to be retrieved from the samples.

The “Studio” site, with its eastern extensions, was the biggest trench excavated in 1978-1980 and provided structural remains and midden-like contexts most likely reflect a period of construction, utilization and abandonment of a building and its peripheries (Fig. 3.11, Morris & Ballin Smith 1996, 76-160). On an irregular grid of 11/12 minor areas (A to E and minor E extension, from 1m² to about 16m²), eighteen different phases were identified (more in Morris & Ballin Smith 1996, 160 & II. 126). Natural sands (Period 1) were firstly disturbed by the construction of enclosure walls (Periods 2 and 4), around which occupation debris started accumulating (Periods 3 and 5). In Period 6 additional rectangular construction was created to the east, possibly a shed, but after some time of usage it collapsed (Period 7). A round kiln was also established and used for some time on the northeast end of the building (Period 8). Later parts of the structures were gradually filled with refuse, clay, sand and organic material (Period 9). The building itself was later demolished and rebuilt into a narrower shape (Period 10). In the end, however, the building also collapsed (Period 11) and was replaced by a smaller enclosure in the western end of the site (Period 12). Later periods (Period 13 to 15) saw mostly refuse dumping over the site, with one enclosing wall crossing the site (Period 14). The final three periods were considered as modern accumulations. Contexts rich in environmental material came mostly from Periods 5, 8-9 and 13-15 and correlated with refuse deposits on the eastern side of the building, predominantly within former ranges of structures present there.

Sampling encompassed a significant part of the “Studio” site (Table 3.02). There was an intention to fully sieve each context encountered through 2mm, 0.895mm and 0.5mm meshes (Rackham 1996), but due to technical issues as well as gradual enlargement of the original trench whole-earth approach could not be properly applied to all parts of the area apart from regions A & B (Rackham 1996, 161; Morris & Ballin Smith 1996, 147-148). While contexts from modern as well as construction phases were not sampled, retrieval by hand was commonplace and some micromammal remains were found in these contexts. More interesting phases, however, related to occupation and deposition of refuse and other human activity within the site, were heavily sampled (216 buckets, approx. 3,000 l, see Table 2.01), with some contexts being essentially whole-sieved (Phases Y, S, R, Q, P, L, relating to Periods 5, 8-9, 13-

15). However, it is not clear how much was sampled in attachments D/E, which were only sparsely sampled and with their own phasing (Morris & Ballin Smith 1996, 97), especially that sample labelling of the stored material did not always correlate fully with data provided on microfiches, what means a significant portion was hand-retrieved and not sampled.

Beachview Burnside Areas 2 and 3 are not as well-known as the “studio” site but still contribute more data to the general knowledge about Birsay village in the past. Investigated in years 1978/79, Area 2 revealed remains of stone constructions (walls?) and midden dump deposits with clay, refuse and industrial waste within or overlaid by sand depositions (more in Morris & Ballin Smith 1996, 52-74). Apart from topsoil (Phase Z) four major phases could be distinguished, from Phase V (rubble, possibly wall or other stone construction), continued by midden-dumping Phases W and X, ending on Phase Y, consisting mostly of natural sands. However, contrary to Area I, only layers from Phases W and X in four specific 1x1 squares were sampled and later sieved while the rest of the trench environmental finds were retrieved by hand (see Fig. 3.12). A similar strategy was also utilized in Area 3, excavated briefly in 1979 (more in Morris & Ballin Smith 1996, 45-51). However, Area 3 had far simpler stratigraphy, with a similar starting Phase with unknown stonework (Phase W) followed by a midden layer (Phase X) covered by natural sand accumulations (Phase Y), ending on topsoil (Phase Z). The only effectively sampled context in area 3 was midden Context UF from Phase X.

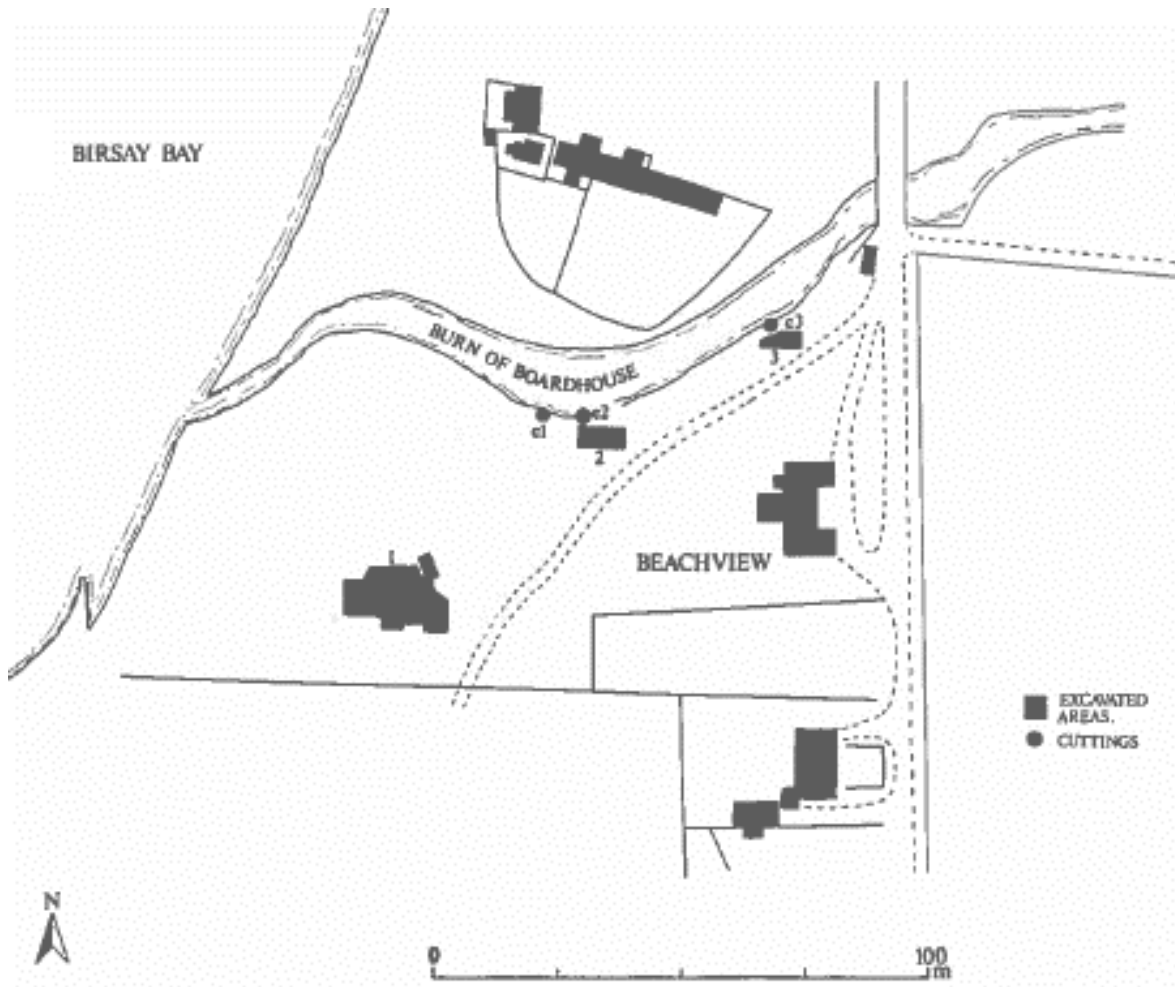


Fig. 3.10 – Birsay Bay plan, including sites/areas 1 to 3 and earlier survey cuttings (c1-3) and its location within modern road and buildings layout (Morris & Ballin Smith 1996, 35 Il. 25).



Fig. 3.11 – Area 1 general plan, including all finds (on the left) and layout of specific sub-sections (on the right) (Morris & Ballin Smith 1996, 76 Il. 55 & 157 Il. 125).

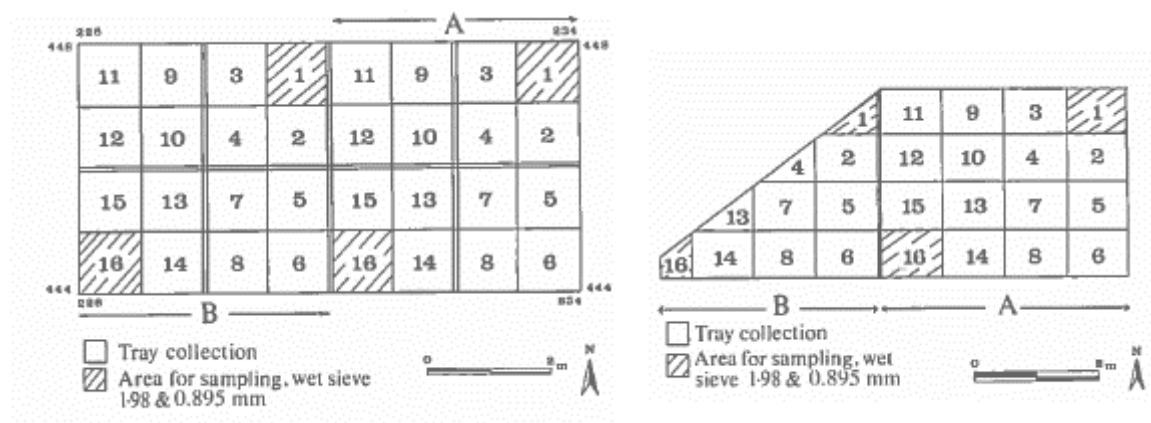


Fig. 3.12 – Sampling strategy in Area 2 (left) and Area 3 (right; Morris & Ballin Smith 1996, 45 Ill. 34).

Table 3.02 – Summary of the studio site (Area 1) sampling, through periods as well as phases relevant to the main trench (based on Morris & Ballin Smith 1996, 147-148).

Phase	Period	Sampling
Z	17-18	only by hand
Y	13-15	48 buckets, 670l
X	12	only by hand
W	12	only by hand
V	11	only by hand
T	10	only by hand
Q	9	180l
R	9	38 buckets, >500l
S	9	79 buckets, 1100l
N	8	only by hand
P	8	13 buckets, 182l
M	6	no finds
L	5	25 buckets, 350l
K	4	only by hand
J	1	no finds

3.2.6. TUQUOY

Tuquoy is a settlement site located on the southern shore of Westray, located near the historic Tuquoy farm, next to the chapel of Crosskirk from 12th century AD (Fig. 3.13). Regional naming, as well as known historical sources, point towards SW part of the Westray once containing an important settlement site, possibly established during early Norse colonization and abandoned around or after late the Medieval period (more in Owen 1993). Tuquoy archaeological site is most likely one of the remains of such settlement. Identified as an archaeological site in 1981, trial digs were scheduled for 1982-1983, followed by one excavation season in 1988. Trial work concentrated on an area less than 100 m², revealing remains of so-called Norse “hall” and “smithy” enclosures, but waterlogged deposits on the base of a nearby cliff were also thoroughly investigated (Fig. 3.14, Owen 1993). While publications about the site are scarce (e.g. Owen & McKinnell 1989; Owen 1993; Owen 2003) unpublished data (e.g. Smith 2017; Hamilton-Dyer 2018), including outlines for specialists working on Tuquoy material (Rackham & Owen 2017), radiocarbon dates (Krus 2017) and stratigraphy report (Owen 2017) was provided to the author by Dr. C. Smith, Dr O. Owen and other specialists currently working on Tuquoy materials as a part of the final monograph publication effort.

Site stratigraphy was established in three stages in order to have a clear picture of any sort and long term activity present on the site. Blocks (contextually, spatially and temporally similar group of contexts) form episodes (blocks representing short time period) which in turn form periods (longer time period, visible throughout the site; more about stratigraphy in Owen 2017). Phase 1 consisted of natural sands, followed by early activity and foundations of minor constructions, dated to as early as 7th – 10th centuries AD (Phase 2). The biggest find from that phase was the waterlogged pit, with a complex sequence of deposition relating to a relatively short period of time around 11th – 12th century AD (Krus 2017). However, Phases 3 and 4 are of major importance, correlating to construction and utilization of the hall (Phase 3) and later rebuild into smithy (Phase 4), with a number of different episodes reflecting construction elements such as walls and floors as well as deposits such as floor spreads, hearth and hearth ash deposits, industrial waste dumps and middens. Finds in the hall included a re-used stone slab with a runic inscription on it (“Thorsteinn Einarsson carved these runes”, see Owen & McKinnell 1989), and kidney-ringed pin that pointed towards eleventh-twelfth century AD (Owen 1993). Bayesian modelling showed, that hall and smithy occupation can be dated to a

relatively short period from 12th to 13th century AD, being contemporary to the church of Crosskirk (Krus 2017). Phase 5 however, starting around 14th century AD, was a time of abandonment, when buildings were used as waste dumping while their elements were gradually collapsing. Considering these dumps, it is most likely that settlement site continued till 15th century AD (Owen 2017; Krus 2017). Later two phases represented agricultural activity in 18/19th century AD (6) and complete abandonment of the site as well as later kelp-burning activity and modern use of the site as pasture (7). It appeared that intrusive burrowing was rare on the site. Contexts from only one block (Block 43, from Phase 4) were identified as being distributed at some point by a rabbit burrow.

Micromammal samples came from both excavation seasons. Most were sieved but retrieval by hand was also occasionally done. During the first season an attempt was made to sieve all context from the trenches through 1mm mesh. However, due to technical issues and time restrictions only small contexts were sieved in full. Before the second year of excavations the approach changed once again and while all material was sieved through 4mm mesh only parts, usually one out of ten buckets of content, was intended to be sieved by 0.5 mm mesh during flotation. The end result was that most contexts were represented by just one bucket of small mammal remains (about 10 litres). Clay contexts could not be properly sieved and in majority of cases only hand-picked remains could be retrieved (C. Smith & O. Owen pers. comm. ; data available in Rackham & Owen 2017). While retrieval of micromammal remains was not a priority one context (Context 33) from Phase 3, was specifically sampled because of the abundance of small vertebrate species.

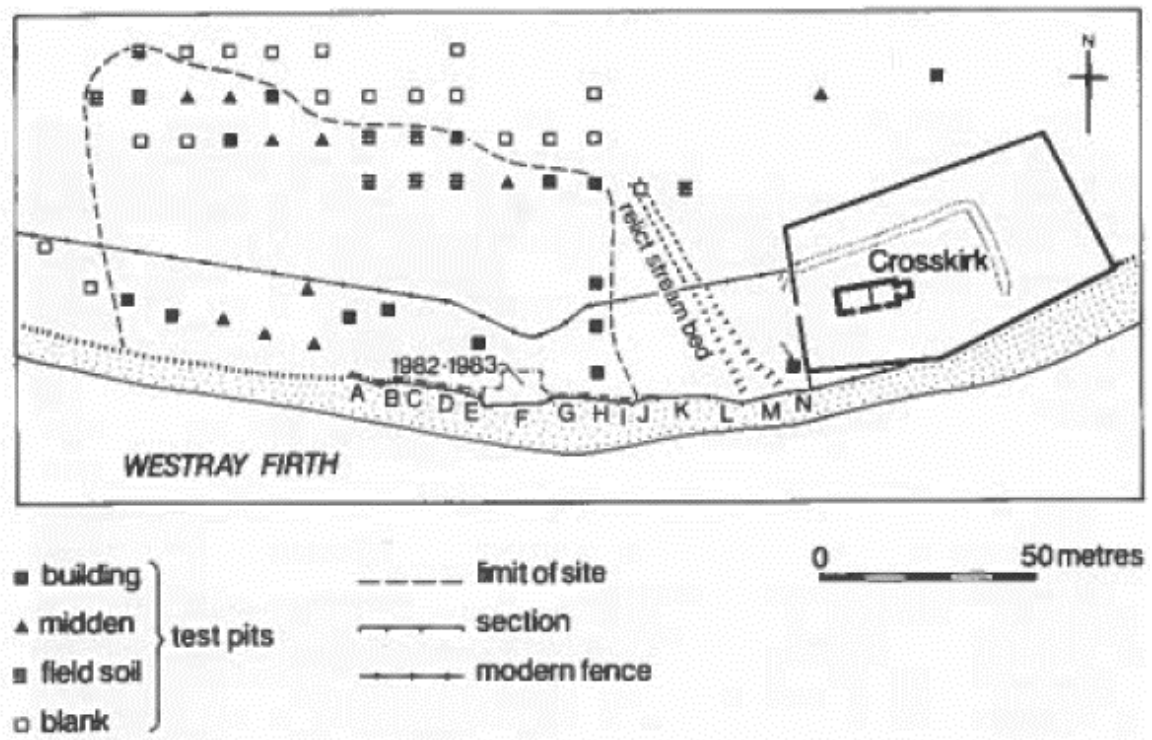


Fig. 3.13 – Plan of the wider area around the Tuquoy site (Owen 1993, 322 Fig. 18.3).

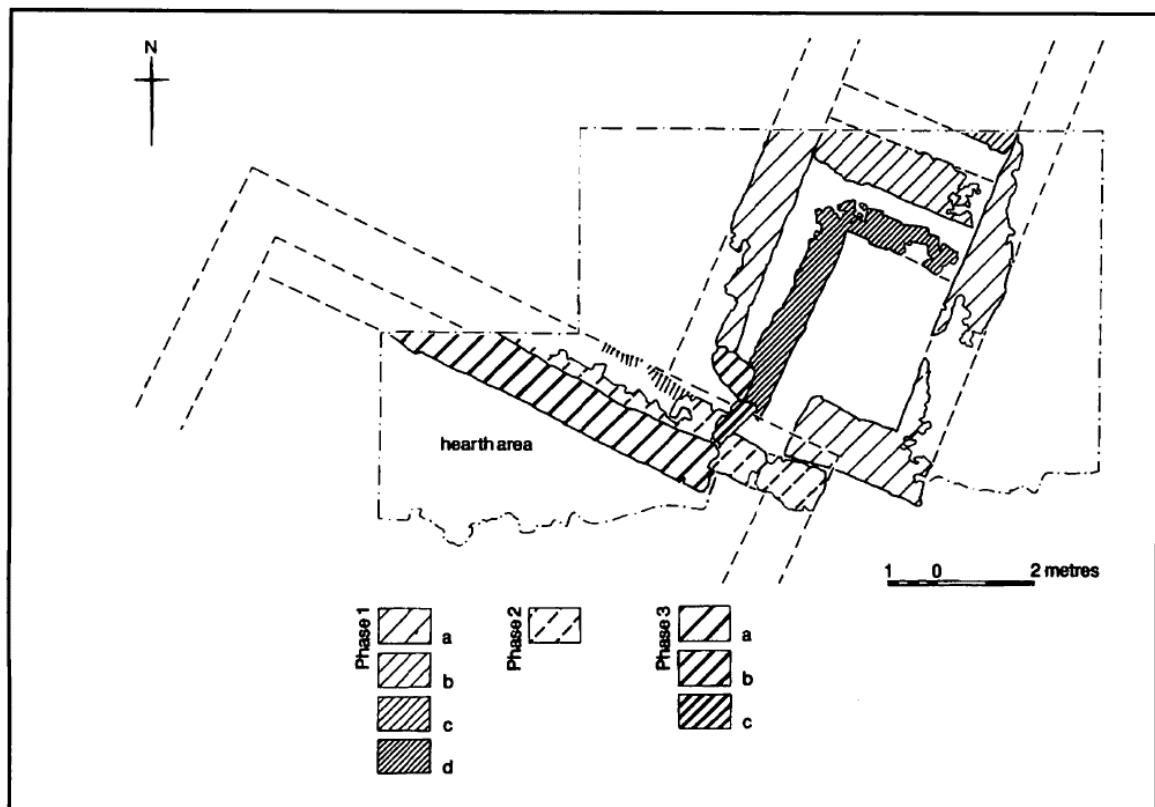


Fig. 3.14 – Tuquoy site plan of a trench containing hall and smithy (from Owen 2003, Fig. 3; Owen 1993, 327 Fig 18.4).

3.2.7. SCAR

Scar is a unique Viking boat burial, discovered in 1985 alongside the north coast of the Sanday isle by a local farmer (Owen & Dalland 1999, 1). Due to a rapid erosion of the site (especially from storms, see Owen & Dalland 1999, 23, 32) rescue excavations, preceded by a survey of the broader area around the site, were scheduled in 1991. Excavations unearthed parts of a boat alongside inhumed human remains of three people (adult male, adult female, child) and a wealth of grave goods assigned to each person (more in Owen & Dalland 1999). While the site monograph (Owen & Dalland 1999), published almost twenty years ago, put stress mostly on explaining the burial aspect of the site unpublished reports containing more data are available to the public (e.g. Dalland 1992&1999; Cerón-Carrasco 1992).

Despite the relatively small size of the site, its stratigraphy is complex, with some details changing over the period of seven years of post-excavational analysis (Fig. 3.15, see Dalland 1992&1999 for more details). Earliest natural contexts, named post-glacial by the excavators, overlaid natural rock surface and consisted mostly of clay and windblown shell sand. That layers however were only investigated in one trial pit (Owen & Dalland 1999, 23). The next set of contexts, directly predating burial, was also mostly natural in origin but also contained stones and stone rubble, coming most likely from some sort of construction activity, and remains of a wall (Owen & Dalland 1999, 24-25). The boat burial itself was created firstly by creating a pit within the soil and putting boat into it, with stone slabs used to put the boat into a proper location, possibly with wooden roof structure above (Owen & Dalland 1999, 26-27). It was radiocarbon dated to 895-1030 cal. AD (Owen & Dalland 1999, dating in 157-163). Originally burial chamber only contained the boat itself, human remains, grave goods and stones, but at some time upper structure collapsed, creating the infill layers from commingled layers formerly being a part of a roof but at some point the chamber could be also infested by otters (*Lutra lutra*, see Owen & Dalland 1999, 31-32 & 36-37). Upper contexts were heavily damaged by erosion, but provided evidence for both natural sand accumulation as well as occasional human activity (Owen & Dalland 1999, 32).

All the contexts were thoroughly sieved through bigger meshes while soil samples (ca. 10 litres) from each of them were taken and sieved through 1mm mesh for later investigation (Owen & Dalland 1999, 22-23). While retrieval of micromammal remains was not a priority many samples, found in all major phases, contained them, even if in small quantities. However,

considering utilization of a burial chamber by otters and other burrowing species (Owen & Dalland 1999, 36-37) it is possible that significant part of the assemblage are of intrusive origin.

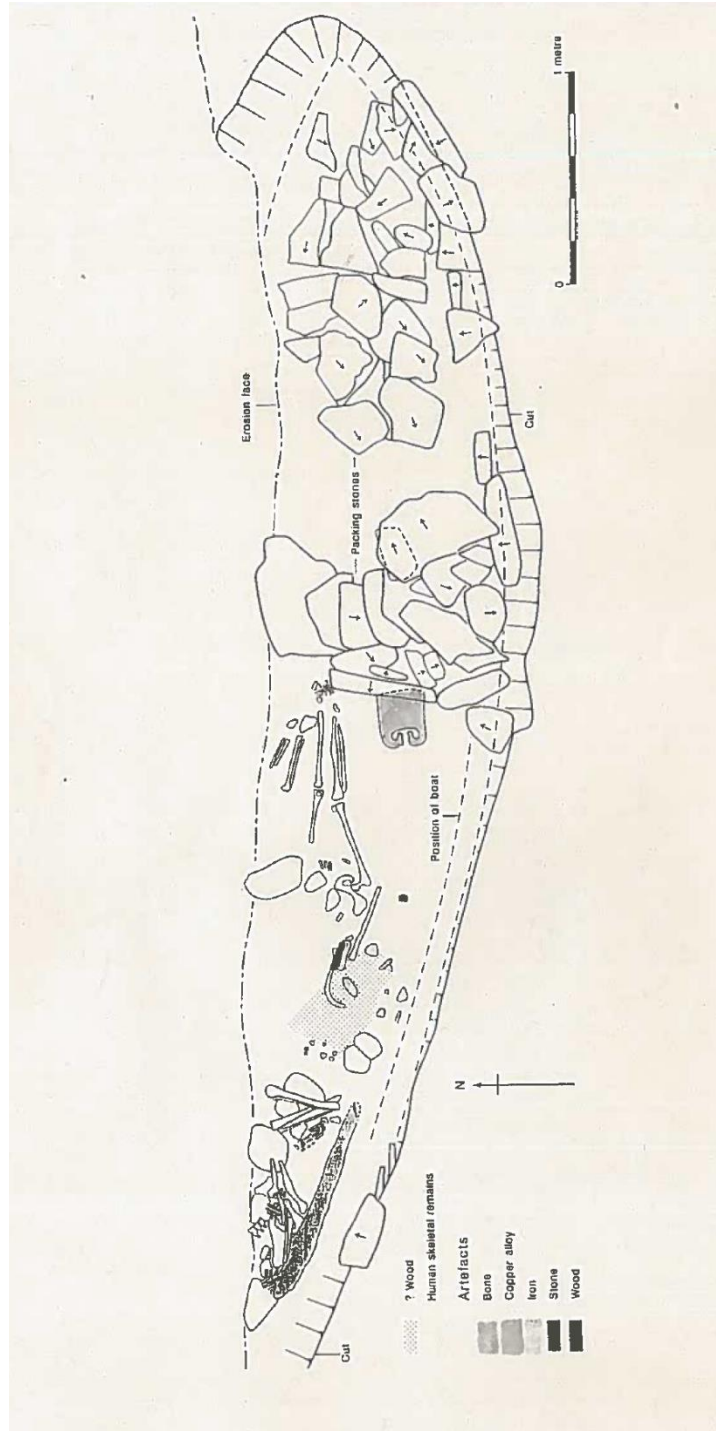


Fig. 3.15 – Scar boat remains stratigraphy (from Dalland 1992&1999, coloured version in Owen & Dalland 1999, 30 fig. 23).

3.3. METHODS – DATA COLLECTION

3.3.1. DATA RECORDING

Microsoft Office software (Microsoft 365, formerly known as Office 365; personal subscription, 64bit version; 2017-2020), specifically MS Excel and MS Word, was used for qualitative and quantitative data recording, resulting in all data being available in a digital form. If not stated otherwise, the recording was attempted up to the smallest unit possible – up to contexts in the case of Skara Brae and individual samples in the case of the other five sites. Higher stratification levels (contexts, episodes, phases/periods, etc.) were later obtained from summing up, or estimating from, relevant samples. All data are available as electronic appendices to this thesis.

3.3.2. SORTING, SIDING AND ANATOMICAL/TAXONOMICAL IDENTIFICATION

As the majority of material chosen for this study either had never been sorted before or sorted only in part, the author had to sort and separate micromammal remains. Sorting was done in a fashion previously employed during Skara Brae analysis in 2015 (Romaniuk 2016a), with anatomical and taxonomic identification of each bone and teeth fragment was performed alongside sorting. Whenever possible, all major bones (mandibles, maxillae, scapulae, humeri, radii, ulnae, pelves, femora and tibiae) were sided either left or right, with loose incisors being attributed to either maxilla or mandible. For the duration of this study sorted micromammal material was bagged in plastic bags, jointly for each context or sample. In the case of bigger samples (NISP >100) material was further segregated, with each anatomical element in its own plastic bag, for the convenience of later analysis.

For the sake of comparison, the author utilized reference collections of historical and modern micromammal specimens currently held in the vertebrate collection, National Museums Collection Centre. As insular environments may profoundly affect micromammal morphology (Angerbjörn 1986; elaborated in the review chapter) the author used references from insular environments whenever possible. Apart from the Twigg Collection, a 40 years old group of 12 Guernsey common voles and 26 field mice from Guernsey, Channel Islands, the author made

use of a collection of Orkney voles, house mice and pygmy shrews of various ages from both sexes, caught with traps or by domestic cats on five islands – Mainland, Rousay, Sanday, South Ronaldsay and Westray.

Beyond the NMS reference collection, a variety of publications were utilized. Those included Hillson (2005) for molars both in sockets and loose, Lawrence & Brown (1973) for teeth, crania and pelvic bones and Ronniger (2009) as well as Vigne (1995) for long bones. Larger skeletal elements (maxillae, mandibles, scapulae, pelves, humeri, femora, tibiae), as well as loose molars, were usually successfully identified either to taxa or category, while smaller bones (vertebrae, ribs, metapodials, phalanges, calcanei, tali, separate cranial bones) as well as most incisors, too similar among species to be taxonomically identified, were recorded only as “unidentified rodent” (roughly similar to vole/mouse in Nicholson 2007). The unique case was presented by ulnae as only fully fused specimens could be differentiated (similar problem mentioned in Ronniger 2009).

The biggest issue to overcome in the case of taxonomical identification (mentioned in the Literature Review) was that species within the same genera or even family have very similar skeletal morphology and may be indistinguishable in absence of other factors. That is why the author attempted firstly to identify teeth as most diagnostic elements and then used that knowledge when identifying more problematic skeletal finds. In the case of absence of any other species within the studied sample within the same family, all remains identifiable to this family were automatically joined under the species present. In the case of two or more species, elements that could not be identified up to taxa would be attributed to a more general category. In the case of this study, the only issue of this sort was encountered when assessing postcranial elements from house and field mice. Apart from complete femoral bones it was near impossible to differentiate between the two, resulting in such finds being recorded as “unidentified mouse”.

Taxonomic assessment of rat remains however required additional methods to be employed. As mentioned in **Chapter 2.2.5.**, brown and black rats are difficult to differentiate, especially in the case of postcranial bones, and additional insular impact could render visual taxonomic identification methods useless. In order to avoid such issues, the author sought to employ the ZooMS method (Buckley 2009; 2016; 2018; Sluis et al. 2014; Harvey et al. 2016), possibly as a part of a collaboration between institutions. Thankfully, Dr David Orton, a zooarchaeologist at the University of York (Department of Archaeology - Bioarchaeology), was working on a bigger project related to archaeological evidence of black rats spread over Europe (Orton et al.

2018) and had funds for utilizing ZooMS and radiocarbon dating (in case of positive identification as a black rat) for his own research.

In November 2018 the author provided Dr Orton with six samples, five from Scar (all single postcranial bones) and one from Brisay. Sample treatment and subsequent analysis were done by Ms. Krista McGrath, a laboratory technician from the University of York. Samples were pre-treated by acid demineralization followed by gelatinization and trypsin digestion to cleave the peptides. The peptides were then cleaned up using ziptips and then run on a matrix-assisted laser desorption/ionisation time-of-flight (MALDI-TOF) mass spectrometer. Results will be discussed in relevant sections of case study II, with joint results table available in this chapter (Table 3.03).

Due to the high fragmentation of studied material sexing could not be consistently applied and was discarded early in the research. The author used references for pelvic morphology from Lawrence & Brown (1973) book but finally only 1-3% of the total MNI could be definitively associated with any sex. However, for the sake of clarification, it is worth noticing, that pelves of both male and female morphology were found for each species present in all sites and in the majority of bigger assemblages. The only exception was pygmy shrews, usually represented by a dozen or so bones from vastly different contexts and thus very difficult to analyse at all.

Table 3.03 – ZooMS results for samples provided to Dr D. Orton (Dr. Orton pers. comm.).

Site	Context	Skeletal Element(s)	Identification
Birsay Area 1	Context 2, commingled/modern layers	right scapula	<i>Brown Rat</i> (<i>R.norvegicus</i>)
	Context 5, predating burial	right scapula	Inconclusive
Scar	Context 5, predating burial	right mandible	<i>Brown Rat</i> (<i>R.norvegicus</i>)
	Context 36, boat infill	right femur + distal epiphysis loose	<i>Brown Rat</i> (<i>R.norvegicus</i>)
	Context 7, predating burial	right tibiofibula + proximal epiphysis loose	<i>Brown Rat</i> (<i>R.norvegicus</i>)
	Context 20, commingled/modern layers	right tibiofibula	<i>Brown Rat</i> (<i>R.norvegicus</i>)

3.3.3. TAPHONOMIC AND PATHOLOGICAL MARKERS

As the analysis of taphonomic changes is crucial for micromammal zooarchaeology the author assessed micromammal remains for the presence of any significant marks. Visual references utilized during the identification of taphonomic marks included *Atlas of Taphonomic Identifications* (Fernández-Jalvo & Andrews 2016), Andrews (1990) and selected case studies (Fernández-Jalvo & Andrews 1992; Crandall & Stahl 1995; Fernández-Jalvo & Dauphin 1995; Denys 2002; Jenkins 2012; Fernandez-Jalvo et al. 2014; Rhodes et al. 2016; Fernández -Jalvo et al. 2016; Fernández et al. 2017). Due to the importance of the established methodology (Andrews 1990, 49-65; Fernández-Jalvo & Andrews 2016, 283-288; see **Chapter 2.2.5-6.**) fragmentation of skulls and long bones was thoroughly studied in every context. The author also attempted to identify all taphonomic marks on bones with clearly visible alterations, especially in cases possibly related to burning. However, due to a sheer amount of micromammal remains, only teeth and proximal (*sensu* Andrews 1990, upper) limb bones (humeri, distal end; femora, proximal end) were fully investigated under the standard optic microscope (4x/10x/40x magnification) for any evidence for digestion/abrasion/weathering.

Once taphonomic data were obtained selected samples, especially of digestion, were studied under higher magnification. Following the example references mentioned in the beginning, BSC 20.00 KV scanning electron microscope (CamScan MX2500), provided by National Museums of Scotland and operated by Dr Lore Troalen (Department of Collections Services, National Museums Scotland), was utilized for that task. At least one micrograph (x14 to x800) of each specimen analysed through SEM was taken for later reference, resulting in 244 micrographs taken. Additionally, in the case of eight possibly burnt specimens from Skara Brae, the author utilized EDS software alongside SEM in order to map their surface chemical composition and establish spectra of specific regions on their surfaces. Then surface chemical composition was then compared with what is known from the literature about chemical alteration specific to burning or staining (carbon vs manganese oxidation; see Fernández-Jalvo & Andrews 2016, 156-158).

An issue connected to scoring digestion marks on teeth was a possible mesowear in micromammals. As mentioned during the literature review, mesowear may sometimes resemble digestion marks on teeth and hypothetically can be identified as such. Especially acid soil corrosion and mesowear should produce hardly distinguishable patterns. However, the problem may be only minor. Out of 108 molars from nine individuals in the NMS reference collection

only three (2.8%) showed any chipping and only two on the lingual side. As way less than 5% of molars displayed any marking of this sort it can be considered inconsequential for further analysis.

The author also recorded pathological data within the studied bone fragments and photographically documented each case. The previous study on Skara Brae found a number of identifiable pathological changes on bones (Romaniuk 2015) but due to a lack of comparative samples and minuscule impact on interpretation such data remained unpublished. However, considering more sites included in the current study, the possible impact of such data on age estimation and a slowly growing set of case studies (see below) the author decided to include pathological changes into the study nonetheless. Pathological changes were identified relying on known literature for animals (Baker & Brothwell 1980; Bartosiewicz 2008; Bartosiewicz 2013), supported by human-based references (Aufderheide & Rodríguez-Martín 1998) and case studies related to micromammal species (Arrizabalaga & Montaugut 1990; Ventura & Götzens 2005; Luna et al. 2017).

3.3.4. DATA QUANTIFICATION

All micromammal material was quantified in a way ensuring the greatest degree of comparability between study sites and reference data in Andrews (1990), as well as other important case studies (Dodson & Wexlar 1979; Andrews & Evans 1983; Hoffman 1988; Kusmer 1990; Matthews 2002; Terry 2007). Even if not directly stated, counting employed in Andrews (1990), and later in studies using his methodology, utilizes NISP as its basis (Lyman et al. 1994A; more in Lyman 2008, 27-38). While there are case studies using MNE instead (Gómez & Kaufmann 2007; Montalvo & Tallade 2009; Montalvo et al. 2012), including the author's former work on Skara Brae (Romaniuk 2016a,b), the author decided to work with NISP on all studied sites. It is due to the possible issues when using MNE (see Lyman 2008, 222-229) and interchangeability of both counts as noticed in Terry's work (2007).

All mandibles, maxillae, scapulae, humeri, radii, ulnae, pelves, femora, tibiae, vertebrae, metacarpals, phalanges, calcanei, tali, ribs as well as loose incisors and molars were counted as NISP. Bones irrelevant to the methodology, like clavicles, sterna or epiphysial plates, were jointly quantified as "other". Isolated cranial bones other than maxilla or cranial fragments not containing maxillae were also included under the "other" label, but the exact number of such

finds was later utilized when quantifying fragmentation. Apart from that, non-NISP counts were also calculated, including incisal and molar teeth found intact (i.e. within the alveolous) as well as empty alveolar spaces. However, mandibular and maxillary differentiation was not employed.

MNI count of each taxon per each context was calculated on a basis on the highest skeletal element NISP from each species in relation to side and author's judgment whether those fragments came from the same or different individual. In the case of bigger species splintered remains of bones can cause some problems in estimating such values (e.g. Marean & Spencer 1991) but when it comes to small mammals bones fragmented beyond some threshold are practically unidentifiable. As Korth (1979) and Andrews (1990, 18-19) have shown, fragmentation of micromammal remains is far more schematic and tiered than bigger species thus making MNI estimation somehow easier.

A number of quantification methods were utilized for the sake of analysis (see Table 3.04). Due to the widespread usage of relative abundances (Andrews & Evans 1983; Andrews 1990, 45-48; Fernández-Jalvo & Andrews 1992; Saavedra & Simonetti 1998; Terry 2007) as well as previous successful utilization of abundances in Skara Brae research (Romaniuk et al. 2016a;b) it was also employed in this work. Values were calculated for selected elements (maxillae, mandibles, loose molars and incisors, scapulae, pelves, humeri, ulnae, radii, femora, tibiae, calcanei, tali, vertebra, metacarpals and phalanges) present in each sample, elaborated on in the literature review (**Chapter 2.2.6.**). Following Terry's (2007) advice, an additional joint abundance value was created for tali, calcanei, metapodials and phalanges in order to avoid data overcomplication for computational methods. In Terry (2007) it was called CTMP, an abbreviation of "Carpals, Tarsals, Metapodials, Phalanges", and the author used this acronym throughout his study. Average abundances values for each sample was calculated as ratio of elements in two ways, one taking into account only bones (to avoid confusion, named "skeletal completeness" in the text and " $\Sigma\%$ " in the appendices) and second including both bones and loose teeth (named "average abundances" in the text and " $\Sigma\%$ with teeth" in the appendices). Jointly, both will be named as "completeness ratios" later in the text.

However, the author also introduced an alternative to abundances. As mentioned in the literature review, the biggest weakness of abundances and a likely source of bias is its reliance on MNI. Moreover, while abundances can be computed easily, their visualisation and explanation may be problematic in the case of large number of contexts analysed. It is due to values being calculated for each element separately, resulting in a group of beyond 10 values.

In order to introduce an alternative, Behrensmeyer's skeletal frequencies (Behrensmeyer 1983; Behrensmeyer & Boaz 1980; presented as in Lyman 1994a, 191 Table 6.14) were adapted. In this method, reworked by the author to fit the same elements as established for abundances, skeletal groups were firstly calculated for three groups of elements (skull, front limbs, hind limbs) and vertebrae, as cumulative NISP for each group (Skulls: maxillas and mandibles, Front Limbs: humeri, ulna, radii and scapula, Hind Limbs: femora, tibiae and pelves). Out of skeletal groups relative frequencies, later called skeletal frequencies, were calculated, as the ratio between each group/element and cumulative NISP of all considered groups/elements in this method. The calculation method was very similar to Andrews skeletal elements proportions (1990, 45) but reduced the number of values to only four, easier to visually compare with other datasets (Lyman 1994a, 191 Table 6.14; Andrews 1990; Table 2.01).

Indices proposed by Andrews were also calculated whenever possible. Those included three skeletal indices (Andrews 1990, 49 Table 3.2) and one teeth index (Andrews 1990, 60 Table 3.9) for each teeth type separately (incisor, molar). Two skeletal indexes compare the NISP of postcranial elements to the NISP of cranial elements, but differ in complexity. The more complex approach (named "complex postcranial to cranial index" in the thesis) divides the NISP all main long limb bones (femur, tibia, humerus, radius, ulna, 10 total for a single complete individual) by the summary of all maxillae, mandibles and molar NISP (16 total for a single complete individual) and then multiplies the result by 5/8 for the better result distribution. The simpler approach (named "simple postcranial to cranial index" in the thesis), in turn, summarizes only maxillae and mandibles NISP and divides it against femora and tibia NISP. The third skeletal index divides distal limb elements NISP (tibia and radius) by proximal limb elements NISP (humerus and femur). For teeth, the percentage of isolated elements is calculated. In this index, loose teeth are divided against the number of teeth missing (empty alveolar sockets). All indices are multiplied by 100% to obtain a percentile result.

The quantification of the cranial and postcranial elements fragmentation (also known as breakage, Andrews 1990) was done in a way similar to Andrews (1990), but with the reworks from later studies. The issue with the breakage quantification described in Andrews (1990, 51 and 54-55, Fig. 3.7 & Table 3.3, 3.5 and 3.7), mentioned before in the literature review, is that some bone fragments can be counted to more than one category, leading to inter or intra observer errors. For cranial elements, the breakage described in Andrews (1990) divides maxillae into ones present in skulls and ones found isolated, but also takes into consideration the presence of zygomatics as a separate breakage state. For mandibles, a similar issue is noted

as the breakage takes into account ramus preservation but in the same time separately calculates cases with inferior border breakage. Due to broken long bones being counted as proximal, distal and shaft, a singular find could be counted twice (e.g. to proximal and shaft category).

That is why the author considered Fernández et al. (2011) as a template for cranial and mandibular breakage (see **Chapter 2.2.6.**) and Terry (2007) for a postcranial breakage. The choice provided a clear division between each breakage state scored, and could be expressed both as NISP of a specific element with this breakage state as well as a percentage of those cases. For cranial fragmentation, it meant the division between complete skulls with maxillary intact, maxillary with zygomatics, maxillary without zygomatics, minor skull fragments. For mandibular fragmentation, it meant complete mandibles, mandibles with broken ramus, mandibles without ramus, mandibles without ramus and inferior border broken. However, mandibular fragmentation can be also easily reduced to complete and broken cases for the ease of calculation. Postcranial bones (humeri, femora, ulnae and tibiae) were only scored as either complete or broken, what would also help during calculations. Apart from fragmentation counts percentages based on them were also calculated by dividing the number of a specific element breakage state NISP (e.g. Broken Humerus NISP) by all NISP for this specific skeletal element (Humerus NISP).

Quantification of other taphonomic marks required a two-stage assessment due to the sheer number of samples. For all samples digestion was quantified as general NISP of as well as % of affected elements, separately for incisors, molars and humeral as well as femoral epiphyses. However, samples containing larger amounts of digested teeth were quantified to a depth prevalent in current methodology, as a four-stage process (light/moderate/heavy/extreme digestion, see Andrews 1990, 65-79; Fernández-Jalvo & Andrews 2016, 238-244, fig. 8.3 & 8.4). The presence of burnt remains was only quantified as present as, apart from Skara Brae, no such finds were found in sufficient numbers to justify further analysis – and in the case of Skara Brae data was already quantified in Romaniuk 2015 and only needed more in-depth analysis.

For the sake of investigating taxonomic diversity in samples and contexts the author created the “number of species classes” and the “number of meaningful species classes”. The first value reflects the number of classes used during taxonomic identification, including both specific species (e.g. “House mouse”) as well as undefined states (e.g. “unidentified rodent”). For example, in a sample with one vole MNI and one MNI coming from an unidentified rodent the “number of species classes” would show two as two classes are present in the sample. In

contrast, second value introduced takes into account only classes that correlate to specific species. In the example previously stated, “number of meaningful species classes” would be one, as only one species-related class is present (vole).

Table 3.04 – Summary of utilized equations, reworked from Andrews (1990), Fernández et al. (2011) and Behrensmeyer (Behrensmeyer 1983; Behrensmeyer & Boaz 1980; Lyman 1994a, 191 table 6.14).

Equation (X 100%)	Full Term	Explanation	Elements considered (Ei value)
$SK_i = NISP_i / NISP$	Skeletal frequencies	Ratio of a specific elements group NISP (NISP _i) to all groups NISP	ELEMENTS GROUP: SKULL (Maxilla+Mandible), Front Limb (Humerus, Ulna, Radius, Scapula), Hind Limb (Pelvis, Femur, Tibia), Vertebra
$R_i = NISP_i / (MNI \times E_i)$	Relative abundance	Ratio of a specific element NISP (NISP _i) to expected anatomical elements numbers (MNI multiplied by a number of elements in an average skeletons, E _i)	BONES: (E _i = 2) Maxilla, Mandible, Scapula, Pelvis, Humerus, Ulna, Radius, Femur, Tibia, Calcaneus, Talus, (E _i = 36) vertebra, (E _i = 20) metapodial, (E _i = 56) phalange LOOSE TEETH: (E _i = 12) molars, (E _i = 4) incisors ELEMENTS GROUP: (E _i = 80) CTMP
$Comp(S \text{ or } T) = \Sigma R_i / NR$	Skeletal Completeness (ComplS) Average abundances (ComplT)	Ratio of the sum of relative abundances (ΣR_i) to the number of relative abundances present (NR)	As in Relative Abundances: ComplS -> only bones ComplT -> bones and loose teeth
$EFr\%_i = EFrNISP_i / EFrNISP$	Fragmentation Percentage	Ratio of a specific element (E) breakage state NISP (EFrNISP _i) to all element breakage states NISP (EFrNISP)	BONES (4 different breakage states): Skull, Mandible BONES (2 different breakage states): Mandible, Humerus, Ulna, Femur, Tibia
$(femurs+humeri+tibiae+radii+ulnae) \times 8 / (mandibles+maxillae+isolated \text{ molars}) \times 5$	Index of postcranial to cranial elements, complex version		As shown in Equation
$femurs+humeri / mandibles+maxillae$	Index of postcranial to cranial elements, simplified version		
$tibiae+radii / femurs+humeri$	Index of distal to proximal limb elements		
$T_{(i, isolated)} / \text{empty alveoli of } T_{(i)}$	Isolated Incisors/Molars	Index of isolated teeth against empty alveolar spaces	LOOSE TEETH: molars, incisors

3.3.5. MEASUREMENTS, AGE SCORING AND AGE ESTIMATION

Von den Driessh (1976) was utilized to standardise measurements taken. Measurements included humeral and femoral length (GL, von den Driessh 1976, 76-77 and 84-85) and mandible molar row length (TRL, similar to the cheek tooth row in von den Driessh 1976, 64). In the case of long bones, the author also noted the stage of epiphyseal fusion and divided measurements into those coming from unfused shafts, partially fused and fully fused specimens.

Age estimation relied on two approaches, one for all species and one tailored for each of major families present on sites. In the case of all species epiphyseal long bone fusion was scored for all humeri, femora, ulnae and tibiae preserved proximal and distal ends. Following Reitz & Wing (2008, table 3.5) and data known from laboratory rats (Dawson 1925) as well as NMS reference collection each region of epiphyseal fusion could be attributed to one of three separate categories: early (distal humerus; distal tibiofibula), middle (distal ulna; proximal femur) and late (distal femur; proximal tibia, humerus and ulna) fusing. Scoring was done jointly for all species but also divided into ones coming from taxonomically unidentifiable specimens, voles, mice (both field and house mice), pygmy shrews and rats. This approach helped in investigating whether samples/contexts contain juvenile, sub-adult or adult specimens as well as estimating their numbers in relation to each other.

In the case of murid molar wear both upper and lower molar teeth were utilized successfully as means of estimating age. Reference models for field mice (originally developed for *Apodemus flavicollis*, Adamczewska-Andrzejewska 1967; used for field mice in Steiner 1967) and house mice (Lidicker 1966; Brothwell 1981) were adjusted in order to be utilizable for single teeth and applicable to Orkney material with the help of Herman (details in Table 3.05). Each molar was scored and obtained data were compared with MNI on context level to provide an approximate age class for each individual. The scoring system was uniform for both species.

Age of voles, due to ever-growing teeth, had to be estimated on a population level by the method described in Lyman et al. (2001) and employed during previous Skara Brae studies (Romaniuk 2016A, Fig. 3). Measurements of vole humeral and femoral bones were plotted in 1mm intervals against their frequency, with the difference between unfused, partially fused and fully fused specimens being colour-coated for easy analysis. However, the method was only utilized in the case of sites that provided enough vole bones.

Table 3.05 – Table summarising wear levels utilized, with description and references for wear scoring used for field (as in yellow-necked mice: Adamczewska-Andrzejewska 1967) and house mice (Lidicker 1966). Expected age relates to the information in the references, known information about the life cycle of both species (House mice in Berry et al. 2008; Field mice in Flowerdew & Tattersall 2008) and personal experience in ageing insular Scottish micromammals (Jeremy Herman pers. comm.). The system is most accurate when the 3rd molar is possible to assess due to 3rd being last to develop molar wear.

Wear Level	Description	...equals to:	Expected age
0	No visible wear	1 and 2 in Lidicker 1966 none or 1 in Adamczewska-Andrzejewska 1967	< 1 month (juvenile)
1	wear areas on cusp tips, isolated from each other	3 in Lidicker 1966 1 or 2 in Adamczewska-Andrzejewska 1967	1-2 months (sub-adult)
2	wear areas on cusp tips, joining in between nearest cusps	4 in Lidicker 1966 2 in Adamczewska-Andrzejewska 1967	3-4 months (adult)
3	each row of cusps worn together	5 in Lidicker 1966 3 in Adamczewska-Andrzejewska 1967	5-7 months (adult)
4	singular wear surface, cusp morphology still identifiable	6 in Lidicker 1966 4 in Adamczewska-Andrzejewska 1967	8-11 months (adult)
5	singular wear surface, cusp morphology lost	7 and 8 in Lidicker 1966 5 in Adamczewska-Andrzejewska 1967	12+ months (adult)

3.3.6. OVERVIEW OF APPENDIX DATA

All quantified data described in **Chapter 3.3.3-4.**, apart from second-stage analysis (complex digestion and burning, displayed only in in-text tables), was included in **Appendix 1 (Data)**. The appendix was created in order to have a possibility to check differences between samples (**Data - Samples**), contexts studied as whole or reconstructed from samples (**Data - Contexts**) and general phases (**Data - General**) of studied sites in dedicated software. The author attempted to include all the data necessary, meaning some values (e.g. Abundances) can be easily calculated from the other values stated (e.g. *Elements NISP* and *MNI*) knowing the necessary equation (Table 3.05). During the analysis all ratio/percentile data was handled as 0 – 1 expected value range, and later transformed to actual percentages (X 100%) for the display.

As the number of columns in **Appendix 1** can exceed 100, data is presented in two stages, firstly by a data group name (e.g. *elements NISP*) and then by individual columns representing a concrete variable (e.g. maxilla NISP; see **Table 3.06** for the overview of data groups and specific column names). Each appendix starts with the *Key Information*, contextual information for samples, contexts or phases. *Basic Quantification* includes data used for general comparisons, such as e.g. general or species-specific NISP or MNI. *Elements NISP* contains NISP values for each skeletal element considered during the identification, counts for intact and missing teeth and cumulative NISP for all minor bones (CTMP). *Skeletal Groups* contain cumulative NISP for specific anatomical groups required to later calculate *Skeletal Frequencies*. *Abundances* contain relative abundances for each element considered during the quantification, as well as for a cumulative value for all minor bones (CTMP) and two averages considered, while *Skeletal Frequencies* and *Indices* columns display four skeletal frequencies and five indices utilized respectively. For *Skull Breakage* and *Mandible Breakage* counts for a specific breakage stage are firstly included, with percentile data following. Similarly, *Fragmentation Counts* include counts, and later *Fragmentation Percentages* contain percentile variables. Last is the *Taphonomy data* group, which contain digestion data, both as counts and percentiles, ending on a column denoting the presence or absence of burnt remains.

Appendix 2 Measurements includes all metric data taken. Raw data is displayed in the second part of this Appendix (2.2) and divided into separate tables depending on a site and specific area within it. Columns denote a measurement (greatest length of Tooth Molar Row, humerus or femur) and side from which it was taken (left or right). The first part (2.1) contains tables summarizing measurements through descriptive statistics (columns) for each measurement

(rows) and separately for sites as well as voles, mice and unidentified categories (separate tables).

All data for fusion scores were included in **Appendix 3 Fusion Scores**, with all molar wear data displayed in the text during the analysis. The fusion data was divided into different tables, depending on the site. Each table contains cumulative counts for each major area or phase as well as selected contexts (row groups). Epiphyses scores shown includes humerus, ulna, femur and tibia, both proximal and distal (specific rows). Counts are scored as fused or unfused for all finds (*Overall*), unidentified remains (*Unidentified*), voles (*Microtus*), mice (*Apodemus* or *Apodemus/Mus*), rats (*Rattus*) and shrews (*Sorex*; columns).

Table 3.06 – Overview of data groups and related columns included in the Appendix 1 (data) for all the sites. Each column relates to a single variable.

* data included in case of references and signatures databases

Data Group	Columns (individual variables)		
Key Information	<i>Contextual data for each site, period, context, sample or reference [differs between sites]</i>		
Basic Quantification	weight (g) * (Σ)NISP * (Σ)MNI *	No. Of Classes (Meaningful) No. Of Classes (All)	Specific group NISP/MNI [differs between sites]
Elements NISP	Maxilla * Mandible * Scapula * Pelvis * Humerus * Ulna * Radius * Femur *	Tibia * Vertebra * Calcaneus Talus Rib Metapodial Phalanx Other	Incisor (loose) * Molar (loose) * Incisor (intact) Molar (intact) Incisor (Missing) Molar (Missing) CTMP *
Skeletal Groups	Skull Elements * Front Limb Elements *	Hind Limb Elements * Vert. Elements *	All. Elements *
Abundances (%)	Maxilla* Mandible* Incisor (loose) * Molar (loose) * Scapula * Pelvis * Humerus * Ulna *	Radius * Femur * Tibia * Vertebra * Calcaneus Talus Rib Metapodial	Phalanx CTMP * $\Sigma\%$ $\Sigma\%$ with Teeth
Skeletal Frequencies (%)	Skull * Vertebra *	Front Limb * Hind Limb *	
Indices (%)	Isolated Incisors Isolated Molars	Postcr. to Crania (complex) * Postcr. To Crania (simple) *	Distal to Proximal *
Skull Breakage, Counts	Max. In Skull Max. With Zygom.	Max. Only Minor Fragm.	
Skull Breakage, Percentages	Max. In Skull Max. With Zygom.	Max. Only Minor Fragm.	
Mandible Breakage, Counts	Complete Ramus Broken	Ramus Missing Inferior Border Broken	
Mandible Breakage, Percentages	Complete Ramus Broken	Ramus Missing Inferior Border Broken	
Fragmentation Counts	Mandible (Complete) * Mandible (Broken) * Humerus (Complete) * Humerus (Broken) *	Ulna (Complete) * Ulna (Broken) * Femur (Complete) * Femur (Broken) *	Tibia (Complete) * Tibia (Broken) *
Fragmentation Percentages	Mandible (Complete) * Mandible (Broken) * Humerus (Complete) * Humerus (Broken) *	Ulna (Complete) * Ulna (Broken) * Femur (Complete) * Femur (Broken) *	Tibia (Complete) * Tibia (Broken) *
Taphonomy	Digestion, Incisors(NISP) Digestion, Molars (NISP) Digestion, Hum. & Fem. (NISP)	Digestion, Incisors(%) Digestion, Molars (%) Digestion, Hum. & Fem. (%)	Evidence of Burning

3.3.7. REFERENCE DATABASE

As mentioned in **Chapter 2.2.**, the majority of taphonomic methods for studying micromammals remains are designed specifically to establish what predator is responsible for the deposition of a specific micromammal bone assemblage. Known modern depositions are often used as references when attempting identification of both modern and archaeological deposition (e.g. Romaniuk et al. 2016) as well as to establish how well the studied species pattern matches already known ones (e.g. Armstrong & Avery 2014). The idea of a specific “pattern” for selected predators or predatory groups has been suggested and elaborated on within the last 40 years (e.g. Andrews & Evans 1983; Andrews 1990; Saavedra & Simonetti 1998; Matthews 2002; Soutttou et al. 2012).

The differences between predators depend on multiple factors related to animal biology and behaviour, though major differences can be noted between three key groups: owls, diurnal raptors and mammals. Owls are known to ingest micromammals in whole and later regurgitate almost complete skeletal remains in a form of a pellet, creating large skeletal assemblages over time with a relatively low amount of digestion marks on their surfaces. Diurnal raptors tend to dismember micromammals prior to or during the consumption, resulting in disarticulated and fragmented remains, deposited in both pellets and droppings. Mammalian carnivores ingest micromammals whole, but have very strong stomach acids, dissolving gracile bones and severely altering robust ones. Moreover, mammals tend to use their faeces to mark their territory, resulting in small but multiple depositions over a wider area. For more see Andrews (1990, the importance of predators in a deposition: 25-44, quantitative analysis: 45-90, animal habits: 178-209).

The utility of the predatory reference data for the intended purpose (i.e. identifying/comparing to specific depositors) can be seen when data is plotted directly. When relative abundances are plotted (for example, see Fig. 3.16) one can notice uniformly high values for both cranial and postcranial elements in the case of owl pattern, with a low number of loose teeth and some loss of minor paw bones and more fragile elements like scapulas. Plotted fragmentation (example in Fig. 3.17) also shows far better preservation for the owl, with the majority of finds for specific elements being found intact. In turn, diurnal and mammalian predator patterns tend to show far less preserved crania, more loose teeth found and less balanced postcranial abundances. The differences between diurnal and mammal predators seem to be less pronounced, but one can

still see some intact finds for diurnal raptors while mammal finds are almost uniformly found broken.

As an integral part of studying and understanding taphonomy, the database of predatory deposition references was built from data displayed in taphonomically-oriented research, either contemporary to Andrews's work (1983-1990) or published later. The choice was inspired by Terry (2007) paper, but the original choice of references (Andrews & Evans 1983; Andrews 1990; Dodson & Wexlar 1979; Hoffman 1988) was broadened by additional sources (Kusmer 1990; Williams 2001; Matthews 2002; Gómez 2007; Gómez & Kaufmann 2007; Montalvo et al. 2007; Montalvo & Tallade 2009; Montalvo et al. 2012; Souttou et al. 2012; Armstrong & Avery 2014; Montalvo et al. 2014; Rudzik et al. 2015, López et al. 2018).

Additionally, a separate group of references was established for species present on Orkney or that have been present at some point in the past. Those included a barn owl, snowy owl, long-eared owl, kestrel, peregrine, hen harrier and red fox. Mean values were taken for Barn owls (Roost site $n = 4$, Andrews 1990, 33 table 2.2), long- and short-eared owls (each $n = 2$, Andrews 1990, 210 App. T 12) as well as kestrels ($n = 4$, Andrews 1990, 212 App. T 12). Singular assemblages were used in the case of Snowy owls (Andrews 1990, 210 App. T 12), peregrine falcons and hen harriers (Andrews 1990, 212 App. T 12) as well as red foxes (Andrews 1990, 213 App. T 13). Those will be referred to as "signatures" later in the thesis.

Data gathered from the references as well as signatures resembled one gathered for the sites (see Table 3.06, columns denoted with *) and is available in **Appendix 1 Data - Reference Data**. Due to fragmentation data presented in Andrews (1990) was differently formatted to other data as well as later references, it was impossible to create a singular table for all the references while still containing examples from Andrews (1990). The author split references into separate tables for data based on NISP (MNI, individual elements NISP, Skeletal groups, Abundances, Skeletal Frequencies and Indices) and fragmentation (Fragmentation Counts and Fragmentation Percentages). In the case of signatures, however, all data could fit into a singular table as all came from Andrews (1990). Due to some variety in the recording between references, if necessary, on an individual basis, the author attempted to recalculate specific values to better fit the recording system utilized in this thesis. For example, for Andrews (1990) the author had to recalculate the complex system of postcranial bone breakage (see **Chapter 2.2.7.** and **Chapter 3.3.4.** for more information) into a complete/broken dichotomy. Moreover, as Andrews (1990) fragmentation was only recorded as percent, the author also had to

recalculate Fragmentation Counts based on known Elements NISP and Fragmentation Percentages.

Statistical reason for the utilization of the selected data can be seen through utilizing Principal Component Analysis, one of the methods reducing multidimensional data to just two variables (Alder 2012, 357-360; e.g. Terry 2007, Fig. 1), on the reference data (Abundances in Fig. 3.18, Fragmentation in Fig. 3.19). In the case of both relative abundances and fragmentation percentages, it is easy to see a clear dichotomy between owls and other species. The difference between diurnal and mammal groups is however less visible, more in case of fragmentation than abundances. It generally confirms results seen in Terry (2007, Fig. 1), though a better division may be available when utilizing more complex algorithms.

For additional investigation between predator accumulation and dispersal/background scattering, the author added contexts from Skara Brae that represented extreme dispersal (all Trench III, most of IV and couple from of I and II, see Romaniuk et al. 2016b) to the database of references and a singular signature. As all those cases show very low values, it is a useful cut-off point between what can be considered as accumulation and non-accumulative scattering. Selected Skara Brae contexts were classified as a third or fourth category – background scattering.

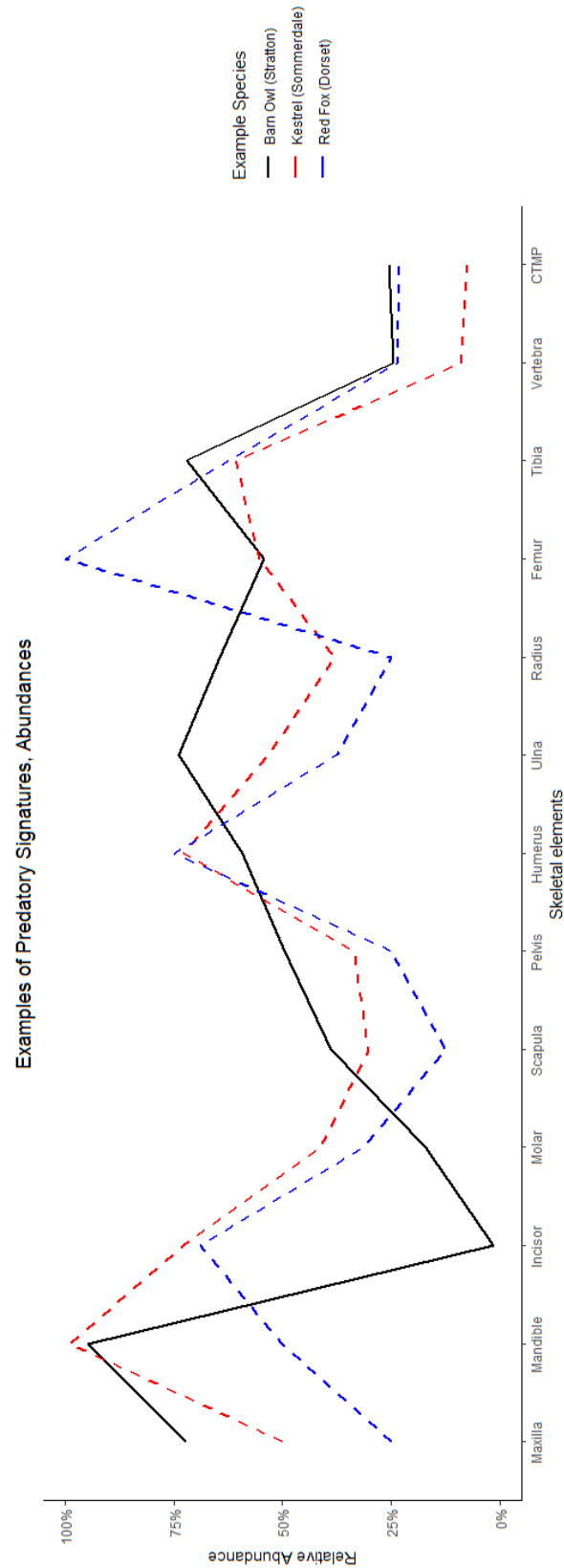


Fig. 3.16 – Example of relative abundances from three different species, representing three major groups of micromammal depositors. This type of visualisation was popularised by Andrews (1990) to highlight differences between specific patterns.

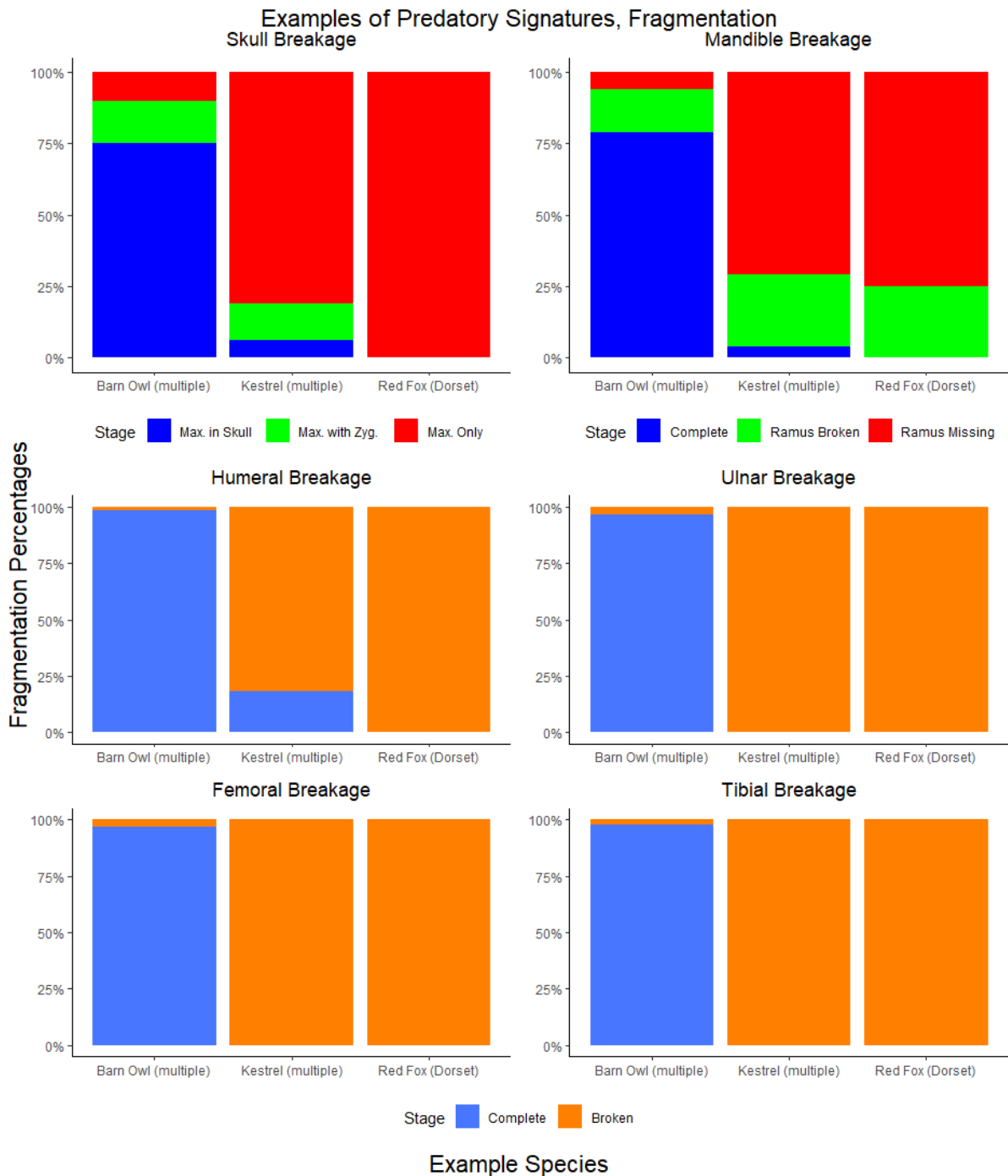


Fig. 3.17 – Example of fragmentation/breakage from three different species, representing three major groups of micromammal depositors, plotted for *Fragmentation Percentages*. The upper row presents the complex breakage of skull and mandible, while the middle and lower row shows the simplified breakage of postcranial elements (explained in **Chapter 3.3.4.**).

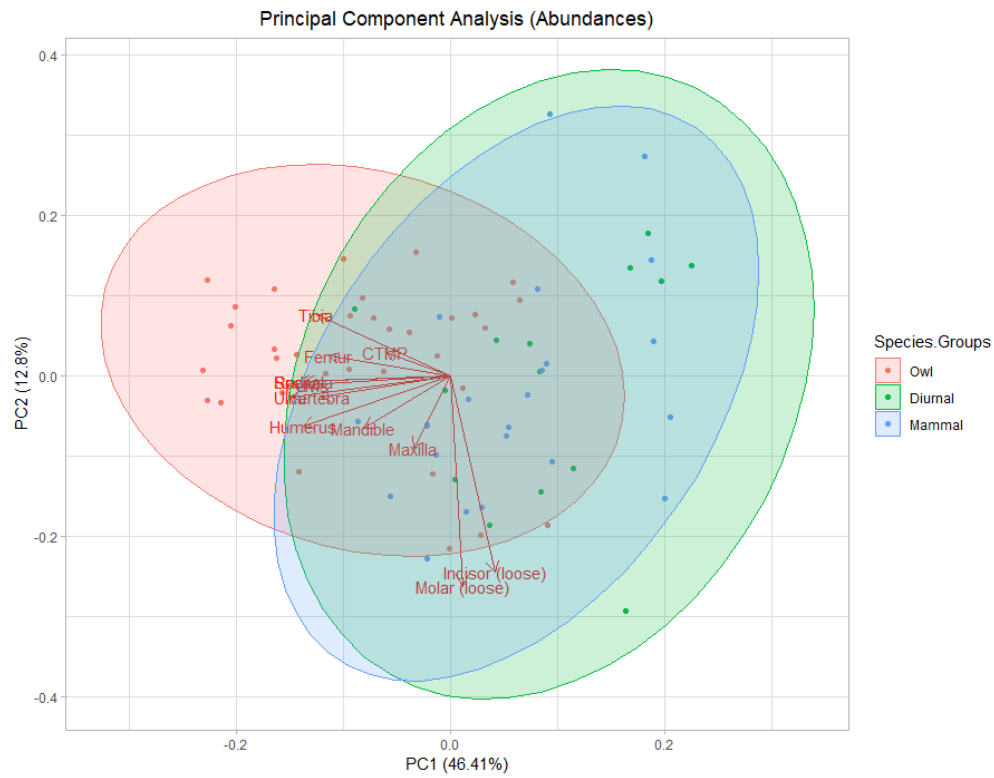


Fig. 3.18 – Principal Component Analysis (PCA) of the references data *Abundances*, including groups theoretical boundaries and trend lines for specific relative abundances.

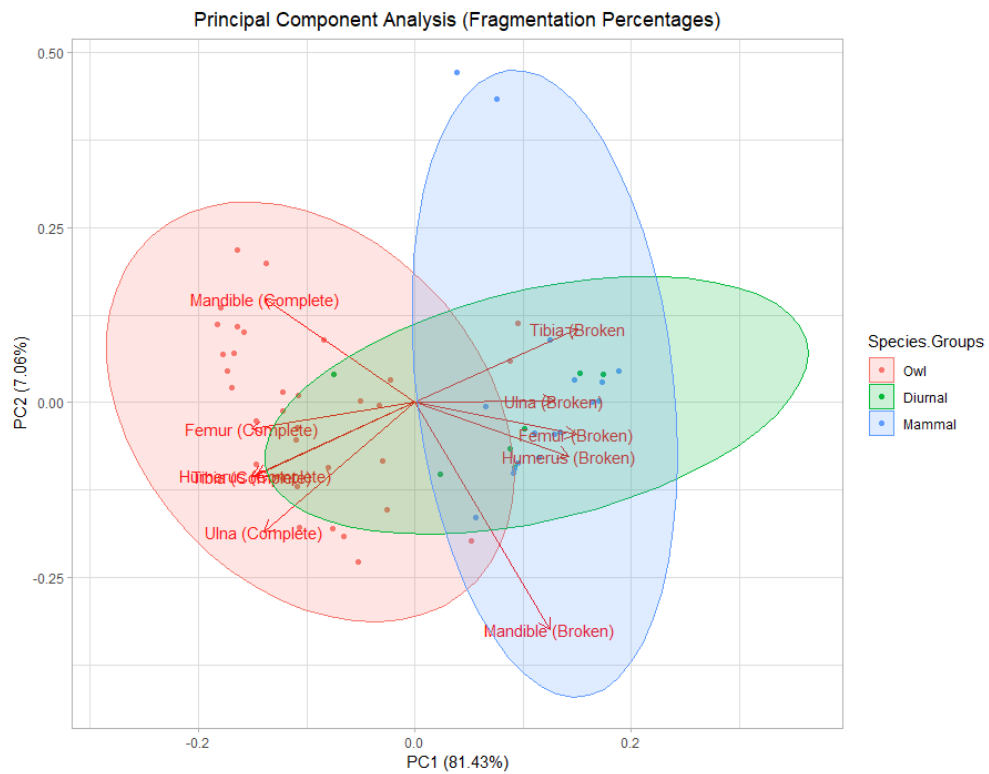


Fig. 3.19 – Principal Component Analysis (PCA) of the references data *Fragmentation Percentages*, including groups theoretical boundaries and trend lines for specific fragmentation percentages.

3.4. METHODS – STATISTICS AND COMPUTATION

3.4.1. RESEARCH STANDARISATION

The majority of analyses and visualisations, including all statistical computations, were coded in R and run in RStudio (RStudio Team 2016; Adler 2012). It was done to standardise the analysis for all quantifiable data and ensure the reproducibility of results. Coding in R was initially done on R version 3.5.1, with RStudio version 1.1.456 and later adapted to R version 4.0.2 and RStudio version 1.3.1073 as a new standard. All relevant results were saved in **Appendix 4 Statistics** and **Appendix 5 Predictions**. Due to the sheer number of computed data, many case studies only summarize or discuss only a key portion of them.

As the research tackles both individual statistical tests as well as compares large amounts of test results, a degree of standardisation was needed when it came to the statistical reporting and display. For examples of how to deal with such a task, the author utilized both biological (Witlock & Schuller 2015) and archaeological (Grayson 1984; Orton 2000) references, with some consideration of what has been done in micromammal taphonomy (Terry 2007; 2008). As during the author's PhD studies the importance of standardised statistical reporting has increased, further changes were included due to Dr Jonny Geber and Dr David Orton suggestions. For all tests relying on either the number of samples or degrees of freedom, the *n* or *df* value is always stated, either alongside the results within the text or in the figures and tables captions. For individual tests discussed, if possible, all results computable in R were stated in the text (**Chapter 3-5**) and included in selected Appendices. However, in the case of multiple tests being performed and/or summarised, only key results were considered (e.g. for correlations, the correlation coefficient). It is predominantly due to the methodological approach taken in such cases, namely searching for trends within a bigger pool of results rather than evaluating specific relationships. However, a practical side was also present, as creating the code to perform and summarize multiple tests was a time-consuming task, with the aim more focused on specific values saving both time and shortening the code necessary to process the results. In the case of data display the author followed Whitlock & Schluter (2015, 25-64) to visualise statistical results, relying on fully described 2d graphs (bar, frequency, box, scatter and mosaic plots) and tables.

While each stage of the analysis deals with different issues, site data could be formatted to a level of individual samples or contexts, with the latter possible to interpret in two ways. Given many contexts were only sampled (Bu Broch, Birsay Bay, Tuquoy, Scar), contexts could be interpreted as completely exclusive from samples by removing single-sample contexts, or partially overlapping with the samples by taking into account all contexts recorded. Due to that, if necessary, three levels were considered: samples only (named “samples” later in the analysis), multi-sampled or retrieved in whole contexts only (named “contexts”), and all the contexts (named “combined” due to the overlap). The division could help in understanding, how different levels or retrieval affect obtained results. In the case of Links of Noltland, where contexts were retrieved as a whole but with a grid-based division into samples, one-sample contexts were not included to “samples” but to “contexts” and “combined” groups due to representing the entirety of micromammal remains found within that context.

3.4.2. EXPLORING DATA

The first step of every statistical analysis should be to understand the nature of studied data, both archaeological and from the references. It could be done by investigating data distribution and significance across the studied sites as well as references. Knowledge about data distribution was required for further statistical research to point out which statistical tests or approaches are suitable for the data. In case of significance, results may show to what degree data vary between the sites (either by comparing means or value ranges) while also providing information on whether those changes are statistically significant.

Sites data investigated included all numeric data (*Basic Quantification, Elements NISP, Skeletal Groups, Abundances, Taphonomy, Skeletal Frequencies, Indices, Fragmentation Counts and Fragmentation Percentages*) besides species-specific NISP and MNI (*Basic Quantification*), element NISP not utilized on its own during the analysis or pointed only for the reference (e.g. “molar (missing)” or “other”, *Elements NISP*; “all elements” in *Skeletal Groups*) or essentially duplicating other values (“vertebra” in *Skeletal Groups* is the same thing as in *Elements NISP*). Applicable data from the references database was also investigated.

Data distribution was investigated through both descriptive statistics, visualisation and the Shapiro-Wilk test results (Whitlock & Schluter 2015, 374-375; Adler 2012, 382). Descriptive statistics included minimum, mean, median, mode and maximum values, as well as standard

deviation and the total range (i.e. from minimum to maximum), with histogram plots as a default visualisation (see Fig. 3.20). For Shapiro-Wilk p values were stated, with $p = 0.05$ considered as a demarcation point between like normal ($p > 0.05$) and non-normal ($p < 0.05$) distribution (see Table 3.07 for an example). Apart from testing raw data the applicability of common data transformations for the sake of normalising archaeological or reference data was also checked. Logarithmic, square root and reciprocal (inverse) transformations were employed to check the possibility of normalising integer data while arcsine was utilized mainly for fractional data with standard value range between 0 and 1 (Whitlock & Schluter 2015, 377-381; see Table 3.08). In the latter case, due to the occasional presence of values impossible to be processed by arcsine equation, testing with extreme data exclusion was used.

Once data distributions were known, tests measuring data significance could be chosen either from one way ANOVA and Levene tests (for normal distribution) or Kruskal-Wallis rank-sum and Flinger-Killeen tests (for non-normal distribution, see Whitlock & Schluter 2015, 460-471; Adler 2012, 378-381 & 387-388; see Table 3.07 for examples). Significance tests were applied to data with consideration of major areas within selected sites being separate entities, resulting in up to eight different areas considered (Skara Brae Trenches I and II, Skara Brae Trenches III and IV, Birsay Area 1, Birsay Areas 2 and 3, Links of Noltland Trench A, and Links of Noltland Trench D, Scar, Tuquoy). Site-based aims were to check if data could be significantly different between site core and off-site trenches (Skara Brae), if a difference could be noted between two different areas or trenches (Links of Noltland, Birsay), and if there is a visible difference between retrieval techniques (Birsay).

The three level system (samples, contexts, combined) was incorporated for more information on differences between samples and contexts as different contextual levels of data quantification, and applied to the reference database, all the sites jointly as well as on individual basis. Due to a large number of results only joint site data (**Table 1a**) and references data (**Table 1b**) were included in the **Appendix 4 (Statistics)**, with further significance tests summaries in text. Test examples, discussed and used for visualisations, were taken from both joint data, separate site data and reference data results.

Additionally, ANOVA or Kruskal-Wallis tests could be applied to check how specific anatomical groups differ between and within the sites. As taphonomy agents can lead to different levels of fragmentation and disarticulation (see **Chapter 2.2.7** and **Chapter 3.3.7.**) significant results for specific groups of anatomical elements may point towards differences between the sites, e.g. between intact depositions and disarticulated ones. While some

importance could be inferred from already defined *skeletal groups/frequencies*, a different approach was utilized. Groups of specific variables were defined in-code, including the skull (*maxilla, mandible*), front limbs (*humerus, ulna, radius*), hind limbs (*femur, tibia*), upper limbs (*humerus, femur*), lower limbs (*ulna, radius, tibia*), flat bones (*scapula, pelvis*) and small bones (*vertebra, CTMP*). Fragmentation data were also included as groupings, either as joint fragmentation for specific bones (e.g. mandible fragmentation containing *mandible (complete)* and *mandible (broken)*) or differences between complete and broken bones (e.g. complete frontal limbs, including *humerus (complete)* and *ulna (complete)*). For anatomic groups significance results see **Appendix 4 Statistics – Table 2**.

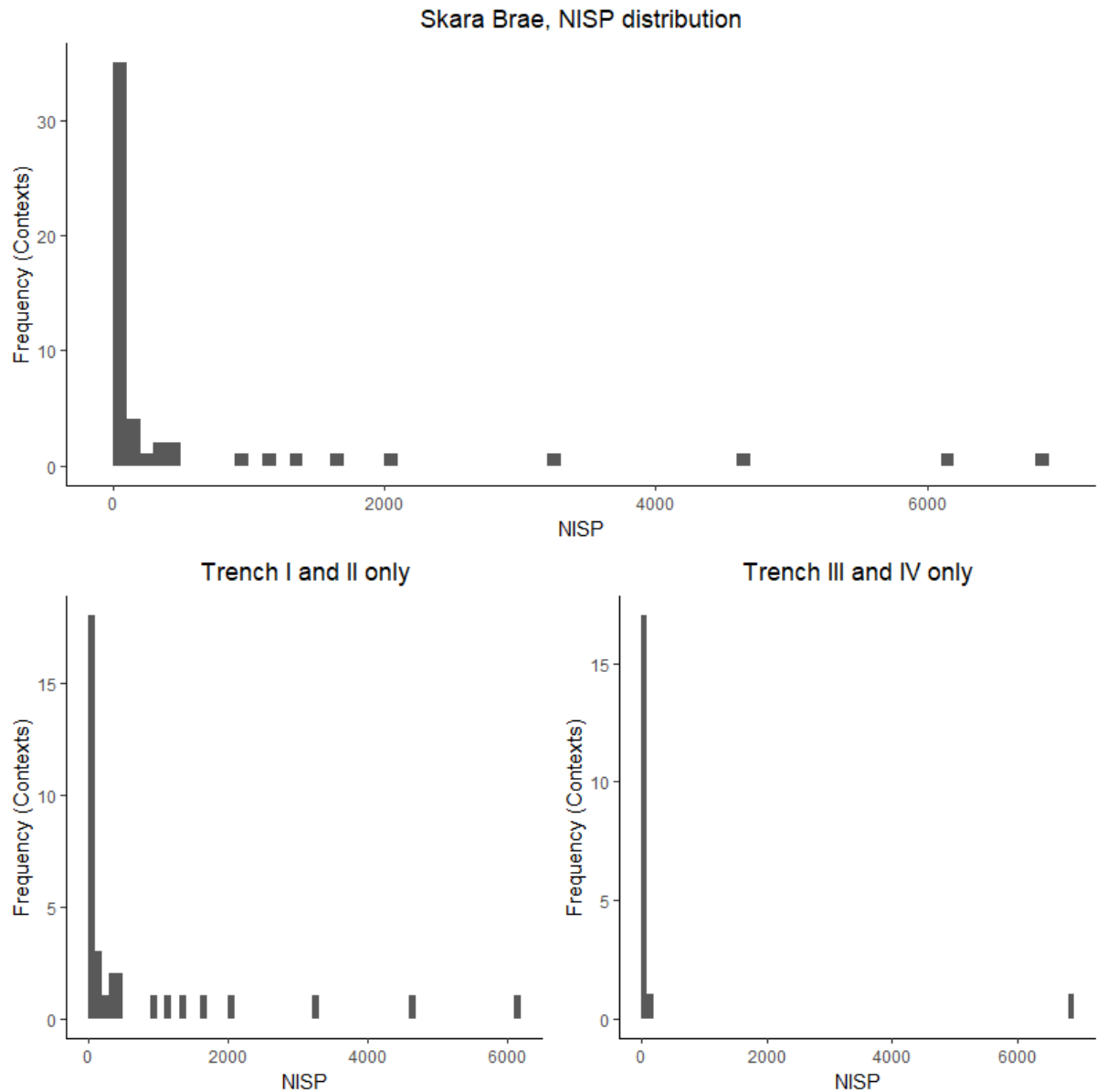


Fig. 3.20 –Example of a distribution visualisation: NISP frequency distribution in contexts from Skara Brae, plotted in intervals of 100 for all the trenches (upper plot), in-site trenches (lower left) and off-site trenches (lower right). It is a visualisation of an example data tested later in Table 3.07. In a general plot one can already notice the majority of values being clustered around the lower-end of the scale (mean = 586, median = 33, standard deviation = 1456) denoting non-normal distribution of the NISP data. For trench-specific plots one can also notice that, while showing a similar trend, off-site trenches have only one large context, perhaps more of an outlier. Compare with Table 3.07 to see how the distribution affects different tests.

Table 3.07 – Summary of the statistical tests used during data exploration, including their application assumptions, type, key R code, obtainable data from each test and reporting depending on individual or multiple testing. Notice, that for whole Skara Brae Shapiro-Wilk value denotes non-normal distribution ($n = 53$, $W = 0.46$, $p < 0.001$), what points towards the applicability of non-parametric Kruskal-Wallis and Flinger-Kileen tests. Those two also suggest differences between tested groups (Trenches I and II against Trenches III and IV, both $p < 0.001$).

Statistical Test	Shapiro-Wilk	one-way ANOVA	Kruskal-Wallis	Levene	Flinger-Kileen
Alternative name	Shapiro-Wilk test for normality	one-way analysis of variance	one-way analysis of variance on ranks	Levene test of homogeneity of variances	Flinger-Kileen test of homogeneity of variances
Application	assessing whether variable is normally distributed	assessing whether samples came from the same distribution	assessing whether samples came from the same distribution (mean as a key value)	assessing whether samples came from the same distribution (variance as a key value)	
Test type	-----	Parametric	Non-parametric	Parametric	Non-parametric
Results	variable is normally distributed variable has a distribution different than normal	samples (likely to be) coming from the same distribution (population)	samples coming from different distributions (populations)		
Function in R	shapiro.test ()	summary(aov())	kruskal.test()	levene.test()	fligner.test()
R package	stats	stats [aov()]	stats	car	stats
Raw test results in R (Skara Brae ΣNISP; Groups = 2, $n = 53$)	W = 0.45914 p-value = 1.08e-12	base [summary()] df = 1 (51) Sum Sq = 1287282 (109017237) Mean Sq = 1287282 (2137593) F-value = 0.602 Pr(>F) = 0.441	chi-squared = 13.913 df = 1 p-value = 0.0001915	df = 1 (51) F-value = 0.4945 Pr(>F) = 0.4851	chi-squared = 12.396 df = 1 p-value = 0.0004303
Individual test reporting	$n = 53$, $W = 0.46$, $p < 0.001$	df = 1 (51), $F = 0.602$, $p = 0.441$	df = 1, Chi = 13.91, $p < 0.001$	df = 1 (51), $F = 0.49$, $p = 0.4851$	df = 1, Chi = 12.40, $p < 0.001$
Multiple tests	$n = 53$ $p < 0.001$	df = 1 (51) $p = 0.441$	df = 1 $p < 0.001$	df = 1 (51) $p = 0.4851$	df = 1 $p < 0.001$

Table 3.08 – List of popular data transformations often utilized to normalize data distribution.

Transformation	Equation
log10	$\log_{10}(x)$
inverted	$1/x$
square root	\sqrt{x}
arcsine	$\text{asin}(\sqrt{x})$

3.4.3. PEARSON/SPEARMAN CORRELATIONS AND χ^2 TESTS

The next stage of the analysis was concerned with the applicability of correlation and χ^2 tests to the archaeological and reference data, both as means of data exploration as well as assemblage identification. It was especially important to assess the utility of methods already used in the literature but never elaborated on their actual effectiveness. However, the establishment of preferable data choice for specific methods given was also important due to data redundancy often encountered in publications (e.g. both NISP and ratio/percentile data for specific elements displayed). In the available literature Pearson correlation test has been often used to establish correlations between contexts (e.g. Hoffman 1988; Andrews 1990, 47 t.3.1), with NISP counts of specific elements being used for that purpose. However, χ^2 test, occasionally used by several authors (e.g. Saavedra & Simonetti 1998), utilized relative abundances, not NISP, to prove or disprove homogeneity. It was also the case in the author's original work on Skara Brae (Romaniuk 2015), which used χ^2 test on relative abundances and fragmentation percentages, expressed in 0 to 100 scale, in the supplementary material to the published article (Romaniuk et al. 2016b, S.3).

Correlations can be calculated either through Pearson or Spearman method (Whitlock & Schluter 2015, 503-519; see Table 3.09). Pearson and Spearman correlations usage is not as strict as in other cases where parametric/nonparametric dichotomy is applied. Pearson is best for ratio/interval scale data but depending on a situation may be utilized for ordinal data that can be treated as an interval. Most important however is whether the relationship between data are linear. Ratio/interval scale plus linearity of relationship are commonly present in data with natural distribution hence Pearson correlation being usually considered as a parametric test. In contrast, Spearman, as a simple rank-based correlation, can be applied quite easily to ordinal data as well as to interval or ratio data. This method check relies on a monotonic relationship between studied data (arranges data from highest to the lowest value in each dataset) in order to draw conclusions but does not score exact rises or decreases of values. Spearman is a better choice for all the data in the case of monotonicity but with the lack of exact linearity thus is often considered as a non-parametric alternative for Pearson correlation.

The analysis started with a direct comparison of correlation tests through their application to archaeological and references data. It was both to check whether data relationships are monotonous or linear in relationship (and thus which method is more applicable for the data), as well as to evaluate the strength of correlations between variables within their own data groups

as well as between them. The data tested was similar as in the case of Data Exploration (**Chapter 3.4.2.** and **Chapter 4.1.**), with sites data including the majority of data groups (*Basic Quantification*, *Elements NISP*, *Skeletal Groups*, *Abundances*, *Taphonomy*, *Skeletal Frequencies*, *Fragmentation Counts* and *Fragmentation Percentages*) with the exception of *Indices*, percentile part of the *Taphonomy* group and several repeating, species-specific or not directly utilized variables. From the references, the entirety of *Elements NISP*, *Abundances*, *Skeletal Frequencies*, *Fragmentation Counts* and *Fragmentation Percentages* was utilized as well as *Skeletal Groups* besides vertebra and cumulative values. Matrices of Pearson and Spearman correlation coefficients were computed for references data as well as site data, in the latter case only considering the combined level of quantification (i.e. data equal to **Appendix 1 Data - Context Data**) for all the sites jointly as well as each site separately.

In the case of obtained Pearson coefficient (r) being higher than Spearman coefficient (ρ) data could be considered not only monotonic but also relatively linear, even if considered non-normally distributed. When the inverse situation is observed, i.e. Spearman ρ being higher than Pearson r , data are still monotonic but less linear than necessary for the utility of parametric tests. In the case of weak correlations data comparison does not show a monotonic relationship – and in extension any linearity. However, due to the sheer number of values for each variable ($n = 916$ for samples, $n = 237$ for multisampled contexts only, $n = 466$ for all contexts) critical values for correlations were by nature very low. For example, for $df = 100$ ($n = 102$) and significance 0.05 the critical value for Pearson is 0.195, for $n = 100$ and significance 0.05 Spearman critical value is 0.197. Considering that it was easy to pass for the vast majority of tests, rendering most if not all tests statistically significant.

Once coefficient matrices were computed, their results were summarized in two ways. The first was to summarize the cases in which a specific correlation returned higher values and provide median values obtained for each method. In appendices (See **Appendix 4 Statistics – Table 3**) it was done up to individual variables, with a more general summary of whole data groups presented in the text. Second, once the preferable method for data correlation was found, was to summarize for each variable the highest and lowest correlation coefficient obtained as well as with which variables those results were obtained. It was recorded separately for within the data group and when considering all the data. The outcome can be seen in **Appendix 4 Statistics – Table 4a-c**.

The next stage of the analysis was to answer, whether chosen statistical tests can be used to identify specific assemblages, for example owl deposition. Testing correlations from that

perspective would help in answering, whether correlations are good enough for assemblages classification as it was implied back in Andrews (1990, 47 Table 3.1) and how detailed such investigations can be given obtained correlation values range and specific sets of data used. For this stage only references and signatures datasets were utilized, with data coming from *Elements NISP*, *Skeletal Groups*, *Abundances*, *Skeletal Frequencies*, *Fragmentation Counts* and *Fragmentation Percentages* (see examples of *Abundances* and *Fragmentation Percentages* data in Table 3.10). In general, the assumption was that a specific method is applicable to a specific data group if the results obtained can be clearly differentiated between four key groups (owl, diurnal, mammal, background scattering), and the majority if not all significant positive correlations can be found when comparing a group with itself. For an example of how to apply the tests and interpret the results see Table 3.11.

For each data group and method a matrix of correlation coefficients was created, either by comparing entries within the references dataset or by comparing references entries to entries in the signatures dataset. Results obtained from comparisons within the references database were summarized in **Appendix 4 Statistics – Table 5a-b**, considering data group used, main group (owl, diurnal, mammal, dispersal) tested, group to which it was compared, the overall number of correlations obtained, descriptive statistics for correlation coefficients, number of strong positive and negative correlations obtained. Moreover, those results were visualised and further summarized in the text. In the case of comparison of the references data to signatures data, those were only summarized in text.

Also, for the sake of context identification, the utility of χ^2 method was checked by following the same approach as in the case of correlations. Data used for χ^2 was slightly different from correlation data. Original data had to be multiplied by 100 as χ^2 test does not work with percentages expressed as ratio/fractions and requires a sample pool resulting in min. 5 per each used value. In previous research, the test was used in two ways. The first was to see whether samples can be considered as homogenous or not where the test was used as suggested (Romaniuk 2015), resulting in discarding the null hypothesis of random deposition. Second, it was used to see the similarity of studied data with predatory contexts, assuming contexts deposited by the same species will be homogenous. Only a few examples showed values lower than χ^2 0.05 threshold but responded to important differences in abundances and fragmentation patterns. By grading values from lowest to highest one could see most to least plausible depositors. The outcome for references is summarised in **Appendix 4 Statistics table 5c**, in a

manner similar to correlations, while a summary for both references and signatures was included in the text.

In the case of applicability of correlations and/or χ^2 tests as a classifier for one or more data groups, the author proceeded with checking their usefulness by establishing the likely accuracy of such approach for each data group and method. It was done by summarizing already obtained matrices to check the categorical provenience of best results. Accuracy was established for each of four main groups (Owl, Diurnal, Mammal, Scattering) as well as all four groups overall. The author also checked how the reduction of groups affects accuracy, with three combining mammal and diurnal as one group and two showing only a dichotomy between owls and other assemblages. Summary for references to references data comparison can be seen in **Statistics – Table 6a & b**, with extracts for both references to references and references to signatures comparison being shown in the analysis.

Table 3.09 – Summary of the three tests utilized: Pearson correlation, Spearman correlation and χ^2 test. The summary includes full name, test application, critical values source, interpretation of results, key information on their computability in R (functions, obtained results from a single test) and reporting. Standard confidence (0.95) and significance ($\alpha = 0.05$) levels for two-tailed testing were utilized.

Correlation/Test	Pearson correlation	Spearman correlation	χ^2 test
Alternative name	Pearson correlation coefficient / Pearson's r	Spearman's rank correlation coefficient / Spearman's ρ (rho)	chi-squared test of independence (homogeneity)
Application	assessing whether there is a linear relationship between two samples	assessing whether there is a relationship between two samples	assessing whether samples are either homogenous or independent
Results	r or $p >$ crit. Value - crit. Value $<$ r or $p <$ crit. Value r or $p <$ - crit. Value	Samples share strong positive correlation Weak or no correlation Samples share strong negative correlation	$\chi^2 >$ crit. Value : samples independent $\chi^2 <$ crit. Value : samples homogenous -----
Critical values in:	Weathington et al. 2012, 451-452 Table B. 7 (rounded to 3 decimal places)	Witlock & Schulter 2015, 722-723 Table G	Witlock & Schulter 2015, 703-705 Table A
Function in R (all from stats package)	cor(method = "pearson") [coefficient] cor.test (method = "pearson") [test] t = 22.84 df = 51 p-value $<$ 2.2e-16 cor = 0.9544347 percent confidence interval: 0.9219951 - 0.9735692	cor(method = "spearman") [coefficient] cor.test(method="spearman") [test] S = 920.98 p-value $<$ 2.2e-16 rho = 0.9628695	chisq.test() X-squared = 333.47 df = 52 p-value $<$ 2.2e-16
Raw test results in R (Skara Brae ΣNISP to ΣMNI, n = 53)			
Individual test reporting	df = 51 r = 0.95 p = $<$ 0.001	n = 53 ρ = 0.96 p = $<$ 0.001	df = 52 χ ² = 333.47 p = $<$ 0.001
Multiple tests/ coefficients only		df = 51 r = 0.95	df = 52 χ ² = 333.47

Table 3.10 – Example dataset, including four references from the references dataset in **Appendix 1 Data – References** and two data groups: *Abundances* and *Fragmentation Percentages*. Contrary to The appendix display as percentages, data here is displayed as computed, i.e. as a ratio with an expected range of 0 to 1. Those examples were used in Table 3.11 to compute example results.

Data Group	Data	Barn Owl (Stratton)	Short-eared Owl (Ross)	Kestrel (Sommerdale)	Red Fox (Dorset)
Abundances	Maxilla	0.72	0.80	0.50	0.25
	Mandible	0.95	0.83	0.99	0.50
	Incisor	0.02	0.07	0.73	0.69
	Molar	0.17	0.26	0.41	0.31
	Scapula	0.39	0.47	0.30	0.13
	Pelvis	0.50	0.73	0.34	0.25
	Humerus	0.59	0.97	0.73	0.75
	Ulna	0.74	0.87	0.53	0.38
	Radius	0.65	0.83	0.38	0.25
	Femur	0.54	0.83	0.55	1.00
	Tibia	0.72	0.90	0.61	0.63
	Vertebra	0.25	0.44	0.09	0.23
	CTMP	0.26	0.24	0.08	0.23
Data Group	Data	Barn Owl (n = 4)	Short-eared Owl (n = 2)	Kestrel (Sommerdale)	Red Fox (Dorset)
Fragmentation Percentages	Mandible (Complete)	0.78	0.24	0.00	0.00
	Mandible (Broken)	0.22	0.76	1.00	1.00
	Humerus (Complete)	0.99	0.88	0.18	0.00
	Humerus (Broken)	0.01	0.12	0.82	1.00
	Ulna (Complete)	0.97	0.92	0.00	0.00
	Ulna (Broken)	0.03	0.08	1.00	1.00
	Femur (Complete)	0.97	0.93	0.00	0.00
	Femur (Broken)	0.03	0.07	1.00	1.00
	Tibia (Complete)	0.98	0.87	0.00	0.00
	Tibia (Broken)	0.02	0.13	1.00	1.00

Table 3.11 – An example of standard statistical tests used as a classifying method. For each data group and method, a barn owl pattern from Table 3.10 was paired with the remaining three patterns: a short-eared owl (Owl and Owl), kestrel (owl and kestrel) and red fox (owl and fox). To properly compute χ^2 , all values from Table 3.10 were multiplied by 100. For correlations, all significant results were obtained only when both owl patterns were tested. χ^2 tests showed homogeneity only when owl and owl pair was tested when using abundances (for $df = 12$ $\chi^2 < 21.03$). In the case of other pairs, it seemed that the barn owl pattern was in overall more similar, to kestrel, a diurnal raptor, than a red fox, a mammalian carnivore. However, for fragmentation both test results were significantly negative.

Data Group	Method	Pair	Result	P-value
Abundances	Pearson ($df = 11$)	Owl and Owl	0.90	<0.001
		Owl and Kestrel	0.49	0.090
		Owl and Fox	0.11	0.716
	Spearman ($n = 13$)	Owl and Owl	0.80	0.001
		Owl and Kestrel	0.43	0.146
		Owl and Fox	0.22	0.468
	χ^2 ($df = 12$)	Owl and Owl	16.50	0.170
		Owl and Kestrel	115.66	<0.001
		Owl and Fox	166.66	<0.001
Fragmentation Percentages	Pearson ($df = 8$)	Owl and Owl	0.82	0.004
		Owl and Kestrel	-0.96	<0.001
		Owl and Fox	-0.98	<0.001
	Spearman ($n = 10$)	Owl and Owl	0.79	0.007
		Owl and Kestrel	-0.68	0.029
		Owl and Fox	-0.88	0.001
	χ^2 ($df = 9$)	Owl and Owl	82.09	<0.001
		Owl and Kestrel	832.54	<0.001
		Owl and Fox	893.97	<0.001

3.4.4. CLASIFFICATION MODELS

Modern programming can offer a range of computing-intensive methods that can be helpful in finding relationships between variables. Most commonly used are so-called multivariate data reduction methods, algorithms that track similarities between multiple variables and translate them into simpler, easier to visually display and analyse forms. Perhaps the best example is the Principal Component Analysis (PCA in short: Adler 2012, 357-360), which results can be easily plotted to visually represent the differences between observations (Adler 2012, 360 Fig. 16-4; Terry 2007, Fig. 1 & 2; see Fig. 3.18-9). More complex methods can go a step further beyond explanation and enable predicting where new or unknown data would fit. Predictive models can be used as means of classifying a specific object to a known category based on data provided. There is a wide selection of dedicated classification models or regression/machine learning models adapted for classification (Adler 2021: 467 – 484), with the most commonly used being Linear Discriminant Analysis (LDA, more in Adler 2012: 472 – 474; example in Terry 2007, Fig. 3 – 5 and mentioned in Fig. 2.04 in **Chapter 2.2.7.**). It relies on normally distributed, continuous data to find the most optimal way through linear regression to separate observations into expected categories (classes). Due to the linearity of results, LDA outcome can be also easily visualised in a way similar to PCA.

While both PCA and LDA have already been used to explore micromammal data, they may not be necessarily the best choice for larger data sets. Terry's work (2007) utilized both PCA and LDA to visualise the distribution of reference data, using a trained LDA model to classify a deposition found at the Homestead Cave (see **Chapter 2.2.7.** for more information). However, the dataset of references used was very small (only 39 entries for *Abundances* and 18 for *Fragmentation*), mostly coming from a single publication (Andrews 1990). Due to that, the stress was put predominantly on a visual side of both methods and the dichotomy between owls and the remaining two predatory groups. LDA usage as a classification method was just a minor point of the research. Additionally, both PCA and LDA can be only effectively applied to normally distributed data. In the case of a non-normal distribution, results would be significantly biased and less informative than in case of methods relying on non-normal distribution or ones being applicable to data regardless of its distribution.

For this thesis, a classification model trained to identify recognisable deposition patterns could help in working with large amounts of data more than a method visualising relationship patterns. The sheer number of contexts recorded in all six sites (n = 466) meant that assessing

likely taphonomic agents could be an arduous task if done in a traditional manner, i.e. by describing, analysing and describing each case separately. Employing classification would provide another way of exploring data and streamline the process of assessing multiple sites. Multivariate data reduction methods were not needed, mostly because descriptive statistics and correlations being already employed to explore both site and references data to great detail, with *Abundances*, *Fragmentation* and *Frequencies* visualised on its own and described in greater detail in **Chapter 5**. PCA was only utilized to showcase the variability within the references dataset and the viability of suggested classes (**Chapter 3.3.7**, Fig. 3.18-9), in a similar way as in Terry (2007, Fig. 1 and 2).

To properly employ a classification model in this study the analysis firstly started with finding what classification method is most suitable for the micromammal data. The author chose five different methods to check (Table 3.12). Apart from already described LDA, methods selection included: K-Nearest Neighbours (Knn), Flexible Discriminant Analysis (FDA), Generalized Linear Model With Penalized Maximum Likelihood (GLMNet) and Radial Kernel Support Vector Machine (SVM; more about the methods in Adler 2012, 424-427 and 464-484). Knn was chosen due to being functionally the most basic classification method, applicable to all data. It draws judgement on an object classification based on how classified are the most similar (“nearest”) objects. In turn, FDA was chosen due to being a variation of LDA, but working on a non-parametric regression instead. GLMNet was chosen as an example of a complex method, which combines multiple statistical methods to draw conclusions. It is also a preferred method to work on very large datasets. Similar to LDA, it was primarily developed for linear data, but can be also applied to a non-linear or a mixed distribution data without the risk of biases. The final choice, the SVM method, was due to a different approach to data and resistance to outliers. SVM sees data as a multidimensional plane and divides that space to create the most optimal way to fit the sought classes.

The comparison of five methods was achieved by training a series of classification models, each using a different method, on a references dataset (10 resampling events with 3 repeats for each) and then comparing the obtained classification models with each other. It was achieved by pooling accuracy and kappa (*Cohen’s kappa*, κ) values from each run to create a range for each method, plottable against each other. Training was done separately for applicable data groups (given the prior results of correlations and χ^2) and considered outcomes for all four classes present in the references dataset (owl, diurnal, mammal, background scattering) as well as shortening the classes to only three (owl, diurnal and mammal, background scattering).

Additionally, in order to check whether data pre-treatment affects (positively or negatively) used methods outcome, each method was run on both raw data and pre-treated one (weighted normalisation). The general outcome of the testing (accuracy, kappa) would answer, alongside data distribution, which method is the best for training a classification model, including whether is a difference between utilizing specific data groups, as well as whether data pre-treatment affects the model training and how the number of groups used affects identification accuracy.

Once the assessment of the methods was done and the best method or methods for the data found, the analysis proceeded with creating final models and assessing their quality. Two classification models for each applicable data group and method were trained on two different seeds. It was achieved firstly by tuning specific key parameters unique to each method (e.g. k value for KNN, see Adler 2012: 445-446 and Table 3.12) and finding the most optimal values, providing the highest accuracy for a classification algorithm. Then the optimal classification model, relying on those parameters, was trained. Once all the models were trained, the algorithms were applied back to the references data. In the case of more than one viable method, the aim was to choose the most optimal one, with accuracy desirably beyond 95% when applied to the references data. Once the choice was made, for each trained algorithm, all false identifications were checked and the reason behind misidentification was discussed.

Once the assessment was done the best method or methods were applied to the site data. When methods could confirm the same class for either sample or context for all data groups utilized, it was considered as a final outcome. In the case of different outcomes, it was scored either as accumulation (when outcomes point towards different predatory classes) or as contested (combination of predatory classes and scattering).

Table 3.12 – Final section of methods used for classification of micromammal data. Information includes the full method name, preferred data distribution for a specific method, pages where those methods are explained in Adler (2012), tuneable parameters and whether the method utilizes random number generation during the learning process. Once optimal parameters for each method are known (through *tune()* function from e1071 package), the final model for each method is generated using either general function (*train()*) or by a dedicated function if available.

Method	LDA	FDA	GLMNet	Knn	SVM Radial
Full name	linear discriminant analysis	flexible discriminant analysis	generalized linear model with penalized maximum likelihood	K-nearest neighbours	radial kernel support vector machine
Data Distribution	Linear data	All data	Linear preferred	All data	All data
Reference in Adler (2012)	472-6	472-6	424-7	477-8	464-5 & 483-4
Tuneable parameters	---	degree n-prune	alpha lambda	k	cost gamma
Uses random number generation (RNG)	No	Yes	Yes	Yes	Yes
Function to compute final model	lda()	fda(method=mars)	train()	train()	svm()
R package	MASS	mda	caret	caret	e1071

3.4.5. SAMPLE REPRESENTATIVENESS

One of the big issues already noted in the literature review (**Chapter 2.2.4.**) and stressed in this chapter is the impact of sampling and sampling regime on data representativeness. Thankfully, data from two sites could be studied from two similar approaches done on a different scale, to establish the degree of representativeness between samples and contexts expected. Many contexts were retrieved in whole from Birsay Area 1 but recorded in separate ~14 litre samples. Whole-sampled contexts, twenty in total, came from the central and squares of the area, representing the interior of an excavated construction. In turn, Birsay Bay Areas 2 and 3 were solely studied through whole-sieving of four selected squares in each case, resulting in a wider area being thoroughly investigated but no context retrieved completely. In the case of Links of Noltland, however, all contexts were sieved, with their material recorded up to the square (2x2m) the material came from. Applicable for analysis were 38 contexts from Trench A and 15 contexts from Trench D.

The first part of the analysis relied on data exploration. In order to be considered as a faithful representation of a context, the sample should have the same taxonomic diversity as well as the same or very similar taphonomic data, indicating the same taphonomic processes. The outcome of this stage of analysis can be seen summarized in **Appendix 4 Statistics** in tables **7a** (Birsay) & **b** (Links of Noltland). Checking taxonomic diversity was tackled by establishing whether taxonomic classes present in MNI estimation (in first case all, in second only ones reflecting specific species) of a sample match those of a context. The author firstly calculated, how many samples per context can be representative in each considered category, and later recalculated those values in percentages. Assuming a strong correlation coefficient means matching data, data groups that were previously proven effective in comparisons (See **Chapter 3.4.3.** and **Chapter 4.3.**) were used in correlations (Pearson or Spearman, depending on the previous stage of the analysis results) between samples and contexts. The number of strong correlations, as well as incomputable cases, were recorded, with the former being also calculated in percentages. Correlation coefficient values were also explored by descriptive statistics, to better understand the nature of obtained correlations, with correlation matrices also analysed later. Digestion was most problematic and due to that match was considered as true in the case of presence or absence matched between sample and context, with results quantification similar to taxonomic diversity. Finally, samples were checked from a perspective of simultaneous representation of all data types, considering results in taxonomic diversity, digestion and

correlations. The effectiveness of classification models, established in previous parts of the analysis, was also checked in a similar fashion. The number of samples matching with the parent context in identification was noted, with an additional calculation of percentile values. In the case of visualisations in-text, calculating the coefficient of determination (r^2) was used to further analyse the relationships between data.

For the second part of the analysis, the author decided to check how the aggregation of samples affects data representativeness. The aggregation of data from smaller “sub-samples” in order to obtain a representative sample is called cumulative sampling in archaeology and associated sciences (Miksicek 1987, Fig. 4.3; Orton 2000, 148-176 & Fig. 6.5, 6.9-10), a method originally designed for archaeobotanical research (Fasham & Monk 1978; Veen & Fieller 1982; Miksicek 1987). The point of the aggregation process is to reach equilibrium in data obtained, where sought data stops to significantly change (“fluctuate”) when new subsamples are added. Sample built in such a way should be as representative as sampled data can be, “adequately” representing its parent context or assemblage. While original investigations considered mainly taxonomic diversity and related data in any quantifiable data could be investigated in such way. For this stage of analysis, the author chose four contexts, two for each studied site, with criteria being primarily highest taxonomic diversity and secondly highest samples count. The sequence of sample aggregation was established randomly, with the outcome visualised as line plots for specific variables and summarized in tables in-text.

3.4.6. TAPHONOMIC PROCESSES

A question that could be investigated alongside the analysis of various methods was how, and to what extent, non-predatory taphonomic factors and processes can affect predatory patterns. Gradual scattering of bone assemblages from primary assemblages, secondary accumulation and the process burial of the assemblage itself, have been several of the key issues considered by Taphonomy as a science (Lyman 1994a). However, as mentioned in the literature review (**Chapter 2.2.6-8.**) micromammal archaeology and taphonomy have rarely investigated deposition patterns beyond modern, relatively well preserved, predatory assemblages and perhaps variability between those assemblages. Especially lack of new data on scattering is surprising, considering the impact of dispersal was already noted in Terry’s 2004 research, with a conclusion that such changes can affect assemblages identifiability.

Due to restricted amount of data, the analysis was divided into two sections, with the first part being a visual exploration of available examples and their comparison to references and site data. Terry (2004) and Behrensmeyer's work (Behrensmeyer 1983; Behrensmeyer & Boaz 1980; Lyman 1994a, 191 table 6.14) were used to obtain examples of specific patterns. Terry (2004) provided micromammal patterns specific to the stages of open-air owl accumulation dispersal, from intact pellets (intact), through partially dispersed pellets (partial dispersal), to deteriorated and dispersed remains (full dispersal). As Terry's work was actually on one large assemblage with different dispersal levels from its centre, a cumulative pattern (named "Whole assemblage" or "Whole" for short) was also considered. In turn, Behrensmeyer's patterns included various assemblages, including buried remains (diagenetic predatory pattern), scattered remains (biostratigraphic dispersal) and predatory patch (kill site accumulation). While those patterns were mostly created by large taxa, a comparison could help in understanding how some assemblages may form. Also, for reference, a pattern representing a complete skeleton (called "complete") was included. For visual comparison, *Skeletal Frequencies* and *Indices* (related to skeletal parts only) were utilized, both due to ease of visualisation of singular and multiple patterns as well as *Skeletal Frequencies* being based on Behrensmeyer's work (see **Chapter 3.3.4.**). All results of visualisation were included in-text.

The second part of the analysis relied on the creation of theoretical datasets, simulating specific stages of scattering or burial, and later checking how identifiable those datasets are given previously checked (correlations, χ^2 , classification models) methods. Theoretical datasets were created by transforming references data (Table 3.13). For *Abundances*, equations were obtained from differences between different stages of dispersal in Terry (2004) and between on-field and buried assemblages in Behrensmeyer (Behrensmeyer 1983; Behrensmeyer & Boaz 1980). For *Fragmentation Percentages*, only Terry (2004) dispersal stages were considered. As the references data came mostly from the investigation of intact pellets or scats found on the ground, the "intact" stage of dispersal (Terry 2004) and "predatory patch" (Behrensmeyer 1983) were considered as most similar to the references database. Due to that "intact & surface" was considered equal to the references database and became the baseline for transformations. Similarly to the visualisation stage of analysis, the "whole assemblage" was also considered when creating theoretical datasets.

The analysis of theoretical datasets was done through similar means as investigating the viability of correlations, χ^2 test values and trained classification algorithms. However, the difference was the omission of the testing phase and the application of the best approach found

specifically for *Abundances* and *Fragmentation Percentages*. In the case of correlations, it meant the choice between Pearson and Spearman correlation based on previous analysis, while in the case of classification the utilization of one or more tested methods. Firstly, the author applied those methods to each of eight theoretical datasets and analysed obtained results. Secondly, the author checked how effective are correlations with signature data, transformed through each equation, and classification model, trained on transformed data simulating partially dispersed, buried assemblage, in identifying site contexts. All results were presented in-text.

Table 3.13 – Transformation equations used to change reference data (assumed to intact/predatory patch deposition being most similar to reference data, hence used as a baseline). For the difference between the types of assemblage see analysis in **Chapter 4.6.**

Type of Data	Type of Assemblage	Source of Data	Abundances													
			Maxillary	Mandibulae	Incisors Loose*	Molars Loose*	Scapulae	Pelves	Humeri	Ulnae	Radii	Femora	Tibiae	Vertebrae	CTMP	
Abundances	Whole assemblage (Intact+Partial+Dispersal)	Terry 2004	x*0.68	x*1	x*1.0.5	x*1.02	x*0.6	x*0.48	x*0.38	x*0.34	x*0.26	x*0.6	x*0.68	x*0.28	x*0.21	
	Intact															
	Partial		x*0.636	x*1	x*1.2	x*1.1	x*0.818	x*0.182	x*0.409	x*0.318	x*0.227	x*0.455	x*0.636	x*0.231	x*0.111	
	Dispersal		x*0.6	x*1	x*0.8	x*0.8	x*0.2	x*0.6	x*0.1	x*0.1	x*0	x*0.6	x*0.6	x*0.038	x*0	
Fragmentation Percentages	Predatory Patch	Lyman (1994A, Fig. 6.14); Behrensmeier (1983); Behrensmeier & Boaz (1980)														
	Burial		x*0.8	x*0.8	x*1.1	x*1.182	x*1.182	x*1.111	x*1.182	x*1.182	x*1.182	x*1.111	x*1.111	x*0.91	x*1.145	
	Whole assemblage (Intact+Partial+Dispersal)															
	Intact															
Fragmentation Percentages	Partial	Terry 2004														
	Dispersal															
	Whole assemblage (Intact+Partial+Dispersal)															
	Intact															

all = x+0.05(broken) x-0.05(complete) (max. 1.0, min. 0)

Baseline for transformations

all = x+ 0.1(broken) x-0.1(complete) (max. 1.0, min. 0)

all = x+0.25(broken) x-0.25(complete) (max. 1.0, min. 0)

3.4.7. MEASUREMENTS, SKELETAL FUSION, WEAR AND PATHOLOGICAL CHANGES

The final methodological approaches relevant for methodological evaluation are those using metric, age and pathology data, summarised in **Appendix 2 Metrics & 3 Fusion Scores**, or, as in the case of molar wear and pathological changes, during the analysis. As already mentioned in the Literature Review (**Chapter 2.2.5-6.**) such data can be gathered but due to the rarity of methods and studies taking advantage of such data their importance and accuracy in archaeology, apart from strict molar morphometrics, is essentially unknown.

Metric and age-related data were assessed first. Metrics were assessed by checking the number of specific measurements obtained from the sites in relation to NISP and MNI and taxonomic differences. The outcome from all the sites was also plotted and its informativeness discussed. The analysis of age data collected was more complex as the three methods suggested had to be assessed separately. Assuming that better methods will include a greater number of individuals the most important factor to check in each case was how much of an overall MNI is being represented in a method. Additionally, methods were checked against each other in order to investigate if any significant differences in interpretation can be seen.

Pathology data were tackled by firstly checking numbers retrieved and calculating average retrieval rates of identifiable cases for each site. The type of pathological changes recorded was also checked to investigate whether there is any significant bias towards specific cases. Once done, specific cases were discussed in length.

3.4.8. INTRODUCING COMPUTATIONAL RESULTS TO SITE ANALYSIS

The outcome of methodological case study should be applicable on several levels to the later sites analysis. Most crucial is what data are actually informative and can be later utilized without a fear of statistically inconclusive outcomes. It was especially important for previously under researched or newly introduced data types, including ones related to age estimation (wear, skeletal fusion), postcranial metrics, pathologies and so on. In the case of quantified data based on NISP it also included *Indices* and *Skeletal Frequencies*. Moreover, additional statistical data on specific quantifications can be later used as reference to showcase the statistical importance of some conclusions. Finally, the search of possible taphonomic agents and differentiation

between predatory and non-predatory patterns can be augmented by classification approaches tested in the first case study. Most classifications based on workable methods, relying on data most suitable for them, can be used to save time and streamline identification of multiple contexts present on six analysed sites. The results of application of those methods to site data were included in **Appendix 5 Predictions**.

3.5. SUMMARY

Micromammal material analysed in this thesis comes from six different sites, including five settlements and one boat burial. All sites chosen were either sampled or sieved in whole. Each of the main periods investigated, Neolithic and Norse/Medieval, is represented by two settlement sites with undisturbed stratigraphy, one on Mainland (central island) and one on Westray (north-western end of the archipelago, on the way to Shetland isles). Two additional sites, a broch from Early Iron Age and boat burial from Norse period, were included in order to represent situations different than that presented in the four main sites. Contextually, one represents a site between two main periods while the other a non-settlement archaeological assemblage. Methodically, both sites were emergency digs, investigated at speed, with sampling and sieving consequently utilized but not a priority. Reference materials in a form of partial or complete micromammal skeletons were also used, chosen from the National Museums Scotland vertebrate collection.

Most of the sorting and all siding and identification was done by the author, firstly over the course of the previous project (Skara Brae) and then during this research (remaining five sites). All the work was done through the visual assessment, with the exception of taphonomic assessment and rat species identification. Data retrieval started from estimating anatomical and taxonomical provenience of all encountered micromammal fragments, with quantification taking into account that not all fragments can be identified up to specific species. In specific cases, such as secondary data based on elements NISP, two methods were introduced in order to include alternative approaches in later methodological analysis. In the case of rat bones selected material was taken to The University of York to be checked through the ZooMS method. Taphonomic changes were also assessed during this stage, alongside measurements and molar wear scoring. Most relevant taphonomic marks, necessary to check whether assemblages were of a predatory origin or altered in any way by humans, were digestion, burning and fragmentation. As abrasion and weathering may cause similar changes to digestion it was also assessed but not quantified. Selected materials were checked under the SEM microscope with EDS functionalities, to confirm the taphonomic identification under better resolution (SEM) and obtain information on samples' chemical composition (EDS, specifically for burnt remains). Metric data were gathered alongside epiphyseal fusion and molar wear scoring, to be used primarily for the recreation of micromammal species age pyramids.

Statistical and computational methods were utilized to assess obtained data and used methods as well as to create and test new approaches to analysis. The assessment started from establishing the distribution of obtained data, including the utility of common transformations for the sake of obtaining gaussian distribution, later proceeded with testing statistical methods and training of classification algorithms on different sets of data. In turn, later analysis concentrated on sampling representativeness, pattern overlap between taphonomic agents and processes and its implication to identifiability, ending on assessing data rarely used with micromammalia (especially wear and skeletal fusion as age markers). However, the most important was the possibility of reapplying the results for the sake of site analysis, which was achieved by a focused discussion at the end of the methodological case study.

4. CASE STUDY 1 – ASSESSMENT OF METHODS

4.1. EXPLORING DATA

Quantifiable data gathered from all six sites did not follow normal (gaussian) distribution (full data in **Appendix 4.1a**). Results obtained from Shapiro-Wilk test for *Basic Data Quantification* (NISP, weight, MNI, Number of Meaningful Species Categories), averages from *Abundances* (Skeletal completeness, Avg. frequencies) and *Taphonomy* (Digestion counts and percentages) showed very low p-values ($p < 0.001$). All medians remained lower than means and mode was almost always the lowest possible value, revealing extremely right-skewed (positive) patterns. The most extreme case of skewness was noted within digestion counts, with most values apart from maximum being 0, revealing in the process that the vast majority of samples and contexts did not have any digested finds.

The best, and perhaps most important, example here is NISP. Given NISP is either related to (e.g. elements NISP) or is the basis in equations (e.g. Abundances) for other variables, its distribution is a good proxy for other data. Regardless if analysed within samples or contexts, jointly or as separate sites, NISP uniformly followed this distribution. This situation is clearly visible in visualisation (Fig. 4.01), descriptive statistics (samples: mean = 46.85 and median = 13, contexts: mean = 364.51 and median = 44) as well as Shapiro-Wilk test results (samples: $n = 916$, $W = 0.41$, $p < 0.001$; contexts: $n = 237$, $W = 0.42$, $p < 0.001$).

Abundances, *Fragmentation Percentages* and *Skeletal Frequencies* data also did not follow normal distributions (see Fig. 4.02 for examples of femoral proportions). All three datasets were quantified to percentages and thus could be considered as proportions with values ranging from 0.00 (0%) to 1.00 (100%). However, due to the system of calculating *Abundances*, adapted from Andrews (1990, 45) and Andrews & Evans (1983), maximal values happened to be higher in the case of heavily fragmented remains. *Abundances* also followed left-skewed distribution, with skewness being more pronounced in the case of samples than contexts, most likely of differences in values range. *Skeletal Frequencies* resembled to some degree abundances, but with context data showing less positive skew and, if not sudden rise in 90-100% values, approaching normal distribution. On the other hand, fragmentation values were correlated in

pairs and thus resulted in a predominantly bimodal pattern, with values allocated mostly on two ends of the proportions spectrum. Extreme distribution was more pronounced with samples, with the low-end extreme being more represented than the high-end one. Contexts contained more middle values but a negative correlation between complete and broken proportions could be noticed for middle values distribution.

Non-normal distribution was also common when analysing each side separately. According to the test, the assumption of normal distribution should not be rejected in the case of a p-value above 0.05. However, the majority of obtained p values were below that threshold. Cases above $p = 0.05$ were suggestive but too rare to be considered as having any impact on non-normal distribution trends already established. Moreover, calculations based on a smaller number of samples or contexts could provide p above 0.05, but visually not resembling actual gaussian distribution (examples in Fig. 4.03). More certain results were relatively frequent only for some *Skeletal Frequencies* and *Indices*, especially for contexts and open areas (e.g. Skara Brae Trenches III and IV contexts, *Distal to Proximal* Index: $n = 19$, $W = 0.93$, $p = 0.344$). For the remaining data, there was no deeper pattern observable between the sites.

Experimentation with data transformation for the whole dataset as well as for selected sites revealed a number of problems with such an approach. In the case of a whole dataset, with the exception of log10 application to weight data from contexts, transformations did not achieve satisfying results in providing normal distribution. It was visible especially for abundances and fragmentation percentages, where Shapiro-Wilk tests, after either square root or arcsine transformation, provided p still remaining within the spectrum of < 0.001 (examples in Fig 4.04). The only case where p was higher were arcsine-transformed average abundances for contexts ($n = 237$, $W = 0.99$, $p = 0.022$), but the value still did not reach $p = 0.05$ threshold. However, it did show arcsine transformation showing better results than square transformation. Inverted transformation proved to not be workable at the level of the whole dataset. Better results with transformation were obtained when working with each site separately. In some cases, primary as well as secondary data could be transformed into a normal distribution, but, similarly to raw p values, results were still too scarce to consider any method as a viable transformation for later analysis.

Encountered issues suggested discarding parametric tests in favour of the non-parametric approach to raw data. The majority of variables belong to a bigger data group (e.g. *Skeletal Frequencies*, *Abundances*, *Fragmentation Percentages*) which has to be either analysed jointly or compared with each other to produce expected results. In such a case, in order to apply

parametric tests, all sets of values within a group should approach a normal distribution. A similar approach should also be taken when comparing data through parametric methods. However, at best, mixed distributions were obtained within those groups, with data transformation results not providing a viable and coherent basis to be applied to the studied data. As mixed data, as well as data transformations, can introduce biases to parametric methods, non-parametric tests on raw data should be ones to be applied to further explore micromammal datasets if potential biases cannot be assessed.

The exploration of the reference data also suggested a non-parametric approach. In contrast to what was noted before for the site data relative abundances, abundances obtained from the references were almost exclusively between the values of 0 (0%) to 1 (100%), with only a couple of exceptions due to fragmentation. Additionally, means and medians were usually higher, around the range 10% to 70%, showing that data was far less skewed towards one end, even though modes were quite often either 0% or 100% (more in **Appendix 4.1b**). However, regardless of whether dispersal data was considered or not, raw values were uniformly below $p = 0.05$ threshold for the Shapiro-Wilk test, for both percentile as well as count data. The only visible difference was relative abundances having a more bimodal pattern than previously observed extreme skewness, with the additional concentration of values around 50% sometimes leading to multimodal pattern emerging (see Fig. 4.05). Similar to site data, arcsine transformation failed at normalising the whole dataset and only partially helped in the case of abundances coming from predatory assemblages only.

As data seemed to be non-parametric, the author used Kruskal-Wallis rank-sum test in conjunction with Flinger-Killeen test of homogeneity of variances, as described in methodology section (see Table 4.01). According to both tests the vast majority of data significantly differed between sites both in terms of means (Kruskal-Wallis test) as well as variation (Flinger-Killeen test), pointing towards the sites being nonidentical as well as the majority of data being possibly informative for the further analysis. For the whole site data, including both multi and one sample contexts, only one variable showed p higher than 0.05 for the Flinger-Killeen test (Mandible relative abundance: $df = 8$, $Chi = 9.67$, $p = 0.289$). Significant results were also common for contexts only and samples levels, but with some differences suggesting level of quantification affecting significance, thus possibly later analysis. For samples, the exceptions were almost exclusively within the *Taphonomy* group for humeral and femoral ends digestion (for percentile data: Kruskal-Wallis $df = 6$, $Chi = 9.03$, $p = 0.172$; Flinger-Killeen $df = 6$, $Chi = 8.52$, $p = 0.203$). It is possibly related to this type of digestion score being extremely rare within

the samples (Mean, median and mode being 0 or 0%). Two additional cases were noted only for Flinger-Killeen test, perhaps due to samples, while showing extreme results, were in overall more often towards the low-end of the established value ranges. Context-only data returned the majority of results above $p = 0.05$, though such results were still in minority across all data groups. It was mostly for the Kruskal-Wallis test, suggesting context-level data, in contrast to samples, showing similar means for the tested variables. Such situation was noted specifically *Abundances*, *Fragmentation Counts* and *Fragmentation Percentages*. With the last showing four different variables out of ten being relatively similar between the sites (e.g. Complete Tibia percentages: Kruskal-Wallis $df = 7$, $Chi = 12.5$, $p = 0.085$). However, fragmentation counter-values (e.g. Broken Tibia percentages: Kruskal-Wallis $df = 7$, $Chi = 40.38$, $p = <0.001$) were always significant, perhaps suggesting the way *Fragmentation Percentages* are obtained affecting the results.

Tests applied to the references data showed very strong and consequent differences between major groups, both as whole with scattering (owls, diurnal/mammal, background scattering) as well as within predator assemblages only (owls and diurnal/mammal; Table 4.01). In the whole dataset, *Elements NISP* proved to be significantly different both in means and variation (e.g. Humerus NISP: Kruskal-Wallis $df = 2$, $Chi = 51.27$, $p = <0.001$; Flinger-Killeen $df = 2$, $Chi = 32.19$, $p = <0.001$) while abundances based on those data only showed similarities in variation in three cases (e.g. loose incisors relative abundance: Finger-Killeen $df = 2$, $Chi = 5.36$, $p = 0.068$). A similar situation was noted for fragmentation, with *Fragmentation Percentages* showing $p > 0.05$ for Flinger-Killeen test for four out of ten variables. It is perhaps due to references data having more balanced variables ranges than what archaeological data have provided. Only *Skeletal Frequencies* showed a different trend, only half showing differences in means but three in variances. When data was narrowed only to predatory groups (owl, diurnal/mammal) differences were still predominant, though to a lesser degree. While both test results were affected far less significant results were obtained for variation, with *Abundances* showing only seven out of 13 variables with Flinger-Killeen test p below 0.05 but ten with Kruskal-Wallis test p below 0.05. Given that, predatory depositions seem relatively similar in each other in terms of value ranges obtainable, definitely more than archaeological data. However, there should be enough difference still in terms of means to main predatory groups to be distinguishable from each other (e.g. tibia relative abundance: Kruskal-Wallis $df = 1$, $Chi = 26.70$, $p = <0.001$; Flinger-Killeen $df = 1$, $Chi = 0.55$, $p = 0.459$).

Interestingly, each site with multiple areas returned a different answer when both tests were applied to obtained data (Table 4.02). Due to Skara Brae having both on-site and off-site trenches (I and II being within the site, III and IV off the site), it was not surprising to find out significant differences between both. Especially NISP/count based data (*Basic Quantification, Elements NISP, Fragmentation Counts*) showed differences in means and, apart from one case (Number of Meaningful Species Classes: $df = 1$, $Chi = 1.32$, $p = 0.25$), a differences in variation. It is most likely due to vastly different number of finds, with trenches I and II providing majority of NISP (Romaniuk 2016a). However, ratio data (*Abundances and Fragmentation Percentages*), also provided variables showing p lower than 0.05 for one or both tests.

Links of Noltland had a relatively similar situation as Skara Brae, but with inside deposition (Trench A) and open-field deposition (Trench D), but examples of significant differences in means or variation were far rarer. Given no significant results for the Basic Quantification group, it may point towards more subtle differences between relatively similar depositions in terms of quantity. Majority of cases were recorded for samples, with tests on a context level providing examples only for specific variables, most notably Indices (e.g. isolated incisors; Kruskal-Wallis $df = 1$, $Chi = 12.55$, $p = <0.001$; Flinger-Killeen $df = 1$, $Chi = 14.64$, $p = <0.001$). However, variables tended to show significant results only for one test but not another (e.g. ulna relative abundances for contexts: Kruskal-Wallis $df = 1$, $Chi = 1.9$, $p = 0.168$; Flinger-Killeen $df = 1$, $Chi = 12.89$, $p = <0.001$).

The most complex situation, however, could be seen with Birsay, partially due to the complexity of the site itself. Similarly to Links of Noltland, different levels returned different results, with the majority significant results on the sample level. However, a mixture of whole-earth sieving and sampling made it even more complex. When all the contexts were tested, significant results were roughly similar to samples (e.g. MNI for samples and Kruskal-Wallis test: $df = 1$, $Chi = 12.96$, $p = <0.001$; for combined: $df = 1$, $Chi = 7.68$, $p = 0.006$), as noted in case of joint sites, due to a multiple of contexts being represented by a single sample. However, when only multicomplex or whole-retrieved contexts were tested, results were often not significant (MNI for contexts and Kruskal-Wallis test: $df = 1$, $Chi = 3.58$, $p = 0.059$), returning similar situation as in case of Links of Noltland contexts. Only indices showed consistent significant results (e.g. complex postcrania to crania index: Kruskal-Wallis $df = 1$, $Chi = 10.01$, $p = 0.002$; Flinger-Killeen $df = 1$, $Chi = 4.15$, $p = 0.042$), with singular cases in other data groups.

The analysis of anatomical group significance through Kruskal-Wallis test provided further information on anatomical relevance in data (**Appendix 4.2**; Table 4.03). For the sites analysed jointly, both samples and all contexts (combined) levels returned significant results ($p < 0.05$) for all groups checked. For multi-sample contexts (contexts), the majority of results were also significant, but with some cases showing p above 0.05. For NISP-based data it happened only for the Complete Hind Limb group ($df = 7$, $Chi = 10.59$, $p = 0.158$). However, for percentile data non-significant results happened for four groups, one representing Skull ($df = 7$, $Chi = 9.91$, $p = 0.194$) and three representing different fragmentations, specifically Complete Hind Limb, Complete Frontal Limb and Mandible Fragmentation. Reference data showed all groups significant for whole data, but in the case of narrowing data to only predatory references, one could notice an inversion of what was noted for contexts. Almost half of the groups were non-significant for NISP, but when percentile data was used only three groups did not show significance, with Skull showing the highest p ($df = 1$, $Chi = 0.02$, $p = 0.902$). It is perhaps due to predatory data being better balanced in terms of NISP values, but with changes still showing in abundances and fragmentation percentages. For the sites, Skara Brae showed a very similar situation noted for the joint analysis context level. In turn, Links of Noltland and Birsay Bay showed the difference between samples and contexts already noted previously in data exploration. Of Links of Noltland, only one group was recorded as significant for percentile data on a context level, namely Isolated Teeth ($df = 1$, $Chi = 16.41$, $p = <0.001$). Birsay Bay showed more significant results, but also with Isolated Teeth showing lowest p ($df = 1$, $Chi = 9.85$, $p = 0.001$).

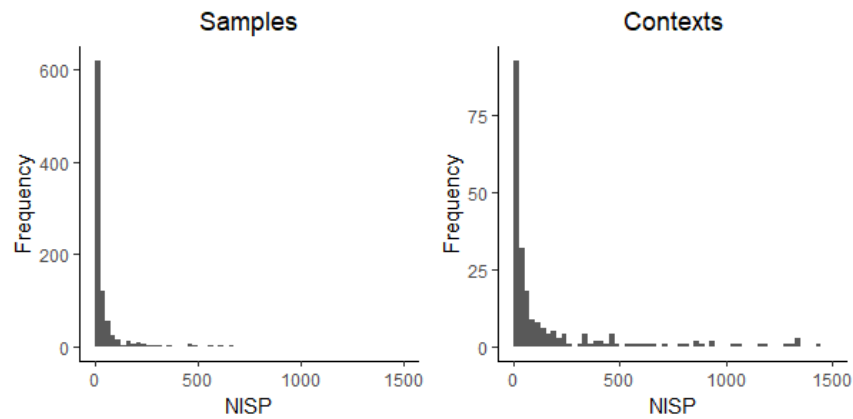


Fig. 4.01 – NISP frequency distribution in samples (left) and contexts (right) from all studied sites, plotted in intervals of 25 from 0 to 1500. Only fourteen contexts contained NISP higher than 1500 and were not shown on the right figure.

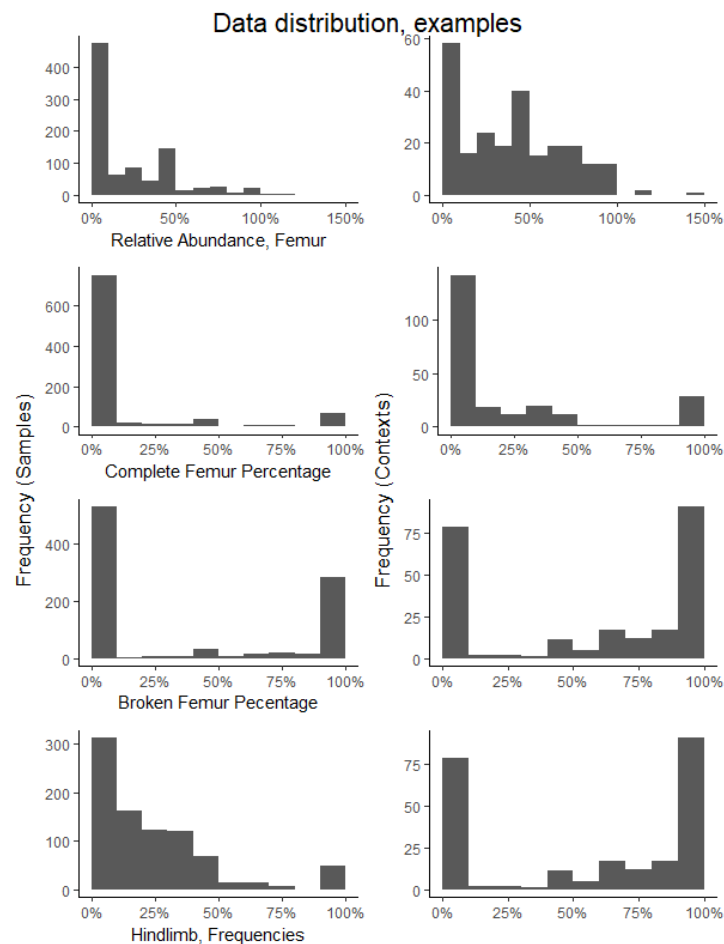


Fig. 4.02— *Abundances* and *Fragmentation Percentages* frequency distribution for femoral bones as well as *Skeletal Frequencies* for hind limbs, plotted for all sites. Note a difference between those distributions, especially in case extreme values between abundances and fragmentation and middle range values between samples and contexts.

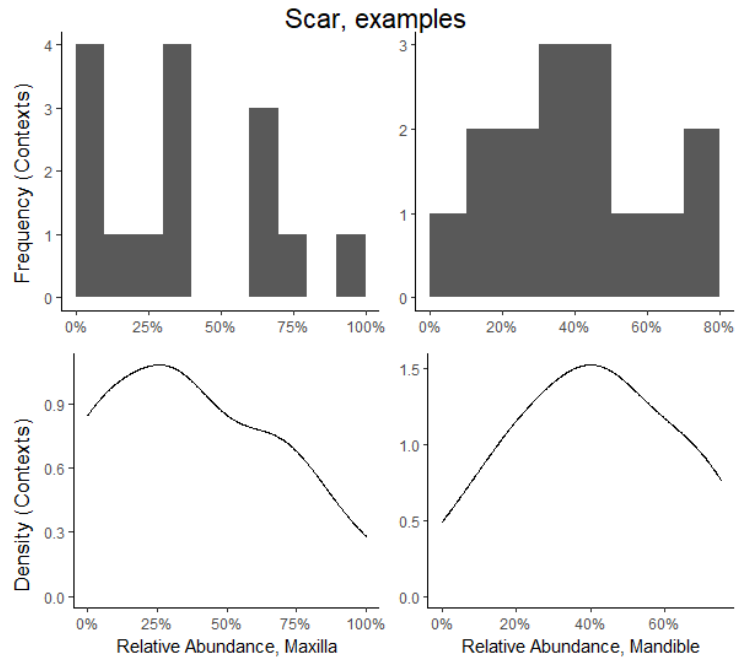


Fig. 4.03 – Frequency and density plots for context data of two relative abundances from Scar. Both variables passed the Shapiro-Wilk test (Maxilla: $n = 15$, $W = 0.91$, $p = 0.139$; Mandible: $n = 15$, $W = 0.98$, $p = 0.919$). Visually both variables differ from a normal distribution, especially in the case of histogram plots. It is perhaps due to a low number of observations affecting the test.

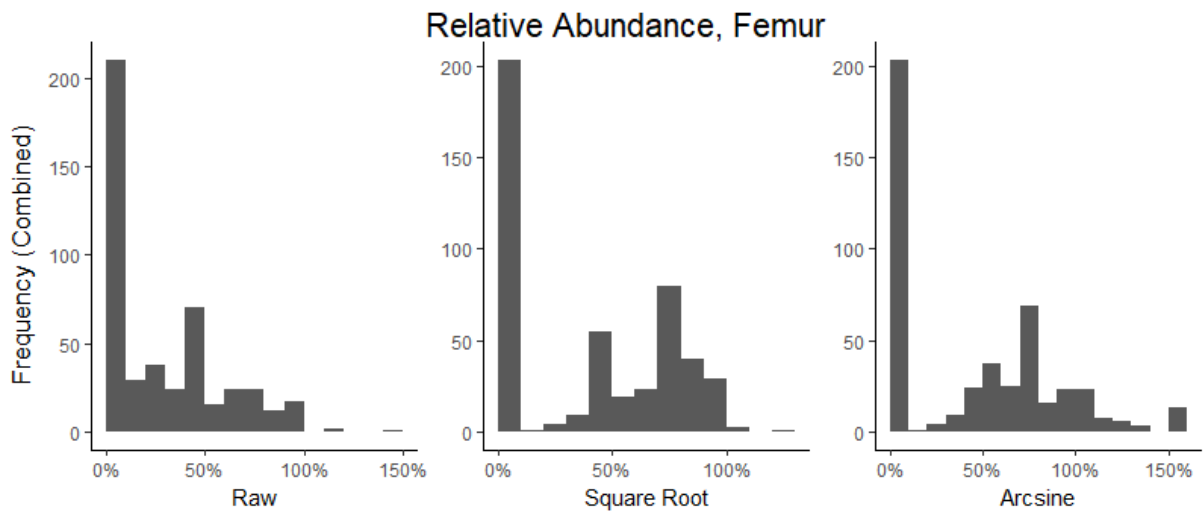


Fig. 4.04 – Frequency distribution of a femur relative abundance from all the studied sites and all contexts (combined level), divided into raw values and two transformations applicable to ratio/proportion data. Square root and arcsine transformations failed to provide better results due to extreme values. For raw data Shapiro-Wilk test results was $n = 466$, $W = 0.84$, $p = <0.001$, for square root $n = 466$, $W = 0.82$, $p = <0.001$, and arcsine unable to compute without removing extreme values (after removal of unknown number of entries result was $W = 0.85$, $p = <0.001$).

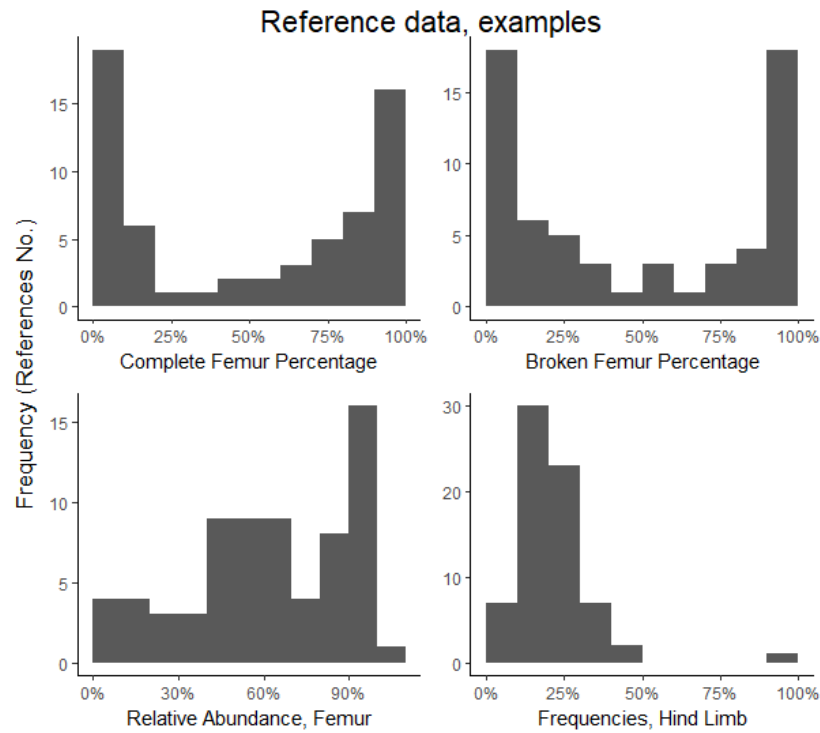


Fig. 4.05 – *Abundances and Fragmentation Percentages* frequency distribution for femoral bones as well as *Skeletal Frequencies* for hind limbs, plotted the predatory-only reference data. In contrast to Fig. 4.02 there is somehow better balance in mid-values number for fragmentation, though Femur relative abundance shows three separate peaks. Still, all four evidently show non-normal distribution, with e.g. Hind Limb skeletal frequencies showing $n = 71$, $W = 0.7592$, $p = <0.001$.

Table 4.01 – Summary of Kruskal-Wallis and Flinger-Killeen tests for the investigated site and reference data, summarized by the number of results lower than $p = 0.05$ and percent of all the test results. Values below $p = 0.05$ most likely point towards significant differences between the studied sites (whole data) or depositor groups (reference data). See **Appendix 4.1a** and **b** for more information.

Data	Data Type	Dataset	KW test - below 0.05	KW below 0.05 as %	FK test - below 0.05	FK below 0.05 as %
Whole Data	Basic Quantification	Samples	4	100%	4	100%
		Contexts	4	100%	4	100%
		Combined	4	100%	4	100%
	Abundances (% , averages)	Samples	2	100%	2	100%
		Contexts	2	100%	2	100%
		Combined	2	100%	2	100%
	Taphonomy	Samples	4	67%	3	50%
		Contexts	6	100%	6	100%
		Combined	6	100%	6	100%
	Elements.NISP	Samples	13	100%	13	100%
		Contexts	13	100%	13	100%
		Combined	13	100%	13	100%
	Abundances	Samples	13	100%	13	100%
		Contexts	10	77%	11	85%
		Combined	13	100%	12	92%
	Fragmentation Counts	Samples	10	100%	10	100%
		Contexts	8	80%	10	100%
		Combined	10	100%	10	100%
	Fragmentation Percentages	Samples	10	100%	10	100%
		Contexts	6	60%	9	90%
		Combined	10	100%	10	100%
	Skeletal Groups	Samples	3	100%	3	100%
		Contexts	3	100%	3	100%
		Combined	3	100%	3	100%
	Skeletal Frequencies	Samples	4	100%	3	75%
		Contexts	3	75%	4	100%
		Combined	4	100%	4	100%
	Indices	Samples	5	100%	5	100%
		Contexts	4	80%	4	80%
		Combined	5	100%	5	100%
References Data	Elements NISP	Whole	13	100%	13	100%
		Predation Only	11	85%	8	62%
	Abundances	Whole	13	100%	10	77%
		Predation Only	10	77%	7	54%
	Fragmentation Counts	Whole	10	100%	10	100%
		Predation Only	6	60%	7	70%
	Fragmentation Percentages	Whole	10	100%	6	60%
		Predation Only	10	100%	5	50%
	Skeletal Groups	Whole	3	100%	3	100%
		Predation Only	3	100%	1	33%
	Skeletal Frequencies	Whole	2	50%	3	75%
		Predation Only	2	50%	2	50%
	Indices	Whole	3	100%	3	100%
		Predation Only	2	67%	1	33%

Table 4.02 – Summary of Kruskal-Wallis and Flinger-Killeen tests for individual site data, formatted similarly to Table 4.01. Values below $p = 0.05$ most likely point towards significant differences within the studied sites.

Data	Data Type	Dataset	KW test - below 0.05	KW below 0.05 as %	FK test - below 0.05	FK below 0.05 as %
Skara Brae	Basic Quantification	Contexts	4	100%	3	75%
	Abundances (% , averages)		2	100%	0	0%
	Taphonomy		2	33%	2	33%
	Elements NISP		13	100%	13	100%
	Abundances		9	69%	3	23%
	Fragmentation Counts		7	70%	9	90%
	Fragmentation Percentages		4	40%	4	40%
	Skeletal Groups		3	100%	3	100%
	Skeletal Frequencies		1	25%	4	100%
Links of Noltland	Indices		1	20%	0	0%
	Basic Quantification	Samples	0	0%	2	50%
		Contexts	0	0%	0	0%
	Abundances (% , averages)	Samples	0	0%	2	100%
		Contexts	0	0%	0	0%
	Taphonomy	Samples	2	33%	2	33%
		Contexts	0	0%	0	0%
	Elements NISP	Samples	5	38%	10	77%
		Contexts	1	8%	3	23%
	Abundances	Samples	7	54%	7	54%
		Contexts	3	23%	5	38%
	Fragmentation Counts	Samples	2	20%	6	60%
		Contexts	0	0%	1	10%
	Fragmentation Percentages	Samples	2	20%	2	20%
		Contexts	0	0%	1	10%
	Skeletal Groups	Samples	0	0%	2	67%
		Contexts	0	0%	1	33%
	Skeletal Frequencies	Samples	3	75%	2	50%
		Contexts	2	50%	0	0%
	Indices	Samples	4	80%	3	60%
		Contexts	3	60%	4	80%
Birsay	Basic Quantification	Samples	3	75%	2	50%
		Contexts	0	0%	0	0%
		Combined	4	100%	1	25%
	Abundances (% , averages)	Samples	2	100%	2	100%
		Contexts	0	0%	0	0%
		Combined	0	0%	0	0%
	Taphonomy	Samples	0	0%	0	0%
		Contexts	2	33%	3	50%
		Combined	4	67%	4	67%
	Elements.NISP	Samples	12	92%	12	92%
		Contexts	2	15%	1	8%
		Combined	8	62%	5	38%
	Abundances	Samples	11	85%	11	85.00%
		Contexts	1	8%	2	15.00%
		Combined	3	23%	0	0.00%
	Fragmentation Counts	Samples	8	80%	9	90.00%
		Contexts	0	0%	1	10.00%
		Combined	4	40%	2	20.00%
	Fragmentation Percentages	Samples	8	80%	6	60.00%
		Contexts	2	20%	3	30.00%
		Combined	3	30%	1	10.00%
	Skeletal Groups	Samples	3	100%	3	100.00%
		Contexts	0	0.00%	0	0.00%
		Combined	2	67.00%	0	0.00%
	Skeletal Frequencies	Samples	1	25.00%	1	25.00%
		Contexts	0	0.00%	2	50.00%
		Combined	0	0.00%	2	50.00%
	Indices	Samples	3	60.00%	3	60.00%
		Contexts	4	80.00%	2	40.00%
		Combined	2	40.00%	0	0.00%

Table 4.03 – Summary of Kruskal-Wallis and Flinger-Killeen tests for anatomical parts, formatted similarly to Table 4.01 and 4.02. For the table see **Appendix 4.2**.

Data Type	Data	Dataset	KW test - below 0.05	KW below 0.05 as %
Anatomical Parts, NISP	Whole Data	Samples	17	100%
		Contexts	16	94%
		Combined	17	100%
	Skara Brae	Contexts	16	94%
		Links of Noltland	3	18%
	Birsay	Contexts	0	0%
		Samples	17	100%
		Contexts	1	6%
	References Data	Combined	5	29%
		Whole	17	100%
		Predatory	9	53%
Anatomical Parts, Percent	Whole Data	Samples	17	100%
		Contexts	13	76%
		Combined	17	100%
	Skara Brae	Contexts	11	65%
		Links of Noltland	5	29%
	Birsay	Contexts	1	6%
		Samples	14	82%
		Contexts	4	24%
	References Data	Combined	4	24%
		Whole	17	100%
		Predatory	14	82%

4.2. APPLICATION OF CORRELATIONS

Comparing Pearson and Spearman correlations was complex but generally in favour of utilizing the Spearman rank correlation method for exploring data. When all site data were analysed jointly (Table 4.04; full breakdown in **Appendix 4 (Statistics) Table 4.3**), Spearman rank-sum was higher in 1402 out of 1891 cases (74%), with median obtained within strong but moderate values ($\rho = 0.45$ for $n = 466$). Pearson correlation not only provided fewer cases where it proved to be more efficient than Spearman correlation but also showed a very low median (median $r = 0.25$ for $df = 464$). However, it was technically strong (over the 0.10 critical value for $df = 300$). It points towards site data in overall being relatively monotonically correlated with each other, perfect to use the Spearman correlation, but not linear to a degree justifying Pearson correlation as means of assessing the whole dataset. In the case of specific sets of data, ratios (*Abundances*, *Fragmentation Percentages*, *Skeletal Frequencies*) were found to follow this observation. For *Skeletal Frequencies* correlations obtained were predominantly negative, reflecting the way those values are interconnected with each other, but Pearson provided a better, even if negative, median. However, the situation was reversed for counts (*Basic Quantification*, *Taphonomy*, *Elements NISP*, *Fragmentation Counts*, *Skeletal Groups*), which were providing higher values predominantly from Pearson correlations. In the case of the *Basic Quantification* group cases were even between both correlations, but with Spearman showing a noticeably higher median ($\rho = 0.67$ for Spearman, $r = 0.52$ for Pearson).

More information about the utility of correlation methods could be inferred from studying each variable results separately (**Appendix: (Statistics) Table 4.3**). In case of variables from the *Basic Quantification* group one could notice, in case of correlations within the group, that all cases where Spearman correlation showed higher coefficients was related with The Number of Meaningful Species Classes (e.g. correlation with NISP: Spearman $n = 466$, $\rho = 0.58$, $p = < 0.001$; Pearson $df = 464$, $r = 0.14$, $p = 0.003$). However, when those variables were compared with variables outside of their data group it revealed a skew towards Spearman correlation. For example, NISP showed 32 cases where the Spearman method provided higher correlation coefficients, with the Pearson method showing higher for about 29 cases. In case of NISP-related correlations, median was also higher for Spearman method (median $\rho = 0.65$ for $n = 466$). Such a situation was repeated in the case of other count data (*Elements NISP*, *Fragmentation Counts*, *Skeletal Groups*) but without cases similar to The Number of Meaningful Species Classes. For ratio data one could notice variables that produced strong

coefficients with other data almost exclusively in the case of Spearman correlation. For *Fragmentation Percentages*, such situation was noted predominantly for complete ratios (e.g. Complete Femur). For relative abundances, the biggest example was CTMP, with all possible pairings showing better coefficient results for Spearman. Moreover, Pearson correlations for CTMP provided a very low median, including one of few weak correlations and second-lowest observed (median $r = 0.05$ for $df = 464$). Such a situation points towards CTMP not being suitable to analyse through methods relying on linearity, such as e.g. Pearson correlation.

In the case of the references data an even stronger skew towards Spearman correlation coefficients was noted. In contrast to sites data, results from both counts and ratio data align with the Spearman method. References data also showed the highest variation in median values, with *Elements NISP* and *Skeletal Groups* providing the highest correlations encountered (both medians above $\rho = 0.8$ for $n = 93$) while *Fragmentation Percentages* and *Skeletal Frequencies* showing weak to moderately strong negative correlations, with the strongest negative being Pearson coefficients median for *Fragmentation Percentages* (median $r = -0.42$ for $df = 83$). Interestingly, individual variables generally follow those trends. The only visible exceptions are maxillary and mandibular abundances. Especially the latter, when correlated with other abundances, in 8 cases out of 12 showed higher coefficients for the Pearson correlation, with the coefficient median being mildly higher than one taken from Spearman correlations ($r = 0.38$ for $df = 91$ to $\rho = 0.34$ for $n = 93$).

As it seemed Spearman correlation was more applicable to trace relationships between variables, matrix of Spearman correlation coefficients was analysed in order to check tendencies within highest and lowest correlations between specific site data (**Appendix: Statistics, Tables 4a-b**). Key variables (NISP, weight, MNI, Skeletal Completeness) were predominantly correlated with each other, with correlation coefficients higher than $\rho = 0.8$ (e.g. NISP to MNI, $n = 466$, $\rho = 0.9$, $p = < 0.001$). Still, their correlations with other data proved to be strong, with lowest recorded being between Skeletal Completeness and the Number of Meaningful Species Classes ($n = 466$, $\rho = 0.20$, $p = < 0.001$). The Number of Meaningful Species Classes itself, while showed strong correlation with MNI ($n = 466$, $\rho = 0.48$, $p = < 0.001$) was in general very loosely correlated with the rest of checked variables, in case of 24 different variables providing lowest obtainable coefficient (e.g. with Femoral relative abundance: $n = 466$, $\rho = 0.05$, $p = 0.232$). Digestion of Molars and Incisors was predominantly correlated with each other ($n = 466$, $\rho = 0.56$, $p = < 0.001$), with lowest coefficients in case of both being with mandibular breakage (for Incisor Digestion: $n = 466$, $\rho = 0.05$, $p = 0.260$).

Elements NISP, *Abundances*, showed best and worst coefficients often between each other, was perhaps due to *Elements NISP* variables being used to calculate *Abundances* (e.g. Maxillary NISP to Maxillary relative abundance: $n = 466$, $\rho = 0.89$, $p = < 0.001$). Similar impact of the way of calculation was noted for *Fragmentation Counts* and *Fragmentation Percentages*, but also included lowest possible correlations (e.g. For NISP of complete mandibles, correlation with the percentage of complete mandibles: $n = 466$, $\rho = 1$, $p = < 0.001$, correlation with the percentage of broken mandibles: $n = 466$, $\rho = -0.13$, $p = 0.005$). *Skeletal Groups* and *Skeletal Frequencies* also showed the impact of how they are calculated on their results. Lowest correlations were exclusively with *Skeletal Frequencies* variables, while positive correlations being mostly with *Elements NISP* and *Abundances* variables (e.g. Skull elements, highest with Mandibular NISP: $n = 466$, $\rho = 0.93$, $p = < 0.001$; lowest with Vertebra frequencies: $n = 466$, $\rho = 0.05$, $p = 0.399$).

In-group Spearman correlations of references data showed many trends, some already noted for the site data (**Appendix: Statistics, Tables 4c**). Specific elements counts within the *Elements NISP* group often showed highest correlation in case of anatomical association (e.g. Maxilla NISP to Mandible NISP: $n = 93$, $\rho = 0.94$, $p = < 0.001$), with lowest being with NISP of loose incisors (e.g. Maxilla NISP to Incisor NISP: $n = 93$, $\rho = 0.75$, $p = < 0.001$). However, all correlations were very strong given the lowest obtained was $\rho = 0.67$ (between Radius NISP and loose incisors NISP) for $n = 93$, for which the critical value is 0.204. In case of *Abundances* a similar association between anatomically associated bones was noted (e.g. Humerus to Ulna relative abundances: $n = 93$, $\rho = 0.85$, $p = < 0.001$), as well as lowest correlations being with loose teeth relative abundance (e.g. Radius to loose incisor relative abundances: $n = 93$, $\rho = 0.02$, $p = 0.881$). However, contrary to *Elements NISP*, *Abundances* showed in overall far lower correlation coefficients, with the majority of lowest correlations recorded being lower than $\rho = 0.204$, suggesting no correlation. In case of *Fragmentation Counts* and *Fragmentation Percentages* highest correlation coefficients were between variables representing elements with the same state of preservation (e.g. complete Humerus NISP to complete Tibia NISP: $n = 85$, $\rho = 0.95$, $p = < 0.001$), and lowest between differing preservation (e.g. complete Humerus NISP to broken Femur NISP: $n = 85$, $\rho = 0.50$, $p = < 0.001$). The difference was that the lowest correlation coefficients noted for *Fragmentation Percentages* were often both strong and negative. For *Skeletal Groups* all correlations were high and strong, with lowest, between vertebrate and skull elements, being $p = 0.831$ ($n = 85$, $p = < 0.001$). *Skeletal Frequencies* were

an inverse of the situation within the *Skeletal Groups*, with correlations being predominantly negative.

Table 4.04 – Summary breakdown of correlation coefficients obtained while applying Pearson and Spearman correlation to the data within specific data groups within the site and references data, with an additional summary for all the variables within the sites data present in the end. The first two columns summarise cases, where each method provided a higher correlation. Latter two columns, in turn, provide the median of correlation coefficients provided by each method. For the summaries related to individual variables see **Appendix 4 (Statistics) Table 4.3**.

Dataset	Data Group	No. (Higher)		Median	
		Pearson	Spearman	Pearson	Spearman
References Data	Elements NISP	6	72	0.811	0.895
	Abundances	21	57	0.412	0.470
	Fragmentation Counts	16	29	0.325	0.686
	Fragmentation Perc.	21	24	-0.293	-0.059
	Sk. Groups	0	6	0.853	0.911
	Sk. Frequencies	2	4	-0.420	-0.180
Sites Data	Basic Quantification	3	3	0.516	0.666
	Taphonomy	3	0	0.762	0.476
	Elements NISP	73	5	0.863	0.667
	Abundances	6	72	0.319	0.407
	Fragm. Counts	43	2	0.769	0.564
	Fragm. Perc.	11	34	0.101	0.282
	Sk. Groups	3	0	0.877	0.725
	Sk. Frequencies	0	6	-0.297	-0.158
	All groups	489	1402	0.249	0.455

4.3. CORRELATIONS AND χ^2 – CONTEXT IDENTIFICATION

Correlations of deposition patterns, both within references data or between references data and signatures, revealed possibilities to use them as an analytical tool for identifying owl deposits. In the case of both *Abundances* as well as *Fragmentation Counts* and *Fragmentation Percentages* Pearson correlation returned strong differences between owls and other investigated groups. Spearman correlation also showed a similar trend, albeit with less marked differences. Looking at references data groups correlations (Fig. 4.06, see also **Appendix: Statistics Table 5a-b**), among six data types tested both *Fragmentation Counts* and *Percentages* showed the majority (76-81%) of strong correlations (i.e. for Pearson and $df = 8$ above $r = 0.632$, for Spearman and $n = 10$ above $\rho = 0.648$) being only within the owl group, with correlations with other groups rarely producing significant results. Moreover, correlations with other predation groups were often providing negative values, especially in the case of fragmentation percentages showing strong negative values (e.g. for half of the mammal references). In the case of *Abundances*, the situation also enabled differentiation of owls from other groups alongside the line of a critical value, but only in the case of positive values. Negative results were rare and other group correlations showed values mostly within the range of weak to moderate correlations ($r/\rho = 0$ to 0.5), thus creating a lesser range of values than in the case of fragmentation. Signature data application to the references data has also shown similar albeit clearer values distribution as in the case of group comparisons, though results could be affected by uneven representation of species groups (four owls vs. three diurnal species, one mammal and one scattering).

In contrast to *Abundances* and *Fragmentation*, *Elements NISP* completely failed to provide a workable range of values, while *Skeletal Groups* and *Skeletal Frequencies* showed better results in the case of Spearman rank correlation. The worst situation was noted for Pearson test application to *Elements NISP*, where the majority of references returned significant correlations, with two groups (owls, mammals) essentially occupying the same range of values. In turn, Spearman correlations provided lower values, resulting in the majority of owl group correlations being below the significance threshold, with the lower range of values within the standard deviation overlapping with the remaining two predatory groups. *Skeletal Groups* and *Frequencies* provided the same results for each correlation, most likely due to frequencies being recalculated directly from skeletal groups. In this case, Spearman rather than Pearson correlation provided more varied mean coefficients for each group. Still, several problems were

identified. The low number of variables (only four) resulted in only the most extreme coefficients ($r = 0.95/-0.95$ or $\rho = 1.0/-1.0$) being considered strong, which, in conjunction with significant overlap between mean and extreme coefficients, resulted in problems with interpretation. Moreover, similar to NISP, the owl and mammal group was hard to differentiate. Still, mean and median values for owls were strongly skewed, beyond the main cluster of mammal values, pointing towards misidentification with other groups being actually less likely than what was computed.

A similar situation to correlations, though harder to interpret and possibly utilize, was encountered when checking χ^2 values computed from references data (Fig. 4.07, see also **Appendix: Statistics Table 5c**). Technically, in the case of references data tests showed the owl group being non-homogenous in *Elements NISP*, *Abundances*, *Fragmentation Counts/Percentages*, *Skeletal Groups* and *Frequencies* data distribution – both within itself as well as against other groups. Only a few χ^2 values obtained were low enough to be considered significant/homogenous ($\chi^2 < 21.03$ for *Elements NISP/Abundances*, $\chi^2 < 16.92$ for *Fragmentation Counts/Percentages* and $\chi^2 < 7.82$ for *Skeletal Groups/Frequencies*), with the biggest number of such cases noted for *Skeletal Frequencies*. Moreover, homogenous assemblages were not necessarily within the checked group (here: owls), but could also happen in case of testing between owls and other groups, usually mammals. For example, two lowest values for owl *Fragmentation Percentages* comparison with the main groups showed two values ($df = 9$, $\chi^2 = 3.4$, $p = 0.946$ and $df = 9$, $\chi^2 = 5.77$, $p = 0.762$), first coming from within the owl group and second from computing with diurnal assemblages.

However, marked differences between specific groups value ranges and clustering were noted in the case of *Fragmentation Percentages* and to a lesser extend *Abundances*. Similarly, as in correlations, owl contexts showed visible differences from other assemblages, having far lower χ^2 values when compared within the group, including all homogenous outcomes in the case of *Abundances* (~ 3% of all χ^2 values). For *Abundances* owl χ^2 values clustered below clusters of other groups, with owl median ($\chi^2 = 80.3$) being about half of other groups median ($\chi^2 = 161.6$ for diurnals, $\chi^2 = 178.6$ for mammals, $\chi^2 = 288.4$ for scattering). Such situation was even more pronounced in the case of *Fragmentation*, where the owl median was $\chi^2 = 85.06$, over four times lower than rest of the groups ($\chi^2 = 434/471/351$). Moreover, despite ranges of diurnal and mammal groups encompassing the range of an owl group, clusters were visibly differing, with the third quartile of the owl group being smaller by about 77 from the first quartile of the diurnal

group. The issue of overlap was however more pronounced in the case of *Skeletal Frequencies*, with owls and mammals providing very similar ranges and values.

However, using correlations or χ^2 to identify assemblages other than owls proved to be problematic. As already noted in the case of correlations with owls, diurnal and mammal groups showed almost the same ranges, especially in the case of *Fragmentation Percentages*. It was especially visible regarding mammals as a separate group, as obtained mean/median correlations within the group and between mammals and diurnal raptors were essentially the same for abundances and fragmentation counts. Not surprisingly, overlap in ranges and means resulted also in an overlap in significant values noted. χ^2 testing showed an even higher overlap between those two groups, with medians for diurnal and mammal groups being essentially the same ($\chi^2 \sim 136$ -162). Finally, correlations of scattering with other groups showed almost uniform low positive/negative values, while in the case of χ^2 computable instances of scattering were sometimes overlapping with other groups.

The beforementioned issues were noticeable when assessing accuracy within references data (Table 4.05, left side), with new problems also emerging. Data chosen included *Abundances* (producing workable results, in contrast to *elements NISP*), *Fragmentation Percentages* (producing better results than *Fragmentation Counts*) and *Skeletal Frequencies* (results either same to skeletal groups or better than them), with Pearson correlation used for former two and Spearman for the latter. In the case of both correlations and χ^2 using the highest correlation coefficient or lowest χ^2 value results in high accuracy within owls, in references dataset reaching from 82 to 94% depending on method and data. However, the accuracy for other groups was uniformly lower, resulting in general accuracy for all four groups being low, on a margin of 70% at best (correlations: *Abundances* and *Fragmentation Percentages*) and below 50% at worst (correlations: *Skeletal Frequencies*). Moreover, the utilization of χ^2 resulted in the computation of a number of tests returning bias warnings or being outright incomputable. As it lowered the choice of references to references or signature to references comparisons it was considered as “missing” accuracy. It predominantly affected scattering assemblages but was also occasionally present across other three groups.

The same issues, to an even greater extent, were also noted when assessing the accuracy when applying signature depositions to model data (Table 4.05, right). In the case of signature data including or excluding non-significant results have a higher impact than when utilizing the whole breath of references data. For all four groups accuracy was at best above 50%. Group-specific accuracy in the case of owls, depending on data, was better than (*Fragmentation*,

Skeletal Frequencies) or on par (*Abundances*) with the diurnal group, with estimation for mammal and scattering groups being least accurate. Interestingly, accuracy followed to some degree the number of signatures for each group, with owls and diurnal groups represented by two to four signatures and mammal as well as scattering by only one.

One means of improving the accuracy when using correlations and χ^2 tests might be the reduction of sought categories to 3 or only 2. The combination of mammal and diurnal groups markedly increases the obtainable accuracy, from 3% up to 15% increase depending on the method. The only case where group reduction did not visibly help were *Fragmentation Percentages* χ^2 tests for signature data. However, the best results are obtainable when there are only two possible groups, one representing owls and the other non-owl assemblages (diurnal/mammal/scattering). In such case, accuracy can reach even 89% for references to references comparison and between 70% to 86% in the case of references to signatures comparison.

Considering the problematic but still possible usage of both correlations and the χ^2 method for studying archaeological contexts, signature data was applied to site data firstly through Pearson correlation (Table 4.06). Due to the most promising results, *Abundances* and *Fragmentation Percentages* were checked, with *Skeletal Frequencies* as an alternative. Correlations could be computed for almost all relative abundance data, with only four samples and one context incomputable. A worse situation was encountered in the case of *Fragmentation Percentages*, with 161 samples impossible to correlate with signatures, but contexts showed only five incomputable cases. Frequencies also could not be computed for a number of samples (n= 52) but only two contexts were affected by it.

In the case of Pearson test on *Abundances* the number of significant positive correlations was relatively high, from 12% in case of samples up to 24% in case of contexts and 17% in overall. Especially in the case of multi-sampled/whole-earth contexts it meant that many showed strong correlations with more than one signature. Similar situation was noted in the case of fragmentation correlations. Combined datasets showed values in between samples and contexts, pointing to samples with strong correlations coming from both single- and multi- sample contexts. *Fragmentation Percentages* showed similar percent of strong positive correlations (12% for samples, 20% for contexts, 15% overall), confirming situation observed in the case of *Abundances*. However, biggest differences between abundances and fragmentation, already noted in previous paragraphs, were the number of strong negative correlations. Abundances showed strong negatives mostly in the case of samples (2%), with only two context correlations

showing similar values. Fragmentation, on the other hand, provided plenty of strong negatives in both samples (10%) and contexts (19%), comparable to the number of strong positive correlations. In contrast to both *Abundances* and *Fragmentation*, *Skeletal Frequencies* provided relatively small amounts of significant values, usually about 2-3% considered strong positive and 1 to 3% as strong negative.

The highest correlations showed strong skew towards diurnal and mammal species. For both samples and contexts *Abundances* as well as *Fragmentation Percentages* showed strong correlations to diurnal species, especially hen harriers and red foxes. *Abundances* samples were best correlated with hen harriers (samples $n = 279$), followed by red foxes ($n = 232$), with scattering being the third most common ($n = 110$). Contexts provided a slightly different distribution, with red foxes (contexts $n = 71$) closely followed by hen harriers ($n = 60$) and kestrels ($n = 50$) and then scattering ($n = 17$). Owls were rarely strongly correlated, with snowy owl being least correlated with a third of samples and contexts (samples $n = 337$ / contexts $n = 99$) and followed by scattering (samples $n = 209$ / contexts $n = 66$) and barn owls (samples $n = 153$ / contexts $n = 32$). Combined data also showed a similar distribution of lowest correlations. *Fragmentation Percentages* showed the predominance of strongest correlations with red foxes (samples $n = 264$ / contexts $n = 79$), followed by kestrels (samples $n = 161$ / contexts $n = 70$) as well as hen harriers (samples $n = 109$ / contexts $n = 26$). Lowest correlations were dominated by owls, especially long-eared owls (samples $n = 391$ / contexts $n = 149$) and snowy owls (samples $n = 117$ / contexts $n = 26$). However, *Skeletal Frequencies* partially differed from both abundances and fragmentation, mostly due to a higher prevalence of owl signatures. In the case of samples, highest correlations were with the red fox ($n = 279$), barn owl ($n = 212$) and hen harrier ($n = 202$) patterns. Context data in turn showed a predominance of high correlations with hen harriers and red fox signatures, followed by almost equal amounts of owls, hen harriers and kestrels. Interestingly, hen harriers were also among the lowest correlations in samples and contexts.

χ^2 test was also applied to site data, with results hard to interpret for *Abundances* and *Fragmentation*, but surprisingly informative for *Skeletal Frequencies* (Table 4.07). The computable number of samples and contexts, without additional biases recorded, were significantly lower than previous correlations, revealing problems especially with sample *Fragmentation* analysis. The ranges obtained were very large and, as expected, very difficult to interpret on their own. In the case of *Fragmentation* only one single sample came out as homogenous to signature data, with *Abundances* coming out as never being homogenous. In

contrast, *Skeletal Frequencies* came out as often homogenic (samples $n = 622$ and contexts $n = 317$), suggesting better alignment with the χ^2 testing method. Most common lowest χ^2 for *Abundances* were with red foxes (samples = 154/ contexts = 56), with *Fragmentation* predominantly showing snow owls (samples = 266/ contexts = 137). Interestingly, for samples *Frequencies* most common lowest values were with barn owls ($n = 262$), kestrels ($n = 252$) or peregrines ($n = 205$). In the case of contexts, however, kestrels and peregrines were the most commonplace ($n = 90$ and 69 respectively).

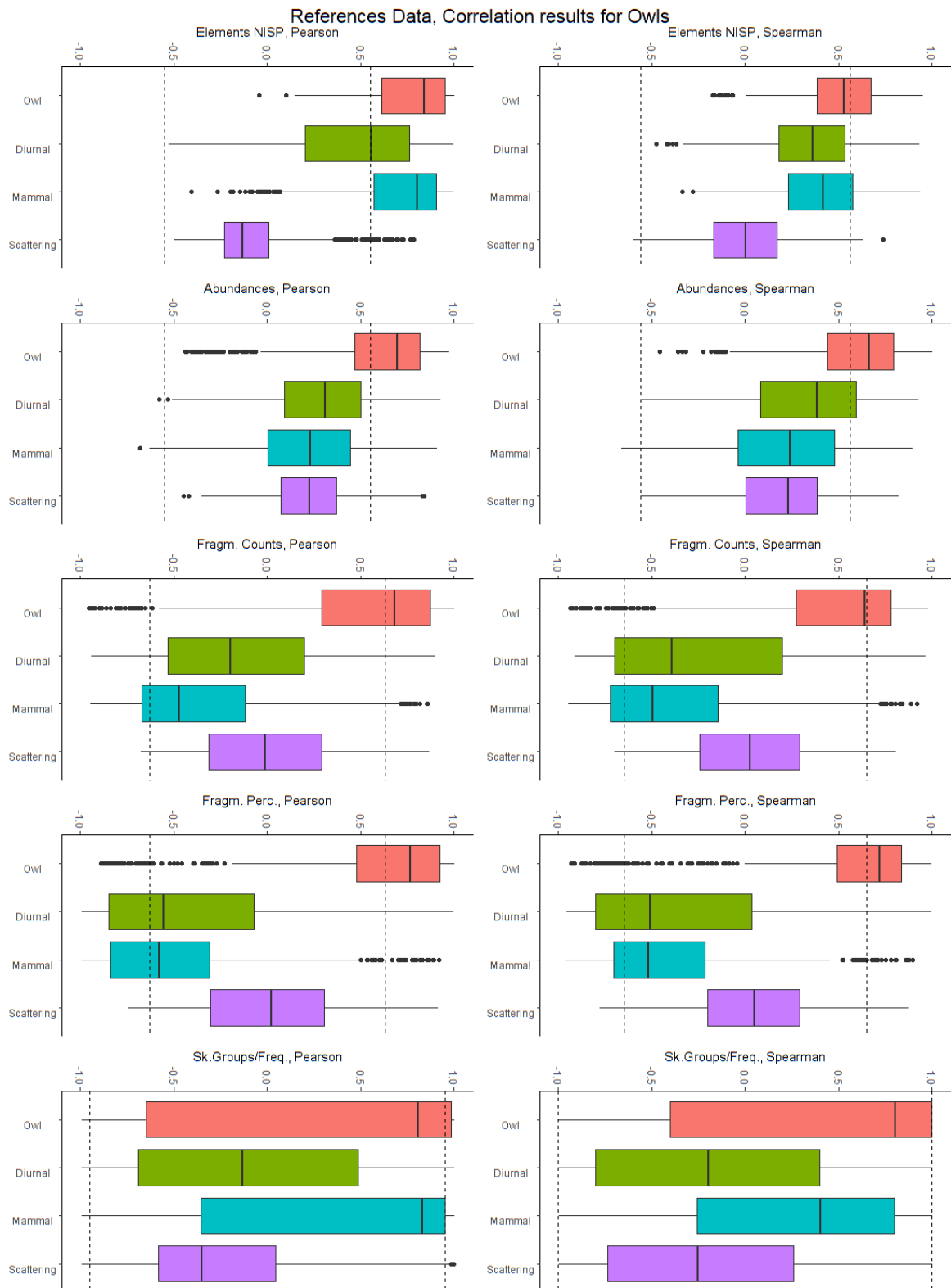


Fig. 4.06 – Boxplots of correlation coefficients received for each data type (*Elements NISP*, *Abundances*, *Fragmentation Counts* and *Percentages*, *Skeletal Groups* and *Frequencies*) and type of test (left column for Pearson, right for Spearman test). Correlations summarized were done from the perspective of one predatory group (owls). Positive and negative critical values for each case are expressed as dotted lines.

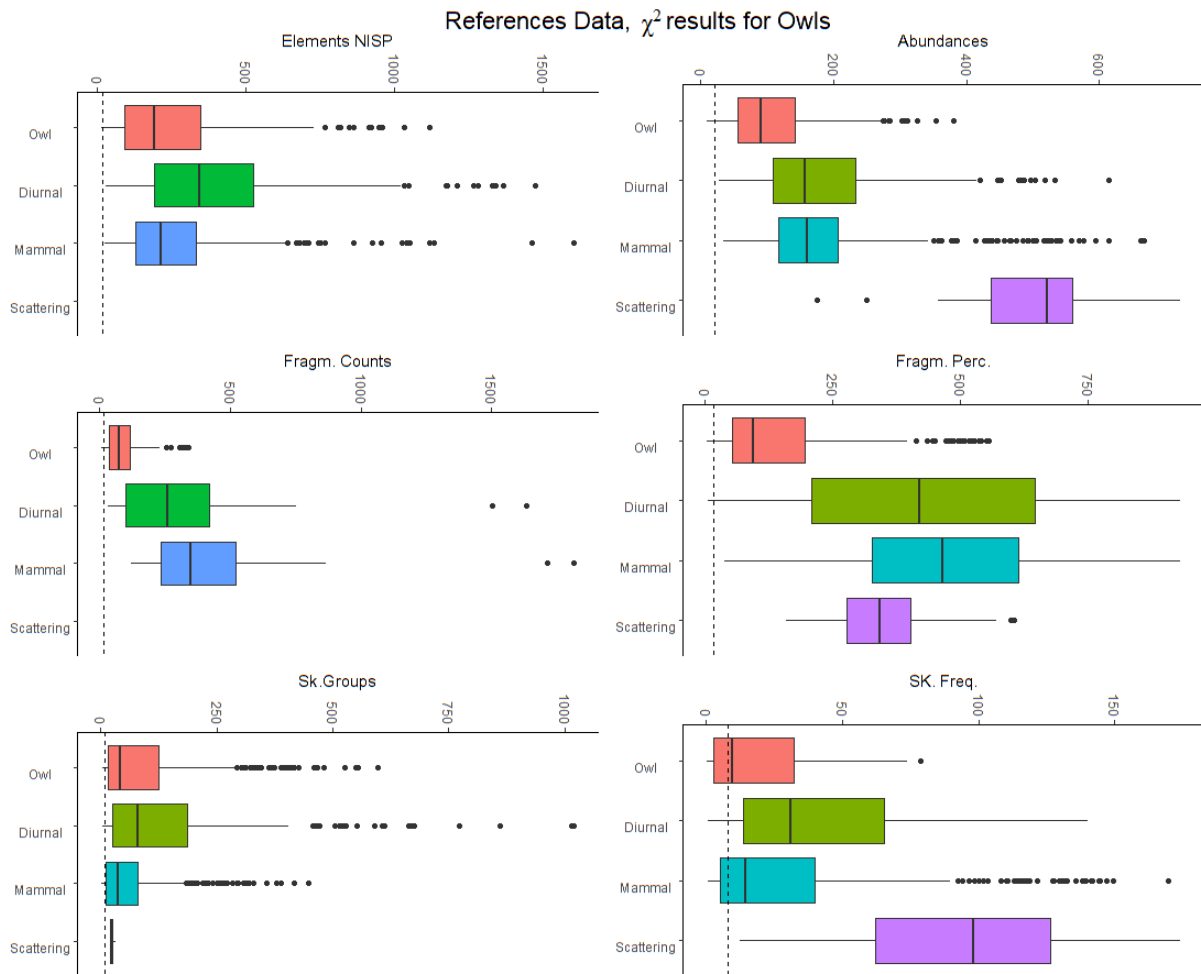


Fig. 4.07 – Boxplots of χ^2 values obtained from each data types (elements NISP, abundances, fragmentation counts & perc., skeletal groups and skeletal frequencies) from the perspective of one predatory group (owls) within model data. Critical values for each case are expressed as a dotted line.

Table 4.05 – Accuracy obtained for references to references as well as signatures to references data using correlations (Pearson for *Abundances* and *Fragmentation*, Spearman for *Skeletal Frequencies*) and χ^2 methods. For χ^2 missing/incomputable values, as % of accuracy, is also shown.

Data		Model to Model				Signatures to Model			
Type	Group	Correlations		χ^2		Correlations		χ^2	
		Accuracy Strong	Accuracy All	Accuracy	Missing	Accuracy Strong	Accuracy All	Accuracy	Missing
Abundances	Owl	88%	88%	88%	0%	76%	76%	61%	21%
	Diurnal	36%	36%	21%	7%	71%	79%	57%	29%
	Mammal	70%	70%	74%	0%	30%	35%	26%	17%
	Scattering	57%	57%	0%	39%	22%	26%	0%	96%
	General (4 cat.)	68%	68%	53%	11%	51%	54%	37%	40%
	General (3 cat.)	73%	73%	65%		63%	69%	48%	
	General (2 cat.)	87%	87%	78%		73%	80%	48%	
Fragmentation	Owl	91%	91%	91%	0%	91%	91%	32%	62%
	Diurnal	30%	30%	0%	0%	50%	50%	10%	10%
	Mammal	50%	50%	44%	6%	33%	44%	0%	11%
	Scattering	68%	73%	0%	27%	18%	18%	0%	100%
	General (4 cat.)	69%	70%	46%	8%	55%	57%	14%	55%
	General (3 cat.)	85%	86%	55%		71%	74%	17%	
	General (2 cat.)	88%	89%	58%		74%	86%	17%	
Frequencies	Owl	88%	94%	79%	0%	55%	58%	64%	0%
	Diurnal	0%	7%	29%	0%	21%	57%	79%	0%
	Mammal	9%	9%	35%	0%	17%	57%	9%	0%
	Scattering	39%	43%	0%	0%	4%	13%	0%	0%
	General (4 cat.)	43%	47%	41%	0%	28%	46%	37%	0%
	General (3 cat.)	55%	60%	46%		28%	48%	39%	
	General (2 cat.)	62%	71%	48%		29%	71%	62%	

Table 4.06 (left) & 4.07 (right) – Summary of comparing signature data to site data through correlations (left, Pearson for *Abundances* and *Fragmentation*, Spearman for *Skeletal Frequencies*) and χ^2 (right) tests.

Data Type	Dataset	Computable Entries	Correlations Obtained	No.		Strong Negative	Strong only	Owl		Diurnal		Fox		Scatter		Most Common Highest	Most Common Lowest
				Strong Positive	Homogenic			Strong	Diurnal	Strong only	All	Strong only	All	Strong only	All		
Abundances	Samples	912	8208	1021	175	25	118	248	452	153	232	69	110	Hen Harrier	Snowy Owl		
	Contexts	236	2124	504	2	11	24	109	124	66	71	12	17	Red Fox	Snowy Owl		
	Combined	462	4158	708	62	18	65	160	238	90	114	32	45	Hen Harrier	Snowy Owl		
Fragmentation	Samples	755	6040	738	627	15	127	141	270	131	264	88	94	Red Fox	Long-Eared Owl		
	Contexts	232	1856	365	355	8	38	66	95	62	79	15	20	Red Fox	Long-Eared Owl		
	Combined	394	3152	480	425	10	68	96	159	75	116	44	51	Red Fox	Long-Eared Owl		
Sk. Frequencies	Samples	864	7776	143	102	27	212	9	325	15	279	11	48	Red Fox	Hen Harrier		
	Contexts	235	2115	47	56	8	28	7	117	7	75	1	15	Hen Harrier	Hen Harrier		
	Combined	443	3987	73	73	13	81	10	197	8	141	3	24	Red Fox	Hen Harrier		

Data Type	Dataset	Computable Entries	No. Tests Obtained	No.		Owl	Diurnal	Fox	Scattering	Most Common Lowest	
				Homogenic	Weak					Common	Lowest
Abundances	Samples	354	1267	0	140	60	154	0	Red Fox	0	Red Fox
	Contexts	147	721	0	39	52	56	0	Red Fox	0	Red Fox
	Combined	195	847	0	72	56	67	0	Red Fox	0	Red Fox
Fragmentation	Samples	304	822	1	278	26	0	0	Snowy Owl	0	Snowy Owl
	Contexts	152	522	0	139	13	0	0	Snowy Owl	0	Snowy Owl
	Combined	190	601	0	174	16	0	0	Snowy Owl	0	Snowy Owl
Sk. Frequencies	Samples	870	6612	622	352	487	31	0	Barn Owl	0	Barn Owl
	Contexts	235	1910	317	56	173	6	0	Kestrel	0	Kestrel
	Combined	444	3432	404	141	285	18	0	Kestrel	0	Kestrel

4.4. APPLICATION OF CLASSIFICATION MODELS

The assessment of classification methods started from checking the performance of chosen five classification models on micromammal data, revealing primarily the impact of identifiable groups number on overall accuracy in the process. Considering *Abundances*, *Fragmentation Percentages* and *Skeletal Frequencies* being most effective in the case of correlations and to some degree during χ^2 tests, as well as have already successfully been used in previous research (Terry 2007), those two groups of data were used to train methods. In the case of four classes (owl/diurnal/mammal/scattering), methods provided very wide ranges of both accuracy and kappa for *Abundances* (Fig. 4.08, left). For the accuracy, the range of was about 0.3 to 0.9, while kappa showed ranges from 0.2 to above 0.8, with a couple of methods providing values up to 1 for both. *Fragmentation Percentages* (Fig. 4.09, left) also showed similarly wide ranges, from 0.5 to 0.9 for accuracy and 0.35 to 0.85 for kappa, a single method obtaining both values on a level of 1. Averages however were quite consistent, with accuracy in the range of 0.6 to 0.8 for relative abundances or 0.6 to 0.85 for fragmentation. Going with McHugh (2012, Table 3) kappa values rating, in all methods kappa could be considered occupying the whole range from no ($\kappa = 0-0.2$) up to perfect ($\kappa = 1$) agreement, with median around weak ($\kappa = 0.4-0.6$) and moderate ($\kappa = 0.6-0.8$) values. However, better-fitted results were obtained when reducing categories sought by combining diurnal and mammal classes together (Fig. 4.08 and 9, right). While overall ranges of the two studied variables did not differ substantially, median values clustered nearer the high-end of the spectrum. In the case of *Abundances* median accuracy for each method was 0.8 or better, with kappa clustering around strong ($\kappa = 0.8-0.9$) values. The difference was even more pronounced in the case of fragmentation, where all methods besides LDA included 100% accuracy and kappa within the interquartile range of obtained values.

Methods were also tested on *Skeletal Frequencies*, with similar albeit less promising results. Similar to abundances and fragmentation, frequencies data showed the marked difference between classification based on four (Fig 4.10 left) and three (Fig 4.10 right) groups, with the latter showing on average higher accuracy and kappa. However, values obtained were also lower than in the case of the other two data groups, by about 0.2 for each variable. It was especially visible in the case of classification based on four categories, where upper ranges for accuracy were at best 0.8, with median values clustering around 0.5. Kappa values were also weak ($\kappa = 0.4-0.6$), suggesting either very low reliability of algorithms trained on frequencies in such a way or frequencies themselves. Workable accuracy ranges and kappa were obtained

for three groups, although even in this case results were still lower than four groups classification for abundances and fragmentation. Considering both, it is likely that data itself is not good enough for training accurate classification algorithms.

Methods choice proved to be of secondary consideration, with pre-processing inconsequential to the results. Some variation of results could be noted between tested methods in the case of *Abundances*, with the SVM method being the most likely choice for four categories, with FDA and SVM being best for three-group classification. Especially the FDA method showed both perfect accuracy and kappa within the interquartile range of obtained results, suggesting being the most optimal method in this case. However, the accuracy of other methods was not far behind, with the upper end of accuracy ranges always including perfect score. In the case of *Fragmentation Percentages*, it was even more pronounced, with almost all methods equally applicable. The only difference was noted for LDA, but mostly due to computed data heavily clustering around a narrow range of results. Additionally, pre-processing of data did not help nor hinder the utility of methods. Apart from the Knn method, no differences in accuracy between algorithms trained on raw and ones trained on pre-processed data were noted. In the case of Knn, classifiers with pre-processing fared better for *Abundances* and worse for *Fragmentation*, although differences were only marginal.

Due to no clear advantage all tested methods were tuned on the references data to create a best fitting algorithm in each case, with two different random seeds considered, and later compared with each other (Table 4.08). The only element of algorithm training dropped during this stage of classifiers analysis was data pre-processing, with *Skeletal Frequencies* being the only data not considered due to a low chance of meaningful results. Differences in accuracy were noted between algorithms tuned on different random seeds, stemming from the random number generation effect on the tuning process. Overall results range between both methods and seeds was relatively wide, with the accuracy of about 74 to 100% in the case of abundances and 80 to 99% in the case of fragmentation. Best results for four groups were obtained through SVM modelling, with perfect 100% fit for *Abundances* (first seed) and lower but workable 85% fit in case of *Fragmentation*. The Knn method also provided perfect fit for *Abundances* but showed lower obtained accuracy for *Fragmentation*. From the perspective of *Fragmentation*, the best method turned out to be FDA, with stable 86% accuracy (both seeds). However, three groups, while showing similar results range, provided overall better results. 90% and over accuracy scores were common, especially for *Fragmentation*. Second best in case for each dataset was the SVM method, providing 96% to 97% accuracy for *Abundances* and 93% to 98%

Fragmentation, with beyond 95% threshold expected for effective identification method. FDA provided third best, and still significant, *Abundances* accuracy of 96% (first seed). FDA also contributed the best model for *Fragmentation*, with 99% accuracy (second seed). The Knn method provided 100% accuracy fit for *Abundances* (first seed), similarly to four groups case, but only 90 or 89% in the case of *Fragmentation*.

After considering the obtained data, the author decided to utilize methods trained for three group identification on *Abundances* and *Fragmentation*, but could not easily decide on specific algorithms to utilize on the data. The decision of using three groups came from two points. First was the fact, that the lesser number of groups resulted in better accuracy for both datasets and only three-group classification could lead to optimal (accuracy of 95% or higher) results. Second was the result of previous analysis of correlations and χ^2 values and Terry's work (2007), which proved the utility of pooling diurnal and mammal assemblages together. In the case of specific methods choice, the author tried to choose ones beyond 95% accuracy or, if not possible, on a verge of it (90-95%). It resulted in rejection of LDA and GLM net. Knn, despite perfect accuracy obtained for *Abundances*, was however rejected due a chance of an algorithm not working at all – Knn tuning always resulted in K tuning parameter equal to 1 in the case of four groups, regardless of what portion of *Abundances* data being included. Moreover, Knn underperformed when utilizing *Fragmentation* as well as the only one showed variation with pre-processing, including a number of possible biases in results replicability. As a result, only SVM and FDA methods could be considered as most suitable for later work.

The application of two chosen methods (SVM due to high accuracy, FDA due to replicability) to references data revealed new information about how data reflects the site, including the importance of contextual data. Tuning parameters were taken from two established seeds, the first one proving best for abundances and the second for fragmentation. Interestingly, cases where trained model failed to properly identify depositor group could be easily explained as an effect of different mode of accumulation and/or dispersal. Misidentified data in each case could be considered either as outliers within their own group or possibly belonging to two groups at once. For FDA results on references data could be successfully visualised. *Abundances* showed a very minimal overlap between the sought classifications for 0.95 confidence threshold (Fig. 4.11), while *Fragmentation* (Fig 4.12) showed a pronounced clustering, with 0.95 confidence threshold showing exclusive grouping.

In the case of *Abundances* one misidentification repeated for both methods, with additional five cases being method-specific (three for FDA, two for SVM; see **Appendix 1 Data – References**

for more information about the contexts discussed). Both SVM and FDA models identified one of two European eagle owl (Andrews 1990, 188-189 & 211) assemblages to diurnal/mammal class. The assemblage consisted of prey remains left after feeding, which contextually would be more likely to be expected from a diurnal than an owl species. It was most likely the reason behind misidentification, as the other European eagle owl assemblage, consisting of specific to Owls regurgitated pellets, was identified to an owl class. Other cases of misidentification also showed a similar trend, contextually differing from a pattern expected for the predatory group. FDA identified one barn owl assemblage as coming from diurnal/mammal species, with southern crested caracara, *Polyborus plancus*, considered as scattering. On the other hand, SVM identified both Chimango caracara, *Milvago chimango*, and cougar, *Puma concolor*, assemblages as scattering. All those assemblages came from the same study by Gómez (2007). The source itself already claimed that the studied patterns showed lower than normal completeness, providing a very low number of NISP and resembling scattered remains. In turn, Coyote, *Canis latrans*, assemblage showed a rare “upward” trend, being identified by FDA as coming from owls. The assemblage was an outlier due to higher relative abundances than normal within diurnal and mammal species.

In the case of fragmentation, however, the situation was more straightforward as only a couple of misidentifications occurred. In the case of Black-backed Jackal, *Canis mesomelas*, two assemblages from this species (Matthews 2002, table 2&3) were included, one identified to diurnal/mammal class and one to background scattering by both methods. The former contained only a handful of bones, most likely representing one micromammal specimen, but the latter provided even fewer bones, including just one tibial fragment, more similar to extreme dispersal from Skara Brae Trenches. One more misidentification occurred for SVM, with Verreaux's Eagle, *Aquila verreauxii*, assemblage (Armstrong & Avery 2014) being considered classified as an owl. The source of misidentification can be seen easily in data, as among tested deposition patterns one coming from Verreaux's Eagle provided more intact bones than other diurnal species. Additionally, Armstrong and Avery (2014) noted the difference in modification patterns between species, suggesting intrinsic differences stemming from a more varied diet.

When the trained SVM and FDA models were applied to the site data one could notice marked differences between samples and contexts as well as the differences between methods themselves (see Table 4.09). Identification as scattering was predominant within samples, consisting of 57% (*Abundances*, 525 entries for SVM) to 74% (*Fragmentation*, 680 entries for SVM) of all samples studied. Contexts also showed a substantial number of dispersals (~38%

for *Abundances* for SVM and 59% for FDA), but not to the extent that samples showed, with combined level showing value in-between the previous two. Overall, FDA was skewed towards scattering in the case of abundances while SVM showed a bigger skew in the case of fragmentation. Identification as diurnal/mammal was the second most common in samples (24% for FDA, 40% for SVM for *Abundances* and 22/21% for *Fragmentation*) and combined datasets. However, considering SVM classification in overall, diurnal/mammal class was predominant with 50% and over of all contexts being identified as such while for FDA it only approached such threshold with *Fragmentation* patterns. Finally, classifying archaeological assemblages as coming from owls was rare. Especially for SVM method only a few dozen samples showed affiliation with owl *Abundances* and *Fragmentation* patterns, with contexts ranging between ten (*Abundances*) up to eighteen (*Fragmentation*). In turn, FDA provided more examples, especially in the case of *Fragmentation* where 33 contexts were identified as coming from owls.

The final results, an outcome of comparing *Abundances* and *Fragmentation* classification, showed the majority of data being either scattering or on the verge of it. Samples showed about half of them being clear scattering assemblage, with another ~30% being identified as one through either *Fragmentation* or *Abundances*. Scattering was also quite common in the case of contexts, where data showed 32-33% contexts resembling a dispersal and another 34% (FDA) or 19% (SVM) likely being one. 47% of all combined data could be considered as scattering, with about 23-25% being between scattering and accumulation. In the case of specific accumulations results from FDA and SVM classifiers strongly differ, with the latter dominated by clear diurnal/mammal category (16% for samples and 40% contexts) to the almost complete exclusion of owls besides a few cases. FDA showed only a moderate number of results for diurnal/mammal class, but also provided accumulations that were simultaneously identified to owl and diurnal/mammal class. Confirmed owl identifications were however still scarce, with only five cases within combined data.

Due to FDA being an easier method to compute, possible to visualise if necessary and provide more varied results for accumulations for both data, it was utilized in later analysis. However, in terms of accuracy on references data alone, SVM seems to be equally eligible for utilization for micromammal data at this point.

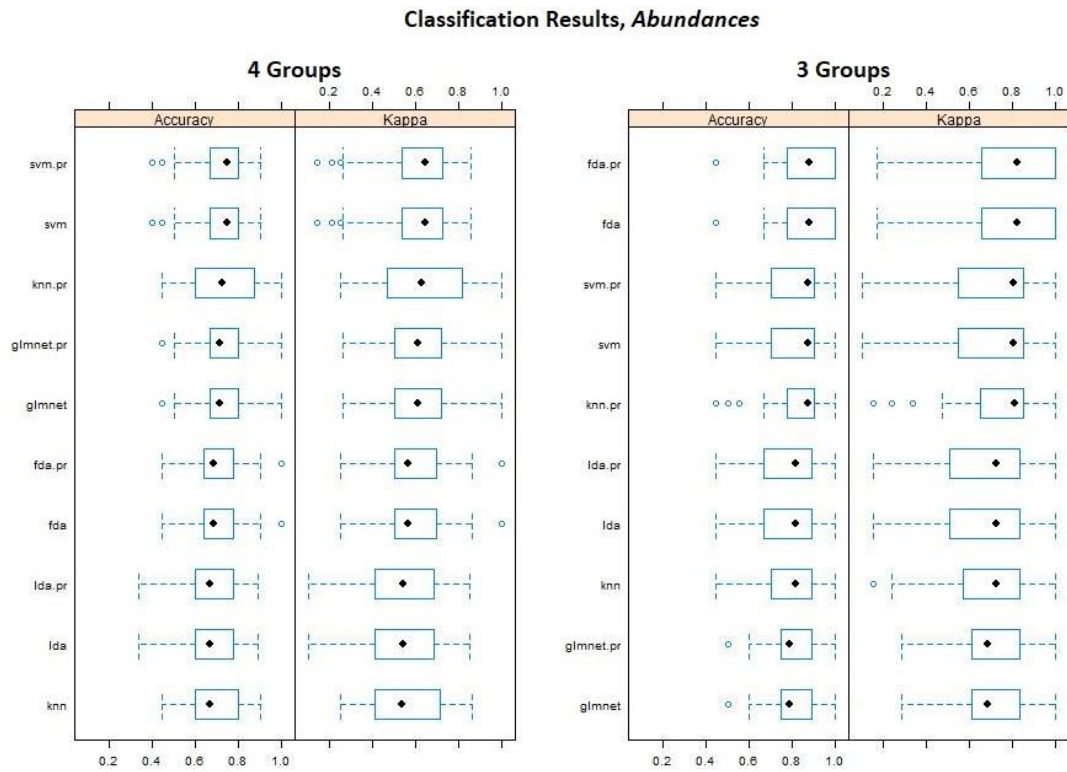


Fig. 4.08 – Data ranges for accuracy and kappa for five methods (ending “pr” indicates data pre-processing) applied to *Abundances*, categorised for 4 (left) or 3 (right) sought groups.

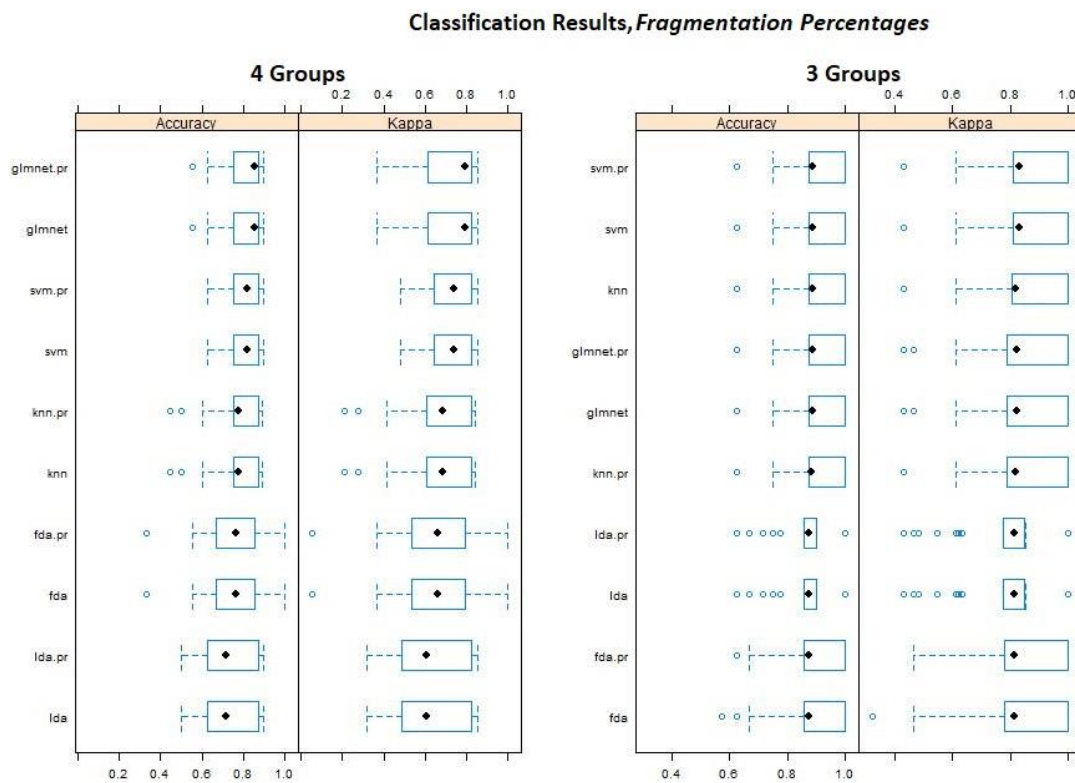


Fig. 4.09 – Data ranges for accuracy and kappa for five methods (ending “pr” indicates data pre-processing) applied to *Fragmentation Percentages*, categorised for 4 (left) or 3 (right) sought groups.

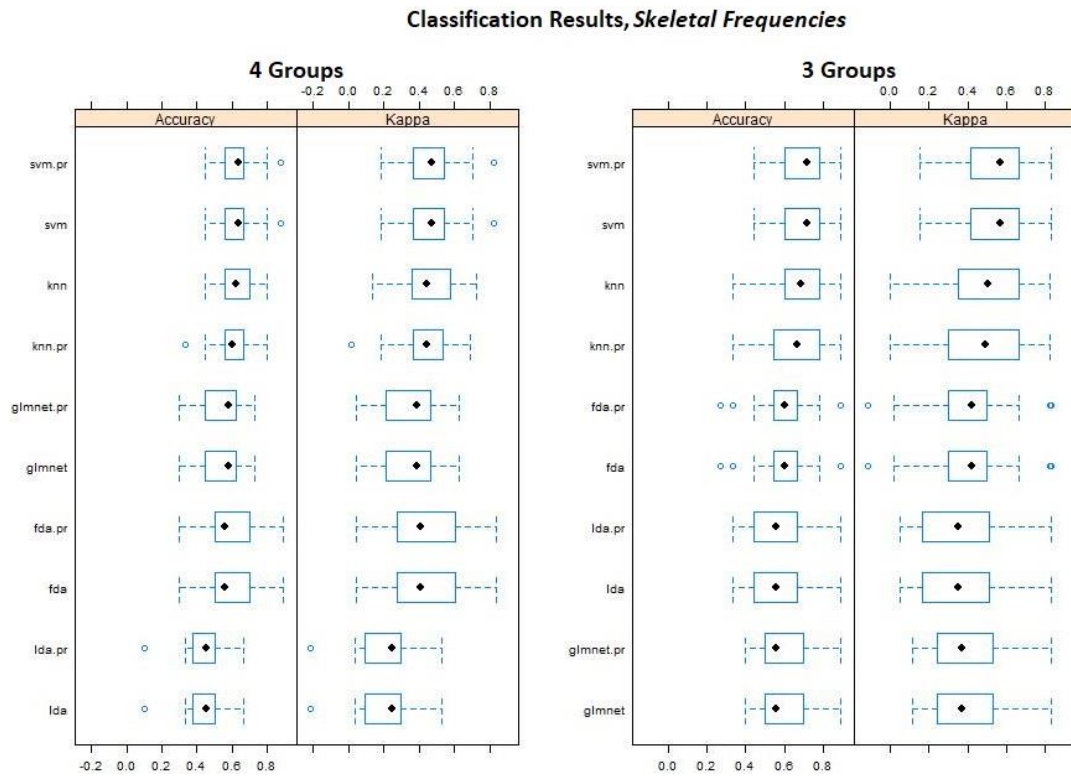


Fig. 4.10 – Data ranges for accuracy and kappa for five methods (ending “.pr” indicates data pre-processing) applied to *Skeletal Frequencies*, categorised for 4 or 3 sought groups.

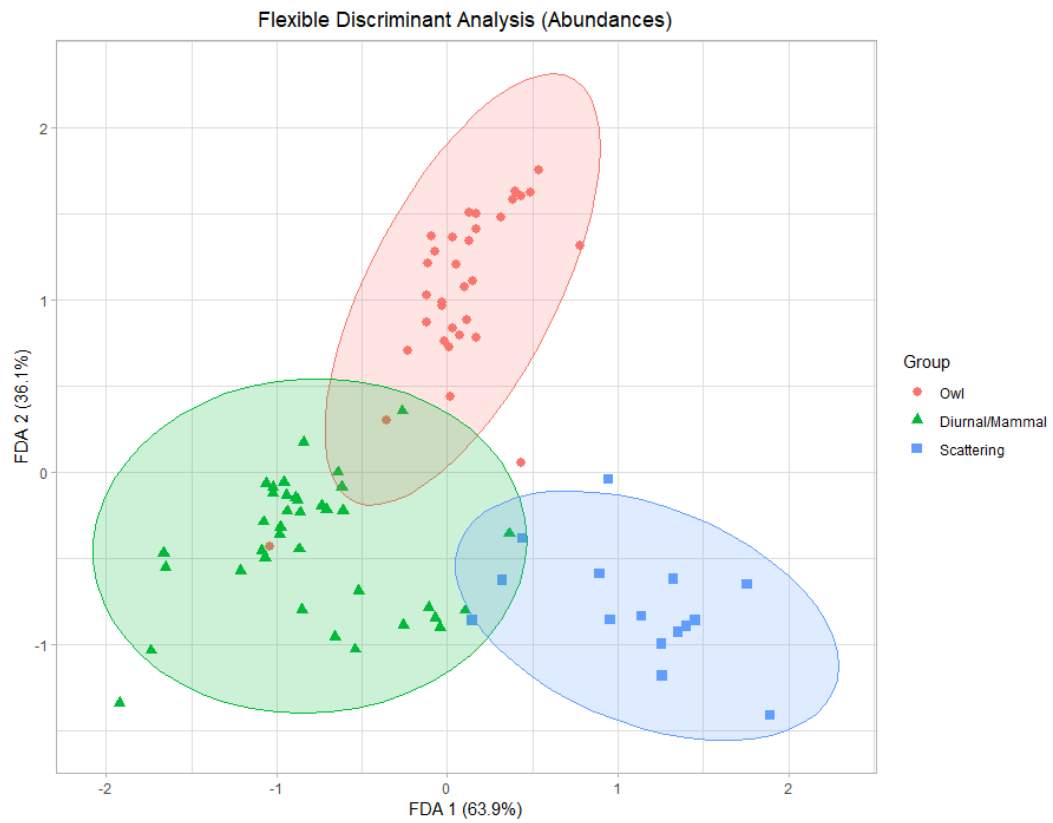


Fig. 4.11 – Visualisation of FDA results on *Abundances* from References Data.

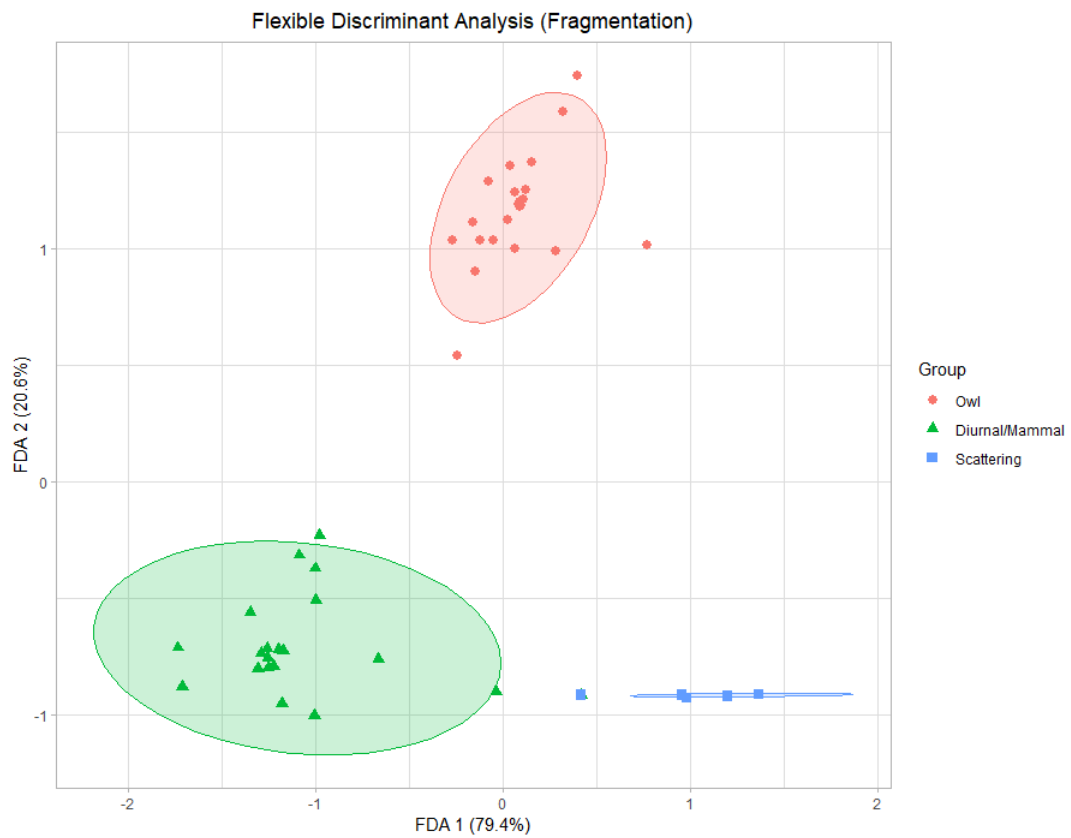


Fig. 4.12 – Visualisation of FDA results on *Fragmentation Percentages* from References data.

Table 4.08 – Best accuracy obtained from trained methods for two sets of data, depending on random seed (7 or 24) and a number of groups utilized for classification. *LDA did not have tuneable parameters nor relied on random number generation, resulting in same accuracy regardless of random seed.

Grouping	Method	Accuracy - Abundances		Accuracy - Fragmentation	
		(Seed: 7)	(Seed: 24)	(Seed: 7)	(Seed: 24)
4 Groups	SVM Radial	100%	94%	85%	85%
	FDA	78%	78%	86%	86%
	GLM Net	84%	74%	80%	82%
	Knn	100%	100%	80%	81%
	LDA		84%*		80%*
3 Groups	SVM Radial	97%	96%	93%	98%
	FDA	96%	94%	95%	99%
	GLM Net	86%	86%	92%	92%
	Knn	100%	82%	90%	89%
	LDA		86%*		92%*

Table 4.09 – Identifications obtained when applying trained *Abundances* and *Fragmentation* model to sample (n = 916), context (n = 237) and combined (n = 466) levels of data, for FDA and SVM methods.

Data	Group	FDA			SVM		
		Samples	Contexts	Combined	Samples	Contexts	Combined
Abundances	Scattering	666	139	324	525	89	246
	Diurnal/Mammal	218	80	120	367	138	205
	Owl	32	18	22	24	10	15
Fragmentation	Scattering	638	100	291	680	107	312
	Diurnal/Mammal	202	104	126	193	112	132
	Owl	76	33	49	43	18	22
Result	Scattering	508	79	244	476	75	224
	Contested	288	81	127	253	46	110
	Accumulation	37	31	38	40	20	23
	Diurnal/Mammal	77	42	52	143	95	107
	Owl	6	4	5	4	1	2

4.5. SAMPLE REPRESENTATIVENESS

The initial overview of two chosen sites, Neolithic Links of Noltland and Norse/mediaeval Birsay Bay, revealed marked differences in samples representativeness between the sites as well as within them. Given results of previous analyses, data groups considered for correlations, apart from taxonomic (no. of species classes, no. of meaningful species classes) and digestion counts, were *Abundances*, *Fragmentation Percentages* and *Skeletal Frequencies*. Classifications based on Pearson (*Abundances*, *Fragmentation Percentages*) and Spearman (*Skeletal Frequencies*) correlations as well as χ^2 test and a trained FDA classification model were also included. In overall, representativeness differed depending on the data checked, from as high as reaching 95% (species match for Links of Noltland Trench A) to as low as 1% to 3%, in the latter case especially for summary categories (full data match for Birsay Areas 2 & 3, see Table 4.10). However, the representativeness of Birsay Bay samples was significantly lower than those obtained from Links of Noltland, with the total percentage of representative samples as well as the average context representation obtained almost universally 10% lower. This situation included both direct matches of data (both binary yes/no as well as on the correlation strength) as well as classification based on correlations, χ^2 and algorithms. Interestingly, further differences could be noted between specific areas, possibly revealing the impact of a wider context of deposition on representativeness. Birsay Bay Area 1 as well as Links of Noltland Trench A, both representing in-structure deposits (i.e. contexts with restricted accumulation/dispersal area), have provided generally more representative samples to their open areas counterparts (no or minor restriction to accumulation and dispersal), Birsay Areas 2 & 3 and Links of Noltland Trench D.

From the context perspective, the most crucial for obtaining representativeness were the taxonomic diversity as well as what portion of a context samples represented. Plotting the representativeness of species match and *Fragmentation Percentages* match against five quantifiable data from the studied contexts (number of species classes, NISP, weight, skeletal completeness, context size expressed in samples) revealed the former to be most correlated with the number of species classes present within the context, while the latter with overall context size measured by a number of samples retrieved (Fig. 4.13). Obtained r^2 between species match and the number of species classes was high ($r^2 = 0.56$), with a decreasing trend line pointing towards more diverse taxonomic composition harder to notice in a sampled material. Representativeness of fragmentation was also impacted by the taxonomic diversity, with more

taxonomically complex contexts less likely to provide many representative samples. However, in contrast to species match, the lower-end of representativeness range was not affected, resulting in r^2 showing only 0.14. Still, considering the number of contexts ($n = 79$), r^2 of 0.1 and more could not be considered as a weak relationship or lack of one. A similar relationship as in the case of fragmentation to species classes was also noted for context sample size, with a gradual decline of the upper end of likely representativeness ranges as the number of samples the context consists rise. However, r^2 for fragmentation was 0.17, the highest obtained among all the data comparisons, suggesting it to be the most likely source of variability of results. Additionally, the second-highest r^2 for species match was obtained with context sample size ($r^2 = 0.25$), especially visible in the case of Birsay contexts and suggesting its high importance for species representativeness.

Relationships with other data have a lesser role in a change of a context providing more representative samples. Interestingly, comparison against skeletal completeness revealed no visible relationship, with r^2 equal to 0.01 for species and even lower 0.001 for fragmentation. In turn, NISP and weight have shown some impact on fragmentation data. While r^2 has shown only minor values, 0.1 and 0.14 respectively, the lower end of representative results was slowly going up as both variables increase denoting a positive correlation. Weight was also noted to have a minimal impact on species match, though it could only be noted in the case of Birsay Bay. Still, it seems NISP data had only an impact on quantifiable data (*Skeletal Frequencies*, *Abundances*, *Fragmentation Percentages*), as species match has shown coefficient of determination basically equal to 0.

Rest of data checked also follow the situation noted in species and *Fragmentation* match in the case of dominant relationships and skeletal completeness (see Fig. 4.14), though their relationship with other variables differs significantly. The declining trend in the case of comparison with context size was also noted when dividing contexts into two groups, large and small contexts, based on the overall number of samples retrieved (1-9 for small samples for Birsay, 1-4 in the case of Links of Noltland, see Table 4.11). The coefficient of determination obtained when checking digestion against species classes showed a clean relationship ($r^2 = 0.32$). An even better value ($r^2 = 0.48$) was obtained with a context size, being the highest observed. *Skeletal Frequencies* match showed a clear negative relationship with both species classes and context size. However, the negatively skewed relationship was also noted in the case of NISP and weight. In turn, the representativeness of *Abundances* shows a far less pronounced tendency for species classes, with r^2 obtained being only 0.08. The relationship of

Abundances with the number of samples within the contexts, while having a similar tendency to other data (r^2 of 0.1), show both low and high end of values range approaching $r^2 = 0.5$ as the number of samples grows. However, *Abundances* also showed a similar relationship with NISP and weight as fragmentation, especially in a second case providing a clear rise of lower end of the representative range as the value rises.

In order to be fully representative, the sample had to be tested as positive in all four main categories, i.e. taxonomic composition, *Abundances* and *Fragmentation* patterns as well as presence or absence of digestion. *Skeletal Frequencies*, as a simplified version of *Abundances*, were discarded from theoretical full representativeness to avoid redundancy. However, even considering differences between the sites, the context size in samples ($r^2 = 0.16$) as well as taxonomic diversity ($r^2 = 0.23$) and presence of digestion were crucial for representativeness. Out of 203 samples in Birsay Area 1, only nine could be considered as fully representative of their parent context. It was even worse for Area 2 and 3, with only five out of 158 samples representative. Both smaller and larger Area 1 contexts were strongly affected, although in the former case on average about 13% of samples were representative per context while in the latter case less than 5%. Area 2 and 3, on average, showed values below 5%, rendering data representativeness essentially unlikely. Links of Noltland however showed far higher representativeness, with 53% from Trench A and 41% from Trench D being considered as fully representative. Especially high were outcomes for smaller contexts (average of about 65/70%), with larger contexts showing values lower than general for samples (50/38%).

Additionally, a series of problems unique to specific data types were noted when checking relationships. One was the presence of samples negatively correlated to their parent context. While all negative correlations obtained were weak, it does not exclude the possibility of strong negative correlation samples not only not representing the parent context but also being misleading to the parent context nature. Additionally, some samples did not provide *Skeletal Frequencies* or *Fragmentation Percentages* that could be correlated with the parent context. For fragmentation about 57 samples from Birsay and 15 from Links of Noltland did not provide any correlation values. Sometimes a large percentage of context content was not possible for establishing correlation. In the case of Trench D context 22, out of six samples, two turned out to be incomputable. A similar situation could be noted with context 134 from Birsay Area 1, where four samples out of 19 did not provide comparisons. However, the most severe case was with the two biggest contexts from Area 2 and 3, which provided 14 non-computable samples each, at worst being about 29% of all retrieved content. While *Skeletal Frequencies* were also

occasionally showing no values (up to 13 samples in Birsay Areas 2&3) there were fewer cases, with the most severe being in the case of Links of Noltland Trench D Context 37 (one of two samples incomputable). It points towards risk of the material from some contexts being so thinly distributed or biased that the majority of samples may turn out incomparable.

Moreover, digestion also showed a unique problem. In both sites, digestion marks were a rarity, with only twelve contexts from Birsay and three from Links of Noltland providing anything at all. Only Birsay Area 2 and 3 provided more contexts than less with digestion (four out of six). That is why for all contexts not containing such data a 100% match between samples and contexts was scored, resulting in the majority of samples in each context being representative.

Classification matches based on correlation (four groups: owl/diurnal/mammal/scattering) and χ^2 (two groups: owl/non-owl) followed patterns noted when comparing data directly, though potentially significant differences could be noted. Most similar were relationships between classification based on specific data and said data relationship with other data, resulting in taxonomic diversity (either encompassing all used classes or taking into consideration only definite species identification) and context size in samples strongly and negatively affecting representativeness. The final prediction for the trained classifier, being a composite score similar to the full match discussed before, also showed very low number of matching results, possibly pointing towards Birsay samples rarely showing full representativeness. However, representativeness provided by matches did not necessarily reflect that noted from direct data comparison. It was especially notable when comparing matches based on *Skeletal Frequencies*, which provided higher accuracy than strong frequencies correlation could. Classification matches based on χ^2 , particularly, provided very high representativeness. In turn, classifications based on *Abundances* showed less representativeness, while fragmentation returned better results for Birsay, but worse for Links of Noltland.

When assessing the situation from the perspective of the samples, one could notice the importance of sample size and quality, though a strong difference between the studied sites affecting relationships between data could also be seen. When plotting species match data distribution depending on match outcome one could notice each site returning a different answer (Fig. 4.15, left plots). For Birsay both NISP and weight provided higher values for positive matches, with mean completeness also higher in those samples. Links of Noltland did not exhibit such correlation, with all values being relatively similar in the case of both negative and positive matches, either reflecting very low taxonomic diversity or generally greater in terms of NISP and weight samples than ones retrieved from Birsay. Still, when data were

divided alongside full match results (Fig. 4.15, right plots), one could notice a visible difference between positive and negative matches on both sites. Samples providing a full match for species, abundances, fragmentation and digestion were almost always more skeletally complete and provided more NISP, with correlated weight also higher.

Noticeable differences between the samples can be also inferred from investigating already obtained correlation coefficients (between samples and parent contexts) and comparing them with other variables through coefficients of determination (table 4.12). *Skeletal frequencies*, *Abundances* and *Fragmentation Percentages* correlations obtained from Links of Noltland samples, when compared against other data have shown quite high coefficient values, with only frequencies providing r^2 lower than 0.1 in a couple of cases (species classes and weight). The coefficients of *Abundances*, in particular, suggested strong relationship between correlations and skeletal completeness ($r^2 = 0.35$) but also with NISP and weight ($r^2 = 0.23$ & 0.24). However, the best obtained values were actually between *Abundances* and *Skeletal Frequencies* correlations ($r^2 = 0.43$) as well as *Fragmentation Percentages* ($r^2 = 0.35$), suggesting general similarities between the samples. In contrast, Birsay Bay correlations provided relatively low values with other data, in case of *Skeletal Frequencies* not providing any r^2 beyond 0.09. However, relationships between data seemed to differ to those noted for Links of Noltland, with *Abundances* showing a less pronounced relationship with frequencies ($r^2 = 0.08$) than to fragmentation ($r^2 = 0.15$). Skeletal completeness also showed less importance to abundances correlations ($r^2 = 0.08$) than NISP ($r^2 = 0.18$) and weight ($r^2 = 0.16$). Interestingly, digestion, as calculated based only on contexts with digestion present, showed relatively high coefficient when compared to NISP and weight ($r^2 = 0.37$ and $r^2 = 0.39$), with third highest result with species classes ($r^2 = 0.12$).

The aggregation process showed visible trends among quantifiable data. The relationship between key quantifiable data proved to be heavily linear (Table 4.13, see Fig. 4.16 as an example). NISP, MNI and Weight showed consistent r^2 from 0.9 to almost 0.99 (e.g. MNI, Fig. 4.11). Only context 16 from Links of Noltland Trench A showed values in the range 0.8 to 0.9 for NISP and MNI when plotted against % of aggregated context. However, skeletal completeness, the only key value with both upper and lower end values (0 to 100%), was mildly correlated in three out of four contexts, showing high variation between early aggregation stages. Only context 28 showed skeletal completeness gradually rising, though with a minor fall around midway through aggregation. Similar variability was also noted in the case of other ratio data, including abundances and fragmentation (Fig. 4.17). Initial variation was usually

very high, often leading to changes of 10% and above between the aggregation steps. In many cases variation started to lower around midway however, ceasing to be a problem around 75% of all samples aggregated. In rare cases, however, variation was still visible beyond this point, especially in the case of maxillary abundances for context 198 (Birsay Bay Area 1) or 16 (Links of Notland Trench A).

Despite deviations from expected results being noted, the aggregation of data confirmed the already visible impact of the percent of context sampled on data representativeness. In the case of abundances and fragmentation correlation to parent context, the relationship proved to be logarithmic (Fig. 4.18). Especially for abundances, values were steeply rising within the first aggregation steps, soon reaching near 1.0 between 20 and 30% of context aggregated. Fragmentation correlation values are also clustered in the same way, although a higher variation than noted in the case of abundances can be noted before reaching midway through the aggregation process. However, among four contexts only two started from a sample with non-significant abundance correlation and only one with non-significant fragmentation correlation, possibly creating a bias towards better results. Correlations with frequencies however showed a more complex situation, with values rising to 25% just to sharply fall until 75% and rise once again. This situation was especially visible in the case of context 198, but a similar pattern was also noted for A16. In the case of context 208 this situation was not noted, while in the case of D13 only one early level of aggregation did not provide a significant (1.0) correlation.

Binary matches between species, digestion and predictions have shown in overall better results than ones noted in sample analysis (Table 4.14), but with a strong variation between studied contexts. The number of levels with representative taxonomic diversity varied, from 100% (context A16) resembling a match being achieved from the first selected sample up to only 11% (context D13) showing that only a complete context (i.e. final level of aggregation) was representative. However, more interesting in this case was Birsay Bay, with the higher number of taxa present in contexts, where results could be achieved relatively early (Context 198) or very late into data aggregation (Context 208). A similar situation for Birsay Bay was repeated in the case of digestion, with variation between 25% and 94%. The majority of predictions based on χ^2 and correlation-based matches were correct from the first samples. Only specific cases were noted and did not show the correlation between the two groups of predictions. Interestingly, trained FDA algorithms showed differences between studied sites, with prediction match being achieved late for Birsay Bay context 198, with context 208 showing the full match in the case of fragmentation but showing the same trend for abundances. In turn,

Links of Noltland showed a match earlier, three out of four cases before reaching 50% of aggregation.

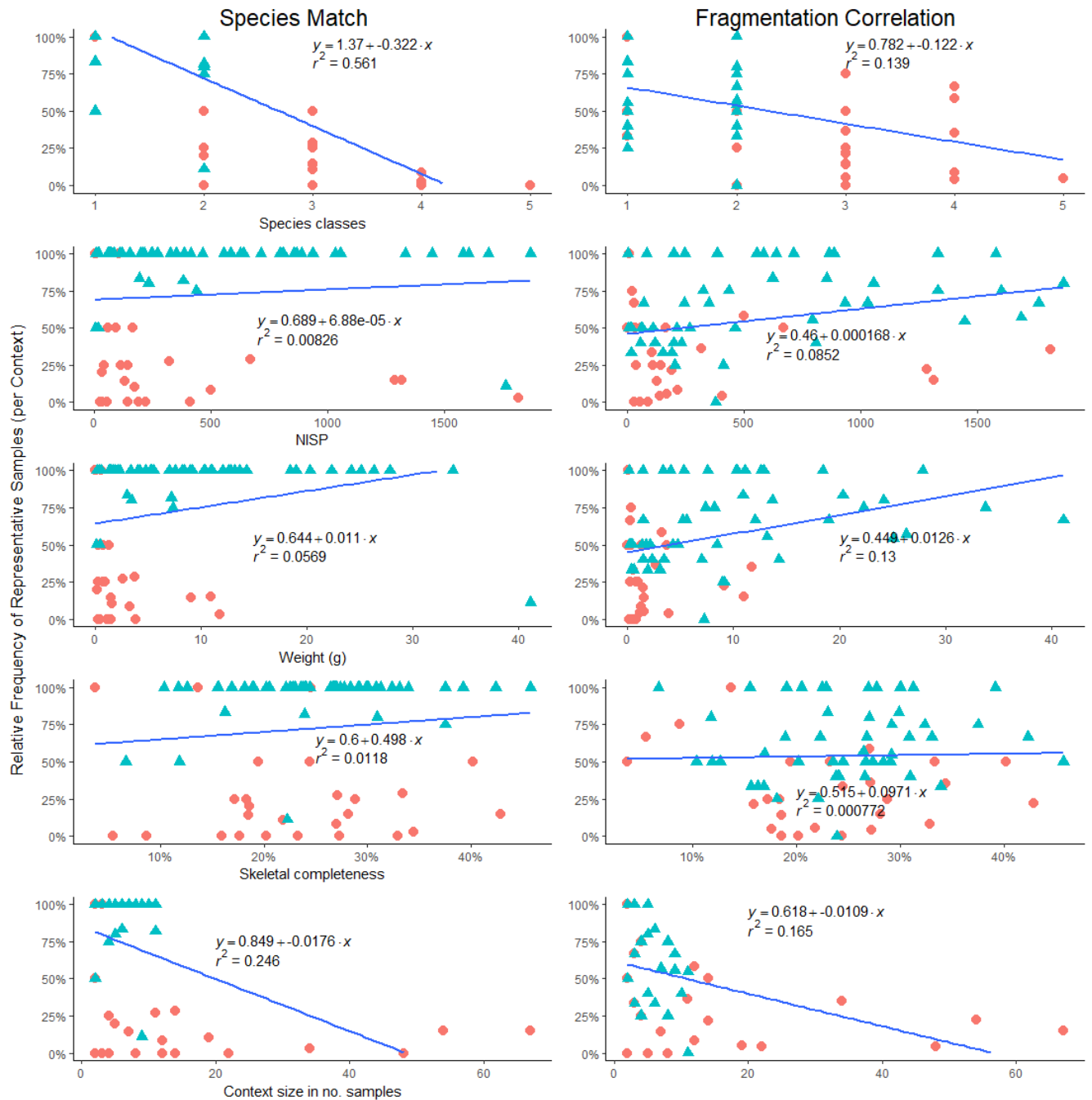


Fig. 4.13 – Comparison between a percentage of representative samples in two categories (species match and *Fragmentation Percentages* correlation) and context number of species classes, NISP, weight, skeletal completeness and context size (measured by a number of samples retrieved). Birsay Bay contexts marked with round shape and red colour, Links of Noltland contexts by triangle and teal colour. Coefficient of determination (r^2), related equation and regression line calculated jointly for both sites.

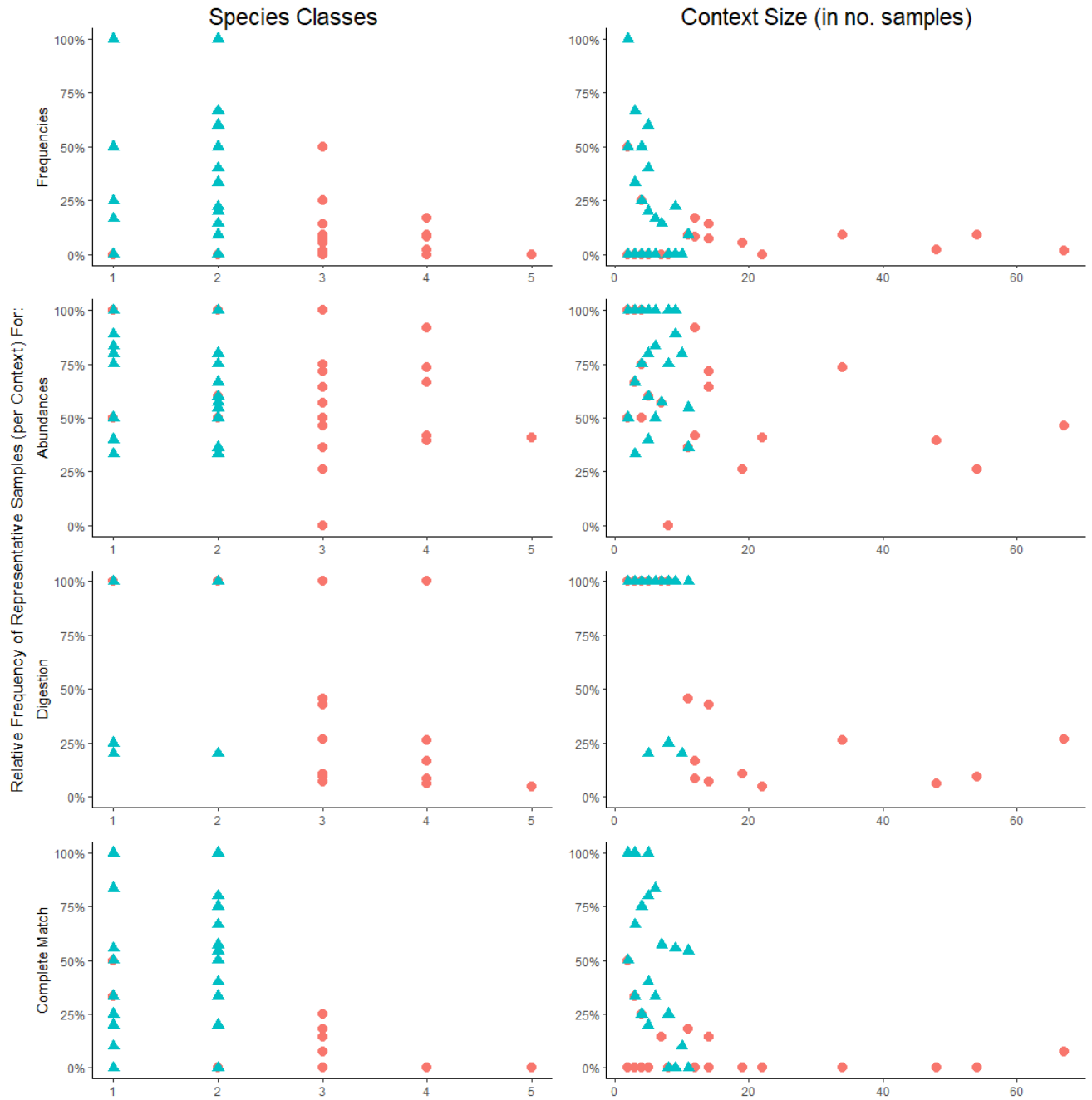


Fig. 4.14 – Comparison between species classes and context size (as number of samples retrieved) to a percentage of representative samples in each category: *Skeletal Frequencies* and *Abundances* strong correlation, digestion match and full match (match in species as well as *Abundances*, *Fragmentation* and digestion). Birsay Bay contexts marked with round shape and red colour, Links of Noltland contexts by triangle and teal colour.

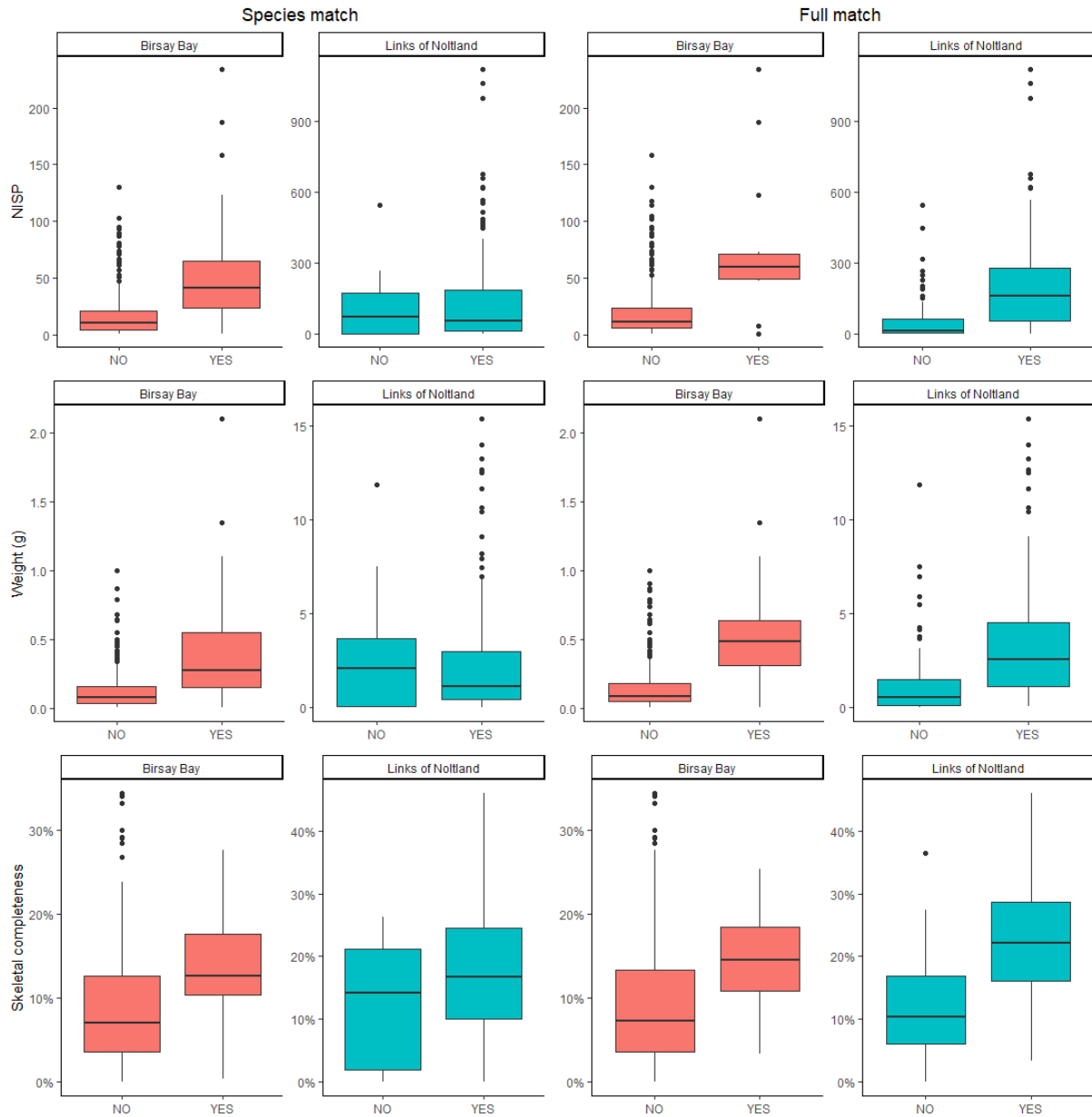


Fig. 4.15 – Differences in samples skeletal completeness, NISP and weight depending on whether there is a sample-context match in the case of diagnostic species (left) as well as if there is a full data match (right). Both sites (Birsay Bay, Links of Noltland) presented separately.

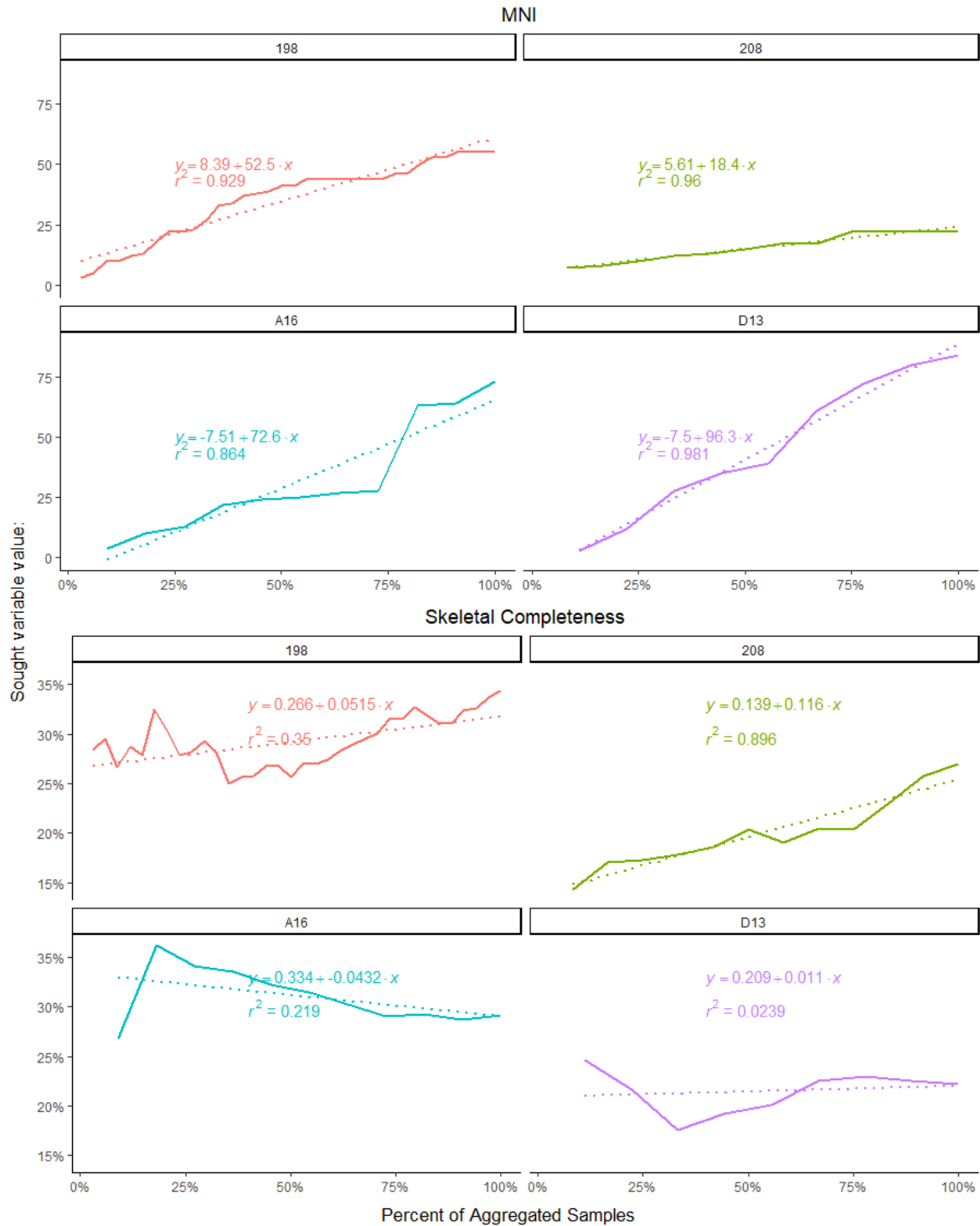


Fig. 4.16 – Impact of aggregation on quantifiable data in example of MNI and Skeletal Completeness. MNI and Sk. Completeness values (y-axis) are plotted against what proportion of the whole context have been aggregated (x-axis).

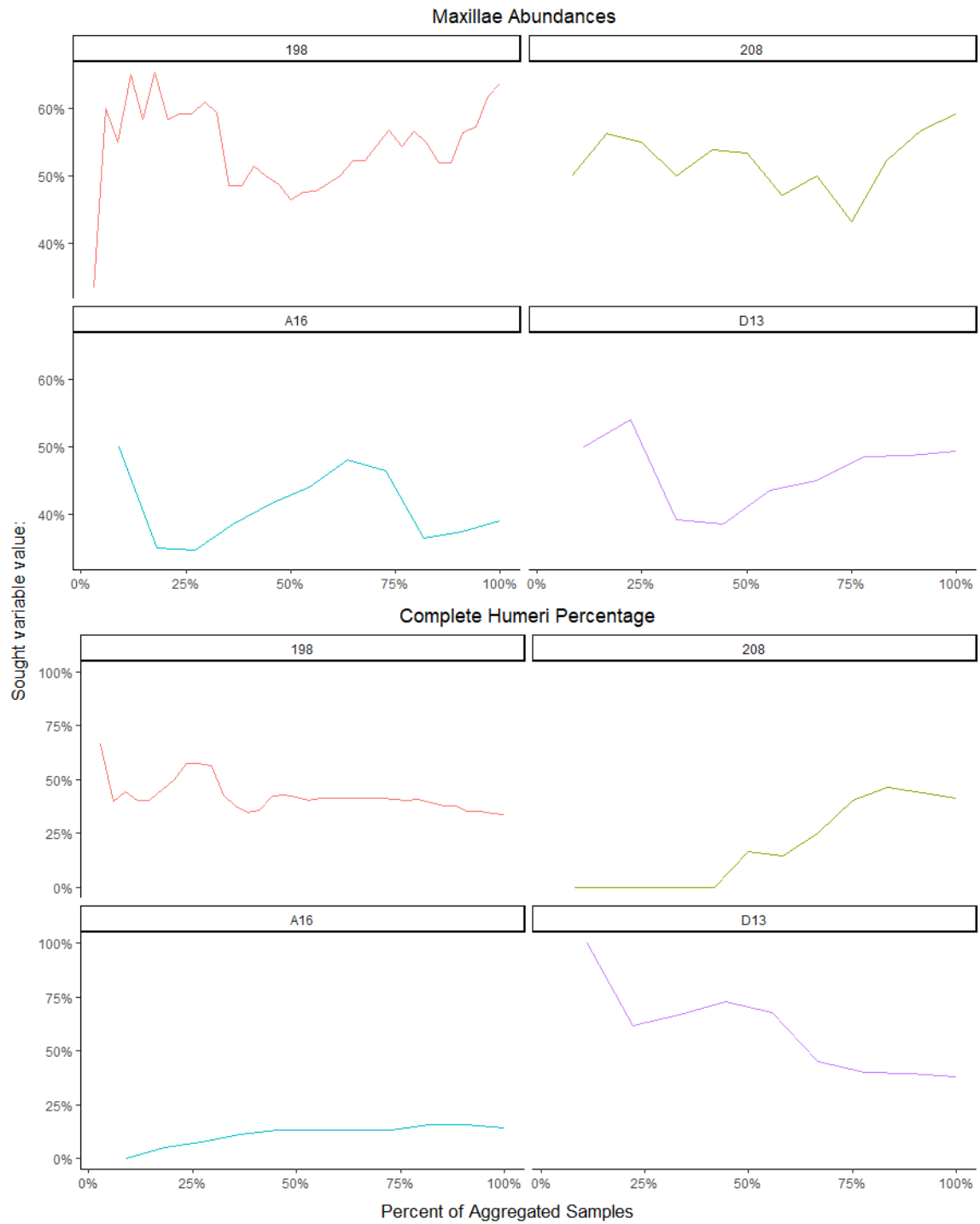


Fig. 4.17 – Impact of aggregation on individual quantified variables, through two examples (maxillae abundances and complete humeri percentage).

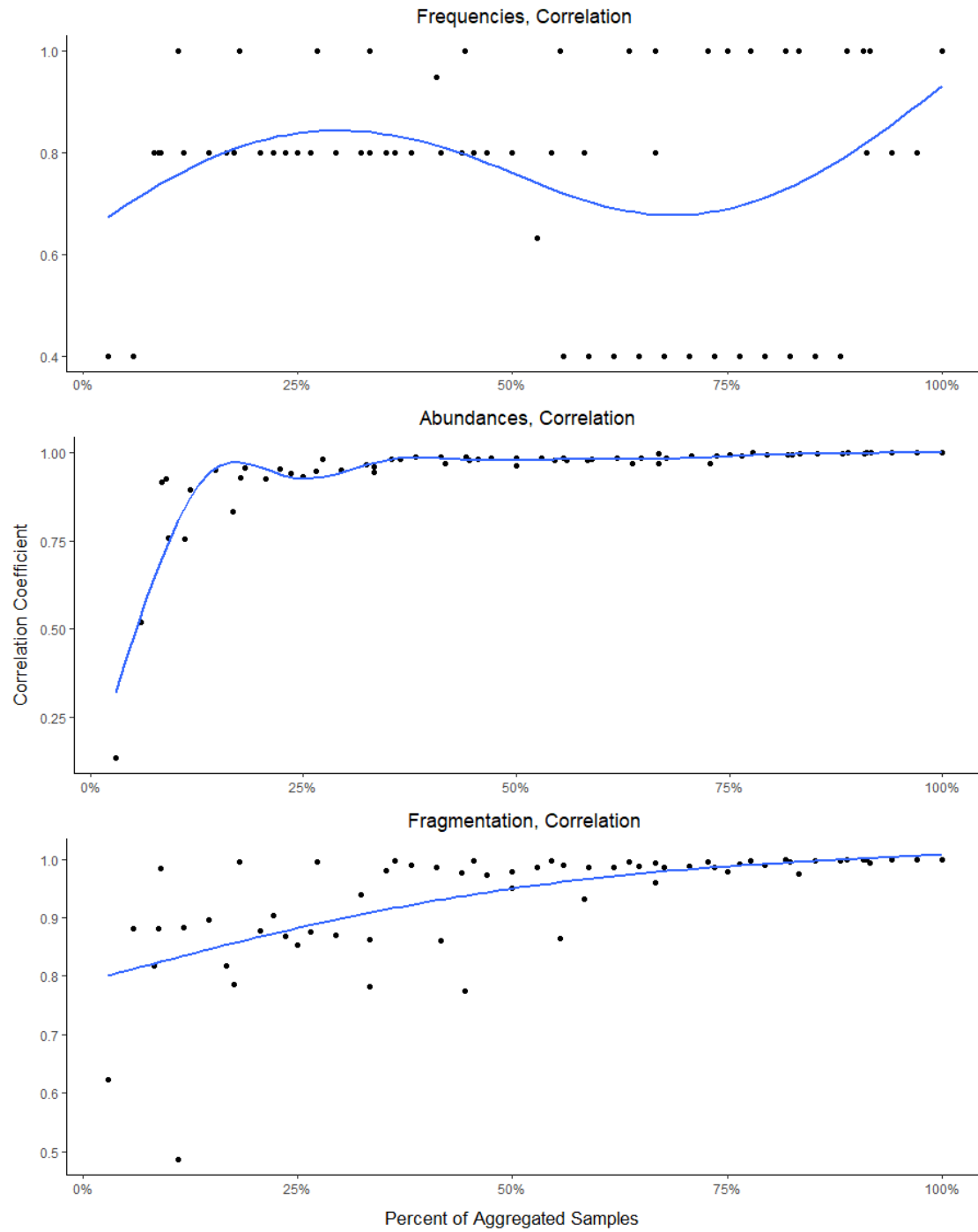


Fig. 4.18 – Impact of aggregation on quantified data correlations. Correlations coefficients between aggregated data and parent contexts for each level of aggregation were plotted against % of aggregated context.

Table 4.10 – Overall number of representative samples for each value group/match investigated as well as means for all contexts, with percentile equivalent. Upper part of the table relates to simple data match, while lower to a classification-type match. Data for Birsay Bay and Links of Noltland areas, extracted from **Appendix: Statistics** table **7a** and **7b**.

Data		Birsay - Area 1		Birsay - Area 2 & 3		Links of Noltland Trench A		Links of Noltland Trench D	
Classes	Samples	31	15.3%	11	7.0%	87	63.5%	54	68.4%
	Avg. Contexts	2	27.2%	2	6.7%	2	66.6%	4	67.4%
Species	Samples	33	16.3%	11	7.0%	131	95.6%	70	88.6%
	Avg. Contexts	2	31.3%	2	6.7%	3	95.7%	5	93.0%
<i>Sk. Frequencies</i> (Corr.)	Samples	18	8.9%	4	2.5%	33	24.1%	5	6.3%
	Avg. Contexts	1	10.7%	1	3.0%	1	29.1%	0	7.6%
<i>Abundances</i> (Corr.)	Samples	102	50.3%	72	45.6%	92	67.2%	67	84.8%
	Avg. Contexts	5	63.0%	12	51.3%	2	70.8%	4	82.8%
<i>Fragm. Perc.</i> (Corr.)	Samples	57	28.1%	19	12.0%	82	59.9%	46	58.2%
	Avg. Contexts	3	34.4%	3	22.8%	2	66.7%	3	59.5%
Digestion	Samples	77	37.9%	30	19.0%	133	97.1%	65	82.3%
	Avg. Contexts	4	73.0%	5	40.8%	4	97.9%	4	89.7%
Full Match (sp.+ab.+fr.+dig.)	Samples	9	4.4%	5	3.2%	73	53.3%	32	40.5%
	Avg. Contexts	0	10.3%	1	1.2%	2	60.4%	2	48.4%
<i>Sk. Frequencies</i> Corr. Match	Samples	95	46.8%	39	24.7%	75	54.7%	36	45.6%
	Avg. Contexts	5	47.7%	6	40.8%	2	57.9%	2	46.0%
<i>Abundances</i> Corr. Match	Samples	97	47.8%	65	41.1%	80	58.4%	56	70.9%
	Avg. Contexts	5	49.0%	11	41.0%	2	61.7%	4	66.4%
<i>Fragm. Perc.</i> Corr. Match	Samples	87	42.9%	55	34.8%	73	53.3%	43	54.4%
	Avg. Contexts	4	45.4%	9	31.4%	2	59.7%	3	55.7%
<i>Sk. Frequencies</i> Chi. Match	Samples	142	70.0%	74	46.8%	131	95.6%	64	81.0%
	Avg. Contexts	7	66.0%	12	54.7%	3	95.1%	4	78.7%
<i>Abundances</i> Chi. Match	Samples	69	34.0%	16	10.1%	78	56.9%	43	54.4%
	Avg. Contexts	3	44.5%	3	20.7%	2	61.0%	3	51.6%
<i>Fragm. Perc.</i> Chi. Match	Samples	81	39.9%	25	15.8%	87	63.5%	60	76.0%
	Avg. Contexts	4	53.0%	4	30.6%	2	68.9%	4	74.1%
<i>Abundances</i> , Classification	Samples	49	24.1%	13	8.2%	99	72.3%	42	53.2%
	Avg. Contexts	2	47.1%	2	34.0%	3	75.9%	3	52.6%
<i>Fragmentation</i> , Classification	Samples	61	30.1%	20	12.7%	87	63.5%	38	48.1%
	Avg. Contexts	3	42.9%	3	24.8%	2	69.9%	3	50.0%
Classification Final Result	Samples	25	12.3%	7	4.4%	81	59.1%	26	32.9%
	Avg. Contexts	1	23.9%	1	26.5%	2	61.9%	2	32.3%

Table 4.11 – Mean number of representative samples as well as percentile representatives for small and large contexts (size difference dependent on a site). Upper part of the table relates to simple data match, while lower to a classification-type match. Data for Birsay Bay (large contexts containing ten or more samples) and Links of Noltland (large contexts containing four or more samples), extracted from **Appendix: Statistics** table 7a and 7b.

Data		Birsay - Area 1		Birsay - Area 2 & 3		Links of Noltland Trench A		Links of Noltland Trench D	
Classes	Avg. Small C.	1	34.7%	0	12.5%	2	68.0%	2	70.0%
	Avg. Large C.	3	13.2%	2	3.7%	4	63.6%	5	66.2%
Species	Avg. Small C.	1	41.1%	0	12.5%	2	96.2%	2	100.0%
	Avg. Large C.	3	13.2%	2	3.7%	6	94.7%	6	89.4%
<i>Sk. Frequencies</i> (Corr.)	Avg. Small C.	0	11.5%	0	0.0%	1	34.0%	0	10.0%
	Avg. Large C.	2	9.2%	1	4.5%	1	18.5%	0	6.4%
<i>Abundances</i> (Corr.)	Avg. Small C.	2	68.6%	2	58.3%	2	72.4%	2	80.0%
	Avg. Large C.	11	52.4%	17	47.8%	4	67.3%	6	84.2%
<i>Fragm. Perc.</i> (Corr.)	Avg. Small C.	1	36.4%	2	45.8%	2	70.5%	2	70.0%
	Avg. Large C.	6	30.8%	4	11.3%	3	58.5%	4	54.2%
Digestion	Avg. Small C.	4	100.0%	4	100.0%	2	100.0%	2	100.0%
	Avg. Large C.	4	22.8%	6	11.2%	6	93.3%	5	84.5%
Full Match (sp.+ab.+fr.+dig.)	Avg. Small C.	0	13.3%	0	0.0%	2	65.4%	2	70.0%
	Avg. Large C.	1	4.6%	1	1.9%	3	49.7%	2	37.6%
<i>Sk. Frequencies</i>	Avg. Small C.	2	48.3%	2	66.7%	1	60.9%	1	43.3%
Corr. Match	Avg. Large C.	11	46.6%	8	27.9%	3	51.5%	3	47.4%
<i>Abundances</i> Corr.	Avg. Small C.	2	48.3%	2	41.7%	2	63.5%	1	50.0%
	Avg. Large C.	11	50.4%	16	40.7%	3	57.8%	5	74.6%
<i>Fragm. Perc.</i> Corr.	Avg. Small C.	2	44.7%	1	25.0%	2	65.4%	2	70.0%
	Avg. Large C.	10	46.6%	13	34.5%	3	47.2%	4	48.6%
<i>Sk. Frequencies</i> Chi. Match	Avg. Small C.	2	66.0%	2	66.7%	2	94.9%	2	73.3%
	Avg. Large C.	16	65.9%	17	48.7%	6	95.5%	6	81.4%
<i>Abundances</i> Chi.	Avg. Small C.	1	50.0%	2	45.8%	2	63.5%	1	46.7%
	Avg. Large C.	7	34.4%	3	8.1%	3	55.8%	4	54.1%
<i>Fragm. Perc.</i> Chi.	Avg. Small C.	2	61.5%	2	62.5%	2	74.4%	2	70.0%
	Avg. Large C.	8	37.1%	5	14.6%	3	57.1%	5	76.1%
<i>Abundances</i> , Classification	Avg. Small C.	2	61.7%	3	87.5%	2	81.4%	1	50.0%
	Avg. Large C.	3	20.1%	2	7.2%	4	64.0%	4	53.9%
<i>Fragmentation</i> , Classification	Avg. Small C.	2	51.3%	2	50.0%	2	75.6%	1	60.0%
	Avg. Large C.	5	27.1%	4	12.2%	3	57.4%	3	44.9%
Classification Final Result	Avg. Small C.	1	32.8%	2	75.0%	2	66.7%	1	30.0%
	Avg. Large C.	1	7.3%	0	2.3%	3	51.6%	2	33.4%

Table 4.12 – r^2 values between quantifiable sample data, including correlations obtained from specific data groups (*Skeletal Frequencies, Abundances, Fragmentation Percentages*).

Data	Birsay Bay				Links of Noltland			Both sites		
	freq. corr.	abund. corr.	fragm. corr.	Dig. sel.	freq. corr.	abund. corr.	fragm. corr.	freq. corr.	abund. corr.	fragm. corr.
No. Species Classes	0.07	0.11	0.06	0.12	0.08	0.13	0.08	0.06	0.05	0.01
Skeletal Completeness	0.02	0.08	0.13	0.06	0.10	0.33	0.25	0.05	0.24	0.26
NISP	0.09	0.18	0.13	0.37	0.10	0.23	0.21	0.06	0.19	0.21
Weight	0.07	0.16	0.09	0.39	0.09	0.24	0.18	0.05	0.18	0.19
<i>Sk. Frequencies</i> corr.		0.08	0.00	0.02		0.43	0.10		0.19	0.04
<i>Abundances</i> corr.	0.08		0.15	0.08	0.43		0.35	0.19		0.29
<i>Fragm. Percentages</i> corr.	0.00	0.15		0.09	0.10	0.35		0.05	0.29	
Digestion, selected corr.	0.02	0.08	0.09							

Table 4.13 – r^2 values between aggregated data in studied contexts.

Data	Birsay, Context 198			
	%Cont.	NISP	MNI	Weight
NISP	0.99			
MNI	0.93	0.96		
Weight	0.98	1.00	0.97	
Sk. Compl.	0.35	0.30	0.14	0.28

Data	Birsay, Context 208			
	%Cont.	NISP	MNI	Weight
NISP	0.99			
MNI	0.96	0.95		
Weight	0.97	0.99	0.94	
Sk. Compl.	0.90	0.91	0.78	0.91

Data	Birsay, Context A16			
	%Cont.	NISP	MNI	Weight
NISP	0.85			
MNI	0.86	0.99		
Weight	0.90	0.99	0.99	
Sk. Compl.	0.22	0.15	0.18	0.18

Data	Birsay, Context D13			
	%Cont.	NISP	MNI	Weight
NISP	0.97			
MNI	0.98	0.99		
Weight	0.97	0.99	1.00	
Sk. Compl.	0.02	0.06	0.03	0.04

Table 4.14 – Percentage of representative aggregation steps for each context (species, digestion as well as *Frequencies*, *Abundances* and *Fragmentation* correlations and χ^2 as well as algorithmic predictions based on *Abundances* and *Fragmentation*).

Context	Species	Digestion	Matches		
			Correlations Predictions		
			Freq.	Abund.	Fragm.
Birsay, 198	82%	94%	100%	100%	100%
Birsay, 208	25%	42%	100%	100%	33%
LoN, A 16	100%	100%	73%	91%	100%
LoN, D 13	11%	100%	100%	100%	100%

	χ^2 Test Predictions			Algorithm Predictions	
	Freq.	Abund.	Fragm.	Abund.	Fragm.
Birsay, 198	100%	100%	41%	32%	26%
Birsay, 208	100%	92%	100%	25%	100%
LoN, A 16	100%	100%	91%	82%	55%
LoN, D 13	100%	100%	100%	33%	89%

4.6. VISUALISING TAPHONOMIC PROCESSES

The analysis of taphonomic processes started from visualising and analysing dispersal patterns from Terry's work (2004; see Fig. 4.19, upper plots). The first detailed studies on micromammal dispersal revealed differences in content between the accumulation of fresh, intact pellets and older material that remains out of partially or fully disintegrated pellets (Terry 2004). Right-skewed bimodal distribution of dispersal from the point of origin (tree trunk) was noted, with proportions of skeletal elements strongly changing due to loss of small and fragile elements. Many taphonomic data were strongly affected by dispersal, with the steady rise in fragmentation and the decrease of markedly altered bones (e.g. digestion). When plotted (Fig. 4.19, upper plots), stages of dispersal showed a gradual decline from intact to dispersal stage in vertebrae as well as front limb bones as a percentage of the whole assemblage, with percentile increase of skull elements, especially mandibles, and hind limb bones. The change was more gradual with skull and vertebral elements, with limb bones changing strongly only in dispersal. Some changes could be explained by a loss of smaller, more fragile bones first, such as vertebrae or distal front limb bones. When all the stages of assemblage dispersal were pooled, the resulting pattern for the whole assemblage revealed values not dissimilar to partial dispersal.

Dispersal patterns were comparable with attractional accumulation patterns obtained for bigger mammals in eastern Africa (Behrensmeyer 1983; Behrensmeyer & Boaz 1980). The strongest observed phenomenon in those patterns were the different percentages of vertebra and long bones in relation to each other and skull elements in surface and buried contexts (Fig. 4.19 lower plots). The "predation patch" (i.e. place where animals were frequently ambushed and occasionally consumed), as well as the "burial" pattern, showed a high number of vertebra in relation to other bones. It was a similar situation to one observed in the case of micromammal intact or partial dispersal patterns from Terry's work (Fig. 4.19, upper plots). In turn, the large-taxa dispersal pattern showed on average very similar numbers of each skeletal group, differing from one noted by Terry. Additionally, intentional accumulations of prey remains (so-called "Hyena den") consisted predominantly of limb long bones, a phenomenon not observed during Terry's work nor in obtained *Skeletal Frequencies* patterns.

The skeletal frequencies provided from model data and signatures revealed the prevalence of patterns unique to specific groups. Within an owl group value ranges for skulls and front limbs were most consistent, with standard deviation ranges between 10 and 20% for skulls and 10 to

25% for front limbs (Fig. 4.20, upper plots). More variability could be noticed in the case of the remaining two groups, especially vertebrae, showing interquartile ranges from about 25 to 55%, visibly dominating assemblages and with only a minor overlap with upper ranges of hind limbs. Not surprisingly, this pattern was very similar to the intact pellets pattern, with vertebrae being most prevalent and followed by firstly front and then hind limbs, ending on skull elements. All associated signatures also showed a similar pattern, from near-perfect fit (barn owls) up to be to some degree similar to partial pellets dispersal (short-eared owls; Fig. 4.20, lower plots). Diurnal species provided a clean contrast to owls, with dominating prevalence of skulls (25-50% within interquartile range), with vertebrae showing a wide range of frequencies (5 to 40%). Limbs showed similar means to owls but with wider ranges for front limbs. Signatures however showed strong variations, from peregrine showing almost the same values for all skeletal parts but skulls and similarity to short-eared owls to hen harriers, with over 50% of all frequencies being skull elements and only minor finds of vertebrae. Not surprisingly, those are more difficult to compare with micromammal assemblages dispersal patterns, at best being similar to partially and fully dispersed assemblages, but Behrensmeyer's dispersed bones pattern may be more similar in this case.

However, a chance of owls and mammal assemblages overlapping in expressed value ranges as well as problems with extreme scattering was noted. Apart from skulls, all *Skeletal Frequencies* showed similar means, with vertebrae being relatively common. Skulls showed however a wider variation, with a 5%-25% range. The red fox signature, used to find assemblages similar to mammals, was very similar to owls. The only difference was a slightly higher prevalence of hind limb bones. Not surprisingly, scattering provided the most extreme values, with 0 to 50% ranges from skulls, front and hind limbs. Vertebrae were absent from all scattering assemblages, resulting in no values present for them. However, identifiability of scattering may be possible due to many assemblages lacking one or more skeletal frequencies. The signature used had only skull and front limb bones, resulting in a 50% split of *Skeletal Frequencies*.

Indices changed depending on species group, but the result is difficult to interpret due to overlap in the range of values (see Fig. 4.21). Complex postcranium to cranium index showed the most consistent answers when used as differentiation between owls and other species as well as scattering. Most values for owls clustered around just above 200%, with the interquartile range encompassing most values within the range 200%-300%. In contrast, the rest of the studied groups had median values on or slightly below 100%, with the interquartile range not encompassing any values beyond 180%. In the case of signatures, all owl species showed this

trend, with the index well over the value of 200% for each of them. However, the red fox signature showed a very similar value, about 200%, showing a possibility of occasional overlap, but remaining signatures provided values around 100%. The simplified postcranial to cranial index and distal to proximal limb bones index did not show differences strong enough to provide clear cut-off points for identification. While owl assemblages provided clear simplified index values, tightly clustered around specific values, diurnal and mammal species showed a higher variation of values, often encompassing the whole range of owl values. It was especially visible in the case of peregrines and kestrels/hen harriers, with peregrines providing a simplified index slightly higher than owl signatures while kestrels and hen harriers showing far lower values. In turn, the distal to proximal index provided relatively narrow ranges for all predatory groups, though with an overlap in their upper/lower ends of standard deviation ranges. As a result, one can notice a gradual decline of the index from owl to red fox signature.

The analysis of *Skeletal Frequencies* across the main sites (Fig. 4.22, upper plots). have suggested. Skara Brae Trenches I and II provided contexts with relatively wide ranges of frequencies, but the majority of values clustered in a manner similar to diurnal species, with skull frequencies being slightly less expressed. A similar pattern, but with slightly higher hind limbs expression, was also found in the case of other Neolithic sites, especially Links of Noltland Trench D. Similar to Trench D, Trench A showed bigger frequencies variation, with a higher prevalence of front or hind limbs and similarity to Behrensmeyer's dispersed bones pattern. Trenches III and IV of Skara Brae, used mostly as an example for scattering, have returned the expected pattern. Interestingly, sites from later periods showed a drift towards an owl-like pattern, which was especially visible in the case of Birsay Area 1. Mean values showed the consistent predominance of vertebrae, followed by front and then hind limbs, ending with skulls. However, the remaining three differences are not big and the majority of values overlap. A similar situation was noted in the case of Areas 2 and 3, with vertebral dominance being consistently within $45 \pm 0.2\%$ value range and the biggest variation within skulls frequencies. Scar also showed the predominance of vertebrae but also bigger ranges for other frequencies, most notably skulls, and higher values of hind limb than front limb bones. The last site, Tuquoy, was dominated by skull frequencies, followed by high numbers of vertebrae and small frequencies of fore and hind limbs. This situation is similar to diurnal species as well as the partial dispersal pattern.

Indices provided additional information not noted when analysing *Skeletal Frequencies* (Fig. 4.22, lower plots). The most similar situation was with Skara Brae, where Trenches I and II

provided values corresponding to ones obtained from diurnal and mammal species and Trenches III and IV were used previously to investigate scattering. Links of Noltland differed from Skara Brae on a number of occasions, from lower complex indices in the case of Trench D to Trench A showing far higher values for complex as well as simplified index, with front/hind index also showing a range of higher values. Norse/mediaeval sites also showed strong differences from each other. Area 1 from Birsay provided complex index values on par with Links of Noltland, strongly in contrast to Area 2 and 3 as well as other Norse sites. In turn, Tuquoy provides a similar range of values for each index, with means however being lower than 0.5. Contexts from Area 2 and 3 varied essentially only in the case of simplified indexes.

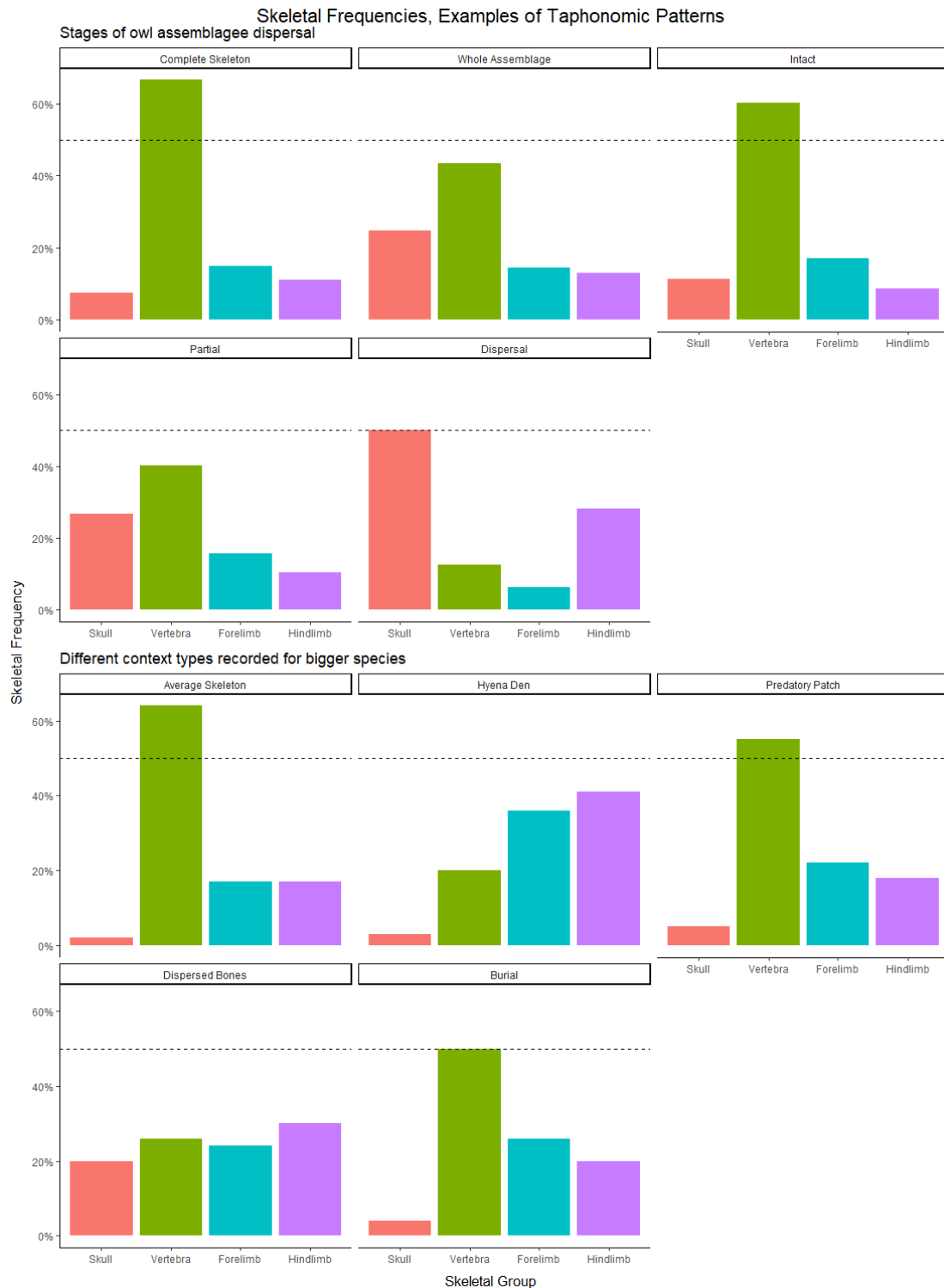


Fig 4.19 – *Skeletal frequencies* for stages of micromammal assemblage dispersal (up, Terry 2004, Fig. 6 plus calculations for the whole assemblage & complete skeleton) and specific contexts from bigger mammals (down, Behrensmeyer 1983; Behrensmeyer & Boaz 1980; Lyman 1994a, 191 Fig. 6.14). Behrensmeyer data were raw values showed in Lyman 1994a Fig.6.14 while Terry's were calculated in the same manner as references and site data in this thesis (See **Chapter 3.3.4.**).

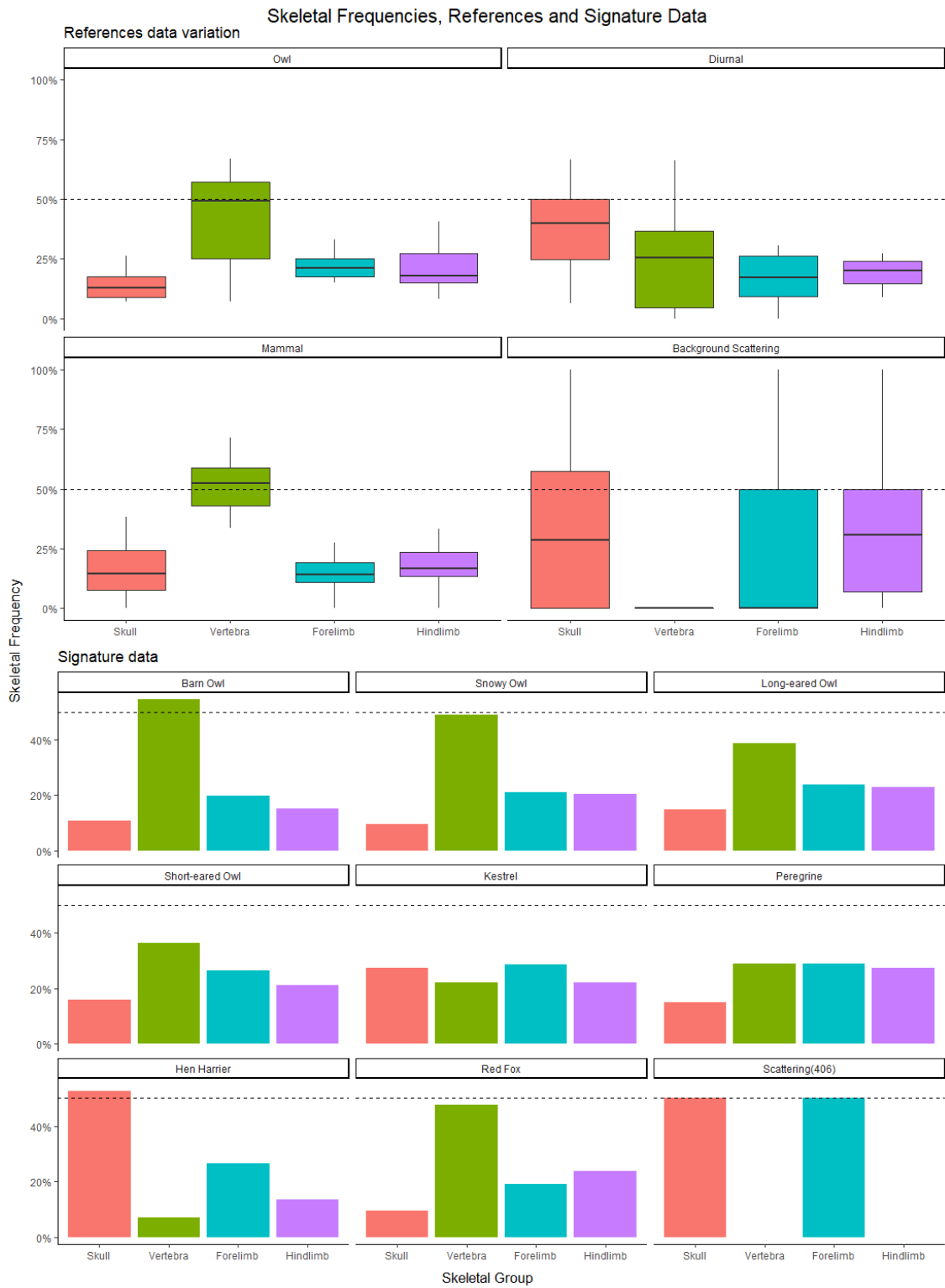


Fig. 4.20 - *Skeletal Frequencies* variation within the references data, shown for each category (upper plots), and frequencies obtained from signatures data (lower plots).

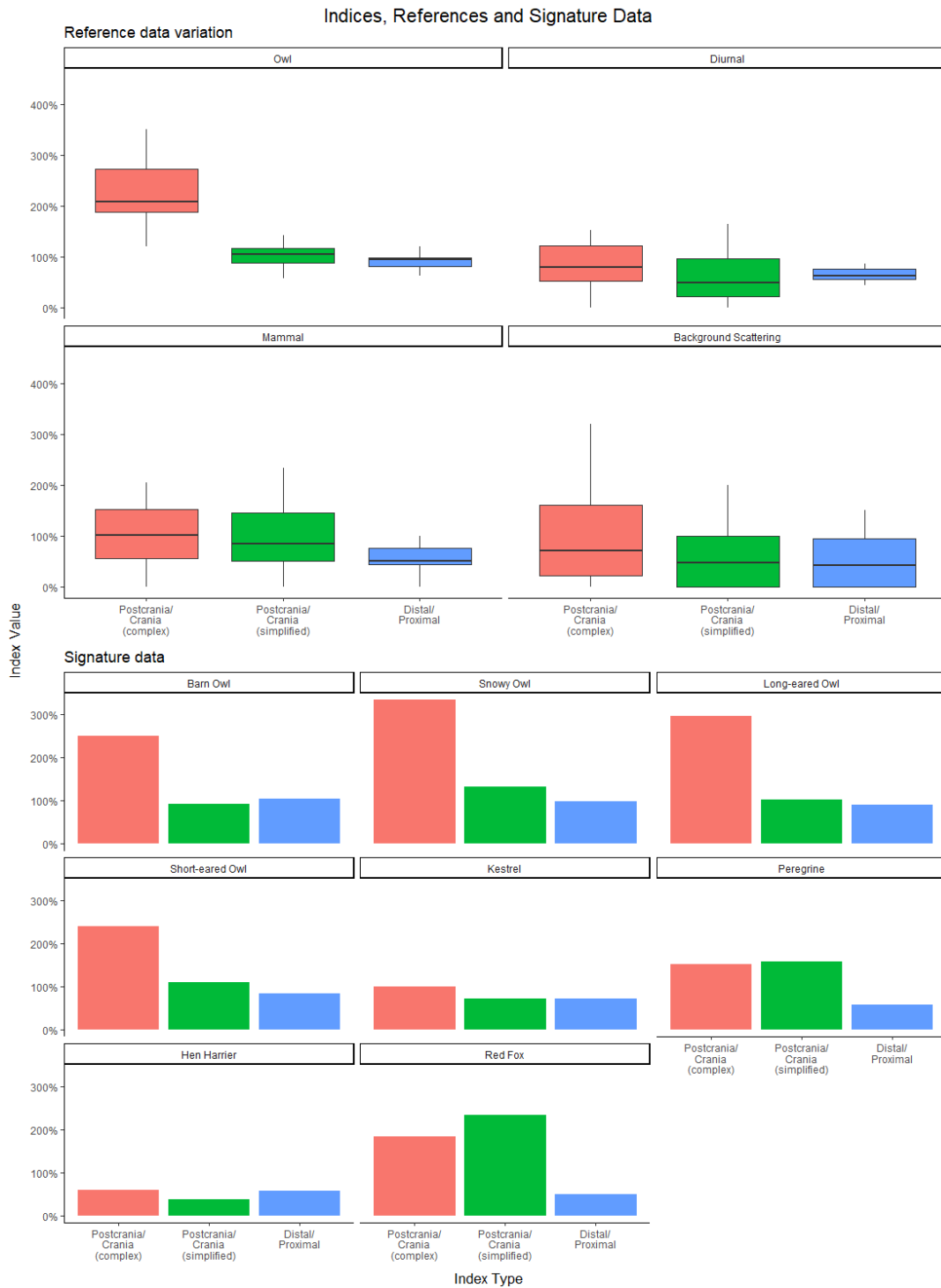


Fig. 4.21 – The variation of three skeletal indices (See **Chapter 3.3.4.**) within the references data , shown for each category (upper plots), and indices derived from utilized signatures (lower plots).

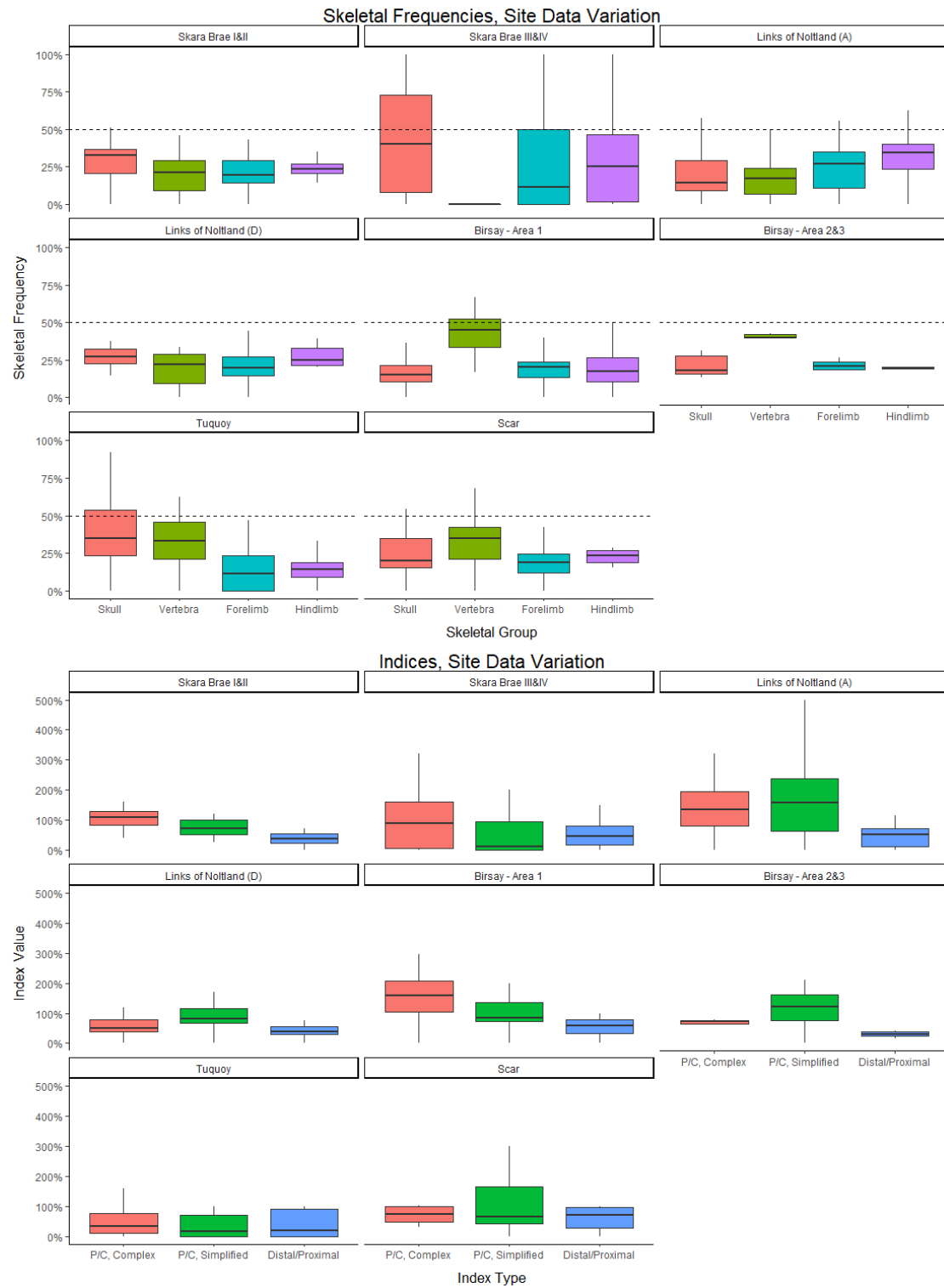


Fig. 4.22 – Variation of *Skeletal Frequencies* (upper plots) and three skeletal indices (lower plots) within and between the sites.

4.7. THE IMPACT OF TAPHONOMIC PROCESSES ON IDENTIFIABILITY

As indicated in **Chapter 4.3.**, Pearson correlation as well as χ^2 test was used in order to explore theoretical datasets simulating different stages of dispersal, using *Abundances* and *Fragmentation Percentages* data groups, with the intention of identifying depositors. In the case of *Abundances* correlations, dispersal showed a marked but predictable impact on assemblage identification attempts, with burial showing rather minor influence (Fig. 4.23). From the perspective of owl deposition theoretical datasets simulating partial and full dispersal, as well as one simulating the whole assemblage, shown to provide on average more homogenous dataset. Within the owl deposition correlations came out being on average stronger than in the case of the original references dataset. However, so did owl correlations with other groups, especially diurnals, which either created or expanded the already existing overlap of significant values between those groups. Interestingly, simulating burial resulted in partial mitigation of the issue. Still, observed changes in dispersal patterns have also applied to burial variations in themselves.

χ^2 results also did not show strong differences in the case of dispersal and burial (Fig. 4.24). The most visible difference was the shortening of obtained values ranges, with owls group interquartile range being below 90 in the case of any pattern variation. Additionally, homogenous cases were slightly more frequent, with some cases of homogeneity between owls and diurnal species patterns. However, the overall pattern of relationships between the non-homogenous results of groups did not differ from a pattern noted for original data.

Correlations of *Fragmentation Percentages* provided different results to abundances (Fig. 4.25), with χ^2 supporting results of correlations (Fig. 4.26). Instead of providing a higher quantity of strong correlations, theoretical datasets provided less of them, leading to all data clustering between positive and negative critical values. The situation was especially visible in the case of data simulating full dispersal, where all groups clustered within similar ranges, with only a minor part of an owl group showing strong positive values. In turn, the least affected were results from the data resembling whole assemblage. One could notice a minor overlap in the main clusters between owls and scattering, although the overlap happened only in the case of weak positive correlations. χ^2 results also differed from what was noted for *Abundances*, though the result was relatively similar. Values ranges shortened, though it did affect outliers and the upper end of value ranges, leaving homogenous results and lower ends of main values

clusters more or less the same. The owl group remained with the lowest values, but other groups showed values clustering within the same ranges. In the case of dispersed assemblage medians for diurnal, mammal and scattering were essentially the same.

However, even if internal consistency is present, as in the case of χ^2 , it does still affect accuracy when data from different stages of dispersal are compared. The accuracy obtained from comparing theoretical datasets to the original one (see Table 4.15) showed a marked decrease in general accuracy, especially for dispersal stages and *Abundances*. Similar results were also obtained when applying signatures to theoretical datasets (see Table 4.16), though with more variation between results. The reduction was most severe for four groups in the case of *Abundances*, which were reduced from 68% (original/intact dataset) to only 41% (surface partial dispersal) for correlations and from 53% to barely 20% for χ^2 tests. Similar though not as dramatic reduction can be also seen for two groups. The situation with buried patterns was more complex. Apart from the intact pattern/original dataset, correlations showed relatively higher accuracy to their surface counterparts. In the case of χ^2 , buried dispersal provided less accuracy than surface dispersal while also showing more incomputable cases, with partial dispersal being slightly more accurate for buried patterns. The least differences in general accuracy were noted for *Fragmentation Percentages*, where the accuracy of correlations lowered no more than 10% in worst cases, though χ^2 tests showed an almost as dramatic decrease as in the case of *Abundances*.

More problems with accuracy could be noted individually for specific groups. Owl *Abundances* have shown the most marked decrease in every case, starting from 88% in the case of intact dataset down to only 33%/0% in the case of full dispersal. In contrast, diurnal and mammal groups showed a varied pattern, with partial dispersal showing an increase in accuracy for the former and a decrease for the latter, with the situation in case of full dispersal reversed. In the case of *Fragmentation Percentages*, owls have also shown correlation results similar to *Abundances*, though with lesser loss of accuracy. The accuracy for mammals showed variation between dispersal stages, but diurnal group showed increased accuracy with heavier dispersals, up to 80%. In the case of χ^2 , owls also showed a visible pattern, repeated by mammals. However, diurnals were almost universally misidentified.

Trained classification models returned different accuracy depending on a dataset they were applied to (Table 4.17). For both *Abundances* and *Fragmentation Percentages*, the accuracy of both classifiers was the highest when applied to original (intact) datasets. For the abundances-based model, the nearest accuracy to original data (96%) was the intact-buried dataset (95%),

with misidentifications being essentially the same as in the case of original data. However, the whole assemblage dataset, with lower accuracy of 83%, provided far more erroneous identifications. Most of the new misidentifications were within the owls group, especially of species with skeletal alteration and digestion more impactful than barn owls, such e.g. tawny owls. Interestingly, some cases, like the little owl assemblage, were also identified as background scattering. Partially and fully dispersed datasets provided even lower accuracy values, between 60% (surface dispersal) to 54% (buried partial dispersal). The least number of positive identifications for owls were on a partial-surface stage, with only five positively identified as such. The remaining were identified mostly as diurnal/mammal species. Dominating identification in the case of full dispersal was scattering, with scattering misidentifications spread through both two other classes.

The fragmentation-based model did not fall with their accuracy as low as abundances-based, but nonetheless similar trends could be noticed. The lowest decrease was about 18% for dispersal, though it still left about 81% accuracy present. Misidentification in the case of a whole dataset encompassed only three mammal contexts identified as coming from owls. In turn, two dispersal stages showed a decrease in positive identifications as owls, though not to an extent seen in the case of abundances. Regarding diurnal/mammal group only four contexts were shown switching groups, with all but one switching “upward” (i.e. to owls).

In order to check how theoretical datasets affect the results of classifiers trained on them, the author utilized partial-buried dataset to train an *Abundances* classifier and partial dataset for a *Fragmentation Percentages* classifier. Both used the FDA method. Once trained classifiers were applied to sites data, with additional differentiation between levels (samples, contexts, combined), and compared with original classifiers results (Table 4.18). Differences between original and new classifiers results were immediately evident. In the case of *Abundances*, one could notice a larger number of samples as well as contexts being identified to owls, with scattering being less pronounced in the case of samples. In contrast, *Fragmentation* provided fewer owl identifications as well as marginally fewer for scattering, with diurnal/mammal class being more pronounced. However, most crucial were both classifiers results when combined into a single analytical tool. The original classifiers provided only six samples, including one representing a whole context, that both in *Abundances* and in *Fragmentation* could be identified as coming from owls. In all, only four contexts could be derived from owls. Classifiers trained on partial/burial dataset, despite differing changes to owl transformations depending on data used, provided more consistent answers, including 16 samples and nine contexts. In turn,

scattering was not as prevalent as in original classifiers results. Most common, however, were cases where one classifier identified a sample or context as a scattering, with another as a form of accumulation.

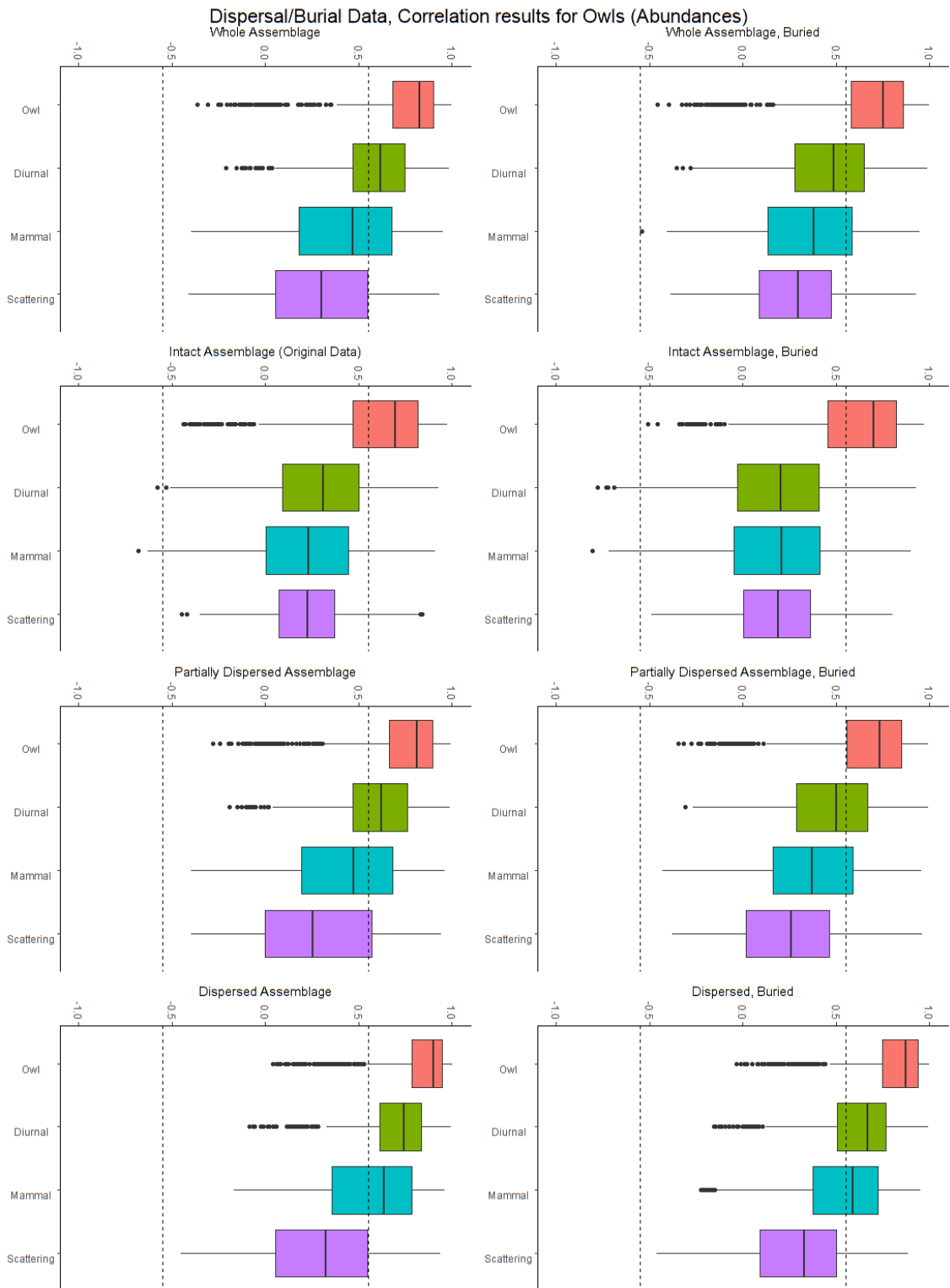


Fig. 4.23 – Results of Pearson correlation on *Abundances* for both original (i.e. “intact” pattern) and theoretical datasets from the perspective of an owl group. Theoretical datasets represent stages of dispersal, a potential impact of transition from biostratinomy to diagenesis (“burial” variations of each dispersal stage) as well as how a whole assemblage would look like when combining all dispersal stages together. See Table 3.13 for more information about how theoretical datasets were calculated.

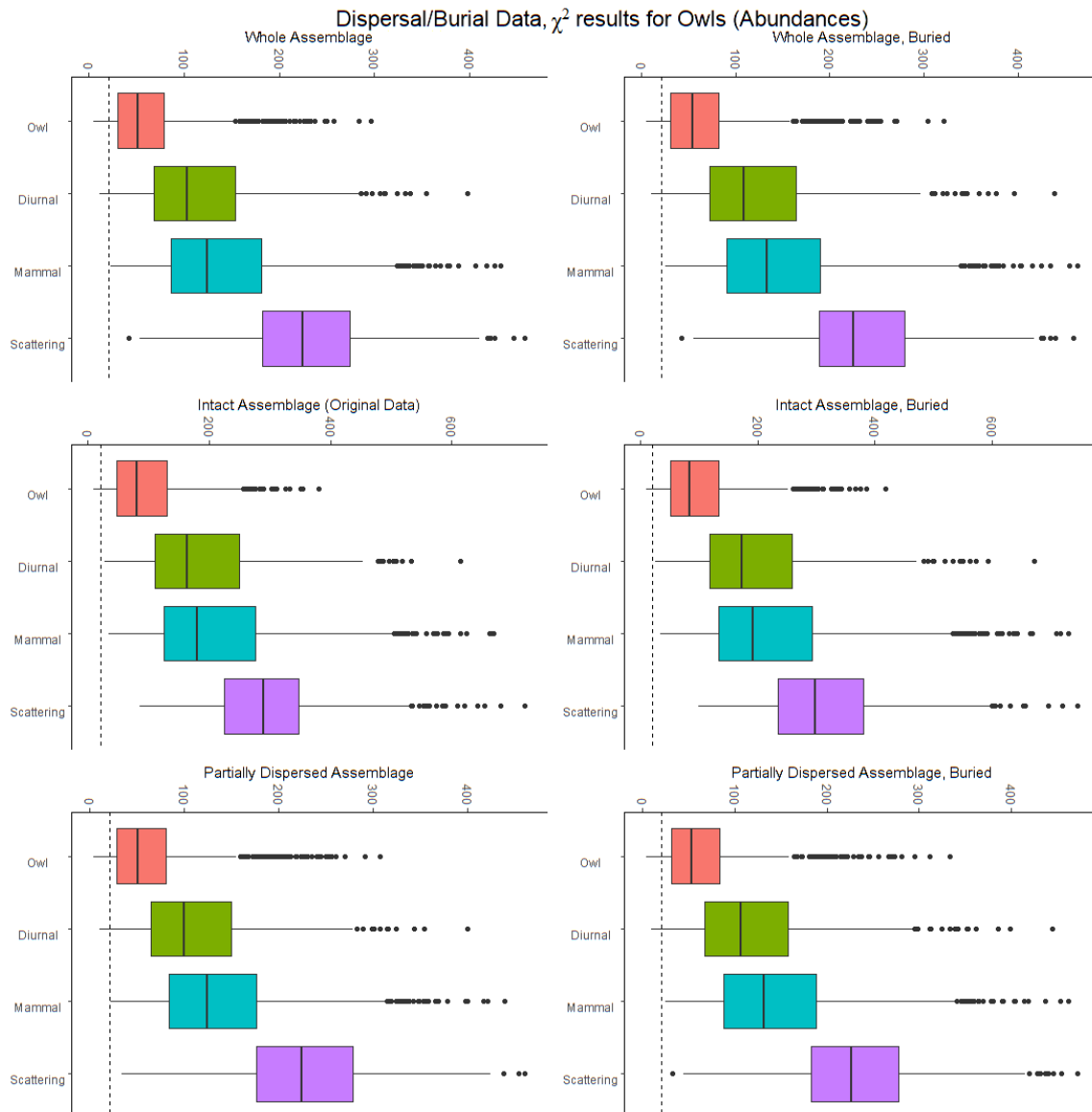


Fig. 4.24 – Results of χ^2 method application to *Abundances* for both original (i.e. “intact” pattern) and theoretical datasets from the perspective of an owl group. See Fig. 4.23 and Table 3.13 for further information.

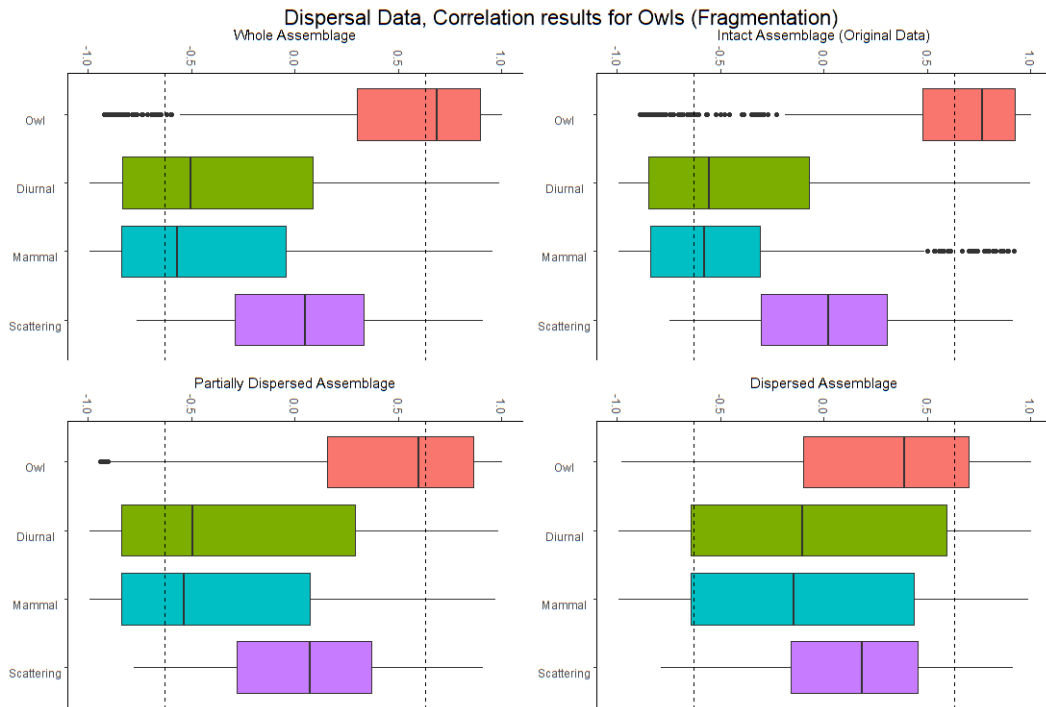


Fig. 4.25 – Results of Pearson correlation on *Fragmentation Percentages* for both original (i.e. “intact” pattern) and theoretical datasets from the perspective of an owl group. See Fig. 4.23 and Table 3.13 for further information.

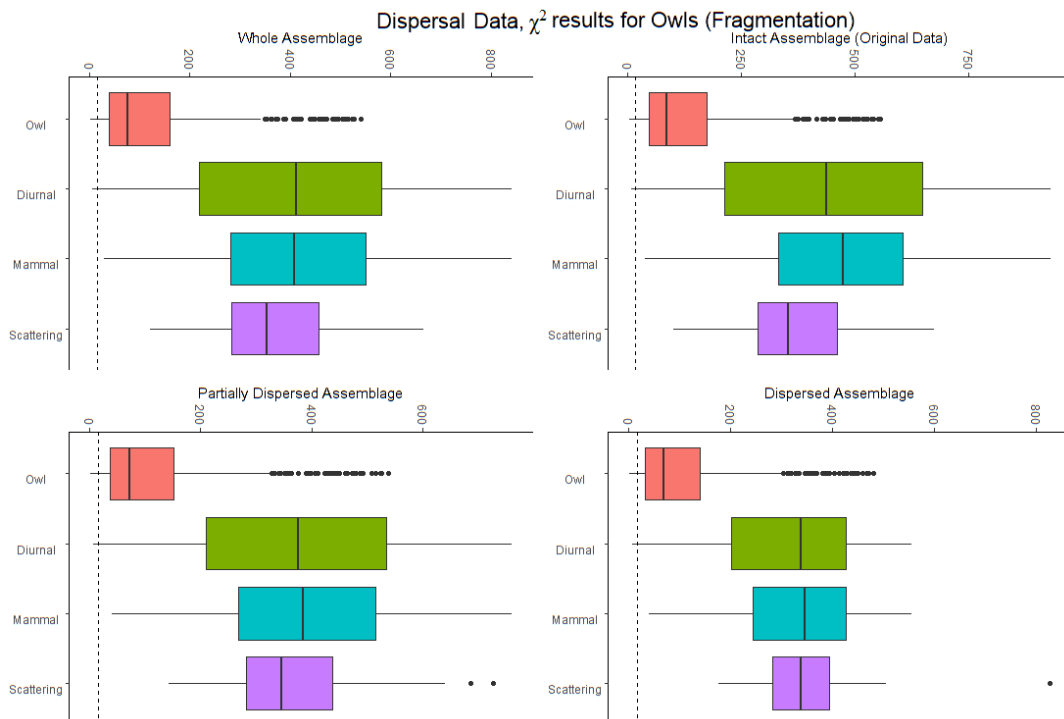


Fig. 4.26 – Results of χ^2 method application to *Fragmentation Percentages* for both original (i.e. “intact” pattern) and theoretical datasets from the perspective of an owl group. See Fig. 4.23 and Table 3.13 for further information.

Table 4.15 – Accuracy obtained using Pearson correlation and χ^2 square method, for both original (i.e. “intact” pattern) and theoretical datasets. Accuracy calculated separately for each main taphonomic group as well as jointly, for all four or reduced to two (Owl, Non-Owl) groups. For χ^2 missing/incomputable values, as % of accuracy, is also shown.

Data	Group	Abundances						Fragmentation Percentages					
		Surface			Buried								
		Corr (strong)	Corr (all)	χ^2 (missing)	Corr (strong)	Corr (all)	χ^2 (missing)	Corr (strong)	Corr (all)	χ^2 (missing)	Corr (strong)	Corr (all)	χ^2 (missing)
Whole Assemblage	Owl	61%	61%	36%	82%	82%	55%	85%	85%	0%	85%	91%	0%
	Diurnal	50%	50%	14%	29%	29%	14%	40%	40%	14%	40%	0%	0%
	Mammal	43%	43%	74%	39%	43%	65%	39%	39%	4%	39%	44%	0%
	Scattering	57%	57%	0%	57%	57%	0%	68%	73%	39%	68%	0%	27%
	General (4 cat.)	54%	54%	33%	57%	58%	38%	65%	67%	13%	65%	46%	7%
	General (2 cat.)	83%	83%	61%	88%	89%	66%	85%	86%		85%	57%	
Intact	Owl	88%	88%	88%	88%	88%	82%	91%	91%	0%	91%	91%	0%
	Diurnal	36%	36%	21%	29%	29%	29%	30%	30%	7%	30%	0%	0%
	Mammal	70%	70%	74%	57%	61%	83%	50%	50%	0%	50%	44%	6%
	Scattering	57%	57%	0%	57%	57%	0%	68%	73%	39%	68%	0%	27%
	General (4 cat.)	68%	68%	53%	63%	65%	54%	69%	70%	11%	69%	46%	8%
	General (2 cat.)	87%	87%	78%	85%	86%	78%	88%	89%		88%	58%	
Partial Dispersal	Owl	39%	39%	27%	52%	52%	42%	79%	79%	0%	79%	68%	0%
	Diurnal	43%	43%	14%	29%	29%	14%	50%	50%	14%	50%	0%	0%
	Mammal	26%	30%	61%	35%	39%	61%	39%	44%	4%	39%	39%	0%
	Scattering	57%	57%	0%	57%	57%	0%	68%	73%	39%	68%	0%	27%
	General (4 cat.)	41%	42%	27%	45%	46%	32%	64%	67%	13%	64%	36%	7%
	General (2 cat.)	73%	74%	57%	76%	77%	59%	82%	85%		82%	48%	
Full Dispersal	Owl	33%	33%	0%	48%	48%	0%	62%	62%	0%	62%	56%	0%
	Diurnal	21%	21%	14%	29%	29%	7%	80%	80%	21%	80%	10%	0%
	Mammal	61%	61%	74%	52%	52%	70%	44%	50%	4%	44%	22%	0%
	Scattering	57%	57%	0%	57%	57%	0%	68%	73%	39%	68%	0%	27%
	General (4 cat.)	44%	44%	20%	48%	48%	18%	62%	64%	14%	62%	29%	7%
	General (2 cat.)	72%	72%	51%	77%	77%	49%	76%	79%		76%	35%	

Table 4.16 – Accuracy obtained using Pearson correlation and χ^2 square method, between signatures data and original (i.e. “intact” pattern) and theoretical datasets. Table formatted similarly to Table 4.15.

Data	Group	Abundances						Fragmentation Percentages					
		Surface			Buried								
		Corr (strong)	Corr (all)	χ^2	Corr (strong)	Corr (all)	χ^2	Corr (strong)	Corr (all)	χ^2	Corr (strong)	Corr (all)	χ^2 (missing)
Whole Assemblage	Owl	33%	33%	30%	27%	42%	33%	82%	88%	47%	82%	88%	41%
	Diurnal	86%	93%	43%	36%	86%	36%	50%	50%	0%	50%	50%	10%
	Mammal	17%	30%	26%	30%	39%	39%	44%	44%	0%	44%	44%	11%
	Scattering	22%	26%	0%	96%	26%	0%	18%	18%	0%	18%	18%	100%
	General (4 cat.)	34%	40%	24%	46%	44%	27%	54%	56%	19%	54%	56%	46%
	General (2 cat.)	61%	69%	35%		72%	38%	70%	82%	21%	70%	82%	
Intact	Owl	76%	76%	61%	21%	85%	64%	91%	91%	32%	91%	91%	62%
	Diurnal	71%	79%	57%	29%	71%	57%	50%	50%	10%	50%	50%	10%
	Mammal	30%	35%	26%	17%	35%	30%	33%	44%	0%	33%	44%	11%
	Scattering	22%	26%	0%	96%	22%	0%	18%	18%	0%	18%	18%	100%
	General (4 cat.)	51%	54%	37%	40%	55%	39%	55%	57%	14%	55%	57%	55%
	General (2 cat.)	73%	80%	48%		75%	49%	74%	86%	17%	74%	86%	
Partial Dispersal	Owl	15%	18%	21%	27%	21%	18%	76%	79%	85%	76%	79%	0%
	Diurnal	86%	100%	21%	36%	86%	29%	40%	40%	0%	40%	40%	0%
	Mammal	9%	17%	30%	30%	13%	35%	56%	56%	0%	56%	56%	0%
	Scattering	22%	26%	0%	96%	22%	0%	18%	18%	0%	18%	18%	100%
	General (4 cat.)	26%	32%	18%	46%	29%	19%	52%	54%	35%	52%	54%	26%
	General (2 cat.)	53%	63%	33%		54%	32%	68%	79%	38%	68%	79%	
Full Dispersal	Owl	27%	27%	21%	61%	36%	21%	59%	62%	85%	59%	62%	0%
	Diurnal	93%	100%	0%	43%	79%	0%	30%	30%	10%	30%	30%	0%
	Mammal	17%	26%	52%	35%	26%	61%	83%	83%	0%	83%	83%	0%
	Scattering	22%	26%	0%	96%	22%	0%	18%	18%	0%	18%	18%	100%
	General (4 cat.)	33%	38%	20%	60%	37%	23%	50%	51%	36%	50%	51%	26%
	General (2 cat.)	60%	67%	25%		61%	27%	62%	74%	37%	62%	74%	

Table 4.17 – Results of the application of trained classifiers (on original data) to theoretical datasets representing stages of dispersal as well as their transition to burial. See Table 3.13 for further information on how the datasets were calculated.

Data	Original Class.	Whole Assembl.	Whole Assembl. (Buried)	Intact (Orig. Pred.)	Predictions					
					Intact (Buried)	Partial Dispers.	Partial Dispers. (Buried)	Full Dispersal	Full Dispersal (Buried)	
Abundances	Owl	33	23	27	32	32	7	11	17	17
	Diurnal/Mammal	37	35	31	37	36	42	31	17	13
	Scattering	23	35	35	24	25	44	51	59	63
	Accuracy		82.8%	82.8%	95.7%	94.6%	54.8%	53.8%	60.2%	57.0%
Fragmentation Percentages	Owl	34	37		34		31		22	
	Diurnal/Mammal	28	25		27		31		39	
	Scattering	22	22		23		22		23	
	Accuracy		96.4%		98.8%		89.3%		81.0%	

Table 4.18 – Results of the application of differently trained classifiers to the original site data, with the consideration of different data levels. Original models were trained on the references data back in **Chapter 4.4.**, with new models being trained on the partial-burial theoretical dataset (*Abundances*) and the partial theoretical dataset (*Fragmentation*). See Table 3.13 for further information on how the datasets were calculated.

Data	Group	Original Model			Model Based on Partial Transformation		
		Samples	Contexts	Combined	Samples	Contexts	Combined
<i>Abundances</i>	Scattering	666	139	324	338	68	176
	Diurnal/Mammal	218	80	120	458	104	208
	Owl	32	18	22	120	65	82
<i>Fragmentation Percentages</i>	Scattering	638	100	291	633	97	286
	Diurnal/Mammal	202	104	126	239	123	156
	Owl	76	33	49	44	17	24
Final Result	Scattering	508	79	244	296	53	152
	Contested	288	81	127	379	59	158
	Accumulation	37	31	38	87	57	69
	Diurnal/Mammal	77	42	52	138	59	77
	Owl	6	4	5	16	9	10

4.8. MEASUREMENTS, SKELETAL FUSION AND WEAR

Quantities of metrical data retrieved for Orkney voles exhibited strong biases towards assemblage size and/or retrieval method as well as site taxonomic composition. Complete and measurable vole long bones as well as mandibles preserved enough to retrieve tooth row length were predominantly found within Skara Brae and Links of Noltland assemblages (Table 4.19). Both sites were fully sieved and contained mostly (Skara Brae) up to almost exclusively (Links of Noltland) Orkney voles. Additionally, mean long bone measurements representativeness was usually higher for those two sites, with the lowest for Links of Noltland Trench A (9%) up to 35% for Skara Brae Trench IV. Sampled sites provided far fewer measurements though representativeness differed between sites. Tuquoy provided the least representative data, on average covering only 3.6% of established vole MNI. Similarly, Birsay Bay did not provide many representative data, with Area 1, where voles were a minority, providing at best 13 measurements of a single element. However, Bu Broch provided comparable representativeness to Skara Brae Trench IV while Scar showed slightly better percentages than Links of Noltland Trench A. Both cases were most likely due to low MNI values, leading to every NISP strongly affecting MNI and skeletal completeness. (e.g. MNI/NISP correlation for Bu Broch: $n = 9$, $\rho = 0.96$, $p = <0.001$).

The impact of retrieval method and taxonomic composition was also noted in the case of murid bone measurements (Table 4.20) but with bigger stress put on species presence and possible relation with differential bone preservation. Most measurements were provided by a site where murids were beyond half of MNI, Birsay Bay Area 1, with the second site being whole-sieved Skara Brae. Sampled sites such as Tuquoy or Scar almost did not provide any intact remains. Bu Broch contained only field mice femora, bones both bigger and sturdier than humeri. However, representativeness was lower than in the case of Orkney voles. Birsay, despite an abundance of murid individuals, had material covering on average only 10% of MNI. Skara Brae showed a higher average due to an overrepresentation of intact left femoral bones. However, most of Skara Brae humeri attributable to field mice were broken, with less than ten on either side barely representing 10% of individuals.

Additionally, the major issue was identified affecting juvenile and murid bones, possibly impacting the usage of complete bones as the means of age estimation for a wider population. The most obvious issue was that features of humeral and femoral bones distinct enough to be

used for species identification were either related to epiphyses or developing no earlier than in sub-adults. In the case of bigger taxonomic diversity only a few juvenile bones could be successfully identified up to species or species groups, resulting in the majority being labelled as unidentified (see Birsay in Table 4.21). Moreover, differentiating between field and house mice bones proved to be impossible for most limb bones, especially humeri. Femora could occasionally be differentiated between those two species but full fusion without severe taphonomic alteration was required. In a result, in order to study measurements from Tuquoy, Birsay and Scar sites, the only possibility was to have all murid bones pooled together.

However, even in the case of relatively high MNI representativeness, a bias in fusion representativeness was noted. Skara Brae Trench IV showed the highest average, as mentioned previously 35%, but it meant about 65% being fragmented remains, often containing epiphyses in different stages of development/fusion, 2% of all intact specimens and three MNI in complete bones. In the case of proximal humeral epiphysis only four complete bones showed their full fusion. However, among all 273 recorded proximal humeri about 31 exhibited proper epiphyseal fusion, with 20 being attributed to voles, two for field mice and nine unidentified. It was about 11% of all scores and at least 16 MNI, in the case of only vole identification 8% and minimum represented MNI of 10. A similar situation happened with early fusing epiphyses, where among two examples of no distal humerus epiphyseal fusion, only one was represented by a complete specimen. However, the situation was more visible within proximal femur fusion, where thirteen proximal femora showed no fusion but only four complete could be taken into account by the metric-fusion method.

Some patterns in Orkney vole size reduction over time can be inferred from metric data (see Fig. 4.27) but low representativeness, a small number of fused bones as well as differences in sample sizes rendered the analysis doubtful. Size reduction was especially visible in the case of mandibular TRL (tooth row length). Modern Orkney measurements were far lower than Neolithic data, with later sites showing middle values. Interestingly, Links of Noltland showed lower values to Skara Brae, possibly exhibiting differences between isles in roughly the same period. However, Bu Broch, Tuquoy, Scar and Birsay barely provided viable measurements and could not be considered as representative of their respective periods. In turn, long bone measurements were mostly coming from still growing specimens, resulting often in more than 50% size difference between the biggest and smallest bones in a group. Some tendency towards size reduction over time was noted in the case of humeri, with Neolithic and modern data once again showing different ranges. However, there was a visible overlap between clusters on both

sides. Femora measurements showed minimal differences between Neolithic and modern data but also exhibited more extreme values in the case of other sites, especially very high values from Scar.

Murid data analysis suffered from many biases, especially the small number of measurements, lack of comparable data and multiple species analysed at once (Fig. 4.28). The author could not obtain modern data from Orkney samples and had to use field mice data from Guernsey for comparison. Interestingly, Guernsey data showed strong similarities with sites showing the presence of only field mice, with combined field and house mice populations showing lower values. It was especially visible in the case of Birsay, where house mice were most common, alongside many juvenile bones. However, both humeri and femora measurements could not be considered as representative due to the relatively minuscule number of measurements.

The epiphyseal fusion data obtained from all limb bones showed on average higher representativeness than complete bones (Table 4.22). On average about 61% of a specific bone NISP was represented by epiphyses resulting in about 24% of general site MNI being represented. In some cases, simple fusion scoring representativeness was far higher than averages would suggest. For example, in Skara Brae's case Trench I representativeness was 49% for distal and 35% for proximal humeri, with Trench IV showing 77% and 56%. It is a far better outcome than when only studying intact bones (Tables 4.19-21), where on average only 22% to 40% MNI could be represented. Additionally, fusion data could be obtained for all studied areas, with fragmentation being less impactful on analysis.

However, the number of observations as well as representativeness differed across sites in a manner similar, though not equal to, the pattern already seen in the case of complete bones. The greatest number of observations, alongside high representativeness, was noted in the case of fully sieved Skara Brae and Links of Noltland. Trench IV provided almost 1840 observations, with the highest average representativeness for all sites being 47% of MNI. However, Trench III showed only 12%, possibly reflecting a very low number of finds in general and the dispersal nature of this part of the Skara Brae site. In turn, sampled sites showed strong differences between each other. Bu Broch and Birsay Bay Area 1 provided similar representativeness to Skara Brae Trench I and II (26/24%). additionally, Area 1 showed quite a high number of observations, over 1000. Tuquoy showed the lowest average representativeness, about 8.3%, but still provided about 600 observations. Scar and Birsay Bay Areas 2 and 3 showed middle values of about 16 to 18%, with the best being 258 observations and worst 24.

Problems with analysing fusion data stemmed mostly from the presence of bone fragments containing epiphyses but not identifiable up to species. The problem with unidentified remains is easily explained while looking at Trench I from Skara Brae (Table 4.23) where one-fourth of observations were unidentified bones. Average representativeness for specific species was lower than one for the whole assemblage, especially in the case of the far less frequent wood mice. However, unidentified bone quantities were more or less in synchronization with vole bones, suggesting the majority of them coming from this species. However, for more taxonomically diverse sites (Tuquoy, Birsay, Scar) unidentified bones barely aligned with any taxa, resulting in possible bias when analysed separately. The already mentioned problem with identifying murid bones created another layer of problems as field and house mice could only be analysed jointly.

Molar wear scoring proved to return the most representative and easiest to interpret data of each site's mouse population (Table 4.24). The house mouse, in particular, showed strong representation, in the worst case 86% (Scar) and in the best comprising all MNI (Birsay Bay Area 2). For field mice, full coverage of MNI was also obtained (Birsay Bay Area 1 & 2) but many values obtained were on average lower than in the case of house mice. Lower values were present in both sampled and fully sieved sites. However, even in the worst case (Bu Broch – 27%), representativeness was better than in the case of other methods utilized. Additionally, due to distinct morphological changes of both mouse species' teeth, identification to specific species was almost guaranteed.

The only issue of molar wear scoring, apart from applicability to only specific species, was the possible bias created during the approximation of score from multiple teeth. The number of raw scores used to establish the age of one MNI ranged from 1, one score per one MNI, up to over 4. A lower number of scores usually meant a lower ratio, possibly showing a strong connection with the number of bones retrieved in overall. Birsay Area 1 provided the majority of *Mus* and many *Apodemus* scores, resulting in the highest scores to MNI ratio. On the other hand, one to one ratio in the case of Bu Broch was due to only three skull fragments with scorable teeth being found. However, extrapolation from four or more scores may result in incorrect results, especially when scores were not including first molars. In some cases, scores were differing to the extent that the author had to assume scores came from different individuals, thus recalculating MNI for the context or sample.

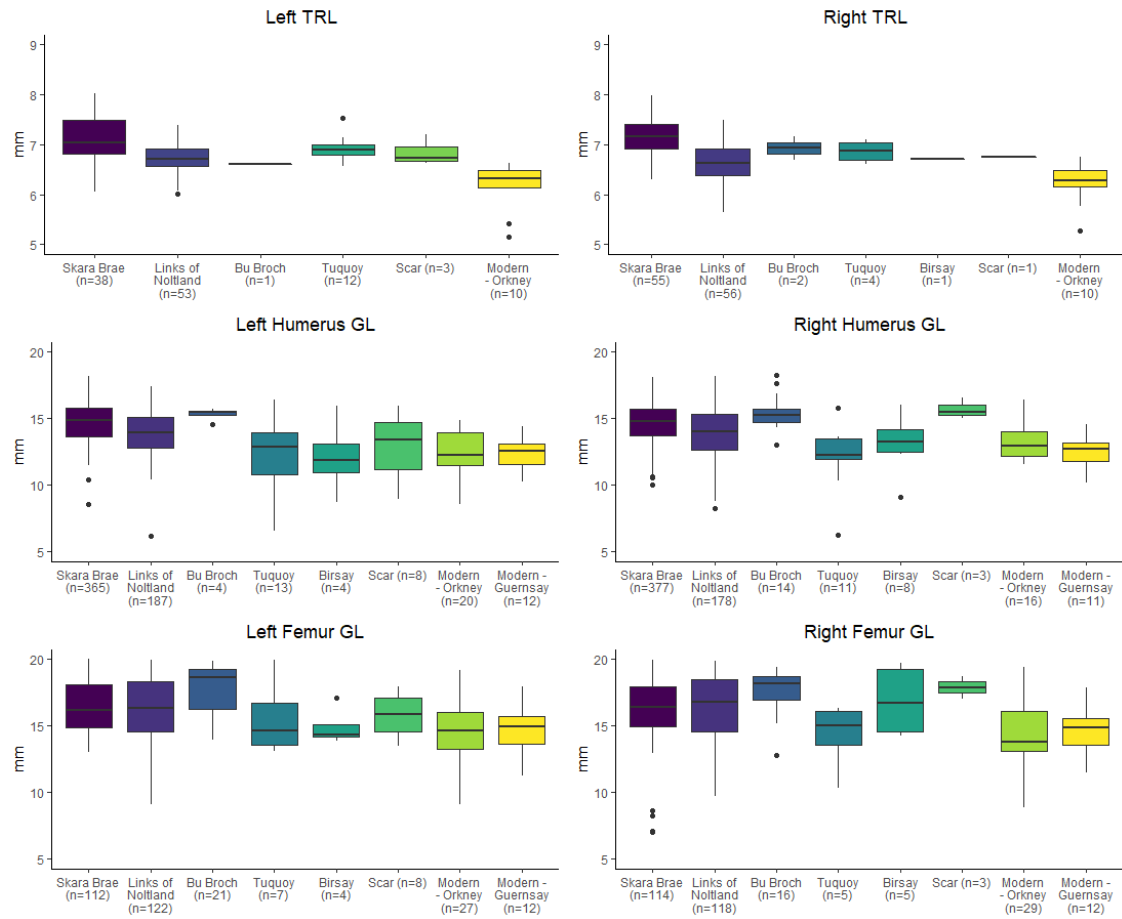


Fig. 4.27 – Boxplots representing Orkney vole measurements from archaeological sites as well as modern samples.

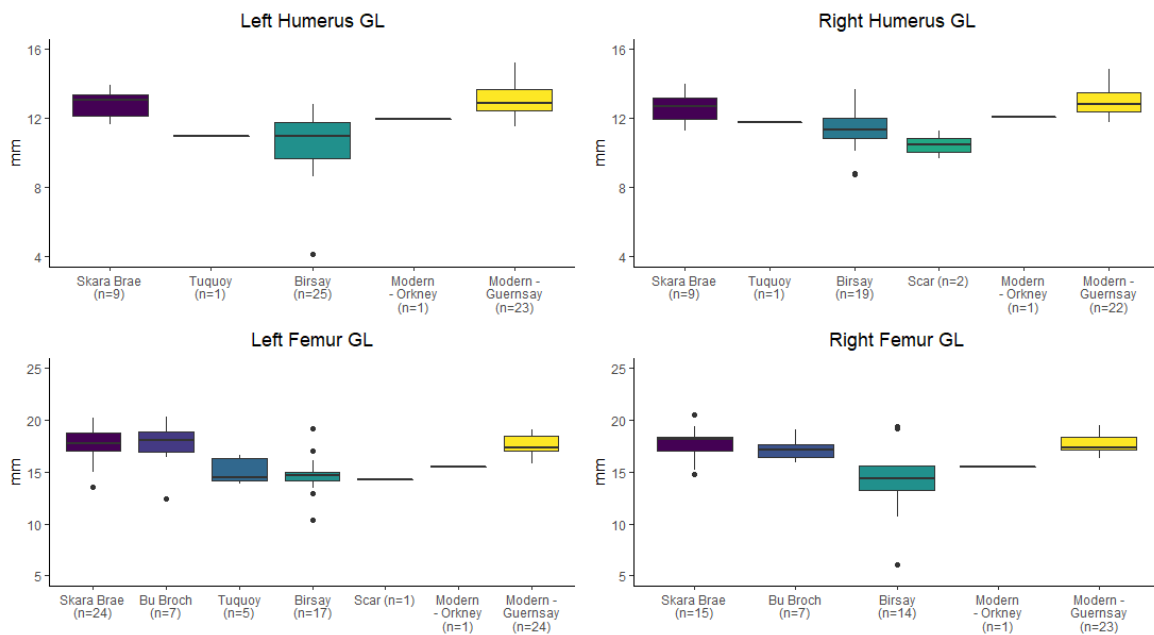


Fig. 4.28 – Boxplots representing field and house mouse measurements from archaeological sites as well as modern samples.

Table 4.19 (A), 4.20 (B) and 4.21 (C) – Tables summing measurements taken from each site. Length measurements were divided into tables in relation to species (A – voles, B – murids, C – unidentified and rats), with further division through bone or features measured (mandibular tooth row, humerus greatest length, femur greatest length), side and state of epiphyseal fusion (unfused, partially fused, fully fused). Apart from the number of measurements percentile representativeness of MNI was included.

(A) Metric data, Microtus																											
Links of Nottland				Links of Nottland (D)				Bu Broch				Tuquoy				Bisay Area 1				Bisay Area 2				Scar		Avg. %MNI	
Skara Brae (I)		Skara Brae (IV)		(A)		(D)		Bu Broch		Tuquoy		Bisay Area 1		Bisay Area 2		Scar		Avg. %MNI									
Material Type	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI					
TRL	Right	55	4.40%	0	0.00%	36	3.65%	20	5.12%	2	3.51%	4	1.59%	1	1.52%	0	0.00%	1	1.79%	2.40%							
	Left	39	3.12%	0	0.00%	27	2.74%	26	6.65%	1	1.75%	12	4.78%	0	0.00%	0	0.00%	4	7.14%	2.91%							
Right Partially Fused	Unfused	0	0.00%	0	0.00%	3	0.30%	0	0.00%	0	0.00%	1	0.40%	0	0.00%	0	0.00%	0	0.00%	0.08%							
	Partially Fused	244	19.54%	95	40.77%	101	10.23%	56	14.32%	12	21.05%	9	3.59%	3	4.55%	3	8.33%	3	5.36%	14.19%							
	Σ	37	2.96%	1	0.43%	13	1.32%	5	1.28%	2	3.51%	2	3.51%	1	1.52%	1	2.78%	0	0.00%	1.58%							
Humerus GL	Unfused	281	22.50%	96	41.20%	117	11.85%	61	15.60%	14	24.56%	11	4.38%	4	6.06%	4	11.11%	3	5.36%	15.85%							
	Partially Fused	0	0.00%	1	0.43%	0	0.00%	1	0.26%	0	0.00%	1	0.40%	0	0.00%	0	0.00%	0	0.00%	0.12%							
Left Partially Fused	Unfused	243	19.46%	82	35.19%	105	10.64%	71	18.16%	4	7.02%	11	4.38%	1	1.52%	2	5.66%	7	12.50%	12.71%							
	Partially Fused	3	2.72%	3	1.29%	7	0.71%	3	0.77%	0	0.00%	1	0.40%	0	0.00%	1	2.78%	1	1.79%	1.16%							
	Σ	277	22.18%	86	36.91%	112	11.35%	75	19.18%	4	7.02%	13	5.18%	1	1.52%	3	8.33%	8	14.29%	13.99%							
Right Partially Fused	Unfused	1	0.08%	4	1.72%	0	0.00%	7	1.79%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0.40%							
	Partially Fused	34	2.72%	67	28.76%	56	5.67%	41	10.49%	16	28.07%	5	1.99%	4	6.06%	0	0.00%	3	5.36%	9.90%							
	Σ	7	0.56%	1	0.43%	7	0.71%	7	1.79%	0	0.00%	0	0.00%	1	1.52%	0	0.00%	0	0.00%	0.56%							
Femur GL	Unfused	42	3.38%	72	30.90%	63	6.38%	55	14.07%	16	28.07%	5	1.99%	5	7.58%	0	0.00%	3	5.36%	10.86%							
	Partially Fused	0	0.00%	0	0.00%	0	0.00%	4	1.02%	0	0.00%	0	0.00%	1	1.52%	0	0.00%	0	0.00%	0.28%							
	Σ	35	2.80%	72	30.90%	50	5.07%	50	12.79%	18	31.58%	6	2.39%	2	3.03%	1	2.78%	6	10.71%	11.34%							
Left Partially Fused	Unfused	3	0.24%	2	0.86%	12	1.22%	6	1.53%	3	5.26%	1	0.40%	0	0.00%	0	0.00%	2	3.57%	1.45%							
	Partially Fused	38	3.04%	74	31.76%	62	6.28%	60	15.35%	21	36.84%	7	2.79%	3	4.55%	1	2.78%	8	14.29%	13.07%							
	Σ	12.77%	35.19%	8.97%	16.05%	24.12%	3.59%	4.92%	5.56%	9.82%	13.44%																
Avg. (Postcranial)																											
(B) Metric data, Murids																											
Links of Nottland				Links of Nottland (D)				Bu Broch				Tuquoy				Bisay Area 1				Bisay Area 2				Scar		Avg. %MNI	
Material Type	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI	Obtained	%MNI					
Right Partially Fused	Unfused	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0.00%						
	Partially Fused	5	5.26%	0	0.00%	0	0.00%	11	6.43%	1	2.13%	2	10.53%	4.06%	0.00%												
Humerus GL	Unfused	4	4.21%	0	0.00%	1	0.80%	7	4.09%	0	0.00%	0	0.00%	1.52%	0.00%												
	Partially Fused	9	9.47%	0	0.00%	1	0.80%	18	10.53%	1	2.13%	2	10.53%	5.58%	0.00%												
	Σ	0	0.00%	0	0.00%	0	0.00%	2	1.17%	0	0.00%	0	0.00%	0.00%	0.00%												
Left Partially Fused	Unfused	6	6.32%	0	0.00%	1	0.80%	13	7.60%	2	4.26%	0	0.00%	3.16%	0.00%												
	Partially Fused	3	3.16%	0	0.00%	8	4.68%	0	0.00%	0	0.00%	0	0.00%	1.31%	0.00%												
	Σ	9	9.47%	0	0.00%	1	0.80%	23	13.45%	2	4.26%	0	0.00%	4.66%	0.00%												
Right Partially Fused	Unfused	1	1.05%	1	9.09%	2	1.17%	2	1.17%	0	0.00%	0	0.00%	1.89%	0.00%												
	Partially Fused	10	10.53%	4	36.36%	3	2.40%	6	3.51%	0	0.00%	0	0.00%	8.80%	0.00%												
	Σ	4	4.21%	2	18.18%	2	1.60%	5	2.92%	1	2.13%	0	0.00%	4.84%	0.00%												
Femur GL	Unfused	15	15.79%	7	63.64%	5	4.00%	13	7.60%	1	2.13%	0	0.00%	15.53%	0.00%												
	Partially Fused	0	0.00%	0	0.00%	0	0.00%	2	1.17%	0	0.00%	0	0.00%	0.00%	0.00%												
	Σ	19	20.00%	7	63.64%	0	0.00%	11	6.43%	0	0.00%	1	5.26%	15.89%	0.00%												
Left Partially Fused	Unfused	5	5.26%	0	0.00%	0	0.00%	4	2.34%	0	0.00%	0	0.00%	1.27%	0.00%												
	Partially Fused	24	25.26%	7	63.64%	0	0.00%	17	9.94%	0	0.00%	1	5.26%	17.35%	0.00%												
	Σ	15.00%	31.82%	1.40%	10.38%	2.13%	3.95%	17.35%	0.00%																		
Avg.																											

Table 4.22 – Table summarizing recorded fusion for long bones (humerus, ulna, femur, tibia). Each case is represented by the number of fusion states recorded (fused + unfused cases), percentile relation to all bones of the same type (fusion no./bone NISP * 100) and general representativeness of MNI (fusion no./MNI * 2[number of epiphyses of this type in skeleton] * 100). For summaries and averages see edges of the table.

Sites	Values	Humerus distal	Tibia distal	Ulna distal	Femur proximal	Ulna proximal	Humerus proximal	Femur distal	Tibia proximal	Σ & avg.%
Skara Brae Trench I	No.	1294	183	305	1270	580	941	519	487	5579
	%NISP	83.16%	25.81%	43.63%	87.83%	82.98%	60.48%	35.89%	68.69%	61.06%
	%MNI	48.10%	6.80%	11.34%	47.21%	21.56%	34.98%	19.29%	18.10%	25.92%
Skara Brae Trench II	No.	58	22	8	62	17	52	38	33	290
	%NISP	77.33%	48.89%	30.77%	86.11%	65.38%	69.33%	52.78%	73.33%	62.99%
	%MNI	39.19%	14.86%	5.41%	41.89%	11.49%	35.14%	25.68%	22.30%	24.49%
Skara Brae Trench III	No.	7	6	2	8	2	7	8	7	47
	%NISP	100.00%	60.00%	66.67%	72.73%	66.67%	100.00%	72.73%	70.00%	76.10%
	%MNI	14.00%	12.00%	4.00%	16.00%	4.00%	14.00%	16.00%	14.00%	11.75%
Skara Brae Trench IV	No.	377	137	48	366	167	273	242	230	1840
	%NISP	82.86%	45.07%	25.67%	98.92%	89.30%	60.00%	65.41%	75.66%	67.86%
	%MNI	77.25%	28.07%	9.84%	75.00%	34.22%	55.94%	49.59%	47.13%	47.13%
Links of Noltland A	No.	1635	1360	308	1308	1035	1174	1033	700	8553
	%NISP	60.85%	60.47%	26.26%	58.31%	88.24%	43.69%	46.05%	31.12%	51.87%
	%MNI	48.81%	40.60%	9.19%	39.04%	30.90%	35.04%	30.84%	20.90%	31.91%
Links of Noltland D	No.	333	164	54	350	163	236	190	173	1663
	%NISP	76.20%	53.59%	28.42%	83.14%	85.79%	54.00%	45.13%	56.54%	60.35%
	%MNI	42.05%	20.71%	6.82%	44.19%	20.58%	29.80%	23.99%	21.84%	26.25%
Bu Broch	No.	22	65	0	71	0	21	64	54	297
	%NISP	100.00%	87.84%	0.00%	93.42%	0.00%	95.45%	84.21%	72.97%	66.74%
	%MNI	15.94%	47.10%	0.00%	51.45%	0.00%	15.22%	46.38%	39.13%	26.90%
Tuquoy	No.	143	59	22	157	65	66	53	51	616
	%NISP	83.14%	59.00%	28.57%	81.77%	84.42%	38.37%	27.60%	51.00%	56.73%
	%MNI	15.38%	6.34%	2.37%	16.88%	6.99%	7.10%	5.70%	5.48%	8.28%
Birsay Area 1	No.	203	134	71	219	134	133	101	99	1094
	%NISP	80.56%	69.07%	43.29%	83.27%	81.71%	52.78%	38.40%	51.03%	62.51%
	%MNI	39.04%	25.77%	13.65%	42.12%	25.77%	25.58%	19.42%	19.04%	26.30%
Birsay Area 2	No.	62	13	16	66	33	44	15	9	258
	%NISP	65.96%	40.63%	34.04%	83.54%	70.21%	46.81%	18.99%	28.13%	48.54%
	%MNI	36.05%	7.56%	9.30%	38.37%	19.19%	25.58%	8.72%	5.23%	18.75%
Birsay Area 3	No.	7	1	1	9	0	3	1	2	24
	%NISP	87.50%	33.33%	100.00%	81.82%	0.00%	37.50%	9.09%	66.67%	51.99%
	%MNI	43.75%	6.25%	6.25%	56.25%	0.00%	18.75%	6.25%	12.50%	18.75%
Scar	No.	29	29	18	37	26	22	30	27	218
	%NISP	74.36%	61.70%	54.55%	72.55%	78.79%	56.41%	58.82%	57.45%	64.33%
	%MNI	16.86%	16.86%	10.47%	21.51%	15.12%	12.79%	17.44%	15.70%	15.84%
Avg.	%NISP	80.99%	53.78%	40.16%	81.95%	66.12%	59.57%	46.26%	58.55%	60.92%
	%MNI	36.37%	19.41%	7.39%	40.83%	15.82%	25.83%	22.44%	20.11%	23.52%

Table 4.23 (A) and 4.24 (B): A: Summary of recorded fusion for long bones from Skara Brae Trench I, with a detailed breakup of species classes (Orkney vole, field mouse, unidentified specimen). B: Summary of wear data scores for all applicable sites, divided by species (Field/ house mouse). Data presented included number of raw scores (1 score = 1 NISP indicating that score), number of scores per one individual, number of raw scores per one scored MNI, number of raw scores per all MNI, MNI per each wear stage, the sum of scored MNI and percentile expression of the scored MNI representativeness.

(A) SKARA BRAE - TRENCH I																					
Trench I, classes	Values		Humerus		Tibia		Ulna		Femur		Ulna		Humerus		Femur		Tibia		Σ & avg.%		
	Overall	No.	distal	%MNI	1294	183	305	1270	580	941	519	487	18.10%	5579	25.92%	3885	19.44%	242	15.92%		
			48.10%			6.80%	11.34%	47.21%	21.56%	34.98%	19.29%	18.10%									
	Microtus	No.	1147	%MNI	45.92%	79	110	773	382	791	205	398	15.93%	3885	19.44%	242	15.92%	1452	9075.00%		
	Apodemus	No.	37	%MNI	19.47%	23	3	65	6	31	42	35	15.93%	3885	19.44%	242	15.92%	1452	9075.00%		
	Unidentified	No.	110	%MNI	5500.00%	81	192	432	192	119	272	54	2700.00%	1452	9075.00%	1452	9075.00%	1452	9075.00%		
	(MNI = 1)	%MNI																			
(B) MURID MOLAR WEAR																					
Species	Site	No. Raw scores	avg. scores per est.	MNI	avg. Scores per all MNI	None	Wear 1	Wear 2	Wear 3	Wear 4	Wear 5	Σ	as % of MNI								
Apodemus	Skara Brae (trench I)	98	2.00	1.03	0.27	3	10	15	12	7	2	49	51.58%								
	Bu Broch	3	1.00	0.27	0	0	1	2	0	0	0	3	27.27%								
	Tuquoy	74	2.31	1.21	1	18	5	5	3	0	0	32	52.46%								
	Birsay (Area 1)	109	2.66	2.66	1	17	14	7	1	1	1	41	100.00%								
	Birsay (Area 2)	62	2.70	2.70	0	11	5	5	5	2	0	23	100.00%								
	Scar	13	1.44	1.08	0	7	1	1	1	0	0	9	75.00%								
Mus	Tuquoy	65	1.14	1.02	3	22	16	6	8	2	2	57	89.06%								
	Birsay (Area 1)	498	4.12	3.83	3	38	37	23	12	8	8	121	93.08%								
	Birsay (Area 2)	37	1.54	1.54	0	8	8	5	2	1	1	24	100.00%								
	Scar	6	1.00	0.86	0	3	2	1	0	0	0	6	85.71%								
Avg.		1.99		1.62		77.42%															

4.9. PATHOLOGICAL CHANGES

Pathological changes were scarce and hardly representative of a wider population, with prevalence rates different between sites (Table 4.25). On average, over 2,000 fragments had to be studied in order to find one pathological bone fragment. The majority of fragments were however obtained from the Neolithic sites. Skara Brae Trenches I and IV provided 17 cases, already identified back in 2015 (Romaniuk 2015) but not published (Romaniuk et al. 2016A). On average, one pathological bone was found per 1521 fragments in Trench I and per 3538 fragments in Trench IV, resulting in prevalence of 0.07% and 0.03% respectively. In Links of Noltland ten pathological bones were retrieved, about one per 2984 fragments in Trench A and per 1085 (0.03%) in Trench D (0.09%). In turn, sampled sites provided few, if any bones. Birsay Bay Area 1 provided two pathological bones (per 2226 fragments, prevalence of 0.04%) while Bu Broch and Tuquoy only a single one each. However, while Tuquoy prevalence was about 0.02%, for Bu Broch it was about 0.22%, ten times higher.

Strong differences could be noted also depending on specific types of pathologies found. Among all the sites Skara Brae provided the most diverse pool of pathologies, including some identified only in Trench I. Links of Noltland showed minor variability but the rest of the sites provided only one type of pathology, possibly reflecting sample size impact on both the amount and diversity of finds. One category, vertebral fusion, was found only in Skara Brae and Links of Noltland. Bones exhibiting identifiable healed fractures, hip dislocation or osteoarthritis were in turn found only in Skara Brae. However, the most common category was pathologies that could not be successfully identified to a specific type or showed only once in the pool of samples. It included e.g. possible fractures that became infected, sometimes leading to a fusion between adjacent long bones.

Overall, seven examples of healed fractures were retrieved. In Skara Brae Trench I, five cases were identified, with Trench IV providing another two. Most showed simple healed fractures with transverse displacement (similar to e.g. Bartosiewicz, 2013, 47 fig. 29, 48 fig. 30, or Baker & Brothwell 1980, 86 fig. 5 & 88 fig. 6), with a fissure line still visible on the shaft surface and cortical bone build-up around it. However, in the case of one right common vole femur fracture (Fig. 4.20, upper-middle) the situation was more complicated, most likely reflecting comminuted/impacted fracture. The fracture line was heavily irregular and most likely the whole bone was shattered into several pieces through most likely compression, which healed in

a currently visible odd shape. The most notable was a bony protrusion, probably a splinter of an original shaft, ending on something resembling a pseudo-joint surface.

Six cases of vertebral fusion were found, two in Skara Brae Trench I and four in both areas of Links of Noltland. Vertebrae fused included cervicals (one case in Skara Brae and one case in Links of Noltland), lumbar (one case in Skara Brae and two cases in Links of Noltland) and caudals (one case in Links of Noltland). In all cases bones were firmly fused, in most without any (cervical & lumbar) or minor (lumbar, fig. 4.29 bottom right) dislocations and/or bony protrusions visible on the surface. Such a situation was similar to one observed in other animals (Bartosiewicz, 2013, 113-115, especially Figure 91) and most likely relates to natural fusion that occurs in older individuals. The only exception was two tailbones, where the fusion exhibited strong dislocation on the sagittal plane and a deep cavity between two bodies on one side of the structure. Additionally, the cranial end of one and the caudal of another seemed to be partially obliterated but covered in cortical bone. Considering the location, it was either fracturing or dislocation of one of the bones, possibly followed by infection, leading to subsequent fusion and cavity creation.

Two examples of osteoarthritis and another two of hip dislocation were identified. Evidence of degenerative joint disease was found on proximal ulnae (see Fig. 4.29 lower left). Such condition could be identified, similarly to humans and animals alike (Aufderheide & Rodríguez-Martín 1998, 93-96; Baker & Brothwell, 1980, 107-134; Bartosiewicz, 2013, 117-129), due to a presence of eburnation within, and bony build-up around, the joint surface. In the case of hip dislocation affected bones were pelvises, exhibiting pathological depression on a degenerated acetabular ridge. Both pathologies could be identified as false acetabula created after a hip dislocation. The dislocation in each case was most likely caused by a traumatic event as original acetabula seemed to be of proper size for adult specimens.

Pathological conditions on 14 specimens were either unique cases or ones that could not be identified with certainty. All those cases encompassed only long limb bones. The majority were malformations alongside distal or proximal epiphysis with possibly related shaft affected, identified on ulnae, radii, tibiae and phalanges/metapodials. Distal tibiae fragments showed visibly distorted distal ends with additional bone build-up beyond what would be considered as natural joint area. Single cases were retrieved from Links of Noltland, Bu Broch and Tuquoy. It is possible that identified pathologies were the result of a healed fracture, possibly including misplacement of tarsal bones, or a prolonged inflammation due to an unknown source. In turn, ulnar/radial malformations found in Skara Brae (one case) and Links of Noltland (three cases)

showed a distal third of bones up to epiphysis visibly enlarged and porous, in one case leading to the fusion of both bones together (fig. 4.29). All most likely were related to either fracture (see Li et al. 2019, Fig. 1 & 6 for comparison) or pathological changes within or next to the wrist joint, such as infection (see Bartosiewicz, 2013, 48 fig. 31), with the possibility of paws being simply amputated due to some traumatic accident. The remaining two similar cases were identified on a metapodial (Links of Noltland) and phalanx (Birsay; Fig. 4.40). The metapodial exhibited enlarged, porous bone over two-thirds of the shaft, ending on a barely functional distal epiphysis. This situation most likely showed some pathological condition happening around the metapodial-proximal phalanx joint, possibly affecting the whole paw. In turn, the proximal phalanx showed a strongly distorted proximal end and half of the shaft, with false articular surfaces present. It might be due to a complex fracture resulting in bone dislocation, possibly ending either on the fusion of bone fragments from more than one bone, prolonged inflammation of the bone.

The remaining cases were three bones from Skara Brae and one from Links of Noltland. All exhibited minuscule bony protrusions, in three cases alongside minor shaft distortion. No other diagnostic features were identified. In some cases a correlation with specific muscle attachment was clearly visible. For example, one humerus from Links of Noltland showed such changes posteriomediaally on the shaft's distal half, within the area where medial head of triceps attaches to the bone. Bone exostases could be an example of Myositis ossificans traumatica (Aufderheide & Rodríguez-Martín 1998, 27), a condition that may happen due to traumatic accidents, while affected shafts could reflect incomplete, greenstick fractures.



Fig. 4.29 – Six out of 15 bones with pathological changes from Skara Brae. From left to right: (upper row): healed fracture of a vole humerus, healed complex fracture of a vole femur, a vole pelvis with false acetabulum. (lower row): a vole ulna with arthritic changes around humeroulnar joint, ulna and radius fused with each other with shafts in a process of healing and/or prolonged infection, clear fusion between two lumbar vertebrae.

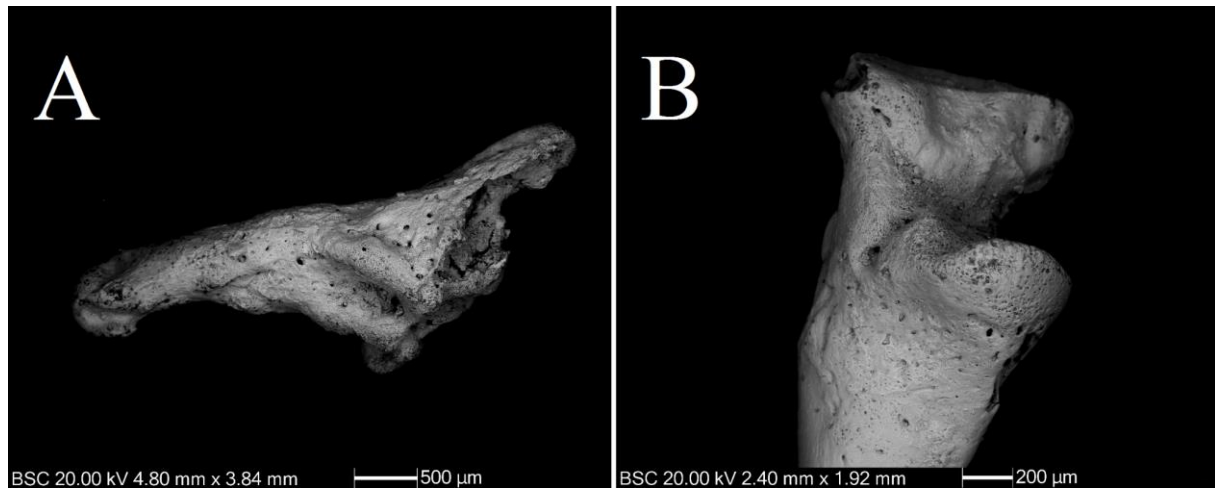


Fig. 4.30 – SEM micrographs showing pathological changes on rodent bones retrieved from the Birsay Bay Area 1: metapodial/phalanx from context 195 (Period 9) with proximal end pathologically changed (A), radius from context 198 (Period 9), with proximal end showing pathological changes in shape of a second head (B).

Table 4.25 – Table summing number of bone fragments showcasing pathological changes from each site, alongside prevalence and a breakdown of main pathology types.

Site	No. All	No. Fractures (healed)	Hip dislocation	Vertebral fusion	Osteoarthritis	Unknown/Other	Prevalence
Skara Brae (Trench I)	15	5	2	2	2	4	0.07%
Skara Brae (Trench IV)	2	2	0	0	0	0	0.03%
Links of Noltland (Trench A)	7	0	0	3	0	4	0.03%
Links of Noltland (Trench D)	3	0	0	1	0	2	0.09%
Bu Broch	1	0	0	0	0	1	0.22%
Tuquoy	1	0	0	0	0	1	0.02%
Birsay	2	0	0	0	0	2	0.04%
Σ	31	7	2	6	2	14	0.05%

4.10. REVISED METHODOLOGY FOR CASE STUDY 2

The methodological case study provided the best means of large-scale data comparison through specific statistical methods. For general comparisons between variables, Spearman rank correlation proved to be best, with Kruskal-Wallis and Fligner-Killeen tests for establishing significant differences in data distribution between groups (sites or site areas). Comparisons for the sake of depositor identification were best done through Pearson correlations for *Abundances* and *Fragmentation Percentages*, Spearman rank correlation for *Skeletal Frequencies* as well as trained SVM and FDA classifying algorithms on *Abundances* and *Fragmentation Percentages*. χ^2 approach could theoretically be adopted but showed either too low accuracy to be truly applicable or visible technical problems. Methods tested and the data obtained from the Case Study 1 are predominantly suited for the search of possible taphonomic agents. The author should make use of Pearson correlations (*Abundances* and *Fragmentation*) for comparing contexts with signature assemblages, with trained FDA classifiers (*Abundances* and *Fragmentation*) also considered as an equal source of information. However, the impact of non-predator taphonomic processes suggests also incorporating alternative explanations assuming their presence. It can be done by using partial/burial transformations on signatures (for alternative correlation results) or trained data (for classification algorithms adjusted for dispersal) when other parts of the analysis justify using them.

The most important revision came to the data intended for age estimation. Such data have rarely been retrieved and studied from micromammal assemblages, chiefly because of such deposits usage as a proxy for specific predators and the environment rather than the population itself. Previously the author used a complex method using two different data types that seemed to work well with micromammal data (see Lyman et al. 2001). However, testing proved that this approach did not represent the majority of estimated MNI, with the additional factor of differential survivorship likely impacting results. In turn, simple fusion scoring and molar wear scoring, even if also biased by differential survivorship, at least proved to represent an assemblage population better, with wear often achieving 100% representation. Due to that, the analysis of age distribution across sites should concentrate only on fusion and wear data.

Additionally, the importance of spatial-related and contextual data was found as a means of tracking additional taphonomic changes that the studied assemblages may have undergone. The site analysis of data should take into account all observable NISP/MNI/weight differences within officially recorded stratigraphy, including taxonomic differences in the first two cases,

but will also attempt to include contextual data (e.g. spatial location within the grid, context type) if available for a specific site.

Most criticism of Case Study 1 related to metrical and to a less extent to pathological data. While some trends could be noticed, both were heavily affected by a strong relationship with the amount of material retrieved, resulting in data being incomparable between sites and trends possibly being biases stemming from the small sample pools for the majority of sites. That is why the author considered both being fully investigated in Case Study 1, with pathologies mentionable only as additional reference data for age estimation due to many of those identified either taking a long time to manifest or is related to old age.

5. CASE STUDY 2 – ASSESSMENT OF SITES

5.1. SKARA BRAE

5.1.1. ASSEMBLAGES QUANTIFICATION AND DISTRIBUTION

The general data did not meaningfully differ from that used for a previous study (Romaniuk et al. 2016a table 1, 2016b). A few previously not integrated subsamples have been added to the site data, mostly to contexts already containing significant amounts of skeletal fragments. New NISP resulted in the additional 14 MNI added to the site, but neither composition nor interpretation of those contexts changed. However, one new context was added to Trench I. Identified species did not differ from the previous studies, which consisted of Orkney voles and field mice. Overall, over 31,000 rodent NISP was found within the four trenches, reflecting 53 different contexts (Table 5.01). Over 73% of NISP came from Trench I, representing the core of the site, while another 3% came from the peripheral Trench II. Off-site trenches differed considerably in NISP amounts. Trench III provided the least material to work with (0.3%), while Trench IV contained assemblages comparable in size with Trench I (over 22%). MNI distribution was similar but the domination of Trench I was more pronounced (79.6%). However, Trench IV contained noticeably less MNI than NISP would suggest (15.9%) while Trench III lacked any *Apodemus* skeletal fragments. The majority of data came from contexts identified as an amalgam made of multiple atrophic and non-anthropogenic sources, such as human refuse, structural remains, windblown soil, clay or stones (Table 5.02). The second most substantial source seemed to be sandy, mostly natural, accumulations, with organic middens and stone-filled features only providing low NISP with similar completeness.

Unique patterns in accumulation could be noticed when stratigraphy of each trench was considered separately as well as in relation with each other (Table 5.01 & Fig. 5.01, plots A & B) and was noticeable during significance testing. Trench I showed the most complex stratigraphy, with four phases representing major changes within the settlement, with additional subphases available for two of them. The oldest phase, relatively small in terms of unearthed volume (4.65 m³) but spanning a long period of time (3500 – 3100 BC), provided moderate amounts of remains, with moderate to high completeness (Skeletal Completeness of 21%,

Average Abundances of 22%). Contexts 168 and 157, both consisting mostly of grey ash clay, contained predominantly Orkney voles. However, evidence for a single field mouse were also found. Following Phase 0, Phase 1 was one of the main settlement periods. However, it provided material comparable in number to Phase 0 and about 3% lower in completeness despite the greater volume (~6 m³). Fourteen contexts, from sand accumulations to rich organic middens and refuse deposits, differed in assemblage size. One from two early contexts, small and sandy Context 164 with stone inclusions (possibly from a stone wall), contained over 300 NISP while the bigger amalgam of clay and refuse, context 151, provided only three. While the majority of individuals came once again from voles, the difference was not as striking as in the previous Phase. Only the three smallest contexts, both in terms of NISP and volume, did not provide any mouse bones, while in the case of Context 150 (refuse amalgam) more mice remains were retrieved than voles. The Intermediate Phase, between Phase 1 and Phase 2, provided a big assemblage of over a thousand bones from its main sandy Context 139 with clay and refuse lances, about 8.6 cubic metres big. Both species were once again present but in proportions more similar to Phase 0 than Phase 1, moreover, completeness recorded was quite high, about 25% (Skeletal Completeness) to 27% (Average Abundances).

However, it was Phase 2 that provided the overwhelming majority of finds in Trench I (84% NISP), with the highest completeness encountered (29% Skeletal Completeness, 31% Average Abundances). It is not surprising considering it consisted of more recent settlement layers, with a volume analysed of over 20 m³. Still, a number of sub-phases divided the assemblage, resulting in a more varied situation. Early Phase 2 consisted of middle to large size micromammal assemblages within either amalgams of clay, sand and refuse or sand accumulations. All contexts contained remains of both species although voles heavily dominated over mice. Interestingly, three assemblages from Middle Phase 2 and two huge accumulations from Late Phase 2 differ significantly from early depositions, each a subphase in its own way. In the case of the middle period, despite similar context sizes, one context provided only one bone while the second one was a very small assemblage. The only large find was one from hearth context (Context 120), containing over sixty voles and one field mouse. The two youngest contexts, representing the late phase of the site utilization, were in turn the first and third biggest micromammal accumulations found in Trench I. Both contexts were refuse and clay amalgams, with a similar percentage split between voles and mice MNI (93% to 7%).

While Trenches II to IV showed simpler stratigraphy all were to some degree comparative with Trench I. Trench II stratigraphy, as a site periphery, could be linked to site overall stratigraphy, with Phases 1 and 2, including subphases, resembling ones present in Trench I. Trench II Phase 1 was represented by assemblages retrieved from two clay and refuse amalgams as well as one rich organic midden and a stonework of unknown purpose. The stonework provided only a few finds but remaining three contexts contained small to high number of micromammal remains, with mice representing about 10 to 50% of all MNI while also showing moderate/high completeness (Skeletal Completeness of 24%, Average Abundance of 25%). On the other hand, three contexts from Phase 2, each representing a separate subphase, did not contain mice. Among them only one from the early subphase could be considered as a moderate accumulation, with the rest from middle and late subphases showing few finds. Completeness was also low (Skeletal Completeness of 14, Average Abundances of 18%).

In contrast to Trench II, off-site trenches do not show clear phases, being predominantly natural sand accumulations with sporadic contexts of mixed anthropic and natural deposition. In the case of Trench III all assemblages were very small in size, containing isolated vole bones and low completeness (9% for both Skeletal Completeness and Average Abundances). Sporadic human involvement was seen as an amalgamation of natural sand with displaced turf and other material but did not provide any deviations from completely sandy contexts. However, Trench IV, while showing predominantly the pattern found in Trench III, contained two specific assemblages. The first was the largest accumulation of micromammal remains found within a single context, more confusing as coming from mostly sand accumulation (Context 408). The next accumulation, of moderate size, was provided by a context containing plough-marks (Context 407). Both jointly showed the highest average completeness obtained from Skara Brae data (39% Skeletal Completeness, 40% Average Abundances). However, mouse bones were found only in major accumulations, one small accumulation and one single bone find.

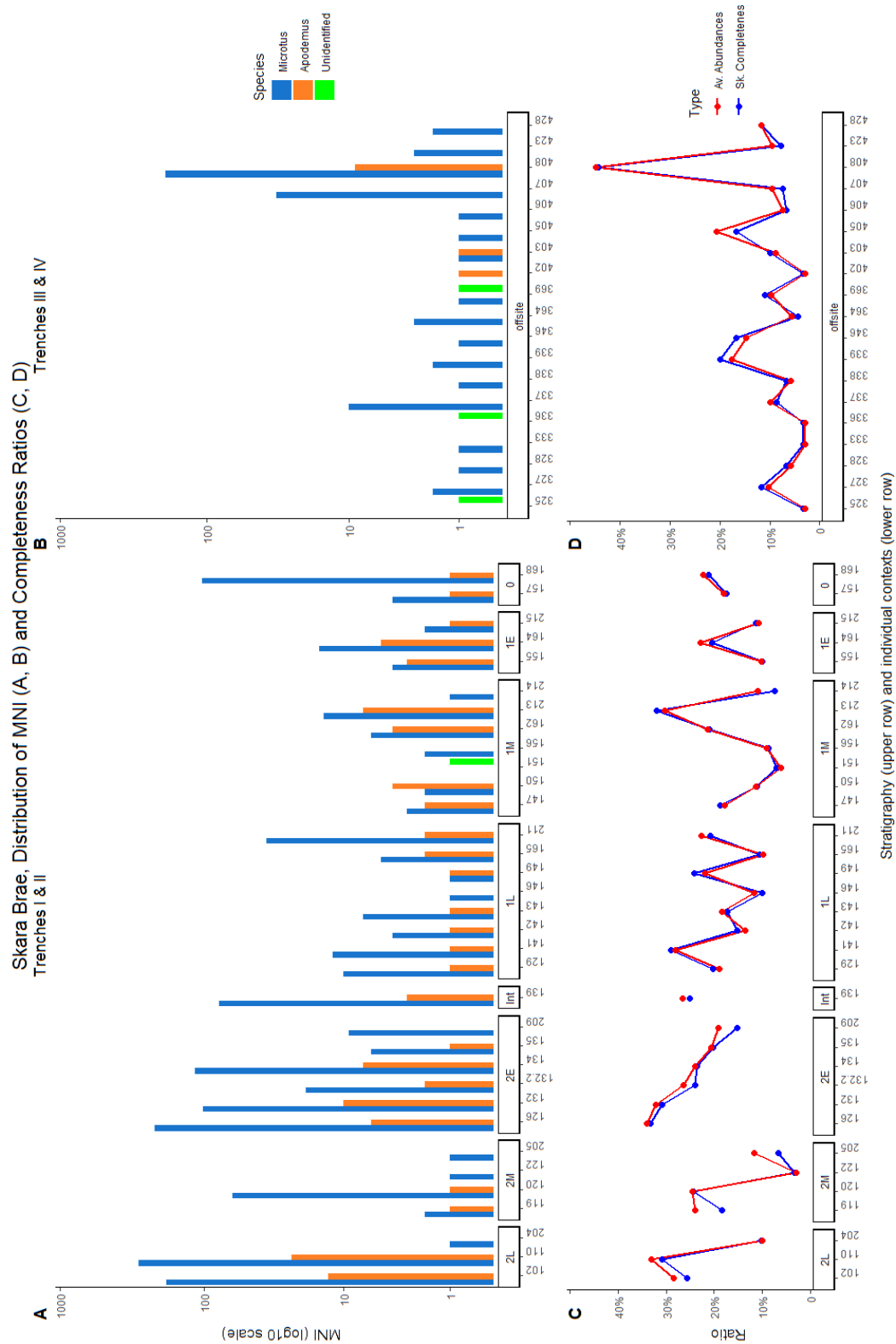


Fig. 5.01 – A and B (upper plots): Distribution of MNI across four trenches. In Trench I and II contexts were arranged according to stratigraphy while trenches III and IV were arranged according to simplified stratigraphy (numbering sequence).

C and D (lower plots): values of completeness ratios (Skeletal Completeness, Average Abundances) for each context in trenches, arranged in the same way as in plots A & B.

Table 5.01 (Upper) – Weight, NISP and MNI counts distribution for Skara Brae trenches, depending on specific species categories. In the case of on-site trenches data was broken down to main phases present.

Phase	Trench	Weight (g)	Size	Contexts	Microtus		Apodemus		Unid. Rodent		ΣNISP	ΣMNI
					NISP	MNI	NISP	MNI	NISP	MNI		
0	I	39.31	4.65	2	851	106	8	2	531	0	1390	108
1	I	37.32	6.18	14	510	72	94	25	502	1	1106	98
Int	I	37.57	8.58	1	636	78	15	3	510	0	1161	81
2	I	518.84	18.01	10	10068	993	339	65	8753	0	19160	1058
1	II	40.03	8.97	4	456	53	38	10	459	0	953	63
2	II	4.74	2.09	3	85	11	0	0	41	0	126	11
	III	4.76	---	11	63	22	0	0	40	3	103	25
	IV	140.27	---	8	3450	233	51	11	3575	0	7076	244
Σ		822.84	---	53	16119	1568	545	116	14411	4	31075	1688

T.5.02 (Lower) – NISP and MNI counts as well as Skeletal Completeness for specific types of contexts, including an amalgam of several sources (e.g. mixture of deposition with natural windblown sand) and plough marks content.

Type	Trenches	Contexts	Weight	Microtus		Apodemus		Unid. Rodent		ΣNISP	ΣMNI	Compl.
				NISP	MNI	NISP	MNI	NISP	MNI			
amalg.	I, II, III, IV	25	522.69	9990	994	369	73	8434	2	18793	1069	28.0%
clay	I	2	5.46	53	11	6	3	37	0	96	14	15.4%
midden	I, II	2	18.68	193	18	31	10	274	0	498	28	26.5%
stone	I, II	5	29.02	514	70	11	3	491	0	1016	73	23.0%
sand	I, II, III, IV	18	246.90	5367	474	128	27	5174	2	10669	503	30.3%
plough.	IV	1	0.09	2	1	0	0	1	0	3	1	6.7%

5.1.2. AGE DATA DISTRIBUTION

Very few long bones without early fusing epiphyses were found, suggesting no, or a very small number, of juvenile individuals in the studied population (Fig. 5.02). Despite humeri being the second-best represented long bone in Skara Brae assemblages, no trace of unfused distal epiphyses was found in Trenches I to III. In Trench IV, only a singular case was found, in Context 408. Slightly better representation was found in the case of the tibia distal epiphysis. In Trench I, values ranged from 9% (Intermediate Phase, context 139) up to 16% (Phase 0) but with no finds from Phase 1. In contrast to Trench I, in Trench II about 10% of all distal tibiae from Phase 1 were found unfused while Phase 2 showed no such finds. No such finds were retrieved from Trench III or the majority of Trench IV contexts. Context 408, once again, contained such remains in small amounts (~ 9%). However, tibial finds were rare in contrast to humeral ones, resulting in joint percentages of early fusing epiphyses being only minority affected by the presence of unfused distal tibiae. The least difference was in the case of offsite trenches, possibly coinciding with Trench IV higher unfused percentages to other trenches.

In the case of middle fusing epiphyses, the situation was similar to early fusing ones. Case with proximal femoral epiphyses was somehow similar to humeri despite more specimens being found. Only four cases were found in Trench I, one from Phase 0 and three from Phase 2. Trenches II and III yielded no such finds while in Trench IV Context 408 provided thirteen cases, four identifiable to voles. In contrast, unfused distal ulnae in small amounts (8-13%) were found in all phases of Trench I. However, despite representing only about 7.5% of all distal ulnae, about twenty specimens were found in Phase 2. Comparable amounts were found in Trench II but only in Phase 1 while, once again, no such finds were recorded from Trench III and all Trench IV, besides Context 408. The relationship between femora and ulnae was however the same as humeri and tibiae, resulting in joint results showing only very small percentages for unfused specimens.

Further analysis of epiphyseal fusion revealed the predominance of individuals approaching adulthood with a significant addition of fully-grown specimens. The highest quantities of late fusing epiphyses being found intact were proximal ulnae, with from 60% to 100% being found in such a state depending on a Trench and Phase. Fused specimens were more frequent in the case of earliest and latest phases of Trench I, with Phase 2 of Trench II and all off-site contexts besides accumulation in Trench IV providing no unfused specimens. In contrast to proximal ulnae the rest of the late fusing epiphyses, proximal tibia and humerus as well as distal femur,

provided more unfused specimens than fused ones. On average percentages of fusion between all three were relatively similar, from 5% to 34%, resulting in joint percentages (with ulnae) around 25% for Trenches I, II and IV. Trench III provided only 8% due to all finds besides two ulna epiphyses being found unfused. On average, distal femora were more often fused than proximal humeri and distal tibiae. However, the difference between femora and humeri was rarely large and only distal tibiae were likely to differ in specific phases (Intermediate Phase, Phase 2) due to providing the least amount of fused specimens. In all three cases the largest quantities in relation to assemblage size were found in Phase 1, beyond 30% for humeri and femora and about 17% for tibiae. In Context 408 all counts were around 10%, but in contrast to Trench I the lowest cases was for femora, while tibiae were the highest (c. 12%).

In the case of field mice molar wear, complementary data were obtained to skeletal fusion. While some problems were encountered when analysing fusion data separately for each species, both seemed to contribute to the same early, middle and late fusion frequencies. Molar wear of field mice in Trench I (Fig. 5.03) did however differ from indications obtained from skeletal fusion, revealing the predominance of adult individuals. The majority of finds came from animals from roughly three (category 2) up to six (category 3) months old, corresponding to adult specimens. However, subadults (category 1) and older adults (category 4) were also present, with juveniles (category 0) and overwintered animals (category 5) most likely present in very small numbers.

Analysis of skeletal fusion does not substantially differ from the previous research results (Romaniuk et al. 2016a, Fig. 3), with molar wear perhaps showing some difference between major species. Although the previously applied method represented only a fraction of finds the overall outline was similar, with the majority of voles approaching maturity. A minor difference between Trench I and IV is also visible in the case of epiphyseal fusion, but it is not as noticeable as the previous method has suggested. However, for voles the difference was the possibility to compare data against Trenches II and III as well as contexts outside 407 and 408 accumulations, providing a better understanding of the fringe and off-site situation. In turn, the molar wear showed field mice population being much older than expected of commensal population, with much more adults and older adults than sub-adults or juveniles.



Fig. 5.02 – Skara Brae, epiphyseal fusion expressed as a relative frequency of NISP (red-unfused, blue-fused) and grouped in three main groups related to individual's age (early/middle/late). Upper plots reflect each trench, with lower plots showing stratigraphy in Trenches I and II as well as differentiation between accumulation in Trench IV and remaining contexts.

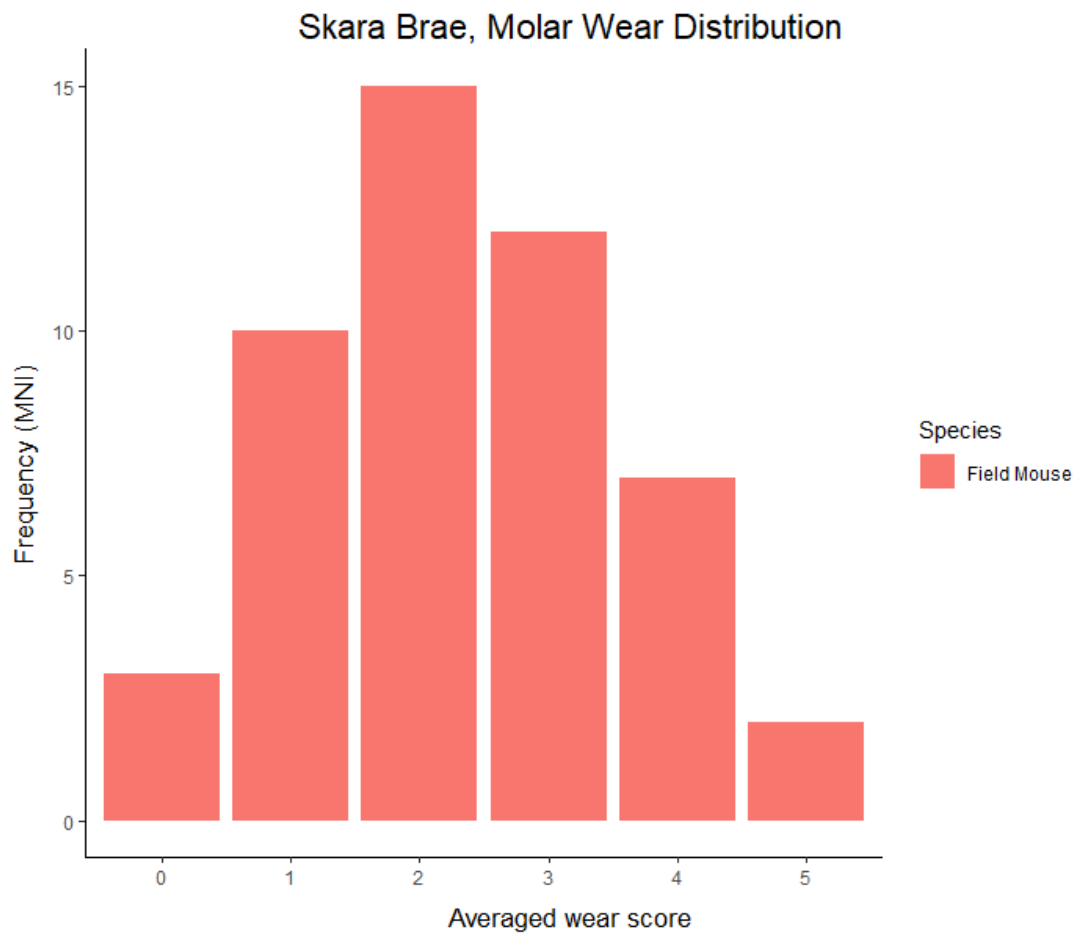


Fig. 5.03 – Skara Brae, frequency distribution of *Apodemus* MNI depending on molar wear scores obtained.

5.1.3. FREQUENCIES, ABUNDANCES AND INDICES

In general, skeletal completeness as well as average abundances correlated to the size of each studied assemblage, with some variation visible in the case of skeletal frequencies. On average, the difference between completeness ratios was slightly greater than 1%, but a number of contexts showed differences bigger than 3%, mostly from Trench II (Contexts 205, 209 and 214) but singular cases were also found in Trench I (Context 119) and IV (Context 405). Correlation with NISP was more pronounced in the case of Trenches I and II (Skeletal Completeness: $n = 34$, $\rho = 0.90$, $p < 0.001$; Average Abundances: $n = 34$, $\rho = 0.90$, $p < 0.001$) than in trenches III and IV (Skeletal Completeness: $n = 19$, $\rho = 0.70$, $p < 0.001$; Average Abundances: $n = 19$, $\rho = 0.77$, $p < 0.001$). Interestingly, while correlation with MNI in site trenches was strong, in off-site ones it was far lower, for Skeletal Completeness on verge of significance ($n = 19$, $\rho = 0.43$, $p = 0.068$) and for Average Abundances slightly beyond ($n = 19$, $\rho = 0.45$, $p = 0.050$). As size differences correlated to some degree with the division between phases and subphases completeness ratios could also fit in the same way.

Skeletal Frequencies varied greatly between trenches, specific phases or even context investigated, resembling temporal and spatial variety present on site (Fig. 5.04). Differences between trenches are clearly visible, with Trench IV showing the predominance of vertebrae in frequencies, Trench I in skull fragments and Trench II showing relatively similar frequencies to all categories. Similarly, Trench III showed an almost complete absence of vertebrae, aligning with the previous identification of these assemblages scattering. However, the most complex case was encountered in Trench I. The earliest phase identified in Trench I, Phase 0, showed a strong predominance of skull remains (>50%), with other frequencies slightly below the 20% threshold. While the phase consisted of only two contexts both showed the same frequencies outline (e.g. Context 168). However, Phase 1 showed a wider variation between retrieved contexts. The general outline indicated an equal prevalence of skull and vertebrae elements (~29% each), with an addition of hindlimb (24%) and frontlimb (19%) bones. Mostly sandy context from early segments of this phase, like Context 164, were showing similar frequencies, with later amalgams of sand, clay and refuse, e.g. Context 141, showing predominance of vertebrae (38%), followed by skulls (25%) and then limb bones (less than 20% for each). The Intermediate Phase was represented by a single Context 139, with frequencies differing from the remaining phases. Skulls and front limbs were most frequent – 36 and 28% respectively. Hind limbs were not far away (24%) but vertebrae were a relative

rarity, considering their number in an average skeleton (13%). Phase 2 resembled Phase 1 but with a minor representation of skulls. The majority of assemblages within this time period showed similar frequencies of hind and front limbs, with either equal representativeness or slightly in favour of front limbs, as well as skulls, which dominated each context. However, the biggest variation was within vertebrae, ranging from under-represented (Context 102) to the second most commonplace finds (Context 110).

Fringe and off-site trenches, while showing a simpler situation, exhibited greater variation of encountered skeletal frequencies. From the outline, Trench II Phase 1 showed similarities with the same phase from Trench I. However, contexts differed from each other, especially in the case of two predominant accumulations. Context 213, an organic-rich midden with well-preserved finds, showed very high vertebral frequencies (46%), followed by hindlimbs (21%). The second biggest Phase I accumulation, Context 211, showed an inverted situation, with skull remains being the most commonplace (35%). More internally consistent was the following Phase 2, with almost 50% frequencies of skulls and only a few cases of vertebrae. Moreover, this phase of Trench II showed similarities with off-site Trench III and minor contexts from Trench IV, both providing no, or only a small number, of vertebrae while mostly consisting of maxillae and mandibular remains. However, as noted back in **Chapter 5.1.1.**, Trench IV Contexts 407 and 408 differed strongly in NISP, with 407 showing almost exclusively skulls and Context 408 providing an outline of frequencies most similar to owl-like accumulation, with skulls being the least common find.

Abundances were similar between Trenches I, II and IV, but were usually far lower in Trench III (Fig. 5.05). In the case of paired bones most commonplace were maxillae and mandibles, followed by proximal limb bones. Over 3,100 mandibles were found in all four trenches, with frequencies around 64% among contexts from trenches I, II and IV. Maxillae were found in lower numbers, about 2,600, with bigger differences in average frequencies between trenches. Humeri fragments were slightly more commonplace than femora, but trenches differed in abundances, with Trench I and IV having higher average humeri abundances while II and III having lower. Mid-range values were mostly of pelves and tibiae, with the latter having consistent relative abundance across trenches (c. 25%), apart from II (16.8%) while the former having more diverse averages, from 9% in Trench III to 25% in Trench I. Lowest counts were observed for scapulae and radii, ranging from no finds (scapulae in Trench III) up to 18% (radii in Trench III). Apart from vertebrae, with frequencies ranging from near 0 up to 5%, only minuscule amounts of other bones were found. Especially surprising was the almost complete

lack of foot bones, such as phalanges or metacarpals, as well as ribs. However, large amounts of loose incisors and molars were found, over 8,000 NISP in total.

Major contexts within site trenches showed moderate deviation from general trench *Abundances*. In Trench I, Contexts 102, 110 (Phase 2) and Context 139 (Intermediate Phase) did not significantly differ, following a similar pattern with roughly 5% difference from each other apart from maxillary relative abundance. However, Context 164 (Phase 1) and Context 168 (Phase 0) deviated from previous contexts, each in a different way. Context 164 exhibited far lower maxillary and mandibular and moderately lower humeral and tibial relative abundances, with other ratios being roughly within the range of main contexts of Phase 2 and Intermediate Phase. The largest difference however was a far higher count of distal limb bones, especially metapodials, in relation to all other contexts. On the other hand, Context 168 provided far higher maxillary and mandibular abundances with the majority of postcranial abundances being lower than ones from Contexts 102, 110 and 139. In the case of Trench II, Contexts 209 (Phase 2), 211 and 213 showed higher deviation from overall trench values. Most similar with each other were Contexts 209 and 211, but they still differed in the case of humeri and hind limb bones. Context 213 differed from the other two especially when it came to high maxillary, pelvis, humeral and distal long bones relative abundances. However, values related to loose incisors, ulnae and radii were far lower.

The largest differences in abundances could be noted in the case of off-site trenches – mostly due to either lack of large contexts or the presence of only single ones, dictating the outline of the whole trench when studied jointly. Trench III provided only one small context that approached MNI of 10 individuals (Fig. 3.14). Context 337 showed higher values (about 20% higher) than the overall trench outline in the case of mandibles and loose incisors, with other values being within the range of comparativeness. Trench IV, on the other hand, provided two relatively big contexts, Contexts 407 and 408. Context 408 was similar to overall trench values but with maxillary and femoral abundances slightly higher and humeral frequencies, due to fragmentation, beyond 100%. However, Context 407 showed strong deviation from both context 408 and Trench IV overall. Only mandible counts were high, with maxillae and loose teeth being moderately lower. Postcranial bones were within the range of 0% to 3%.

Indices obtained from Skara Brae contexts showed clustering around specific values but the variation was very high (Fig. 5.06). In the case of percentages of isolated teeth, the situation differed between incisors and molars. The quantities of isolated incisors differed heavily from context to context, occupying most of the scale between 0% up to 460%, with the majority of

contexts either within the 0-50% or 100-200% brackets. The latter resembled major contexts, with only one of lower value (Context 168) and two beyond 200% (Context 139 & Context 164). On the other hand, isolated molars values were within 0% to 80% range but with the majority of contexts lower than 40%. Size affected that percentage, with larger contexts being above 40%. Complex index of postcranial to cranial elements provided a range of values far wider from what was known from predatory assemblages, even beyond 700%. However, the majority of contexts showed ranges between 0 up to 250%, with higher counts being only found in single cases. In this case the largest contexts were within the middle of that range, between 50% and 150%. In the case of the simplified index of postcranial to cranial elements the situation was similar, but with fewer outliers present. The index of proximal to distal limb elements also had a wide range, up to 180%, but with the majority clustered around 0-60% values including main contexts.



Fig. 5.04 – Skara Brae *Skeletal Frequencies*, plotted for main site trenches (upper plots), stratigraphy of Trenches I and II as well as specific accumulation types in Trench IV (middle plots) and selected main contexts identified in areas I, II and IV (lower plots).

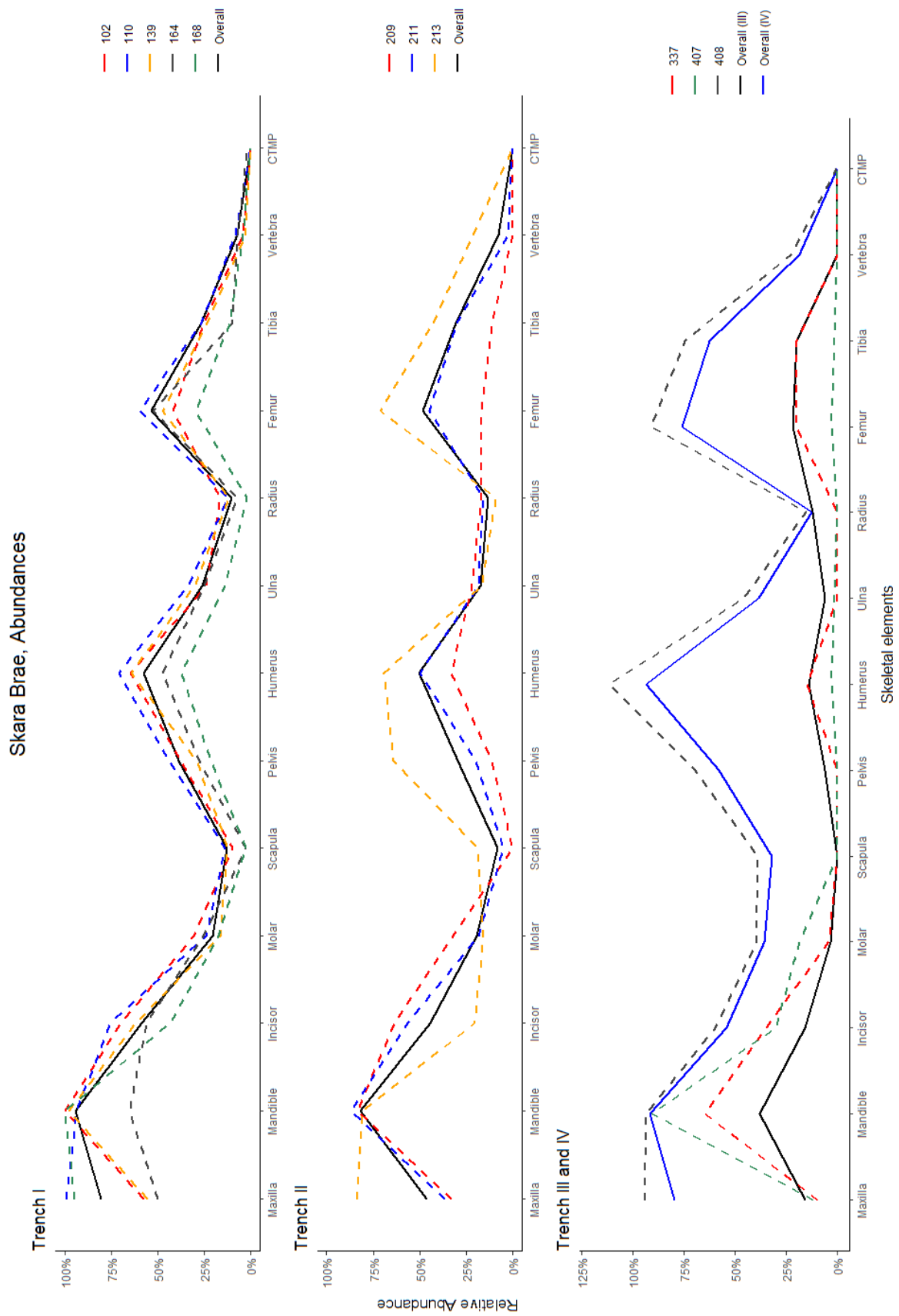


Fig. 5.05 – Skara Brae *Abundances* of specific skeletal elements, plotted for overall trench data as well as most important contexts of these trenches presented.

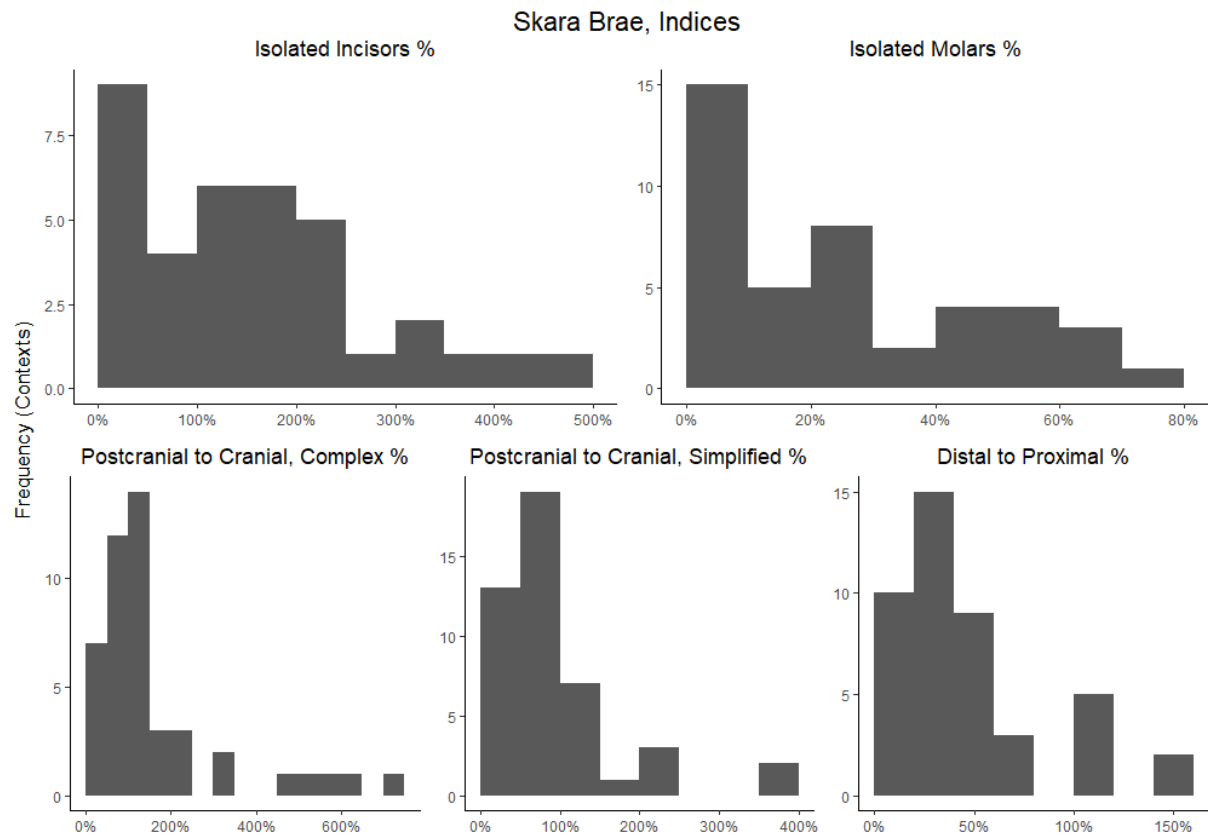


Fig. 5.06 – Skara Brae, frequency distribution of index results for *Indices*.

5.1.4. FRAGMENTATION

Skull breakage differed only slightly between the four studied trenches (Fig. 5.07). Only one percent of cranial finds, either from Trench I or IV, were skulls with maxillae (53 NISP). All those crania were broken, lacking parts of calvarium and additional fragmentation visible on preserved parts. In Trench I, only two phases contained broken skulls – Phase 2 ($n = 32$) and Phase 1 ($n = 6$). The next stage of fragmentation was represented by maxillae still connected to zygomas, occasionally with other bones present (e.g. nasals). All trenches provided such finds, consisting from 8% in the case of Trench IV up to 25% of all cranial finds in Trench III. The majority of other cranial finds (75-90%) were either maxillae isolated from other cranial bones, often heavily fragmented, as well as other single cranial bones, notably nasals, occipitals, temporals and parietals. Intact mandibles, similarly to broken skulls, were only found in Trenches I and IV but in the latter case their contribution to mandible NISP was more substantial (less than 4% in I, over 10% in IV). On the other hand, mandibles with minor breakages alongside ramus were found within all trenches, being 14% up to 19% of all mandibular finds. Heavier examples of breakages (mandibles missing ramus and fragmented mandibular bodies) followed a similar trend but consisted of a bigger number of finds. With the exception of Trench IV, the most commonplace were heavily fragmented mandible remains, with ramus-less mandibles being second most common.

In a similar way to skull bones, postcranial fragmentation differed between trenches in specific cases. Humeral breakage percentages were most similar between trenches as well as between phases in Trench I. Percentage of intact bones ranged from 39% to 48%. Higher percentages were only found in Trench III (all finds intact) and Trench II Phase 2 (67%). Similar to humeri, intact ulnae also were predominantly within a specific range of 17% to 33%, with the exception of Trench III (67%). In the case of femoral bones, the percentage range was quite large, with some cases containing over 40% of intact femora (Trenches III and IV) while others approaching 10% (Phase 0, Trench I) or having all finds broken (Phase 2, Trench II). However, in that case site and off-site trenches differ quite significantly and a similar situation was repeated in the case of tibiae. Complete tibiae were relatively rare in Trench I (12%), with the highest percentages in Phase 1 (24%) and lowest in Phase 2 (10%). Percentages for Trench II were similar to Trench I (16%) but both Trench III and IV provided far higher values, 50% and 31% respectively.

Minor differences in fragmentation between individual contexts were also noticeable (Fig. 5.08). Most noticeable was the difference between youngest context deposited on site, Context 102 (Late Phase 2), and other major assemblages. Context 120 contained less fragmented postcranial bones, with complete humeral, ulnar and femoral counts being on average 20% higher. Interestingly, tibial fragmentation provided less pronounced differences, with some contexts (e.g. Context 164) containing far better proportions. Skull breakage did not differ substantially apart from the fact that only context 102, among the major contexts, contained broken skulls. Interestingly, other cases of broken skulls came mostly from mid to large size contexts. Mandible counts were almost identical, with some variation of complete ones (highest for Context 139) as well as fragmented remains (bigger numbers for older contexts). In contrast to Trench I, major contexts from Trench II followed the outline of cranial and postcranial breakage already noted for each phase without much deviation. On the other hand, Context 337 from Trench III was not comparable with the overall trend, mostly due to low counts creating extreme values. Lesser case of such an issue could also be noticed when comparing Context 407 to Context 408 or overall Trench IV proportions. Context 407 showed all key elements being 100% complete, most likely due to a single-digit number of postcranial bones found.

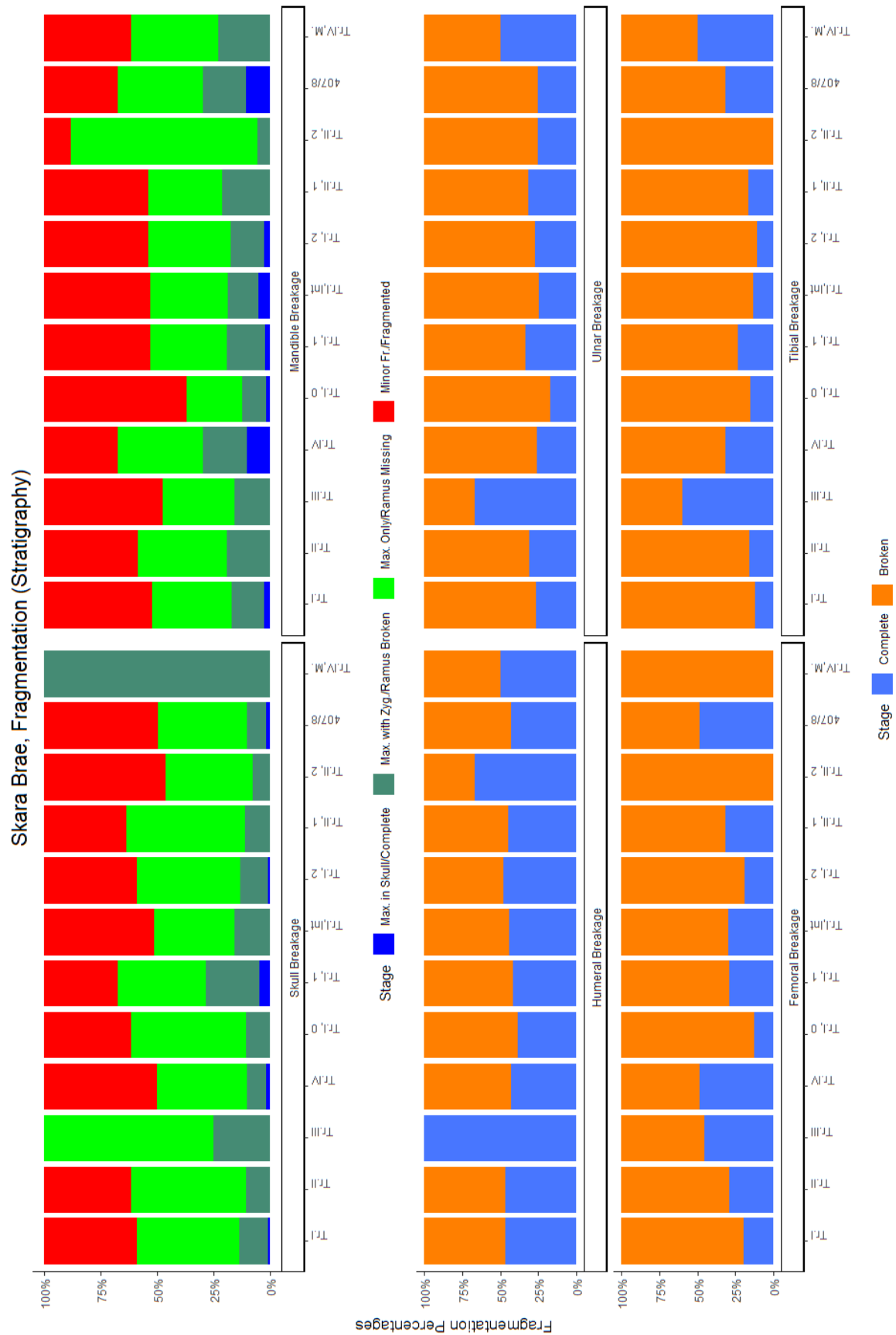


Fig. 5.07 – Skara Brae, skull (upper row) and postcranial (two lower rows) breakage for major phases in Trench I and II, overall for Trench III and smaller and major contexts division for Trench IV.

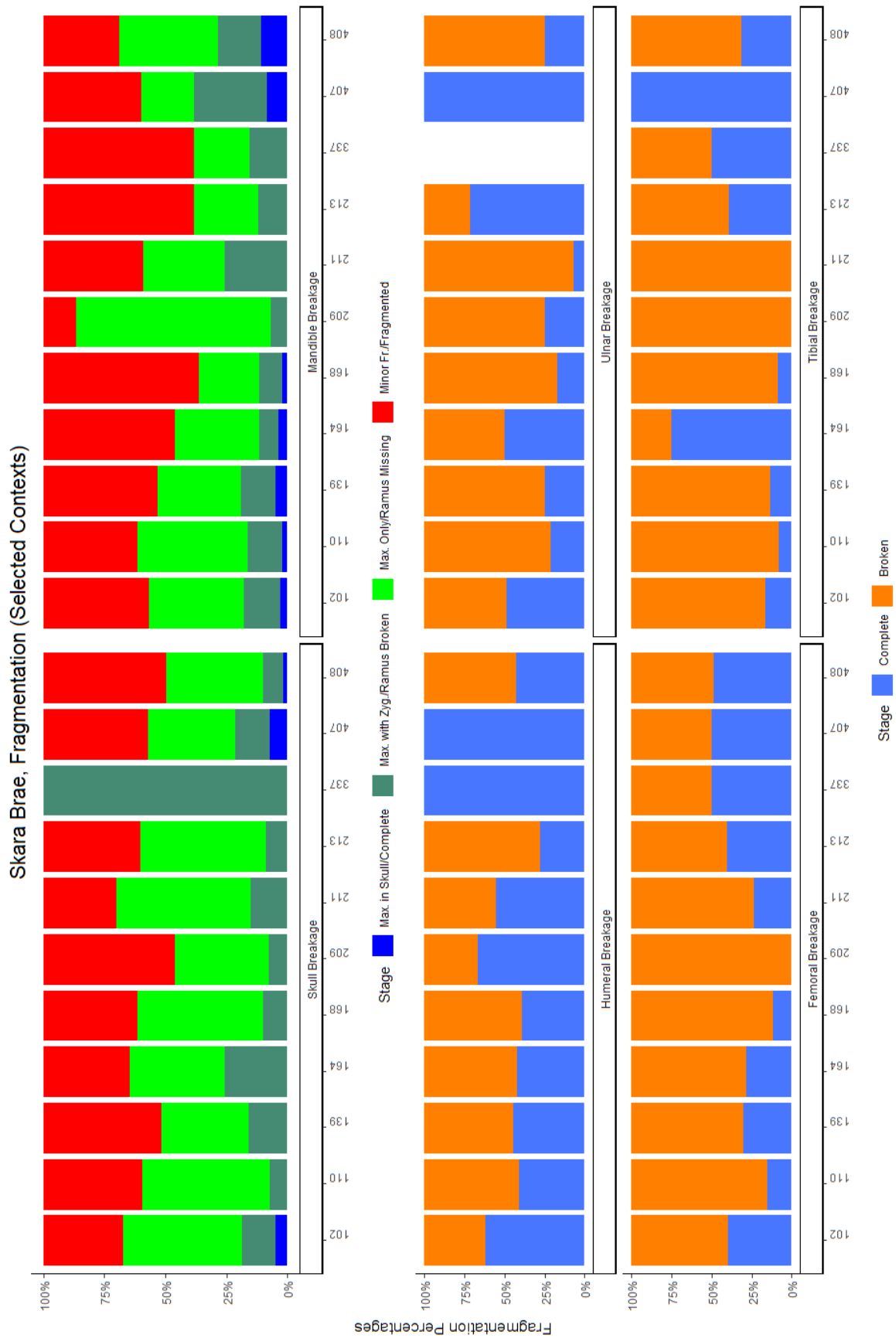


Fig. 5.08 – Skara Brae, skull (upper row) and postcranial (two lower rows) breakage for major contexts from Trenches I to IV.

5.1.5. DIGESTION AND BURNING

Digestion marks were identified on the Skara Brae material but other taphonomic alterations were more prevalent. The majority of finds exhibiting digestion came from the latest phase of Trench I but all phases from Trenches I and II as well as Trench IV overall provided small amounts of finds; only Trench III lacked such finds. However, percentage representation of digestion differed from raw counts, with smaller assemblages having higher proportions of digested material (Table 5.03). Light molar digestion was most common, with moderate digestion being found in smaller quantities. Only two examples of heavy molar digestion were found, one in Context 110 and another one in Context 139. Incisor digestion, on the other hand, was found only in Trenches I and IV, and scored predominantly as light, with some moderate specimens and one heavy example. Epiphyseal digestion, despite the wide presence of femoral heads as well as distal humeri, was rarely found. Digestion marks on molars, even in heavy cases, did not expand beyond the alveolar line, suggesting tooth loss after digestion rather than during. Heavier digestion provided specimens with wedge-like tooth matter loss between tooth crown and alveolus, exposing internal tooth cavity (Fig. 5.09 A). Additionally, many specimens showed a combination of chipping and digestion as well as transverse dentine cracking on silent edges (Fig. 5.09 B). Heavy incisor digestion could be once present at the site in larger numbers but due to other processes such finds ended up either broken or heavily weathered. A similar problem was also noted in the case of epiphyseal digestion, with some possible examples of digestion not being counted due to more prevalent signs of other processes. Additionally, some incisors were covered in a layer of substances, most likely a combination of soil with biological matter, obfuscating digestion assessment (Fig. 5.09 E).

As it was already mentioned in previous research (Romaniuk et al. 2016A), Skara Brae provided evidence of burning in two site trenches. Burn marks were almost as common as digestion, especially prevalent in Phase 2 main Contexts 110, 132 and 134 (Table 5.04). Some correlation between the quantity of burnt remains and the assemblage size could be noted, but it was not a strict rule. Context 102, despite being about a half of 110 in terms of NISP, provided almost ten times fewer burnt elements. The majority of fully burnt specimens were either vole mandibles (Fig. 5.10) or long limb bones, especially humeri. Additionally, charred teeth found in Trench I were in majority fully burnt, with possible remaining unburnt surfaces on parts previously covered by alveolus. Other bones, for example vertebrae (see Fig. 5.10 A), exhibited partial burning on most exposed processes and elements, rarely being fully discoloured. The

overwhelming majority of burnt elements were carbonised, around stages two and three (as described in Cáceres 2002, after Fernández – Jalvo & Andrews 2016, 157 Fig. 5.2), with only handful examples of calcination, mostly partial (stage four). However, the examples of calcination were brittle and easily breakable during examination (e.g. Fig. 5.10 B).

SEM was used to check to what extent visually assessed burn-like discolouration actually truly represented thermal alteration. The enamel of assessed teeth (Fig. 5.11 A) was visibly cracked, with a network of shallow longitudinal and transverse cracks going all the way from top to bottom of its body. Additionally, sections of cementum, located between salient edges, were shrunk and transversely cracked into several parts. Finds were also brittle and usually fragmented into several parts. In the case of molars burned while still within the mandible, exposed parts were fragmented into smaller pieces, while rooted parts remained as one piece, resulting in a broken and irregular profile. Surface bone layer cracking was also present on long limb bones but in specific places. The femoral head exhibited a combination of cracking emerging radially from *fovea capitis* and irregular pitting alongside cracks (Fig. 5.11 B, C). Apart from the head, cracking was also present on epiphyses but the rest of shaft was usually pitted with elongated depressions, sometimes joined together. A network of such depressions could also be seen on mandibular inferior borders, with occasional transverse cracking (Fig. 5.11 D). Interestingly, while some charred samples investigated under the SEM exhibited weathering and other taphonomic processes, digestion seemed not to be present on burnt bones.

SEM combined with EDS was used to check the chemical composition of a blackened surface of possibly burnt specimens and, in combination with previous assessment, guarantee proper identification. Two teeth, molar and incisor, as well as two bones, mandible and femur, were checked with that method, alongside unburnt specimens for comparison. Elements identified predominantly consisted of those common in bone and dentine matrix (e.g. calcium, phosphorus), earth soil (e.g. silicon, manganese) or both (oxygen, see Fig. 5.12). However, manganese staining coming from soil inclusions could not be considered a significant problem. Larger amounts of manganese were encountered only on a studied incisor. Soil-related elements, including manganese, were confined to surfaces with visible soil inclusions, with surfaces of uncontaminated dentine and enamel almost free of any significant manganese accumulations. However, varying amounts of carbon, which numbers seem to roughly correlate with oxygen, suggested carbon staining (either by direct burning or from other burnt material) as most possible from the chemical perspective.

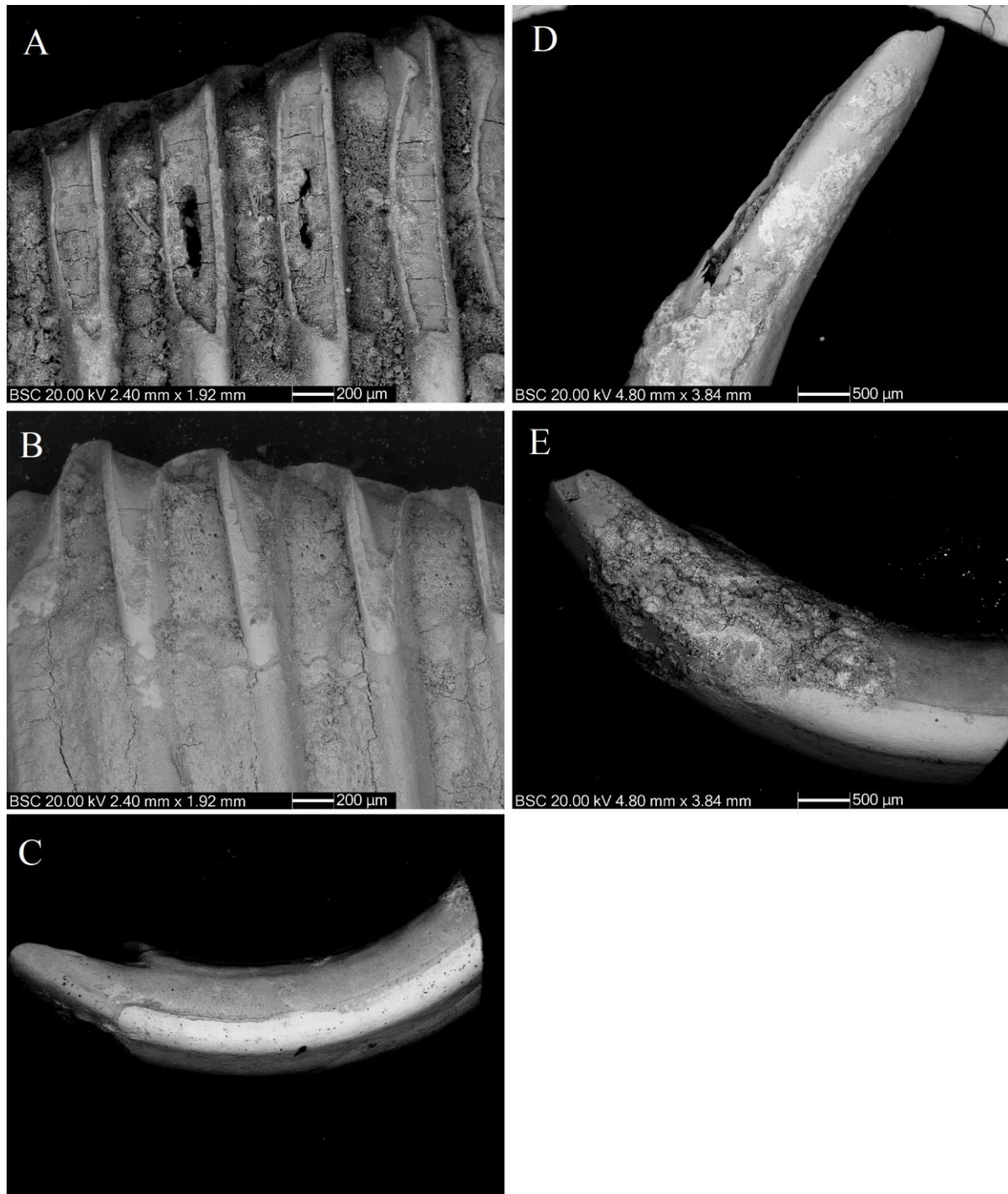


Fig. 5.09 – SEM images of Skara Brae material from Trench I: (A, Context 102) vole molar with chipped and digested salient edges, (B, Context 110) vole molar with heavy digestion between its top and location of alveolus ridge, (C, Context 110) upper incisor with light dentine loss on its tip, (D, Context 110) lower incisor with digestion loss of dentine and dentine cracked inwards, latter due to additional breakage and weathering, (E, Context 110) incisor with a combination of soil and organic matter around its tip.



Fig. 5.10 – (A) Completely charred left vole mandible, Context 110, and partially charred axis, Context 211 (Romaniuk et al. 2016A, Fig. 6). (B) Fragmented remains of partially calcinated vole mandible and molar, Context 102.

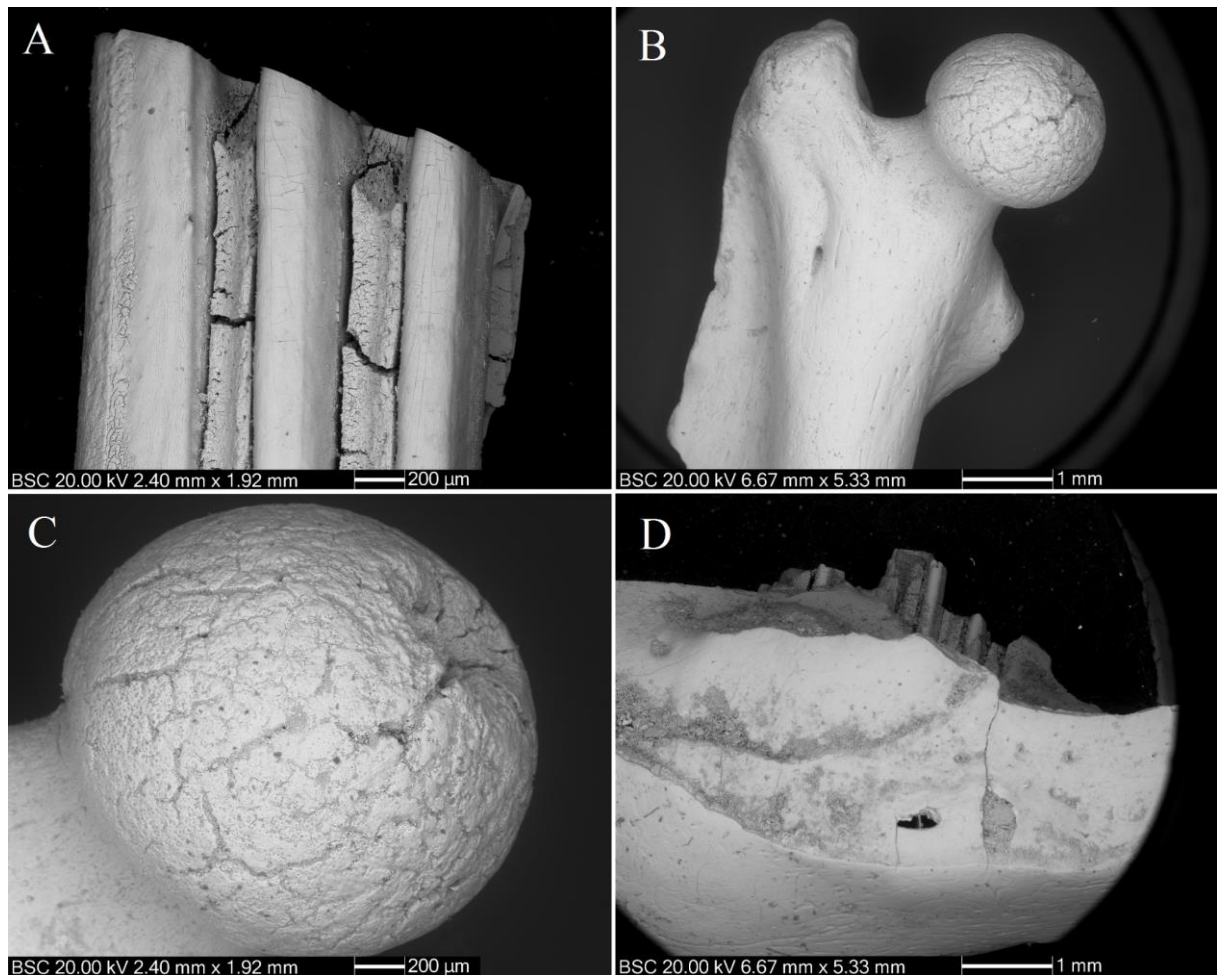


Fig. 5.11 – (A) calcinated molar, (B, C) carbonated/calcinated femur and (D) carbonised mandible from Context 110.

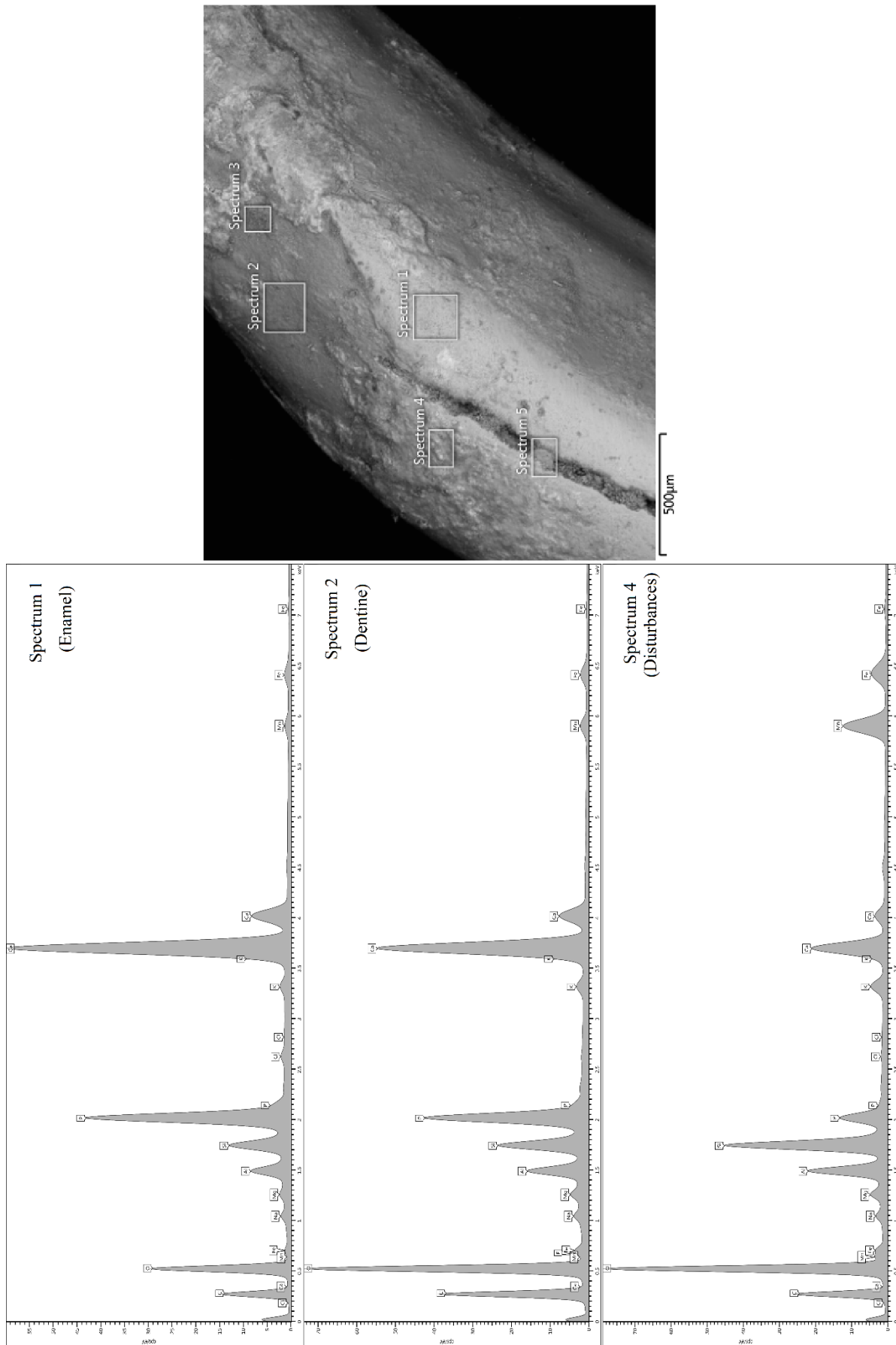


Fig. 5.12 – Three spectra of five taken from the burnt incisor, representing different surface features.

Table 5.03 – Percentage of digested specimens of each category for Trenches I to IV, including phases in Trenches I and II as well as accumulation types in Trench IV. For teeth both loose and intact finds were considered.

Phase/Acc	Trench	Percent of digested elements		
		Incisors	Molars	Epiphyses
0	I	0.93%	1.97%	2.07%
1	I	3.11%	4.78%	0.63%
Int	I	4.04%	12.67%	3.87%
2	I	4.47%	3.01%	0.48%
1	II	0.00%	0.61%	0.00%
2	II	0.00%	4.44%	0.00%
Main Acc.	IV	0.77%	0.71%	0.37%
Minor C.	IV	10.00%	0.00%	0.00%
	I	4.18%	3.71%	0.77%
	II	0.00%	1.43%	0.00%
	III	0.00%	0.00%	0.00%
	IV	1.04%	0.69%	0.36%
All Trenches		3.54%	2.99%	0.65%

Table 5.04 – NISP of remains showing burn marks in each trench and context, divided into heavily burnt (>75% surface), partially burnt (<75% surface) and charred loose teeth.

Trench & Context		Charred bone remains			Overall
		Charred bone fragment s >75%	Charred bone fragment s <75%	Charred teeth (loose)	
	102	4	6	5	15
	110	35	21	49	105
	119	0	0	1	1
	120	4	2	1	7
	126	12	6	4	22
	129	0	2	0	2
	132	28	17	16	61
	132.2	3	1	2	6
	134	16	21	15	52
Trench I	135	3	1	1	5
	139	1	2	2	5
	142	1	0	0	1
	146	0	1	2	3
	147	1	1	0	2
	155	0	1	0	1
	156	0	1	0	1
	157	1	1	1	3
	162	0	2	1	3
	164	1	3	0	4
	168	8	1	2	11
Trench II (211 & 213)		2	2	0	4
Σ		120	92	102	314

5.1.6. POSSIBLE TAPHONOMIC AGENTS

While the classification model was trained partially on Skara Brae data, it nevertheless provided more information about possible predators as well as a possible impact of non-predator related taphonomy (see Table 5.05). In Trench I, almost all bigger accumulations were classified as coming either from a diurnal raptor or a carnivorous mammal. In the case of the earliest Phase 0 and its key Context 168, algorithms trained on both original (“normal” method) and transformed data (“adjusted” method) returned such identification. Subsequent Phase 1 showed a more nuanced situation, with abundances showing scattering in for original and owl for transformed data-trained classification. More contexts were identified as scattering than ones originally used to train algorithms, with some showing partial identification as such. Accumulations with diurnal/mammal identification were present (e.g. Context 143 and 162) but occasional partial owl identification was also present. Only Context 141 showcased owl identification in the case of both data, though with adjustment moving identification to diurnal/mammal category. In turn, Context 149 showed complete owl match only in the case of adjusted approach, with the original one showing owl abundances but fragmentation more akin to scattering. Intermediate Phase and Phase 2, in turn, returned to results being predominantly diurnal/mammal, though adjusted classifiers often identified abundances as coming from owls, possibly due to better preservation than Phase 0. It was especially visible in the main contexts, especially the largest accumulations within late Phase 2 (Contexts 102 and 110).

In the case of Trench II, classification was dictated mostly by how many of these contexts were used to train models as well as general preservation of the assemblage. The general outline followed the one noted in Trench I, with both Phase 1 and 2 reflecting Phase 2 identification in main site stratigraphy. When it came to specific contexts however three out of seven (Contexts 204 and 205 from Phase 2, Context 214 from Phase 1) were included as an example of scattering and returned the same identification. The remaining contexts however showed some variety. Especially the midden deposition of Context 213 provided a combination of owl (*Abundances*) and diurnal/mammal (*Fragmentation Percentages*) groups, with adjusted algorithm providing owl as a result for both. Other two main accumulations (Contexts 209 and 211) were categorised as diurnal or mammal, with transformation changing identification in the case of *Abundances* to an owl. The oldest context (Context 215) showed a combination of scattering and owl identification, possibly due to a small general NISP ($n = 19$).

Off-site trenches followed the situation shown in Trench II. All contexts from Trench III and all minor ones from Trench IV were used in modelling as dispersal, leaving only two with other affiliation in Trench IV. Overall, Trench III provided classification highlining scattering, with adjustment showing a rather erroneous owl classification for *Abundances* but scattering for *Fragmentation Percentages*. Trench IV showed consistency in fragmentation towards owl classification and diurnal/mammal/owl variation for abundances, with adjustments showing identification of both as owl. All contexts from Trench III and all minor contexts from Trench IV showed scattering, with only two other classifications obtainable only in the case of adjustments. However, most interesting were identifications for Contexts 407 and 408. Context 408 was identified as diurnal/mammal accumulation when considering abundances, but as owl in the case of fragmentation. Adjusted algorithms however clarified the identification further, with both identifications being owl. Context 407 was unique due to combining very low relative abundances, leading to be considered as dispersal, but also low levels of fragmentation, ending with being considered as an owl in this regard. However, adjusted methods showed both data being classified as scattering.

The majority of *Abundances* and *Fragmentation Percentages* correlations coefficients came out as significant, pointing towards kestrels, hen harriers or short-eared owls. Almost all contexts previously identified to diurnal/mammal category showed the highest correlation to kestrels for both data groups, often beyond $r = 0.8$ in the case of original methods and $r = 0.7$ to $r = 0.8$ in the case of adjusted methods. Second most commonplace were correlations with hen harriers, with short-eared owls more common for transformed abundances data. Outliers from that pattern usually had lower but still significant correlation in the case of highest correlations, around $r = 0.6-7$, and a similar range of values for weakest obtained correlations. For Trench I, correlations for *Abundances* drifted from kestrels (Normal, $df = 11$, $r = 0.90$, $p = <0.001$) towards hen harriers (Adjusted, $df = 11$, $r = 0.75$, $p = 0.003$), resulting in Trench I also going towards this direction. In contrast, Trench II and contexts within drifted from kestrels towards short-eared owls, especially in the case of Context 211. Surprisingly, correlation with owls was found for joint Trench III and its biggest Context 337, possibly reflecting how small samples affect correlation rather than showing true similarity. Generally, lower correlation values than in other cases seem to confirm such notion. In extension, main context from Trench IV, Context 408, showed similarity with Trench II, providing best correlations to either kestrels (Normal) or short-eared owls (Adjusted).

Table 5.05 – Highest correlations (upper table) and classification outcomes (lower table) for *Abundances* and *Fragmentation Percentages*, based either on original references/signature data (Normal) or ones simulating partial dispersal/burial (Adjusted). The upper section of each table includes overall for trenches and site stratigraphy while the lower section includes major contexts. In the case of Trench IV major and minor contexts were also represented jointly.

Trench, Phase or Context	Highest Corr. Abundances				Highest Corr. Fragmentation			
	Normal		Adjusted		Normal		Adjusted	
Trench I	0.90	Kestrel	0.75	Hen H.	0.97	Kestrel	0.97	Kestrel
Trench II	0.93	Kestrel	0.85	Owl(Sh)	0.96	Kestrel	0.95	Kestrel
Trench III	0.91	Kestrel	0.89	Owl(Sh)	0.60	Owl(Sh)	0.70	Owl(Sh)
Trench IV	0.86	Kestrel	0.78	Owl(Sh)	0.88	Kestrel	0.86	Kestrel
Tr. I, Phase 0	0.95	Hen H.	0.75	Hen H.	0.97	Kestrel	0.99	Kestrel
Tr. I, Phase 1	0.91	Kestrel	0.82	Owl(Sh)	0.98	Kestrel	0.97	Kestrel
Tr. I, Interm.	0.94	Kestrel	0.82	Owl(Sh)	0.95	Kestrel	0.95	Kestrel
Tr. I, Phase 2	0.90	Kestrel	0.74	Hen H.	0.96	Kestrel	0.97	Kestrel
Tr. II, Phase 1	0.93	Kestrel	0.84	Owl(Sh)	0.96	Kestrel	0.94	Kestrel
Tr. II, Phase 2	0.83	Hen H.	0.91	Hen H.	0.91	Kestrel	0.90	Kestrel
Tr. IV, major	0.86	Kestrel	0.77	Owl(Sh)	0.87	Kestrel	0.86	Kestrel
Tr. IV, minor	0.82	Kestrel	0.86	Owl(Sh)	0.88	Kestrel	0.82	Kestrel
102	0.90	Kestrel	0.83	Hen H.	0.84	Kestrel	0.78	Kestrel
110	0.90	Hen H.	0.75	Hen H.	0.96	Kestrel	0.98	Kestrel
164	0.85	Kestrel	0.76	Hen H.	0.67	Kestrel	0.58	Kestrel
168	0.95	Hen H.	0.76	Hen H.	0.96	Kestrel	0.99	Kestrel
209	0.87	Hen H.	0.93	Hen H.	0.91	Kestrel	0.90	Kestrel
211	0.94	Kestrel	0.88	Owl(Sh)	0.90	Kestrel	0.91	Kestrel
213	0.74	Owl(Sh)	0.65	Owl(Lg)	0.91	Hen H.	0.82	Hen H.
337	0.80	Kestrel	0.88	Owl(Sh)	0.45	Owl(Sh)	0.55	Owl(Sh)
407	0.73	Hen H.	0.79	Hen H.	0.86	Owl(Sh)	0.87	Owl(Sh)
408	0.82	Kestrel	0.72	Owl(Sh)	0.87	Kestrel	0.86	Kestrel

Trench, Phase or Context	Abundances Classification		Fragmentation Classification		Final Result	
	Normal	Adjusted	Normal	Adjusted	Normal	Adjusted
Trench I	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Trench II	Scattering	Owl	Diurn./Mamm.	Diurn./Mamm.	Contested	Accumulation
Trench III	Scattering	Owl	Scattering	Scattering	Scattering	Contested
Trench IV	Diurn./Mamm.	Owl	Owl	Owl	Accumulation	Owl
Tr. I, Phase 0	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.
Tr. I, Phase 1	Scattering	Owl	Diurn./Mamm.	Diurn./Mamm.	Contested	Accumulation
Tr. I, Interm.	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Tr. I, Phase 2	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Tr. II, Phase 1	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Tr. II, Phase 2	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Tr. IV, major	Diurn./Mamm.	Owl	Owl	Owl	Accumulation	Owl
Tr. IV, minor	Scattering	Scattering	Scattering	Diurn./Mamm.	Scattering	Contested
102	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
110	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
164	Diurn./Mamm.	Diurn./Mamm.	Scattering	Owl	Contested	Accumulation
168	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.
209	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
211	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
213	Owl	Owl	Diurn./Mamm.	Owl	Accumulation	Owl
337	Scattering	Scattering	Scattering	Scattering	Scattering	Scattering
407	Scattering	Scattering	Owl	Scattering	Contested	Scattering
408	Diurn./Mamm.	Owl	Owl	Owl	Accumulation	Owl

5.2. LINKS OF NOLTLAND

5.2.1. ASSEMBLAGES QUANTIFICATION AND DISTRIBUTION

Links of Noltland has provided the biggest quantity of micromammal finds among all studied sites, over 42,000 NISP and 2,000 MNI (Table 5.06). Especially Trench A (the “Grobus”) contained massive assemblages, often beyond 1000 NISP, resulting in 34,000 NISP obtained from the area of about 140 m². In turn, Trench D, a 48 m² trench through anthropic layers of cultivation and refuse, provided over 8,000 NISP. It is a relatively high quantity considering the other sites (3rd considering trenches as separate sites, after Trench A and Skara Brae Trench I) but about 30% smaller than expected considering Trench A density per m², 172 vs 244 NISP/m². While both sites showed relatively similar, high completeness ratios (Skeletal Completeness of 26% and Average Abundances of 29% for Trench A, respectively 24% and 27% for Trench D), it was on average lower than observed in Skara Brae Phase 2 of Trench I or main accumulations within Trench IV. Additionally, both provided exclusively (Trench A) or almost exclusively (Trench D) bones and tooth fragments of an Orkney vole, with remains of a single field mouse found only in Trench D. However, in the case of non-species-specific classes, Trench A provided far more unidentified rodent MNI, consisting of over a third of all MNI counted. In contrast, Trench D has shown only four unidentified MNI, only a minor addition to the trench overall MNI. However, significance testing did not show strong results for either trench.

In terms of stratigraphy, Trench A was only explored to a restricted degree, resulting in all data coming mostly from the abandonment and refuse phase. As context relationships could not be reconstructed for this long, but relatively consistent, period (Fig. 5.13), it seemed best to follow spatial data obtained alongside data retrieval. While spatial recording was not exclusive for specific squares, resulting in a sample sometimes relating to up to three squares, the visualisation of assemblage ranges was possible. The localisation of the largest and best-preserved contexts was informative (see Fig. 5.14), being often found nearby structure entries and cells/passages within its northern part. The largest assemblage encountered, Context 48, provided about 5,500 NISP as well as high completeness (30% for Skeletal Completeness, 34% for Average Abundances). It was found in the so-called Hazel’s cell, a rounded room with an opening to a Passage B, in turn leading from Square HO89 to HQ 90 (eastern entrance). Hazel’s cell also provided other large contexts, such as for example Context 58, not as complete (27%

Skeletal Completeness and 32% Average Abundances) but often occupying not only the room but also Passage B nearby. However, the northern passages, beforementioned Passage B as well as A (Squares HO89, HO90 and HP90) also provided large accumulations, including some showing completeness ratios comparable to Skara Brae contexts from Phase 2, such as Context 120 (Passage A, 31% Skeletal Completeness, 36% Average Abundances), 29 (Passage A), 34 (Passage B) and 195 (Passage B). However, not all large contexts showed such high completeness, with some, for example Context 60 (Passage B), showing far lower preservation (12% Skeletal Completeness, 17% Average Abundances).

The southern entrance to the Grobust (Squares HN85 and HO85), including adjacent squares (Squares HP8, HQ85, HO86, and HQ86), was also filled with micromammal remains. Especially the entrance provided relatively small and undispersed contexts containing massive assemblages (Contexts 170 and 185) but with relatively moderate completeness (21-22% for Skeletal Completeness, 26% for Average Abundances). The southern and central squares of the southern chamber were also filled with micromammal remains (Contexts 16 and 193), covering a relatively wide area but providing surprisingly high completeness ratios (up to 47% Average Abundances in Context 193). The smaller contexts that provided less NISP also varied in completeness but higher values usually corresponded with the presence of larger contexts nearby. The largest and best-preserved were within the beforementioned passages and Southern Chamber, with the link between those regions in a form of Passage C also providing some finds (e.g. Contexts 14 and 26). Finds on the outside of the Grobust were rare, with single finds at best, although retrieval of material from outside of the structure was not a priority during the excavations.

In contrast to Trench A, Trench D was explored thoroughly up to the bedrock, thus providing both complex stratigraphy (Fig. 5.15) as well as a clear spatial location of all retrieved micromammal material (Fig. 5.16). Micromammal finds were obtained from all contexts apart from natural, possibly not sieved, Contexts 39 and 40 and most recent, single abandonment Context 1. Some contexts spanned over the majority of Trench D, showing the lack of natural constraints as well as a context simply forming gradually on top of older ones, with the majority of disturbances and intrusive stratigraphy coming either from cultivation efforts or wall construction and later deterioration. The earlier phase, related solely to farming and refuse disposal, provided multiple small contexts with complex stratigraphic relationships. Among nine recorded layers, six provided micromammal remains, with the site coverage ranging from small deposits within one square (e.g. Context 35, only 14 NISP; 17% Skeletal Completeness

and 20% Average Abundances) up to assemblages present over a half (Context 33) or majority (Context 32) of the studied area. Additionally, the size and location of samples from Contexts 32 and 33 that provided micromammal remains showed a tendency to concentrate within just one or two squares, with adjacent squares providing fewer finds with lower overall completeness. In the case of 32 squares which provided over 200 NISP, including one with far higher completeness ratios than others found (FR89, 32% Skeletal Completeness and 36% Average Abundances), with other samples showing far lower NISP as well as completeness. Context 33 also provided a similar situation, with two samples visibly more complete (samples from Squares FR87 and FR88), with completeness ratios above 20% and minor samples present in adjacent squares. However, in both contexts one could notice the presence of finds within Square FQ83, away from the concentration. It may indicate a spread over a wider area from the same assemblage but may also be a sign of more than one assemblage present within one context.

Data from later phases repeats the pattern seen in Phase I, especially contexts covering wider areas having a noticeable concentration within specific squares. This situation is repeated in Phase II, with half of all NISP coming from only one square, with moderate/high completeness ratios (Square FQ89, 25% Skeletal Completeness, 30% Average Abundances). In the remaining eight squares covered by the assemblage each showed less than 100 NISP and six had far lower completeness. Interestingly, two minor samples showed completeness equivalent to the main sample, including one adjacent to it (Square FR89, 22% Skeletal Completeness, 25% Average Abundances) and one at the verge of the assemblage (Square FR87). Another period, representing only refuse deposition, provided more contexts showing a similar pattern. However, NISP were on average far lower than in the first two phases. In turn, Phase IV, wall construction, showed minor deposition or dispersal alongside the constructed wall but of moderate completeness ratios (~20%). The biggest concentration however was found within the Disturbance Context 13, where a famous concentration of deer remains was found (see Sharples 2000, Clarke et al. 2017). It provided a concentration of micromammal remains roughly in the middle of the excavated area, exhibiting relatively high completeness (25% Skeletal Completeness, 30% Average Abundances). All but one adjacent square provided samples, with seven showing lesser completeness and one similar to the main sample. However, Phase V, where deposition of deer remains might have actually happened alongside a minor stone construction, did not provide any remains but one bone, although possibly because of the low volume the phase actually occupied within the stratigraphy. Following contexts within

Phase VI, a temporary abandonment of the area, did not show any big concentrations apart from one context containing two samples, most likely separate assemblages.

The last two phases of site utilization also have shown the repetition of observed deposition patterns, but with better average completeness among retrieved samples. It was visible in Contexts 4 and 8 of Phase VII, the last phase of known cultivation of the wider area within the Neolithic period. Context 8, the second biggest micromammal accumulation on the site, also provided a dominating sample in the north-western end of the excavated area, with very high completeness (38% Skeletal Completeness, 39% Average Abundances), highest observed in Trench D. Context 4, was unique due to the assemblage running across the midline of the area but even though three biggest samples came from adjacent squares, with completeness ratios ranging from 21% to 32%. The latest recorded Context 2, from Phase VIII, provided only a small amount of NISP but with average to high completeness ratios.

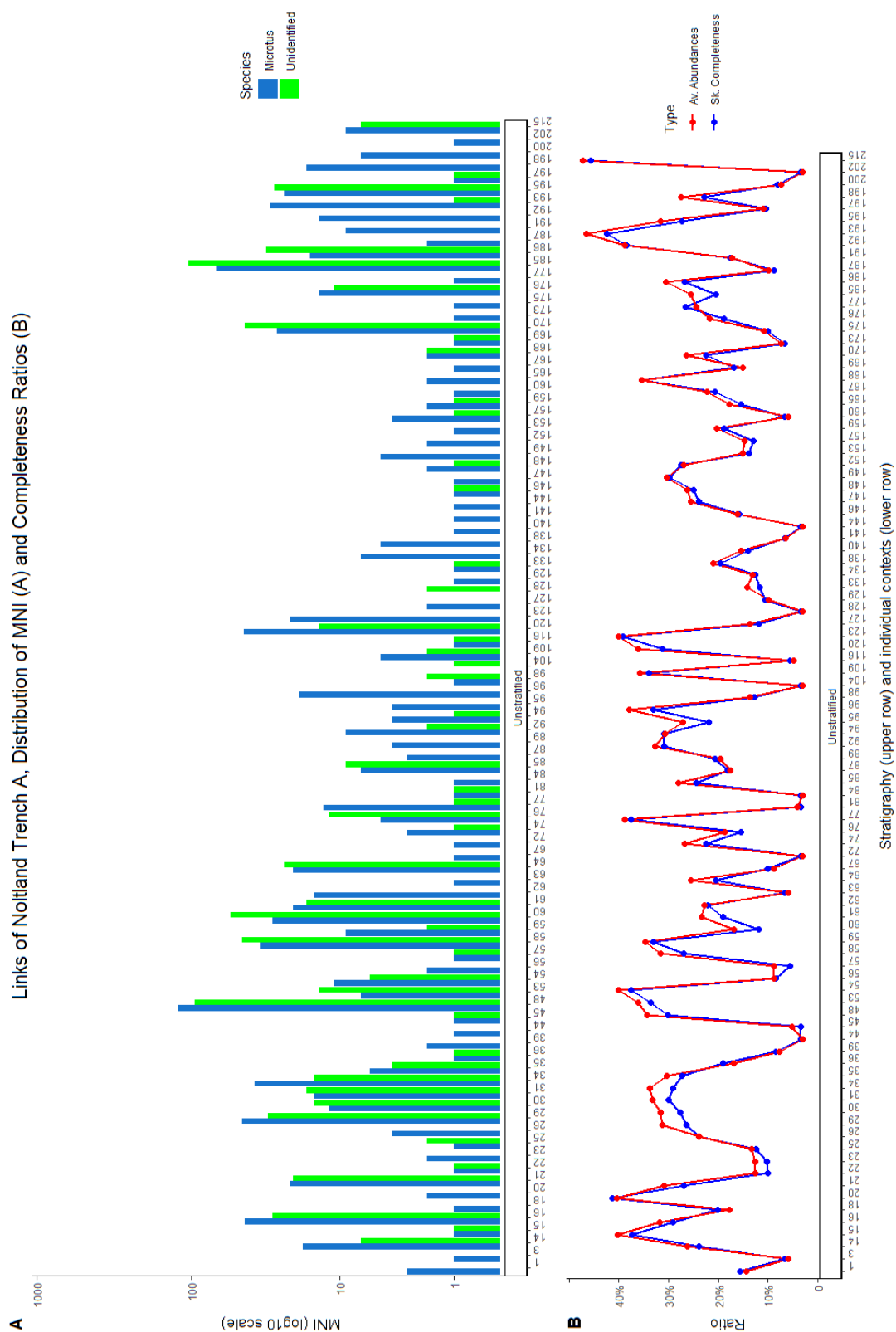


Fig. 5.13 – A (upper plot): Distribution of MNI in Trench A. Due to no stratigraphy being reconstructed data are presented alongside context number.

B (lower plot): values of completeness ratios (Skeletal Completeness, Average Abundances) for each context in Trench A, arranged in the same way as in plot A.

Links of Noltland Trench A
NISP allocation of selected contexts within the site grid

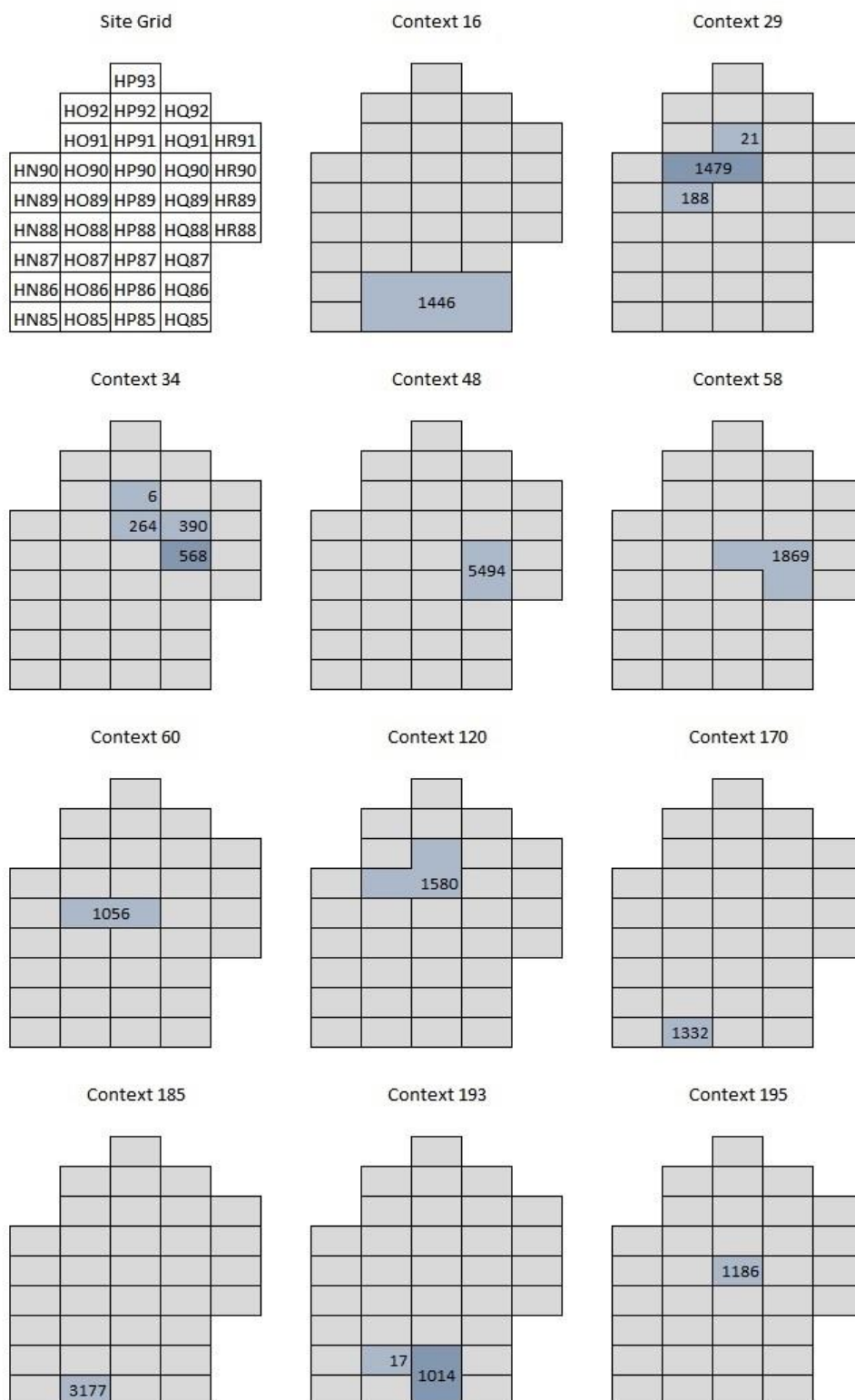


Fig. 5.14 – Spatial distribution of NISP according to square grid in Trench A, shown for all contexts beyond 1000 NISP in size. If applicable, main area of deposition in dark blue. Due to several samples being recorded for a more than one square values are sometimes calculated jointly for up to six squares.

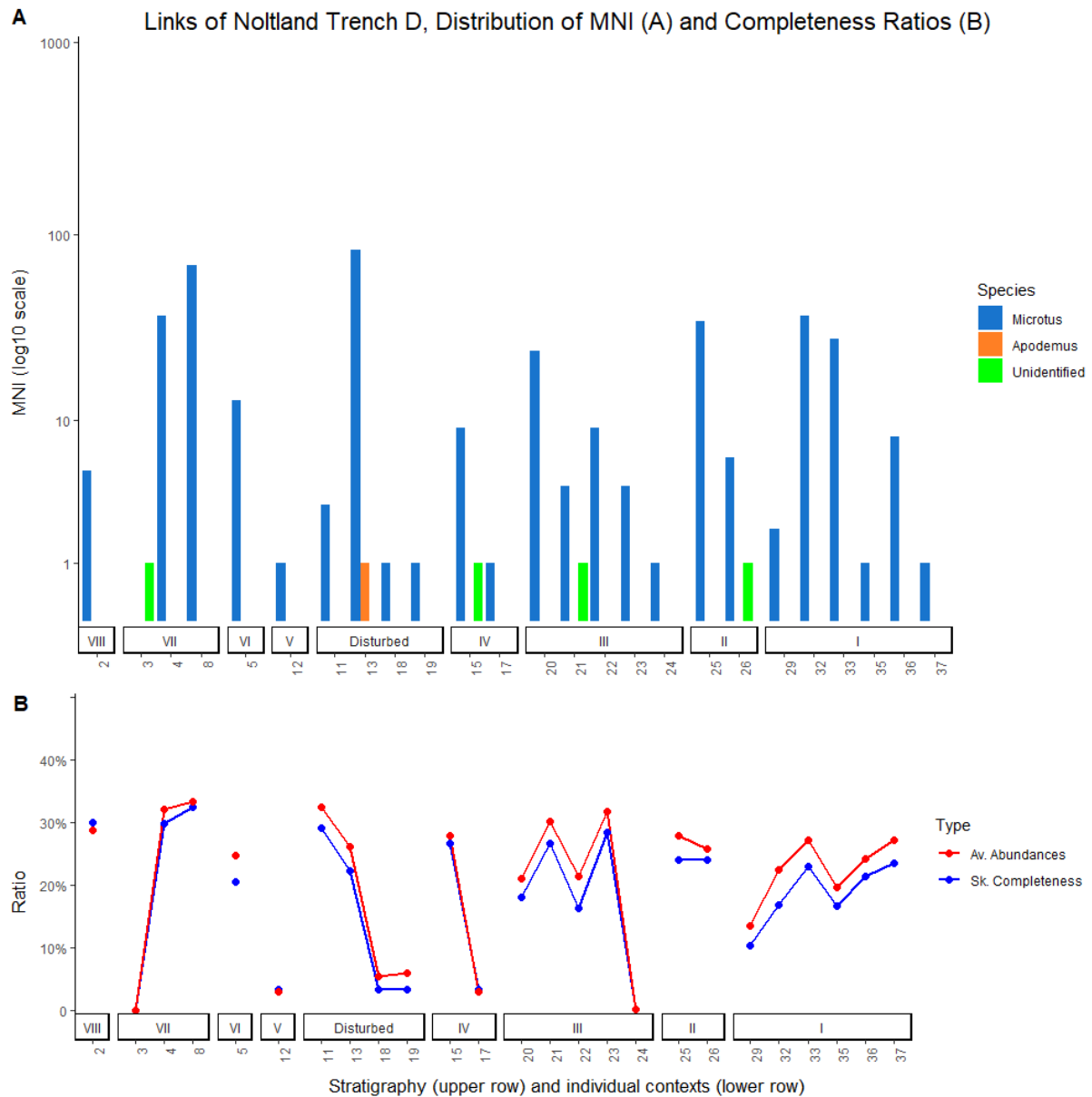


Fig. 5.15 – A (upper plot): Distribution of MNI in Trench D. Contexts were arranged according to site stratigraphy.

B (lower plot): values of completeness ratios (Skeletal Completeness, Average Abundances) for each context in Trench D, arranged in the same way as in plot A.

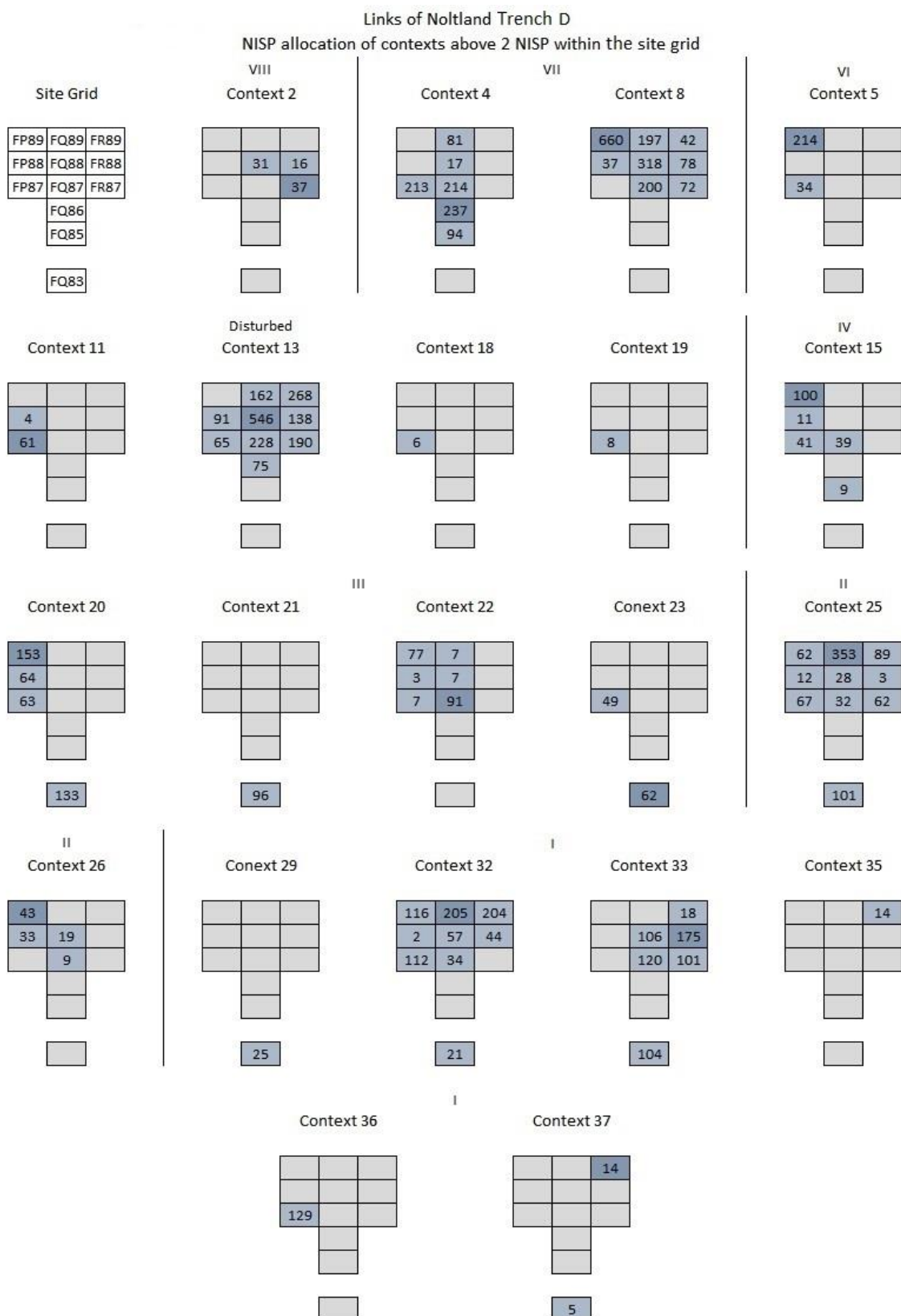


Fig. 5.16 – Spatial distribution of NISP in Trench D, shown for all contexts apart from the smallest four (Contexts 3, 12, 17 and 24). If applicable, main area of deposition in dark blue.

Trench	Phase	Description	Dating	Weight (g)	Contexts	Samples	Microtus		Apodemus		Unid. Rodent		ΣNISP	ΣMNI	
							NISP	MNI	NISP	MNI	NISP	MNI			
A	---	---	max ~ 2855/2480-2005 BC	545.02	92	206	13309	987	0	0	20890	688	34199	1675	
	I	cultivation & refuse deposition	start 3160 ~ 2870 BC	27.3	6	20	1028	77	0	0	0	578	0	1606	77
	II	cultivation	end 2850-2640 BC	16.61	2	15	616	41	0	0	0	312	1	928	42
	III	Refuse deposition	max ~ 2830-2300 BC	14.99	5	14	491	42	0	0	0	323	1	814	43
	IV	wall construction	~ 2500-2250 BC	7.19	2	6	121	10	0	0	0	80	1	201	11
D	Disturbed	deposits around phase IV wall	---	42.62	4	13	1253	88	2	1	587	0	1842	89	
	V	deer deposition & stone constr.	max ~ 2280-2130 BC	0.1	1	1	1	1	0	0	0	0	1	1	1
	VI	possible abandonment	---	4.05	1	2	136	13	0	0	112	0	248	13	
	VII	ard & spade cultivation	max ~ 2200-1930 BC	54.11	3	15	1250	106	0	0	1211	1	2461	107	
	VIII	wall construction	---	1.44	1	3	34	5	0	0	50	0	84	5	
no match		---	0.85	---	5	90	8	0	0	2	0	92	8	8	
		Σ		169.26	25	94	5020	391	2	1	3255	4	8277	396	
		Σ		714.28	117	300	18329	1378	2	1	24145	692	42476	2071	

Table 5.06 – Weight, NISP and MNI counts distribution for Links of Noltland trenches, depending on specific species categories. In the case of Trench D, further breakdown based on the recorded stratigraphy was also shown.

5.2.2. AGE DATA DISTRIBUTION

Both trenches provided marginally more varied situations in the case of early fusing epiphyses than Skara Brae Trenches (Fig. 5.17). overall, only about 2.5% of all epiphyses falling in this category were found unfused in Trench A, with Trench D providing relative frequency almost four times larger (9%). This suggests some, although restricted, presence of juveniles within Trench D. The least represented were unfused distal humeri, with only 12 such finds in Trench A and 18 in Trench D. Unfused distal tibiae were most common in Trench D, with about 16% of all finds being found in this state. Phases that provided enough data to analyse in Trench D showed a similar outline as the whole trench, with the noticeable exception of Phase IV and VI. In the former, retrieved epiphyses were always scored as fused, while in the latter, out of 14 early epiphyses finds, half were found unfused. This included five humeral ends, over a quarter of all found in this trench.

The difference between trenches was also noticeable in the case of middle fusing epiphyses. Once again, Trench A showed predominantly fused specimens, with about 2.7% cases being found unfused. However, Trench D unfused cases showed relative frequency of 13%, about 4% higher than in the early fusing category and five times more than in Trench A. It may signify a minor contribution, but greater than in Trench A or Skara Brae, of the overall presence of young individuals within Trench D assemblages. This outcome was due to both middle fusing epiphyses differing between trenches, both providing higher ratios of unfused to fused specimens. However, on top of that, unfused proximal femora were numerically more common in Trench D, with 41 unfused cases in contrast to only 17 fused ones found inside the Grobust. Middle fusing epiphyses distribution across Trench D phases was similar to joint overview. However, Phase VI provided far more unfused specimens, approaching but not achieving about 50%.

Late fusing epiphyses resembled the situation already encountered in Skara Brae, although with additional variation between both trenches. Overall more than half of recovered late fusing epiphyseal surfaces did not show any traces of fusion, which was more pronounced in the case of Trench D (77%) than Trench A (62%). Similar to Skara Brae, best ratio of fused cases were with proximal ulnae, with Trench A showing about 9% more in relative frequencies than Trench D (61% against 52%). In the case of the remaining three scored epiphyses Trench A showed a roughly similar outline to Skara Brae, with Trench D showing differences to other Neolithic areas and trenches. Distal femora and proximal humeri showed roughly similar ratios, with

about 37-38% being found fused, while proximal tibiae were rarely found in such state, in about 4% of all times. In the case of Trench D however femoral cases were most pronounced (18%), with proximal humeri (13%) and tibiae (15%) not far behind. A minor variation between phases could be noticed but, once again, Phase VI showed strong deviation from observed patterns. It is due to a fact that only one late fusing epiphysis was found within associated contexts, resulting in an over 95% relative frequency of unfused elements.

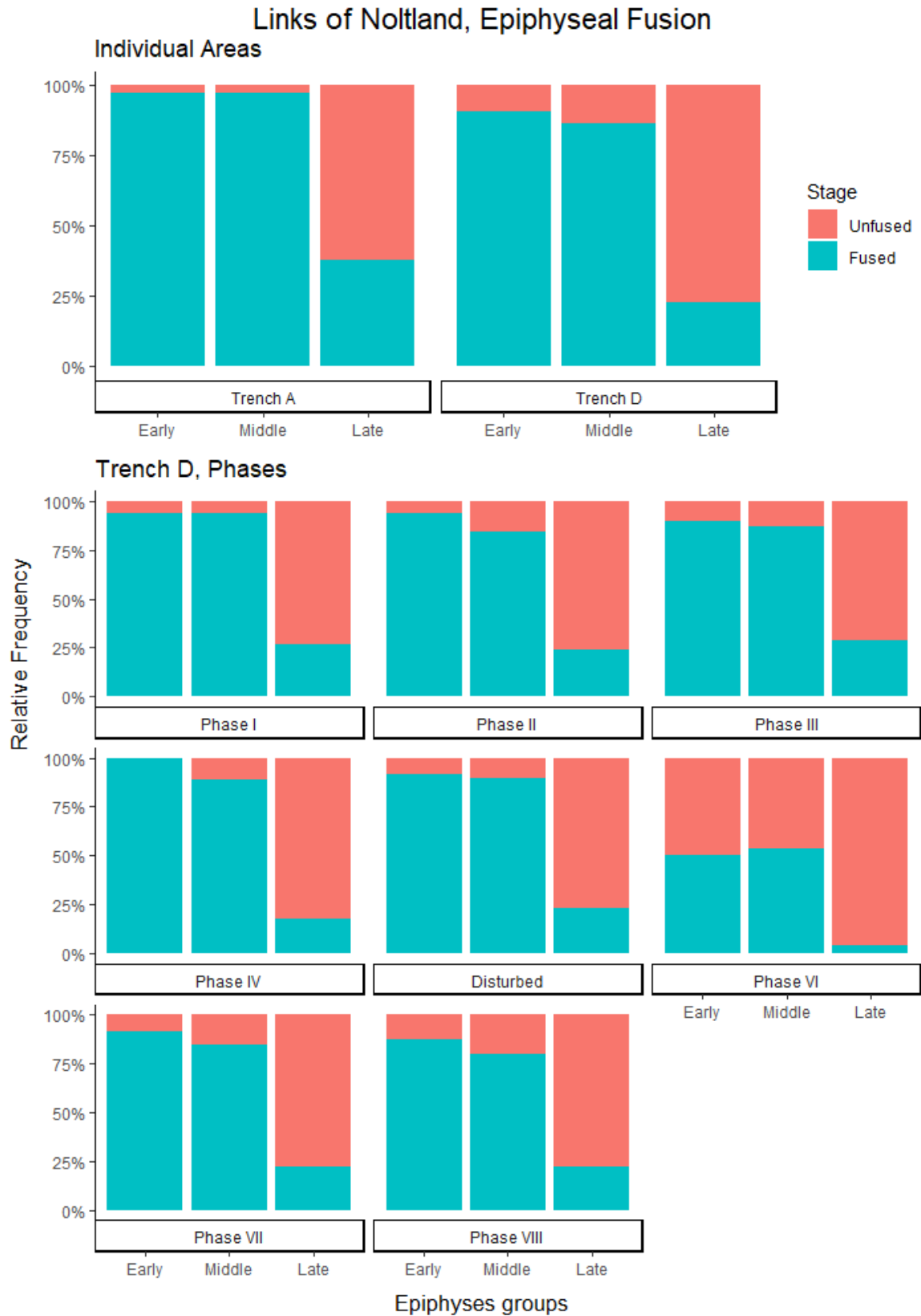


Fig. 5.17 – Links of Notland, epiphyseal fusion expressed as a relative frequency of NISP (red-unfused, blue-fused) and grouped in three main groups related to individual's age (early/middle/late). Upper plots reflect each Trench, with lower plots showing stratigraphy in Trench D.

5.2.3. FREQUENCIES, ABUNDANCES AND INDICES

Trench A and Trench D differed consistently between each other in the case of *Skeletal Frequencies* obtained (Fig. 5.18). Trench A was dominated by front and hind limb finds, 32% and 34% respectively, with vertebrae (19%) and skull fragments (15%) being far less common. This pattern was quite consistent across major accumulations from both northern (e.g. Contexts 29, 48 and 58) and southern (e.g. Context 185) sections of the site, with visible but minor variation in the case of vertebrae. In turn, Trench D has shown all groups beyond 20%, with maxillary/mandibular fragments most common (28%). Variation within the trench was also higher, with only Phases II and possibly VI showing no major deviations from the relationships between *Skeletal Frequencies* seen for the whole trench. Phase I, the oldest cultivated layer, had frequencies of skulls and vertebrae inverted, although one major individual context (Context 32) did show almost uniform frequencies distribution. Most unique were disturbed layers, with a far higher relative presence of skulls, 35% in general as well as in the case of biggest context (Context 13), followed by hind limbs, front limbs and finally vertebrae. Phase VII, the last proper cultivation layer, has shown a far bigger role of vertebral remains (31%) with skulls (25%), which was especially visible in the biggest context retrieved from this phase (Context 8). The latest archaeological layer provided mostly hindlimb bones (35%) although more fragile elements were not that rare (e.g. vertebrae, 23%).

Abundances obtained from Trench A showed consistency across much of the retrieved assemblages (Fig. 5.19). In general, maxilla and mandible relative abundances were low both on-site, respectively 26% and 42%, as well as when compared with other sites, especially Skara Brae. The majority of contexts followed such values, especially in the case of maxillae, with deviations usually showing even lower values (e.g. Context 185 – 10% and 27%). Loose incisors were comparable to Skara Brae, with 75% relative abundances, while molars showed slightly higher values, around 38%. However, larger contexts were the main source of such finds, with all unique cases investigated showing similar or higher values. Scapulae, pelves, radii, vertebrae and minor limb bones (CTMP) showed minor variation around mean values, rarely providing values higher than 20% (for larger bones) or 5% (for smaller bones). However, the main limb bones were commonplace, with the highest values usually obtained for humeri. On average, humeri provided relative abundances of about 80%, with some contexts beyond 100% (e.g. Context 48 or 58) due to humeral fragmentation. Femora and tibiae showed 67% in each case, with a positive skew towards larger contexts in the case of former and negative in

the latter. Ulna relative abundances were very consistent across contexts, with about 35 +- 5% variation.

Trench D however provided far different *Abundances*, with further differentiation between phases and specific contexts, often within the 10% range. The least differences were among minor limb bones (CTMP), most likely due to a small NISP of such finds to expected numbers. However, in the case of other small bones, like vertebrae, the variation was quite substantial – from close to 0% up to over 11%, especially if checked against the overall value of 6.7%. Skull elements such as maxillae and mandibles were a good example of differences within bigger anatomical groups. The cumulative relative abundance of maxillae was 55%, with variation from 5% to about 75% depending on a phase, while in the case of mandibles it was 76%, with variation covering almost all of the range from 50% to 100%. However, maxillary abundances did not show a consistent pattern across the phases while mandibular abundances strongly differed between early (Phase I to IV) and later (Phase VI-VIII and disturbed) phases, with about 30% better results in the case of the latter. Interestingly, some resemblance of this can also be tracked for isolated teeth, with latter phases generally showing more incisal abundances (especially Phase VI) and fewer molar abundances. The latest contexts (VIII) showed, however, both far fewer incisors and fewer molars (25% and 15% respectively), far lower than average on the site (39% and 61%). In the case of the remaining skeletal elements only the latest two phases have shown an anomaly – with tibial abundances above 50% (Phase VII) or exactly on 100% threshold (Phase VIII). However, the latter may be due to smaller NISP and MNI numbers biasing the results. It may be the case as the comparison of individual contexts provided fewer complex abundances, with any significant differences noted within beforementioned maxillary/mandibular and isolated teeth abundances.

The analysis of indices was a confusing task due to both trenches providing very different patterns both to Skara Brae as well as to each other (Fig.5.20), sometimes resulting in incomparability. Isolated incisor % range in the case of Trench A was very wide, three times as much as in Skara Brae or Trench D. It was most likely an impact of relatively low maxillary/mandibular abundances in relation to high numbers of incisor fragments found. Moreover, many larger contexts, for example Context 48, provided very high values (here 628%), resulting in their automatic incomparability with data obtained in Andrews (1990) due to overshooting the established scale. In the case of Trench D, with a similar scale of values as Skara Brae, the majority were between 100% and 200%. Moreover, data obtained from main contexts was also included in this range (e.g. 149% for Context 13). A similar situation occurred

in the case of complex index of postcranial to cranial bones, where obtained values, with calculation including teeth, showed a range about three times of Skara Brae and Trench D. However, clustering was mostly within a specific range, with the majority of contexts falling into 0 to 150% range, as is the case in other Neolithic sites. A minor difference could be noted, with Trench A showing bigger values around 50-150% range and Trench D predominantly within 0%-50%. Similarly, while isolated molars have also shown a far larger range of values than Skara Brae, the obtained data fell mostly within the same values, with the majority of values from 0% to 20% for both trenches. The remaining two indices were not as complex to interpret, usually with Trench D contexts showing smaller ranges and lower values to Trench A.

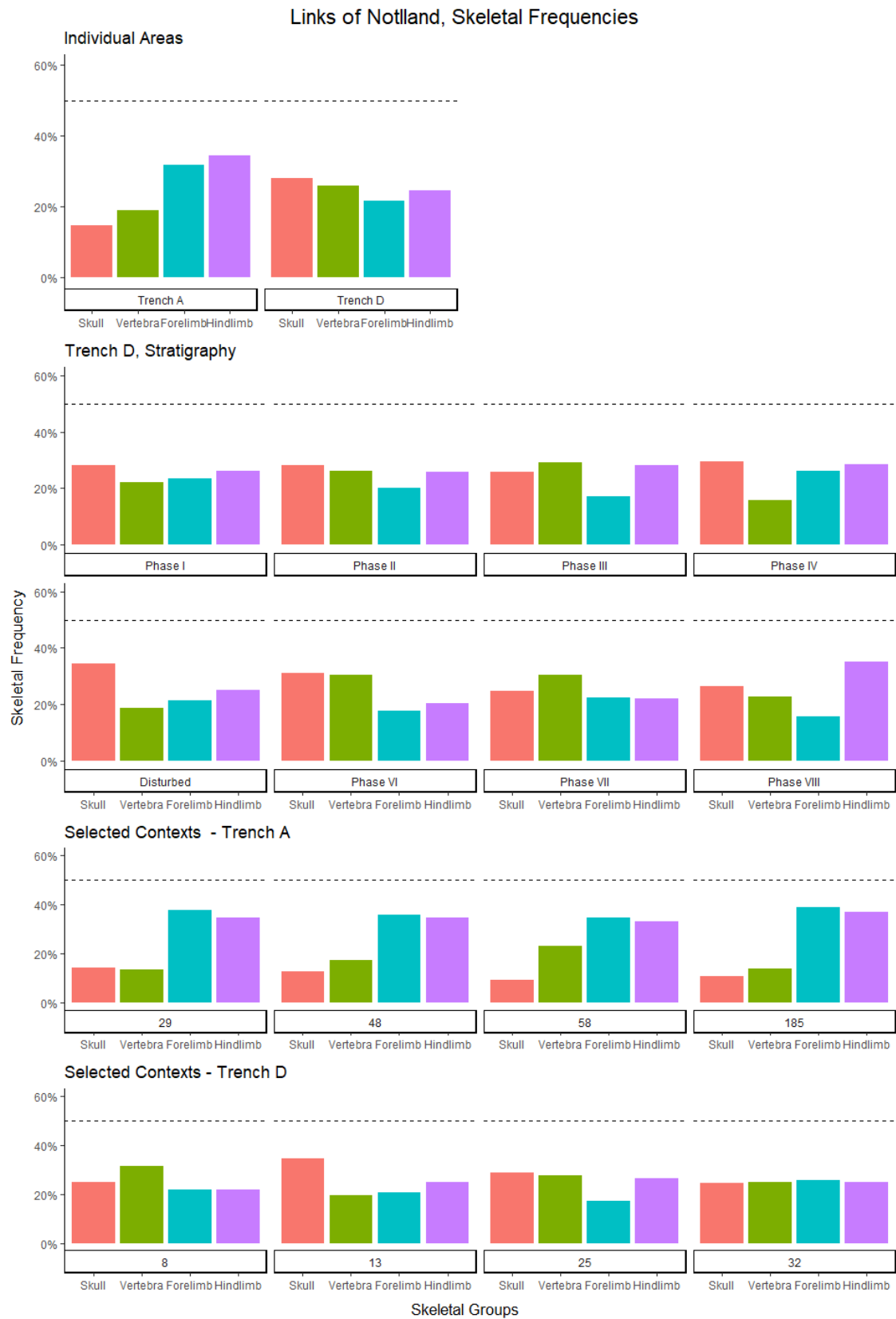


Fig. 5.18 – Links of Notland *Skeletal Frequencies*, plotted for main trenches (upper plots), stratigraphy in Trench D (middle plots) and selected contexts from each trenches (lower plots).

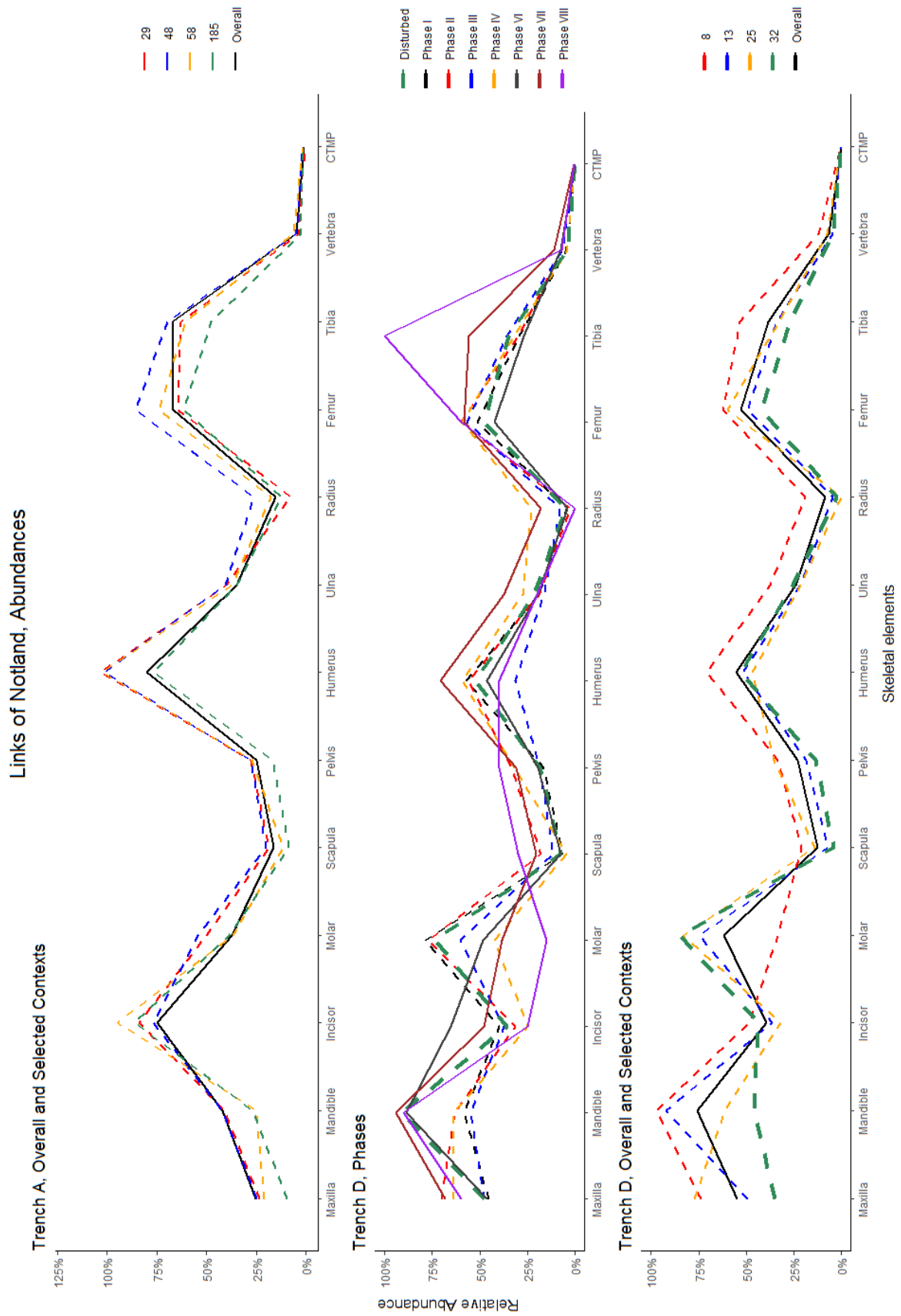


Fig. 5.19 – Links of Noltland *Abundances* of specific skeletal elements, plotted for Trench A and D (overall plus major contexts) as well as the stratigraphy of Trench D.

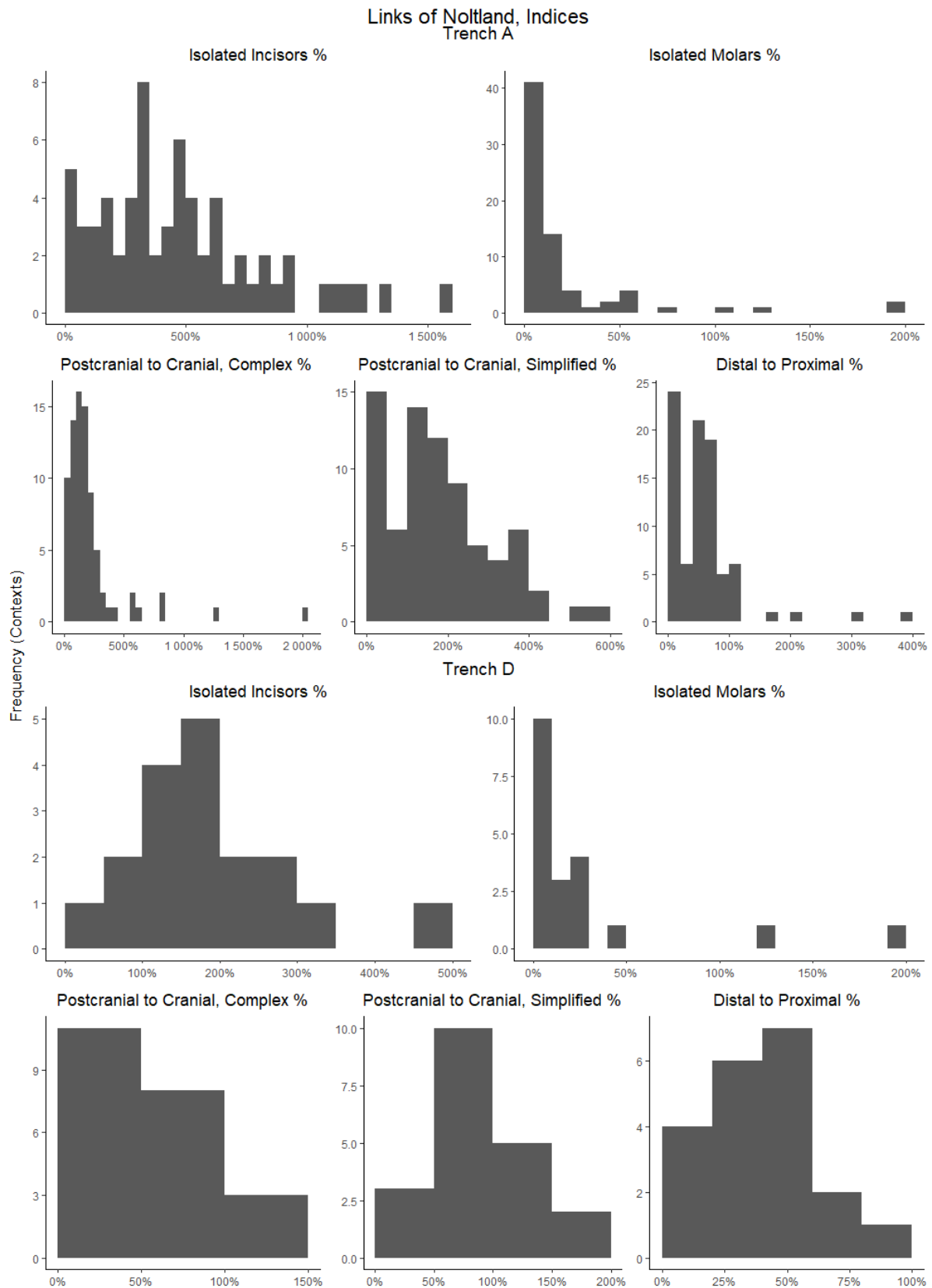


Fig. 5.20 – Links of Noltland, frequency distribution of index results for Trench A (upper) and D (lower plots) *Indices*.

5.2.4. FRAGMENTATION

The skull elements breakage pattern was vastly different from one established for Skara Brae, representing on average far more altered remains (Fig. 5.21). While both trenches provided more maxillae in relatively intact although broken skulls than Skara Brae ($n = 63$ for Trench A, $n = 28$ for Trench D), overall these constituted only a minor percentage of maxillary finds. Moreover, maxillae with zygomas were also present in roughly the same numbers, resulting in remaining finds being either only maxillary bone or a skull fragment, with predominance of the latter. Variation between trenches was minor, with better-preserved cases more common in Trench D. In turn, stratigraphy within Trench D showed differences in preservation between phases in terms of percentages but not necessarily raw numbers. In the case of Phase IV, maxillae found in skulls are several times more common than in other phases. However, the same number of such finds came from Phases II, IV and disturbed layers. In turn, no such finds came from Phases VI and VIII, with the latter also not providing any maxillae with zygoma intact.

Mandibular elements also provided a pattern with more severe breakage than Skara Brae did. The pattern was very similar to skull breakage, with minuscule percentages of well-preserved specimens, the predominance of fragments and relatively better preservation in Trench D. The only difference on trench level was that the number of complete bones retrieved was smaller than in the case of Skara Brae, just 28 NISP. Variation between phases was however greater than in the skulls, with once again Phase IV showing best preservation overall and Phase VIII lowest obtained.

The postcranial bones also followed skull pattern of heavy fragmentation. In all four investigated cases Trench A provided far fewer complete cases than Trench D, with the smallest difference in the case of the ulna (13% to 17%) and biggest in that of the humerus (10% to 35%) bones. Within specific phases, the best preservation could be found within Phases IV, VI, VII, with less preserved either being early (Phases I, II and III), Disturbed or late (Phase VIII) phases. The only difference is noticeable for ulnae, with the most complete pattern emerging in the latest phase. It is likely due to a small number of ulnar finds in overall ($n = 2$).

The largest assemblages within Trench A and D also differed along established patterns (Fig. 5.22). Contexts within Trench A almost completely consisted of fragmented remains, visible in the case of both cranial and postcranial elements. Maxillae showed better preservation than

mandibles, although in all cases over 75% of all finds were just skull fragments. Mandibles pattern was more extreme, with over 90% being fragmented remains. In the case of postcranials, the best preservation was found in the case of forelimb bones, especially ulnae which showed values between 5% to 10%. The least preserved were hind limb bones, with almost all finds being fragments. Noticeably, the preservation of the main accumulations within Trench D was clearly aligned negatively with context age. The best-preserved was possibly Context 8 from Phase VII, showing mandibles (less than 50% being heavily fragmented) and proximal limb bones (42% of all humeri and 35% of femora found intact) being least altered. In stark contrast, Context 32 from the first phase showed universally worst preservation, with no intact ulnae found. Some variation was however present in distal limbs, with Context 13 showing the highest number of ulnae and Context 25 of tibiae preserved.

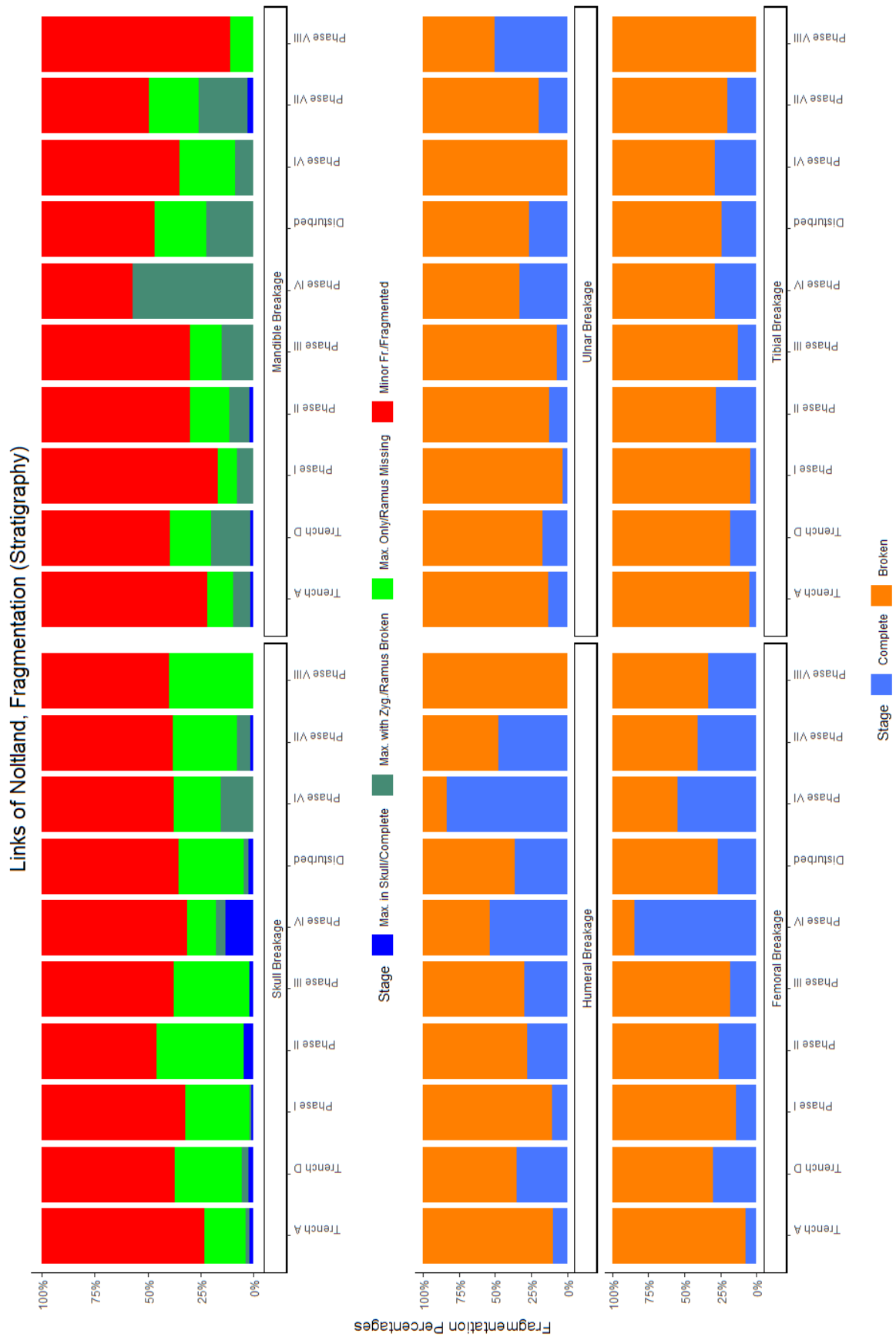


Fig. 5.21 – Links of Noltland, skull (upper row) and postcranial (two lower rows) breakage for Trench A and D (overall) as well as stratigraphy of Trench D.

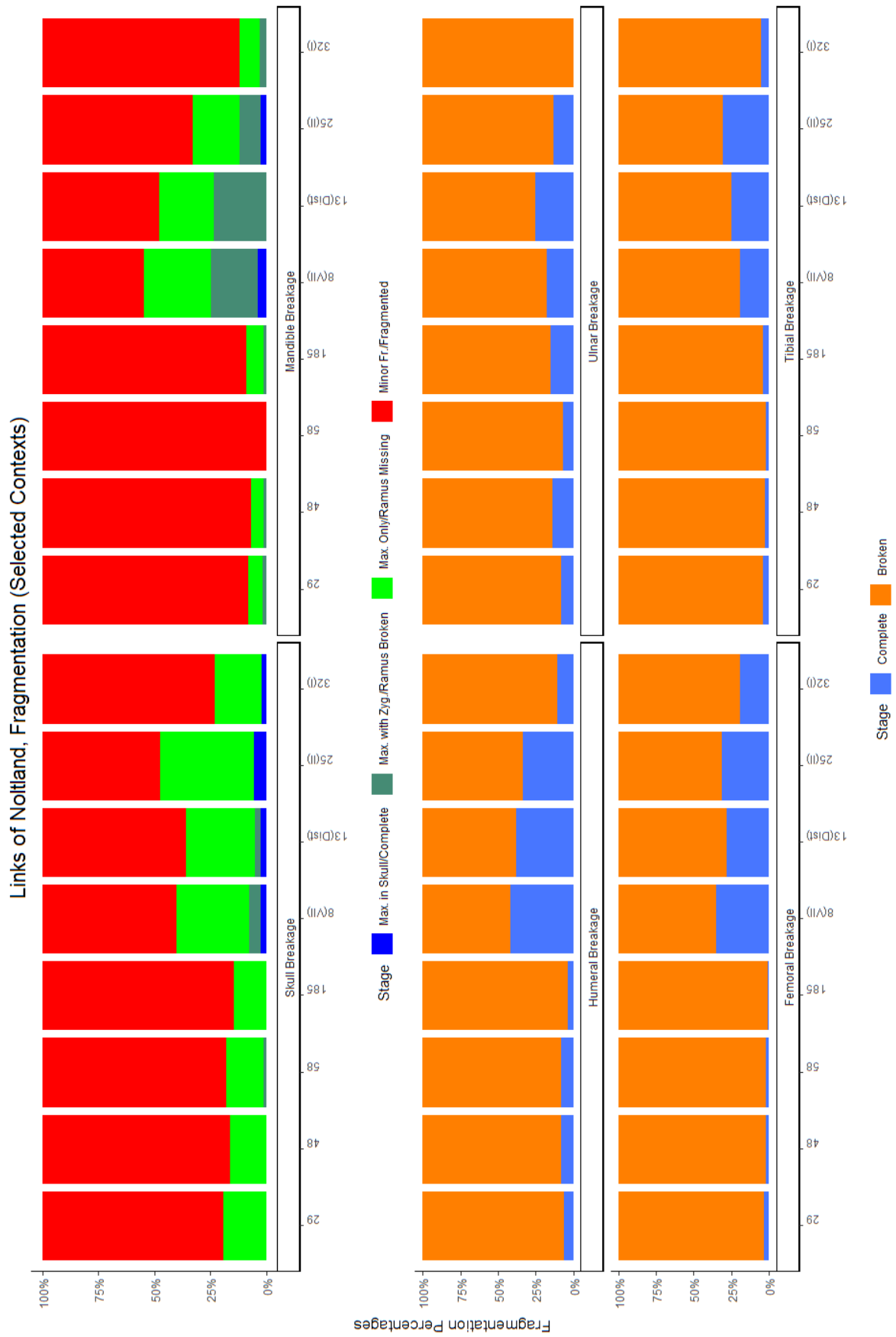


Fig. 5.22 – Links of Noltland, skull (upper row) and postcranial (two lower rows) breakage for major contexts in Trenches A and D.

5.2.5. DIGESTION AND BURNING

Despite both trenches providing large amounts of teeth and epiphyses digestion was identified with certainty on 17 molars, eight from Trench A and nine from Trench D. This amount was barely visible when plotted as percentages, with the largest concentration (six cases) barely being 1% of all molar finds. Moreover, those were either in early or middle stages of digestion, with alterations visible around salient edges. However, abrasion and weathering were visible on many bones retrieved from Links of Noltland, correlating with high fragmentation observed in a previous subchapter. It is very possible that light digestion was more prevalent in both trenches but due to other taphonomic changes, any diagnostic elements were removed from the tooth surfaces.

Minor evidence of burning was found in both trenches but evidence for likely discolouration was also recorded. 14 contexts showed evidence of burning, seven for each trench (8% of all in Trench A and 28% in Trench D). Total or near-total bone carbonisation was identified on a couple of finds (e.g. Fig. 5.23 C), with no evidence for partial or total calcination found. However, discolouration was much more frequent, often providing very similar results to burning. Mandibles and associated teeth have shown a particular tendency towards manganese-like staining (Fig. 5.23 A), especially visible through a contrast between dentine/cementum and enamel. However, staining on long bones was harder to identify. The difference was often found between shaft and epiphyses colour (see Fig. 5.23 B), but in the case of heavily fragmented remains it was not possible to differentiate between staining and proper burning.

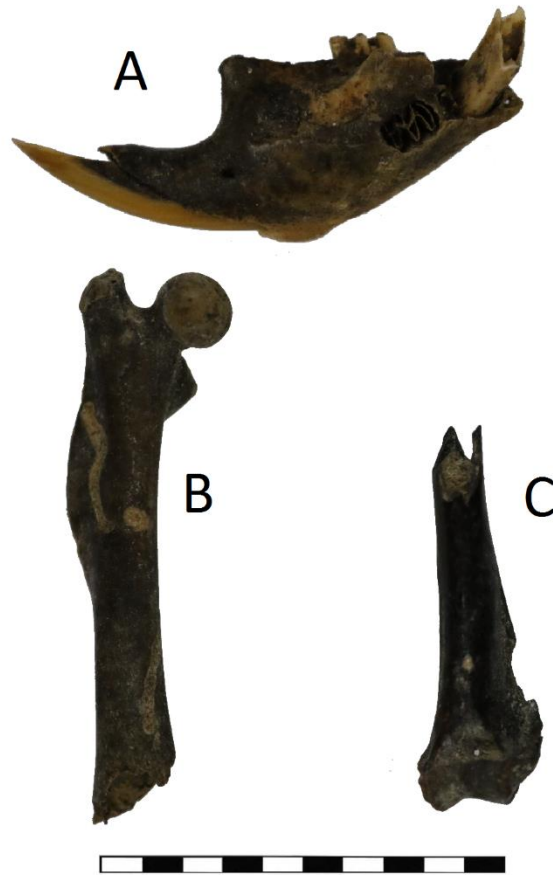


Fig. 5.23 – Examples of effects of staining (A & B) and burning (C) on Links of Noltland material.

A – Mandible, Trench A Context 48

B – Femur, Trench D Context 33

C – Distal Humerus, Trench A Context 134

5.2.6. POSSIBLE TAPHONOMIC AGENTS

The majority of data was classified as either being a scattering or coming from diurnal/mammal species, hinting towards owls in the case of specific phases (Table 5.07). Both trenches showed fragmentation akin to diurnal/mammal group, with a variation being noticeable mostly within *Abundances*-based classifications. Trench A showed scattering for this type of data, with the algorithm trained on the theoretical dataset suggesting owl-like accumulation. Trench D showed originally a different result (diurnal/mammal) but was also classified as an owl pattern in the case of adjustment. However, the internal stratigraphy of Trench D has shown to be more complex, with possible phases of accumulation and subsequent dispersal. The first three phases indicate predominantly diurnal/mammal type of deposition, with Phases II and III showing owl identification in the case of *Abundances* (former for normal approach and latter for adjusted one). Phase IV strongly differed from the previous three phases, with *Fragmentation Percentages* showing uniform owl identification and *Abundances* also resulting in the same identification after adjusting. The latter disturbances showed uniform diurnal/mammal result, with Phase V being also uniformly identified as scattering. However, Phases VI and VII were repetitions of previously noted patterns, namely disturbed contexts for former and Phase IV for latter, possibly reflecting new accumulations. The last Phase, VIII, showed owl identification for *Abundances*, with *Fragmentation Percentages* most similar to diurnal/mammal predatory group.

Major contexts also followed patterns established for Trench A and D. In Trench A over half of all context-related identifications were ones related to scattering, both in the case of *Abundances* and *Fragmentation Percentages*. While the majority of such identifications were for contexts with low NISP, several main contexts have also provided scattering, notably in the case of *Abundances* (Contexts 29, 48, 58 and 185). However, diurnal/mammal identification was also encountered often, especially for fragmentation and adjusted classifiers. Owl identification was rare, with a full identification as owl being found only for smaller contexts, once for unadjusted classifiers (Context 26) and four for adjusted ones (Contexts 14, 22, 89 and 153). Trench D showed a different situation, with scattering identification being present but not to the extent as in Trench A, with NISP less than 25. Most contexts showed quite uniform diurnal/mammal identification (e.g. Context 13). Owl identification was occasionally present in both original and adjusted results, but mostly alongside diurnal/mammal identification (e.g. Context 8 or 25). Phase-based identifications did not reflect specific contexts. For example,

Phase IV classification results were almost exclusively owls. However, among the specific Phase IV contexts one (Context 15) showed similarity in their own classification only on two cases, while another (Context 17) completely differed, being uniformly identified as scatter.

Correlations provided data either similar or differing from ones observed in Skara Brae, depending on a trench discussed. The biggest difference was the prevalence of strong correlations with red foxes in Trench A, both in the case of overall data as well as individual contexts. In some cases, correlations were even approaching $r = 1.0$ (e.g. Trench A fragmentation, on original data: $df = 8$, $r = 1.00$, $p = <0.001$). Main contexts from both the northern and southern part of the trench were consequently similar to red foxes although the exact correlation value ranged from $r = 0.6$ up to over $r = 0.9$, with lower values, similarly to Skara Brae, obtained from adjusted correlations. Trench D, being more similar to Skara Brae, showed more variation in correlation results. Especially similar to Skara Brae was the predominance of kestrel/hen harrier correlation as the strongest one, with short-eared owl occasionally present for adjusted correlation, especially for later contexts.

Table 5.07 – Highest correlations (upper table) and classification outcomes (lower table) for *Abundances* and *Fragmentation Percentages*, based either on original references/signature data (Normal) or ones simulating partial dispersal/burial (Adjusted). The upper section of each table includes overall for trenches and site stratigraphy while the lower section includes major contexts. 1.0 correlation value due to rounding up 0.995 – 0.999 scores.

Trench, Phase or Context	Highest Corr. Abundances				Highest Corr. Fragmentation			
	Normal		Adjusted		Normal		Adjusted	
Trench A	0.89	Red Fox	0.84	Red Fox	1.00	Red Fox	1.00	Red Fox
Trench D	0.81	Kestrel	0.76	Owl(Sh)	0.95	Kestrel	0.96	Kestrel
Phase I	0.64	Kestrel	0.72	Peregrine	0.99	Red Fox	0.99	Red Fox
Phase II	0.63	Hen H.	0.64	Peregrine	0.95	Red Fox	0.96	Kestrel
Phase III	0.68	Kestrel	0.78	Peregrine	0.96	Red Fox	0.98	Kestrel
Phase IV	0.84	Kestrel	0.65	Owl(Sh)	0.49	Kestrel	0.42	Kestrel
Disturbed	0.76	Kestrel	0.74	Owl(Sh)	0.98	Kestrel	0.98	Kestrel
Phase V	0.65	Red Fox	0.30	Peregrine	0.43	Owl(Sn)	0.46	Owl(Sn)
Phase VI	0.84	Hen H.	0.90	Kestrel	0.66	Kestrel	0.61	Kestrel
Phase VII	0.95	Kestrel	0.88	Owl(Sh)	0.91	Kestrel	0.90	Kestrel
Phase VIII	0.70	Kestrel	0.88	Owl(Lg)	0.93	Hen H.	0.94	Hen H.
A - 29	0.82	Red Fox	0.80	Red Fox	1.00	Red Fox	1.00	Red Fox
A - 48	0.89	Red Fox	0.77	Red Fox	0.99	Red Fox	0.99	Red Fox
A - 58	0.86	Red Fox	0.80	Red Fox	1.00	Red Fox	1.00	Red Fox
A - 185	0.86	Red Fox	0.87	Red Fox	0.99	Red Fox	0.99	Red Fox
D - 8	0.96	Kestrel	0.87	Owl(Sh)	0.93	Kestrel	0.94	Kestrel
D - 13	0.76	Kestrel	0.74	Kestrel	0.98	Kestrel	0.98	Kestrel
D - 25	0.61	Hen H.	0.63	Peregrine	0.94	Kestrel	0.95	Kestrel
D - 32	0.52	Kestrel	0.73	Peregrine	0.99	Red Fox	0.99	Red Fox

Trench, Phase or Context	Abundances Classification		Fragmentation Classification		Final Result	
	Normal	Adjusted	Normal	Adjusted	Normal	Adjusted
Trench A	Scattering	Owl	Diurn./Mamm.	Diurn./Mamm.	Contested	Accumulation
Trench D	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Phase I	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.
Phase II	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Diurn./Mamm.
Phase III	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Phase IV	Diurn./Mamm.	Owl	Owl	Owl	Accumulation	Owl
Disturbed	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.
Phase V	Scattering	Scattering	Scattering	Scattering	Scattering	Scattering
Phase VI	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Phase VII	Diurn./Mamm.	Owl	Owl	Owl	Accumulation	Owl
Phase VIII	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Diurn./Mamm.
A - 29	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.
A - 48	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.
A - 58	Scattering	Owl	Diurn./Mamm.	Diurn./Mamm.	Contested	Accumulation
A - 185	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.
D - 8	Diurn./Mamm.	Owl	Owl	Diurn./Mamm.	Accumulation	Accumulation
D - 13	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.
D - 25	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Diurn./Mamm.
D - 32	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.

5.3. BU BROCH

5.3.1. QUANTIFICATION, DISTRIBUTION AND AGE DATA

Bu Broch data was problematic to study mostly because of the limited material available, contrasting with both the overall size of the site and other studied sites. Bu Broch provided only 455 bone and teeth fragments in just nine samples, each from a different context, representing roughly 69 rodent individuals (Table 5.08, Fig. 5.24). However, similar to Skara Brae, only two species were identified: Orkney voles and field mice. Apart from the earliest Phase I, most likely not sampled at all, all phases provided at least a small amount of micromammal NISP. The original Broch usage Phase IIa provided only two samples with few vole bones, in each sample representing a single individual, and no evidence of mice. Both samples came from contexts identified as middens (Context L80 – eastern midden, Context L43 – western midden). The first abandonment Phase IIb provided samples of rodent bones from three layers. In the case of two (Context L50 – silt layer, Context L68 – rubble next to the entrance) only single vole individuals were identified. However, Context L17, essentially a thin layer showing an effectual short-term abandonment (silt and blow tumbled stones in the central area), provided almost 50% of all micromammal bones, overall highest skeletal completeness (above 20%) and evidence for both voles and mice. All later phases provided only one sample in each case. Phase III, a later period of utilization, was represented only by Context L65, a grey floor deposit with singular individuals of each species; while Phase IIIb (final abandonment and later intrusions) Context L14 (rubble within wall Context L13) provided the second-biggest sample in terms of NISP, both of voles and field mice. Additionally, Context L2 (central area, tumbled stones), spanning possibly between IIb and IIIb, provided the second heaviest sample, while unstratified Context L1 (mostly topsoil) provided remains of two voles.

Similar to the general information, the scarcity of samples and the small pool of assessable finds negatively impacted the possibility of exploring age-related data. The overall view of epiphyseal fusion suggested the majority of individuals being sub-adults, with minuscule amounts of fully grown as well as juvenile animals (Fig. 5.25). Early fusing epiphyseal surfaces retrieved were predominantly found fused and, as in Skara Brae Trenches I to III, only retrieved unfused cases were distal tibiae. The biggest amount of such finds were obtained from Phase II b, with a ratio of unfused cases slightly lower than 10%. The highest ratio was found in Phase III b (20%), mostly due to the small number of finds obtained ($n = 5$). Epiphyseal fusion

representative of a midway stage of growth was only represented by proximal femora as no ulnar finds were retrieved from Bu Broch assemblages. Obtained scores contributed to the fused cases relative frequencies, with only two unfused femora found in Phase II b. The most varied situation, despite no proximal ulnae found, was in the case of late fusing epiphyses. Only about 6.5% of those finds were scored as fused and, as in the Neolithic sites, the majority of those were distal femora. Only Phases IIB,II/IIIB and IIIB returned those finds, with the majority found within Phase II b.

Scoring of field mouse molar wear was attempted, but in the end only a handful of scores were established. Only three individuals could be scored by molar wear, resulting in two being assessed third and one second level of wear.

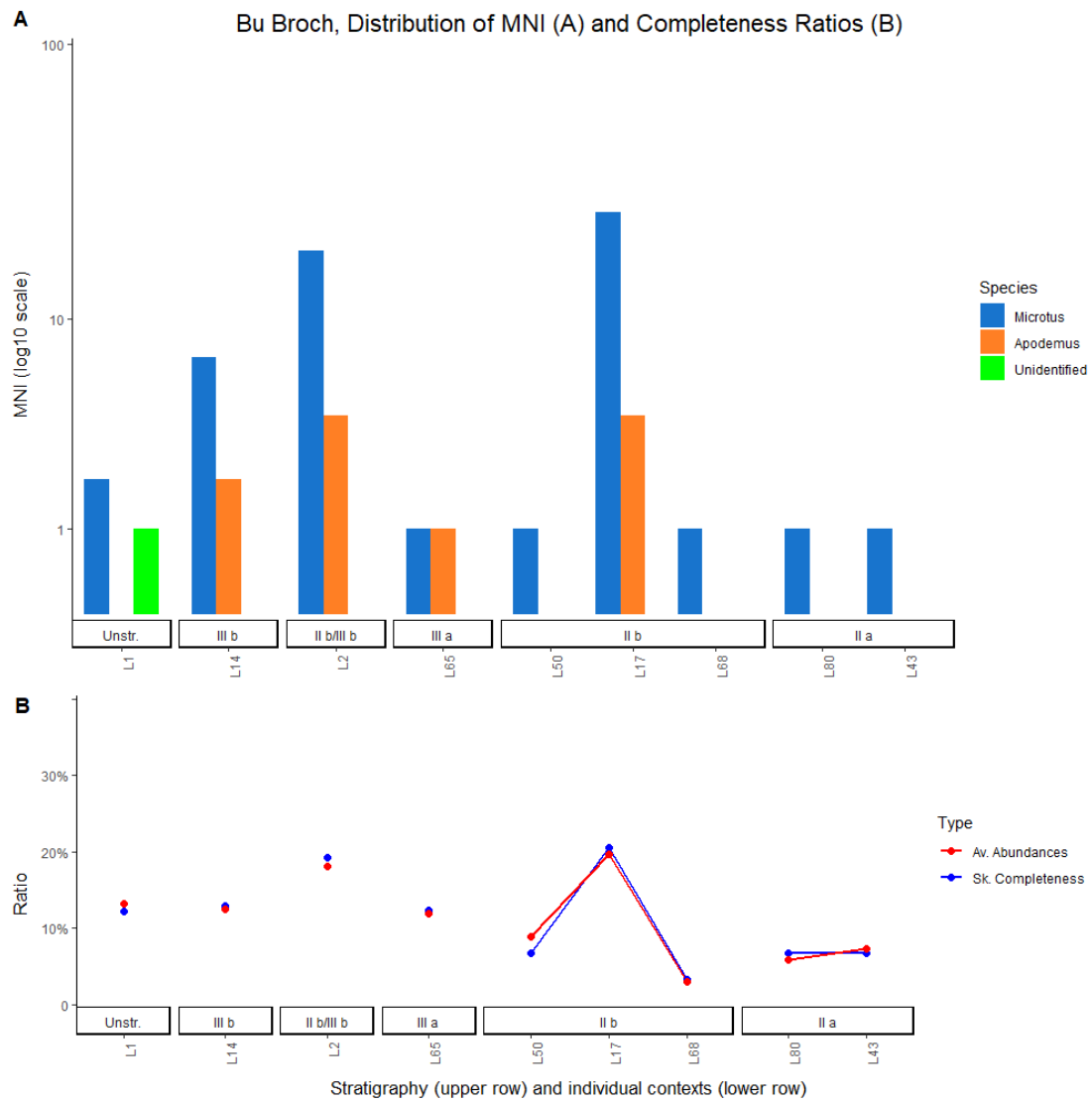


Fig. 5.24 – A (upper plot): Distribution of MNI in Bu Broch, arranged according to site stratigraphy.

B (lower plot): values of completeness ratios (Skeletal Completeness, Average Abundances) for each context in Bu Broch, arranged in the same way as in plot A.

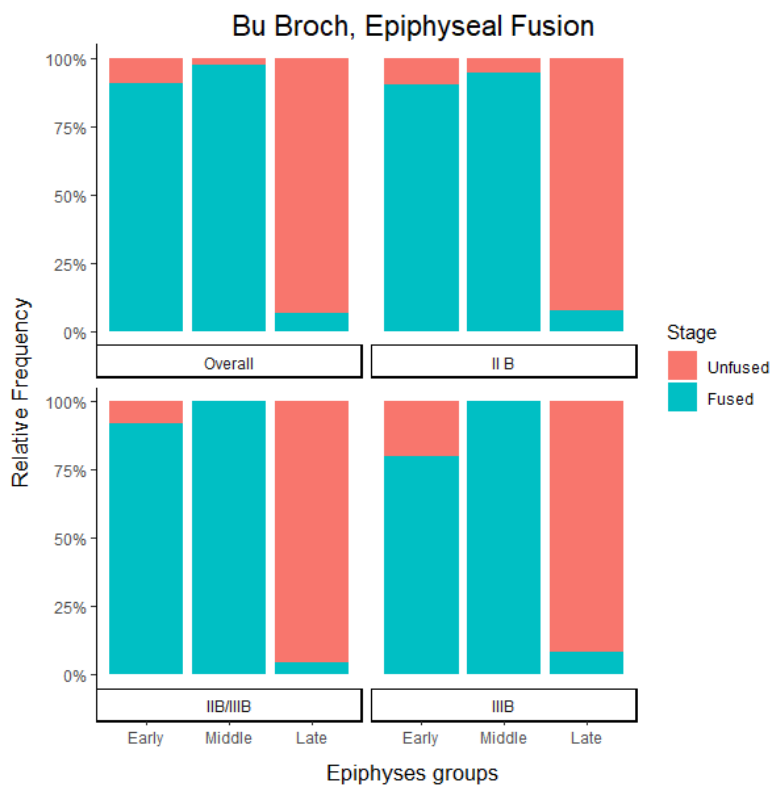


Fig. 5.25 – Bu Broch, epiphyseal fusion expressed as a relative frequency of NISP (red-unfused, blue-fused) and grouped in three main groups related to individual's age (early/middle/late). Presented plots reflect the whole site (overall) and three largest phases that provided enough remains.

Table 5.08 – Weight, NISP and MNI counts distribution for Bu Broch and its stratigraphy, depending on specific species categories.

Phase	Weight (g)	Contexts	Samples	Microtus		Apodemus		Unid. Rodent		ΣNISP	ΣMNI
				NISP	MNI	NISP	MNI	NISP	MNI		
II a	0.31	2	2	3	2	0	0	2	0	5	2
II b	16.52	3	3	157	27	20	4	48	0	225	31
III a	0.29	1	1	3	1	1	1	11	0	15	2
II b/III b	13.32	1	1	118	18	7	4	27	0	152	22
III b	4.17	1	1	31	7	3	2	7	0	41	9
Unstr.	1.16	1	1	11	2	0	0	6	1	17	3
Σ	35.77	9	9	323	57	31	11	101	1	455	69

5.3.2. SITE TAPHONOMY AND IDENTIFICATION

Low NISP values and very selected sieving resulted in possibly uninformative *Skeletal Frequencies*, *Abundances* (Fig. 5.26) and *Indices*. The majority of finds were either skull or hind limb remains, with almost no vertebral or small bones found. Additionally, overall as well as phase-specific *Skeletal Frequencies* were almost equal, with the only difference between Phase II b, Phase II/III and Phase III b being which specific group of the two main (skull, hindlimb) is higher. The lack of small and front limb bones diminished the usability of relative abundances to skull and hind limb elements, whose counts did not significantly differ between overall data and largest Contexts L17 and L2, apart from maxillary (slightly more) and humeral (slightly less) bones in the latter. Indices provided informative results when computable but similar to other approaches could be impacted by a loose sieving regime. Isolated molar percentages were uniformly low, within 0 to 15 %. Considering a high number of maxillae and mandibles with almost complete molar rows, it could indeed reflect a low dispersal of such elements. However, it could also be impacted by sieving biased towards bigger elements, mostly because longer incisors showed a wider range of values. In contrast, both postcranial/cranial indices were similar. Distal to Proximal Limb Bones index provided almost the whole range of possible values. However, this could be impacted by the lack of radii retrieved.

Fragmentation was of restricted use due to similar reasons as in previous sections (Fig. 5.27). However, it proved to be slightly more informative, despite the lack of ulnae. Overall, about half of maxillae came from mostly fractured skulls. Maxillary only finds were rare, similar to minor cranial fragments. The biggest difference between major contexts could also be noted, with Context L2 providing predominantly broken but preserved skulls. Mandibular breakage also differed between contexts, with Context L2 having the majority of intact finds while the rest of Bu Broch contained mandibles with broken ramus. For postcranial bones the situation was similar across contexts, with the majority being intact finds. The lowest amounts of fragmented remains were within humeri, possibly also due to these elements being less abundant than femora and tibiae.

No traces of burning were found in Bu Broch assemblage. Similarly, apart from Context L17, no traces of digestion could be noted. The only finds were two molars, representing light digestion, but considering the circumstances it could be also a misidentification of abrasion.

Correlations and classifications provided somewhat conflicting data (Table 5.09). Classification results were heavily skewed towards scattering in the case of *Fragmentation Percentages*, with adjusted methods providing somehow confusing skew towards owls. Transformation from scattering towards owl identification might be another example of low NISP samples skewing results. In turn, *Abundances* results were mostly within diurnal/mammal group, with some showing scattering classification in the case of original data. Correlations showed generally lower values than in the case of Neolithic sites, with best being around or just below $r = 0.8$ (e.g. Unadjusted Abundances for Phase IIIb: $df = 11$, $r = 0.80$ $p = 0.001$). The lowest results were weak positive correlations, especially common for *Fragmentation Percentages*-based correlations. In contrast to Skara Brae and Links of Noltland, the most common were high matches with owls, especially short- and long-eared. However, due to best correlations being often so low it is not certain, whether best correlations are informative at all.

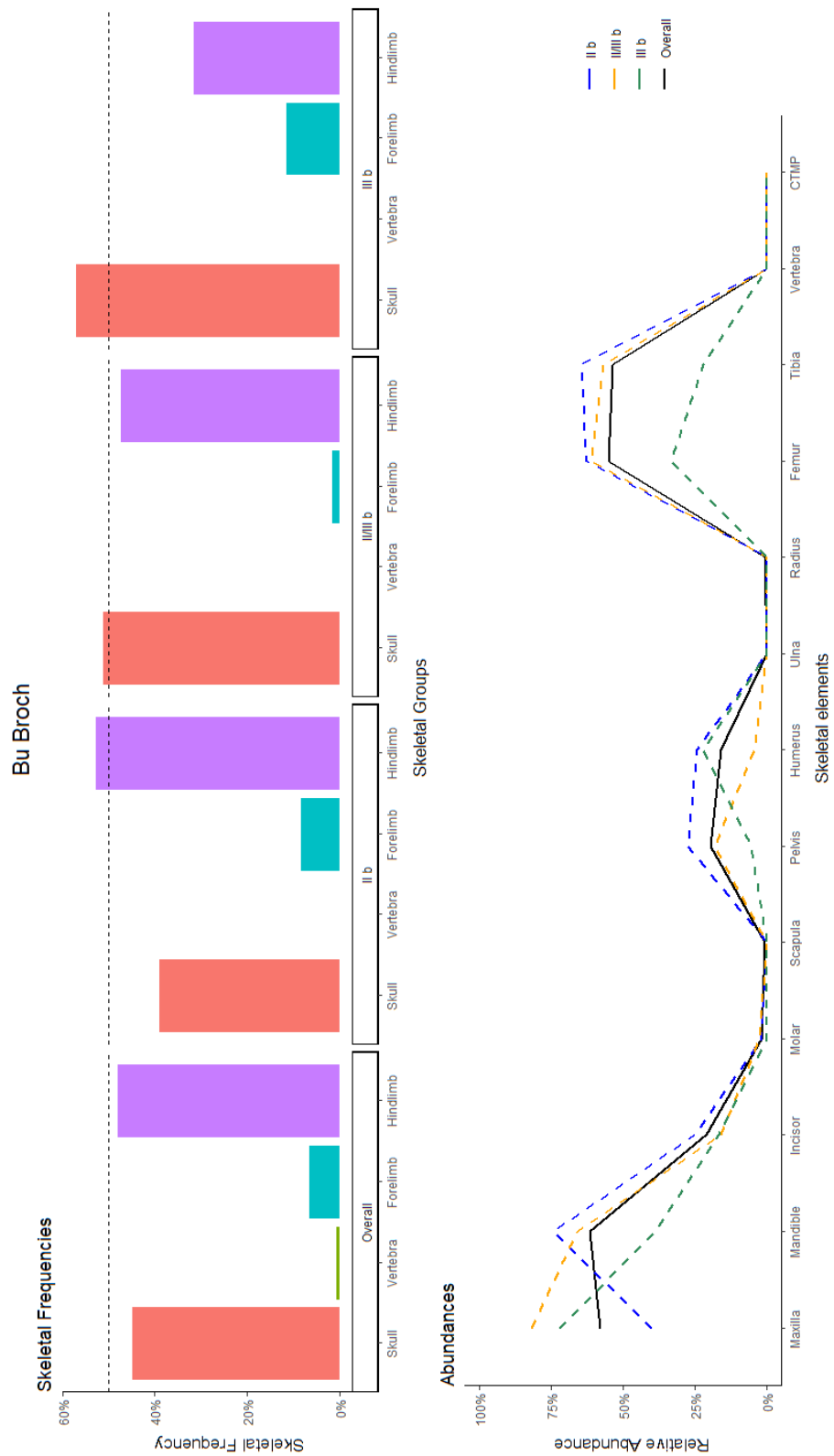


Fig. 5.26 – Bu Broch *Skeletal Frequencies* (upper plot) and *Abundances* (lower plot), site overall as well as main phases.

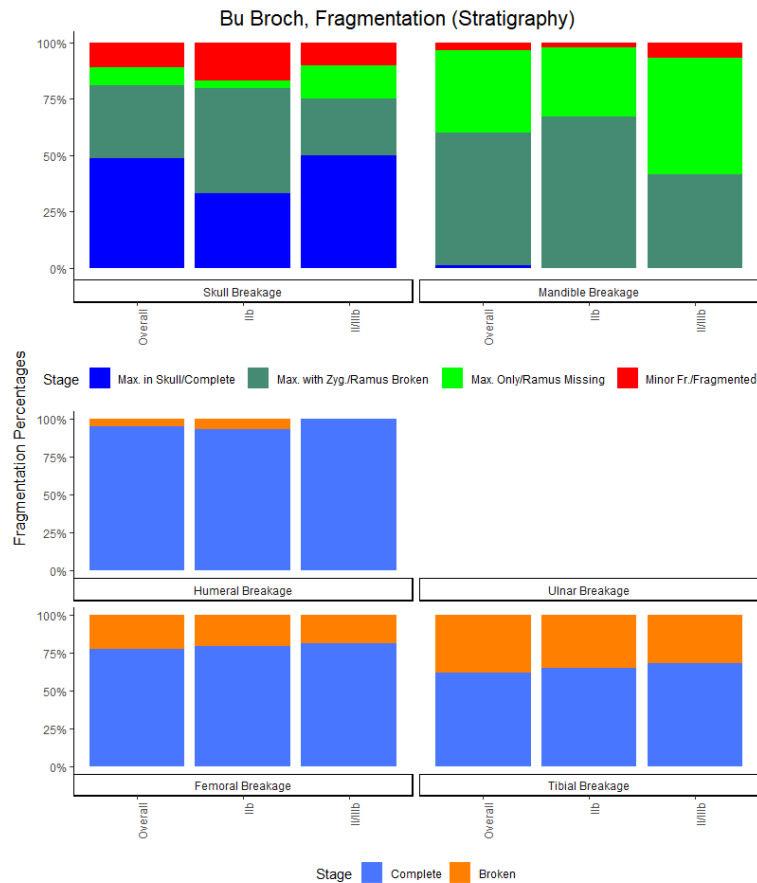


Fig. 5.27 – Bu Broch, skull (upper row) and postcranial (lower rows) breakage for overall data as well as two phases with best representativeness.

Table 5.09 – Highest correlations (upper section) and classification (lower section) for *Abundances* and *Fragmentation Percentages*, based either on original references/signature data (Normal) or ones simulating partial dispersal/burial (Adjusted).

Phase	Highest Corr. Abundances				Highest Corr. Fragmentation			
	Normal		Adjusted		Normal		Adjusted	
Overall	0.73	Kestrel	0.75	Owl(Lg)	0.64	Owl(Sh)	0.71	Owl(Sh)
II a	0.75	Hen H.	0.54	Hen H.	0.61	Hen H.	0.59	Hen H.
II b	0.74	Kestrel	0.79	Owl(Sh)	0.66	Owl(Sh)	0.72	Owl(Sh)
III a	0.62	Owl(Sn)	0.56	Owl(Sn)	0.54	Owl(Sh)	0.55	Owl(Lg)
II b/III b	0.66	Kestrel	0.69	Owl(Lg)	0.68	Owl(Sh)	0.74	Owl(Sh)
III b	0.80	Hen H.	0.57	Owl(Lg)	0.32	Owl(Sh)	0.41	Owl(Sh)
Unstratified	0.68	Hen H.	0.58	Hen H.	0.10	Kestrel	0.08	Kestrel

Phase	Abundances Classification		Fragmentation Classification		Final Result	
	Normal	Adjusted	Normal	Adjusted	Normal	Adjusted
Overall	Diurn./Mamm.	Diurn./Mamm.	Scattering	Owl	Contested	Accumulation
II a	Diurn./Mamm.	Diurn./Mamm.	Scattering	Scattering	Contested	Contested
II b	Scattering	Diurn./Mamm.	Scattering	Owl	Scattering	Accumulation
III a	Scattering	Owl	Scattering	Scattering	Scattering	Contested
II b/III b	Diurn./Mamm.	Diurn./Mamm.	Scattering	Owl	Contested	Accumulation
III b	Diurn./Mamm.	Diurn./Mamm.	Scattering	Owl	Contested	Accumulation
Unstratified	Diurn./Mamm.	Diurn./Mamm.	Owl	Scattering	Accumulation	Contested

5.4. BIRSAY

5.4.1. ASSEMBLAGES QUANTIFICATION AND DISTRIBUTION

All three areas provided micromammal data (Table 5.10). Birsay Bay Area 1, the main excavation site, provided 244 sieved and six hand-picked samples from around 50 sampled contexts. Together, the samples contained 6,136 identifiable bone and tooth fragments of micromammal species. In the case of samples taken alone, the MNI could be estimated to be about 540, but when whole contexts are taken into account this number was reduced to just 260. Species identified in Area 1 included predominantly house mice (MNI 130) and to a lesser extent field mice (MNI 41) and Orkney voles (MNI 66). Additionally, evidence for three pygmy shrew individuals was found, while the topsoil contained a single hand-retrieved scapula of a rat. Both physical examination and ZooMS analysis showed it to be a brown rat. In the case of unidentified individuals, eight individuals were identified as murids while another 11 could only be described as a rodent. Areas 2 and 3 also provided samples albeit in smaller numbers. Six sampled contexts from Area 2 provided 86 samples, containing 2059 NISP. Sample-based MNI could be estimated as high as 257 (samples only), but context-based MNI estimation reduced the number to just 86. Species identified included Orkney voles (MNI 36), field mice (MNI 23) and house mice (MNI 24) as well as pygmy shrews (MNI 2). No rat bones were retrieved and only one MNI came from an unidentified rodent. In contrast, area 3 provided only 22 samples from a single context, with only 142 NISP and 8 MNI. However, the species identified were the same as in Area 2. In terms of significance, the areas mostly differed in mean values between contexts rather than ranges, although mostly on the verge of significance (**Appendix: Statistics 1e**).

The distribution of micromammal material differed between various contexts, most likely reflecting differences in sampling, although other factors could not be excluded (Fig. 5.28 A & C). Due to the sampling regime changing from whole-sieving to selective sampling, however, the initial dig area (squares A and B, see Fig. 3.11), had contexts that provided multiple samples while 24 peripheral or late contexts were only sampled once, including four with only hand-retrieved material. No samples were taken from the two earliest documented periods, including natural sands and the earliest evidence for human activity (Period 1) as well as the earliest enclosure wall (Period 2). Sieving included only material spanning from early occupation

deposits (Period 3) up to post-abandonment sands deposits (Period 15). The latest material was hand-retrieved from the soil connected with modern-day activity (Period 18).

The first occupation deposits provided relatively few remains but later periods of occupation (Periods 5, 7 and 8) provided a variety of different micromammal assemblages within and sometimes around the studied enclosure. However, apart from sandy/clay layers 210 and 212 corresponding to Period 5, those contexts were usually of small size and had low counts of skeletal completeness. The largest assemblages, containing over 50% of all Area 1 micromammal finds, came from contexts 164, 182, 195, 198, and 208, located in beforementioned Squares A and B (within the enclosure) and dated to Period 9. Those contexts were also most skeletally complete among all those found in area I, with skeletal completeness in a range from 27% (Context 164) to 43% (Context 182) and slightly but noticeably higher average abundances. However, as noted in the previous case study (**Chapter 4.5.**) material distribution within the contexts was not even, suggesting strong accumulation in specific but impossible to pinpoint (lack of spatial data) parts of the occupied area. Period 9 was characterised by gradual abandonment of a rectangular structure, with layers of rubble and infill slowly accumulating within. Contexts 182, 198 and 208 were a sequence of midden-like layers rich in a variety of finds, from pottery shards and industrial waste, through rich plant matter, to shells and bone fragments of a variety of species. Contexts 164 and 195 were more sandy layers corresponding to Context 182 and similar composition of inclusions. Period 11, of total structural collapse, did not provide much data but later periods (Periods 13 to 15), representing sand and midden accumulations with only a brief period of human activity, provided a relatively high number of finds, both within the former structure (Context 65) as well as in contexts outside of it (e.g. Context 134). Completeness ratios did not significantly differ between themselves but fluctuated from as high as over 30% (e.g. 32% for both ratios from Context 65) to below 10% depending on the context. The most recent contexts were not sieved, resulting in only two incomplete samples retrieved.

Species composition in Area I differed both between time periods and single contexts within them (Fig. 5.28 A, Table 5.10). The early occupation deposits from south of the enclosure did only provide evidence for voles and field mice. However, evidence of mice appears in Period 5 and was present through Periods 7 and 8, in numbers higher than or roughly similar to voles. In turn, during these periods the number of field mice seemed to dwindle in relation to other species. Especially in the case of Period 8, only a single element attributable to field mice was found, in Context 171, infill of a round kiln. Pygmy shrews only appeared once in those

occupation periods, in Period 7 Context 55, stones south of the enclosure. Period 9 differed vastly from older periods, with a strong predominance of house mice remains. However, voles and field mice were still present in relatively large quantities. Smallest Context 206, indoor small pit infill with remains of steatite, pottery, mammal/fish bone and shell, provided only house mouse bones. In contrast, all other contexts showed evidence of all three species, with Context 198 providing the largest numbers of house mice. Contexts 198 and 208 also contained remains of a pygmy shrew – the latest evidence of this species to occur in Birsay archaeological assemblage. The following Period 11 did not provide any evidence besides several vole remains but later Periods 13 to 15 provided several contexts differing in species compositions. While overall MNI's were roughly similar between both murid species and voles, more bones were attributable to the latter than the former. Context 65 contained more murid remains, being more similar to Period 9 contexts, while Context 134, having a similar composition, contained more vole bones and teeth. Modern contexts of Period 18 showed evidence only of voles and a singular brown rat bone, possibly showing a different species composition than one visible in the archaeological assemblage. However, due to being hand-retrieved, it might be simply a retrieval bias towards bigger species.

Area 2 showed differences in both assemblage sizes and completeness as well as their species composition to the main site (Fig. 5.28 B & D, Table 5.10). Full sieving of selected squares resulted in 5 out of 6 contexts in Area 2 being sampled multiple times. Two phases in Area 2 were sampled, Phase X (younger phase) containing both more NISP as well as more skeletally complete assemblages (26% Skeletal Completeness, 33% Average Abundances) than Phase W (older phase; 12% Skeletal Completeness, 16% Average Abundances). In the case of specific samples only a handful provided high completeness, with the majority showing less than 10%. Still, similarly to Area 1, there was no possibility to track to which sampled square those samples belonged. Both phases had similar species composition, with majority of material and more MNI coming from Orkney voles but mice also contributing strongly to both counts. However, in Phase X both murid species showed similar amounts of material but in later Phase W there were fewer field mouse remains in relation to house mice than in Phase X. Additionally, younger phase contributed remains of a pygmy shrew.

Area 3, in contrast to 1 and 2, had only one context effectively sampled, resulting in a lack of comparative contexts within the same area. Still, Area 3 materials seemed to follow a distribution similar to Area 2 Phase X, which is not surprising considering both cover relatively similar timeframes. The dominating role of voles in context MNI was followed by murids and

singular remains of a pygmy shrew. Completeness was on an average level (18% for Skeletal Completeness, 22% for Average Abundances). Some samples have shown greater completeness but the difference within the context were not as pronounced as in other contexts investigated.

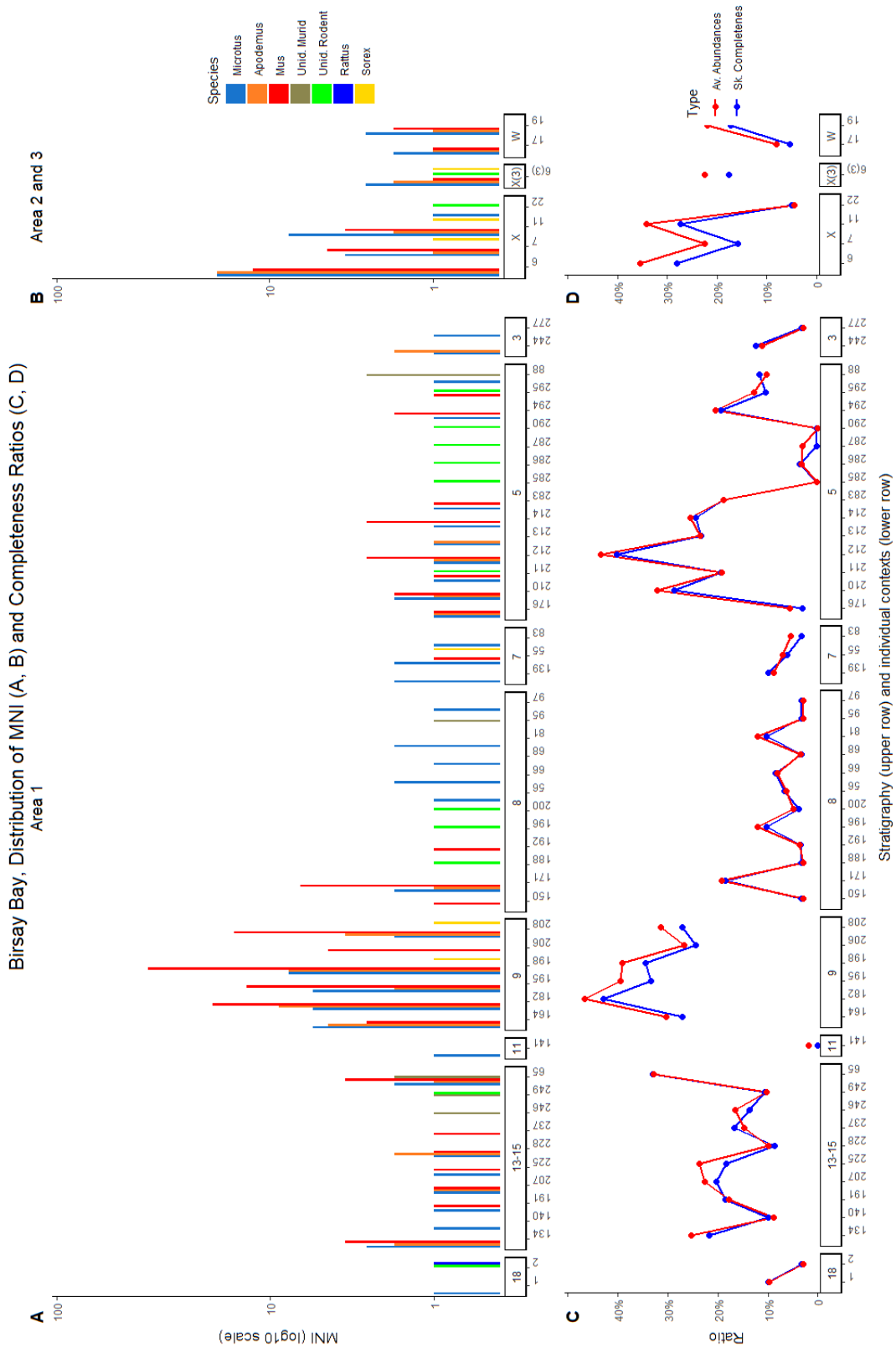


Fig. 5.28 – A & B (upper plot): Distribution of MNI across three areas, arranged alongside known stratigraphy (periods for Area 1, phases for 2 and 3).
C & D (lower plot): values of completeness ratios (Skeletal Completeness, Average Abundances) for each context in Birsay Bay, arranged in a way as in plots A & B.

Table 5.10 – Weight, NISP and MNI counts distribution for Birsay Bay areas and their stratigraphy, depending on specific species categories.

Area	Period	Phases	Weight (g)	Contexts	Samples	Microtus		Apodemus		Mus		Unid. Rodent		Unid. Mouse		Rattus		Sorex		ΣNISP	ΣMNI
						NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI		
1	3	---	0.26	2	3	2	2	5	2	0	0	7	0	2	0	0	0	0	0	16	4
	5	L	5.11	14	24	43	10	9	4	45	14	484	6	48	3	0	0	0	0	629	37
	7	---	1.13	3	6	17	5	0	0	1	1	13	0	0	0	0	0	2	1	33	7
	8	N, P	3.47	12	21+2(h.r)	39	9	1	1	21	9	113	3	6	1	0	0	0	0	180	23
	9	Q, R, S	31.08	6	127+1(h.r)	310	28	106	28	541	93	3553	0	182	0	0	0	4	2	4696	151
	11	V	0.04	1	1(h.r)	4	1	0	0	0	0	2	0	0	0	0	0	0	0	6	1
	13-15	Y	4.65	10	57	72	10	11	6	37	13	419	1	30	4	0	0	0	0	569	34
	18	Z	0.63	2	2(h.r)	5	1	0	0	0	0	1	1	0	0	1	1	0	0	7	3
	Σ		46.37	50	244	492	66	132	41	645	130	4592	11	268	8	1	1	6	3	6136	260
	---	W	1.26	2	7	43	5	2	2	10	3	84	0	2	0	0	0	0	0	141	10
2	---	X	16.46	4	130	509	31	106	21	93	21	1185	1	23	0	0	0	2	2	1918	76
	Σ		17.72	6	137	552	36	108	23	103	24	1269	1	25	0	0	0	2	2	2059	86
3	---	X	1.16	1	22	45	3	6	2	7	1	83	1	0	0	0	0	1	1	142	8
	Σ		65.25	57	403	1089	105	246	66	755	155	5944	13	293	8	1	1	9	6	8337	354

5.4.2. AGE DATA DISTRIBUTION

The analysis of epiphyseal fusion revealed the presence of all stages of skeletal development but in different quantities depending on area location (Fig. 5.29). In contrast to the other sites as well as Areas 2 and 3, assessable epiphyses from Area 1 were predominantly either of murid provenience or taxonomically impossible to identify, with only a minuscule contribution from voles. Differences between Area 1 and 2 as well as 3 also included differing quantities of fused and unfused finds. The most noticeable example was with early fusing epiphyses. About 20% of all distal humeri and 40% of tibiae from Area 1 were found unfused, resulting in a relative frequency of about 28%. It may be a sign for a relatively significant part of the on-site rodent population being juveniles. In contrast, fringe areas provided fewer such finds, with relative frequencies of unfused specimens being from 11% to 13%. It was still a higher amount than found on Neolithic sites. In the case of specific stratigraphy, however, the situation did vary between periods or phases. In Area 1 periods 8 and 13-15 unfused bones comprised over 40% of all juvenile finds. Period 9 showed values more similar to joint data, most likely due to providing the majority of finds for the whole area. Within Area 2, all unfused specimens came from one Phase X, showing about 12% relative frequency of unfused cases.

Middle fusing epiphyses provided similar results to early fusing ones but with higher ratios of unfused cases, suggesting a high percentile of older juveniles and sub-adults within the rodent population. About 43% of finds from Area 1 showed lack of fusion, visible especially in the case of proximal femora (relative frequency of 47%). Similar to early fusing data, Periods 13-15 also showed far higher relative frequencies, with the majority of finds (68%) being unfused, while most representative Period 9 showed ratio comparable to joint data (41%). Area 2 also saw an increased ratio for middle fusing epiphyses, with about 29% finds unfused, predominantly femora (30%). All those finds, as was the case with early fusions, came from Phase X. Area 3 however differed from both Area 1 and 2, showing a decrease of unfused cases, with only 10% relative frequency obtained.

Late fusing epiphyses suggested the predominance of sub-adults within the site, with site fringes providing values more similar to those from the Neolithic sites. About 80% of all late fusing finds from Area 1 did not exhibit fusion. In contrast to previously observed data, the majority of proximal ulnae found were unfused, with humeri showing the least number of unfused cases (68%). Still, proximal tibiae showed the fewest examples of fusion. Similar to previous fusion stages, Periods 11-15 provided only three cases of a late-stage fusion, resulting in a 95% relative

frequency for the lack of fusion. In turn, Period 9 exhibited a relative frequency of 77% for unfused cases, slightly lower than the area overall. Areas 2 and 3 did not provide as many unfused bones but such finds were still more common than fused cases (69/67%). For Area 2, the majority of fused finds came from Phase X, with Phase W showing only a single fused specimen. Proximal femora and ulnae were the most frequent fused cases, with humeri and tibiae exhibiting fusion much more rarely.

Molar wear proved to be the best way of ageing murid population in Birsay (Fig. 5.30). Due to molars being widespread in Area 1, molar wear scoring could encompass all field mice and the majority of house mice population. Interestingly, despite differences in sample pools, both murid species seemed to have similar age distribution. The distribution itself seemed as expected from a natural population, with a negative correlation between score number and number of individuals. The majority of wear scores obtained reflected specimens within first three months of their lives (category 1 and 2), but category 3, representing fully grown specimens, was also quite frequent. Wear reflecting older individuals were present but far less frequent. In the case of field mice they were very rare, being represented by single specimens. Unworn molars, most likely juvenile individuals, were present in the case of both species in very small numbers. Area 2 also provided similar distribution of wear scores despite a smaller sample pool. However, no unworn molars were found while field mouse distribution was steeper, with more individuals within category 1 and no heaviest wear present on the site. Area 3 did not provide enough data to create a distribution. However, a single house mouse in that area seemed to have molars around score 2 while two field mice provided wear around category 1 and 3 respectively.

Additional evidence for the presence of juvenile specimens was found through SEM analysis (Fig. 5.31). A small fragment of alveolus bone retrieved from the kiln infill Context 171, Period 9, was rattling when touched, suggesting the presence of an unerupted tooth inside. After breaking the alveolus and investigating its insides, firstly visually and then under the SEM, a house mouse first maxillary molar was identified. It consisted only of a crown, with no roots yet formed, with its surface covered by still developing dentine and enamel layers. Considering the state of development, it is most likely that this specimen died during the late stage of pregnancy or within the first few days after birth.

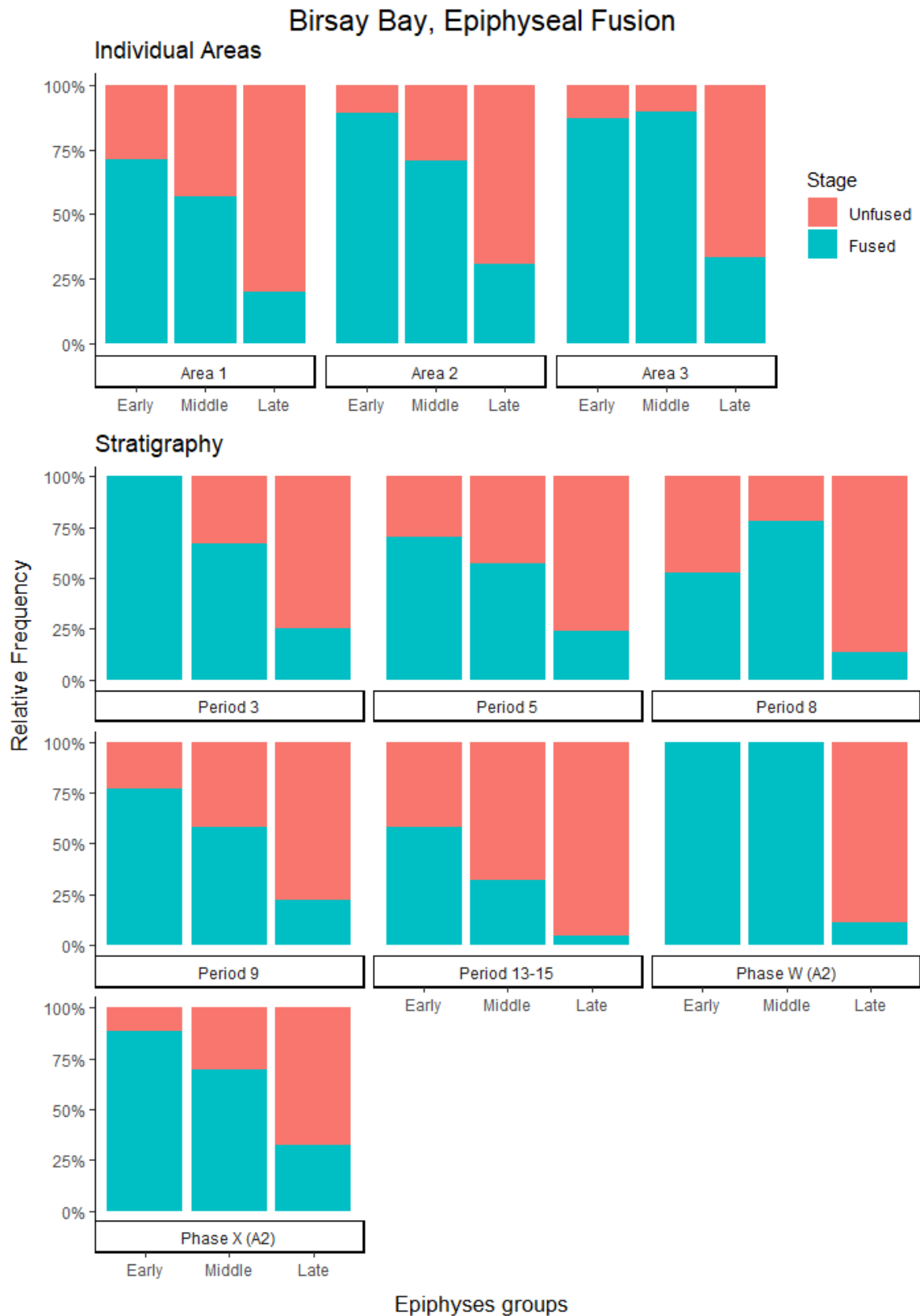


Fig. 5.29 – Birsay Bay, epiphyseal fusion expressed as a relative frequency of NISP (red-unfused, blue-fused) and grouped in three main groups related to individual's age (early/middle/late). Upper plots represent three main areas of Birsay Bay, with lower plots showing stratigraphy in Area 1 and 2.

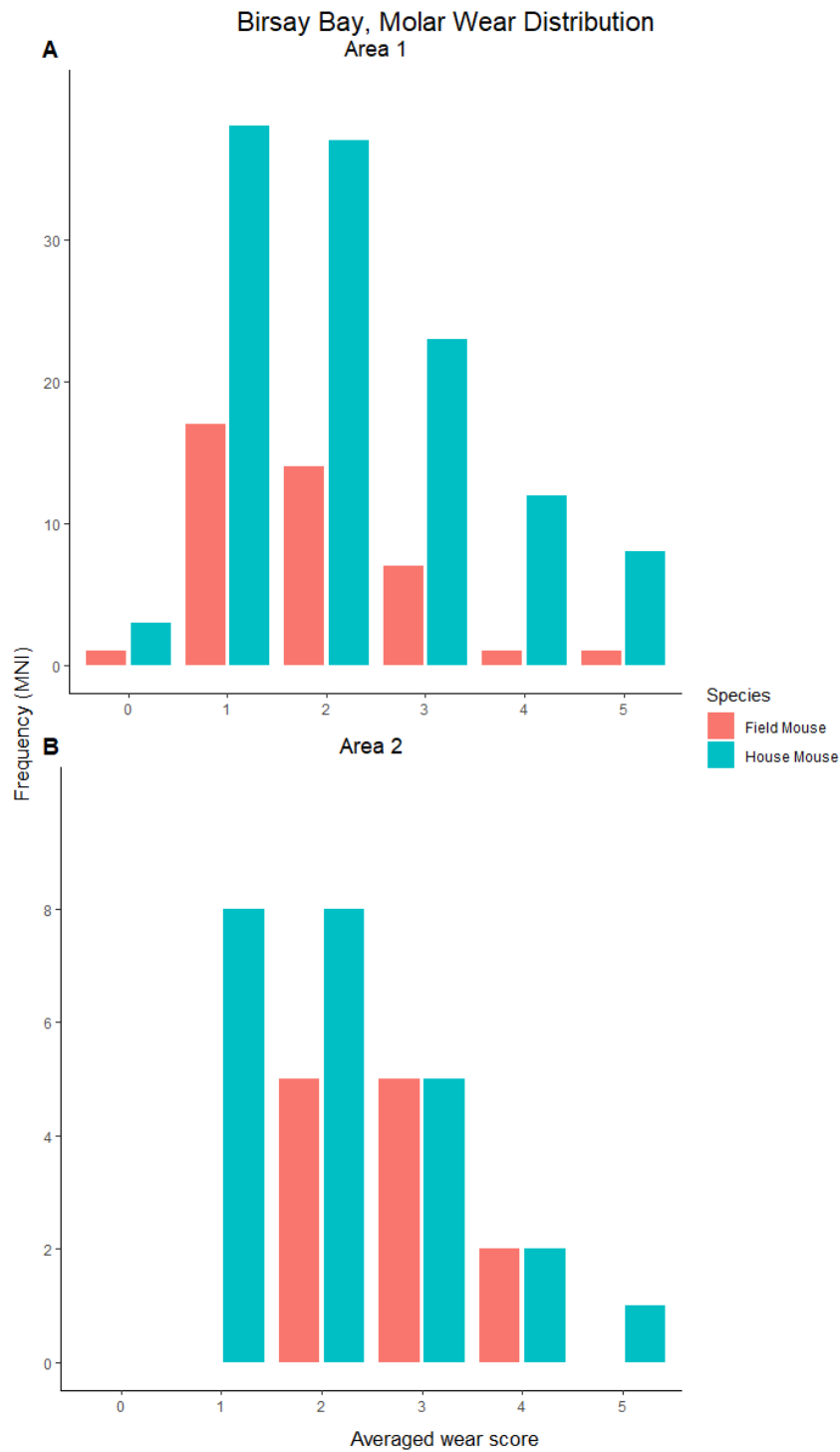


Fig. 5.30 – Birsay Bay, frequency distribution of *Apodemus* and *Mus* MNI depending on molar wear scores obtained for Area 1 (A) and Area 2 (B).

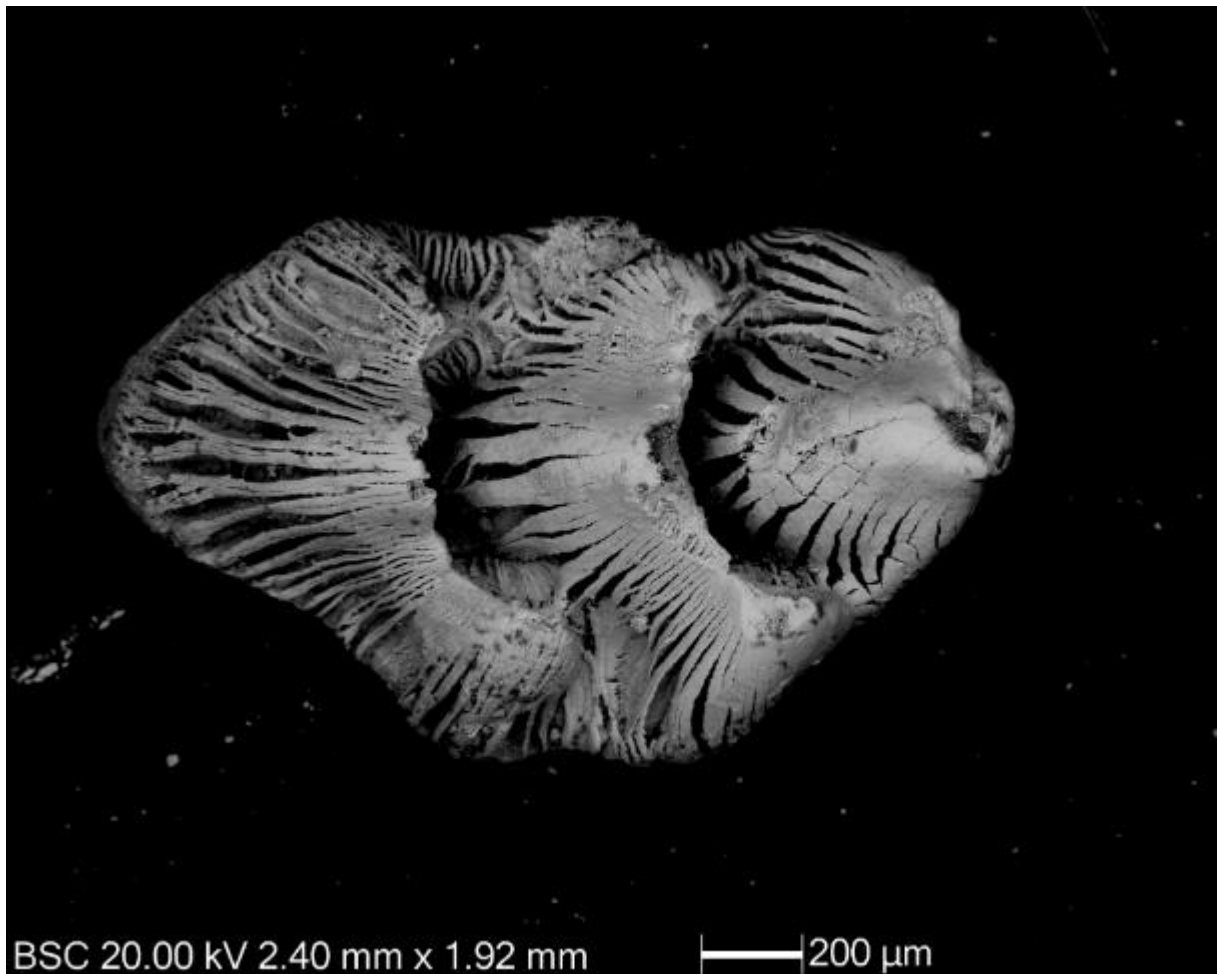


Fig. 5.31 – SEM micrograph of a still developing crown of a house mouse first maxillary molar, retrieved from Context 171 (Period 8).

5.4.3. FREQUENCIES, ABUNDANCES AND INDICES

Skeletal Frequencies retrieved from Birsay Bay Areas were vastly different from the other sites (Fig. 5.32), most resembling owl stages of dispersal from Terry (2004). The best example was Area 1, with vertebral frequencies of 51%, followed by front limbs (17%) and skull as well as hind limb elements (16%). Area 2 also provided many vertebral finds, though to a lesser degree considering the whole assemblage (40%), and showed a stronger presence of skull remains (23%). Area 3, in turn, showed stronger presence of hindlimb elements rather than skulls (25%) with vertebral and front limb frequencies being similar to Area 2.

While Area 2 was uniform in pattern across known phases, the stratigraphy of Area 1 showed some variation. The majority of periods followed general Area 1 *Skeletal Frequencies*. Especially Period 9 contributed to the site pattern, with vertebrae frequency around 53% and the remaining three frequencies around 15% - 16%. However, even within Period 9 there was a minor variation between contexts. Context 198 provided the highest NISP, in result affecting heavily obtained *Skeletal Frequencies* and *Abundances*. Context 182, second biggest, showed values more similar to ones obtainable from intact specimens, with 52% vertebrae followed by 20% front and 16% hindlimbs, with skull elements being noticeably least common (12%). The other three big Contexts, 164, 195 and 208, showed a stronger presence of skull elements and hind limb bones. The previous Periods 7 and 8 differed from the established frequencies, with Period 7 even showing predominance of skull elements (41%) rather than vertebrae (19%). However, Period 5, and especially Context 215, showed a pattern already noted for Period 9 being present in earliest occupation periods, perhaps aiming at a long-lasting trend. The trend may be also seen in later Periods 13-15, mostly because of Context 65 repeating a similar pattern. Most differing was Period 3, with a pattern determined by a very low NISP (only 16) of most robust elements, possibly showing the impact of differential preservation.

Abundances obtained from Birsay material showed relatively high values for various skeletal elements but differed from a similar situation in Skara Brae (Fig. 5.33). In general, Area 1 had moderate relative abundances of maxillary and mandibular bones (50-60%) but far lower than ones observed in Skara Brae Trench I. However, high amounts of loose incisors contrasted with low percentages of loose molars, a pattern also visible in the case of Skara Brae. All larger limb bones were present, with the predominance of humeri and femora (circa 50%) followed by ulnae and tibiae. The smaller bones were also quite common, with relatively high relative abundances of calcanei and tali. Metapodials were also present but ribs and phalanges were

rarely found. Period 5, the earliest to provide enough material to have *Abundances* properly plotted, differed substantially only in the case of far lower cranial abundances. A similar situation occurred in the span of Periods 13 to 15, but with mandibles being more similar to original distribution as well as tibial relative abundance being more pronounced than femoral ones. Period 9, which contributed most data for overall calculations, was very similar to the Area 1 *Abundances* outline but with relative abundances on average 5-10% higher. For incisors, the difference was however much higher, with values exceeding 100% due to both a high number of finds as well as fragmentation providing more than one 1 NISP for a singular element. In contrast, Periods 7 and 8 were far less skeletally complete, with abundances being from 5% to 70% lower than generally in Area 1. Moreover, while period 8 still followed a distribution similar to the overall data, period 7 lacked some bones, including radii and tibiae. In the case of the other two areas, period 2 exhibited very similar abundances to Period 9, including very high isolated incisors percentages. In contrast, Area 3, despite similarity with Areas 1 and 2, showed more extreme abundances due to a sample pool lacking some bones.

Abundances estimated for specific contexts showed more deviations from the overall estimations than those seen in the case of periods. Contexts 182, 198 and 208 had very similar skull bones and loose teeth relative abundances, especially with loose incisors percentages beyond 100%, reflecting their provenance to Period 9. However, postcranial relative abundances differed, with Context 182 having higher percentages than Period 9 in general. Contexts 198 and 208 had lower postcranial relative abundances, with Context 208 showing lower results especially in the case of minor bones such as tibiae. Context 212, the largest assemblage from Phase 5, provided fewer small bones but at the same time showed high relative abundances of long bones, especially ulnae (100%). Loose teeth and maxillae were within ranges similar to other contexts but fewer mandibles were retrieved in relation to MNI. Context 65 (Period 13-15) in general provided abundances distribution similar to its parent period, with the exception of humeral bones showing higher results.

Apart from isolated incisors, *Indices* obtained from Birsay resembled data from Skara Brae (Fig. 5.34). Isolated incisors predominantly showed values beyond 250%, with major contexts from period 9 beyond 300%. Isolated molars values ranged mostly between 0 and 50%, including major contexts, but far higher values were also present, especially in the case of Area 2 and 3. Indices of cranial to postcranial elements, both complex and simplified, were almost exclusively within 0-200% range. The highest values were shown by main contexts of Periods 5 and 13-15, while main contexts from Period 9 showed being more moderate. Apart from one

context, proportions of limb elements were within 0-120% range, with some outliers within Area 1.



Fig. 5.32 - Birsay Bay *Skeletal Frequencies*, plotted for main areas (upper plots), stratigraphy in Area 1 and 2 (middle plots) and selected contexts from Area 1 (lower plots).

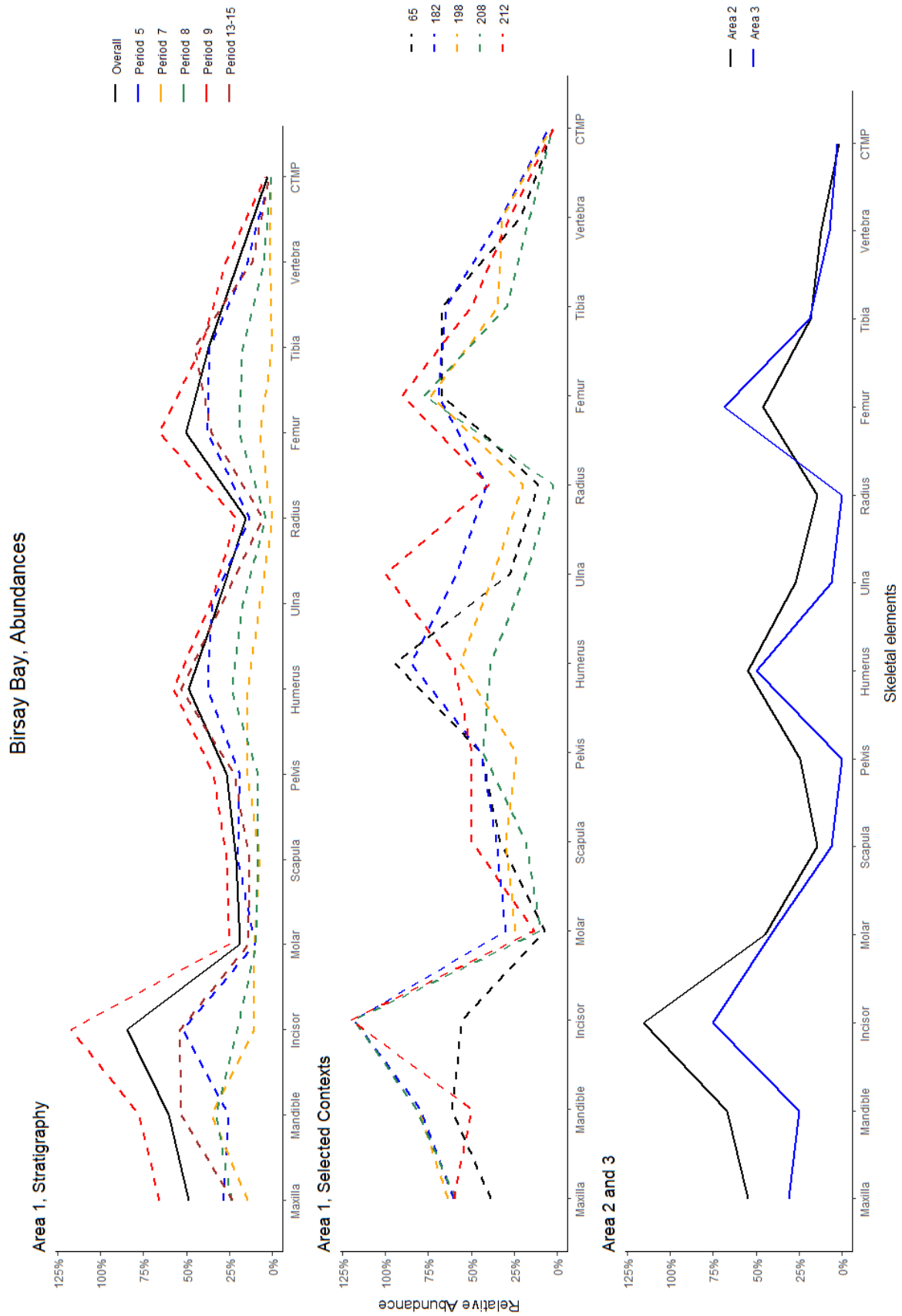


Fig. 5.33 – Birsay Bay *Abundances* of specific skeletal elements, plotted for Area 1, including its stratigraphy (upper), specific contexts from Area 1 (middle) and general for Area 2 and 3 (lower).

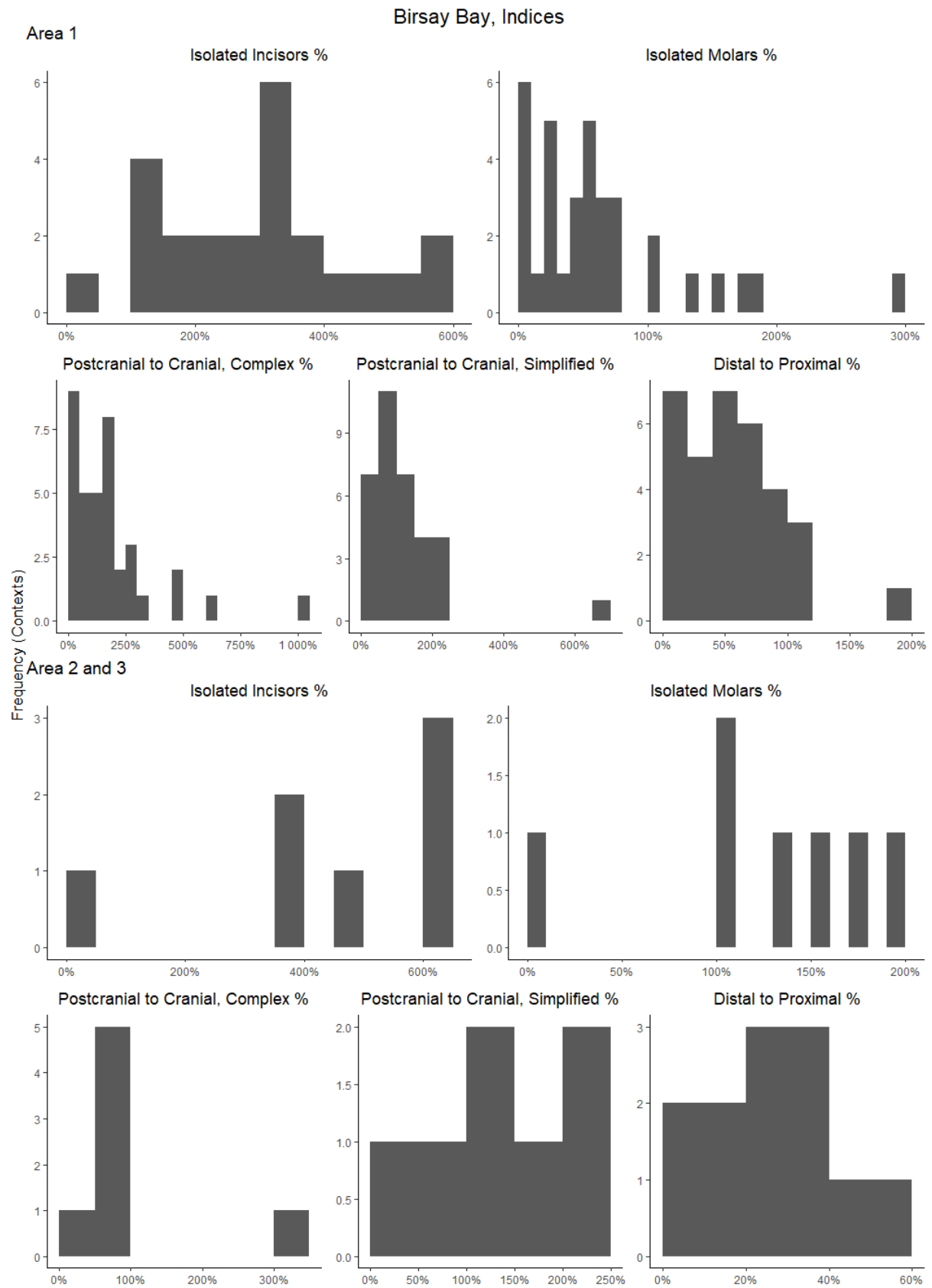


Fig. 5.34 – Birsay Bay, frequency distribution of index results for Area 1 (upper) and 2 as well as 3 (lower plots) *Indices*.

5.4.4. FRAGMENTATION

Fragmentation did not significantly differ from the patterns observed from Skara Brae but differences between areas could be noted (Fig. 5.35). In the case of skull elements majority of finds (>90%) were isolated maxillae and other cranial bones. Maxillae with zygomas and adjacent bones still attached, especially with complete viscerocranium, in Area 1 and 2 were rare while in 3 no such remains were found. The same situation repeated in the case of mandibles, with a predominance of highly fragmented remains in both Areas 1 and 2 and completely no more intact finds in Area 3. Postcranial elements such as ulnae, femora and tibiae also repeated this pattern. However, humeral fragmentation was lower than of the other postcranial bones, up to providing complete cases even for Area 3. Interestingly, when specific periods are taken into account fragmentation seemed to strongly differ. Period 5 differed mostly by a bigger amount of intact femoral finds while in Period 8 more than half of the humeri were found intact with half of ulnae and tibiae being evenly divided between fragmented and intact finds. In contrast, Period 9 followed closely overall Area 1 distribution. Periods 13-15 provided slightly more intact humeri, femora and tibia but the majority of ulnae finds were fragmented.

Most representative contexts usually followed specific period fragmentation distributions (Fig. 5.36). Context 212 exhibited similarities with its parent period but provided no skulls or maxillae with cranial bones attached. Mandibles showed either full completeness or heavy fragmentation while distal limb bones (ulnae, tibiae) showed the predominance of intact specimens. In four out of six contexts from Period 9, the majority of cranial elements seemed to have similar fragmentation for the most part. However, in contrast to Contexts 182 and 198, Contexts 206 and 208 did not have any skull remains more complete than isolated maxillae. In the case of mandibular fragmentation, Context 206 had more intact specimens or some with just lightly altered ramus than the rest of Period 9 contexts. Postcranial bone breakage in Contexts 182, 198 and 208 differed but not to a significant degree. Only Context 206 showed noticeably higher humerus and tibia intactness but provided no intact femora. Interestingly, Context 65 fitted well with the Period 13-15 breakage pattern, with only minor changes in the case of skull breakage, due to the lack of maxillae with only zygomatic bones retrieved.

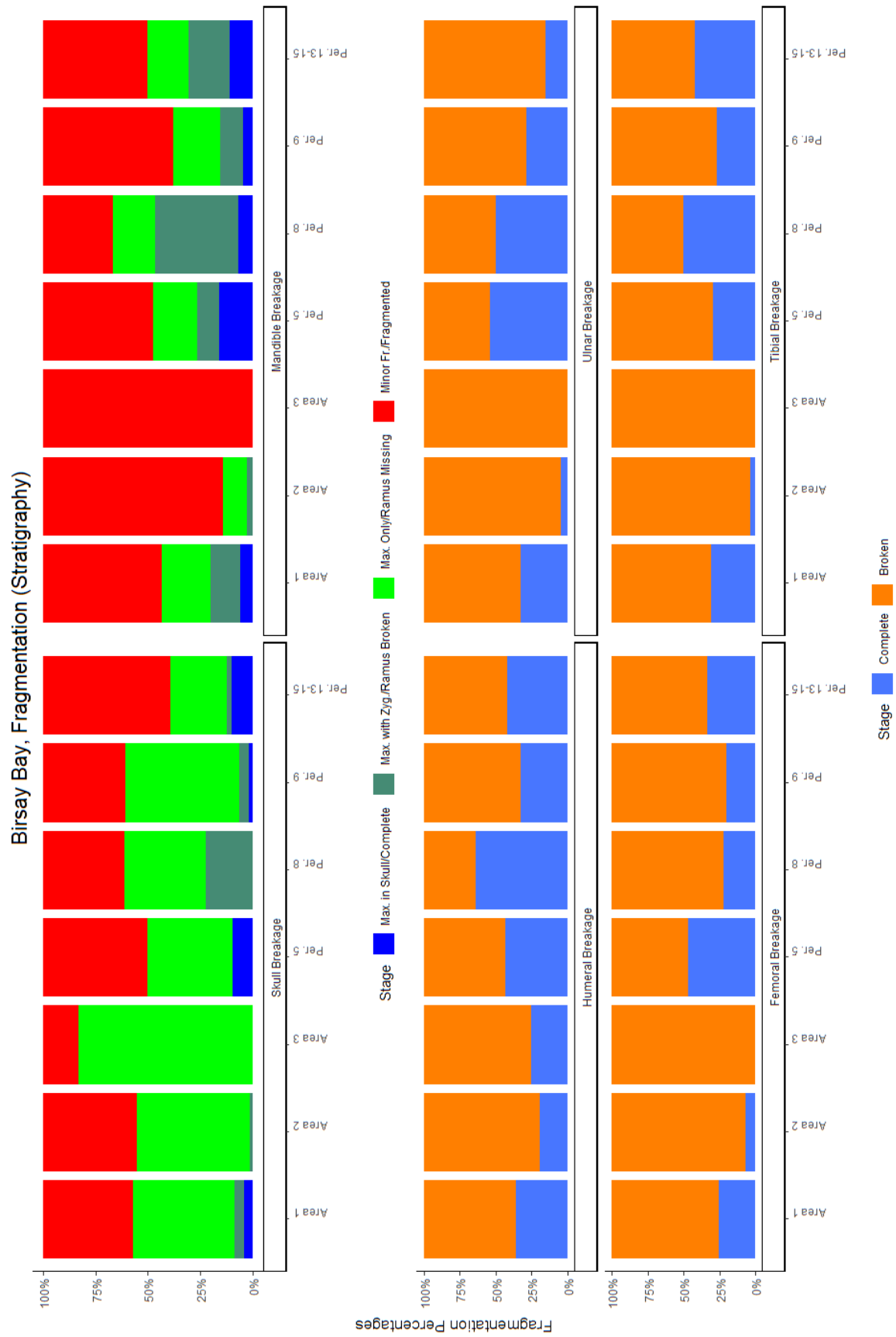


Fig. 5.35 – Birsay Bay, skull (upper row) and postcranial (two lower rows) breakage for Areas 1 to 3 (overall) and the stratigraphy of Area 1.

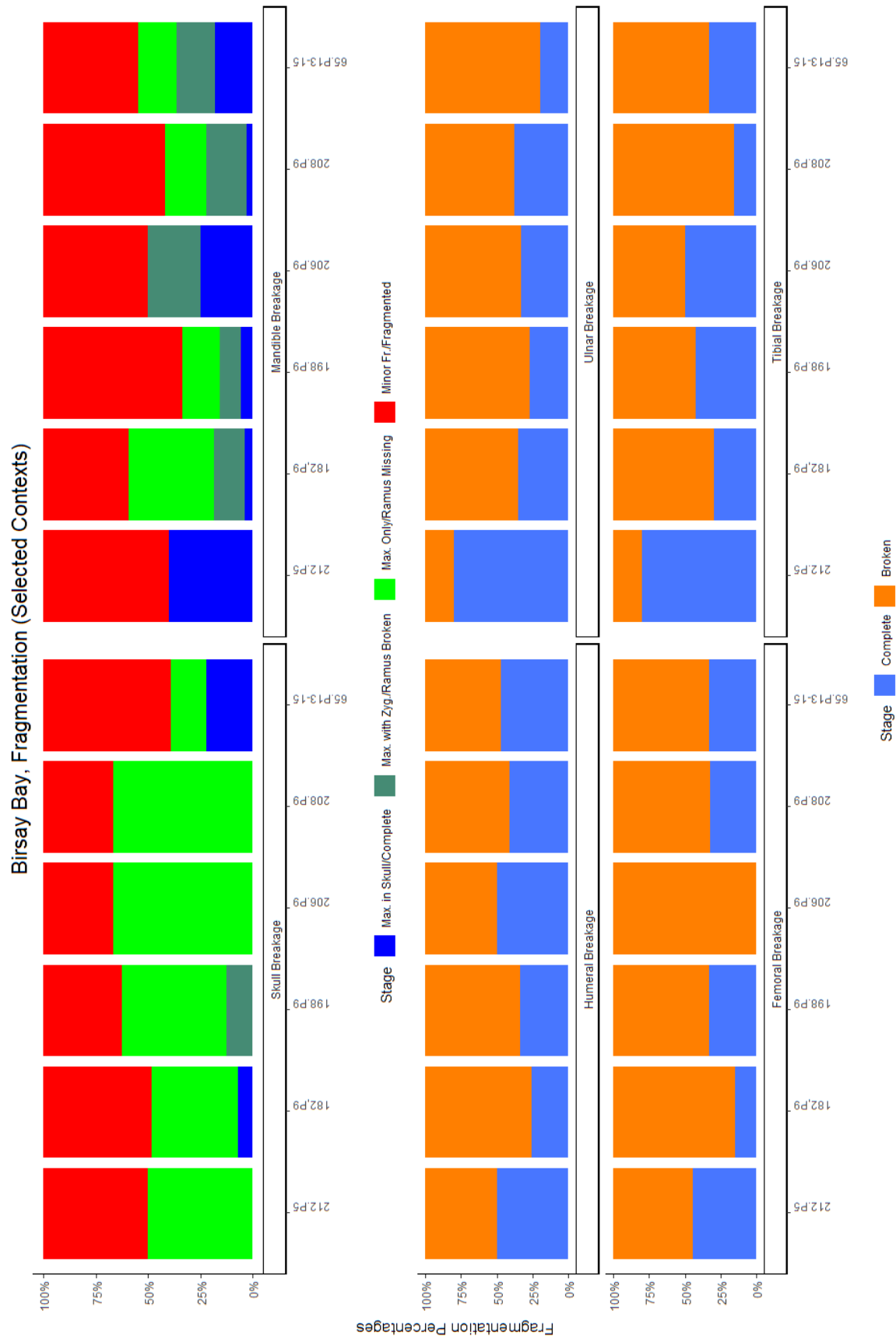


Fig. 5.36 – Birsay Bay, skull (upper row) and postcranial (two lower rows) breakage for representative contexts from Area 1.

5.4.5. DIGESTION AND BURNING

Evidence for digestion is present but scarce within all three areas (Table 5.11, Fig. 5.37). No extreme cases of digestion were found while several molars macroscopically showing signs of heavy digestion turned out to be a product of abrasion rather than digestion. Similarly, many moderate or light cases proved to show more similarities to abrasion/weathering than to digestion. Additionally, the majority of identified cases were related to vole molars, with murid molars not exhibiting such changes. Incisor digestion was very low and present only in bigger assemblages such as Period 9 Contexts 164 (~ 6%) and 182 (~ 2%). Molar digestion was occasionally higher, up to about 18% in Context 164, but overall results for Areas 1 and 2 showed similar amounts of incisors and molars with digestive changes. Confirmed digestion of epiphyseal surfaces of long bones was noted only on the one skeletal element from Area 2.

Evidence for burning was present within Birsay assemblages, contextually connected with areas of peat ash and household waste deposits. Six assemblages from Area 1 provided singular skeletal elements that were either carbonised or calcinated. While two among them were the biggest contexts encountered on site (Contexts 182 and 198) or within their respective period (Context 65) three contexts from period 5 were represented by singular buckets/samples retrieved. Those contexts were Context 176, burnt peat filled with organic remains, Contexts 294 and 295, peat ash layers with fish and shell remains. Area 2 provided two cases of burning in Contexts 19, rich clay sand, and 7, a midden layer.

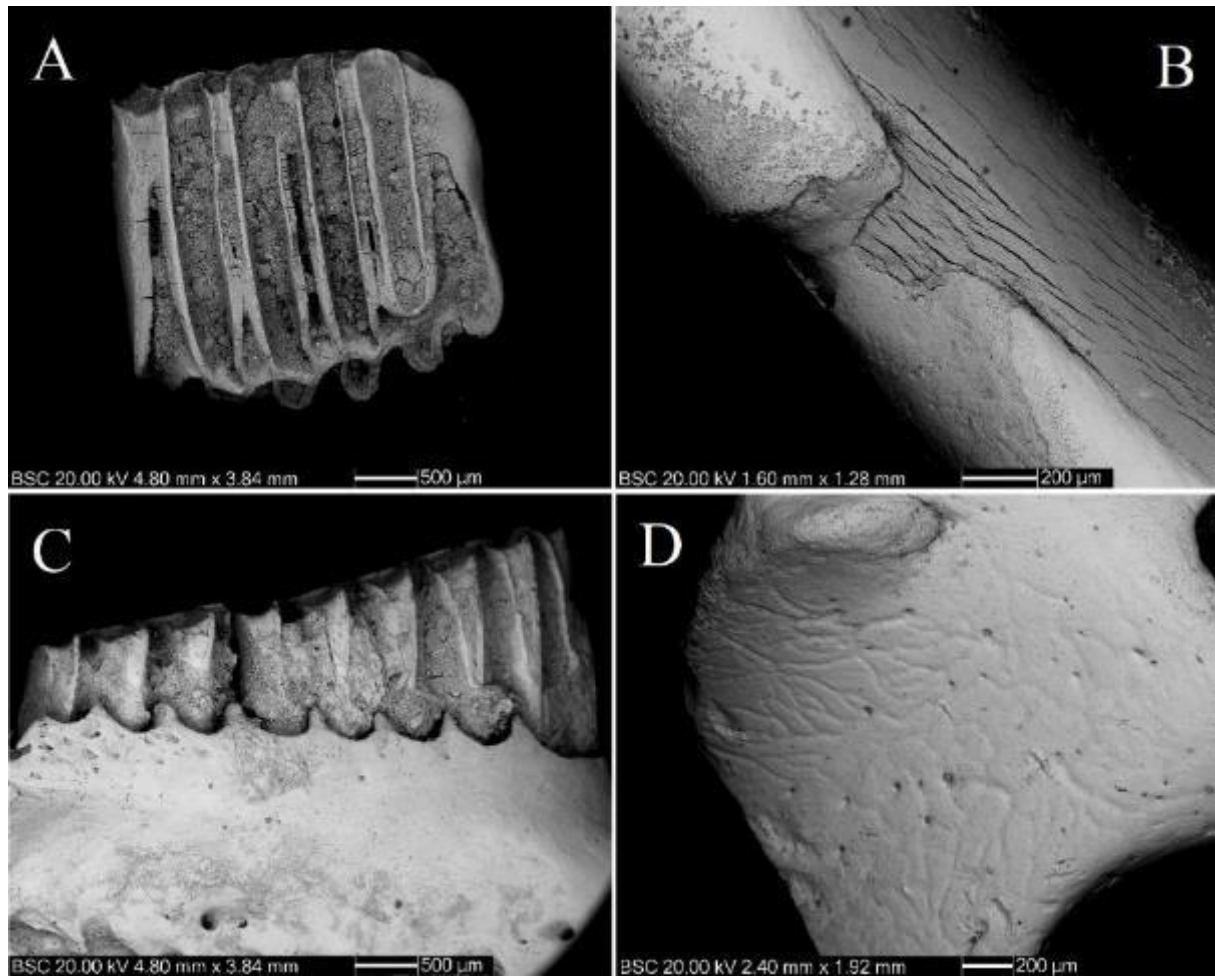


Fig. 5.37 – SEM micrographs of selected samples: heavily abraded molar (A), abrasion on incisor on the alveolous line (B), digestion or abrasion of vole mandibular molars (C), the surface of burnt mouse maxilla (D).

Table 5.11 – Percentage of digested specimens of each category for Areas 1 to 3, including periods and phases in 1 and 2. For teeth both loose and intact finds were considered.

Area	Period/Phase	Percent of digested elements		
		Incisors	Molars	Epiphyses
1	3	0.00%	0.00%	0.00%
	5	3.49%	1.20%	0.00%
	7	0.00%	0.00%	0.00%
	8	0.00%	0.00%	0.00%
	9	2.59%	4.51%	0.00%
	11	0.00%	0.00%	0.00%
	13-15	0.00%	6.00%	0.00%
	18	0.00%	0.00%	0.00%
		2.34%	4.13%	0.00%
2	W	0.00%	0.00%	0.00%
	X	3.87%	5.57%	0.62%
	Σ	3.62%	5.21%	0.58%
3	X	4.17%	2.38%	0.00%
All Areas		2.76%	4.47%	0.14%

5.4.6. POSSIBLE TAPHONOMIC AGENTS

The classification algorithm provided data correlating to some extent with the number of samples per context as well as general NISP (Table 5.12). On area level, Birsay showed predominantly classifications to diurnal/mammal group. Owl identification was noted however for *Abundances* of Area 1 and 2, with the former showing it only in the case of adjusted results and the latter in both cases. The internal structure of both areas showed some variation, mostly connected with general NISP retrieved from each phase. Contexts from Area 1 Periods 3, 11 and 18, showing a small number of NISP (< 33), were identified as scattering in the majority or entirety. Period 7 also showed scattering, but only for methods trained on original data. In the case of Area 2 only *Abundances* for Phase W showed scattering as identification. The remaining stratification showed a combination of scattering with diurnal/mammal and owl identification. For Area 1 Period 8 showed predominantly diurnal/mammal identification, with scattering visible only in the case of *Abundances*. In turn, Periods 13-15 showed *Fragmentation Percentages* more similar to owls while Period 5 adjusted results showed owls in both cases. Area 1 Period 9 and Area 2 Phase X, both providing the largest amounts of micromammal remains, showed continuous owl identification for *Abundances* as well as diurnal or mammal identification for *Fragmentation Percentages*.

While many contexts were identified as scattering, all large assemblages showed similarity to owl/diurnal/mammal identification noted in the case of periods/phases. The majority of contexts from Area 1 and both contexts of Phase W in Area 2 showed scattering as identification in at least one of two datasets, predominantly reflecting their low NISP values. However, larger contexts from better explored periods (Periods 5,9 and 13-15) showed identification very similar to their parent periods, with owl identification being more common. Especially one of the earlier contexts, Context 212, showed full identification as an owl, with transformation showing differences only in the case of *Abundances*. The remaining main contexts showed owl identification either for *Abundances* (e.g. Contexts 182, 198 and 208) or for *Fragmentation Percentages* (Contexts 65 and 206).

Correlations provided a range of outcomes, from exact matches to weak negative correlations. Main areas visibly differed from each other, with Area 1 being consistent with kestrel signature (regardless of whether adjusted or not), Area 2 showing tendencies towards hen harriers (*Abundances*, highest for adjusted: $df = 11$, $r = 0.91$, $p = < 0.001$) and red foxes (*Fragmentation Percentages*, same result for both cases: $df = 8$, $r = 0.99$, $p = < 0.001$) and Area 3 being best

correlated with the red fox signature. Some differences could be noted within Area 2, but once again most varied responses were obtained for Area 1 and associated contexts. The earliest recorded period correlated with long-eared owls (*Abundances*) and kestrels (*Fragmentation Percentages*) though only in the former case were values significant. Next three periods showed a variety of responses, up to correlations with scattering pattern on a verge of strength for Period 7 fragmentation (unadjusted: $df = 8$, $r = 0.61$, $p = 0.06$). The largest context from Period 5, Context 212, showed a similar pattern in the case of *Abundances* but differed in fragmentation, with both methods pointing towards owl species (for unadjusted: $df = 8$, $r = 0.65$, $p = 0.044$). Period 9, in turn, showed predominantly hen harrier (*Abundances*) kestrel (*Fragmentation Percentages*). Out of four main contexts, three showed exactly the same pattern, with Context 182 differing only in the case of *Abundances*. The last periods with NISP comparable to Period 9, Periods 13-15, showed the same correlation results, though some variation was found in the case of Context 65 *Abundances* results. Period 18 was the only one with definitively weak correlations, especially for fragmentation, possibly confirming the scattering classification.

Table 5.12 – Highest correlations (upper table) and classification outcomes (lower table) for *Abundances* and *Fragmentation Percentages*, based either on original references/signature data (Normal) or ones simulating partial dispersal/burial (Adjusted). The upper section of each table includes overall for areas overall and site stratigraphy while the lower section includes major contexts.

Trench, Phase or Context	Highest Corr. Abundances				Highest Corr. Fragmentation			
	Normal		Adjusted		Normal		Adjusted	
Area 1	0.79	Kestrel	0.84	Kestrel	0.99	Kestrel	0.99	Kestrel
Area 2	0.76	Hen H.	0.91	Hen H.	0.99	Red Fox	0.99	Red Fox
Area 3	0.80	Red Fox	0.87	Red Fox	0.98	Red Fox	0.98	Red Fox
Period 3	0.71	Owl(Lg)	0.78	Owl(Lg)	0.35	Kestrel	0.29	Kestrel
Period 5	0.74	Red Fox	0.75	Red Fox	0.90	Hen H.	0.85	Hen H.
Period 7	0.75	Hen H.	0.66	Hen H.	0.61	Scatt.	0.61	Scatt.
Period 8	0.96	Kestrel	0.88	Owl(Sh)	0.85	Kestrel	0.74	Kestrel
Period 9	0.75	Hen H.	0.85	Hen H.	0.98	Kestrel	0.99	Kestrel
Period 11	0.29	Hen H.	0.76	Red Fox	---	---	---	---
Period 13-15	0.82	Kestrel	0.85	Owl(Sh)	0.91	Kestrel	0.91	Kestrel
Period 18	0.56	Hen H.	0.42	Owl(Lg)	0.42	Owl(Sh)	0.50	Owl(Sh)
Phase W (A2)	0.61	Hen H.	0.84	Red Fox	0.93	Kestrel	0.94	Kestrel
Phase X (A2)	0.77	Hen H.	0.92	Hen H.	0.99	Red Fox	0.99	Red Fox
212 (P5)	0.57	Red Fox	0.60	Red Fox	0.65	Owl(Sh)	0.63	Owl(Sh)
182(P9)	0.78	Kestrel	0.81	Red Fox	0.96	Kestrel	0.98	Kestrel
198 (P9)	0.72	Hen H.	0.84	Hen H.	0.96	Kestrel	0.96	Kestrel
206 (P9)	0.68	Hen H.	0.63	Hen H.	0.82	Kestrel	0.82	Kestrel
208 (P9)	0.68	Hen H.	0.79	Hen H.	0.94	Kestrel	0.94	Kestrel
65 (P13-15)	0.77	Red Fox	0.73	Owl(Sh)	0.93	Kestrel	0.94	Kestrel

Trench, Phase or Context	Abundances Classification		Fragmentation Classification		Final Result	
	Normal	Adjusted	Normal	Adjusted	Normal	Adjusted
Area 1	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Area 2	Owl	Owl	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Accumulation
Area 3	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.
Period 3	Scattering	Scattering	Scattering	Scattering	Scattering	Scattering
Period 5	Scattering	Owl	Diurn./Mamm.	Owl	Contested	Owl
Period 7	Scattering	Diurn./Mamm.	Scattering	Diurn./Mamm.	Scattering	Diurn./Mamm.
Period 8	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.
Period 9	Owl	Owl	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Accumulation
Period 11	Scattering	Scattering	Scattering	Scattering	Scattering	Scattering
Period 13-15	Scattering	Diurn./Mamm.	Owl	Diurn./Mamm.	Contested	Diurn./Mamm.
Period 18	Scattering	Diurn./Mamm.	Scattering	Scattering	Scattering	Contested
Phase W (A2)	Scattering	Owl	Diurn./Mamm.	Diurn./Mamm.	Contested	Accumulation
Phase X (A2)	Owl	Owl	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Accumulation
212 (P5)	Owl	Diurn./Mamm.	Owl	Owl	Owl	Accumulation
182(P9)	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Diurn./Mamm.
198 (P9)	Owl	Owl	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Accumulation
206 (P9)	Diurn./Mamm.	Diurn./Mamm.	Owl	Diurn./Mamm.	Accumulation	Diurn./Mamm.
208 (P9)	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation	Diurn./Mamm.
65 (P13-15)	Diurn./Mamm.	Owl	Owl	Diurn./Mamm.	Accumulation	Accumulation

5.5. TUQUOY

5.5.1. ASSEMBLAGES QUANTIFICATION AND DISTRIBUTION

Both excavation seasons together provided 228 samples containing micromammal material, retrieved from 205 contexts (Table 5.13). About 4484 identifiable skeletal fragments, coming from at least 465 individuals, were documented. Among the samples, 216 were sieved as described in the materials section while 12 samples were retrieved by hand. Among by-hand retrieval, only five were taken from contexts not sampled for sieving. The breadth of identified micromammal species was larger than in Neolithic Skara Brae and Early Iron Age Bu Broch but did not differ from species inhabiting Westray today. Orkney voles were over half of the micromammal population observed (MNI 251), followed by field and house mice (MNI 61 and 64 respectively). Pygmy shrews occasionally appeared in 19 samples (MNI 21). About 5 MNI were attributed to mice but not to specific species while 63 could only be described as an unidentified rodent. Only one sample (Context 1061) containing a single rodent bone was retrieved from contexts of Block 43 (intrusive rabbit burrowing). In general, completeness counts were very low, possibly due to small sample sizes, with a few noticeable exceptions. One of these exceptions was Context 1112, an outdoor fill with a Skeletal Completeness of 32% for just one individual.

The distribution of finds was not uniform. Regardless of phase, most samples provided only a dozen or fewer skeletal fragments, quite often only teeth, vertebrae or other small elements (Table 5.14). NISP median for all samples was just eight, with an observable deviation from the norm of the two largest Contexts 33 and 28, both from Block 29, Phase 3. Both were statistical outliers but Context 28 contained just 83 NISP, representing five individuals, while Context 33 provided 1138 NISP, 42 individuals in total, about a quarter of the total number of micromammal finds at Tuquoy and about 9% of all MNI. Context 33 also provided high completeness, about 24% in the case of Skeletal Completeness and 30% in the case of Average Abundances. Context 28 also provided high completeness in relation to other contexts, but about 4% lower than Context 33. Overall, the majority of finds come from phases corresponding to initial human activity within the area (Phase 2), construction and utilization of two buildings found during the excavations (Phases 3 and 4) and gradual abandonment of the site (Phase 5). Blocks/contexts that provided the largest quantity of samples with micromammal remains were especially furnace and floor spreads within the smithy, walls and other contexts within the hall,

external deposits and abandonment layers (dumps) after the smithy abandonment. On average, samples from Phases 3 to 5 had more NISP and higher weight, which might reflect a genuinely higher density of skeletal fragments in these samples than in those coming from either natural soils predating Tuquoy (Phase 1), or from layers that followed the settlement (agriculture in Phase 6, kelp burning in Phase 7). However, completeness ratios in Phases 3 to 5 were noticeable higher only in the case of Phase 3. Phases 4 and 5 proved to have lower average completeness than agricultural Phase 6. Considering the sample pools ($n = 163$ for Phases 4 and 5, $n = 7$ for Phase 6), it may point towards more through context sampling not necessarily leading to higher completeness values. Additionally, a bias towards sampling anthropogenic contexts could not be fully excluded.

Differences between species could be seen in their distribution throughout the site (Fig. 5.38 & 9). Due to a well-studied stratigraphy both temporal and spatial differences could be found, including proportions in general areas of the settlement as well as in specific context types. Orkney voles were present from Phase 1 (Context 1022) until Phase 7 (Context 1042), comprising the majority of finds in each of seven phases. Their bones were found both inside the studied structures, within specific constructions and in a variety of outside contexts. Their MNI dominated especially Contexts 28 and 33, with the largest accumulations also found in outdoor windblown contexts, but not a huge difference was found between indoor and outdoor areas in general. Interestingly, the presence of voles was relatively lower in abandonment/rubble/later structure areas, windblown contexts and foundations of studied constructions. In contrast, field mice earliest appearance was Context 1171 (Block 9, Phase 2), an early pit infill, and they were present on the site until Context 108, Phase 5. Most finds were heavily scattered, representing, apart from Context 33, at best one or two individuals. Blocks that provided higher numbers of field mice were floor spreads within smithy while more complete cases were retrieved from other deposits as well as walls; their remains were also found within the hall entrance. Phase 5 finds came almost entirely from abandonment layers, with collapse contexts containing bigger amounts of these species than other types of contexts. House mice appeared slightly later than field mice, in Context 306, Block 13, a pit containing organic material and charcoal. Similar to field mice, their remains usually represented single individuals, with some relationship with floor layers and collapse contexts but also wall fillings. Notable exceptions were Blocks 77 and 97, with a relatively high number of house mice in either outside contexts or midden/rubble deposits, and a single bone retrieved from a drain/trench context. There were no remains from Phase 6, apart from a few murid bones

unidentified to a taxon, but house mice could be once again seen in Block 106, within the windblown sands. Finally, pygmy shrew bones appeared in Block 2 Context 1022, in natural sediments, and appeared sporadically until Context 1101, Phase 7. Most finds come from Phase 3 single finds and were retrieved from the construction contexts, but natural sands and predatory contexts also provided a number of different fragments.

The majority of samples contained only one or two species; higher counts were a rarity. Only context 137, an early rubble deposit from Phase 5, contained MNI of one for each of the four species. Samples that had three species differed between Phase 3 and later phases. Both Contexts 28 and 33, Phase 3, contained voles, field mice and pygmy shrews in windblown sand commingled with products of human activity like rubble or charcoal. All but one of the later contexts include a mixture of voles and two murid species within anthropogenic content, with other faunal remains and some carbonized material present, such as cereal grain (Context 91).

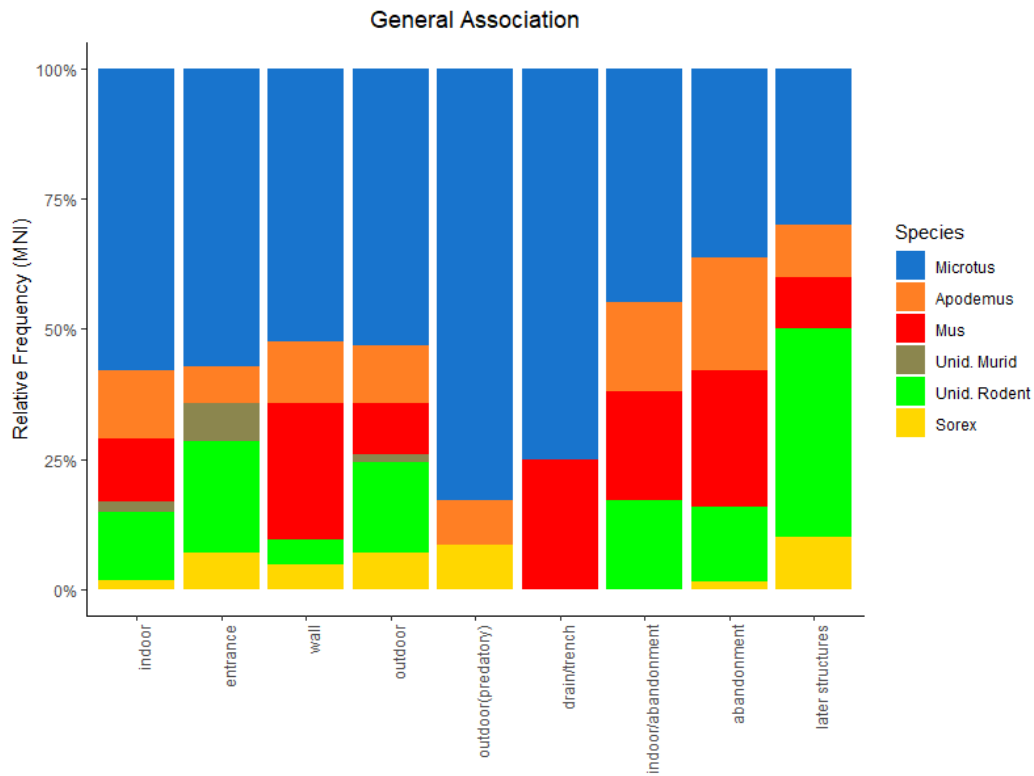


Fig. 5.38 – Tuquoy, relative frequency of MNI per species (including undetermined categories) in relation to general area of the site.

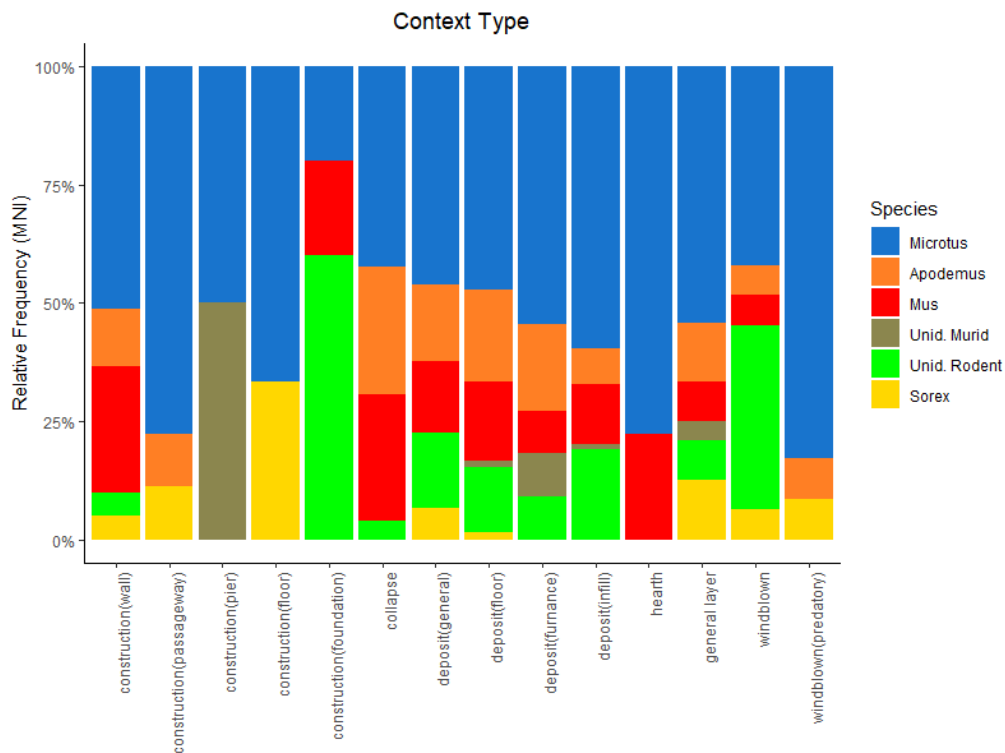


Fig. 5.39 – Tuquoy, relative frequency of MNI per species (including undetermined categories) in relation to specific context type.

Table 5.13 (left) – Weight, NISP and MNI counts distribution for Tuquoy and its stratigraphy, depending on specific species categories.

Table 5.14 (right) – Average weight, NISP and completeness ratios (Skeletal Completeness and Average Abundances), separately for samples and for contexts, for all phases besides the earliest recorded.

Phase	Weight	Contexts	Samples	Microtus		Apodemus		Mus		Unid. Rodent		Unid. Mouse		Sorex		Σ NISP	Σ MNI
				NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI		
1	0.06	1	1	1	1	0	0	0	0	4	0	0	0	1	1	6	2
2	2.67	16	16	76	18	10	3	5	2	78	3	2	0	2	1	173	27
3	29.53	29	32	850	74	40	13	21	7	912	13	6	0	12	8	1841	115
4	33.43	111	129	542	117	63	29	73	34	1041	26	48	4	8	7	1775	217
5	7.44	32	34	119	28	25	16	35	19	372	14	17	0	2	2	570	79
6	1.06	7	7	14	5	0	0	0	0	32	1	1	1	1	1	48	8
7	1.12	9	9	22	8	0	0	5	2	39	6	4	0	1	1	71	17
Σ	75.31	205	228	1624	251	138	61	139	64	2478	63	78	5	27	21	4484	465

Phase	Weight	Average, samples		Average, contexts	
		NISP	Skeletal Completeness	NISP	Skeletal Completeness
2	0.17	11	4.6%	11	4.6%
3	0.92	58	9.9%	63	10.2%
4	0.26	14	6.8%	16	7.1%
5	0.22	17	7.1%	18	7.1%
6	0.15	7	8.7%	7	8.7%
7	0.12	8	5.3%	8	5.3%

Phase	Weight	Average, samples		Average, contexts	
		NISP	Average Abundances	NISP	Average Abundances
2	0.17	11	6.3%	11	6.3%
3	0.92	58	11.2%	63	11.5%
4	0.26	14	8.0%	16	8.4%
5	0.22	17	8.0%	18	8.0%
6	0.15	7	8.7%	7	8.7%
7	0.12	8	5.7%	8	5.7%

5.5.2. AGE DATA DISTRIBUTION

The situation encountered on the Tuquoy site resembled Neolithic sites rather than roughly contemporary Birsay Bay (Fig. 5.40). It was especially visible in the case of early fusing epiphyses as examples of this group were predominantly found well fused. The relative frequency of unfused bones was about 8%, similar to Links of Noltland Trench D. The majority of unfused finds from this category however were distal humeri (10%), with unfused distal tibiae found only in three cases. Tuquoy showed some internal variation but specific phases differences were hard to judge, due to often small pool of obtained scores (similarly to Bu Broch, issue coming from how the data was retrieved). Still, singular finds coincide with possible periods of site utilization and later abandonment. The earliest find of an unfused vole humerus came from a sandy Context 279 (Block 11 Phase 2), predating the smithy, but apart from that there is no other evidence of juvenile specimens. In Phase 3, rodent finds of a similar nature appeared in Contexts 226 and 1205, mixtures of sandy and clay soils with remains of human activity. Surprisingly, none were recovered in the biggest accumulation found, Context 33 and 28. More finds appeared in Phase 4 but mostly outside of the smithy and hall, for example Contexts 96 and 107, Block 77. Unfused bones of voles and mice appeared in relatively high numbers in Block 97, Phase 5, but none could be retrieved from Phase 6. The last finds were proximal unfused femora within Block 106, Phase 7.

The middle fusing range of epiphyses provided a roughly similar number of examples as early fusing epiphyses but with an increased relative frequency of unfused finds. Overall, about 16% of all finds from this category were unfused, with the majority being unfused proximal femora ($n = 23$) and unfused distal ulnae only occasionally found ($n = 5$). Some variation between phases can be noted (see Fig. 5.19) though similarly to early fusions more can be inferred from contexts where those were found rather than phases in general. The earliest case of an unfused proximal femur, identifiable to a vole, came from Phase 2 Context 306 (pit fill) though the majority of finds came from Phases 4 and 5. Once again, however, the major assemblage consisting of Contexts 28 and 33 did not provide any such finds.

Fusion in the case of the late range was however rare, similarly to all sites discussed. 72% of all late fusing finds did not show fusion in any capacity, with relative frequencies of unfused finds highest in the case of proximal tibiae (80%) and proximal humeri (75%). Such finds were more common than early and middle cases, resulting in a little bit better understanding of their distribution across phases. However, differences were not large, with an average relative

frequency of fused cases oscillating around 25%. Even major assemblage, known to not contain any early and middle fusing cases that could be scored as unfused, did provide roughly similar ratios of fusion. Some differences could be noticed between species. In general, a greater proportion of the voles were sub-adult specimens while pygmy shrews and murids showed more fully grown adults. However, this could be due to a sample pool bias, especially in the case of the shrews.

Dental attrition revealed the presence of murids of various ages, from the unworn molars of juvenile animals to the extreme attrition found in old individuals (Fig. 5.41). In the case of both mandibular and maxillary molar wear, most individuals lied within the categories of 1 to 4, reflecting individuals of 1 month up to 10-11 months old. House mice provided sufficient numbers of unworn teeth to be sure of the presence of at least three young individuals and enough with heavy wear to indicate the presence of overwintered animals in the sample. In contrast, field mice mostly belonged mostly to a single category (Category 1, about 1 to 2 months old), with some older specimens occasionally present in random contexts. Only one possible juvenile was found. While house mice MNI was represented in 84% of cases, more bones than teeth of field mice were present and only 50% MNI could be assessed by this method, leading to a potential bias in the results for ageing. Nevertheless, despite the potential bias, tooth wear supplements long bone fusion data, showing that young house mice were indeed present in Phases 3 to 5 (Context 295, block 22; Context 163, block 55; Contexts 84 and 164, block 97).



Fig. 5.40 – Tuquoy, epiphyseal fusion expressed as a relative frequency of NISP (red-unfused, blue-fused) and grouped in three main groups related to individual's age (early/middle/late). Upper plot is the overall situation for Tuquoy, with stratigraphy shown in lower plots. Additionally, data for context 28 and 33 is shown separately.

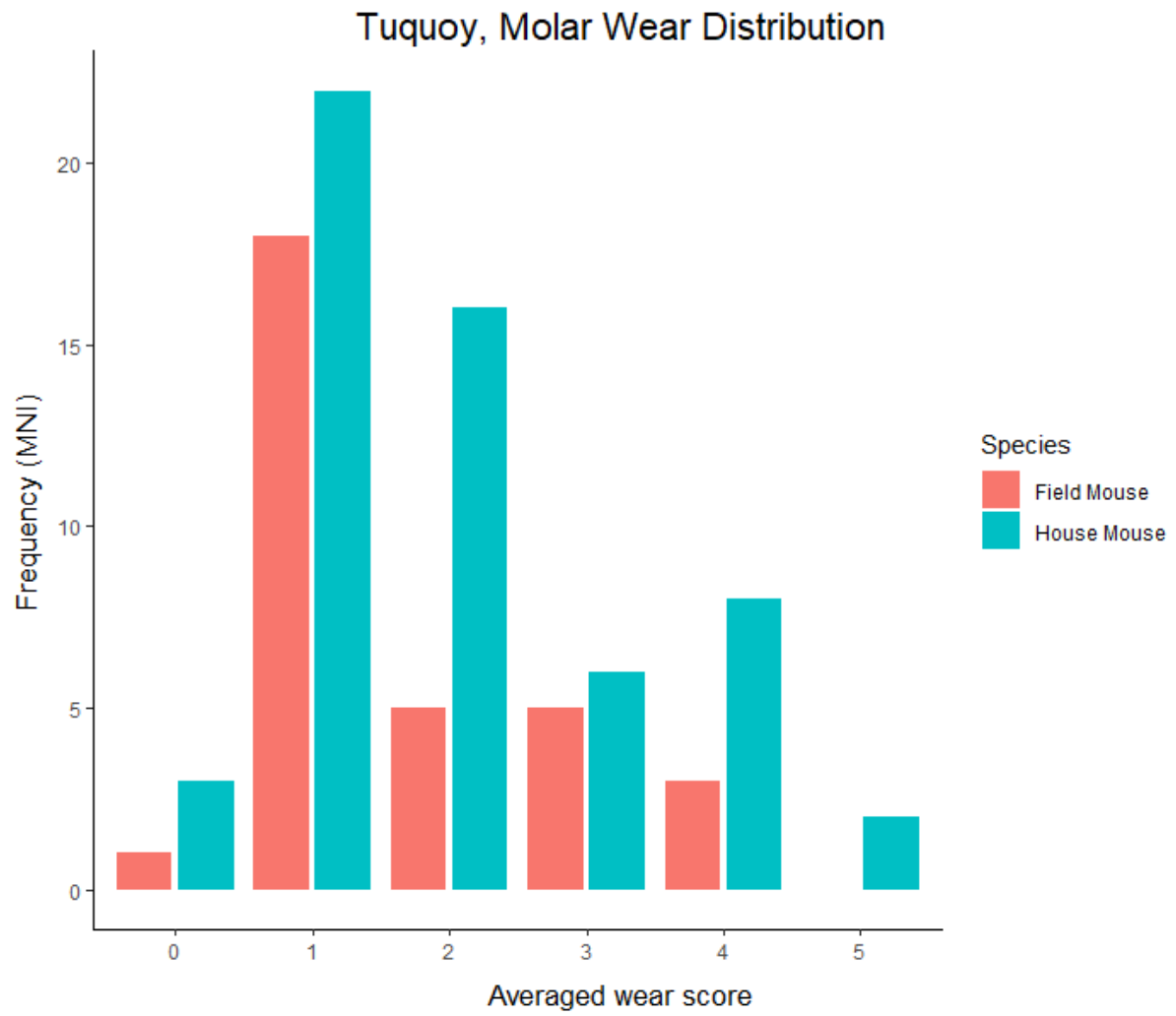


Fig. 5.41 – Tuquoy, frequency distribution of *Apodemus* and *Mus* MNI depending on molar wear scores.

5.5.3. FREQUENCIES, ABUNDANCES AND INDICES

Skeletal Frequencies obtained from Tuquoy, similar to the *Abundances* discussed later, are difficult to interpret, due to one context heavily affecting any joint calculations. Overall frequencies showed vertebrae being most commonplace (40%), followed by skull fragments (26%), hind limbs (19%) and finally front limb elements (16%, Fig. 5.42). However, such a pattern came mostly from Phase 3, specifically Context 33. Its frequencies were even more pronounced, with vertebrae on a level of 46%, skull elements around 24% and hind and front limbs difference of 5%. However, this outline was actually quite rare, with Context 28, context adjacent to Context 33, showing high differences between the front and hind limbs (of about 23%) but small between skulls and vertebrae (~7%). The second best-sampled Phase, IV, did not provide too different frequencies, with 40% of vertebrae, 27% of skull fragments and respectively 16 and 17% of remaining limb bones. However, it was a commingling of multiple small samples, resulting in actual contexts differing quite strongly from this pattern. For example, Context 107 provided almost 50% frequencies for front limbs while Context 181 was almost exclusively skull and vertebral fragments. The earliest known Phase 2 showed the dominance of skull frequencies (46%), reinforced by several samples, such as one coming from Context 306. Phase 5 saw a large contribution of vertebrae but general frequencies distribution more even, with at best 10% differences between major body regions, similar to e.g. Context 73 of this phase but more muted. Phase 6, in turn, and its contexts separately (1112) provided frequencies similar to a degree to Terry's (2004) partial dispersal, but with a smaller number of hind limbs. The latest Phase 7 was dominated by limb bones, with heavily incomplete remains in explored contexts (e.g. Context 1015).

In the case of *Abundances*, while a general trend was noticeable as in frequencies, several phases differed from it to a significant degree (Fig. 5.43). Only Phase 1, represented by a single sample, did not provide any data to work with. While general *Abundances* were similar to Skara Brae data, including spikes in humeral, femoral as well as cranial relative abundances, peak values were about 20-30% lower, with some being at best around 30% mark. The biggest difference from the established trend could be seen in Phase 3, where skull elements, loose teeth, femora and multiple small bones had values slightly (e.g. vertebrae) to much bigger (femora twice as abundant) to what was noted for overall values. On the other hand, Phases 6 and 7 had lower abundances of crania and teeth but showed a pronounced spike in humeri and

tibiae. Phase 2 showed generally lower values than overall data but followed the general trend, similarly to Phase 4 and 5.

Abundances of diagnostic contexts differed strongly, possibly related to differing taphonomic histories but equally likely to be a result of small sample pools. While taphonomic data pooled on phase level could be investigated in-depth, on the context level samples rarely provided enough information for further study. Due to a low NISP number samples represented very incomplete specimens, on median about 5.5.% when considering Skeletal Completeness and 6.3% in the case of Average Abundances. Not surprisingly, the larger samples contained remains that were more skeletally complete, often beyond 20% values as in beforementioned contexts 28 and 33. Context 33 showed *Abundances* pattern of its parent Phase 3, reflecting context providing the majority of finds. The only difference was higher relative abundances for most of the skeletal elements. Context 28 also to some degree followed Phase 3 and Context 33, especially in the case of femoral abundances, but differed due to higher pelves relative abundances as well as the complete lack of scapulae and ulnae. The remaining contexts showed small to no relation to their parent phases. As mentioned before, the most complete sample came from context 1112, a paving passageway infill from Phase 6 that provided a single Orkney vole. Despite high relative completeness, including only minuscule molar loss, it lacked hind limb bones. Contexts 107, 200, 753, 1072 and 1078, found near Smithy/Hall entries or inside those buildings and belonging to Phase 4, with the exception of the last one (Phase 5), provided relatively high completeness. Context 107 was estimated from more than one sample, creating a relative abundances graph with no maxillary bones but high relative abundances of loose incisors and humeri. In contrast, outdoor Context 181 from Phase 4 was estimated from four samples, leading to *Abundances* showing mostly skull elements and almost no postcranial ones. A very specific situation was noted in Context 1015, where the sample provided a high number of humeri of just one side but only minuscule amounts of other bones, leading to high MNI and very low relative abundances.

The analysis of *Indices* provided data but showed signs of being restricted by the small sample pool, resulting in either a lack of or extreme scores (Fig. 5.44). The majority of contexts had the percentages of isolated incisors relatively low, below 100% threshold, with the distribution similar to that seen in Skara Brae. However, some values came out as very high (over 700%). Molar percentages not only provided a wide range but also differed markedly from Skara Brae, showing results in hundreds of percent instead of tens. Still, most contexts were within 0-100% range, with only a portion of them going beyond that threshold. Individually, larger contexts

provided values only slightly higher than 100% (Context 33) or below it (Context 28), which could be informative on some level. In the case of cranial to postcranial and distal to proximal counts, Tuquoy material provided on average far lower percentages to Skara Brae. The largest Contexts 28 and 33, especially, showed very low values in all three indices, showing percentages far below all reference material from Andrews' research (1990). In contrast, Contexts 107 and 1015 showed very high values for cranial to postcranial elements index while being in the middle range of distal to proximal elements index.

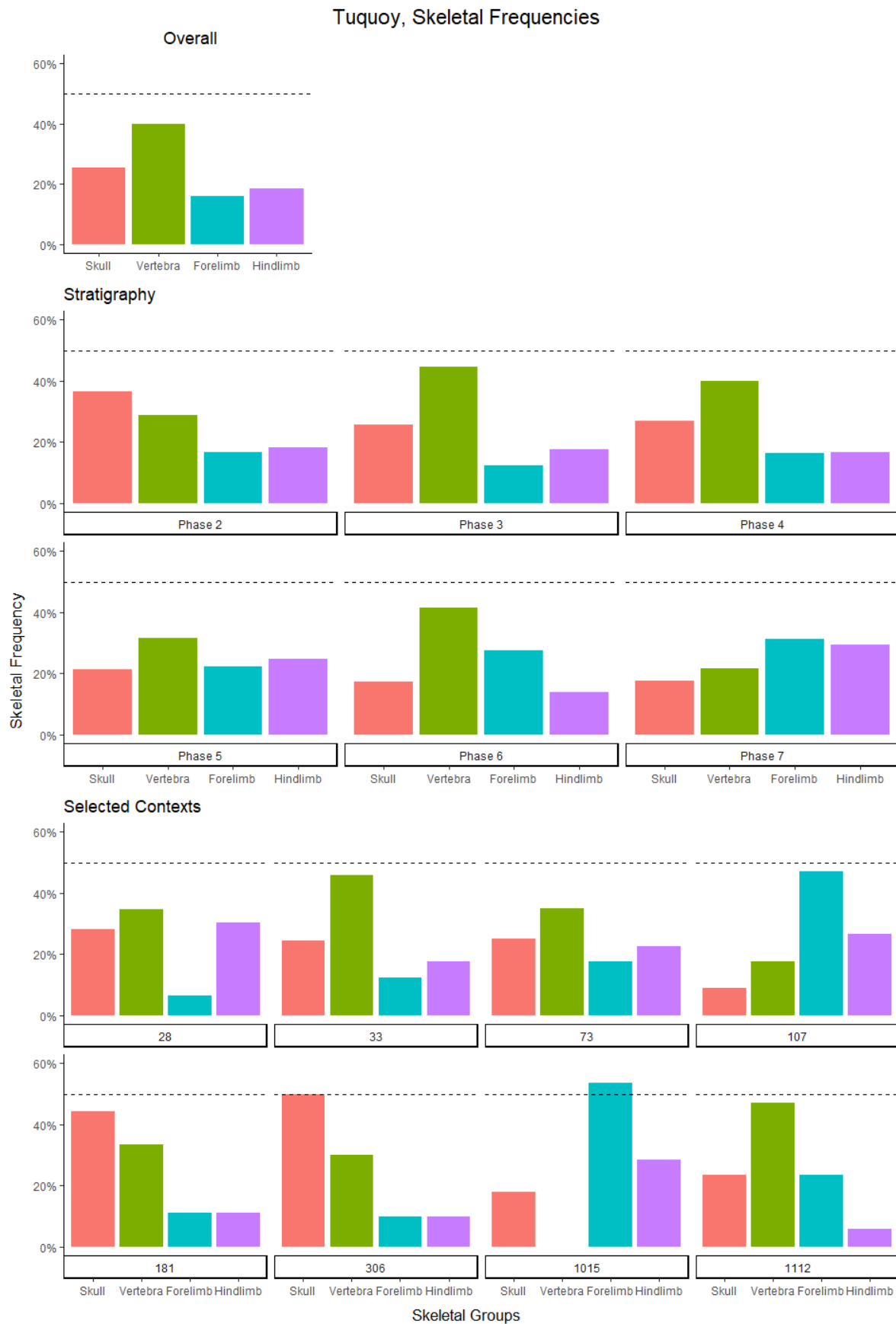


Fig. 5.42 – Tuquoy, *Skeletal Frequencies*, plotted for overall data (upper plot), stratigraphy (middle plots) and selected contexts (lower plots).

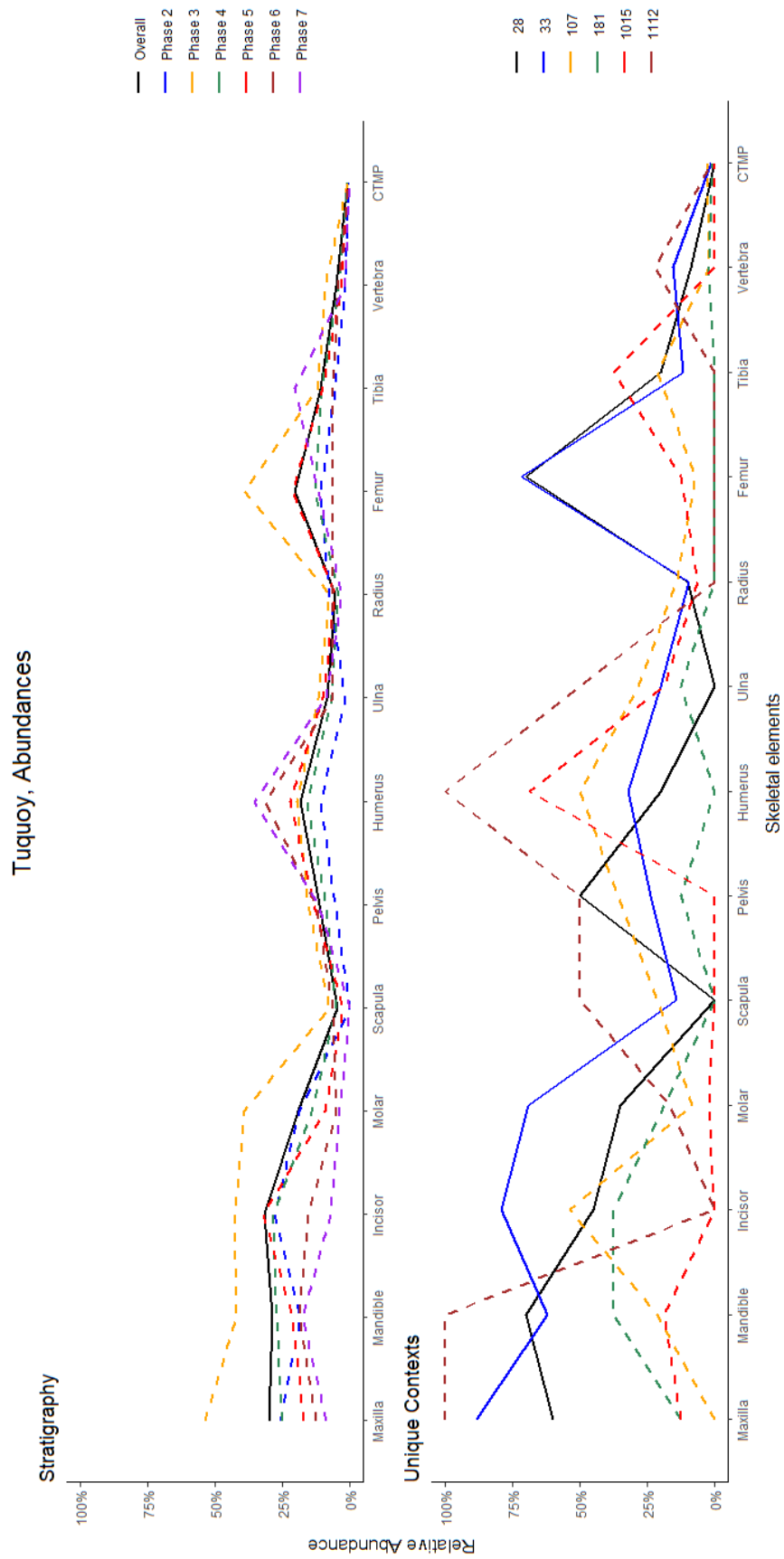


Fig. 5.43 – Tuquoy, *Abundances* of specific skeletal elements, plotted for the whole site and its stratigraphy (upper) as well as specific contexts (lower).

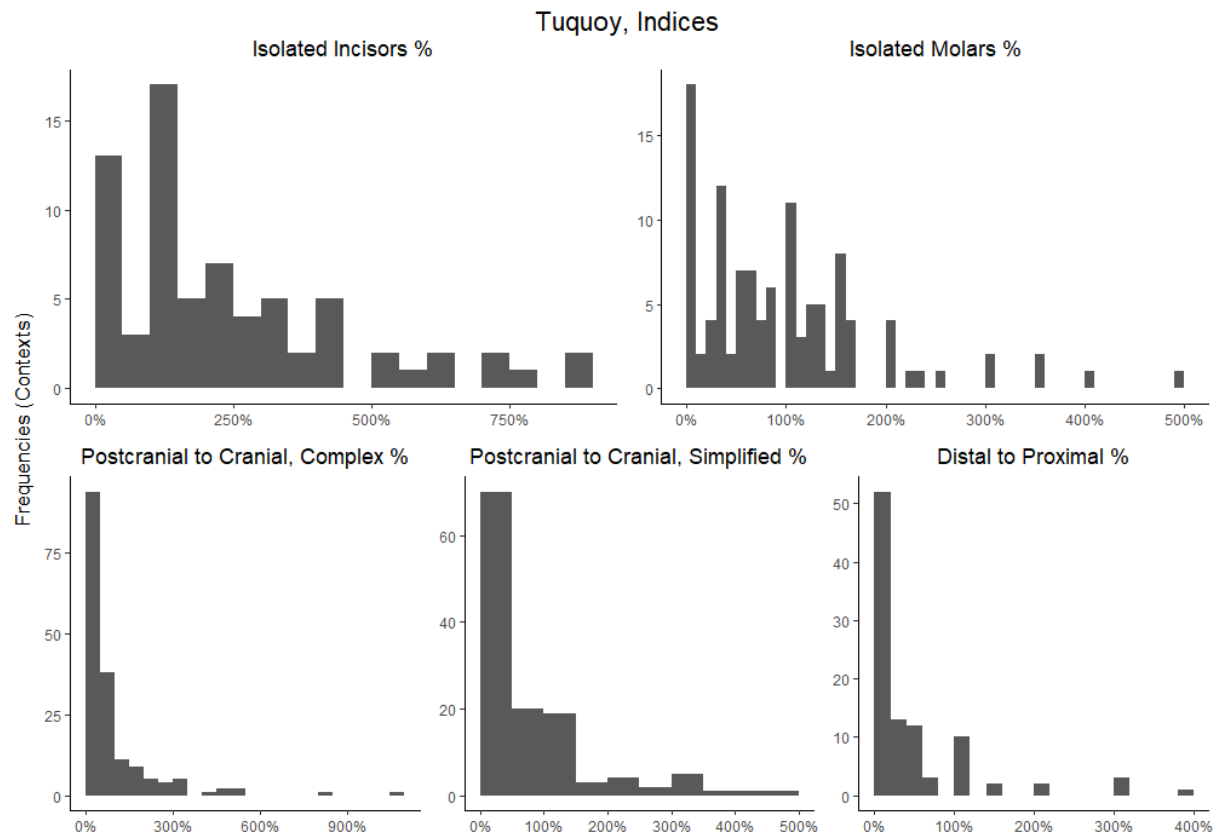


Fig. 5.44 – Tuquoy, frequency distribution of index results for the site *Indices*.

5.5.4. FRAGMENTATION

The skull fragmentation pattern present in Tuquoy was visibly different from the other sites (Fig. 5.45). In general, a minuscule number of cranial finds were skulls, all only viscerocrania with minuscule remains of other cranial bones. Only Phases 3,4 and 5 provided such finds, with Phase 5 showing more in terms of percentage but providing the same NISP as the other two. The majority of finds were only separate maxillae which were also the only finds from later Phases 6 and 7. Minor fragments were also quite common, to a similar degree as seen in Skara Brae. In contrast, the vast majority of mandibles found were fragmented up to very small pieces, with all lesser types of alteration and intact specimens being in the distinct minority. Only Phase 7 provided different proportions. Interestingly, completeness was not necessarily bound to the assemblage size, with major contexts providing similar or more fragmented patterns. While context 28 was similar to Phase 3 Context 33 provided only isolated maxillae and loose skull fragments. However, both contexts contained only (Context 28) or predominantly (Context 33) heavily fragmented mandibles, far more severe to what Phase 3 in overall had shown. Smaller contexts provided too few materials to be properly studied.

Postcranial fragmentation was higher than in Skara Brae material. Humeral breakage was high across all phases, reaching from 60% in Phase 6 to over 80% in Phase 2. Ulnar breakage was generally similar but differed heavily between phases, from no intact finds in Phase 2 up to majority intact in Phase 7. Femoral breakage was even more pronounced, with Phases 6 and 7 not providing any intact specimens. Tibial breakage was not as severe as femoral but followed to some degree its pattern in Phases 2 to 6, with 7 providing some intact bones. Once again, a significant difference could be noted in samples from Contexts 28 and 33, having fewer complete specimens than what overall Phase 3 data would suggest. In the first case (Context 28) no intact bones were retrieved while in (Context 33) complete cases were only found for humeri and femora.

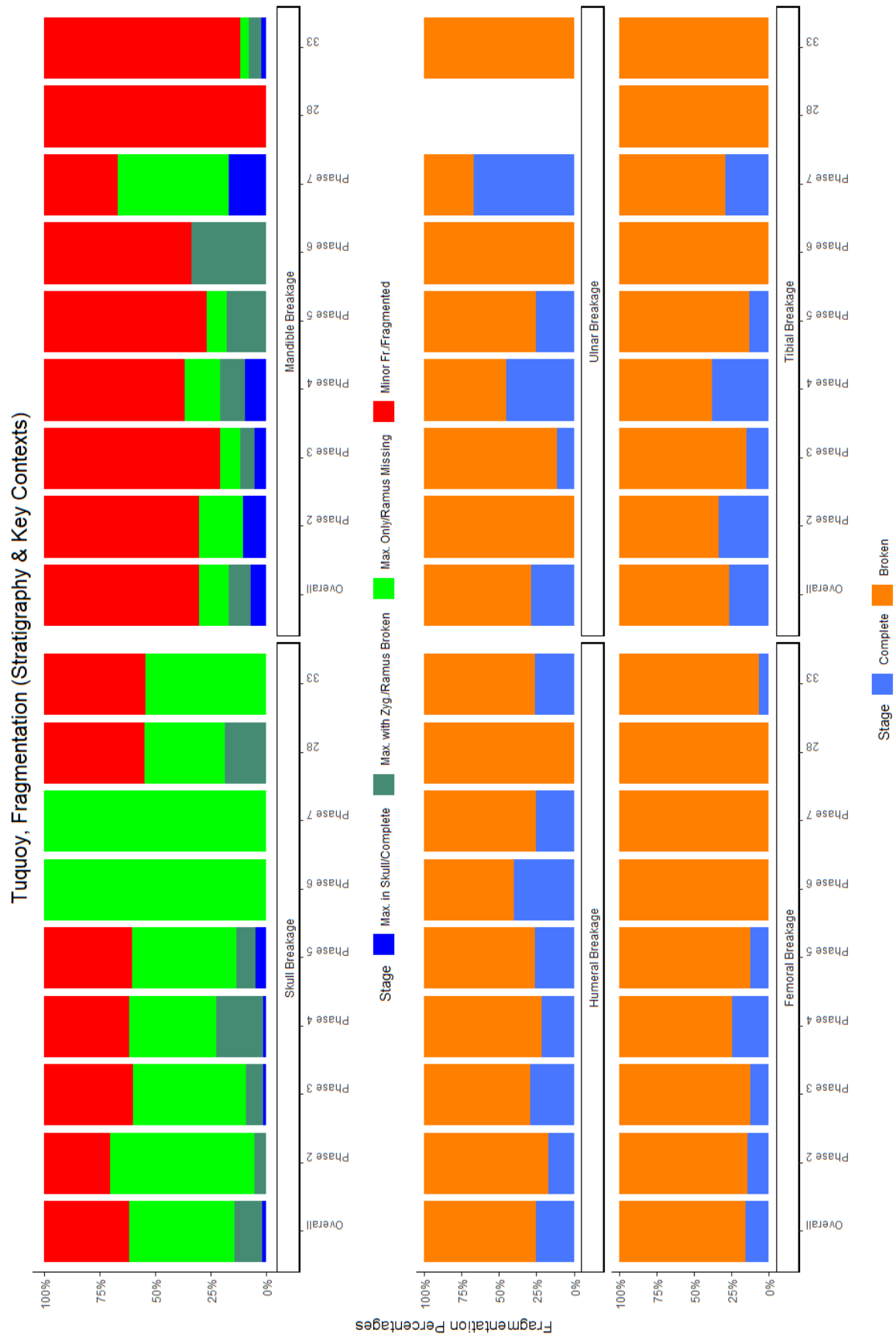


Fig. 5.45 – Tuquoy, skull (upper row) and postcranial (two lower rows) breakage for overall site data, stratigraphy and representative contexts.

5.5.5. DIGESTION AND BURNING

In contrast to Skara Brae, significant quantities of digested bones and teeth had been found within the site of Tuquoy (Table 5.15/6, Fig. 5.46). Overall, samples from 27 contexts contained evidence for digestion, among them 12 contained digested incisors, 23 digested molars and only four digested epiphyses of humeri and femora. Those contexts came mostly from outdoors of Phase 2, 3 and 4, early floor deposits of Phase 4 and abandonment/collapse layers of late Phase 4 and 5. The latest find was from the passageway in Phase 6. Among 10 biggest contexts about seven contained digested material, suggesting possibly a correlation between such finds and assemblage size in NISP. The correlation between overall NISP and all digested elements count was about $\rho = 0.22$ ($n = 205$, $p = 0.002$), low but given the high number of observations (critical value for $n = 100$ being $\rho = 0.20$) considered strong. It is not surprising given Contexts 28 and 33 provided the overwhelming majority of elements found on the site.

A variety of digestive alterations were spotted on teeth and epiphyseal surfaces. The majority of vole molars had only minuscule changes alongside silent ridges, predominantly around tooth's top, seen as enamel thinning or disappearance, exposure of dentine and, to some degree, dentine loss on top and along salient edges as well as cementum rounding or slight loss. Rarely did such changes include enamel and dentine layers below the alveolus line, suggesting molar loss not occurring during digestion. However, more severe cases had salient edges altered over their whole length, with enamel completely eroded away, dentine loss resulting in its inwards collapse to the hollow tooth interior and visible fragmentation and loss of cementum. Field mouse teeth also showed digestion-related changes, with enamel cracking longitudinally and peeling off the dentine beneath at its end at the crown neck. In turn, shrew teeth showed almost no taphonomic changes on their surface, in stark contrast to the mandibular bone. Similar to the vole molars, rodent incisors also showed mostly light digestion, with rounding of the tip and enamel retraction from it. Heavier cases existed, with enamel being reduced to irregularly located "isles" on the dentine surface which showed wavy, weathering-like longitudinal cracking. Epiphyseal digestion was best pronounced on proximal femora, with femoral head often reduced to trabecular bone or cortical layer porous enough to show the trabecula beneath. Additionally, various bones showed semi-circular, microscopic cracking on their surface and rounding of thinner bone parts. Weathering as well as abrasion however was also present on both teeth and bones and not always easy to distinguish from digestion. Moreover, all possible

alterations overlapped with each other, sometimes creating very complex and difficult to decipher cases.

All extreme cases of digestion, and all digested humeri, were found within contexts 28 and 33 (Table 5.16). It is possible that such disparity came solely from differences in size between those two assemblages and the rest of the contexts containing such material, but additional data puts more stress on digestive changes within Context 28 and 33 – and in Block 29 in overall. While sporadic staining of bone or tooth surfaces was noted in some samples, especially on those retrieved from material-rich sediments, bones from Block 29 were evenly stained in dull to dark brown colours. Additionally, only two cases of possible burning were found in Context 28, though chemical burning was more likely.

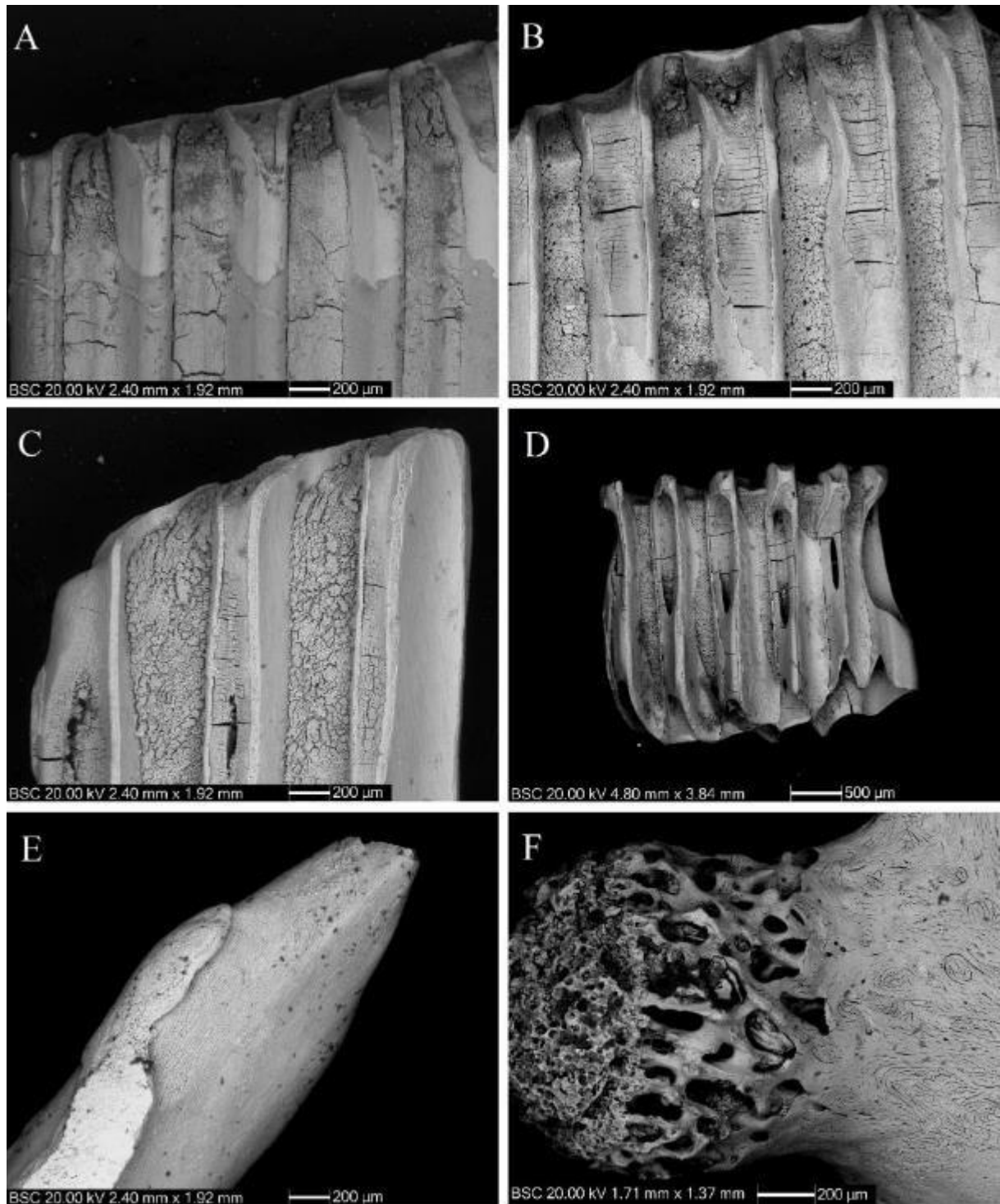


Fig. 5.46 – Selected micrographs showing evidence for digestion: light molar digestion with chipping (A), moderate molar digestion with dentine cracking (B), heavy digestion with inward dentine collapse (C), extreme digestion or/combined with abrasion/weathering (D), light digestion or weathering of the incisor tip (E), heavy digestion and/or weathering of the femoral head and its peripheries with additional taphonomic changes on its tip (F)

Table 5.15 – Percentage of digested specimens of each category for all the site as well as specific phases.
For teeth both loose and intact finds were considered.

Phase	Percent of digested elements		
	Incisors	Molars	Epiphyses
1	0.00%	0.00%	0.00%
2	0.00%	3.85%	0.00%
3	38.10%	30.37%	14.81%
4	2.24%	2.60%	0.79%
5	0.00%	1.73%	1.45%
6	11.11%	0.00%	0.00%
7	0.00%	0.00%	0.00%
Whole Site	13.39%	14.26%	6.04%

T.5.16 – Breakdown of specific elements digestion for all the site as well as two contexts that contributed the majority of finds.

Element	Dig. Level	Overall		Context 28		Context 33	
		No.	% finds	No.	% finds	No.	% finds
Molars	light	151	10.35%	3	12.50%	125	33.42%
	moderate	50	3.43%	1	4.17%	36	9.63%
	heavy	22	1.51%	6	25.00%	14	3.74%
	extreme	3	0.21%	0	0.00%	3	0.80%
Incisors	light	73	10.21%	4	44.44%	62	43.97%
	moderate	13	1.82%	2	22.22%	9	6.38%
	heavy	7	0.98%	1	11.11%	4	2.84%
	extreme	4	0.56%	1	11.11%	3	2.13%
	Humeri	3	1.75%	0	0.00%	3	11.11%
	Femora	19	9.55%	0	0.00%	16	26.67%

5.5.6. POSSIBLE TAPHONOMIC AGENTS

Tuquoy was an even more extreme case than observed on Birsay Bay, with the majority of contexts providing too few skeletal remains to be identified by an algorithm as anything but scattering (Table 5.17). Among 206 contexts about 77% (158) were identified as such in the case of *Abundances*, and about 81% (167) in the case of *Fragmentation Percentages*, resulting in 139 contexts having confirmed classification and further 46 having one identification as scattering. As a result, only 20 contexts were identified as any predatory group, with only two examples of owl classification. The adjusted classifiers returned significantly less conclusive scattering (80, about 39% of all contexts), but were still prevalent in separate cases, resulting in a further 93 inconclusive results (45%).

The predominance of scattering identification among contexts heavily affected joint classification for specific phases. The whole site showed *Abundances* predominantly reflecting scattering, though with adjustment and *Fragmentation Percentages* also showing diurnal/mammal identification. Not surprisingly, the least explored Phase 1 provided scattering regardless of the approach used, but all but one phase have also shown scattering in the case of *Abundances*. The only case without scattering as identification was Phase 3, which showed mostly diurnal/mammal identification, with fragmentation also showing similarities with owl deposition. It is quite surprising considering the dominating contexts (Contexts 28 and 33) provided predominantly diurnal/mammal classification apart from adjusted *Abundances*. Diagnostic contexts from Phases 4 to 7 have shown scattering either in *Abundances* (Contexts 107 and 1015) or *Fragmentation Percentages* (Context 1112) or both (Context 181).

Analysis of correlations was a complex task due to a number of samples/contexts retrieved from Tuquoy. In about half (*Abundances*) up to 75% (*Fragmentation Percentages*), no correlations, or only weak negative ones, were obtained, mostly from contexts already classified as scatterings, suggesting no resemblance to recognisable assemblage arrangements. For *Abundances*, predominant correlations were with hen harriers (83, 40% of all contexts), also visible for overall results (unadjusted: $df = 11$, $r = 0.89$, $p = <0.001$). For fragmentation, most common was lack of any correlation due to no data retrieved (60, 29% of all contexts), but red fox identification was also quite common, including overall results (unadjusted: $df = 11$, $r = 0.96$, $p = <0.001$). Interestingly, correlations with adjusted signatures did provide differences only in twelve cases. In the case of overall data, phases and specific context correlations provided more concise answers. It showed almost exclusively diurnal birds, hen harriers and

kestrels, with red foxes in the case of fragmentation correlations. Most differing was the last two phases, showing short-eared owls as most similar assemblages in the case of *Abundances*. Individual contexts within this phase also showed similar patterns (Contexts 1015 and 1112) despite wide differences in skeletal completeness. Interestingly, major accumulation (Context 33) showed essentially the same results as its parent Phase 3, despite other contexts with different results, such as Context 28, also contributing to it.

Table 5.17 – Highest correlations (upper table) and classification outcomes (lower table) for *Abundances* and *Fragmentation Percentages*, based either on original references/signature data (Normal) or ones simulating partial dispersal/burial (Adjusted). The upper section of each table includes area overall and site stratigraphy while the lower section includes major contexts.

Trench, Phase or Context	Highest Corr. Abundances				Highest Corr. Fragmentation			
	Normal		Adjusted		Normal		Adjusted	
Overall	0.89	Hen H.	0.88	Hen H.	0.96	Red Fox	0.99	Kestrel
Phase 1	0.50	Kestrel	0.76	Kestrel	0.61	Hen H.	0.59	Hen H.
Phase 2	0.85	Hen H.	0.88	Hen H.	0.96	Red Fox	0.96	Red Fox
Phase 3	0.80	Hen H.	0.77	Hen H.	0.98	Red Fox	0.98	Kestrel
Phase 4	0.93	Hen H.	0.94	Hen H.	0.95	Hen H.	0.96	Hen H.
Phase 5	0.78	Kestrel	0.81	Red Fox	0.97	Red Fox	0.99	Kestrel
Phase 6	0.69	Kestrel	0.57	Owl(Sh)	0.93	Red Fox	0.97	Kestrel
Phase 7	0.79	Owl(Sh)	0.65	Owl(Sh)	0.93	Hen H.	0.92	Hen H.
28 (P3)	0.65	Hen H.	0.59	Hen H.	0.88	Hen H.	0.91	Hen H.
33 (P3)	0.74	Hen H.	0.75	Hen H.	0.98	Red Fox	0.98	Red Fox
107 (P4)	0.37	Red Fox	0.51	Red Fox	0.74	Kestrel	0.74	Kestrel
181 (P4)	0.68	Hen H.	0.88	Hen H.	1.00	Scatt.	1.00	Scatt.
1112 (P6)	0.60	Hen H.	0.50	Owl(Bn)	0.59	Kestrel	0.56	Kestrel
1015 (P7)	0.72	Owl(Sh)	0.54	Owl(Sh)	0.95	Hen H.	0.92	Hen H.

Trench, Phase or Context	Abundances Classification		Fragmentation Classification		Final Result	
	Normal	Adjusted	Normal	Adjusted	Normal	Adjusted
Overall	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.
Phase 1	Scattering	Scattering	Scattering	Scattering	Scattering	Scattering
Phase 2	Scattering	Owl	Owl	Diurn./Mamm.	Contested	Accumulation
Phase 3	Diurn./Mamm.	Diurn./Mamm.	Owl	Diurn./Mamm.	Accumulation	Diurn./Mamm.
Phase 4	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.
Phase 5	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.
Phase 6	Scattering	Owl	Diurn./Mamm.	Diurn./Mamm.	Contested	Accumulation
Phase 7	Scattering	Scattering	Diurn./Mamm.	Diurn./Mamm.	Contested	Contested
28 (P3)	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
33 (P3)	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.
107 (P4)	Scattering	Owl	Diurn./Mamm.	Diurn./Mamm.	Contested	Accumulation
181 (P4)	Scattering	Diurn./Mamm.	Scattering	Scattering	Scattering	Contested
1112 (P6)	Owl	Diurn./Mamm.	Scattering	Scattering	Contested	Contested
1015 (P7)	Scattering	Scattering	Diurn./Mamm.	Diurn./Mamm.	Contested	Contested

5.6. SCAR

5.6.1. ASSEMBLAGES QUANTIFICATION AND DISTRIBUTION

In total, 60 micromammal samples were retrieved from Scar (Table 5.18). Among them 57 came from 24 different contexts, representing all main phases of the site. Three samples came from unstratified, most likely recent, layers. All samples provided in total 1079 NISP, in the case of samples analysed separately resulting in 118 MNI but in the case of whole contexts only 85 MNI. Four species were identified, including mostly Orkney vole (MNI 56) but also field mice (MNI 12) and house mice (MNI 7) as well as rats (MNI 6). Rat remains were identified, both visually as well as through ZooMS, as belonging exclusively to brown rats, thus being considered as intrusive to Scar archaeological contexts. The lack of pygmy shrews possibly reflects lack of such species on Sanday, at least not in numbers providing confirmation of the population existence.

The distribution of the material shows that sampling efforts concentrated mainly on contexts related directly to the burial (Fig.5.47 A & B). Natural (postglacial) contexts predating human activity were only seldom sampled, with only two hand-retrieved samples from the same context containing micromammal remains. Jointly they provided moderate quantities of NISP as well as average completeness ratios. On the other hand, unstratified contexts, most likely from modern times, provided even less NISP in two hand-retrieved and one sieved samples and exhibited low skeletal completeness. In the case of more intensively sampled periods, 18 samples were retrieved from three contexts directly predating the boat burial. Despite providing more bone fragments, two out of three contexts exhibited very low completeness ratios, with only one context (Context 49) skeletal completeness similar to the natural layer (24% Skeletal Completeness as well as Average Abundances). The later two main stratigraphic elements, the boat infills and later contexts covering them, were sampled in a similar manner but contained more contexts that provided micromammal remains. Completeness ratios were at best around 20% and often below 10%. The only exception was Context 47, estimated on the base of three samples, which had 27% Skeletal Completeness and 30% Average Abundances.

The species distribution seemed to be similar in the case of periods related to the boat burial but individual contexts showed different taxonomic compositions, possibly reflecting intrusive burrowing (Fig.5.47 A). Natural contexts, as well as unstratified modern ones, showed the

presence of only Orkney voles, while pre and post burial segments of stratigraphy showed the presence of predominantly voles, followed by both murid species and brown rats. The only difference was that house mouse bones were found mostly within contexts directly predating burial, with only a couple of bones retrieved from the infill and later contexts. Individually, only two contexts showed the presence of all species, including five predating burial and 12 atop the burial. Most common were contexts containing voles and field mice, with rats and house mice being found in only four contexts each. Interestingly, the majority of rat and house mouse bones were found each within two contexts disturbed most likely by intrusive burrowing of a rabbit. Rabbit bones were found in 11 samples coming from five contexts, two predating the burial (sandy, possibly windblown Contexts 5 and 7), one being stone packing outside of the boat (Context 55) and two being later layers covering the burial (Context 1, modern ground, and Context 20, windblown sand). Additionally, a cat mandible of about 4 to 5 months-old specimen was found within the boat uppermost infill (Context 33), suggesting cat nesting (Fig. 5.48). Considering the evidence, it is likely, that burrowing was especially severe in rubble-like deposits, such as Contexts 55 (already mentioned) or 36 (stones filled inside eastern end of the boat). It is also possible, that vole and field mice remains found more often than other species, could be a relatively contemporary fauna. However, considering previous research, the bone assemblage could have contained more remains of these animals in samples that did not provide micromammal material and were not studied by the author.

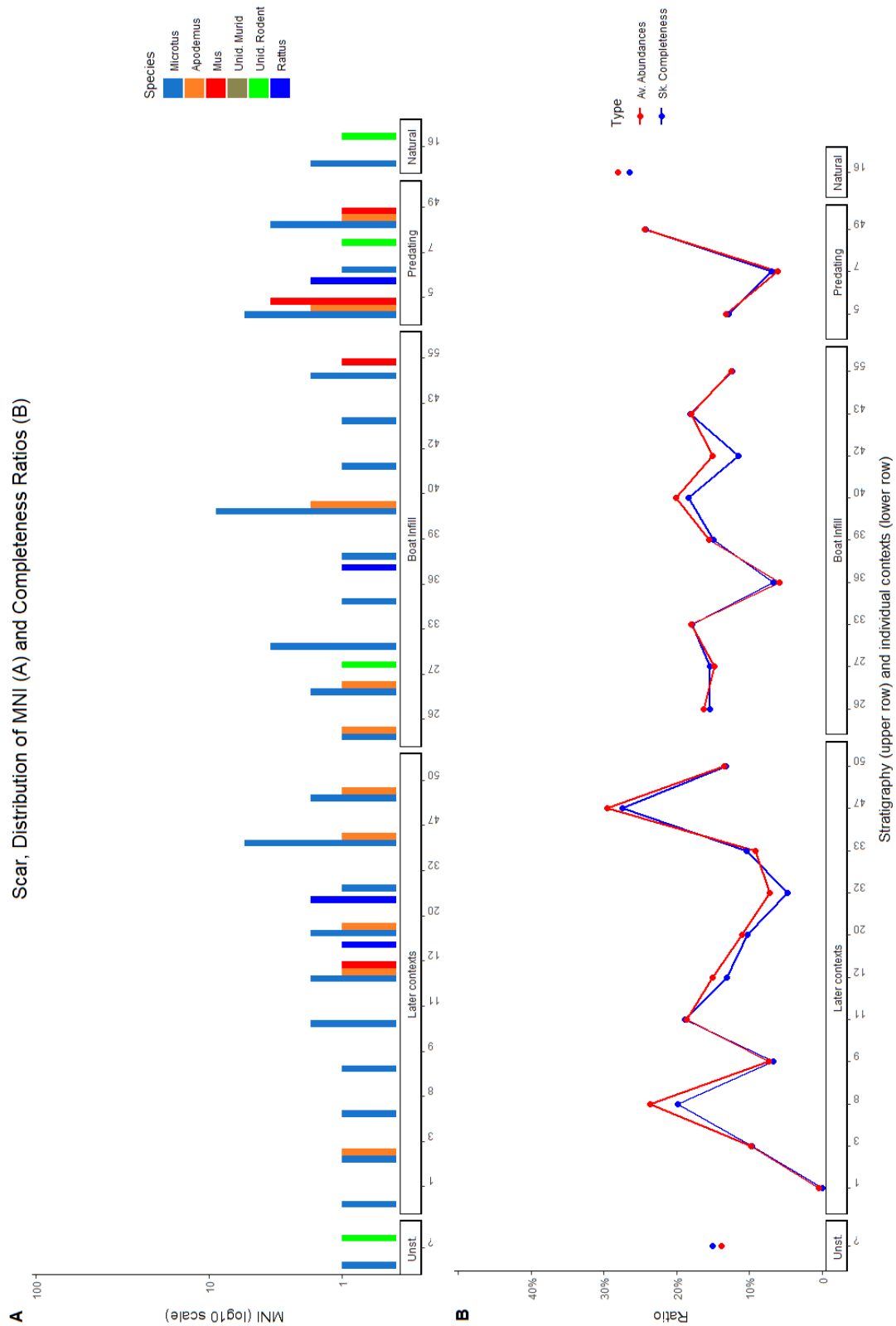


Fig. 5.47 - A (upper plot): Distribution of MNI within the site, arranged alongside known stratigraphy.

B (lower plot): values of completeness ratios (Skeletal Completeness, Average Abundances) for each context in Scar, arranged in the same way as in plot A.



Fig. 5.48 – Scar, a juvenile cat mandible from Context 33, scale in 5mm intervals. Deciduous premolars are present, but permanent canine and first molar are already formed within the bone and visible from the outside (for comparison see Hillson 2005, 59 Fig. 1.36).

Table 5.18 - NISP and MNI counts for Scar stratigraphy, separately for all (upper) and specific (lower) species.

Location	Weight	Contexts	Samples	ΣNISP	ΣMNI
Natural context	0.99	1	2	71	3
Predating Burial	6.62	3	18	252	22
Boat Infill	8.3	9	20	358	29
Later contexts	7.94	11	17	383	30
Unstratified	0.31	---	3	15	2
Σ	24.16	24	60	1079	86

Location	Microtus		Apodemus		Mus		Unid. Rodent		Unid. Mouse		Rattus	
	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI	NISP	MNI
Natural context	26	2	0	0	0	0	45	1	0	0	0	0
Predating Burial	91	11	12	3	8	5	128	1	2	0	11	2
Boat Infill	169	22	10	4	2	1	172	1	3	0	2	1
Later contexts	138	20	7	5	2	1	230	0	0	0	6	3
Unstratified	6	1	0	0	0	0	9	1	0	0	0	0
Σ	430	56	29	12	12	7	584	4	5	0	19	6

5.6.2. AGE DATA DISTRIBUTION

Judging from the epiphyseal fusion, all age classes were present in Scar in a pattern already noticed on the other sites (Fig. 5.49). However, NISP retrieved was low in comparison to other sites, resulting in each individual case having a potential to significantly shift obtained patterns. Generally, enough early fusing epiphyses were found to suggest the presence of juvenile remains in boat infill and later contexts though no assessable finds were retrieved from pre-burial contexts. Overall, about 10% of scorable early fusing epiphyses were found unfused, with burial and later contexts providing higher results (13% and 15% relative frequencies respectively). Middle fusing epiphyses provided almost three times higher percentage of unfused cases (29%), though the number of scorable epiphyses was slightly lower than in the case of early fusing ones. A couple of such finds were retrieved from contexts predating burial, but as in the previous case, the infill and later contexts provided the same (infill: 28%) or better relative frequencies (later: 30%). In contrast, late fusing epiphyses were rarely found fused, being either proximal ulnae or distal femora, suggesting only a minuscule amount of fully adult individuals and prevailing amounts of sub-adults. Additionally, considering the distribution in each phase, pre-burial contexts seemed to contain less fully adult bones (10% relative frequency) than the other two main phases.

However, epiphyseal scoring seemed to show an older population than some singular finds would suggest. While finds from Context 27s (infill) and 40 (shell sand, lowest boat infill) containing juvenile material were included in epiphyseal data unique finds in one sample (Find no. 74 from pre-burial Context 5) contained two vole juvenile mandibles with the third molar present but not yet erupted, accompanied with molars without cementum yet developed. This could suggest at some point Orkney vole burrowing/nesting within at least a couple of Scar contexts. Similarly, rat finds could also point towards this species nesting within discussed features, as find no. 63 from the later deposit (Context 20) contained juvenile rat mandible.

Molar wear estimation for murids could also point towards a young population but MNI was too small to be certain (Fig. 5.50). Six out of seven house mouse individuals and nine out of 12 field mice had assessable molar finds, resulting in scores within the range of 1 to 3. No presence of high attrition was found (categories 4 & 5), suggesting no presence of overwintered specimens, but also no unworn specimens were found. The house mice provided a more natural age distribution, predominance of category 1 with a gradual decline to category 3. In contrast,

Apodemus specimens were almost exclusively young, circa 1-2 months old (category 1), with only singular MNI in categorized to 2 and 3 respectively.

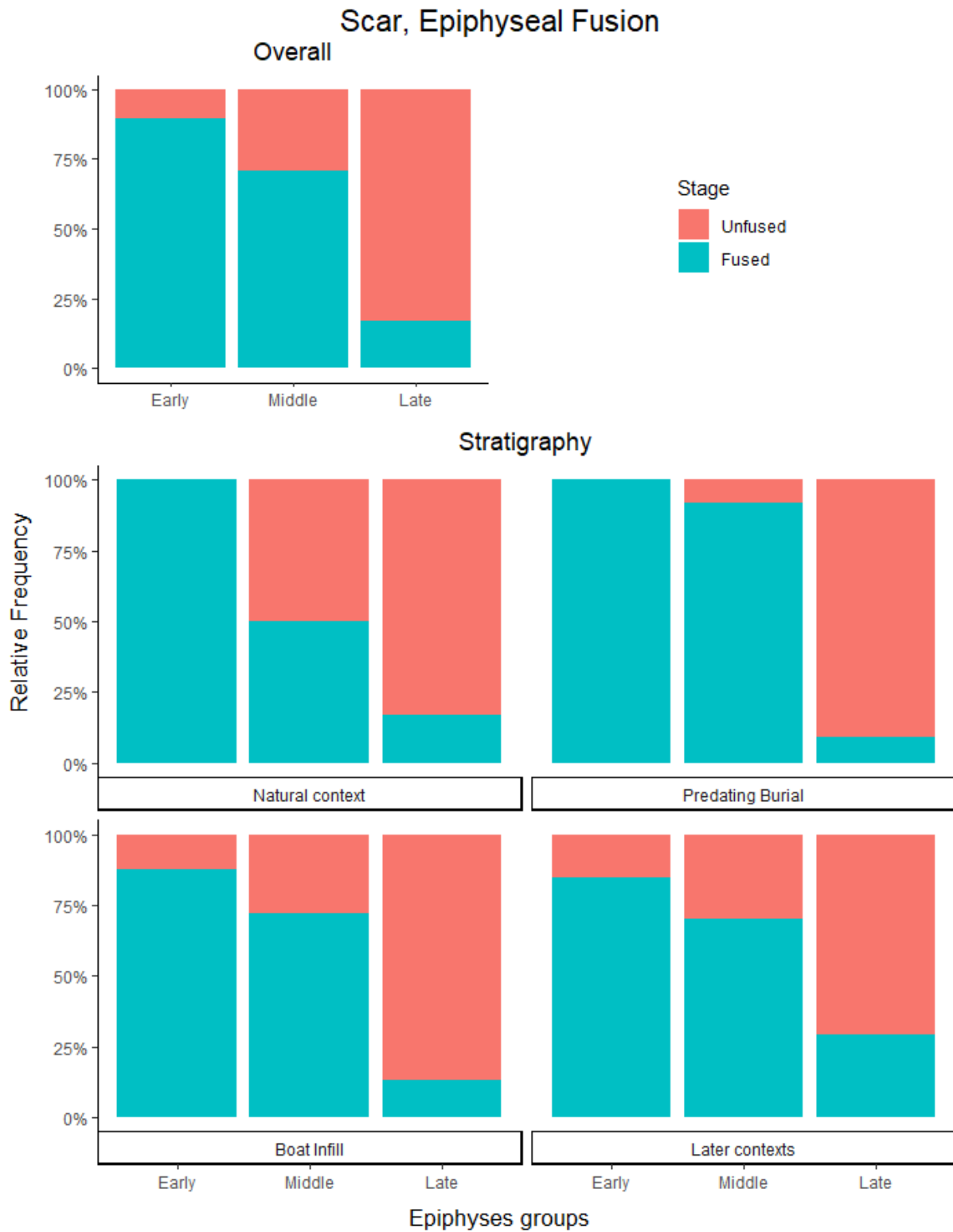


Fig. 5.49 – Scar, epiphyseal fusion expressed as a relative frequency of NISP (red-unfused, blue-fused) and grouped in three main groups related to individual's age (early/middle/late). The upper plot showcases the overall situation for Scar, with stratigraphy plotted below.

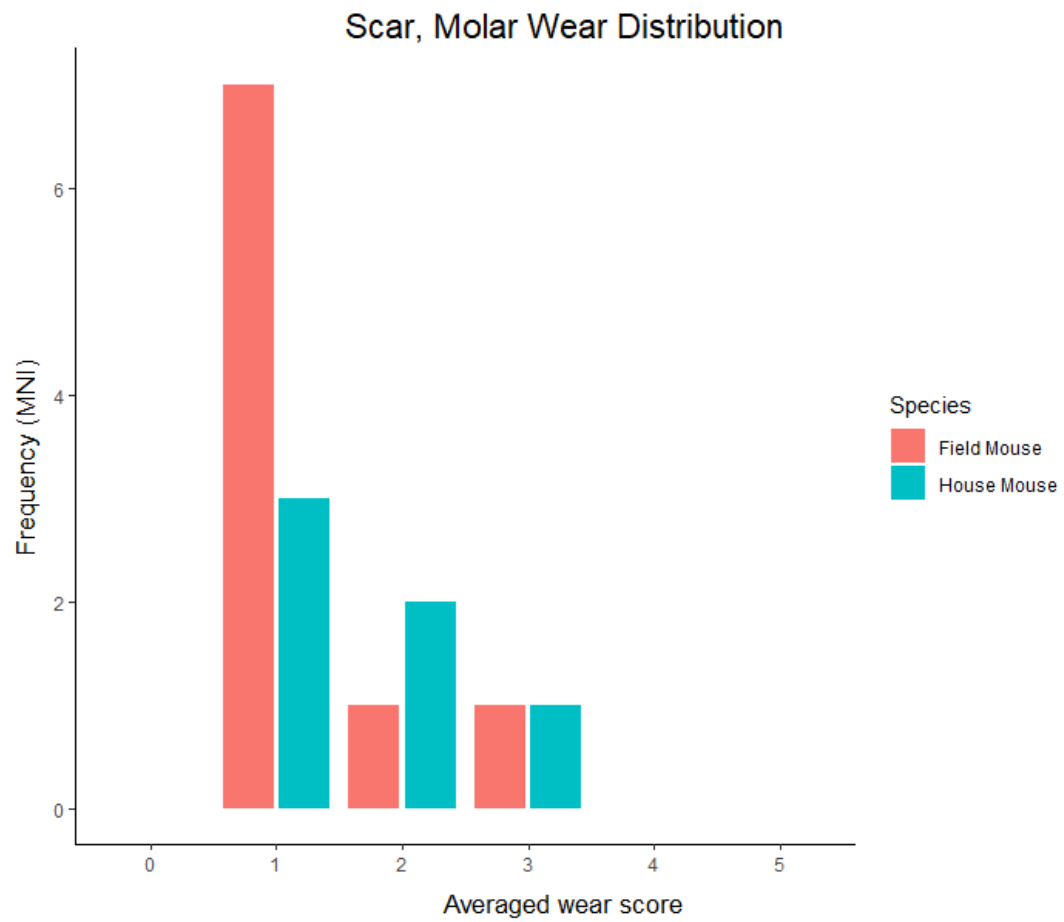


Fig. 5.50 – Scar, frequency distribution of *Apodemus* and *Mus* MNI depending on molar wear scores.

5.6.3. FREQUENCIES, ABUNDANCES AND INDICES

The site overall *Skeletal Frequencies* represented best contexts that are either natural or following burial, rather than burial itself or directly predating it (Fig. 5.51). Similarly to Tuquoy frequencies, vertebrae were most common among elements calculated in frequencies (35%), followed by skull fragments (24%), hindlimb bones (22%) and forelimb elements (19%). However, each of the main periods established in the site stratigraphy differed to some degree from the general values. Natural contexts did not provide much NISP but showed relatively similar frequencies, with vertebrae being most commonplace (45%), but showed higher variation between fore and hind limb bones. In contrast, contexts predating burial showed skull elements providing the highest relative frequencies, mostly due to a single Context 5. Boat infill itself showed similar frequencies to the whole site but with forelimb elements more represented than hindlimb ones. However, the largest Context 40, showed frequencies approaching an even distribution, showing boat infill contexts strongly differing from combined data. Finally, later context frequencies showed similarities in all but skull frequencies, on a par with forelimbs. But, once again, the largest context did not represent the period in overall, with context 47 showing an outline more similar to the boat infill.

Core phases of the site exhibited very similar *Abundances* while extreme ones deviated strongly from each other and the core itself (Fig. 5.52). In general, the majority of relative abundances showed low percentages. Mandibles, despite being the most common finds and present in all core phases in almost the same proportions, produced a relative abundances of only 42%. The only other element that provided relative abundances above 40% in other phases were maxillae, though only in a phase directly predating burial as well as in boat infill – later contexts provided lower results. Loose molar relative abundances were almost the same, about 20%, but loose incisors ranged between just below 20% up to 30%. Scapulae and pelvis differed only slightly, both around or above 10%. Lower limb bones produced almost uniform abundances, in a range between 20 to 30%, but upper limb bones, apart from radii, showed relatively high variation (10-30%). Smaller bones were represented mainly by vertebrae (below 10%) and distal limb main tarsals, with a small addition of metapodials, phalanges and ribs. Within small bones biggest differences were within calcanei, ranging from 5 to 20%. In contrast to the main phases, natural postglacial contexts showed higher relative abundances, up to above 60% for mandibles and tibiae. Humeri and calcanei were also quite common, around 50%. Other *Abundances* were generally higher or on a par with overall values for Scar but no ulnae nor scapulae were found.

Unstratified finds also deviated heavily from other phases, though in this case it could be due to a very low NISP pool. Skull and teeth relative abundances were very low, and no small bones were found apart from a single vertebra. Other bones, such as scapulae and radii, were also missing. Ulnae and distal limb bones showed relatively high relative abundances of 50% but humeri were below 30%.

The most diagnostic contexts showed larger differences than those observed over longer time frames. Context 5, unique due to providing the largest MNI among all contexts (14), exhibited average to high relative abundances in the case of skull bones, especially maxillae (~70%), but the rest of elements showed low to very low values. Apart from loose incisors, which had a relative abundance beyond 20%, and distal limb bones, slightly below this threshold, the rest showed at best 10%, with calcanei, ribs and phalanges missing. In contrast, Context 40, which contained the highest NISP count, showed abundances similar to ones generally exhibited by burial infill. Maxillae, incisors, scapulae, pelves, most of the long limb bones and all small bones were roughly the same but mandibles, molars and tibiae were about 20% higher. Context 47, most skeletally complete context found, also to a restricted degree followed later contexts relative abundances but showed higher values on a number of occasions, especially up to 70% for ulnae.

Apart from molars, *Indices* provided data within the range firstly seen in Skara Brae (Fig. 5.53). Isolated incisors showed a range up to over 350% but the majority of phases and diagnostic contexts were within the range of 150%-250%. All but two contexts in the case of isolated molars showed a range up to 140%, with an overall value slightly below 100% but with Context 5 exhibiting a lower count, below 50. Postcranial to Cranial indices were relatively low, in both complex and simplified form showing values mostly below 100%. In contrast, unstratified material showed value beyond 300%. In the case of distal to proximal limb bones, indices values were the highest for the natural (postglacial) context as well as diagnostic Contexts 5 and 40, all oscillating around 100%. In contrast, boat infill, altered contexts and unstratified material showed values of 60% and less.

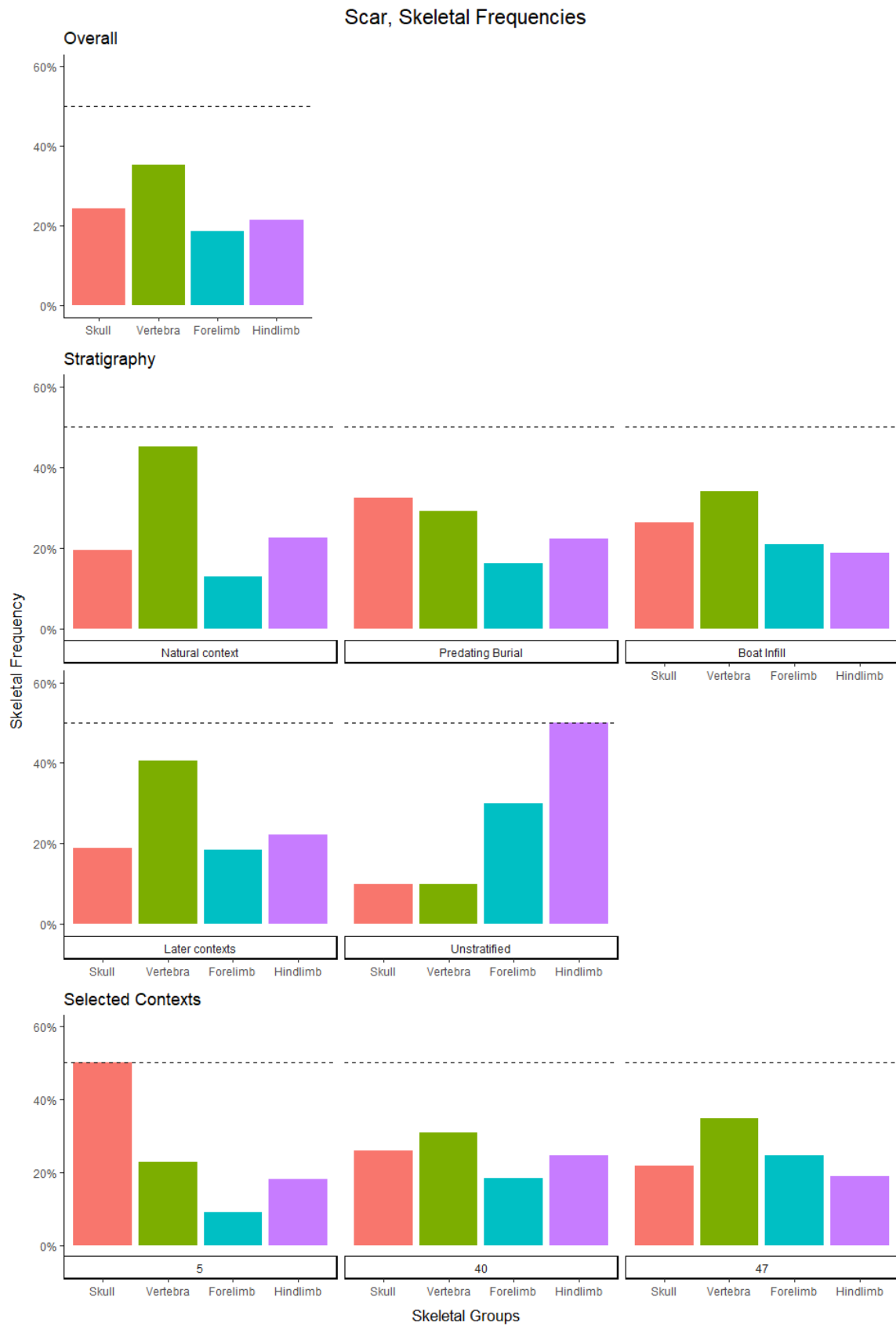


Fig. 5.51 – Scar, *Skeletal Frequencies*, plotted for overall data (upper plot), stratigraphy (middle plots) and selected contexts (lower plots).

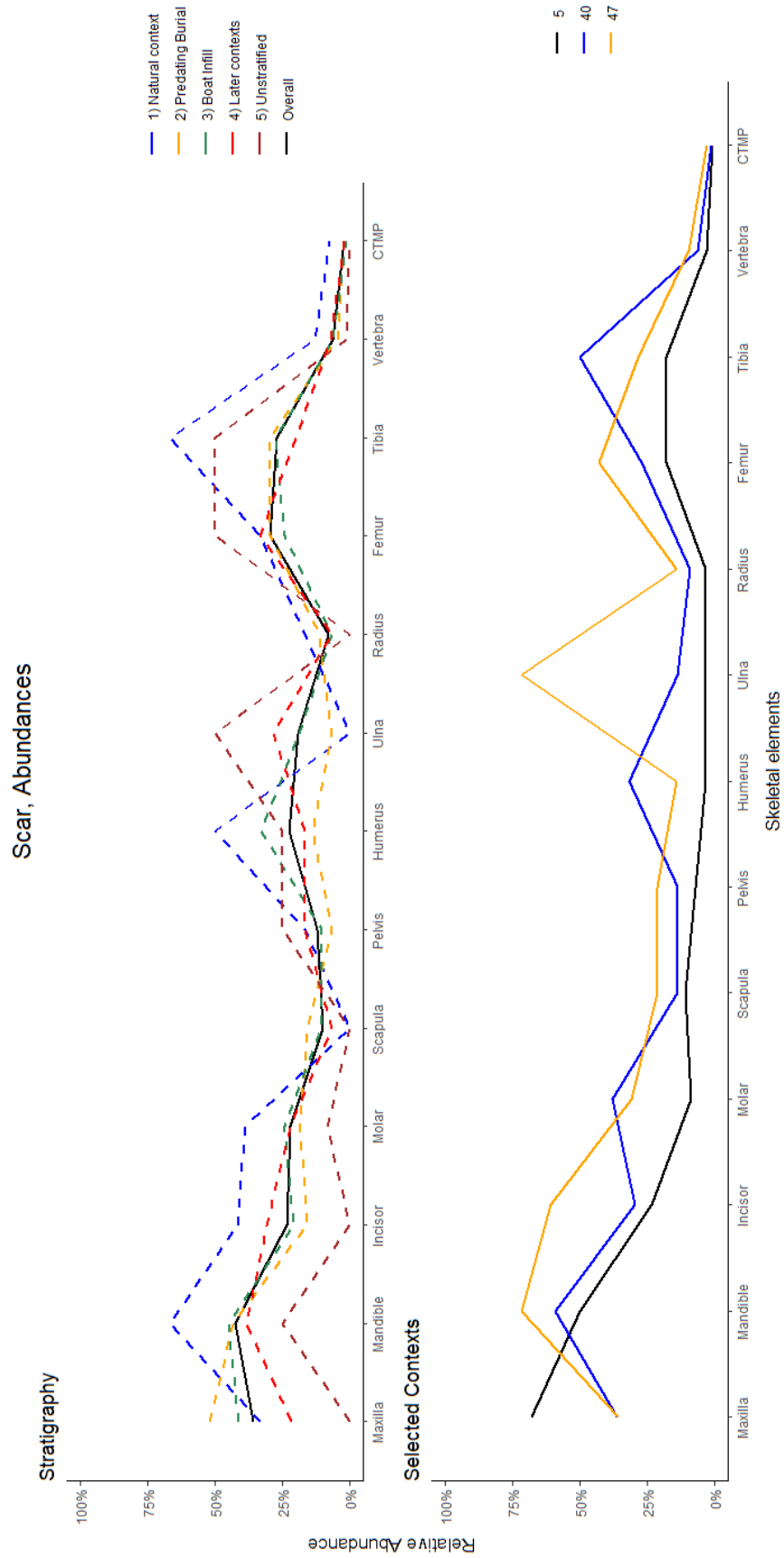


Fig. 5.52 – Scar, *Abundances* of skeletal elements, plotted for site stratigraphy (upper) and specific contexts (lower).

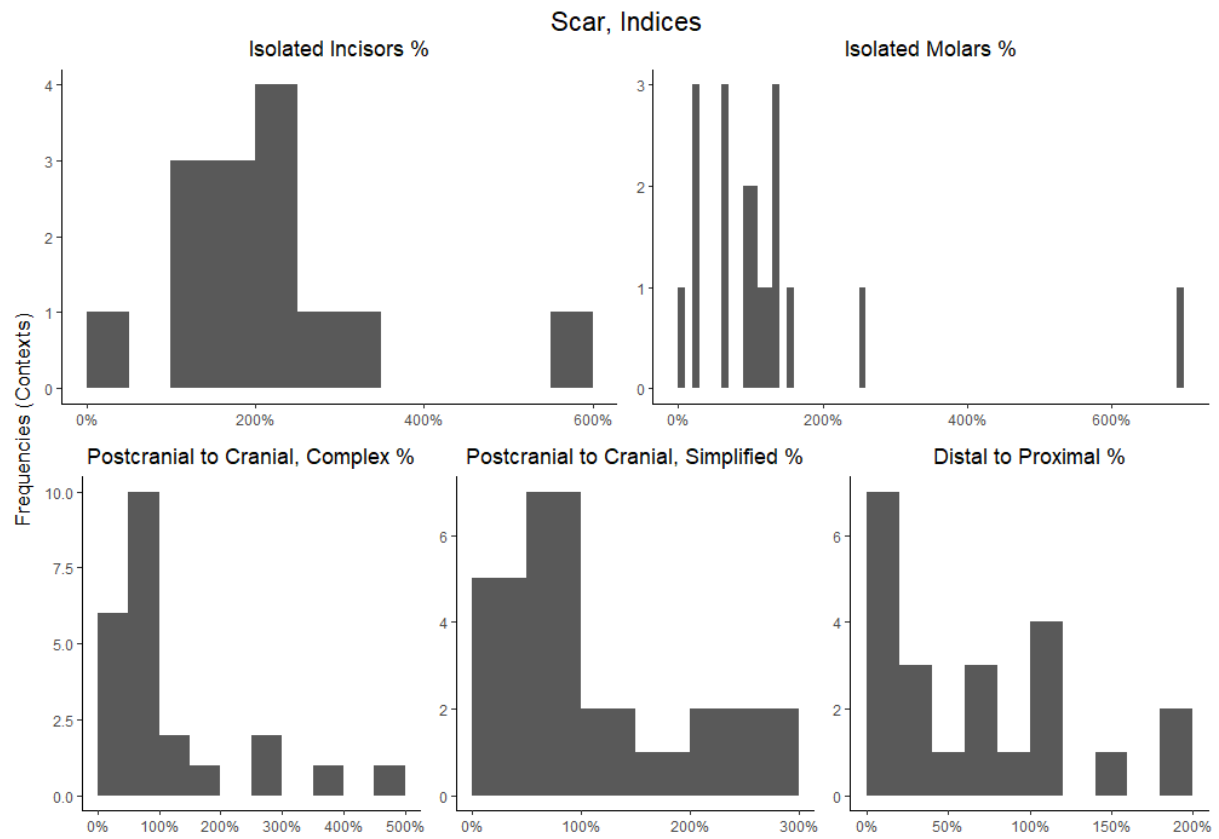


Fig. 5.53 – Scar, frequency distribution of index results for the site *Indices*.

5.6.4. FRAGMENTATION, DIGESTION AND BURNING

Fragmentation differed between major phases as well as between diagnostic contexts (Fig. 5.54). Skull breakage contained more isolated maxillae and small cranial fragments than more intact finds, but in terms of percentages more preserved skulls were retrieved than on the other sites. Especially in the case of contexts predating the burial, one could notice quite high percentages of relatively well-preserved skulls, with infills providing fewer such finds and later contexts containing mostly fragmented remains. Similarly, Context 5 had predominantly preserved viscerocrania and maxillae with zygomas, with other cranial remains being a minority of NISP. Contexts 40 and 47, on the other hand, did not contain viscerocrania and had more heavily fragmented remains. Mandibular breakage was generally similar to that seen in Skara Brae. Intact finds were only retrieved from infills, with other contexts providing ones at with at least broken ramus. However, earlier contexts showed in overall less fragmented remains, which was also reflected in Context 5. In stark contrast, Contexts 40 and 47 showed more heavily altered mandibles. In the case of long limb bones fragmentation, intact finds showed a wide range, from as high as 50% for humeri retrieved from Context 47 down to no such finds for tibiae from the same context. Similar to cranial fragmentation, contexts predating burial provided more intact remains, especially in the case of humeri and ulnae where intact finds were above 50%. The only difference was femoral fragmentation, where boat infills showed beyond 50% of intact NISP. Context 5 provided only intact bones for forelimbs, with hindlimbs being more fragmented but not to a significant degree. Besides tibiae, Context 40 had lower percentages of intact finds than Context 47, inverting the relationship between infills and later contexts.

No signs of burning were found but possible digestion was identified on three incisors and 12 molars, spread thinly within nine contexts from preburial to postburial contexts (Table 5.19). Only vole teeth were affected and apart from two molars, all exhibited only a light form of digestion. Moderate forms of digestion were found isolated in small contexts within boat infill and later stratigraphic layers. Some correlation between assemblage size and finds were noted, but in overall digestion percentages were around 2-5%. However, more evidence for abrasion/weathering and root etching was found.

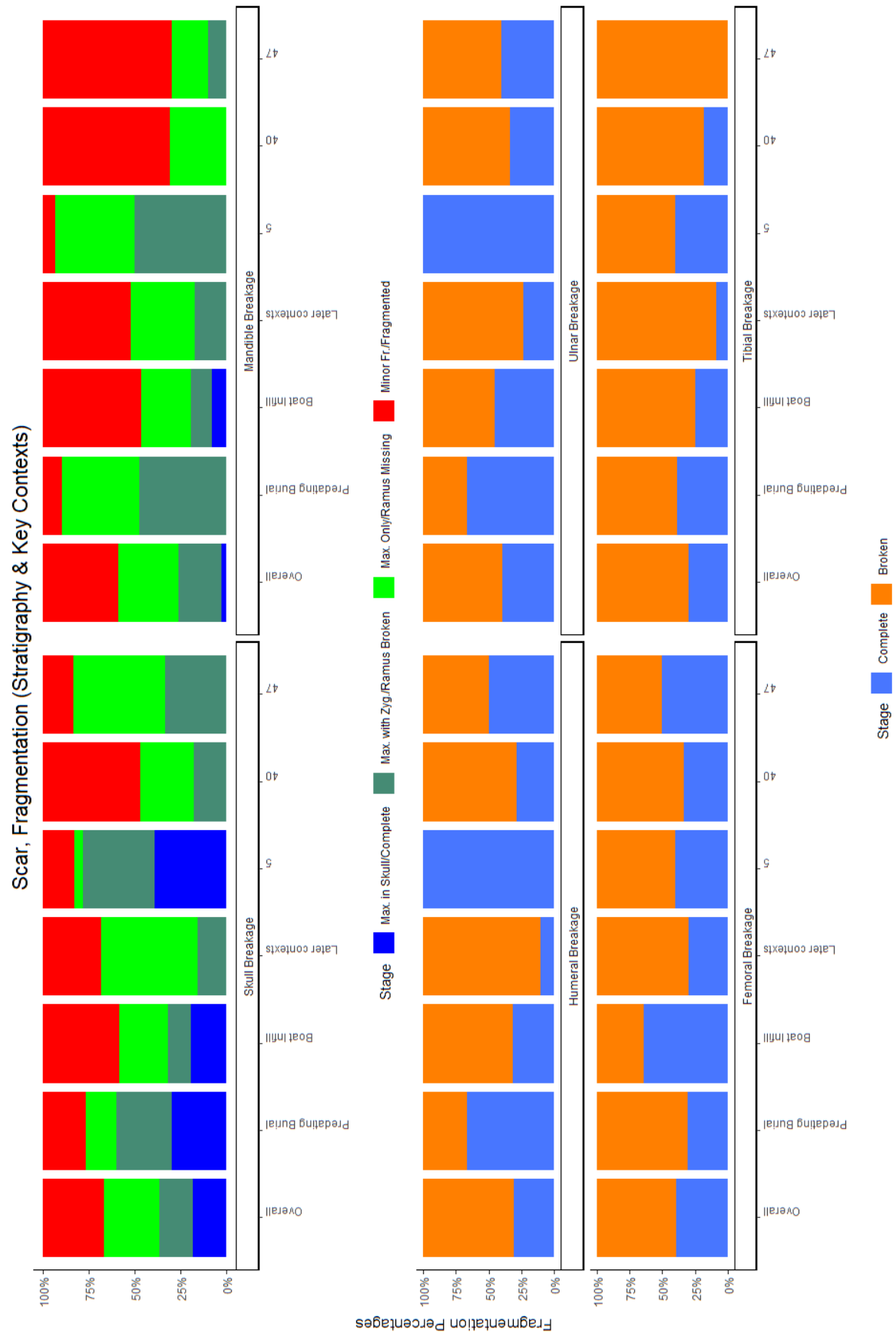


Fig. 5.54 – Scar, skull (upper row) and postcranial (two lower rows) breakage for overall site data, stratigraphy and representative contexts.

Table 5.19 – Percentage of digested specimens of each category for all the site as well as specific phases.
For teeth both loose and intact finds were considered.

Period	Percent of digested elements		
	Incisors	Molars	Epiphyses
Natural context	0.00%	0.00%	0.00%
Predating Burial	0.00%	2.00%	0.00%
Boat Infill	2.27%	4.29%	0.00%
Later contexts	4.00%	3.45%	0.00%
Unstratified	0.00%	0.00%	0.00%
Whole Site	2.11%	3.19%	0.00%

5.6.5. POSSIBLE TAPHONOMIC AGENTS

In most cases, the classification provided similar answers for main phases and both approaches utilized (Table 5.20), but the issue encountered in Birsay and Tuquoy was also present in Scar. The majority out of 26 studied contexts were either fully (9) or partially (6) identified as a scattering, with adjusted classification showing an even more extreme situation (2 and 15 respectively). Contexts identified as such were mostly estimated from just one or two samples. Larger contexts were usually identified as diurnal/mammal or as between this group and owls. It is reflected in stratigraphy, resulting in the whole site being identified as diurnal/mammal, with major contexts (e.g. Contexts 40 and 47) and most parent phases also showing this classification. However, a tendency was also noted towards adjusted data showing definite owl classification. It was also seen in the case of the overall site result as well as natural, predating burial and boat infill contexts. Individual contexts did not provide a definite owl identification, but in two cases (Contexts 16 and 47) adjusted methods hinted towards such classification. Not surprisingly, unstratified data provided easy to identify scattering pattern, with later contexts, including modern ones, showing scattering in case *Abundances*.

Correlations were often weak and did not provide answers as concise as classification, although results were similar as on the other sites. Over 10 out of 25 contexts showed weak correlations, often in cases where classification showed scattering. *Fragmentation Percentages* provided a minor dominance of kestrel signature in best correlations while *Abundances* showed more varied results, including hen harrier and peregrine. Interestingly, *Abundance* correlations in the case of adjusted methods returned better correlations with owls, especially short and long-eared owls. In turn, fragmentation correlation for adjusted methods showed mostly the same species and similar strength.

Table 5.20 – Highest correlations (upper table) and classification outcomes (lower table) for *Abundances* and *Fragmentation Percentages*, based either on original references/signature data (Normal) or ones simulating partial dispersal/burial (Adjusted). The upper section of each table includes area overall and site stratigraphy while the lower section includes major contexts.

Trench, Phase or Context	Highest Corr. Abundances				Highest Corr. Fragmentation			
	Normal		Adjusted		Normal		Adjusted	
Overall	0.90	Kestrel	0.83	Owl(Sh)	0.92	Kestrel	0.91	Kestrel
Natural context	0.71	Kestrel	0.81	Owl(Sh)	0.59	Hen H.	0.54	Hen H.
Predating Burial	0.77	Hen H.	0.71	Owl(Lg)	0.75	Kestrel	0.62	Scatt.
Boat Infill	0.89	Kestrel	0.81	Owl(Sh)	0.73	Hen H.	0.70	Hen H.
Later contexts	0.80	Kestrel	0.75	Kestrel	0.96	Red Fox	0.96	Red Fox
Unstratified	0.78	Peregrine	0.52	Owl(Lg)	0.56	Hen H.	0.50	Scatt.
5	0.86	Hen H.	0.66	Hen H.	0.64	Scatt.	0.68	Owl(Sh)
40	0.79	Kestrel	0.87	Owl(Sh)	0.93	Kestrel	0.94	Kestrel
47	0.87	Scatt.	0.87	Scatt.	0.79	Kestrel	0.77	Kestrel

Trench, Phase or Context	Abundances Classification		Fragmentation Classification		Final Result	
	Normal	Adjusted	Normal	Adjusted	Normal	Adjusted
Overall	Diurn./Mamm.	Owl	Diurn./Mamm.	Owl	Diurn./Mamm.	Owl
Natural context	Diurn./Mamm.	Owl	Diurn./Mamm.	Owl	Diurn./Mamm.	Owl
Predating Burial	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
Boat Infill	Diurn./Mamm.	Owl	Owl	Owl	Accumulation	Owl
Later contexts	Scattering	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Contested	Diurn./Mamm.
Unstratified	Scattering	Scattering	Scattering	Diurn./Mamm.	Scattering	Contested
5	Diurn./Mamm.	Diurn./Mamm.	Owl	Scattering	Accumulation	Contested
40	Diurn./Mamm.	Owl	Diurn./Mamm.	Diurn./Mamm.	Diurn./Mamm.	Accumulation
47	Diurn./Mamm.	Owl	Diurn./Mamm.	Owl	Diurn./Mamm.	Owl

6. DISCUSSION

6.1. METHODOLOGY

6.1.1. RELATIONSHIPS BETWEEN MICROMAMMAL DATA

The obtained site data strongly points towards the use of non-parametric tests for exploring data relationships (**Chapter 4.1.**). This is not surprising considering the nature of much archaeological data, which often do not pass one or more criteria for parametric tests (see Gifford-Gonzalez 2018, 389). Firstly, the data rarely show normal distribution, being a predominantly more or less left-skewed form of Poisson distribution (Gifford-Gonzalez 2018, 387 Fig. 18.2). Secondly, NISP and related MNI, due to multiple problems associated with them, have for some time been considered by researchers as functionally ordinal scale despite interval scale appearance and might exhibit interdependence between skeletal parts (see discussion in Grayson 1984, 17-92 & 93-115; Lyman 2008, 22-82, Gifford-Gonzalez 2018, 396-409). Two necessary points to use parametric tests, apart from having or being able to obtain normal distribution, is to use interval or ratio scale data as well as being certain that studied observations are independent (Gifford-Gonzalez 2018, 389). In the observed micromammal data, extreme right-skewing was indeed noted, especially in the case of primary data, with secondary data showing also bimodal to near-uniform distribution (**Chapter 4.1.**, Fig. 4.01-2). Normalising data was hardly possible, both for the archaeological sites as well as references depositional data. In addition, most data were either correlated with (e.g. weight, similarly bigger species: Lyman 2008, table 3.10) or derived from NISP and/or MNI, resulting in likely inheritance of NISP/MNI biases by secondary data as well as the presence of the same biases in primary data. Apart from very specific taphonomic changes (e.g. digestion), much of the data could be considered as interdependent, even if minimally. Considering how many points necessary for the usage of parametric tests have been violated, it is safe to assume that possible data transformation will not resolve all of them, rendering any data transformation method inconsequential.

From the perspective of methods utilization, application of non-parametric tests proved to be more effective to explore data, although from the perspective of pattern-seeking, parametric methods may be sometimes used when proven more effective (**Chapter 4.1-3.**). For ordinal

scale and non-normal distribution, Gifford-Gonzalez (2018, 390) suggested using a specific range of tests, including χ^2 , Fisher, Wilcoxon, Kendall, Spearman, Kolmogorov-Smirnov. Among those Spearman rank-sum correlation was proven to work when comparing individual variables, partially due to the monotonic nature of obtained data, and provided correlation on average better than the Pearson method, reliant on strict linearity to properly work. Similarly, classification methods explored in the case of machine learning showed LDA, a method also reliant on linearity, could not achieve the accuracy of other methods, either adapted to or developed to work with strongly skewed data (**Chapter 4.4.**, Fig. 4.08-10 & Table 4.08). However, the violation of normal distribution of data can be sometimes ignored when specific conditions arise, e.g. when a very large sample has a distribution relatively similar to normal (Withlock & Schluter 2015, 375-376), or when in the wider population normal distribution is considered a fact. Sometimes when a specific application is needed the parametric method may be adopted – given a sound reason is found. In the case of exploring correlations of data between archaeological contexts and known species patterns, it was found that Pearson correlation application to *Abundances* and *Fragmentation Percentages* showed a range of values that is easier to explain considering sought species groups, especially in the case of bimodal-like distribution of fragmentation (**Chapter 4.3.**, Fig. 4.06). Spearman correlation did not provide strong negative values as well as showing more overlap between strong correlations between groups. Data analysed by those correlations, even if not normal in distribution on their own, tended not to show too much deviation from normality considering the Shapiro-Wilk test when analysed as a string of data. Considering that, for the sake of pattern-seeking, Pearson might be a better method than Spearman rank correlation. The only exception is correlations application to *Skeletal Frequencies*, although it seems such data are better used in visual rather than statistical analysis.

From the statistical analysis perspective, the relationship between data and differences between sites can be surely explored, but internal relationships between data should be acknowledged first. Using the χ^2 method to establish differences between trenches NISP disposition was already done in Romaniuk et al. 2016a (Table 1) but significance tests like Kruskal-Wallis or Flinger-Killeen also showed similar potential in either establishing or disproving homogeneity between sites (**Chapter 4.1** Tables 4.01-3). It could be argued that significance tests are even better due to the applicability to a whole range of data, including proportions/percentile counts, which may also be better to search in what specific way sites differ from each other. It was especially visible in the case of references data, for which the main groups (owls,

diurnal/mammal predators, scattering) showed a lack of homogeneity in both variations and means.

Still, homogeneity or lack of it may be due to how data are related with other data rather than any external pattern. For example, *Fragmentation Percentages* usually showed the lowest correlation between complete and fragmented values of the same bone. It is self-explanatory considering complete and broken percentages are always a sum of 1 (100%), which results in a decrease of one value when the other goes up. It may be the reason why Pearson correlation showed to be more effective for fragmentation data – more linearity in data relationship resulting in a more linear outcome of the correlation test. In turn, *Abundances* seem to be impacted by fragmentation, resulting in registered values beyond 1 (100%). It is also not surprising considering micromammal *Abundances* calculation used here relies on NISP in order to be comparable with main sources (e.g. Andrews 1990) and NISP count itself can be artificially increased through fragmentation. MNI is also a part of the equation when estimating relative abundances and is also affected to some degree by fragmentation (see Lyman 2008, 43-44). The Kruskal-Wallis test revealed that maxillary/mandibular relative abundances and mandibular fragmentation were quite often very similar between sites, differing in the case of samples but not contexts. Fragmentation is possibly the heaviest during first years after deposition and later far more uniform due to material being buried. Still, variation between individual bones seems more pronounced than between groups, suggesting other factors, such as differences in bone density and/or survivability (Lyman 1994a: 234-281) affecting tests.

Checks between sample and context data also revealed the impact of sample size on statistical tests and the necessity of considering its impact before performing statistical testing. Data retrieved from samples showed on average far higher variation, with a relatively broad range of values. Context data, on the other hand, did provide data suggesting similarities in ranges, possibly more predictable than in the case of samples. Especially when investigating Birsay Bay, differences between levels could be noted, with the combined level dataset (containing fully and partially retrieved contexts as well as ones sampled only once) strongly skewed towards sample data pattern. Considering how often fully sieved and partially sieved contexts have to be compared, it points towards a strong bias likely to restrict the use of such comparison. That is most likely why Bu Broch and Tuquoy, and to a lesser extent Scar and Birsay, provide hard to interpret and compare data (see **Chapter 5.3-6.**). The reason for this issue will be explored later on in the discussion section but it might be another reason to be cautious when exploring sites with different retrieval methods.

6.1.2. USING STATISTICS FOR MICROMAMMAL DATA CLASSIFICATION

Considering results obtained when evaluating correlation and classification methods on references and site data, the use of specific statistical methods for seeing patterns in archaeological material is a valid but not necessarily straightforward approach (**Chapter 4.3-4**). The data obtained from classification algorithms were easiest to interpret. It was mostly due to the definite nature of responses and lack of overlap between them as only four or three groups were sought (owls, diurnal, mammal, scattering) within two sets of data. In turn, a combination of results from *Abundances* and *Fragmentation Percentages*, for three groups sought, created five specific responses: confirmed scattering (both classified as scattering), confirmed diurnal/mammal (both as diurnal/mammal), confirmed as owl and additional two mid-stages: accumulation (one returning as owl, one as diurnal/mammal) and contested (one owl or diurnal/mammal, one as scattering). Moreover, method application proved to be straightforward, with the majority of methods being a valid choice and a possibility to effectively work on non-processed data. Results revealed relatively high accuracy alongside acceptable kappa ranges. Moreover, after tuning specific parameters and checking the obtained accuracy on references data it turned out that 95% accuracy threshold, or one on a verge of significance, was likely reached. The only issues noted were related to the utilization of random number generation in algorithm testing, possibly affecting the replicability of a training process. Still, algorithms usually work on specific tune values, which means likely reproduction of final results, even if a process of finding such values may be problematic to reproduce.

In turn, using correlations coefficients or χ^2 values to establish similarities or differences between data proved to be possible, although a more complex task. Even before checking signatures of specific Orkney species the analysis of the whole dataset showed problems with overall and more than one correlation/chi test providing significant values. The references dataset showed that only owls as a group can be effectively differentiated from the other groups through the line of strong positive/negative correlations or lowest χ^2 test values (**Chapter 4.3**, Fig. 4.06-7). While diurnal and mammal groups showed marked differences from owls, established ranges also strongly overlapped with each other. Scattering, in turn, did not provide many strong correlations and did provide very high chi test values, being perhaps most uniform in responses both as a group as well as a signature. In the case of correlations, the best way of dealing with it was the reduction of studied classes, from full owl/diurnal/mammal/scattering to owl/diurnal&mammal/scattering, if not simply dividing into owl and non-owl patterns.

However, an issue with strong and weak results remained. Uniform weak correlations might be a diagnostic element of scattering, though how low is low enough is debatable. This situation may lead to the decision being more related to other correlations obtainable than by assuming the best correlation to be accurate. Still, the issue was proven to be most impactful in the case of the χ^2 approach, as only a two-group differentiation provided any accuracy for references data (**Chapter 4.3**, Fig. 4.07 & Table 4.05). The attempt when using signatures returned at best 50% accuracy, rendering the method essentially useless for further work. Another issue found was with correlations and χ^2 computing requiring at least a basic amount of data being present, else resulting in biased test results or no results at all. This problem was visible especially in the case of archaeological data, but even in the case of references datasets, testing could narrow the choice of comparable signatures simply by data being incomputable.

However, analysis of correlations and χ^2 test results and classification outcomes were arguably more informative on references and site data nature than methods tested. Ratios (*Abundances* and *Fragmentation Percentages*) proved to be a more optimal choice for statistical analysis than NISP/counts (*Elements NISP* and *Fragmentation Counts*) regardless of a method used, possibly because of a finite range of interpretable values thus less impacted by the assemblage size itself. It is interesting also from this perspective, that especially *Elements NISP* has been used for some time to prove or disprove similarity between contexts. However, it did not necessarily mean that ratios are not affected at all. Some species provided more than one pattern, differing enough to be classified in two separate groups, such as e.g. European eagle owl (Andrews 1990, 188-189 & 211) or black-backed jackals (Matthews 2002, table 2&3). In the latter case, it might be due to one assemblage being smaller, thus providing less workable data. However, the former also shows additional biases, impossible to identify through classification alone.

The analysis of *Indices* and *Skeletal Frequencies* had comparable issues as ones noted in the case of correlations and χ^2 , though could be utilizable to some extent to explain obtained patterns (**Chapter 4.3.** and **Chapter 4.6.**). Specifically, frequencies did show the same problems to *Abundances* and *Fragmentation Percentages* in the case of correlation, but with values further exaggerated due to groups showing far higher levels of variation. Correlations were predominantly weak due to the usage of Spearman rank correlation on only four variables present ($\rho = 1.0$, i.e. only complete correlation being strong). However, visualisations of *Skeletal Frequencies* are shown to be an easy analytical tool, though rather for initial analysis and discussion on obtained patterns rather than their definite identification (**Chapter 4.6.** Fig.

4.19-20). A similar situation to *Abundances*, *Fragmentation Percentages* and *Skeletal Frequencies* was also noted in the case of *Indices*. Complex crania to postcrania index was proven to be most responsive to changes between groups, though mostly in differentiating owl deposits to other predator groups. The other two indices provided more overlap between groups. Still, if utilized jointly, those can be useful to some degree due to the owl group showing the least varied range of values. However, variation between sites suggests other factors contributing to obtained patterns.

The application of statistical methods to site analyses encountered a discrepancy between obtained matches or classifications and digestion levels recorded, most likely stemming from factors affecting *Abundances* and *Fragmentation Percentages* (**Chapter 5.**). Especially in the case of older assemblages, the most common identification was diurnal/mammal for classifications and kestrel for correlations, but the majority of studied contexts lacked digestion on a level of a diurnal raptor (e.g. Skara Brae, **Chapter 5.1.5.**). It conflicted with established knowledge about predatory taphonomy (Andrews 1990) and was most likely showing a strong bias, either in digestion recording or in statistical classification approach. However, despite encountering issues when working with and scoring digestion, underscoring was most likely not responsible for such a situation. Issues stemmed mostly from the presence of additional taphonomic changes during the assessment, such as abrasion and weathering, often leading to similar marks on teeth. An experienced observer would often reject those as digestion (Fernández-Jalvo & Andrews 2016) although there is no guarantee both were not the case (see **Chapter 5.5.5.** Fig. 5.46 D and E). Additionally, a inter-observer error when scoring digestion of owl species has been noticed by recent research (Comay & Dayan 2008b), while some previous research has noticed discrepancies with data recorded in Andrews (1990) and their own research (Matthews 2002). However, even if the author would consider such material as digestion, it would be at best categorised as light or, rarely, moderate form. It would still be different from the expected predominance of medium to extreme digestion expected from diurnal or mammal species, not to mention the high percentage of digested material required. Moreover, the only accumulation with large quantities of digested material, Context 33 from Tuquoy, showed a quite considerable amount of highly digested teeth while, at the same time, being classified as diurnal/mammal and highly correlated with hen harrier and red fox patterns (**Chapter 5.5.**). As a result, the issue was most likely within *Abundances* and *Fragmentation Percentages*, which was confirmed by applying adjusted methods (i.e. relying on data

transformed to simulate partial dispersal and burial). Adjusted results showed identification more similar to those obtained from digestion, with owls being much more common results.

Another issue was when to apply the methods based on the original references dataset and when those using references dataset transformation to mediate the impact of scattering on micromammal assemblages. As pointed out in the paragraph above, digestion may be an additional suggestion, but contextual evidence should also be considered, especially due to digestion not always being a definite indicator (Matthews 2002). Contexts known from good preservation of biological remains, such as waterlogged pits/middens, can be considered as a good benchmark for assemblages roughly contemporary to them. In the case of Skara Brae, midden Context 213 *Skeletal Frequencies* and *Abundances* were noticeably different from the rest of the contexts within the site, leading to highest *Abundances* correlations and *Abundances*-based classifications being with owls (**Chapter 5.1**, Fig. 5.04-8 and Table 5.0.5; or, considering low digestion, non-predatory accumulation, such as self-trapment). Another point of reference can be off-site undisturbed accumulations, such as Context 408 from Skara Brae, showing quite a high number of complete bones, pointing towards owl-like fragmentation. Timescale is also an important factor as Neolithic sites showed deterioration requiring transformed methods in order to return answers more consistent with other data or contextual evidence, while Norse/mediaeval contexts did not require much of it (e.g. Tuquoy Context 33; **Chapter 5.5.6**, Table 5.17).

6.1.3. DATA REPRESENTATIVENESS, RETRIEVAL AND SAMPLING

Taxonomic diversity affecting sample representativeness often reflects how the rarity of specific species influences ecological, paleontological and archaeological sampling results (Grayson 1984, 131-167, Reitz & Wing 2005, 113-4; Reitz & Shackley 2012, 89-91). The existing methodology is well aware the relationship between numbers of taxa/genera and other key variables describing sample size (e.g. MNI, Reitz & Wing 2005, 114 Fig. 4.6.; NISP, Reitz & Shackley 2012, 90 Fig. 3.7) is logarithmic rather than linear. Sample size increments rise with the rarity of species, with most commonplace taxa usually included early on and rarer requiring progressively bigger samples taken.

Such a situation was noted predominantly within the Birsay Bay site, but even in the case of the seemingly uniform assemblage from Links of Noltland, the impact of taxa rareness was

noted (**Chapter 4.5.**). Especially the representativeness in the case of data aggregation showed its reliance on specific samples. As mentioned in the Literature Review (**Chapter 2.3.5.**), pygmy shrew mean density per ha is the lowest among Orkney species. Moreover, they do not constitute a significant or regular part of the Orkney predators diet (see Reynolds 1992). Pygmy shrew bones inclusion in an assemblage is either an incidental catch or non-predatory death, both possibly correlated with low density. In all of Birsay Bay Area 1, evidence for only three *Sorex* MNI were found, two within wholly sampled contexts and one in a partially sampled one (**Chapter 5.4.1.**). Despite both tested contexts having about nine soil samples, only a single one in each case was taxonomically representative. In a wider context, it also meant that only three samples out of 244 (~ 1%) taken from Birsay Area 1 were representative of the site's taxonomic diversity. Birsay Bay Area 2 and 3 also presented such cases, though to an even more extreme degree. Three *Sorex* bones were found, each in a separate context as well as sample. In Links of Noltland Trench D, field mouse remains were found only in a single sample of Context 13 (**Chapter 5.2.1.**). It meant only one individual, compared with 391 voles and four unidentified MNI. Such rarity was rather unexpected considering that in Skara Brae, field mice were found to be about 7% of the whole micromammal population.

While factoring in key quantifiable data into taxonomic data analysis reveals yet another layer of issues, they seem to be only affecting predominantly unidentified material. In aggregation analysis, the visibly linear relationship between NISP, MNI, weight and percent of context sampled confirms notions about NISP and MNI being in a linear relationship and usually being unaffected or only mildly by aggregation (Grayson 1981, 49-68). However, it does not mean that all species classes used also have a linear relationship within the confines of those variables. Considering aggregated data (Fig. 6.01, MNI plot), unidentified rodent class has been steadily rising until about midway through the aggregation process, then steadily declining until vanishing once all data has been aggregated. Unidentified NISP was being still amassed, as suggested by Stahl (1996, T.1), but with less impact on MNI with each sample. Such process pointed towards the slower aggregation of remains identifiable up to species than other remains, at least during the first half of the aggregation. However, the issue seems not to affect the ordinal relationship between species MNI. In extension, utilizing taxonomic abundances (e.g. Miksicek 1987, Fig. 4.3) based only on identified species MNI seems to work as expected (Fig. 6.01, abundances plot), with taxonomic abundances values stabilizing before reaching midway point in the aggregation process.

Sampling may also work against other key finds, such as scorable taphonomic marks. For micromammal taphonomy, identifying the presence and severity of digestion is the key for a successful identification of a taphonomic agent responsible for the studied assemblage (Andrews 1990, see **Chapter 2.2.5-6.**). However, the presence of any digested remains from Birsay Bay was rarely acknowledged, with aggregation necessary to obtain at least a minimal amount of evidence. While it may not be a big issue in the case of Birsay Bay, for which the contexts site analysis suggested mainly non-predatory origin, it may also work when a more complex analysis of digestion is employed. The severity of digestion is not even, with amounts of less and more altered remains differing between species (see Andrews 1990, Fig. 3.29). It is possible that sampling will omit less common stages of alteration, possibly biasing digestion data.

Sample size also proved to be a crucial issue from two different perspectives. First was the minimal number of finds required to be, if not representative, at least comparable with the parent context. The lower representativeness of Birsay Bay samples (**Chapter 4.5.** Table 4.10-1) is partially caused by the site having generally far smaller sample sizes in terms of NISP/MNI than Links of Noltland. The impact of low NISP and weight values was visible already in the case of taxonomic matches, but was especially prevalent for quantifiable data correlations and prediction matches. *Fragmentation Percentages* were heavily dependent on just a few samples, usually of a far higher NISP count than the rest of samples within the studied context (e.g. in Birsay Bay Contexts 65, 134 or 171). Context could be divided into too small samples to be even possible to effectively compare with the parent context or each other. NISP of the whole Birsay Bay Context 207 was barely 54 bone and teeth fragments. It resulted in samples being on average having only seven NISP, not enough to provide ratios besides 0% for the majority of bone elements. However, even in the case of larger Links of Noltland samples the same issue could occasionally occur, especially in the case of more spatially extensive contexts.

The second issue relates to how large a part of a parent context the sample forms, both in terms of size as well as the amount of data retrieved. Stahl (1996, T.1) has already suggested the sample size as being a key factor, affecting much of the retrievable data. From the perspective of samples, one could notice higher NISP/weight often being required in order to obtain a match for quantifiable data, such as *Abundances* and *Fragmentation Percentages* (**Chapter 4.5.** Fig. 4.15-8). Additionally, samples representing a bigger percentage of the parent context had in overall a better chance to be representative. It was fully confirmed by cumulative sampling, with both calculations and the majority of predictions getting more accurate with more steps in

aggregation. While the representativeness of metric and pathological data was not tested, later analysis pointed towards more sampling effort producing more representative samples. Pathological changes (**Chapter 4.9.**), especially, showed a strong relationship between the number of NISP retrieved from the site and the overall amount of identified cases. Metric data also showed such a pattern, but with a bigger impact of other data affecting the results, e.g. fragmentation (**Chapter 4.8.**). Both Links of Nolthland and Skara Brae, sites sieved in full, provided the majority of data available. In turn, restricted sampling or the combination of sampling with the whole-earth approach did not produce enough data to be considered as comparable, often only singular finds.

Considering the above, the application of sieving to the majority up to the entirety of studied contexts showed to be best from the perspective of data retrievability and representativeness as well. Shaffer (1992b) provided evidence that differential recovery strongly impacts comparability between species, especially if a size difference is present between them. This observation can be reinterpreted from the perspective of the obtained results. Sample and context data provided visible differences in data distribution, grouping and correlations, while analysis of representativeness suggested samples being at best representative of a specific data facet of a context rather than context overall. As a result, samples can be considered as incomparable to contexts and likely to create biases due to differential recovery. The only way might be narrowing the aim of the research to only very specific data, though it might not work for micromammal taphonomy requiring a variety of different data for accurate judgements. Moreover, as noted in the case of *Skeletal Frequency* correlations as well as selected predictions within aggregation analysis, data representativeness, once reached, does not necessarily remain as such and may lapse back to unrepresentativeness with another sample added.

Interestingly, the difference between sampling and whole sieving profoundly impacted site analyses. Systematic but simple sampling as noted in Tuquoy and to a lesser extent Scar, provided consistent and relatively comparable results but only on the most general level possible (**Chapter 5.5-6.**). However, the problem with such sampling was made obvious when comparing Tuquoy predatory accumulation with the rest of the site. It was identified by excavation teams and sampled almost entirely due to a high density of micromammal remains visible with the naked eye. Other samples have shown a possibility of other large accumulations within the site. However, due to not being easily identifiable, possibly related to higher dispersal, special attention was not taken and only a small part of them was retrieved. A combination of simple sampling with whole sieving of selected contexts also showed a similar

problem in case of Birsay Bay Area 1, with detailed situation within the construction but outside contexts severely under searched (**Chapter 5.4.**). Interestingly, Bu Broch provided an extreme case of non-informative data, with only a few, even if relatively large, samples provided too little to be comparable with any other site or on any level (**Chapter 5.3.**).

The comparison with non-micromammal-oriented research is challenging due to the inapplicability of some widespread notions to micromammal data as well as differences in data sought. Most of the discussion on sampling and representativeness in archaeology is dominated by paleozoological/paleontological research interested in a reconstruction of past fauna and their comparison with modern animal populations. That is why the discourse is mainly interested in creating methods that maximize taxonomic representativeness when reducing possible redundancy and related sampling effort (Lyman 2008, 141-171; e.g. Wolff 1975; Jamniczky et al. 2003). Specific techniques are also used to compare taxonomic composition between isles and mainland populations (“nestedness”, see Lyman 2008, 167-170; e.g. Cutler 1991). However, analysis of nestedness was devised mostly for natural dispersal of species among the isles, usually along natural land bridges, not fitting mostly anthropic composition of Orcadian fauna. In the case of taxonomic composition, the taxonomic diversity from both sites, especially Links of Noltland, already proved to be barely representative, with any less sampling effort most likely resulting in a lack of representativeness. Additionally, if a strong correlation of the sample in relation to the whole context is considered as reaching the point beyond which adding new samples can be considered redundant then studied data provided evidence for such approach being not applicable, at least not for species data. Finally, discussion on sample redundancy may be simply irrelevant to in-depth analysis of micromammal assemblages. Most discussion on redundancy does not consider the uneven distribution of data, which is a basic fact of micromammal research and is essentially built into taphonomic research. Establishing patterns of deposition requires repeatable, “redundant” data, enabling comparability on a fundamental level with other assemblages.

However, even if the results cannot be directly compared, conclusions can still show similarities, especially if the likely impact of spatial sampling is discussed. In the case of Mitchell et al. (2016), while species representation of molluscs was studied and redundancy in sampling was sought, the authors have noted the spatial aspect of sampling biasing expected results. While the identification of all species was achieved in the study, the conclusions suggested species proportions being biased by the area chosen by the research. It was devoid of noticeable mollusc concentrations, which were present elsewhere within the site. This is not

surprising, considering zooarchaeology sees spatial relationships between remains of bigger species as key information, up to being discussed when introducing new audiences to zooarchaeological investigations (e.g. Gifford-Gonzales 2018, 151-152). However, it is often omitted when investigating smaller species or very large assemblages. In the case of micromammals it seems that differences between samples reflect at least to some degree differential accumulation, and related dispersal, of their remains within both archaeological and natural contexts. However, it will be covered in a later subchapter.

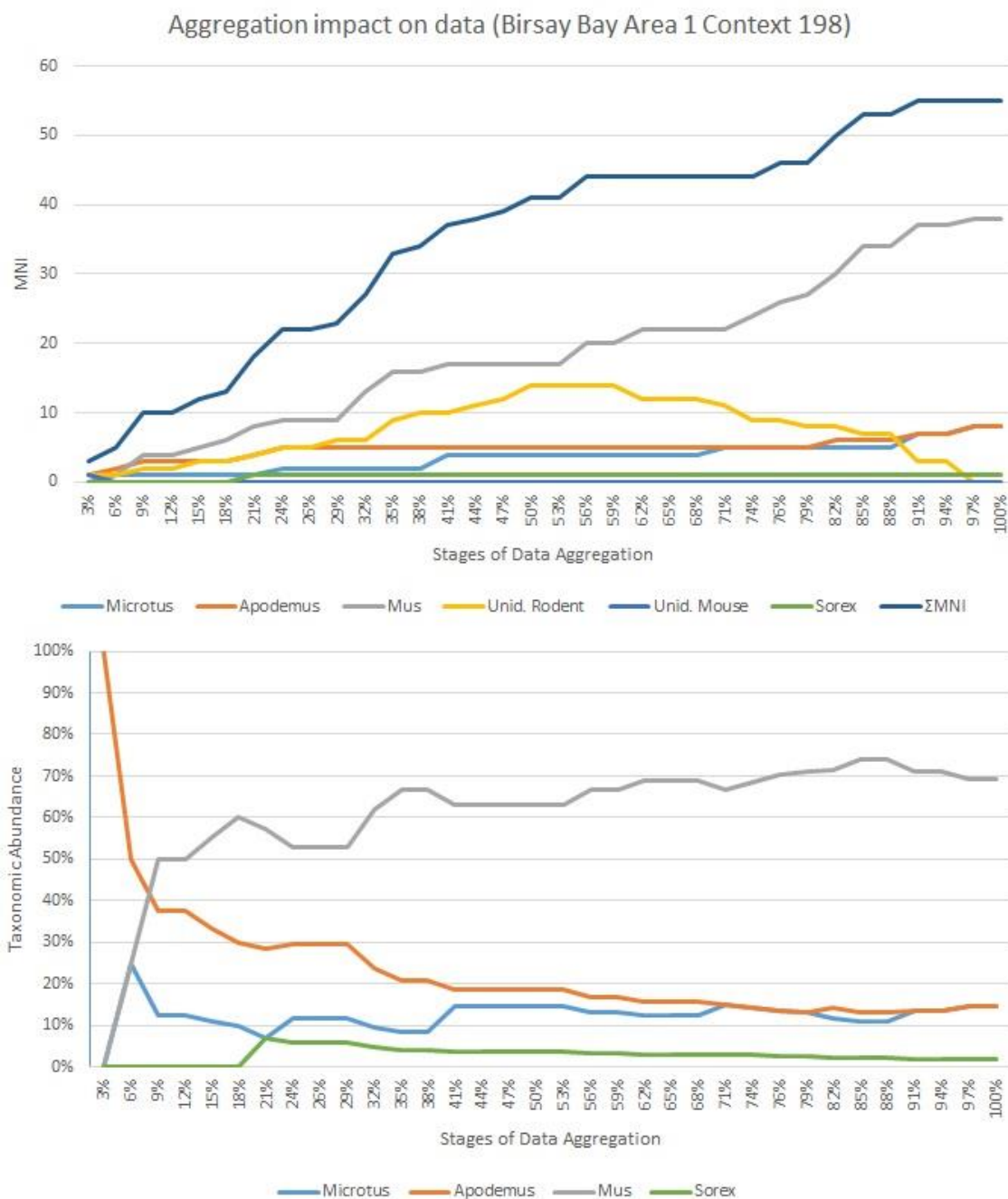


Fig. 6.01 – Relationship between specific species categories MNI/ taxonomic abundances based on MNI and levels of data aggregation for Birsay Bay context 198. MNI for all species classes were shown, with taxonomic abundances encompassing only ones related to specific taxa.

6.1.4. RECONSTRUCTING AGE DYNAMICS AND RELATED DATA

The analysis of the proposed methods of obtaining diagnostic data for age estimation primarily revealed method simplicity and reliance on elements with a high chance of survivorship to be two crucial factors in data representativeness. The best example was molar wear, which provided the highest representativeness ratios for murids, sometimes reaching 100% of all estimated MNI (**Chapter 4.8**, Table 4.24). It is not surprising considering that teeth, especially molars, are one of the most durable elements of the human or animal body (Lyman 1994a, 79-80) and can withstand biostratinomic and later diagenetic processes for longer than any skeletal parts. Murid molars retrieved from all the studied sites were generally well preserved, scorable and found in relatively high numbers. For example, in the case of Birsay Context 182, about 68 out of 153 murid bone and tooth fragments retrieved were loose molars. Additionally, all mandibles (NISP 32) and almost half of maxillae (NISP 9) also had preserved molars *in-situ*. It resulted in about 71% of NISP containing diagnostic data for age estimation. Finally, molar wear scoring on area level seemed to work with both sampling and whole-context sieving, though better results were obtained by the latter.

However, even full representativeness may not guarantee the absence of possible biases. One of the issues is the necessity of approximation of a final score/age category for an individual from multiple scores recorded for each molar individually. In the case of better-preserved specimens, it might be just maxillary and mandibular teeth rows retrieved in full, enabling easy attribution to the same individual. However, more fragmented remains, especially isolated molars, have to be attributed to an individual based on researchers' judgement, thus introducing a possible bias. Another problem, specific to the application of this method to the Orkney population, is the lack of knowledge on how local conditions affect molar wear. Tooth wear has been used for a long time in both humans and animals (Hillson 2005, 218-219). The biggest issue encountered so far have been differing diet across the same species, resulting in populations exhibiting differing wear pattern to the same age class. However, the impact of this specific bias on the analysis may be mediated with a cautious approach and provision of raw data for re-examination in the future. Additionally, extreme scores (lack of wear or extreme wear) should still denote juvenile and fully adult specimens, with the biggest impact being in the case of intermediate scores. A similar situation is often the case in fusion scoring (Reitz & Wing 2008: 193-197, see later paragraphs) and is usually accepted in absence of better methods of age estimation.

Methods based on fusion suffered from the impact of differential survivorship, fragmentation and issues with taxonomic identification of taphonomically altered bones (**Chapter 4.8.** Table 4.22-3). Simple binary scoring of long bone epiphyses showed tolerable levels of representativeness of specific bone elements and related NISP. However, MNI was often calculated from better preserved maxillary or mandible fragments or even surviving teeth, resulting in lower representativeness of MNI in the end. Skara Brae provided relatively high numbers of long bones, but the relative abundances for all four trenches were on average 30% lower than ones obtained for maxillae and mandibles. The only exception were samples from Bu Broch, where distal limb bones represented MNI almost as high as skull elements. Additionally, problems with taxonomic identification also affected fusion recording, resulting in murids being grouped together and bones too altered to be identifiable creating a vast “unidentified micromammal” category. In contexts dominated by a single species it is safe to assume unidentified elements also coming from the same species, but in the case of more diverse composition it may lead to a lack of conclusive information on any of the studied taxa. Issues with identification also affected the identification of some unfused specimens. The retrieved bones from Birsay which visibly belonged to juveniles often could not be identified to species or species group. Finally, while sub-adult and adult markers may be retrievable, but structurally weaker juvenile bones may vanish from the archaeological record (Lyman 1994a, 288-289). While it is a more theoretical, difficult to prove bias, it nevertheless should be considered as an alternative explanation for estimations based on epiphyseal fusion.

Adding metrical data to fusion data could theoretically add a new dimension to the analysis but in practice just introduce more biases to the study and restricts overall representativeness for less well-preserved assemblages. Considering that the fusion scoring currently used is more informative in the case of early or late fusing epiphyses (Reitz & Wing 2008: 193-197), such a method would help in getting additional data from the middle fusing stages, allowing to see skewing of measurements towards older or younger individuals even if no such situation is visible from fusion scoring only (Lyman et al. 2001, fig. 1 & 2). That is also why it was used previously by the author for Skara Brae (Romaniuk et al. 2016, fig. 3a-d; see Fig. 4.23), to prove population skew towards adult size specimens. However, the usage of this method may be justified only in cases where the taphonomic history of remains is not altering the assemblage too much. Metrical data are obtainable only in the case of complete bones without much taphonomic alteration visible on the surface. Differential survivorship of juvenile bones, as mentioned in the previous paragraph, also affects the degree of bone fragmentation. As a result,

juvenile bones are more prone to fragmentation and thus less likely to be measurable than better developed, fused bones of adults. Such a situation was observed when comparing the state of fusion of complete bones to the whole population of scorable epiphyses, revealing biases in the case of both early and late fusing epiphyses representativeness. It was further exaggerated by the fact, that, following the initial idea (Lyman et al. 2001), the method should take into account only bones identifiable to species. As elaborated in the previous paragraph, it was not possible to achieve for many bone fragments. In the result, the previously observed trend towards larger specimens in Skara Brae (Fig. 6.02) may just represent differential survivorship in each trench and impact of identification bias towards better developed, thus older, specimens.

Interestingly, pathological data showed some alignment with age estimation but cannot be studied further due to a lack of comparable research from modern populations (**Chapter 4.9**). Osteoarthritis and vertebral fusion are the type of finds often caused by the natural aging process (Aufderheide & Rodríguez-Martín 1998, 93-96; Baker & Brothwell, 1980, 107-134; Bartosiewicz, 2013, 113-115 & 117-129), though other factors (e.g. trauma or prolonged infection) may also be involved. Additionally, many pathological conditions identified were either healed or possibly in a process of healing, all essentially related to locomotion restrictions. Individuals having such markers had to survive quite long (in relation to average rodent timespan) after the traumatic incident or contracting infection in order for a bone structure to exhibit such changes, additionally avoiding predators that might take advantage of restricted locomotion. However, it is impossible to extrapolate the importance of such finds in absence of data covering pathological occurrences in a living micromammal population affecting bone tissue.

However, micromammal samples did not provide pathological changes common in species with indefinite tooth growth, e.g. overgrowth of incisors or molars (Miles & Grigson 1990, 355-362). It may point towards a relatively healthy population, with food providing optimal hardness in relation to the wearing process of teeth. However, more likely is that such finds were present but either investigated places simply did not contain any example or retrieval methods could not retrieve an identifiable specimen. Differential preservation can affect pathological changes, for example resulting in increased fragmentation of overgrown teeth and the disappearance of such finds from the archaeological record. Many incisors were broken or found outside of sockets, so it is impossible to establish how far such finds were protruding from the alveolus.

Interesting results were obtained from age-related data when analysed on the site level, especially considering how rarely it is being obtained for micromammal finds (**Chapter 5.**). Data were especially important in identifying possible nesting/non-predatory deposition in Birsay Bay (**Chapter 5.4.**). A lower number of early fusing epiphysis and evidence of no wear was noticeable on the site, as elaborated in the site discussion. In the case of molar wear, frequencies of specific wear groups are very similar between sites, with Birsay Bay being not too different to Tuquoy if not for unerupted molars being identified in one case. The biggest difference was in the case of Skara Brae, where molar wear revealed a population older than on Norse/mediaeval sites (**Chapter 5.1.2.**). In turn, epiphyseal scoring showed almost uniform results for all sites besides Birsay Bay, with minor percentages of unfused early and middle fusing epiphyses followed by mostly unfused late fusing epiphyses. Area 1 showed a not too radical difference, with unfused juvenile specimens and still growing sub-adults forming a quarter to slightly less than half of the group. In the case of Tuquoy, the data seemed to be contradictory if not combined with contextual evidence. Still, both methods' results were workable, showing the potential in such data retrieval.

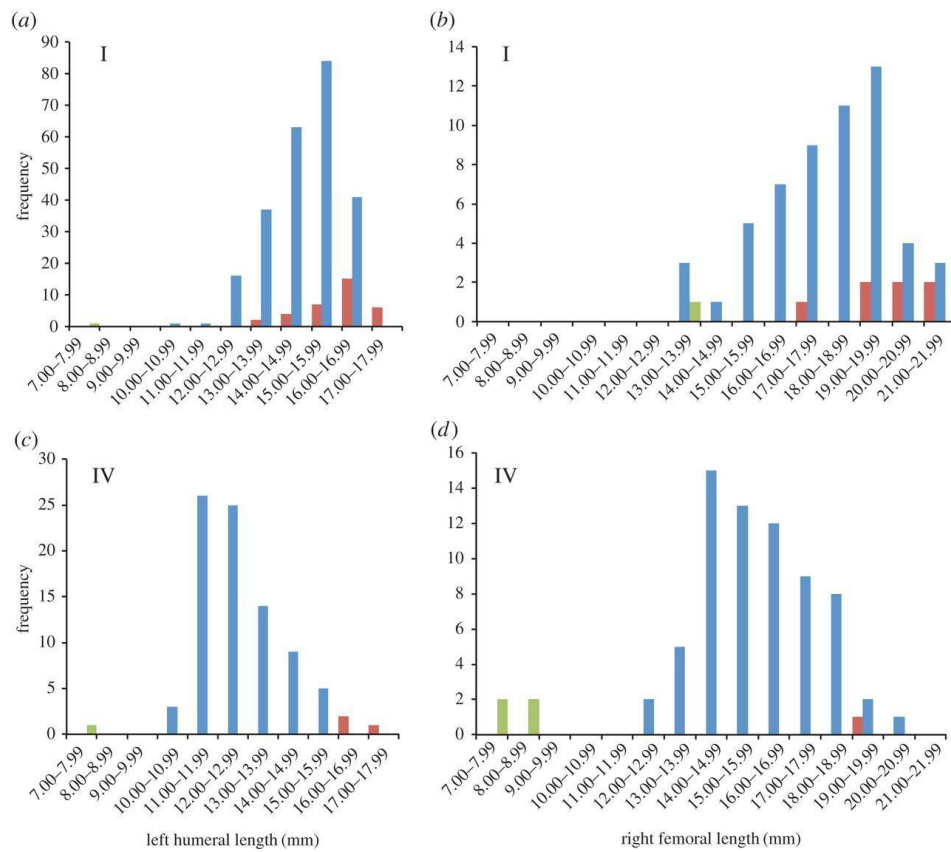


Fig. 6.02 - Lengths of Orkney vole humeri and femora from Trenches I and IV. Both epiphyses fused (red), proximal epiphysis unfused (blue) and both epiphyses unfused (green). Figure from Romaniuk et al. (2016, Fig. 3).

6.1.5. NATURE OF ACCUMULATION, DISPERSAL, SCATTERING AND BURIAL

The analysis of sampling, even before proper analysis of dispersal, as well as later analysis of Links of Noltland and Birsay Bay sites revealed the possible impact of dispersal and scattering (**Chapter 4.5.** and **4.7.**, also elaborated on in **Chapter 5.2.** and **5.4.**). Differences between samples in Birsay Bay are clearly visible when NISP, number of species or even degree of fragmentation, are considered (Fig. 6.03). For example, Context 195 was dominated by a single sample, one of two taxonomically representative as second most complete, which was responsible for about half of NISP retrieved. Spatial evidence for gradual dispersal of micromammal remains over a wider area and/or uneven accumulation by one or more taphonomic agents are also noticeable in the case of Links of Noltland samples (**Chapter 5.2.1.**, see Fig. 5.14 and 5.16). For Trench D highest density samples were usually neighbouring also higher density areas, with smaller samples being located further away. The prominent example was Context 13, with the large accumulation in Square FQ88 being encircled by smaller samples, with the smallest being located two squares away. A similar orientation of densities was noted also for Contexts 4, 8, 15 and 32. Moreover, as in Contexts 25 and 33, the presence of spatially distant samples within one context may point towards the presence of separate but contemporary accumulations.

Samples can also show variation when assessed through skeletal frequencies (**Chapter 4.6.**). Fully sieved contexts from Birsay Bay Area 1 were predominantly retrieved from contexts within a building and adjacent structures, with dispersal area being restricted by structural walls. This situation possibly resulted in contexts maintaining their integrity even after the building collapse, being gradually buried by activity or refuse layers. Larger samples from Context 198 (Fig. 6.04, upper plots) provided very similar *Skeletal Frequencies*, resembling owl deposition and mostly intact assemblage. The only differing sample showed a more dispersal-like structure, with more evenly distributed frequencies. Additionally, due to very small samples in terms of volume, many smaller contexts provided strongly skewed frequencies due to very low NISP, making any comparisons hard to perform. In turn, Links of Noltland Trench D was predominantly open space, with assemblages deposited mostly on a surface layer used frequently as an arable field or refuse deposit, with occasional construction activity. Assemblages in such environments could end up being gradually dispersed on their own over a wider area, with a possibility of human activity being a contributing factor. Contexts obtained

(e.g. Context 13, Fig. 6.04 lower plots) showed either dispersal-like frequencies known from Terry (2004) or diurnal assemblages variation, with skull remains dominating the sample.

Observed differences among *Skeletal Frequencies* were especially noticeable on site and context level, which was proven valuable when assessing sites and investigating patterns. Apart from the differences already identified at Skara Brae between on-site and off-site trenches, unique site-wide tendencies could be noted in the case of Links of Noltland and Birsay Bay (**Chapter 5.2.3. & 5.4.3.**). For Links of Noltland Trench A provided very specific frequencies, with a very high prevalence of limb bones (e.g. Contexts 28 or 48), while Trench D showed more equally distributed frequencies, resembling diurnal deposition or partial owl dispersal. In turn, Birsay Bay Area 1 showed very strong similarities with owl-like *Skeletal Frequencies*, including Terry's intact and partial dispersal examples. In contrast, Areas 2 and 3, on the edge of the site, provided contexts showing frequencies similar either to diurnal or owl species groups. Not surprisingly, analysis on context level highlighted more differences, usually aligned with correlation and classification data. Contexts 141 and 213 had an owl-like appearance of frequencies as well as selected classification hinting towards owl or similar depositor.

Skeletal Frequencies obtained from different sites also strongly suggested a long-term impact of dispersal and later diagenesis, including human-mediated dispersal, on micromammal assemblages integrity. A trend could be noted between the main time periods investigated (Fig. 6.05), with frequencies more akin to dispersal in the case of Neolithic sites and partial dispersal or even intact assemblage within Norse/mediaeval areas. In a similar way to vertebrae, minor elements (CTMP) were much more prevalent in later sites, with *Abundances* noticeably higher. Fragmentation data only loosely followed that pattern, with better and worse preservation seen in both groups. However, some sites, where stratigraphy encompassed long timeframes, such as Skara Brae Trench I or Links of Noltland Trench D, provided a noticeable in-site example of changes in fragmentation. In the latter case one especially, could notice a strong connection between the level of completeness and fragmentation and time spent within the assemblage. In both cases an additional biasing factor was most likely human activity, most likely interfering with deposited assemblages and thus introducing new changes and removing the smallest finds (e.g. phalanges or tali).

The necessity of factoring in dispersal and scattering when studying zooarchaeological material is widely known though rarely implemented in micromammal studies. Most research on micromammal taphonomy has so far concentrated on accumulations (Andrews 1990 *passim*),

with dispersal being considered only as an explanation for anomalous assemblages (e.g. Weissbrod et al. 2005 Fig. 15). Recent papers discuss spatial distribution (e.g. Fernández - Jalvo & Avery 2015 Fig. 8 to 12) but mostly as a proxy for other changes (e.g. paleoclimate). Only recently a necessity to study dispersal as such has been suggested (Terry 2004). Similarly, studies on larger species in the 1970s and 1980s were initially mostly concentrated on forces leading to bone accumulation (see Lyman 1994a, 161-168). However, initial research led to the necessity of further studies also on the impact of dispersal on bone assemblages, in time leading to seeing both accumulation and dispersal as processes mirroring each other (Lyman 1994a, 168-222).

Comparison between Terry (2004) and Behrensmeyer (1983) *Skeletal Frequencies* showed similarity between micromammals and larger species taphonomy. Any observed differences are most likely a result of bone survivorship differences between taxa or differences in species approach to predation, ingestion or deposition. Dispersal contexts as such usually represent a terminal stage of bone survivorship, with bones already being altered through animal and non-animal taphonomic agents in both their biostratigraphic and diagenetic phases (see Lyman 1994a, 223-293). The remaining bones, either whole or their fragments, will most likely represent elements of highest structural density, least likely to be affected by external factors and from regions of the body least interesting for predators. It is especially visible if the bone mineral density is plotted against survivorship (Lyman 1994a, 249 Fig. 7.7.). In the case of larger rodent species, marmots (yellow-bellied, *Marmota flaviventris*, and groundhog/woodchuck, *Marmota monax*), many bones proved to be denser than in the case of ungulates, especially humeral and femoral bones, though in a relatively linear fashion (see Lyman et al. 1992, table 2). Even if traditional correlation fails to note a relationship between density and survivorship, additional research and contextual clues can help in establishing the link (Lyman et al. 1992). The strong predominance of skull and hind limb fragments, especially mandibles and femora, in micromammal dispersal most likely reflects the durability of those bones.

Terry's data comes exclusively from an intentional accumulation of whole carcasses remains by owls, which explains why some modes of deposition seen in Behrensmeyer's work are incomparable with available micromammal data. Larger prey is usually taken by carnivores of comparable or slightly smaller size (e.g. hyenas preying on zebras and other ungulates as in Behrensmeyer 1983) and simply cannot be eaten whole. That is why their carcasses are disarticulated by their predators and later scavengers, with specific body parts remaining on the kill site ("predation path") scattered across the wide landscape ("dispersal") or selected body

fragments accumulated in specific places (“hyena den”). In turn, the body difference between micromammals and their predators is often quite big. For example, owl’s average weight is 260g, while voles are circa 40g of weight. That is why often micromammals are ingested as a whole, with their remains later either regurgitated in pellets or left in scats (Andrews 1990, 28, 34-44). From that perspective, the majority up to all deposited remains can be considered as intentional accumulation, usually reflecting individual predator behaviour (e.g. roosting and nesting sites in barn owls, Andrews 1990, 33 table 2.2).

However, owls are not the only species consuming and depositing micromammals. What was already noted in the case of elements NISP during correlation testing and later discussed in the skeletal frequencies analysis, mammal and owl groups exhibit roughly similar frequencies of specific skeletal parts – akin to intact and partial stages of dispersal from Terry (2004). In contrast, diurnal species, technically in between of those groups considering established knowledge about the destructive impact on micromammal remains (Andrews 1990, 90 Table 3.16), showed differing skeletal frequencies as well as elements NISP. It may be due to the fact that both owls and mammals are more likely to eat prey of a micromammal size as a whole, while diurnal tend to be more selective with ingested elements. Such a situation was already noted by Andrews (1990, 178-108) for diurnal and mammal species, though the size difference between micromammals and mammal carnivores may be bigger thus making ingestion in whole more likely. In extension, owl weak digestion cannot break down whole skeletons, thus regurgitating it whole, while all remains that can survive mammal digestion are deposited within scats, on their own having mild preserving properties during coprolitisation (Bradley 1946, Hollocher et al. 2010, Pesquero et al. 2014). Diurnals, being in the middle of those modes of deposition, can be strong enough to break down specific elements and others not, resulting in some being deposited as pellets and others as fully digested remains. As a result, owl pellet deposition sites and mammal scats may, despite different destructiveness of digestion process, tend to have a more similar selection of elements, while diurnal species can noticeably differ from both.

Another issue connected to the dispersal process is the idea of gradual soil saturation with animal remains. Dispersal and scattering over a prolonged period of time may lead to bone fragments being retrievable from the majority of contexts over a wider area. A pattern of “background scattering” between proper accumulations or even secondary accumulations can be mistaken for assemblages created by e.g. predation, human or other processes (Behrensmeyer 1983). Even in the case of micromammals, known to be predominantly eaten

by predators than naturally expiring (e.g. Behrensmeyer & Boaz 1980; Andrews 1990 *passim*), a saturation of natural contexts with occasional bone fragments dispersed from predatory assemblages may be possible. In the case of Orkney voles, the yearly population cycle includes the death of about 3 million voles (Reynolds 1992). Given the archipelago land area of 990 km² and possible continuous deposition for 6000 years a ratio of 18000 individuals being deposited per 1m² can be calculated. Even assuming 0.1% of those individuals' bones being retrievable it still results in an assemblage of about 288 diagnostic bones or their fragments (complete skeleton being ~160 bones).

Analysis of background scattering requires the in-depth analysis of natural contexts. In the case of data obtained from Orkney only Skara Brae properly explored off-site areas and natural deposition to a satisfactory degree. That is also why the author originally used Trench III and most of Trench IV contexts as examples of scattering for classification analysis. Trench III covered about 50m² nearby the eroding cliff edge, consisting almost entirely of sand deposits with occasional anthropic sediment and ploughmarks. Only 103 bone fragments were retrieved out of 11 contexts, showing very low completeness and no signs of any accumulation-like pattern. A similar situation was noted in the majority of contexts from Trench IV, where 6 out of 8 contexts provided only 50 NISP.

In essence, the studied data revealed the necessity to put statistical analysis into a wider contextual frame. The importance of contextual data for micromammal methodology has been acknowledged in the past, from cave contexts formation (Andrews 1990, 91-106) up to ecological niches of the anthropic environment (Weissbrod et al. 2017a), proving to be a necessity also in the case of discussion on accumulation and dispersal. Despite multiple quantification methods employed in taphonomy (see Lyman 1994a) contextual evidence should always be a determining factor in the choice of methods and changes sought. Interesting is the recent occasional usage of the so-called "contextual taphonomy" term to describe contextual data-dependent studies, especially when discussing food refuse (e.g. Yeshurun et al. 2014) or funerary practices (e.g. Borrini et al. 2012 & 2014). In this study contextual evidence had to be brought to explain accumulation and dispersal on two sites, one representing an open seminatural environment and the other a manmade enclosure. Context 13 from Links of Noltland Trench D, with dispersal-like structure through the whole site, may be a faithful representation of an assemblage in a natural or seminatural open environment (Fig. 6.06). Primary accumulation was, for the most part, not limited or shielded by any other accumulations, resulting in wide and relatively regular spatial dispersal. In turn, depositions in

Birsay are located within a walled structure. Especially in the case of artificial contexts, dispersal may be highly restricted from the majority or even all directions (Fig. 6.06) resulting in a relatively intact accumulation with only minor areas of dispersal present.

However, it also shows the potential of using micromammal data from natural depositions to reconstruct site stratigraphy and provide correlating data for periods of site usage and abandonment. Manmade contexts in particular, such as ditches or walls, can create stratigraphically fragmented terrain which cannot be easily reconstructed by the analysis solely based on the superposition paradigm. In zooarchaeology, the correlation of animal remains with the stratigraphic record is important, with changes over time being a contributing, if not key, factor in establishing site stratigraphy itself (Reitz & Wing 2008, 15 fig. 2.1.; Daniel 1981, 63). However, human practices are quite complex and may create different, changing patterns without the relation with shorter or long timespans (see discussion in Reitz & Wing 2008, 260-266), which restricts usage to very specific accumulations (e.g. food refuse contexts: Yeshurun et al. 2014). In turn, natural contexts, or even anthropic contexts based on alteration of natural ones, could still contain natural data. Micromammal assemblages, even if on a surface level, may not be significantly affected by the construction of a wall or other dividing structure and still maintain spatial relationship expected by an open-area accumulation with a sphere of dispersed bones around it. In the case of Fig. 6.07, if dispersal identified within the enclosure would match the outside area next to a wall it could mean, that both came from the same accumulation. Given no other accumulation than one within it would possibly mean that wall was built after the micromammal bones' deposition. Similarly, micromammal accumulations within contexts related to human activity may differ from ones deposited within abandonment layers, which may help in pinpointing the start of an abandonment process and gradual filling of the structure.

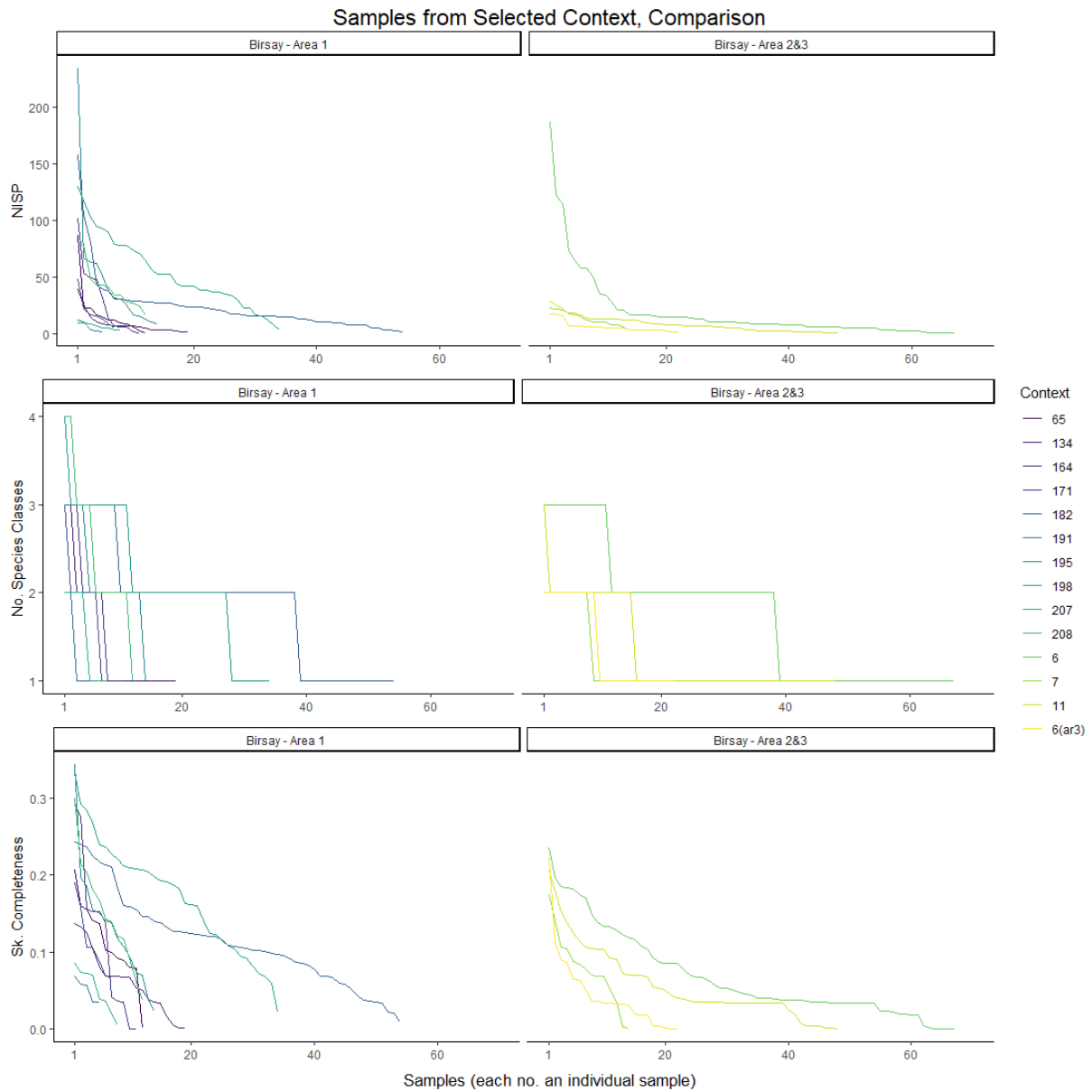


Fig. 6.03 – Specific sample data plotted from highest to lowest for Birsay contexts of five and more samples. Data includes NISP (left plot), Number of Diagnostic Species Classes (middle) and Skeletal Completeness (right). Each plot was arranged separately and while there is a significant overlap between plots, a specific sample number in a context does not necessarily reflect the same sample in all plots.

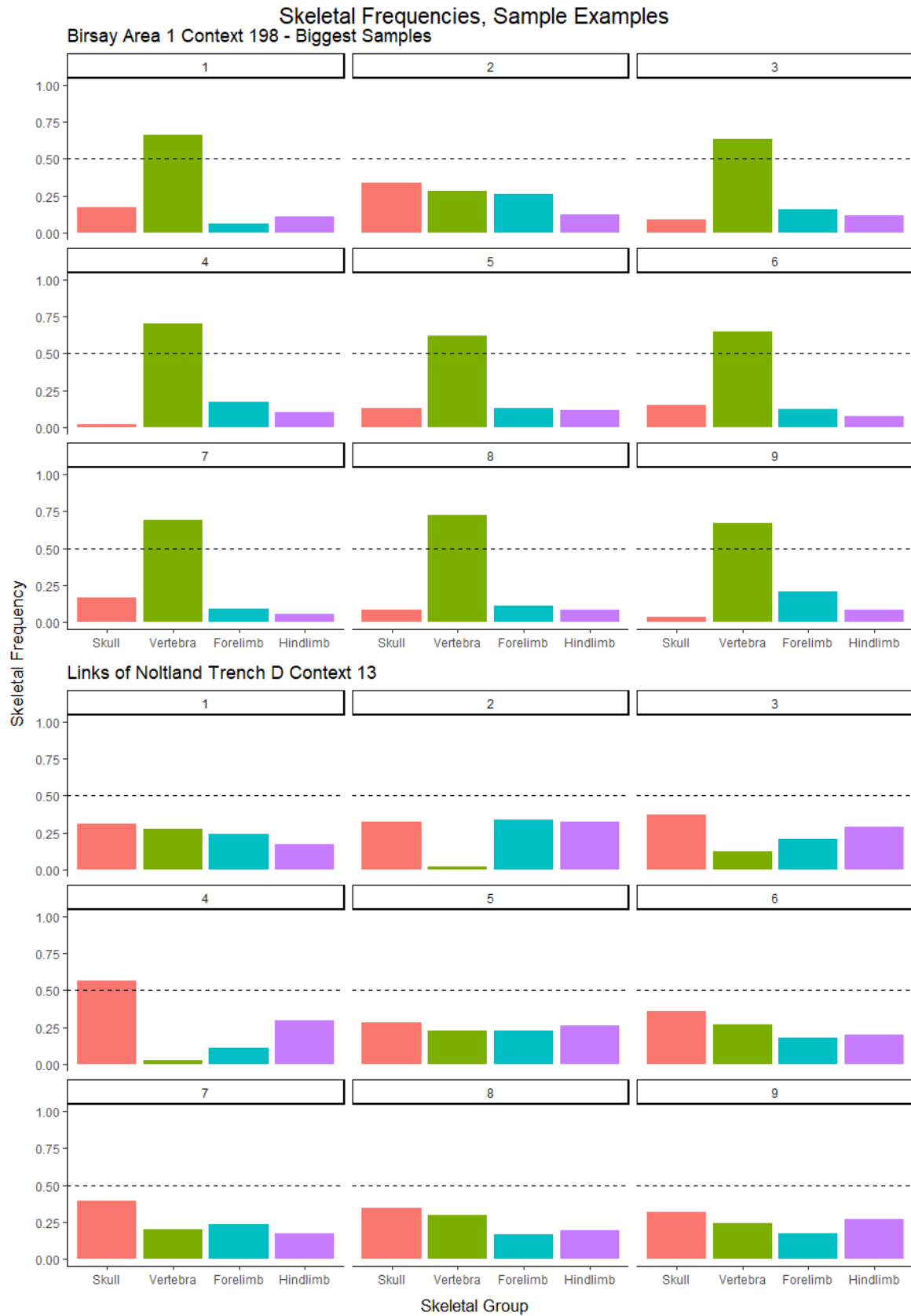


Fig. 6.04 – Sample *Skeletal Frequencies* from two different contexts. Upper plots show nine biggest samples from Birsay Bay Context 198, while lower plots show all the samples available from Links of Noltland Context 13).

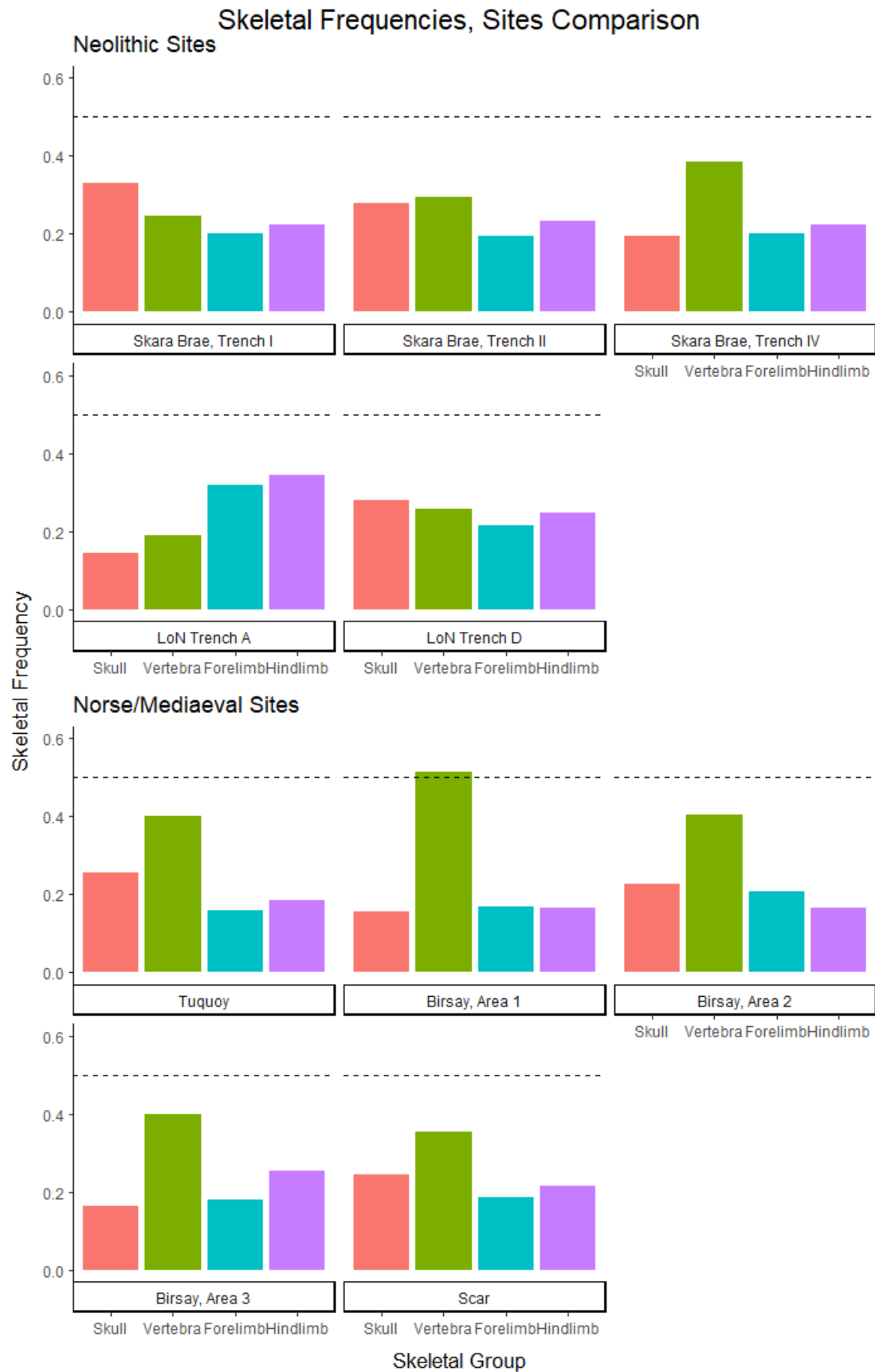


Fig. 6.05 – Comparison of Neolithic to Norse/mediaeval sites through *Skeletal Frequencies*, including specific areas within those sites.

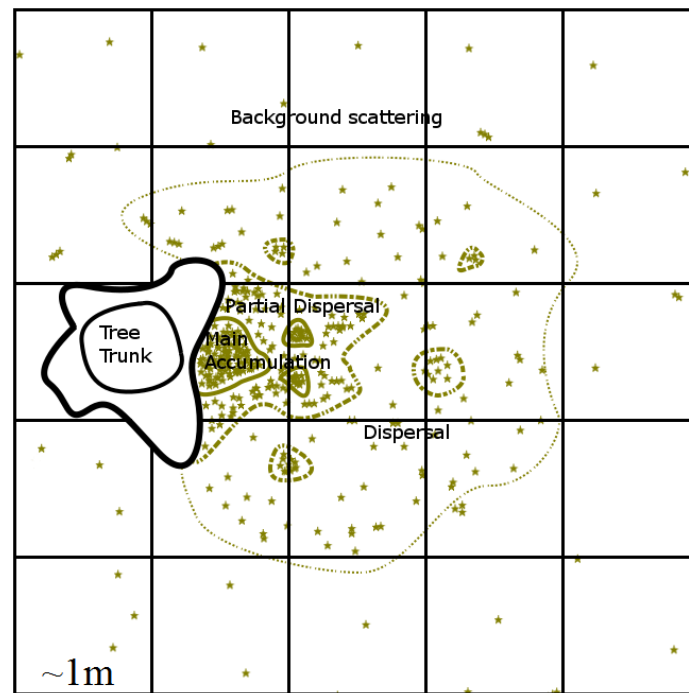


Fig. 6.06 – Illustration of dispersal within the natural, open environment. The majority of remains are within primary accumulation but due to a lack of pronounced borders for dispersal area affected by each stage of dispersal is relatively large, with the difference between dispersal from accumulation and background scattering from previous accumulations or natural death being barely recognisable.

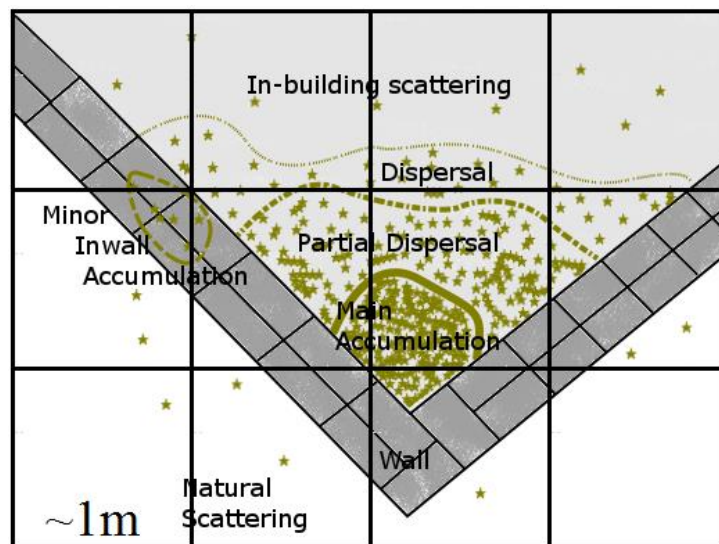


Fig. 6.07 – Illustration of dispersal within the manmade structure. Walls restrict the dispersal process, resulting in a stronger dispersal tendency towards available open space but also accumulation enclosed on a much smaller area. Dispersal front from the accumulation is also easier to differentiate from the in-building and natural scattering through the presence of additional contexts (walls) as well as a more pronounced dispersal edge. An extreme form of accumulation would be in-wall entrapment, possibly resulting in a lack of dispersal.

6.1.6. IMPACT OF NON-PREDATOR TAPHONOMY ON ADOPTED METHODOLOGY

As already seen in Terry's analysis (2004; see fig. 4.14), animal patterns may strongly differ between accumulation and related dispersal, with other research (Behrensmeyer 1983; Behrensmeyer & Boaz 1980; see fig. 4.11) pointing out the assemblage burial further biasing the results. It can be easily visualised just by checking how Terry's dispersal stages, gathered on the surface level, would look after going through the burial process (Fig. 6.08). Some linearity of pattern transformation or extremization of already present patterns can be observed. For linearity, complete and intact surface patterns resemble intact and partial dispersal after burial. For extremization, buried dispersal showcases the same outline but higher frequencies of skulls than surface dispersal. However, previously unrecorded patterns may emerge. In this case partial dispersal did not degrade into full dispersal after burial, but instead showed relatively similar frequencies to ones found during the analysis of diurnal assemblages, with a marked predominance of skulls, minor presence of front limbs and relatively even amounts of forelimbs and vertebrae. As a result, depending on which part of it is studied, an accumulation of one specific depositor may result in the appearance of several different patterns, possibly more similar to other species better-preserved accumulations than the original depositor.

Diagenetic loss could especially affect fragile elements' retrievability and fragmentation pattern, though site analysis was not fully conclusive possibly because of human involvement. In theory and known patterns from both micromammal and large species research (Lyman 1994a, 405-433; Andrews 1990, 10-24), once the deposition is sealed within the context, robust and most likely complete bones would survive the longest, with fragile and fragmented remains disappearing as the time passes. Weathering or abrasion affects first already fragmented or less dense remains, with complete bones or fragments of sturdy elements withstanding outside factors for more time (Korth 1979; Andrews 1990, 18-19). As a result, a very old deposition should show a deceptively high number of complete finds, with fragmented robust bones, if present, as second (see Fig. 6.09). The problem is the biggest loss observed was noted for most durable elements within CTMP group, namely calcanei and tali, while some thin and relatively easily broken metacarpals were still present in bigger assemblages. Moreover, tali (as well as phalanges) also did not appear in Trench D in Links of Noltland while being present in Trench A (**Chapter 5.2.3.**), suggesting prolonged exposure to a human activity being one of the factors contributing to their loss.

Understanding that species patterns are a range rather than a single set of values may be required for the preparation of methods, adjusting obtained answers to match the archaeological record and avoiding further possible errors in interpretation. As already noted in Terry's work (2004), under the current idea of considering modern deposition as a whole or only its very specific part as the species pattern may result in incorrect pattern being sought. Such a situation was validated by the analysis of adjusted correlations and classifications of and their later application to site data (**Chapter 5**). Tinkering with data transformation revealed that statistical methods would provide different answers depending on dispersal and to a lesser extent burial, ranging from more contexts or samples being identified as coming from owls up to far more identified as background scattering. Moreover, the analysis of proportions and other data have revealed visible tendencies within sites, or specific areas or trenches within, towards a very specific form of deposition. An especially strong difference was noted between Neolithic and mediaeval sites, a result of different contextual factors, retrieval process, additional impact of time on assemblages or even predators change over time. Evidence of taphonomic factors possibly differing between trenches/areas of specific sites was also identified.

The issue of identification bias is visualised in Fig. 6.10. Three samples used as a pattern for general groups for owls, diurnal raptors and mammals in actuality may represent more the overall level of preservation rather than the group itself. As a result, samples from archaeological contexts are matched with the wrong group. Misidentification can also happen when comparing buried assemblages with each other. For example, in Bocek's research on the impact of burrowing on a site formation (1986) the difference between skeletal pattern of burrowing versus non-burrowing rodents was one of the elements studied (Bocek 1986, Fig. 3). Although the body parts used in Bocek's research differed from ones used by Terry (2004) or in this thesis, patterns of burrowing rodents resembled more those visible in buried dispersal (Fig. 4.14) while one noted for non-burrowing species resembled buried partial dispersal. Noted differences Bocek considered as evidence in different deposition between two species groups. While it is not necessarily wrong it definitely shows different levels of dispersal between groups.

From the perspective of patterning, the least impacted would be species that create large assemblages of relatively unaltered bones. That is why owl deposits also showed a marked difference to other species, being better correlated between each other than diurnal or mammal species. However, the diurnal/mammal group shows the variety of different accumulations, often according to specific behaviour (e.g. territory marking by using own scats, see viverrids

in Andrews 1990, 41-42), which in turn creates a spectrum of different levels of taphonomic alterations, further impacted by environmental conditions. While actualistic studies are expected to investigate relatively recent depositions, without many environmental changes or of a predictable kind being present, their gradual decomposition and scattering remains a rarely touched subject. While some patterns can be expected, as noted in a previous paragraph, more research into the taphonomy of small species assemblages should be performed in order to be sure of the identification. However, within-species variation of deposition is recently being investigated in more detail (e.g. Andrews et al. 2018).

Considering the above, spatial and contextual data retrieval has to be included in any sampling effort in order for it to properly and faithfully represent the site. In a fully or partially open environment it is generally advised to spread sampled space over a studied region and fragment it into smaller areas to have more diverse samples, less correlated with each other (Orton 2000, 31-32 & Fig. 2.4). The idea may be better than sampling based solely on contextual data as search for specific accumulations will most likely return only the highest concentrations of micromammal material, without much data on background scattering or dispersal area, but at the same time may result in completely non-representative samples and a complete loss of contextual data. Counter to this, one larger area, even if does not cover all accumulations present, may be a better choice. In one illustrated example (Fig. 6.11), only one among four accumulations is being investigated in such a way but the data obtained includes a proper accumulation area as well as associated dispersal, ending on background scattering. However, considering deposition dynamics and the effort needed to be used in retrieving small remains, it would be best to employ more complex and flexible approaches, such as adaptive sampling (Orton 2000, 34-38). Once the presence of an accumulation area is known either through random sampling or contextual evidence, researchers can adapt the sampling regime to gradually include the area beyond the arbitrary threshold of expected background scattering NISP.

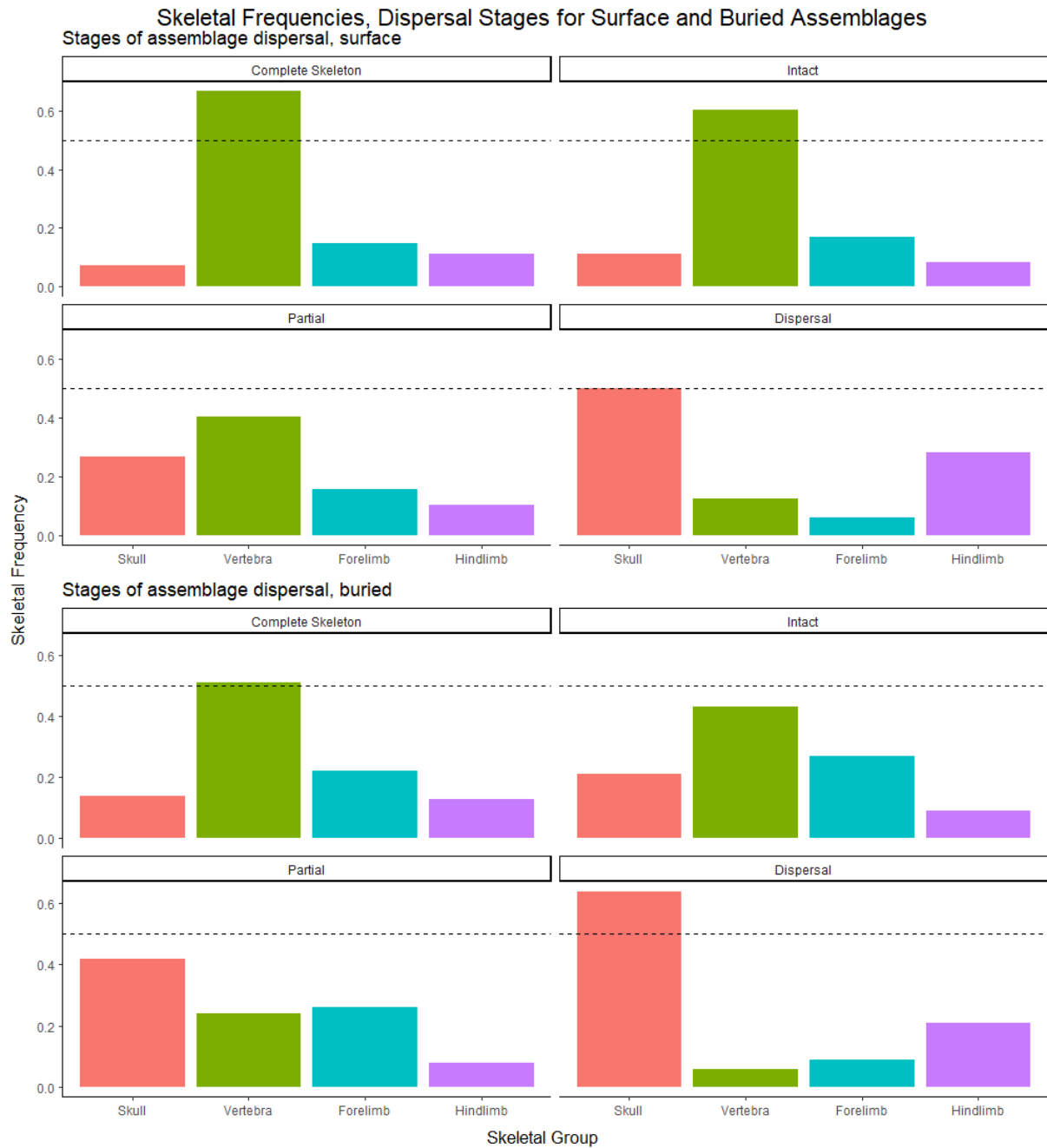


Fig. 6.08 – Example of likely differences between stages of dispersal between surface and buried assemblages expressed in *Skeletal Frequencies*. Surface data as in Terry (2004, Fig. 6), with buried data estimated from surface data by transformation shown in T. 3.13.

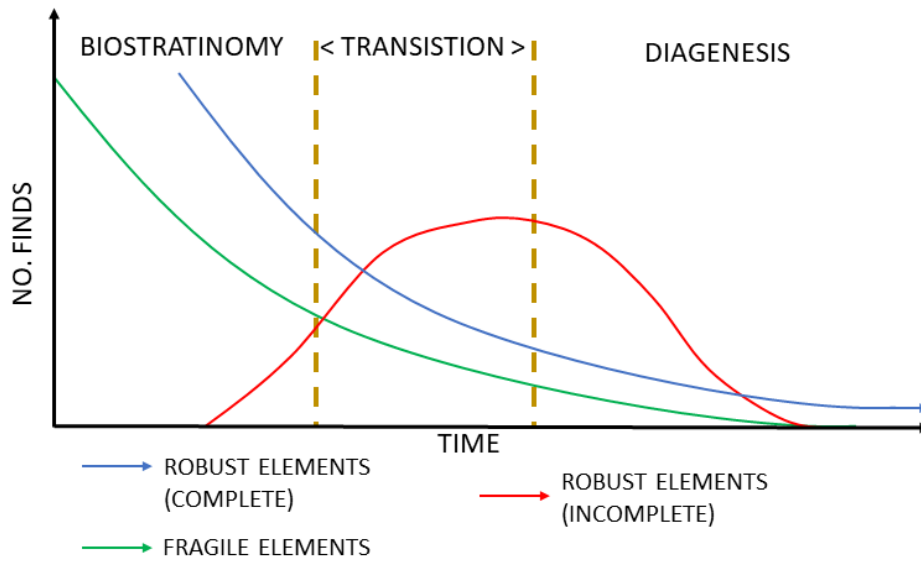


Fig. 6.09 – Graph showing a hypothetical number of finds of robust elements (complete and fragmented) as well as fragile elements depending on a taphonomy stage of a specific deposit.

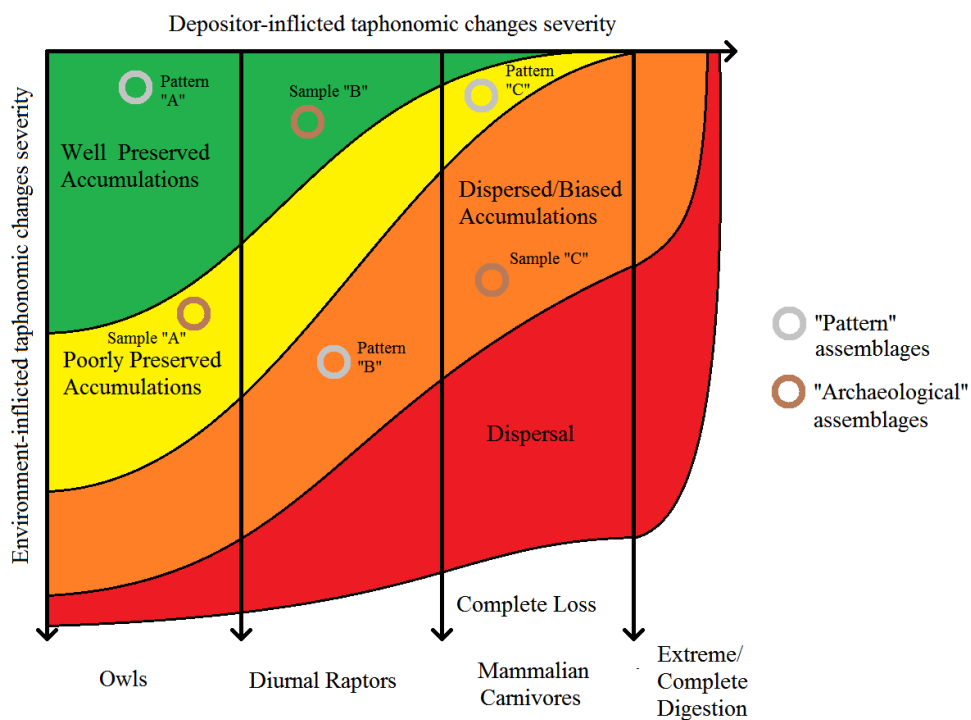


Fig. 6.10 – Illustration of relation between a depositor inflicted taphonomy and environmental based taphonomy on a micromammal assemblage. Assuming area covered by a specific accumulation type within species group roughly represents their abundance in the wild, even in presence of dominating level of preservation, it still creates 4 different patterns for each group. “Pattern” and “Archaeological” samples taken in each group most likely do not correlate with each other and will most likely match better the accumulation within specific accumulation type in a separate group (pattern A to sample B, pattern B to sample C and pattern C to sample A).

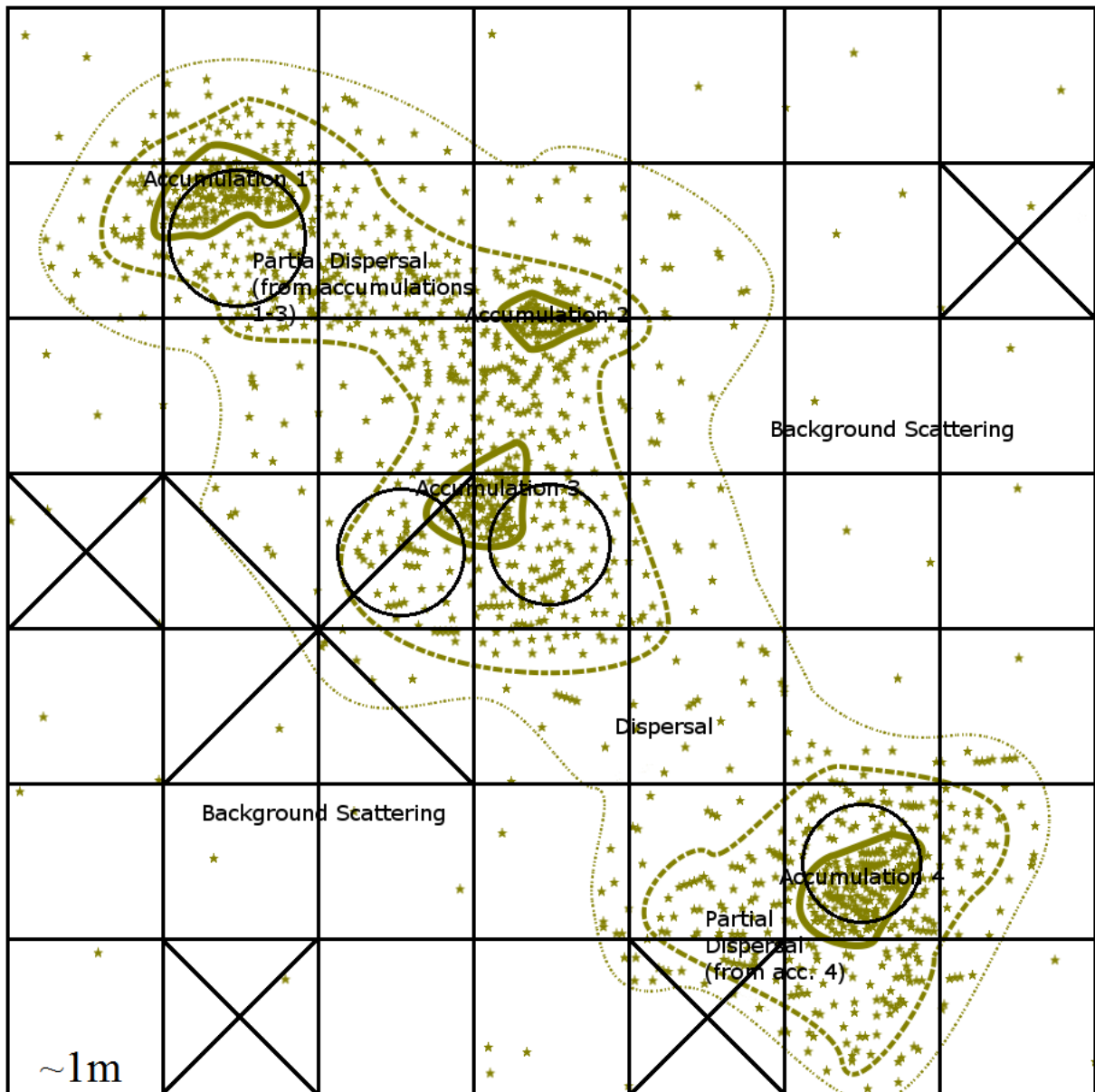


Fig. 6.11 – Illustration representing different approaches to sampling in an open environment. Each method includes four squares out of 49. The contextual-only approach of sampling (circles) includes only densest areas (accumulation), without any change of comparison with less dense areas or background scattering. In turn, random sampling of four separate squares (small crosses) may fail in getting specific type of accumulation/dispersal, in this case showing only background scattering (3 samples) and an edge of dispersal area from the fourth accumulation. The random sampling of a bigger area (single large cross) enables to see both accumulation proper as well as dispersal area and background scattering.

6.2. SITE IDENTIFICATION AND IMPORTANCE

6.2.1. SKARA BRAE

Previous research at Skara Brae (Romaniuk et al. 2016a;b; Romaniuk 2015) suggested a far less complex situation on the site micromammal assemblages. This original analysis already noted major differences between trenches, with anomalous well-preserved deposition in IV and general scattering represented by Trench III, including the possibility of dispersal affecting studied contexts. It was also established that only two species were present, with quasi-commensal field mice present mostly in small amounts within the site and non-commensal Orkney vole dominating assemblages both on-site and off-site. The finds skewed towards the predominance of adult individuals, with a lack of identifiable nesting suggesting species not being native to anthropic sites. However, differences between specific phases within the site and on its fringe remained underexplored, mostly due to phases not showing too high deviation from reach other in the case of fragmentation. Additionally, the differences found in the case of abundances in Phase 0 and early Phase 1 were later repeated by minor contexts in Phase 1 (mid to late) to 2, downplaying their importance. Due to a lack of comparisons outside of the predatory range, massive accumulation found within Skara Brae was assumed to be due to good preservation conditions. In a result, most of the deposition was considered consistent throughout Trench I and associated with most likely a single depositor. Considering abundance differing from patterns found by Andrews (1990), a minuscule number of digested remains and the presence of burning, human involvement in vole deposition was highly possible.

The consideration of dispersal, background scattering and differential survivorship, with the employment of methods tailored to track their impact on bone assemblage completeness, have provided a new layer of relationships between contexts (**Chapter 5.1**). In Trench I, differences mostly reflected the stratigraphic sequence and occupational/transition phases, resulting in main Phases 1 and 2 seeming further from full dispersal than Phase 0 that preceded them. Both Phase 0 and Intermediate Phase provided far lower vertebral and higher to far higher skull frequencies, with similar (Intermediate Phase) or lower (Phase 0) frequencies of limb bones, thus resembling surface or buried dispersal in the case of Phase 0 contexts or buried partial dispersal in the case of Context 139. However, better preserved and skeletally more complete Phases 1 and 2 did not represent complete specimens nor intact assemblages, being similar to buried partial dispersal,

albeit better preserved. Alternatively, a similarity with the whole assemblage could be noted, possibly reflecting contexts being a combination of intact as well as dispersed remains.

However, contexts with data more similar to undispersed assemblages were indeed found, though not in Trench I, expanding on the idea of how the form of a context itself helps preserving micromammal remains. In the case of Trench II, Context 213 provided frequencies more similar to an intact pattern albeit with overrepresentation of hind limb bones. Apart from frequencies, completeness was similar to best-preserved Trench I contexts, above 30% regardless of counting mode used, and postcranial fragmentation was in overall better than Trench I assemblages. It was not surprising considering the context was a waterlogged midden, with anaerobic conditions favourable for long-term preservation of organic remains. A similar frequency profile was also found in Context 408, the main accumulation in Trench IV and largest (below 7 thousand NISP) as well most skeletally complete (44-45%) amongst all trenches studied. Fragmentation was also lower than the other main assemblages, especially in the case of mandibular breakage.

Still, even considering Contexts 213 and 408 as the overall best preserved, minor bones were underrepresented through the site, suggesting dispersal and survivorship impact through the site. Ribs, calcanei, tali, metapodials and phalanges were very rare, present mostly in the largest accumulations. Lack of such finds could be explained by a sieving regime not including them (e.g. too big mesh or additional fragmentation introduced for smallest bones) but considering how many vertebra, both complete and fragments, were retrieved it could be an actual absence of more fragile finds within contexts. Andrew's (1990) study often attributed their low values to the severity of the predator's digestion process, but Terry's (2004) research suggested terminal dispersal affecting survivorship towards more robust bones. It may be correct considering fragmentation within and around the site is more similar to each other than other sites. The lack of moderate to heavy digestion of remains and only scarce evidence for light digestion may point to the latter, though digested remains themselves may be also affected because of weakened structural state (salient edges erosion) affecting survivorship.

The known comparisons with unaffected predatory assemblages may be misleading, and as already pointed out in **Chapter 6.1.2**, the approach to identification had to accommodate this. Romaniuk et al. (2016a) considered obtained patterns coming from either kestrels (Andrews 1990) or even humans (Fernández et al. 2011), but knowing the impact of dispersal it is likely both judgements are incorrect. Indeed, comparison with original signatures, through correlations and classification algorithms or even analysis of indices, provided results

highlighting species within diurnal/mammal class, predominantly kestrels and in second place hen harriers. Still, it does not correlate well with very low digestion, even considering the seasonal variation in digestion severity that some species exhibit (notably owls, see Andrews & Fernández-Jalvo 2018), and does not answer how diurnal raptor deposits would end up in anthropic or mixed contexts given being less likely to roost or nest near humans than owls. However, in specific cases, like beforementioned Contexts 213 and 408, classifiers also tended to identify one of the sets as coming from owls, with the former also showing short-eared owls within the top correlations. Contexts correlations indicating owls, while usually not as high as those indicating kestrels, often showed significant values. Not surprisingly, the utilization of adjusted methods either trained on transformed datasets or correlations with transformed signatures returned more owl patterns in the case of *Abundances* (all methods) as well as *Fragmentation Percentages* (classification). Context 213 fell clearly into the owl category, with fragmentation only slightly higher than usual.

Assuming Skara Brae Trenches I (whole) and II (Phase 2) were filled with partially dispersed owl assemblages that underwent destructive burial process, or both owls and diurnal raptors involvement in deposition (reported for e.g. short-eared owls and hen-harriers: Craighead & Craighead 1956; Watson 1977), may be correct considering noted dynamics between phases. Phase 1 was built on the previous phase, with some contexts and structures being removed and others added. It most likely introduced additional material scattering, further deteriorating the assemblages. A seemingly similar situation could also occur after the Intermediate Phase. However, two main Phases (1 and 2), after early stage with construction activity remained relatively unscathed, with the latest ending in site abandonment. It also answers the preservation difference as Phase 2, best preserved, was not intruded by later construction attempts. Similarly, Trench II Phase 1 saw the majority of human activity, with Phase 2 being mostly thin layers of human deposition, windblown sand and occasional construction activity, with one minor pit found. In relation to Trenches I and II, off-site trenches are mostly an example of already established background scattering, with accumulation within Trench IV providing evidence for predatory deposition of an owl species within a mostly natural, partially open environment and lesser impact of disturbance by human activities.

From a contextual perspective, owls can and often deposit pellets nearby or even within a manmade environment, especially when space within roof structures, disused/abandoned buildings or even on the ground is available (Andrews 1990, 178-194, see a roosting/nesting list for barn owls in Williams 2001, 50-51). This situation is known in the case of archaeological

sites, often resulting in the introduction of additional tectonomic changes, for e.g. further fragmentation due to trampling (e.g. Weissbord 2005). Kestrels are also known to occasionally coexist with humans, on Orkney even nesting on a group due to the absence of natural predators (Andrews 1990, 194), though on average tend to provide far better-digested remains. Owls can occasionally roost even in disused burrows or natural/self-made hollows (see Williams 2001,50). It may explain the presence of a massive assemblage in the off-site trench – the only one also containing evidence of burrowing by rabbit-sizes species.

Additional evidence previously thought to be a sign of human or related involvement, such as burning or coprolite matrix presence on some bones, could be explained by additional work (Romaniuk et al. 2020) or contextually with the aid of available literature. Several small mammal bones were identified within matrices of fragmented coprolites from Context 110. Among them one find was a maxillary bone fragment with first molar intact, clearly identifiable to an Orkney vole (Fig. 6.12). The identification of coprolites as coming from the local dog population showed the contribution of material from a non-avian predator, partially explaining occasional anomalies within micromammal data. However, heavy examples of digestion were found only within the material retrieved from said coprolites, strongly contrasting the non-digested nature of all research assemblages and pointing out towards canids being at best occasional contributors during assemblages creation. In turn, burning, while proven to be of human origin due to the presence of calcination throughout the site, would be easier to explain as accidental rather than intentional human involvement – though neither can be fully excluded. The number of burnt finds was relatively low, slightly less than 1% of NISP, and did not show such prevalence, especially on incisors, as some research (e.g. Henshilwood 1997) would suggest. Accidental burning of animal remains is known in archaeology (Bennett 1999) and considering possible reinterpretation of a depositor as being one of the owl species it is highly likely. The mingling of owl deposition with human refuse and occasional canid scats could occur over a longer period of time, thus producing encountered assemblages.

Interestingly, previous research (Romaniuk et al. 2016a) suggested field mice being commensal species in Skara Brae, but new evidence may point against it. Molar wear revealed a predominance of category 3, suggesting many individuals being full adults. On its own it could be dismissed but when compared with other sites it seems that the most common wear scoring shows a predominance of 1 and 2 categories, with 3 and later being progressively less common. This pattern points towards older specimens and may represent either temporary occupation, e.g. overwintering adults entering human habitation in search for food, or size selection by a

predator involved in Skara Brae deposition. However, the additional taphonomic impact of prolonged diagenesis cannot be excluded.

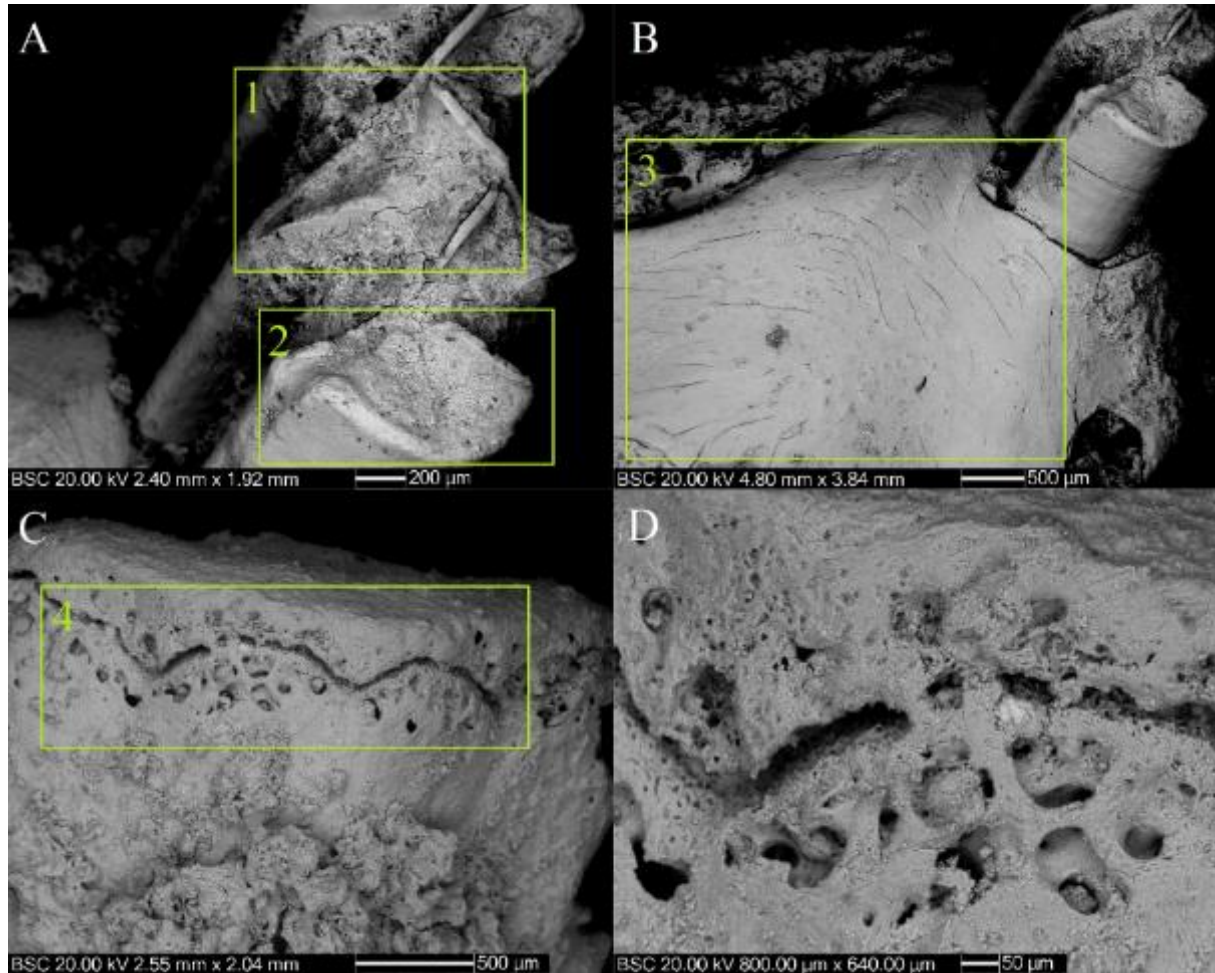


Fig. 6.12 – SEM micrographs of micromammal finds from coprolites in context 110, Orkney vole maxilla (A & B) and rodent (vole?) vertebral body (C & D). Figure taken from Romaniuk et al. (2020, Fig. 4).

6.2.2. LINKS OF NOLTLAND

Links of Noltland provided the most taxonomically uniform micromammal assemblages, with complete lack of field mice save one individual in Trench D (**Chapter 5.2.**). It could be interpreted in a number of ways. The easiest and possibly best would be to assume there was no population of this species on Westray at that time. However, it would be surprising considering non-commensal common vole being in actuality faster to spread through the archipelago than a commensal species. Both species often coinhabit the same environments (see **Chapter 2.3.2-3.**), and the presence of voles on Westray may point towards the isle natural environment already being possible to settle. Alternatively, a population was present but could not be properly assessed by excavations due to methodological or population dynamics reasons. Mainland Skara Brae site provided evidence for field mice presence mostly within the settlement site, with no finds in Trench II Phase 2 and III and only a small number of finds off-site. In the case of Links of Noltland only the latest period of Grobust building history, reflecting late abandonment/refuse accumulation, was investigated during Clarke's work. For some reason, for example due to predators nesting inside or lack of easily accessible food, field mice might have abandoned nesting within the structure after its abandonment by humans. However, more recent research so far has not found any evidence of rodents besides Orkney voles (Fraser 2011), despite more in-depth investigations being done (Moore & Wilson eds. 2011). Alternatively, it could be a result of a very low density of the population (densities depend on habitat and could be even lower than those of pygmy shrews, see Flowerdew 1991) and/or no commensal population on site. The third possible explanation is that singular mice remains retrieved could be brought to the site by an avian depositor from a different island. Such explanation was used in the case of micromammal accumulations within a chambered cairn at Holm of Papa isle (also named Holm of Papa Westray, see Cucchi et al. 2009; Ritchie 2009). Still, Holm of Papa is, till today, mostly a moss-covered rock formation while Westray itself shows the evidence of a vast Orkney vole population already in Neolithic, refuting the necessity of travel by local predators. Finally, singular introductions over the Neolithic provided at best singular cases that failed to establish lasting populations.

This site also provided data reflecting similar patterns to those seen in Skara Brae, visible mostly in age based on skeletal fusion and digestion. A pattern that repeated in both trenches was the predominance of sub-adult individuals when assessing epiphyseal fusion, with some addition of fully grown finds and a slightly bigger but still very minuscule amount of finds

equal to juveniles. Also, as observed in Skara Brae Trenches, there was a tendency for open areas (Trench D) to provide slightly younger specimens than finds within or nearby settlement buildings (Trench A). In the case of digestion, as in Skara Brae, only minuscule amounts of light digestion and a couple of more severe examples have been found. What also repeated were other taphonomic changes, notably abrasion and weathering, leaving similar changes as digestion as well as affecting same finds, resulting in the author's issues with proper digestion identification. However, no biases were found between trenches in this case.

However, quantifiable data such as *Elements NISP*, *Skeletal Frequencies*, *Abundances* and *Fragmentation Counts* and *Percentages* have shown a vastly different situation compared to Skara Brae. On one hand, far greater fragmentation of skulls and selected postcranial bones was found in the case of Trench A, with skull difference only in Trench D. Surprisingly, the bigger the context in Trench A the lesser percentile contribution to better-preserved bones was found. As a result, many long bones seemed to be overrepresented in *Abundances*. The *Skeletal Frequencies* pattern obtained in Trench A was quite reminiscent of the hyena den from Behrensmeyer's work (Behrensmeyer 1983; Behrensmeyer & Boaz 1980), with the prevalence of firstly hind and then front limbs followed by vertebrae and then skulls. On the other hand, both trenches contained more small paw bones, like metapodials or calcanei, as well as ribs than Skara Brae, showing *Abundances* outline more similar to ones observable in Andrews (1990) work. It is especially surprising considering both sites employed essentially the same sieving techniques, thus both providing the presence of additional biasing factor in Skara Brae and the possible absence of one in Abandonment Phase of Links of Noltland grobust structure.

The greatest contribution to understanding how assemblages formed within Links of Noltland trenches was spatial data retrieved alongside whole-earth sieving and sample retrieval. In Trench A, the majority of assemblages formed within small chambers and passageways connected to either identified entrances within the North-East or South-West end of the site. While the Grobust roof collapse was most likely gradual, with the bigger chambers falling down first, it is likely that those areas were also accessible for the longest period of time. It is not surprising considering such a pattern has already been observed multiple times in the case of abandoned Orcadian structures and associated with nesting of predators (e.g. beforementioned Holm of Papa Westray, Ritchie 2009, or Point of Cott, Barber 1997; Halpin 1997; Coy & Hamilton-Dyer 1997). The lack of younger rodents also points towards predatory deposition, but complex deposition pattern makes specific species hard to pinpoint. Overabundances of limb bones and absence of skulls, in addition to high fragmentation, usually reflects mammal

species. Such a situation is seemingly supported by statistical methods, with correlations/chi values pointing towards red foxes and classifiers returning diurnal/mammal class as predominant one. However, lack of a heavy level of digestion, as well as absence of coprolite material on bones or coprolitic finds overall, renders such interpretation most likely wrong. Interestingly, the abundances classifier trained on transformed data classified many contexts as scattering, possibly showcasing the assemblages being heavily dispersed despite their overall NISP size. Going further with this idea, what can be seen within Trench A may be a terminal form dispersal within a closed environment – or within one that relatively rapidly entered diagenesis and was not later disturbed in any way.

Trench D, in turn, represented an interesting case of an open space, unrestricted deposition in a mixed natural/anthropic environment. *Skeletal frequencies* as well as *Abundances* showed patterns similar to Skara Brae Phases 1 and 2, with skewing towards skull elements that visibly contrast data in Trench A. However, what is most important is a connection between a sequence of deposition and *Abundances* and fragmentation data. The site shows fragmentation impact increasing with time, with major contexts within older phases being more affected than ones within younger depositions. It seems to especially impact cranial and main limb bones abundances, though minor elements like vertebrae also show better representation within latter contexts. Considering the human impact on Trench D ranging from agriculture and refuse dumping to constructions and stone removal it could accumulate over time, with newer activities affecting already deposited layers. It would also explain why the best-preserved context came from the latest cultivation phase, which was later followed by a minor construction phase and recent natural layers. Additionally, a spatial dispersal could be noted in each context, correlating to some degree with the idea of a centre of accumulation and dispersal from it as the time proceeds. Considering the impact of dispersal and lack of digestion it is very likely that assemblages came from an owl or related species, especially in the case of Context 8.

6.2.3. BU BROCH

Among all the sites analysed in the thesis, the least informative was Bu Broch, predominantly due to how few samples were retrieved and their composition (**Chapter 5.3.**). While a sieving regime was utilized in Bu Broch it seems only major rodent bones were deposited in the

museum, resulting in remains incomparable to other sites. Additionally, sampling was highly selective, resulting in the majority of samples being taken from contexts unrelated directly to each other. It was visible especially in the almost complete lack of fragmented postcranial bones despite the site age as well as smaller or more fragile bones. In turn, it impacted *Skeletal Frequencies, Abundances* (lack of vertebrae, scapulae) and epiphyseal scoring (no ulnae) and possibly resulted in incorrect MNI being recorded. Finally, vital taphonomic changes, digestion and burning, could not be established, both because of lack of finds and by a lack of comparable cases of other taphonomic changes, like abrasion or weathering.

The only informative part of Bu Broch sample data was the taphonomic composition but even it was hindered by the encountered situation. Taxa identified included species already known from Neolithic sites, namely Orkney voles and field mice. However, the 1st millennium BC should be a likely introduction point for pygmy shrews to Orkney (Vega Bernal 2010). Considering shrew bones are smaller than unretrieved rodent ulnae it is highly likely that such finds, if present on the site, could not be retrieved or were lost during post-excavation sorting.

6.2.4. BIRSAY BAY

Species MNI distribution within and nearby the human structures (Area 1) proved to be key evidence for a different mode of deposition than one observed at the site fringes (Area 2 & 3) as well as other studied sites (**Chapter 5.4.**). The identified species included all confirmed species known from modern Orkney populations, including Orkney voles, field and house mice as well as pygmy shrews. In surface level intrusions, brown rat bones were identified, possibly reflecting relatively recent but temporary infestation at Birsay. Cumulatively, Area 1 as well as Areas 2 and 3 had the same taxonomic diversity but differed fundamentally in the amount of NISP and MNI. MNI for Areas 2 and 3 roughly followed the expected density of populations in natural or seminatural environments, with the domination of Orkney voles (e.g. 42% MNI in the case of Area 2) followed by wood and house mice (27/28% MNI), with only a minor addition of shrews (2% MNI). A similar outline was noted in the case of Tuquoy, with Skara Brae also showing some similarity despite lower taxonomic diversity. In turn, the majority of identifiable finds, and in extension established MNI, in Area 1 came from house mice (50% MNI), with voles and field mice representing second (25%) and third (16%) most common species. Such proportions are even more extreme in the case of the most researched Period 9,

which 62% of MNI was established to be house mice, with the remaining 37% being distributed equally among field mice and voles. Interestingly, two out of three *Sorex* MNI also came from these contexts, though this species' contribution to counts most likely reflects average values.

A dichotomy between the studio site (Area 1) and fringe areas, as well as to other sites, could be also tracked in quantitative data. Area 1 has shown *Skeletal Frequencies* unique amongst all sites investigated, resembling best complete or intact surface assemblages. Completeness was also high, on a par or slightly better than observed on Neolithic sites. It is likely, that in-building deposition resulted in very restricted dispersal. Fragmentation was present, comparable to Skara Brae though slightly more pronounced. Postcranial *Abundances* were also most similar to Skara Brae, but with far better representation of small or fragile bones, such as scapulae, radii, vertebrae and minor limb bones. However, skull bones show lesser values than Skara Brae, being slightly higher than observed in Links of Noltland. In turn, Area 2 and 3, as expected from unrestricted, open-air places, provided more dispersed frequencies outline, with higher postcranial fragmentation than one observed in on a studio site. Interestingly, Area 2 seemed more like a transition between Area 1 and 3, with *Abundances* more similar to the former.

The data of most importance for the site interpretation proved to be age-related, revealing nesting of murids within or nearby the site. In contrast to any other site, Area 1 provided a substantial quantity of unfused epiphyses reflecting juvenile individuals. Moreover, singular finds included an unerupted molar, most likely coming from a very young juvenile. Previous age-related research was interested in attritional and catastrophic mortality within the population (Korth & Evander 1986) or predation selectivity (Lyman et al. 2001). However, selectivity, as understood in Lyman et al. (2001) work is often skewed towards adult specimens, which seems to be the case for Skara Brae. Lack of juveniles can be explained by simply smaller size (either harder to catch or less profit from such catch) or/and the tendency for youngest individuals to spend some time within the nest and later nearby it, with roaming time relatively short and not to great distances. All age classes were represented within Area 1, including most likely nesting juveniles, which can be seen especially in the case of mouse molar wear. Molar wear fits perfectly within the expected attrition mortality of rodent species (Korth & Evander 1986, Fig. 2), which, due to short lifespan, create a steep decline from the youngest age group towards the oldest observed. Considering that period 9 covers abandonment and periodical refuse gathering within the building interior, and is shielded from predation and with human activity still present not too far from it, the obtained age profiles within Area 1 may faithfully represent expected non-predatory attritional mortality (see Lyman et al. 1994a, 118-120). It

would be not surprising that even in the absence of predators rodents can compete with other rodent species as well as each other for territory and food resulting in mortality (see e.g. house mice in **Chapter 2.3.4.**).

The above data, alongside lack of severe digestion, points towards non-predatory deposition within Area 1. The majority of digestion was found within Period 9, with no cases beyond moderate, and plenty of evidence of active abrasion, possibly soil bioturbation. Classifiers and correlation results showed values not dissimilar to other sites, usually ranging within diurnal species and rarely showing owls. However, as mentioned before, it is unlikely those species nested or roosted within still standing building, even if some parts of it were no longer fully utilized. Evidence of burning on a handful of bones may also be a sign that such assemblages accumulated already within the timespan of this area usage.

While Area 1 shows signs of non-predatory deposition and nesting, Area 2 and 3 contrast it with an open area dispersal, some possibly of predatory origin. The presence of digestion mostly within one context (Context 6, Area 2) and its almost complete absence in other contexts may point to dispersal contexts being mostly sampled. There is a variation between samples, similar but not to a degree spatial data from Links of Noltland, suggesting the presence of bigger accumulation nearby. However, the quantitative data still differ from what is known from older sites, suggesting the impact of time also contributing to how the patterns are formed.

The biggest obstacle in understanding the site is that the sampling regime in Area 1 concentrates almost exclusively on two periods. It provides much-needed information on non-predatory accumulation patterns, but because adjacent off-building squares were only sparsely sampled it is not known how in and outside accumulations within Area 1 have differed. Additional information could also show a more gradual change between Area 1 samples and Area 2.

6.2.5. TUQUOY

The biggest issue encountered when studying Tuquoy samples was in essence the same as in Bu Broch (**Chapter 5.5.**). While Tuquoy was not as big as the broch, and had all archaeological contexts sampled, simple sampling resulted in data hardly comparable to other sites on context level, with a chance of no representativeness on general level considering what was established during statistical analysis in case study 1 (**Chapter 4.5.**). It is problematic, as the retrieved data to some degree correlates with observations made on other sites (e.g. Birsay in taxonomy) and

do not seem to be too skewed from the expected values. It is possible that consistent sampling of a small portion of each context encountered reconstruct means on phase level but nevertheless fails to do so on more localised context level. It is especially visible in the case of molar wear analysis, which suggests the minor presence of juvenile specimens of both murid species within the site. However, epiphyseal data do not seem to support this apart from some contextual evidence following retrieved unfused remains.

Such problems especially restrict the usefulness of the taxonomic composition of the site, which is arguably the most informative of all the sites studied. Tuquoy seems to provide the earliest archaeological evidence of pygmy shrews on Orkney (Phase 1, ~ 7th century AD or earlier), although at that time their population within much of the Orkney have already been established for at least a millennium (Vega Bernal 2010). House mice also appeared relatively early (Phase 2, 7-10th centuries AD), possibly within a similar time frame to Birsay Bay (period 5). Neolithic introductions to Orkney were encountered either since the earliest natural contexts (Orkney voles) or in earliest anthropic accumulations (field mouse), identifying the appearance of field mice on Westray somewhere between Links of Noltland definite abandonment (mid. 2 millennium BC) and Tuquoy settling before 7th century AD. NISP/MNI outline of identified species differs from each phase but correlates between species density in nature and quantities encountered within the site. The anomalies happened within abandonment Phase 5, with collapse and abandonment layers providing more house than field mice, and Phases 6 to 7, first showing no mouse species and second only the house mice. Still, the majority of samples came from only 3 phases, resulting in early as well as late finds being least trustworthy, including established introduction sequence.

However, relatively accurate judgements could be made in the case of specific contexts when retrieved to a significant extent (~ 50% of all content), either by multiple samples or samples covering the majority of the said context. An important finding was a predatory accumulation on the outskirts of the site, consisting of two single sampled contexts within Phase 3. Considering one of those contexts provided a quarter of all NISP (Context 33) within just one sample of about ~14 litres, it definitely represented quite dense accumulation, including also non-micromammal remains of a small passerine bird and one of a gull (Hamilton-Dyer 2018). *Skeletal Frequencies* showed relatively minor dispersal for Context 33, with Context 28 being possibly a related dispersal. Moreover, those two contexts provided almost all cases of confirmed heavy and extreme forms of digestion. The site provided remains of owl species (Hamilton-Dyer 2018) as well as a domestic cat, but digestion and other finds, including

classifications and statistical tests, suggest rather diurnal raptor. Contextually, most likely depositors are kestrels as they are known to roost and nest on rock faces along the coast, sometimes on human structures (Orta 1994; White 1994), with hen harriers also a possibility. The location of Contexts 28 and 33, located on the flagged passageway, may represent such a situation. The predominance of voles in Context 33 also reflected a taxonomic composition of known kestrel assemblages studied by Reynolds (1992), though is not too far from what could be found within hen harriers deposits. Other species, such as peregrines, predominantly deposit bird bones and are rarely responsible for substantial micromammal deposits (Andrews 1990, 1996). However, kestrel remains have not been found in Tuquoy while remains of peregrine bones were found within Phase 4 (context 1020, Hamilton-Dyer 2018). Other raptors found within the site (buzzards *Buteo buteo* and white-tailed eagles *Haliaeetus albicilla*) are unlikely to be a source of such accumulation due to heavier fragmentation, digestion and prey species both would provide. It is not possible to perfectly pinpoint the predator species, but a label of a “diurnal raptor” and category 4 predator according to Andrews scale (Andrews 1990, table 3.16) seems certain. Other unique contexts may point towards the predominance of self-trapping of micromammals or natural death and subsequent dispersal of their remains (see Whyte 1991, Stahl 1996). One of the most specific was Context 1112 (Block 99, Phase 6), coming from a paved passageway, with high completeness (34%) despite representing only one Orkney vole individual.

Small size of samples especially affected the interpretation of other contexts containing digestion. Evidence of digestion was found in several samples that were smaller than predatory accumulations within Contexts 28 and 33. It is likely, that more assemblages were present on the site and the aforementioned samples represent either scattering of remains from these assemblages or a retrieved fragment of one. In the case of scattering being a factor, the disturbance of primary assemblages was most likely due to human agency, probably connected with everyday activity, as well as smithy and hall construction and maintenance. Single digested teeth are present within building features, such as the hall wall (Context 99, Phase 3) or early and middle smithy spreads, including pit hearth ash (Context 737, Phase 4). Considering the lack of primary assemblages after Phase 3 and that almost all dispersed samples come from Phases 3 and 4, predator activity on the fringe of the settlement may have moved in response to the construction of the smithy. However, it is also possible that sampling simply omitted other predatory activity within the site or downplayed the importance of some context in this regard.

6.2.6. SCAR

Scar shows similarities to the selective sampling at Tuquoy, resulting in difficulties for interpretation, though informative finds (**Chapter 5.6.**). The encountered issues were not as severe as in the Bu Broch analysis as the obtained data showed some comparability with other sites. This is possibly because of the simple stratigraphy that covers a relatively brief period of site creation and the later period of disturbance, which enabled multiple sampling of the same contexts. Data predominantly followed patterns already found within other sites.

However, the unique case was its taxonomic composition and how it reflected the nature of intrusive assemblages. On other sites, if intrusiveness was identified, it usually included very few finds, mostly relating to rat remains. On Scar intrusions into contexts have been identified before (Owen & Dalland 1999, 31-32 & 36-37), but it seems the introduction of non-contemporary fauna to archaeological assemblages was not of single intrusive species but rather groups of those. Often brown rat bones were found alongside house mice in features also providing rabbit bones, showing a group of modern commensal and non-commensal species (rat and rabbit) or ones that were most likely not yet introduced to Sanday at that time, or were a recent commensal introduction (house mice). It is further elaborated by a find of a juvenile cat mandible. Once an intrusion is established (such as a burrow), it is highly likely to be utilized by multiple species sharing similar living conditions (not necessarily burrowers), visibly increasing taphonomic diversity. In the case of feral cats or rats it likely indicates rabbit burrows. Such “packages” may be traced through Scar, suggesting extensive intrusions not necessarily being one single, burrowing species.

7. CONCLUSIONS

7.1. SUMMARY OF THE RESEARCH RESULTS

As the literature review and later studies confirmed, methodology related to studying micromammal remains can be very wide in scope of possible research questions despite the relative obscurity of the subject itself (**Research question 1**, see Table 7.01; **Chapter 2.4.**). The breath and nature of data obtainable from micromammals are essentially similar to the generated when studying archaeological populations of bigger species, just not as well explored. Arguably, one could consider archaeological micromammal assemblages retrieved as a whole, alongside background dispersal, as even better case studies on taphonomy than bigger mammals could provide. Employing whole-earth sampling to site contexts often results in tens of thousands of remains being retrieved, enough to provide data on the representativeness of specific elements in relation to either the whole assemblage or its parts as well as showing wider relationships between assemblages and dispersed remains. However, the difference in scale that seems to be working in favour of micromammal research also forces the researchers to include a wider thematic approach to their research. A detailed study on specific aspects of the archaeological assemblage may be skewed due to the nature of micromammal taphonomy and the identified importance of recording spatial relationships between accumulations and dispersed remains.

Statistical reasoning can effectively be utilized for the sake of micromammal research, though additional factors have to be considered when working on non-actualistic data (**Research question 2; Chapter 4.1-4&7. and Chapter 6.1.1-2.**). Statistical analysis of data proved to be crucial for reinforcing identified patterns, as it already showed differences between the sites before the proper assessment. Moreover, given the sheer size of the sites database, it could be the only option of proving the relative importance or not of specific data. In the case of the methodological research, even more successful was the application of statistical tests and trained classification algorithms as a means of identifying two to three main predatory groups as well as differentiating predatory accumulation from extreme scattering. This approach can be successfully used when comparing modern zoological finds – especially when freshly deposited. However, application to archaeological data revealed the impact of other, non-predatory factors, as well as the possibility of wrong conclusions from only partially retrieved

assemblages. The approach used to mitigate at least the first found issue partially helped in identifying possible predators.

Among possible data not usually obtained, the most useful proved to be that relating to age-related methods (**Research question 3; Chapter 4.8-9. and Chapter 6.1.4.**). Mortality profile reconstruction, despite visible issues in their application and sometimes representativeness, can work in the case of short-lived micromammals. The majority of wear data showed similar outcomes, with multiple finds of younger specimens and minor presence of older ones. In turn, skeletal data showed predominantly fusion of early to middle fusing epiphyses, with late fusing epiphyses showing greater variation. However, assemblages representing likely nesting showed greater quantities of unfused epiphyses, with completely unworn teeth being more abundant. Non-quantifiable finds, such as e.g. unerupted molars, were also quite useful in identifying nesting. In turn, metrical or pathological data showed major issues in representativeness, either related to assemblage size (pathological changes) or degree of assemblage fragmentation (metrical data).

One of the two biggest issues when applying the current methods to archaeological data was proven to be restricted/simple sampling, an issue relatively prevalent throughout archaeological research in general (**Research question 4; Chapter 4.5. & Chapter 6.1.3.**). The established methods have been created to deal with assemblages retrieved in full, thus showed far less accuracy in the case of only partial retrieval. The representativeness of a sample generally scaled with how large a part of an original context was collected, as well as how many taxonomical units had to be utilized to properly catch parent context taxonomic diversity, especially in the case of standard quantitative data such as abundances or fragmentation. NISP of a sample in overall also showed a positive impact, but mostly when comparing samples far smaller by size. However, the issue was that assemblages were not evenly distributed within the analysed contexts. Due to that, restricted sampling may simply omit crucial areas while contextual sampling may not show the contrast between context deposition patterns. Considering the above, if whole-site sieving is not viable for whatever reason, it should be advised to fully sieve as big part of the site as possible. The aim should be to sieve contexts in whole (or no less than 50% their contents) from a larger section of the site, thus maximising the chance of catching all possible deposition patterns present on site as well as obtaining crucial spatial data.

Non-taphonomic factors, such as dispersal and scattering, impact the identifiability of specific contexts (**Research question 5; Chapter 4.7. and Chapter 6.1.5-6.**). As sampling has shown,

the assemblage does not equal context and accumulations with related dispersal areas can be seen in data as well as spatially within and between contexts. In combination with burial, the process of gradual dispersal creates a range of patterns from one accumulation, possibly showing similarities to ranges of patterns obtained from a different taphonomic depositor/factor. Due to that retrieval needs to take into account a need for obtaining a range of patterns, from remains of primary accumulation up to what can be considered as background dispersal. Only that way original depositors can be successfully traced.

As expected by statistical assessment, site assessments provided conclusive evidence of differences between studied contexts and sites (**Research question 6; Chapter 5. & 6.2.**). The pattern seen in Neolithic settlements visibly differed from later Norse to mediaeval ones while natural contexts located in the open and partially or fully enclosed spaces also showed their own patterns. Moreover, a gradual increase of fragmentation from later to earlier phases could be noted in Links of Noltland Trench D, with occasional presence on other sites, suggesting diagenesis also contributing to *Fragmentation Percentages* pattern – and in extension most likely to *Abundances* pattern as well.

The sites studied here provide evidence for a number of different factors being responsible for deposition, but a number of issues have to be studied further in order to deliver a more certain answer (**Research question 7; Chapter 5. & 6.2.**). Traditional taphonomic focus on predatory depositions is possible within archaeology. However, due to numerous issues already discussed, additional efforts have to be included in order to properly identify a depositor. The majority of studied sites most likely showed owl or mixed species related deposition, with abundances and fragmentation strongly skewed towards hen harriers or kestrels but digestion pointing towards predominantly owls. Making judgements out of data transformed to reflect the impact of dispersal showed greater consistency with owls, though left an area of uncertainty. The only conclusive case of purely diurnal deposition was found within Tuquoy contexts of mostly natural origin. It confirmed their contribution to assemblage formation, but in natural layers usually related with times before or early in the intensification of human activity within the region. Still, considering the issues with differentiating between digestion and abrasion or weathering, it is likely the author himself downplayed the presence of digestion or it was obscured by the additional presence of strong mechanical and chemical alterations related to biostratinomy and later diagenesis.

Evidence for other taphonomic factors is prevalent within the analysed assemblages. The most visible case was Birsay Bay Area 1 contexts found within the building utilization and

abandonment layers. The identification of nesting within or roughly contemporary with those contexts was possible with quantifiable data, with a visible skew towards younger specimens not found in predatory depositions. Moreover, non-quantifiable and contextual data also contributed to such identification. While other sites did not provide such conclusive evidence, similarities can be also seen in Tuquoy. Early abandonment, especially, might be linked with commensal species living nearby moving in while still having access to active human dwellings elsewhere on the site. Related to nesting might be self-trapment, though identifiable evidence from the studied sites might be obscured by other processes. Additionally, dispersal from primary assemblages, predatory or not, can be seen especially in the open areas, creating wider patches of micromammal remains concentration.

An assemblage spatial location of and related contexts is paramount in its creation, later dispersal and a number of taphonomic factors affecting those processes (**Research question 8; Chapter 6.1.5-6.**). In archaeology, assemblages can, and often do, form as a result of actions related to multiple taphonomic agents. It was especially visible in the case of Skara Brae, where at least two predators (owls and dogs) have deposited micromammal remains over time. Additionally, occasional burnt remains may be also evidence of a human-related deposition, possibly related to pest control or assemblage movement e.g. through regular area cleaning or construction activity. Contextual evidence is very important in the analysis, as once again shown in Skara Brae. Remains were deposited in places where refuse was deposited, possibly also enriched by pellets of owls nesting on structures given the presence of building walls and roof plastering in the same assemblages. Similarly, Birsay Bay and Tuquoy showed the importance of early abandonment layers, being a perfect place for nesting micromammals. However, a further history of an assemblage heavily depended on spatial location and possible restrictions in dispersal. Enclosed spaces showed high concentrations remaining even after considerable time while open areas were far more prone to a dispersal of material across the wider area, thus creating a large spectrum of possible patterns.

Finally, the study has mostly confirmed assumptions about micromammal species introduction to and dispersal through the Orkney archipelago (**Research question 9; Chapter 2.3. & 6.2.**). Orkney voles seemed to be well established on the main islands of the archipelago by the mid-Neolithic period. In extension, it suggests the abundance of optimal habitats, most likely low vegetation like grasslands, on both Mainland and Westray at that time. This contrasts strongly to field mice, which seemed to be introduced at more-or-less the same time to the Mainland, but does not have archaeological evidence for a stable population on Westray by the Middle

and Late Neolithic (Links of Noltland). The Norse/mediaeval period provided the earliest evidence in this study. It points towards field mice and voles being introduced most likely by different means or the presence of environmental factors differently affecting those species. However, the Norse period provides plenty of new species, introduced most likely between 1st mill. BC till mid-1st mill. AD, including house mice as well as pygmy shrews. Vole and combined vole and field mice deposition usually points towards predatory deposition, suggesting both species predominance in the Orcadian wild and predation on them by owls and possibly diurnal raptors since the Neolithic. However, the field mice remains can also point towards commensalism, similar to house mice. House mice, found in and around human habitation and refuse/abandonment accumulations, were definitely existing as commensal species, often intermingled with field mice, showing cohabitation of both species in such environment. Similarly, pygmy shrews showed some correlations with anthropic environments, but too few examples were obtained to be fully sure about it. Interestingly, no evidence for rat species until 19-20th centuries AD was found, with Scar finds also showing rat remains as mostly intrusive. It may point towards all rat finds so far recorded by other researchers being most likely intrusive.

Table 7.01 – Summary of key research questions alongside the answers provided by this thesis.

	Research Question	Result
1	How developed is micromammal taphonomy and archaeology and what areas remain omitted or under-researched?	Well developed, in spite of subject obscurity and scarcity of research. Lack of holistic, long-term studies, especially from the zooarchaeological perspective.
2	Can the application of statistical testing and classification help in the archaeological interpretation of micromammal finds?	Yes, especially considering the comparison of large sets of data and confirming or displaying noticeable patterns. However, taphonomic history has to be considered prior to analysis.
3	Can reconstructing mortality profiles and investigating pathological changes help in analysing short-lived micromammal populations?	Age-related data are informative when searching for commensality or nesting. Pathological changes are assessable but primarily correlated to sample size.
4	How do different retrieval methods impact obtained datasets?	Retrieval in full results in easier assessment. Sampling informativeness is reliant on a percentage of a context represented. Samples can be too small to be comparable with whole assemblages or other samples.
5	Do different taphonomic factors create similar patterns, or can one factor create multiple patterns over time?	Yes, as predatory activity is just one of many taphonomic factors affecting remains taphonomic history. Especially dispersal and scattering may result in a range of patterns from a single assemblage over time, overlapping with other known patterns.
6	Are there any noticeable differences in micromammal accumulations between studied sites and/or between specific time periods?	Yes. On a general level, visible differences can be noted between the Neolithic and later Norse/Mediaeval period. Within sites, the impact of long-term diagenesis can also be noted.
7	Can differences identified between micromammal assemblages retrieved across chosen sites be attributed to specific factors?	Yes, both of predatory and non-predatory origin. Predators responsible most likely include avian species. Commensalism is most likely an important factor for natural death and self-trapment.
8	How do micromammal assemblages form within different anthropic contexts?	Context accessibility important in early formation. Refuse and early abandonment layers are most likely to contain depositions from multiple sources while open-area and late abandonment assemblages relate more to typical predatory activity.
9	How does micromammal data correlate to previous research on Orcadian microfauna?	Confirms already estimated introduction dates. Vole population well established by late Neolithic, field mice present on Mainland but mostly absent from fringe isles. More traditional commensal populations were established during the Norse period.

7.2. FURTHER RESEARCH POSSIBILITIES

The research has clearly shown a number of different venues for further micromammal study within archaeology as well as biology and paleoecology. Further research is needed to fully understand how to properly differentiate predatory and non-predatory micromammal assemblages within anthropic contexts, both in terms of quantifiable and non-quantifiable data. Additionally, dispersal and scattering as contributing factors should be firstly studied in depth through actualistic research on modern depositions and only then applied back to archaeological assemblages. Such an approach would help in making any predictions more accurate. Examples of statistical programming used throughout this thesis can also be developed further, with accuracy and applicability to deposits of specific taphonomic history taken into account.

Beyond what has been assessed and discussed in this work, there are still plenty of approaches that have yet to be properly assessed for micromammal remains, on Orkney material as well as beyond. One of these approaches is stable isotope analysis, which the author hopes to work on one day in the future. As the current knowledge about the Neolithic Orcadians points towards a diet relying mainly on breeding livestock and fishing (Childe 1931; Clarke 1976a;b) with a minor contribution of agriculture (Clarke & Sharples 1985) more commensal and omnivorous rodents should exhibit tendencies towards higher trophic level and marine diet while non-commensal ones would drift towards a terrestrial diet with lower trophic levels. While differences between species can be considered as expected, the most interesting would be to check whether some species commensal status changed over time.

LIST OF ELECTRONIC APPENDICES

All appendices to this thesis are included as electronic materials: eight excel files and a zipped coding project in R. Excel files are going to be available as soon as the thesis itself is made available for the wider audience by the University of Edinburgh. For the R project, it is going to be available a year after that, for the author to be able to publish key aspects of the research.

Appendix 1 – Four excel files, containing the majority of quantifiable data used in this thesis (*Key Information, Basic Quantification, Elements NISP, Skeletal Groups, Abundances, Skeletal Frequencies, Indices, Skull Breakage, Counts, Skull Breakage, Percentages, Mandible Breakage, Counts, Mandible Breakage, Percentages, Fragmentation Counts, Fragmentation Percentages, Taphonomy*). Data are summarized separately for each site for stratigraphy (*General*), contexts (*Contexts*) and samples (*Samples*), as well as for reference and signature data jointly (*References*). See **Chapter 3.3.** and Table 3.06. for more details.

Appendix 2 – A single excel file, containing the metrical data. Both raw values and data summaries are displayed, obtained or calculated for each site and, if applicable, a specific area/trench. See **Chapter 3.3.5.** for more details.

Appendix 3 – A single excel file, containing the epiphyseal fusion data. Fusion scores counts are summarized for each site, separately for key areas, stratigraphy and, if applicable, individual contexts. See **Chapter 3.3.5.** for more details.

Appendix 4 – A single excel file, containing statistical tables generated in R for the sake of methodological analysis. See **Chapter 3.4.** and **Chapter 4.** for more details.

Appendix 5 – A single excel file, containing correlation and classification-based predictions, based either on original reference and signature data or one transformed to resemble partial dispersal combined with burial. Summarized separately for the sites, including related stratigraphy, and individual contexts. See **Chapter 3.4.** and **Chapter 4.** for more details.

RProject – A zipped R project. It includes R script files, entry data and full expected output. Details about the project are enclosed in the README file.

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